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PDB ID 7P6Z: EMDB ID : EMD-13234 Title : Mycoplasma pneumoniae 70S ribosome in untreated cells Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J. Deposited on 2021-07-18 : 3.50 Å(reported) Resolution : 4V7C, 7OOC, 7OOD, 3J9W Based on initial models :

This is a Full wwPDB EM Validation 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:

EMDB validation analysis	:	0.0.1. dev 43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f EM\ structures}\ (\#{ m Entries})$
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 $\leq=5\%$ 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	3	2907	7%80%	19% •
2	4	108	5%	27% •
3	W	111	23%	11%
4	a	287	6% 99%	
5	с	212	99%	
6	е	184	46% 96%	
7	k	151	98%	
8	i	146	99%	



Continued from previous page...

Mol	Chain	Length	Quality of chain	
9	m	124	<u>6%</u> 96%	·
10	α	100	99%	
11	<u> </u>	104	13%	170/
	u	104	83%	17%
12	У	57	98%	•
13	0	48	98%	•
14	2	37	8%	
15	1	59	10%	
16	0	119	97%	•
17	s	237	6% 39% 61%	
18	V	65	97%	
10		07	40%	
19	X	97	45% 55% 13%	
20	Z	53	92%	• 6%
21	d	180	97%	• •
22	b	287	80%	20%
23	1	139	9%	•
24	р	127	88%	• 10%
25	i	122	15%	
20		116	22%	
20	11	110		•
27	t	111	86%	14%
28	r	159	87%	13%
29	В	273	78%	21%
30	D	219	70%	30%
31	F	155	97% 99%	
32	А	294	65%	15%
		_01	86%	1370
33	Н	132	96%	• •



Mol	Chain	Length	Quality of chain	
	т	101	80%	
34	J	121	93%	• 6%
35	С	205	99%	
			64%	
36	S	87	87%	• 11%
37	0	04	11%	70/
- 57	0	34	91% 50%	• /%
38	K	139	97%	••
		01	77%	
39	M	61	98%	•
40	I	108	93%	• 6%
	-	100	90%	
41	L	124	94%	• 5%
40	NT	0.0	58%	
42	N	86	97%	•
43	R	87	07%	
			67%	
44	Т	60	87%	• 12%
45	C	149	72%	
40	G	142	99%	••
46	Q	104	62% 38	3%
			71%	
47	E	215	77%	22%
18	D	85	/9%	
40	1	00	96%	• •
49	5	1520	80%	18% •
	-	_	40%	
50	Z	5	100%	
51	7	76	72%	26%
	•	10	1270	2070
52	Y	9	67%	33%
50	r	140	85%	
- 33	I	149	96%	••
54	h	137	92%	•• 7%
			77%	
55	g	161	75%	22%

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2 Entry composition (i)

There are 57 unique types of molecules in this entry. The entry contains 142534 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 23S ribosomal RNA.

Mol	Chain	Residues			AltConf	Trace			
1	3	2879	Total 61690	C 27566	N 11236	O 20009	Р 2879	0	0

• Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	4	105	Total 2245	C 1003	N 409	0 728	Р 105	0	0

• Molecule 3 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	W	99	Total 798	C 505	N 149	0 144	0	0

• Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	285	Total 2199	C 1370	N 433	O 390	S 6	0	0

• Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	с	210	Total 1613	C 1026	N 294	O 290	$\frac{S}{3}$	0	0

• Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	е	176	Total 1349	C 867	N 240	O 242	0	0



• Molecule 7 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	k	148	Total 1138	C 722	N 223	O 193	0	0

• Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues		At	oms			AltConf	Trace
8	i	144	Total 1158	C 733	N 212	O 208	${ m S}{ m 5}$	0	0

• Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues		At	oms			AltConf	Trace
9	m	119	Total 957	C 609	N 175	0 170	${ m S} { m 3}$	0	0

• Molecule 10 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues		At	oms			AltConf	Trace
10	q	99	Total 809	C 525	N 148	0 133	${ m S} { m 3}$	0	0

• Molecule 11 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues		At	oms			AltConf	Trace
11	u	86	Total 641	C 397	N 127	0 116	S 1	0	0

• Molecule 12 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues		Ato	\mathbf{ms}		AltConf	Trace	
12	У	56	Total 436	C 262	N 96	O 73	${ m S}{ m 5}$	0	0

• Molecule 13 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues		Ato	\mathbf{ms}			AltConf	Trace
13	0	47	Total 377	C 234	N 81	O 61	S 1	0	0

• Molecule 14 is a protein called 50S ribosomal protein L36.



Mol	Chain	Residues		Atc	\mathbf{ms}			AltConf	Trace
14	2	37	Total 303	C 189	N 65	0 45	${f S}$ 4	0	0

• Molecule 15 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace		
15	1	59	Total 477	C 300	N 99	O 77	S 1	0	0

• Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues		At	oms	AltConf	Trace		
16	О	115	Total 895	C 568	N 169	O 157	S 1	0	0

• Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues		At	oms			AltConf	Trace
17	S	92	Total 714	C 470	N 121	0 122	S 1	0	0

• Molecule 18 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues		Ate	oms			AltConf	Trace
18	v	63	Total 504	C 312	N 107	0 84	S 1	0	0

• Molecule 19 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues		Aton	ıs		AltConf	Trace
10	v	4.4	Total	С	Ν	0	0	0
19	А	44	218	130	44	44	0	0

• Molecule 20 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues		Ato	\mathbf{ms}			AltConf	Trace
20	Z	50	Total 408	C 255	N 81	O 68	${S \atop 4}$	0	0

• Molecule 21 is a protein called 50S ribosomal protein L5.



Mol	Chain	Residues		At	oms			AltConf	Trace
21	d	175	Total 1244	C 797	N 214	O 229	$\frac{S}{4}$	0	0

• Molecule 22 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues		Ate		AltConf	Trace		
22	b	229	Total 1758	C 1116	N 317	0 318	${f S}{7}$	0	0

• Molecule 23 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues		At	oms			AltConf	Trace
23	1	136	Total 1057	C 680	N 193	0 177	${f S}{7}$	0	0

• Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues		At	oms			AltConf	Trace
24	р	114	Total 941	C 600	N 185	0 154	${ m S} { m 2}$	0	0

• Molecule 25 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues		At	oms			AltConf	Trace
25	j	122	Total 944	C 595	N 178	0 167	S 4	0	0

• Molecule 26 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues		At	oms			AltConf	Trace
26	n	112	Total 853	С 534	N 169	0 149	S 1	0	0

• Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues		At	oms			AltConf	Trace
27	t	96	Total 706	C 449	N 132	0 122	${ m S} { m 3}$	0	0

• Molecule 28 is a protein called 50S ribosomal protein L22.



Mol	Chain	Residues		At	oms			AltConf	Trace
28	r	139	Total 1068	C 663	N 207	0 191	${ m S} 7$	0	0

• Molecule 29 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues		Ate		AltConf	Trace		
29	В	215	Total 1682	C 1063	N 308	O 306	${ m S}{ m 5}$	0	0

• Molecule 30 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues		At	oms			AltConf	Trace
30	D	153	Total 1153	C 731	N 222	0 197	${ m S} { m 3}$	0	0

• Molecule 31 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues		At	oms			AltConf	Trace
31	F	154	Total 1231	C 777	N 234	0 215	${ m S}{ m 5}$	0	0

• Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues		Ate	AltConf	Trace			
32	А	249	Total 1917	C 1224	N 331	O 355	S 7	0	0

• Molecule 33 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues		At	oms	AltConf	Trace		
33	Н	128	Total 993	C 634	N 184	0 174	S 1	0	0

• Molecule 34 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues		At	oms	AltConf	Trace		
34	J	114	Total 828	C 514	N 153	0 155	S 6	0	0

• Molecule 35 is a protein called 30S ribosomal protein S4.



Mol	Chain	Residues		At	oms			AltConf	Trace
35	С	203	Total 1605	C 1015	N 306	O 280	$\frac{S}{4}$	0	0

• Molecule 36 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
36	S	77	Total 629	C 383	N 135	0 111	0	0

• Molecule 37 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues		At	oms	AltConf	Trace		
37	Ο	87	Total 690	C 445	N 128	0 115	$\frac{S}{2}$	0	0

• Molecule 38 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues		At	oms	AltConf	Trace		
38	K	136	Total 1055	C 667	N 209	0 177	${ m S} { m 2}$	0	0

• Molecule 39 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues		Atc	\mathbf{ms}			AltConf	Trace
39	М	60	Total 473	C 302	N 96	0 71	$\frac{S}{4}$	0	0

• Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues		At	oms			AltConf	Trace
40	Ι	101	Total 803	C 518	N 141	0 143	S 1	0	0

• Molecule 41 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
41	L	118	Total 922	C 576	N 186	O 160	0	0

• Molecule 42 is a protein called 30S ribosomal protein S15.



Mol	Chain	Residues		Ato	\mathbf{ms}		AltConf	Trace
42	Ν	83	Total 673	C 428	N 125	O 120	0	0

• Molecule 43 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues		At	oms	AltConf	Trace		
43	R	84	Total 654	C 419	N 119	0 114	${S \over 2}$	0	0

• Molecule 44 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace		
44	Т	53	Total 439	C 275	N 93	O 70	S 1	0	0

• Molecule 45 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues		At	oms			AltConf	Trace
45	G	141	Total 1103	C 720	N 192	0 189	${ m S} { m 2}$	0	0

• Molecule 46 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues		Ate	oms	AltConf	Trace		
46	Q	65	Total 535	C 342	N 103	O 86	S 4	0	0

• Molecule 47 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues		At	oms	Atoms						
47	Е	167	Total 1211	С 762	N 219	O 229	S 1	0	0			

• Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
48	Р	83	Total 675	C 425	N 135	0 115	0	0

• Molecule 49 is a RNA chain called 16S ribosomal RNA.



Mol	Chain	Residues		I	Atoms			AltConf	Trace
49	5	1493	Total 31952	C 14279	N 5792	O 10388	Р 1493	0	0

• Molecule 50 is a protein called nascent peptide.

Mol	Chain	Residues	A	Aton	ns	AltConf	Trace	
50	Ζ	5	Total 26	C 15	N 5	0 6	0	0

• Molecule 51 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues		\mathbf{A}	toms			AltConf	Trace
51	7	76	Total 1618	C 723	N 289	0 531	Р 75	0	0

• Molecule 52 is a RNA chain called mRNA.

Mol	Chain	Residues		At	\mathbf{oms}	AltConf	Trace		
52	Y	9	Total 177	C 81	N 18	O 70	Р 8	0	0

• Molecule 53 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
53	f	144	Total 713	C 425	N 144	0 144	0	0

• Molecule 54 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
54	h	128	Total 630	C 374	N 128	O 128	0	0

• Molecule 55 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace	
55	g	125	Total 617	C 367	N 125	0 125	0	0

• Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).



Mol	Chain	Residues	Atoms	AltConf
56	3	24	Total Mg 24 24	0
56	У	1	Total Mg 1 1	0

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

Mol	Chain	Residues	Atoms	AltConf
57	У	1	Total Zn 1 1	0
57	2	1	Total Zn 1 1	0
57	Z	1	Total Zn 1 1	0
57	М	1	Total Zn 1 1	0
57	Q	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: 23S ribosomal RNA





 \bullet Molecule 4: 50S ribosomal protein L2







Chain q:	99%	
M1 G8 S9 K10 E16 H17 E23	E26 A27 E32 E32 E33 K37 K37 K37 K37 K52 K52 K52 K52 K52 K52 K52 K52 K52 K52	
• Molecule 11: 50	0S ribosomal protein L27	
Chain u:	83%	17%
MET ASN ASN ASN I YR TYR PHE LEU I LEU ASP I LEU	PHE PHE ALA 817 817 817 622 622 622 622 622 622 672 978 970 978 978 978 1102 878 1102 878 ASP ASP	
• Molecule 12: 50	0S ribosomal protein L32	
Chain y:	98%	
MET A2 D20 K32 K32 M47 L51	RS2 X67 X67	
• Molecule 13: 50	0S ribosomal protein L34	
Chain 0:	98%	•
H1 E47 ARG		
• Molecule 14: 50	0S ribosomal protein L36	
Chain 2:	100%	
M D1 3 K28 Q37 G37		
• Molecule 15: 50	0S ribosomal protein L35	
Chain 1:	100%	
M1 L13 K33 K33 K53 K53 K53 K53 K53 K53 K53 K5		
• Molecule 16: 50	0S ribosomal protein L19	
Chain o:	97%	•









V154 T155 L156 N161 K162 S164 S164 A166 L167 A166 L167 A168 L167 A168 L173 M174 L173 M174 C177 UX1 UX1 UX1 UX3

• Molecule 22: 50S ribosomal protein L3

10%

Cha	in	b:								8	0%									20%	6							
••	*	•	•	٠	•	*	•	*	*	*	•	•	••	•	•	••	•	*	*	••	•	•	•					
M1 E2	N21	E32	E42 A43	K44 DAE	K46	D55	E58	K61	E71	E83	T88	G89 F90	E91 M92	E106	D109	D185 E186	M189	E201	K212	I220 E221	L222	T226	E227 K228	PRO	ALA	PRO	LEU LEU	LYS
		_				_				_							_											

LIYIS GIUU CIUNS CIUUTS CIUUTS CIUUTS ALLA ALLA ALLA ALLA ALLA CIUUTS CI

• Molecule 23: 50S ribosomal protein L16

Chain l:	98% •
M1 K20 D43 T61 K77	E30 E31 C399 C499 F316 E135 E135 E135 ALA
• Molecule 24:	50S ribosomal protein L20
Chain p:	88% · 10%
M1 G5 E70 K83 H85 H85	189 E96 199 199 199 199 199 199 199 199 199 199 199 199 199 190 1108 8114 6LU 6LU 6LU 6LU 6LU 6LU 6LU 6LU 8114 9 8114 9 8114 9 8114 9 9 113 9 114 9 113 9 114 115 114 114 114 114 114 114 114 114 114 114 114
• Molecule 25:	50S ribosomal protein L14
Chain j:	100%
M1 D12 K17 Q18 D37	848 848 G50 G70 R71 K72 K72 K72 B80 B80 B80 B80 C106 K104 E105 E105 K104 C106 K104 K104 K104 K106 K105 K105 K11 K11 K11 K12 K11 K12 K12 K12
• Molecule 26:	50S ribosomal protein L18
Chain n:	97%
M1 K2 T3 R4 R9 H24 H24	ILAG LASE NIG 4 NIG 4 NIG 4 NIG 4 NIG 9 NIG 9

 \bullet Molecule 27: 50S ribosomal protein L24



Chain t:	86%	14%
M1 G7 K18 S21 A30 K31	K41 K47 K47 LYS AK6 GLN GLN ALA ALA ALA ALA ALA ALA ALA ALA CLN SER CLN SER CLN SER CLN SER CLN	Б66 F70 078 479 K80 K80 K81 K82 Q83 Q83 Q83 Q83 Q83 V92 V92
N109		
• Molecule 28: 50S	ribosomal protein L22	
Chain r:	87%	13%
M1 D31 M65 G66 D67 E73 E73 E73 C1A	LTS ALA VAL SER SER SER VAL LYS SER ALA ALA CLN GLN GLN GLN GLY CLN CLN GLY	
• Molecule 29: 30S	ribosomal protein S3	
Chain B:	52% 78%	21%
MET GLY GLY K4 K1 F12 F12 M15 M15	223 ₩22 A24 ₩27 N255 %26 H27 H27 H27 E38 E38 E38 E38 E44 E45 F44	N446 N447 Y448 A449 A51 Q52 Q52 Q52 C554 N555 V555 E57 E557 E559 E559 E559 E559
L77 178 679 581 881 881 883 883 883 884 185 986	188 189 189 189 192 192 195 195 196 196 196 196 196 199 1102 1102 1102	1105 1106 N107 E108 (1109 6110 8111 N113 S115 S115 A116 N117 1119
A147 C148 A149 A150 C151 A150 L160 N161 C162 A163	E164 • 1165 • 1165 • 1165 • 1165 • 1165 • 1165 • 1167 • 1167 • 1172 • 1172 • 1172 • 1172 • 1172 • 1172 • 1172 • 1172 • 1172 • 1175 • 1175 • 1187 • 1188 • 1188 • 1186 • 11	A188 E190 K191 A192 A193 A195 A195 A195 A195 A195 A195 A195 A195
ILEU HIS PRO GLN CYS CYS CIN GLN ASN ASN GLN GLN	PLAN PLAN PLES PLES PLES PLES ASN CLN CLN CLN CLN CLN CLN CLN CLN CLN CL	SER SER CLIN CLIN CLIN ALA ALA ALA ALA CLN CLN CLN CLN CLN CLN CLN CLN CLN CLN
• Molecule 30: 30S	ribosomal protein S5	
Chain D:	70%	30%
MET THR ASP GLN GLN GLN CLN GLN GLY GLY GLY LEU	CLN THR THR LEU CLU CLN CLN CLN ALA ALA ALA ALA ALA ALA ALA ALA CLN CLN CLU CLU CLU CLU CLU CLU	LYS LYS ALA VAL VAL VAL LYS CLU CLY CLV CLV CLV CLV CLV CLV ASN ASN ASN ASN ASN ASN ASN ASN ASN ASN
ALA PHE LYS SER CLU F66 E67 E68 R69 R69 TTO	K78 K81 K81 C82 C82 C82 C83 M85 M85 M85 M85 M85 K98 K98 K98 K115 M118	H123 N124 L129 E130 H132 K133 K133 K133 K137 H138 F139 V140 V140
1158 159 1160 163 164 164 165 1165 1169	S176 D177 K181 K181 N182 L183 C184 R185 C184 R185 C184 C198 C198 C198 C198 C198 C198 C198	2204 P205 R205 R207 I210 I211 R212 R213 R214 N215 I216 N215 I216 S218 I216 L216 L216 L216 L216 L216 L218 L218

 \bullet Molecule 31: 30S ribosomal protein S7





• Molecule 34: 30S ribosomal protein S11



• Molecule 38: 30S ribosomal protein S12







 \bullet Molecule 47: 30S ribosomal protein S6



wiw

PDB IN DATA BANK



• Molecule 53: 50S ribosomal protein L9







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	77539	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT $(4k \ge 4k)$	Depositor
Maximum map value	0.009	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.0024	Depositor
Map size (Å)	571.368, 571.368, 571.368	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7004999, 1.7004999, 1.7004999	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).

Mal	Chain	Bo	ond lengths	Bond angles			
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5		
1	3	0.26	1/69100~(0.0%)	0.80	21/107749~(0.0%)		
2	4	0.22	0/2511	0.79	0/3910		
3	W	0.27	0/806	0.52	0/1080		
4	a	0.25	0/2241	0.47	0/3013		
5	с	0.26	0/1639	0.51	0/2209		
6	е	0.26	0/1373	0.45	0/1854		
7	k	0.35	0/1155	0.55	0/1541		
8	i	0.25	0/1180	0.47	0/1585		
9	m	0.25	0/972	0.48	0/1308		
10	q	0.27	0/826	0.53	0/1109		
11	u	0.25	0/649	0.52	0/867		
12	У	0.24	0/440	0.52	0/582		
13	0	0.24	0/380	0.43	0/501		
14	2	0.24	0/305	0.50	0/401		
15	1	0.24	0/484	0.47	0/637		
16	0	0.28	0/905	0.51	0/1211		
17	s	0.27	0/726	0.49	0/981		
18	V	0.23	0/510	0.46	0/684		
19	Х	0.25	0/217	0.48	0/301		
20	Z	0.24	0/412	0.47	0/547		
21	d	0.26	0/1264	0.54	0/1719		
22	b	0.26	0/1791	0.50	0/2408		
23	1	0.27	0/1082	0.49	0/1456		
24	р	0.25	0/955	0.43	0/1271		
25	j	0.26	0/953	0.52	0/1275		
26	n	0.25	0/861	0.50	0/1156		
27	t	0.24	0/712	0.49	0/954		
28	r	0.27	0/1077	0.46	0/1441		
29	В	0.27	0/1705	0.52	0/2304		
30	D	0.26	0/1168	0.49	0/1568		
31	F	0.27	0/1250	0.51	0/1682		
32	А	0.26	0/1951	0.50	0/2652		



Mol Chain		Bo	ond lengths	E	Bond angles
	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5
33	Н	0.26	0/1009	0.50	0/1354
34	J	0.30	0/843	0.57	2/1136~(0.2%)
35	С	0.26	0/1635	0.50	0/2202
36	S	0.30	0/631	0.62	0/838
37	Ο	0.25	0/703	0.49	0/945
38	Κ	0.25	0/1073	0.55	1/1445~(0.1%)
39	М	0.27	0/482	0.48	0/643
40	Ι	0.26	0/814	0.57	0/1096
41	L	0.30	0/933	0.62	2/1254~(0.2%)
42	Ν	0.25	0/679	0.43	0/907
43	R	0.27	0/670	0.52	0/904
44	Т	0.39	0/442	0.61	1/582~(0.2%)
45	G	0.26	0/1119	0.53	0/1508
46	Q	0.26	0/545	0.52	0/730
47	Е	0.28	0/1229	0.51	0/1670
48	Р	0.24	0/684	0.51	0/913
49	5	0.23	0/35777	0.80	8/55776~(0.0%)
51	7	0.25	0/1808	0.89	3/2817~(0.1%)
52	Y	0.89	3/194~(1.5%)	1.11	0/298
53	f	0.44	0/711	0.75	0/988
54	h	0.62	0/629	1.00	1/873~(0.1%)
55	g	0.76	0/616	1.03	1/856~(0.1%)
All	All	0.26	4/154826~(0.0%)	0.74	$40/231691 \ (0.0\%)$

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	Y	2	U	C1'-N1	6.47	1.58	1.48
52	Y	9	U	C1'-N1	6.20	1.58	1.48
52	Y	1	U	C1'-N1	6.00	1.57	1.48
1	3	1201	А	O3'-P	-5.30	1.54	1.61

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
41	L	41	PRO	CA-N-CD	-8.81	99.16	111.50
1	3	1486	U	C2-N1-C1'	8.30	127.66	117.70
1	3	1659	С	N3-C2-O2	-7.93	116.35	121.90
1	3	1659	C	N1-C2-O2	7.80	123.58	118.90
1	3	14	U	C2-N1-C1'	7.73	126.98	117.70
41	L	41	PRO	N-CD-CG	-7.66	91.71	103.20
1	3	426	U	C2-N1-C1'	7.39	126.57	117.70



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	$Ideal(^{o})$
1	3	1211	U	C2'-C3'-O3'	7.35	125.67	109.50
51	7	73	С	N1-C2-O2	7.28	123.27	118.90
49	5	843	С	N3-C2-O2	-7.26	116.82	121.90
38	К	31	LEU	CA-CB-CG	6.94	131.27	115.30
1	3	1486	U	N1-C2-O2	6.92	127.64	122.80
1	3	1211	U	N1-C1'-C2'	-6.43	104.93	112.00
1	3	1486	U	N3-C2-O2	-6.38	117.74	122.20
1	3	14	U	N1-C2-O2	6.23	127.16	122.80
34	J	119	ARG	CG-CD-NE	6.22	124.85	111.80
49	5	189	С	N3-C2-O2	-6.15	117.59	121.90
51	7	73	С	N3-C2-O2	-6.09	117.64	121.90
1	3	14	U	N3-C2-O2	-5.97	118.02	122.20
34	J	119	ARG	CA-CB-CG	5.76	126.06	113.40
1	3	1303	U	C2-N1-C1'	5.75	124.61	117.70
1	3	1341	U	C2-N1-C1'	5.65	124.47	117.70
49	5	468	G	C5-C6-O6	-5.64	125.22	128.60
1	3	2668	А	P-O3'-C3'	5.57	126.38	119.70
49	5	974	С	C2-N1-C1'	5.54	124.89	118.80
1	3	1303	U	N1-C2-O2	5.49	126.64	122.80
54	h	23	PRO	CA-C-N	5.36	128.99	117.20
1	3	426	U	C6-N1-C1'	-5.29	113.79	121.20
49	5	1034	G	N3-C4-N9	-5.29	122.82	126.00
49	5	335	С	N3-C2-O2	-5.29	118.20	121.90
1	3	2305	С	C2-N1-C1'	5.26	124.58	118.80
1	3	1486	U	C6-N1-C1'	-5.22	113.89	121.20
55	g	56	ASN	CB-CA-C	-5.22	99.96	110.40
51	7	17	U	C2-N1-C1'	5.18	123.92	117.70
49	5	1088	С	N3-C2-O2	-5.17	118.28	121.90
49	5	974	С	N1-C2-O2	5.14	121.98	118.90
1	3	1206	U	N1-C1'-C2'	-5.11	106.38	112.00
1	3	2111	U	N1-C2-O2	5.11	126.38	122.80
1	3	1486	U	C5-C6-N1	5.11	125.25	122.70
44	Т	36	LEU	CA-CB-CG	5.05	126.92	115.30

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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	Perce	ntiles
3	W	95/111~(86%)	91 (96%)	4 (4%)	0	100	100
4	a	283/287~(99%)	265~(94%)	18 (6%)	0	100	100
5	с	208/212~(98%)	190 (91%)	18 (9%)	0	100	100
6	е	174/184~(95%)	168~(97%)	6 (3%)	0	100	100
7	k	146/151~(97%)	126 (86%)	20 (14%)	0	100	100
8	i	142/146~(97%)	133~(94%)	9~(6%)	0	100	100
9	m	117/124~(94%)	113 (97%)	4 (3%)	0	100	100
10	q	97/100~(97%)	88 (91%)	9~(9%)	0	100	100
11	u	84/104 (81%)	79~(94%)	5 (6%)	0	100	100
12	У	54/57~(95%)	49 (91%)	5 (9%)	0	100	100
13	0	45/48~(94%)	44 (98%)	1 (2%)	0	100	100
14	2	35/37~(95%)	33~(94%)	2(6%)	0	100	100
15	1	57/59~(97%)	55~(96%)	2(4%)	0	100	100
16	О	113/119~(95%)	101 (89%)	12 (11%)	0	100	100
17	s	90/237~(38%)	84 (93%)	6 (7%)	0	100	100
18	v	61/65~(94%)	58~(95%)	3~(5%)	0	100	100
19	х	42/97~(43%)	38~(90%)	4 (10%)	0	100	100
20	Z	48/53~(91%)	46~(96%)	2(4%)	0	100	100
21	d	173/180~(96%)	156 (90%)	17 (10%)	0	100	100
22	b	227/287~(79%)	217 (96%)	10 (4%)	0	100	100
23	1	134/139~(96%)	127 (95%)	7 (5%)	0	100	100
24	р	112/127~(88%)	109 (97%)	3 (3%)	0	100	100
25	j	120/122~(98%)	106 (88%)	14 (12%)	0	100	100
26	n	108/116~(93%)	102 (94%)	6 (6%)	0	100	100
27	t	92/111 (83%)	83 (90%)	9 (10%)	0	100	100



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
28	r	137/159~(86%)	127~(93%)	10 (7%)	0	100	100
29	В	213/273~(78%)	200 (94%)	13 (6%)	0	100	100
30	D	151/219~(69%)	142 (94%)	9 (6%)	0	100	100
31	F	152/155~(98%)	135 (89%)	17 (11%)	0	100	100
32	А	247/294~(84%)	228 (92%)	19 (8%)	0	100	100
33	Н	126/132~(96%)	104 (82%)	22 (18%)	0	100	100
34	J	112/121 (93%)	105 (94%)	7 (6%)	0	100	100
35	С	201/205~(98%)	191 (95%)	10 (5%)	0	100	100
36	S	75/87~(86%)	72 (96%)	3 (4%)	0	100	100
37	Ο	85/94 (90%)	79 (93%)	6 (7%)	0	100	100
38	К	134/139~(96%)	117 (87%)	17 (13%)	0	100	100
39	М	58/61~(95%)	55 (95%)	3 (5%)	0	100	100
40	Ι	99/108~(92%)	87 (88%)	12 (12%)	0	100	100
41	L	116/124 (94%)	103 (89%)	13 (11%)	0	100	100
42	N	81/86~(94%)	80 (99%)	1 (1%)	0	100	100
43	R	82/87~(94%)	77 (94%)	5 (6%)	0	100	100
44	Т	51/60~(85%)	44 (86%)	7 (14%)	0	100	100
45	G	139/142~(98%)	122 (88%)	17 (12%)	0	100	100
46	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
47	Е	165/215~(77%)	148 (90%)	17 (10%)	0	100	100
48	Р	81/85~(95%)	75 (93%)	6 (7%)	0	100	100
53	f	140/149~(94%)	124 (89%)	15 (11%)	1 (1%)	22	61
54	h	126/137~(92%)	116 (92%)	8 (6%)	2 (2%)	9	43
55	g	123/161 (76%)	115 (94%)	4 (3%)	4 (3%)	4	28
All	All	5814/6670 ($87%$)	5364 (92%)	443 (8%)	7 (0%)	54	84

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All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
53	f	115	ASP
54	h	20	LYS
55	g	45	PHE
55	g	110	CYS
54	h	23	PRO



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Mol	Chain	Res	Type
55	g	88	GLU
55	g	47	ASN

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	Perce	ntiles
3	W	83/98~(85%)	83 (100%)	0	100	100
4	a	233/243~(96%)	233 (100%)	0	100	100
5	с	174/184~(95%)	174 (100%)	0	100	100
6	е	138/159~(87%)	138 (100%)	0	100	100
7	k	118/126~(94%)	118 (100%)	0	100	100
8	i	124/128~(97%)	124 (100%)	0	100	100
9	m	104/109~(95%)	104 (100%)	0	100	100
10	q	88/91~(97%)	88 (100%)	0	100	100
11	u	64/85~(75%)	64 (100%)	0	100	100
12	У	45/49~(92%)	45 (100%)	0	100	100
13	0	39/41~(95%)	39 (100%)	0	100	100
14	2	35/35~(100%)	35~(100%)	0	100	100
15	1	51/51~(100%)	51 (100%)	0	100	100
16	О	91/105~(87%)	91 (100%)	0	100	100
17	\mathbf{S}	80/208~(38%)	80 (100%)	0	100	100
18	v	55/60~(92%)	55~(100%)	0	100	100
20	Z	47/50~(94%)	46 (98%)	1 (2%)	53	79
21	d	111/154~(72%)	110~(99%)	1 (1%)	78	90
22	b	185/233~(79%)	185 (100%)	0	100	100
23	1	107/115 (93%)	$107 \ (100\%)$	0	100	100
24	р	99/108~(92%)	97~(98%)	2(2%)	55	79
25	j	103/103~(100%)	103 (100%)	0	100	100



Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
26	n	85/99~(86%)	85~(100%)	0	100	100
27	t	69/96~(72%)	69~(100%)	0	100	100
28	r	116/132~(88%)	116 (100%)	0	100	100
29	В	176/232~(76%)	175 (99%)	1 (1%)	86	94
30	D	117/178~(66%)	117 (100%)	0	100	100
31	F	128/132~(97%)	128 (100%)	0	100	100
32	А	200/262~(76%)	199 (100%)	1 (0%)	88	94
33	Н	101/115~(88%)	100 (99%)	1 (1%)	76	88
34	J	91/97~(94%)	91 (100%)	0	100	100
35	С	164/183~(90%)	164 (100%)	0	100	100
36	S	70/77~(91%)	69~(99%)	1 (1%)	67	85
37	Ο	71/82~(87%)	70~(99%)	1 (1%)	67	85
38	Κ	111/120 (92%)	111 (100%)	0	100	100
39	М	47/48~(98%)	47 (100%)	0	100	100
40	Ι	93/99~(94%)	92~(99%)	1 (1%)	73	88
41	L	92/105~(88%)	91~(99%)	1 (1%)	73	88
42	Ν	76/78~(97%)	76 (100%)	0	100	100
43	R	66/77~(86%)	66 (100%)	0	100	100
44	Т	43/56~(77%)	43 (100%)	0	100	100
45	G	121/124 (98%)	120 (99%)	1 (1%)	81	91
46	Q	56/94~(60%)	56 (100%)	0	100	100
47	Е	107/196~(55%)	106 (99%)	1 (1%)	78	90
48	Р	73/75~(97%)	72 (99%)	1 (1%)	67	85
All	All	4447/5292 (84%)	4433 (100%)	14 (0%)	92	97

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All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	Z	15	ARG
21	d	30	ARG
24	р	84	LYS
24	р	85	HIS
29	В	90	LYS
32	А	27	ARG



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Mol	Chain	Res	Type
33	Н	110	LYS
36	S	9	LYS
37	0	49	LYS
40	Ι	97	LYS
41	L	78	LYS
45	G	68	ARG
47	Е	80	LYS
48	Р	60	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
5	с	130	GLN
5	с	156	ASN
6	е	21	GLN
6	е	107	ASN
7	k	5	GLN
25	j	18	GLN
28	r	120	GLN
29	В	42	ASN
32	А	70	ASN
32	А	119	ASN
33	Н	52	GLN
35	С	37	GLN
35	С	52	GLN
35	С	70	GLN
35	С	171	ASN
36	S	63	ASN
48	Р	25	GLN
48	Р	62	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	2877/2907~(98%)	532 (18%)	37~(1%)
2	4	103/108~(95%)	28 (27%)	2(1%)
49	5	1490/1520~(98%)	274 (18%)	6 (0%)
51	7	75/76~(98%)	20 (26%)	1 (1%)
52	Y	8/9~(88%)	0	0
All	All	4553/4620 (98%)	854 (18%)	46 (1%)


All (854) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	17	G
1	3	37	G
1	3	48	G
1	3	53	G
1	3	64	U
1	3	65	А
1	3	73	А
1	3	76	А
1	3	77	G
1	3	85	U
1	3	102	А
1	3	103	G
1	3	111	G
1	3	119	A
1	3	121	U
1	3	124	А
1	3	126	С
1	3	132	G
1	3	146	G
1	3	163	А
1	3	164	А
1	3	166	А
1	3	180	А
1	3	184	А
1	3	186	А
1	3	200	А
1	3	203	А
1	3	208	А
1	3	219	G
1	3	220	A
1	3	225	A
1	3	226	A
1	3	230	G
1	3	232	A
1	3	233	U
1	3	234	G
1	3	237	A
1	3	245	U
1	3	251	G
1	3	252	G
1	3	259	A
1	3	270	G



\mathbf{Mol}	Chain	Res	Type
1	3	276	А
1	3	283	А
1	3	284	U
1	3	286	А
1	3	295	U
1	3	296	U
1	3	297	G
1	3	298	U
1	3	299	А
1	3	310	U
1	3	312	U
1	3	315	A
1	3	316	С
1	3	319	G
1	3	325	G
1	3	336	С
1	3	341	G
1	3	343	А
1	3	345	А
1	3	346	G
1	3	363	G
1	3	364	А
1	3	402	А
1	3	403	U
1	3	404	С
1	3	409	А
1	3	411	U
1	3	418	G
1	3	422	A
1	3	424	G
1	3	425	U
1	3	426	U
1	3	427	A
1	3	432	G
1	3	437	A
1	3	447	G
1	3	448	A
1	3	460	G
1	3	484	U
1	3	485	A
1	3	487	С
1	3	491	А



Mol	Chain	Res	Type
1	3	493	А
1	3	501	G
1	3	509	G
1	3	513	А
1	3	514	А
1	3	515	А
1	3	517	G
1	3	544	U
1	3	545	С
1	3	548	А
1	3	554	U
1	3	562	С
1	3	565	C
1	3	566	G
1	3	567	U
1	3	568	G
1	3	581	А
1	3	583	U
1	3	596	G
1	3	598	G
1	3	602	U
1	3	606	G
1	3	608	А
1	3	620	G
1	3	636	U
1	3	637	U
1	3	638	А
1	3	648	G
1	3	649	А
1	3	650	G
1	3	663	A
1	3	670	G
1	3	673	A
1	3	681	А
1	3	682	A
1	3	689	U
1	3	691	G
1	3	705	A
1	3	706	С
1	3	721	G
1	3	752	С
1	3	765	A



\mathbf{Mol}	Chain	Res	Type
1	3	782	U
1	3	792	G
1	3	799	А
1	3	800	С
1	3	810	G
1	3	811	G
1	3	817	А
1	3	818	А
1	3	819	U
1	3	820	U
1	3	825	U
1	3	828	А
1	3	829	А
1	3	840	G
1	3	847	С
1	3	854	A
1	3	862	U
1	3	881	А
1	3	882	С
1	3	883	А
1	3	887	А
1	3	895	G
1	3	902	U
1	3	903	А
1	3	904	С
1	3	924	С
1	3	926	U
1	3	932	U
1	3	936	G
1	3	944	U
1	3	947	A
1	3	949	С
1	3	951	С
1	3	952	U
1	3	953	G
1	3	970	U
1	3	981	A
1	3	982	G
1	3	994	U
1	3	995	А
1	3	997	G
1	3	1008	А



Mol	Chain	Res	Type
1	3	1009	А
1	3	1010	G
1	3	1016	А
1	3	1026	А
1	3	1032	А
1	3	1039	G
1	3	1049	U
1	3	1055	А
1	3	1057	G
1	3	1058	U
1	3	1061	А
1	3	1068	U
1	3	1075	G
1	3	1080	A
1	3	1081	A
1	3	1082	A
1	3	1083	А
1	3	1102	А
1	3	1103	G
1	3	1104	А
1	3	1105	А
1	3	1106	G
1	3	1107	С
1	3	1112	А
1	3	1123	А
1	3	1124	G
1	3	1125	U
1	3	1126	G
1	3	1130	А
1	3	1131	А
1	3	1132	C
1	3	1140	U
1	3	1146	A
1	3	1147	G
1	3	1148	U
1	3	1151	U
1	3	1154	U
1	3	1161	A
1	3	1164	A
1	3	1165	U
1	3	1166	G
1	3	1167	U



Mol	Chain	Res	Type
1	3	1168	А
1	3	1169	A
1	3	1170	С
1	3	1171	G
1	3	1176	U
1	3	1177	А
1	3	1178	А
1	3	1186	А
1	3	1192	U
1	3	1204	А
1	3	1206	U
1	3	1207	U
1	3	1208	A
1	3	1209	U
1	3	1210	A
1	3	1211	U
1	3	1212	С
1	3	1217	G
1	3	1234	U
1	3	1235	U
1	3	1236	G
1	3	1242	G
1	3	1250	А
1	3	1251	G
1	3	1255	G
1	3	1268	U
1	3	1277	A
1	3	1283	А
1	3	1286	G
1	3	1295	А
1	3	1298	A
1	3	1301	G
1	3	1302	С
1	3	1303	U
1	3	1304	U
1	3	1315	A
1	3	1325	С
1	3	1328	A
1	3	1329	U
1	3	1330	U
1	3	1369	U
1	3	1380	U



Mol	Chain	Res	Type
1	3	1393	А
1	3	1406	А
1	3	1407	U
1	3	1412	А
1	3	1414	С
1	3	1423	А
1	3	1424	U
1	3	1431	А
1	3	1436	С
1	3	1444	С
1	3	1445	U
1	3	1448	U
1	3	1455	A
1	3	1456	C
1	3	1466	U
1	3	1480	A
1	3	1481	U
1	3	1483	G
1	3	1485	A
1	3	1486	U
1	3	1487	U
1	3	1504	G
1	3	1508	G
1	3	1509	U
1	3	1510	A
1	3	1513	A
1	3	1514	U
1	3	1515	A
1	3	1518	С
1	3	1519	A
1	3	1520	A
1	3	1522	U
1	3	1523	C
1	3	1532	A
1	3	1533	U
1	3	1534	A
1	3	1535	A
1	3	1541	A
1	3	1557	G
1	3	1558	A
1	3	1559	A
1	3	1571	G



Mol	Chain	Res	Type
1	3	1581	U
1	3	1584	U
1	3	1585	А
1	3	1586	U
1	3	1587	U
1	3	1588	А
1	3	1589	А
1	3	1600	А
1	3	1601	А
1	3	1603	А
1	3	1612	U
1	3	1616	G
1	3	1618	U
1	3	1619	A
1	3	1641	A
1	3	1643	А
1	3	1644	А
1	3	1651	С
1	3	1653	С
1	3	1668	G
1	3	1680	А
1	3	1681	G
1	3	1682	С
1	3	1688	А
1	3	1695	G
1	3	1706	C
1	3	1708	G
1	3	1727	U
1	3	1741	G
1	3	1748	U
1	3	1764	U
1	3	1765	G
1	3	1769	A
1	3	1770	A
1	3	1771	С
1	3	1780	A
1	3	1783	G
1	3	1789	С
1	3	1791	A
1	3	1807	C
1	3	1808	С
1	3	1815	U



Mol	Chain	Res	Type
1	3	1823	U
1	3	1836	A
1	3	1842	G
1	3	1854	A
1	3	1866	G
1	3	1869	G
1	3	1876	G
1	3	1891	А
1	3	1910	G
1	3	1913	G
1	3	1920	А
1	3	1921	С
1	3	1936	G
1	3	1938	U
1	3	1945	A
1	3	1962	U
1	3	1972	С
1	3	1977	А
1	3	1978	U
1	3	1979	G
1	3	1998	U
1	3	2000	U
1	3	2004	G
1	3	2010	А
1	3	2027	G
1	3	2030	А
1	3	2037	А
1	3	2038	А
1	3	2040	А
1	3	2050	G
1	3	2057	С
1	3	2059	G
1	3	2062	С
1	3	2063	G
1	3	2067	A
1	3	2068	G
1	3	2069	А
1	3	2076	G
1	3	2099	U
1	3	2100	G
1	3	2106	G
1	3	2107	A



Mol	Chain	Res	Type
1	3	2108	С
1	3	2110	U
1	3	2111	U
1	3	2112	А
1	3	2114	С
1	3	2115	А
1	3	2117	G
1	3	2123	А
1	3	2124	А
1	3	2125	U
1	3	2128	G
1	3	2130	А
1	3	2133	A
1	3	2139	С
1	3	2141	A
1	3	2151	G
1	3	2153	U
1	3	2164	G
1	3	2166	U
1	3	2171	А
1	3	2172	А
1	3	2180	U
1	3	2181	А
1	3	2193	U
1	3	2195	U
1	3	2196	G
1	3	2198	G
1	3	2199	С
1	3	2200	U
1	3	2202	U
1	3	2206	А
1	3	2207	А
1	3	2211	G
1	3	2212	U
1	3	2219	U
1	3	2220	A
1	3	2222	С
1	3	2233	A
1	3	2246	G
1	3	2247	G
1	3	2274	A
1	3	2276	А



Mol	Chain	Res	Type
1	3	2286	А
1	3	2291	U
1	3	2294	А
1	3	2295	А
1	3	2313	U
1	3	2316	G
1	3	2317	А
1	3	2324	А
1	3	2327	U
1	3	2328	А
1	3	2329	G
1	3	2333	G
1	3	2334	U
1	3	2335	А
1	3	2341	G
1	3	2342	U
1	3	2343	А
1	3	2344	А
1	3	2352	U
1	3	2355	С
1	3	2358	U
1	3	2366	А
1	3	2369	G
1	3	2391	G
1	3	2393	С
1	3	2401	U
1	3	2410	С
1	3	2411	С
1	3	2414	U
1	3	2422	G
1	3	2430	C
1	3	2433	A
1	3	2437	G
1	3	2438	A
1	3	2440	А
1	3	2449	U
1	3	2455	G
1	3	2456	А
1	3	2472	G
1	3	2478	G
1	3	2484	A
1	3	2486	А



Mol	Chain	Res	Type
1	3	2499	U
1	3	2502	G
1	3	2505	А
1	3	2506	С
1	3	2507	С
1	3	2509	С
1	3	2510	G
1	3	2512	U
1	3	2513	G
1	3	2521	А
1	3	2526	А
1	3	2528	С
1	3	2543	G
1	3	2562	U
1	3	2563	U
1	3	2574	A
1	3	2575	G
1	3	2580	A
1	3	2593	U
1	3	2594	С
1	3	2605	G
1	3	2610	А
1	3	2617	U
1	3	2621	U
1	3	2622	A
1	3	2629	G
1	3	2637	А
1	3	2638	G
1	3	2644	U
1	3	2649	G
1	3	2654	U
1	3	2668	А
1	3	2669	G
1	3	2687	A
1	3	2697	С
1	3	2698	U
1	3	2722	G
1	3	2732	A
1	3	2734	С
1	3	2737	G
1	3	2741	A
1	3	2752	G



Mol	Chain	Res	Type
1	3	2756	А
1	3	2765	А
1	3	2773	А
1	3	2785	G
1	3	2786	А
1	3	2797	С
1	3	2798	А
1	3	2799	U
1	3	2801	U
1	3	2808	А
1	3	2811	G
1	3	2812	U
1	3	2813	A
1	3	2822	С
1	3	2824	A
1	3	2829	G
1	3	2839	A
1	3	2853	U
1	3	2863	G
1	3	2865	U
1	3	2871	G
1	3	2876	G
1	3	2883	А
1	3	2884	С
1	3	2888	U
1	3	2890	G
1	3	2897	G
1	3	2898	А
2	4	9	С
2	4	10	С
2	4	11	A
2	4	13	G
2	4	14	U
2	4	22	G
2	4	23	А
2	4	28	C
2	4	33	U
2	4	34	U
2	4	35	С
2	4	40	U
2	4	41	С
2	4	42	G



Mol	Chain	Res	Type
2	4	48	А
2	4	49	G
2	4	54	U
2	4	55	А
2	4	60	С
2	4	65	G
2	4	77	G
2	4	78	С
2	4	86	G
2	4	88	G
2	4	89	А
2	4	99	А
2	4	106	А
2	4	108	С
49	5	7	U
49	5	8	G
49	5	9	А
49	5	10	G
49	5	33	А
49	5	40	G
49	5	48	С
49	5	49	С
49	5	52	А
49	5	61	А
49	5	62	G
49	5	66	А
49	5	75	А
49	5	93	А
49	5	106	С
49	5	114	С
49	5	115	A
49	5	117	U
49	5	120	A
49	5	128	A
49	5	130	G
49	5	134	G
49	5	136	U
49	5	149	G
49	5	154	G
49	5	156	U
49	5	157	А
49	5	159	U



Mol	Chain	Res	Type
49	5	163	G
49	5	167	А
49	5	168	А
49	5	169	G
49	5	171	А
49	5	189	С
49	5	197	А
49	5	198	А
49	5	199	А
49	5	208	А
49	5	210	G
49	5	220	U
49	5	223	G
49	5	236	С
49	5	241	C
49	5	243	G
49	5	247	G
49	5	262	G
49	5	263	С
49	5	285	G
49	5	294	А
49	5	296	А
49	5	297	А
49	5	301	G
49	5	302	А
49	5	324	С
49	5	325	А
49	5	326	С
49	5	328	G
49	5	341	С
49	5	342	G
49	5	343	G
49	5	344	G
49	5	345	А
49	5	347	G
49	5	348	C
49	5	359	А
49	5	363	U
49	5	365	U
49	5	368	С
49	5	369	A
49	5	373	А



Mol	Chain	Res	Type
49	5	374	G
49	5	377	А
49	5	378	А
49	5	393	А
49	5	401	U
49	5	402	G
49	5	407	А
49	5	409	G
49	5	410	А
49	5	417	U
49	5	418	U
49	5	419	A
49	5	420	A
49	5	425	G
49	5	426	U
49	5	435	U
49	5	448	A
49	5	449	А
49	5	450	U
49	5	452	A
49	5	453	С
49	5	457	A
49	5	461	G
49	5	463	U
49	5	464	A
49	5	465	A
49	5	468	G
49	5	473	A
49	5	476	U
49	5	478	G
49	5	481	U
49	5	482	G
49	5	488	U
49	5	489	U
49	5	490	U
49	5	493	A
49	5	494	A
49	5	495	U
49	5	496	A
49	5	509	C
49	5	516	C
49	5	525	G



Mol	Chain	Res	Type
49	5	529	U
49	5	530	А
49	5	531	А
49	5	545	А
49	5	557	А
49	5	562	U
49	5	570	А
49	5	574	С
49	5	575	А
49	5	579	G
49	5	586	G
49	5	594	A
49	5	619	А
49	5	620	A
49	5	628	A
49	5	638	A
49	5	646	A
49	5	662	G
49	5	671	G
49	5	672	A
49	5	680	G
49	5	682	G
49	5	699	A
49	5	715	A
49	5	719	G
49	5	720	U
49	5	721	G
49	5	731	A
49	5	745	U
49	5	746	A
49	5	747	C
49	5	752	G
49	5	787	A
49	5	790	U
49	5	791	A
49	5	811	A
49	5	812	A
49	5	814	C
49	5	815	G
49	5	818	A
49	5	825	A
49	5	829	G



Mol	Chain	Res	Type
49	5	838	А
49	5	839	U
49	5	840	С
49	5	841	С
49	5	842	С
49	5	865	U
49	5	879	G
49	5	883	А
49	5	896	G
49	5	908	А
49	5	910	С
49	5	911	G
49	5	921	G
49	5	922	G
49	5	929	С
49	5	930	А
49	5	953	А
49	5	955	U
49	5	964	А
49	5	970	А
49	5	971	А
49	5	972	А
49	5	977	U
49	5	984	А
49	5	987	U
49	5	988	G
49	5	999	С
49	5	1000	А
49	5	1002	А
49	5	1003	G
49	5	1013	С
49	5	1014	А
49	5	1015	U
49	5	1016	А
49	5	1033	U
49	5	1036	С
49	5	1037	А
49	5	1044	G
49	5	1045	С
49	5	1047	U
49	5	1055	G
49	5	1056	U



Mol	Chain	Res	Type
49	5	1072	G
49	5	1075	G
49	5	1076	U
49	5	1082	U
49	5	1085	G
49	5	1086	U
49	5	1089	С
49	5	1092	А
49	5	1113	U
49	5	1118	А
49	5	1119	С
49	5	1122	U
49	5	1123	G
49	5	1128	G
49	5	1134	С
49	5	1135	U
49	5	1141	U
49	5	1142	G
49	5	1143	С
49	5	1158	А
49	5	1159	А
49	5	1171	А
49	5	1172	А
49	5	1173	А
49	5	1187	U
49	5	1188	А
49	5	1197	G
49	5	1199	U
49	5	1200	G
49	5	1201	С
49	5	1203	А
49	5	1211	A
49	5	1232	С
49	5	1233	G
49	5	1235	С
49	5	1243	A
49	5	1245	A
49	5	1255	A
49	5	1260	U
49	5	1261	А
49	5	1271	U
49	5	1274	G



Mol	Chain	Res	Type
49	5	1276	U
49	5	1279	G
49	5	1296	С
49	5	1312	G
49	5	1314	А
49	5	1320	А
49	5	1321	G
49	5	1327	G
49	5	1337	U
49	5	1338	А
49	5	1353	С
49	5	1354	G
49	5	1356	U
49	5	1373	A
49	5	1394	G
49	5	1397	G
49	5	1400	А
49	5	1403	А
49	5	1404	U
49	5	1417	U
49	5	1426	U
49	5	1429	G
49	5	1433	G
49	5	1464	G
49	5	1467	А
49	5	1468	А
49	5	1478	А
49	5	1480	G
49	5	1481	U
49	5	1492	G
49	5	1495	С
49	5	1504	G
49	5	1505	G
49	5	1506	A
49	5	1508	С
49	5	1509	A
51	7	9	U
51	7	16	G
51	7	17	U
51	7	19	G
51	7	20	G
51	7	21	U



\mathbf{Mol}	Chain	Res	Type
51	7	22	А
51	7	23	G
51	7	24	А
51	7	43	G
51	7	44	U
51	7	47	G
51	7	49	С
51	7	50	G
51	7	54	G
51	7	58	G
51	7	71	А
51	7	72	C
51	7	75	С
51	7	77	А

All	(46)	RNA	pucker	outliers	are	listed	below:
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Mol	Chain	Res	Type
1	3	315	А
1	3	410	G
1	3	425	U
1	3	500	U
1	3	508	А
1	3	513	А
1	3	514	А
1	3	688	U
1	3	881	А
1	3	901	С
1	3	903	А
1	3	952	U
1	3	980	С
1	3	996	А
1	3	1048	А
1	3	1082	А
1	3	1207	U
1	3	1209	U
1	3	1210	А
1	3	1211	U
1	3	1297	U
1	3	1302	С
1	3	1507	G
1	3	1519	А



Mol	Chain	Res	Type
1	3	1570	А
1	3	1583	G
1	3	1585	А
1	3	1587	U
1	3	1588	А
1	3	1618	U
1	3	2342	U
1	3	2504	С
1	3	2506	С
1	3	2604	U
1	3	2668	А
1	3	2764	U
1	3	2862	U
2	4	54	U
2	4	59	А
49	5	168	А
49	5	419	A
49	5	449	A
49	5	838	А
49	5	999	С
49	5	1075	G
51	7	16	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 30 ligands modelled in this entry, 30 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 (i)

This section contains visualisations of the EMDB entry EMD-13234. 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 (i)

6.1.1 Primary map



6.1.2 Raw map



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



6.2 Central slices (i)

6.2.1 Primary map



X Index: 168



Y Index: 168



Z Index: 168

6.2.2 Raw map



X Index: 168

Y Index: 168

Z Index: 168

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: 142



Z Index: 163

6.3.2 Raw map



X Index: 142

Y Index: 160



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



6.4 Orthogonal surface views (i)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0024. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.



Mask visualisation (i) 6.5

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

$emd_{13234}_{msk_{1.map}}$ 6.5.1



Υ



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 852 nm^3 ; this corresponds to an approximate mass of 770 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 0.286 \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 0.286 $\mathrm{\AA^{-1}}$



8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.52	4.10	3.61
Unmasked-calculated*	4.65	7.12	4.91

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.65 differs from the reported value 3.5 by more than 10 %



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-13234 and PDB model 7P6Z. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.0024 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 (0.0024).



9.4 Atom inclusion (i)



At the recommended contour level, 69% of all backbone atoms, 66% 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 (0.0024) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	$\mathbf{Q} extsf{-score}$
All	0.6556	0.3850
0	0.7403	0.4890
1	0.6245	0.4890
2	0.6554	0.4960
3	0.8261	0.4190
4	0.7902	0.3920
5	0.6653	0.3330
7	0.4135	0.2870
А	0.2557	0.3130
В	0.3258	0.3640
\mathbf{C}	0.1811	0.2840
D	0.4444	0.3790
E	0.1366	0.2990
F	0.0727	0.2520
G	0.2906	0.3320
Н	0.1408	0.2910
Ι	0.1610	0.3110
J	0.1814	0.3320
K	0.3930	0.3910
L	0.0730	0.2260
М	0.2418	0.3610
Ν	0.3157	0.2880
О	0.1967	0.3180
Р	0.1887	0.2940
Q	0.2515	0.3370
R	0.0326	0.2340
S	0.2770	0.2470
T	0.3009	0.3340
Y	0.7684	0.4050
Z	0.4615	0.4520
a	0.6718	0.4760
b	0.6264	0.4640
С	0.6011	0.4470
d	0.3719	0.3530
e	0.4138	0.4210

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Chain	Atom inclusion	Q-score
f	0.1360	0.2600
g	0.0146	0.1680
h	0.0000	0.0500
i	0.6361	0.4600
j	0.5837	0.4740
k	0.6073	0.4580
1	0.6544	0.4710
m	0.6385	0.4660
n	0.5487	0.4160
0	0.6018	0.4660
р	0.6542	0.4630
q	0.6110	0.4780
r	0.6663	0.4580
S	0.5761	0.4550
t	0.4692	0.4420
u	0.6074	0.4830
V	0.6214	0.4680
W	0.5147	0.3970
X	0.2294	0.3570
У	0.7031	0.4800
Z	0.6005	0.4670

