

wwPDB EM Validation Summary Report (i)

Apr 27, 2024 – 03:58 PM EDT

PDB ID	:	8UU6
EMDB ID	:	EMD-42561
Title	:	Cryo-EM structure of the ratcheted Listeria innocua 70S ribosome in complex
		with p/E-tRNA (structure II-A)
Authors	:	Seely, S.M.; Basu, R.S.; Gagnon, M.G.
Deposited on	:	2023-10-31
Resolution	:	3.30 Å(reported)
Based on initial model	:	7NHN

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:

EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 3.30 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f EM} {f structures} \ (\#{f Entries})$		
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	a	1550	• 81%	17% ·
2	b	249	90%	10%
3	с	218	93%	7%
4	d	200	100%	
5	е	167	93%	7%
6	f	97	96%	·
7	g	156	91%	• 8%
8	h	132	99%	·

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Mol	Chain	Length	Quality of chain	
9	i	130	96%	.
10	j	102	• 95%	5%
11	k	129	88%	12%
12	1	137	• 99%	
13	m	121	94%	6%
14	n	61	93%	5% •
15	0	89	98%	
16	р	90	97%	
17	r Q	87	91%	. 8%
18	r	79	900/	10%
10	r c	02	8%	120/
20	+	92	88%	12%
20	U	04	96%	•
21	X	76	58% 36%	<u> </u>
22	W	21	24% 5% 71%	
23	А	2932	81%	18% •
24	В	116	87%	11% •
25	a			
	C	277	99%	
26	D	277 209	99% 99%	
26 27	D E	277 209 207	99% 99%	
26 27 28	D E F	277 209 207 179	99% 99% 99% 25% 93%	•
26 27 28 29	C D E F G	277 209 207 179 178	99% 99% 99% 25% 93%	• • 7% 10%
26 27 28 29 30	C D E F G L	277 209 207 179 178 145	99% 99% 25% 93%	• • 7% 10%
26 27 28 29 30 31	C D E F G L M	277 209 207 179 178 145 122	99% 99% 99% 25% 93% 90% 99%	• • • 7% 10%
26 27 28 29 30 31 32	C D E F G L M N	277 209 207 179 178 145 122 146	99% 99% 99% 25% 93% 90% 90%	
26 27 28 29 30 31 32 33	C D E F G L M N	277 209 207 179 178 145 122 146 144	99% 99% 99% 25% 93% 90% 90%	· · 7% 10% ·

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Mol	Chain	Length	Quality of chain	
34	Р	135	• 90%	• 10%
35	Q	119	5% 94%	6%
36	R	114	99%	
37	S	119	98%	
38	Т	102	99%	
39	U	118	94%	6%
40	V	94	98%	
41	W	103	 99%	
42	Y	96	78%	22%
43	Z	62	94%	• 5%
44	1	63	92%	• 6%
45	2	59	93%	• 5%
46	3	81	<u>48%</u> 94%	6%
47	4	57	93%	7%
48	5	49	98%	
49	6	44	98%	·
50	7	66	97%	
51	8	37	97%	·

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2 Entry composition (i)

There are 55 unique types of molecules in this entry. The entry contains 136923 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 16S Ribosomal RNA.

Mol	Chain	Residues		1	AltConf	Trace			
1	a	1516	Total 32515	C 14504	N 5960	O 10535	Р 1516	0	0

• Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
2	b	224	Total 1228	C 757	N 236	O 235	0	0

• Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	с	203	Total 1395	C 880	N 254	O 259	${S \over 2}$	0	0

• Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	199	Total 1429	C 893	N 269	O 266	S 1	0	0

• Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	е	156	Total 1087	$\begin{array}{c} \mathrm{C} \\ 685 \end{array}$	N 196	O 204	${ m S} { m 2}$	0	0

• Molecule 6 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	93	Total 652	C 419	N 117	0 114	${S \over 2}$	0	0



• Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues		At	oms			AltConf	Trace
7	g	143	Total 1015	С 634	N 191	0 186	$\frac{S}{4}$	0	0

• Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues		At	oms			AltConf	Trace
8	h	131	Total 929	C 597	N 159	0 171	${ m S} { m 2}$	0	0

• Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues		At	oms	AltConf	Trace		
9	i	125	Total 920	$\begin{array}{c} \mathrm{C} \\ 578 \end{array}$	N 183	0 158	S 1	0	0

• Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues		At	\mathbf{oms}			AltConf	Trace
10	j	97	Total 714	C 449	N 129	0 135	S 1	0	0

• Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues		At	oms			AltConf	Trace
11	k	114	Total 681	C 415	N 131	0 133	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues		At	\mathbf{oms}	AltConf	Trace		
12	1	135	Total 935	C 584	N 184	O 166	S 1	0	0

• Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues		At	oms			AltConf	Trace
13	m	114	Total 780	C 483	N 157	0 139	S 1	0	0

• Molecule 14 is a protein called Small ribosomal subunit protein uS14.



Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total 463	C 295	N 89	0 74	${ m S}{ m 5}$	0	0

• Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues		At	oms	AltConf	Trace		
15	О	87	Total 635	C 393	N 124	0 116	${S \over 2}$	0	0

• Molecule 16 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues		At	oms	AltConf	Trace		
16	р	88	Total 641	C 406	N 120	0 112	${ m S} { m 3}$	0	0

• Molecule 17 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues		Ator	ns	AltConf	Trace	
17	q	80	Total 558	C 350	N 113	O 95	0	0

• Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues		Ato	\mathbf{ms}			AltConf	Trace
18	r	64	Total 449	C 288	N 84	O 75	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues		Ate	oms	AltConf	Trace		
19	S	81	Total 502	C 314	N 100	0 87	S 1	0	0

• Molecule 20 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues		Ator	\mathbf{ns}	AltConf	Trace	
20	t	81	Total 493	C 298	N 95	O 100	0	0

 $\bullet\,$ Molecule 21 is a RNA chain called p/E Hybrid State Phenylalanine tRNA.



Mol	Chain	Residues		-	Atom	IS			AltConf	Trace
21	x	74	Total 1591	С 713	N 285	O 517	Р 74	${ m S} { m 2}$	0	0

• Molecule 22 is a RNA chain called F-Stop mRNA.

Mol	Chain	Residues		At	\mathbf{oms}	AltConf	Trace		
22	W	6	Total 126	C 57	N 22	0 41	Р 6	0	0

• Molecule 23 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues			AltConf	Trace			
23	А	2904	Total 62385	C 27841	N 11542	O 20098	Р 2904	0	0

• Molecule 24 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues		A	AltConf	Trace			
24	В	114	Total 2428	C 1082	N 428	0 804	Р 114	0	0

• Molecule 25 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues		At	AltConf	Trace			
25	С	273	Total 2059	C 1276	N 405	0 371	${ m S} 7$	0	0

• Molecule 26 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues		At	oms			AltConf	Trace
26	D	206	Total 1545	C 974	N 287	O 280	$\begin{array}{c} \mathrm{S} \\ \mathrm{4} \end{array}$	0	0

• Molecule 27 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
27	Е	205	Total 1515	C 960	N 279	O 276	0	0

• Molecule 28 is a protein called Large ribosomal subunit protein uL5.



Mol	Chain	Residues		At	oms			AltConf	Trace
28	F	167	Total 1142	С 724	N 195	O 218	${ m S}{ m 5}$	0	0

• Molecule 29 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues		At	oms	AltConf	Trace		
29	G	160	Total 1085	C 684	N 201	O 199	S 1	0	0

• Molecule 30 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues		At	oms	AltConf	Trace		
30	L	143	Total 1084	C 689	N 201	0 191	${ m S} { m 3}$	0	0

• Molecule 31 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues		At	AltConf	Trace			
31	М	122	Total 914	C 566	N 173	0 170	${ m S}{ m 5}$	0	0

• Molecule 32 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
32	Ν	145	Total 1022	C 633	N 205	0 184	0	0

• Molecule 33 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues		At	oms	AltConf	Trace		
33	Ο	134	Total 1025	C 658	N 194	0 167	S 6	0	0

• Molecule 34 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues		At	AltConf	Trace			
34	Р	122	Total 952	C 596	N 188	0 167	S 1	0	0

• Molecule 35 is a protein called Large ribosomal subunit protein uL18.



Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace	
35	Q	112	Total 701	C 431	N 139	0 131	0	0

• Molecule 36 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues		At	AltConf	Trace			
36	R	113	Total 843	С 534	N 161	0 147	S 1	0	0

• Molecule 37 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues		At	oms	AltConf	Trace		
37	S	117	Total 930	C 590	N 181	0 155	$\frac{S}{4}$	0	0

• Molecule 38 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues		At	oms			AltConf	Trace
38	Т	101	Total 762	C 492	N 131	0 138	S 1	0	0

• Molecule 39 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
39	U	111	Total 843	C 532	N 160	O 151	0	0

• Molecule 40 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues		At	oms			AltConf	Trace
40	V	92	Total 724	C 460	N 122	0 140	${ m S} { m 2}$	0	0

• Molecule 41 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues		At	AltConf	Trace			
41	W	102	Total 735	C 464	N 135	0 133	${ m S} { m 3}$	0	0

• Molecule 42 is a protein called Large ribosomal subunit protein bL27.



Mol	Chain	Residues		At	AltConf	Trace			
42	Y	75	Total 549	C 338	N 106	0 104	S 1	0	0

• Molecule 43 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms			AltConf	Trace		
43	Ζ	59	Total 439	C 271	N 90	O 76	${ m S} { m 2}$	0	0

• Molecule 44 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms			AltConf	Trace		
44	1	59	Total 467	C 286	N 92	O 88	S 1	0	0

• Molecule 45 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms			AltConf	Trace		
45	2	56	Total	С	Ν	Ο	S	0	0
40	2	50	429	269	81	78	1	0	0

• Molecule 46 is a protein called Large ribosomal subunit protein bL31B.

Mol	Chain	Residues	Atoms			AltConf	Trace	
46	3	76	Total 529	C 332	N 92	O 105	0	0

• Molecule 47 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms			AltConf	Trace		
47	4	53	Total	С	N	0	S	0	0
			425	259	87	74	\mathbf{b}		

• Molecule 48 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms			AltConf	Trace		
48	5	48	Total 380	C 233	N 75	O 68	${S \atop 4}$	0	0

• Molecule 49 is a protein called Large ribosomal subunit protein bL34.



Mol	Chain	Residues	Atoms			AltConf	Trace		
49	6	43	Total 361	C 219	N 87	O 53	${ m S} { m 2}$	0	0

• Molecule 50 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms			AltConf	Trace		
50	7	64	Total 512	C 316	N 112	O 79	${f S}{5}$	0	0

• Molecule 51 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms			AltConf	Trace		
51	8	36	Total 292	C 183	N 59	0 44	S 6	0	0

• Molecule 52 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
52	a	18	Total Mg 18 18	0
52	q	1	Total Mg 1 1	0
52	А	78	Total Mg 78 78	0
52	D	1	Total Mg 1 1	0

• Molecule 53 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
53	n	1	Total Zn 1 1	0
53	4	1	Total Zn 1 1	0
53	5	1	Total Zn 1 1	0
53	8	1	Total Zn 1 1	0

• Molecule 54 is POTASSIUM ION (three-letter code: K) (formula: K).



Mol	Chain	Residues	Atoms	AltConf
54	О	1	Total K 1 1	0

• Molecule 55 is water.

Mol	Chain	Residues	Atoms	AltConf
55	a	2	Total O 2 2	0
55	А	3	Total O 3 3	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: 16S Ribosomal RNA



• Molecule 2: Small ribosomal subunit protein uS2

Chain b:

90%

MET PR0 V3 PR0 V1111 01111 01111 01111 01123 01123 01236 0124 V128 V128 V128 V128 C124 C150 C150 C150 C150 C150 C115 C115 C115	ALA GLU VAL PRO PRO CLU CLU CLV GLU CLU CLU CLU CLU CLU CLU CLU CLU CLU
\bullet Molecule 3: Small ribosomal subunit protein uS3	
Chain c: 93%	7%
MET C2 C2 C2 C2 C1 C1 C1 C1 C1 C1 C1 C1 C1 C1	
• Molecule 4: Small ribosomal subunit protein uS4	
Chain d:	
MET A2 8159 € R200	
\bullet Molecule 5: Small ribosomal subunit protein uS5	
Chain e: 93%	7%
MET PRO GLU CLU CLU CLN ASN CLN CLN CLN CLN CLN CLN CLN CLN CLN CL	
\bullet Molecule 6: Small ribosomal subunit protein bS6	
Chain f: 96%	
MET ALA R3 B18 R79 D86 B85 CLU ALA	
\bullet Molecule 7: Small ribosomal subunit protein uS7	
Chain g: 91%	• 8%
MET P2 KF79 KF79 KF79 C881 C881 C881 C881 A884 A884 A884 A884 A884 A884 A884 A	
• Molecule 8: Small ribosomal subunit protein uS8	
Chain h: 99%	
WET V2	
• Molecule 9: Small ribosomal subunit protein uS9	



Chain i:	96%	•
MET ALA GLN VAL VAL G K129 ARG		
• Molecule 10	: Small ribosomal subunit protein uS10	
Chain j:	95%	5%
MET ALA LYS GLN K5 A34 A34 K101		
• Molecule 11	: Small ribosomal subunit protein uS11	
Chain k:	88%	12%
MET ALA ARG LYS LYS THR THR ARG LYS ARG	ARG VAL LYS LYS ASS A63 A63 A63 A63 A63	
• Molecule 12	: Small ribosomal subunit protein uS12	
Chain l:	99%	
MET P2 R33 K136 LYS		
• Molecule 13	: Small ribosomal subunit protein uS13	
Chain m:	94%	6%
MET ARG ARG 14 D68 D68 V115	All7 GLY LVS LVS LVS	
• Molecule 14	: Small ribosomal subunit protein uS14	
Chain n:	93%	5% •
MET A2 E25 K38 K38 K38 K38 K38 K38 K38 K38		
• Molecule 15	: Small ribosomal subunit protein uS15	
Chain o:	98%	· ·
MET ALA L3 L3 L87 R88 R88 R89		

WORLDWIDE PROTEIN DATA BANK • Molecule 16: Small ribosomal subunit protein bS16 Chain p: 97% • Molecule 17: Small ribosomal subunit protein uS17 Chain q: 91% • 8% MET ALA ASF ALA VAL TLE TLE • Molecule 18: Small ribosomal subunit protein bS18 Chain r: 80% 19% MET ALA GLY GLY ARG ARG GLY ARG ARG ARG ARG ARG ARG GLU GLU GLU • Molecule 19: Small ribosomal subunit protein uS19 8% Chain s: 88% 12% MET GLY ALA GLY ASF ASF ASF LYS • Molecule 20: Small ribosomal subunit protein bS20 Chain t: 96% ALA LYS • Molecule 21: p/E Hybrid State Phenylalanine tRNA 14% Chain x: 58% 36% • Molecule 22: F-Stop mRNA Chain w: 24% 5% 71% 00400

• Molecule 23: 23S Ribosomal RNA Chain A: 81% 18% :5 E A14 G15 G45 C46 <mark>A90</mark> C91 C92 U93 A49 A50 <u>U89</u> A13 G51 U74 G75 A198 A199 C200 A201 **V231** 422(1224 U552 U553 A323 U371 A372 A373 C374 G410 A411 U412 4406 0433 6434 G457 A458 G575 U576 A577 G578 A591 A592 U593 C594 C554 C555 **J**891 C931 0000000 1973 A1119 155 00000 A1344 A1345 J1346 J1346 1557 <mark>C1593</mark> G1594 G1595 A1596 A1701 1946 G2139 C2140 U2141 U2142 U2143 G2143 A2146 C2146 C2146 A2147 G2148 :2149 2150 2165 G2173 2138 •••• 32175 02176 J220 PDB TEIN DATA BANK

A2320 42329 42339 42339 42339 42341 42342 42342 42342 42343 42343 42344 42355 42355 42343 423555 42555 42555 42555 42555 42555 425555 425555 425555 425555 425555 42555555 42555555 4255555555	
C2 485 C2 485 C2 498 C2 498 A2 509 A2 509 A2 536 C2 508 A2 536 C2 538 A2 551 A2	
A2809 G2811 G2812 G2813 G2813 G2813 G2813 G2813 G2823 G2833 G2833 G2833 G2833 G2833 G2833 G2833 G2833 G2833 G2833 G2833 G2833 G2833 G2835 G2833 G2835 G2837	
• Molecule 24: 5S Ribosomal RNA	
Chain B: 87% 11% .	
U 110 1110 1110 1110 1110 1110 1110 111	
\bullet Molecule 25: Large ribosomal subunit protein uL2	
Chain C:	
AET A2 A2 A2 A4 LYS LYS LYS LYS	
• Molecule 26: Large ribosomal subunit protein uL3	
Chain D: 99% ·	
MET 12 ALA LLYS LLYS	
• Molecule 27: Large ribosomal subunit protein uL4	
Chain E: 99%	
ALA ALA	
\bullet Molecule 28: Large ribosomal subunit protein uL5	
25% Chain F: 93% 7%	
MET N2 N2 N2 N2 N2 N2 N2 N2 N2 N2 N2 N2 N2	G131
V132 R133 R133 R135 R136 R141 ASP ASP ASP ASP ASP ASP ASP ASP	
VORLDWIDE PROTEIN DATA BANK	

• Molecule 29: Large ribosomal subunit protein uL6 Chain G: 90% 10% E 5 Z • Molecule 30: Large ribosomal subunit protein uL13 Chain L: 99% GL Y • Molecule 31: Large ribosomal subunit protein uL14 Chain M: 100% • Molecule 32: Large ribosomal subunit protein uL15 Chain N: 99% • Molecule 33: Large ribosomal subunit protein uL16 Chain O: 93% 7% GLU GLU GLY GLY GLY ALA ASN GLU SER SER • Molecule 34: Large ribosomal subunit protein bL17 Chain P: • 90% 10% V76 ASP ALA LYS GLY LYS ASP GLY SER YAL SER THR VAL VAL MET GLY • Molecule 35: Large ribosomal subunit protein uL18 Chain Q: 94% 6%





• Molecule 36: Large ribosomal subunit protein bL19

Chain R:	99%	
M1 E34 G35 T36 M102 M113		
• Molecule 37:	Large ribosomal subunit protein bL20	
Chain S:	98%	•
MET P2 A118 LYS		
• Molecule 38:	Large ribosomal subunit protein bL21	
Chain T:	99%	
M1 D44 M101 ALA		
• Molecule 39:	Large ribosomal subunit protein uL22	
Chain U:	94%	6%
MET ALA SER SER GLU V5 V5 V5 CLV GLU GLU GLY		
• Molecule 40:	Large ribosomal subunit protein uL23	
Chain V:	98%	•
M1 F92 GLU VAL		
• Molecule 41:	Large ribosomal subunit protein uL24	
Chain W:	99%	
M1 150 K74 G87 D102 LVS		

• Molecule 42: Large ribosomal subunit protein bL27



Chain Y:	78%	22%	
MET MET LEU LEU LYS PHE ASP TLE GLN HIS HIS HIS LYS LYS CLY	GLY GLY CUN GLU GLU GLU ALA		
• Molecule 43: Larg	ge ribosomal subunit protein bL28		
Chain Z:	94%	• 5%	
MET A2 L54 B60 ARG VAL			
• Molecule 44: Larg	ge ribosomal subunit protein uL29		
Chain 1:	92%	• 6%	
MET LYS A3 A3 A1 E6 LEU ALA			
• Molecule 45: Larg	ge ribosomal subunit protein uL30		
Chain 2:	93%	• 5%	
MET ALA K3 K57 E58 VAL			
• Molecule 46: Larg	ge ribosomal subunit protein bL31B		
Chain 3:	48% 94%	6%	
MET LVS 123 64 64 818 719 721 721 721 721 723	L24 K29 S30 S31 S32 S31 S32 S32 S32 K23 M37 M37 S33 M37 M37 S33 M37 M37 S33 S31 S32 S31 S32 S31 S32 S31 S32 S31 S32 S31 S32 S31 S32 S31 S32 S32 S31 S32 S32 S31 S32 S32 S31 S32 S32 S31 S32 S32 S32 S32 S32 S32 S32 S32 S32 S32	D5 3 D5 3 S5 4 S5 4 Y5 8 Y5 8 G6 0 G6 0 K6 1 K6 1 K6 1 K6 3 K6 3 K6 5 K6 5	T66 A67 D68 D68 D71 D72 N72 N75 CLY
LEU			
• Molecule 47: Larg	ge ribosomal subunit protein bL32		
Chain 4:	93%	7%	
MET A2 K52 V53 V54 ALA ALA ASN SER			
• Molecule 48: Larg	ge ribosomal subunit protein bL33		
Chain 5:	98%	·	
M1 T48 LYS			



• Molecule 49: Large ribosomal subunit protein bL34

Chain 6: 98% . E SE • Molecule 50: Large ribosomal subunit protein bL35 Chain 7: 97% . E SE

 \bullet Molecule 51: Large ribosomal subunit protein bL36

Chain 8: 97% •





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	15497	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	40.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III $(4k \ge 4k)$	Depositor
Maximum map value	25.559	Depositor
Minimum map value	-12.278	Depositor
Average map value	0.001	Depositor
Map value standard deviation	1.072	Depositor
Recommended contour level	3.2	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles $(^{\circ})$	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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, PSU, 7MG, 4SU, 5MU, MIA, K

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	a	0.68	1/36403~(0.0%)	0.87	12/56778~(0.0%)	
2	b	0.26	0/1241	0.41	0/1721	
3	с	0.40	0/1418	0.56	0/1939	
4	d	0.34	0/1453	0.53	0/1976	
5	е	0.35	0/1100	0.55	0/1496	
6	f	0.33	0/663	0.51	0/904	
7	g	0.35	0/1028	0.58	1/1396~(0.1%)	
8	h	0.39	0/942	0.55	0/1284	
9	i	0.40	0/936	0.59	0/1267	
10	j	0.42	0/726	0.56	0/988	
11	k	0.28	0/691	0.49	0/955	
12	1	0.37	0/949	0.57	0/1290	
13	m	0.36	0/786	0.57	0/1064	
14	n	0.53	0/472	0.60	0/631	
15	0	0.32	0/643	0.55	0/872	
16	р	0.37	0/654	0.54	0/888	
17	q	0.32	0/565	0.58	0/768	
18	r	0.37	0/454	0.55	0/613	
19	s	0.36	0/514	0.51	0/707	
20	t	0.26	0/495	0.43	0/682	
21	Х	0.39	0/1605	0.87	1/2497~(0.0%)	
22	W	0.41	0/140	0.80	0/215	
23	А	0.66	0/69894	0.84	9/109035~(0.0%)	
24	В	0.42	0/2711	0.79	0/4224	
25	С	0.38	0/2095	0.58	0/2821	
26	D	0.41	0/1567	0.56	0/2111	
27	Ε	0.37	0/1536	0.56	0/2082	
28	F	0.30	0/1156	0.54	0/1579	
29	G	0.31	0/1102	0.55	0/1508	
30	L	0.37	0/1107	0.52	0/1495	
31	М	0.37	0/921	0.57	0/1236	
32	N	0.34	0/1032	0.55	0/1381	



Mal	Mol Chain		ond lengths	E	Bond angles
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
33	0	0.37	0/1047	0.56	0/1406
34	Р	0.37	0/963	0.63	1/1294~(0.1%)
35	Q	0.28	0/709	0.51	0/966
36	R	0.37	0/855	0.56	0/1158
37	S	0.41	0/943	0.56	0/1258
38	Т	0.42	0/775	0.52	0/1045
39	U	0.37	0/853	0.55	0/1156
40	V	0.40	0/733	0.54	0/988
41	W	0.33	0/745	0.51	0/1005
42	Y	0.37	0/556	0.58	0/744
43	Ζ	0.34	0/444	0.62	1/593~(0.2%)
44	1	0.31	0/468	0.57	0/628
45	2	0.34	0/432	0.60	0/581
46	3	0.28	0/542	0.48	0/743
47	4	0.41	0/433	0.58	0/577
48	5	0.33	0/384	0.58	0/518
49	6	0.39	0/364	0.66	0/475
50	7	0.35	0/519	0.63	0/677
51	8	0.36	0/295	0.61	0/387
All	All	0.60	1/149059~(0.0%)	0.79	25/224602~(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
14	n	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	a	95	А	C1'-N9	-5.05	1.39	1.46

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
7	g	12	VAL	C-N-CA	-6.66	105.06	121.70
1	a	970	U	C2-N3-C4	-6.35	123.19	127.00
1	а	544	С	C2-N1-C1'	6.12	125.53	118.80
23	А	1358	С	C2-N1-C1'	5.97	125.37	118.80
23	А	231	А	O4'-C1'-N9	5.93	112.94	108.20



There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Group
14	n	42	ILE	Peptide

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
2	b	222/249~(89%)	202 (91%)	19 (9%)	1 (0%)	29	61
3	с	201/218~(92%)	179 (89%)	22 (11%)	0	100	100
4	d	197/200~(98%)	178 (90%)	19 (10%)	0	100	100
5	е	154/167~(92%)	138 (90%)	16 (10%)	0	100	100
6	f	91/97~(94%)	84 (92%)	7 (8%)	0	100	100
7	g	141/156~(90%)	136 (96%)	5 (4%)	0	100	100
8	h	129/132~(98%)	122 (95%)	7 (5%)	0	100	100
9	i	123/130~(95%)	114 (93%)	9 (7%)	0	100	100
10	j	95/102~(93%)	88 (93%)	7 (7%)	0	100	100
11	k	112/129~(87%)	106 (95%)	6 (5%)	0	100	100
12	1	133/137~(97%)	119 (90%)	14 (10%)	0	100	100
13	m	112/121~(93%)	103 (92%)	9 (8%)	0	100	100
14	n	58/61~(95%)	53 (91%)	5 (9%)	0	100	100
15	0	85/89~(96%)	83 (98%)	2 (2%)	0	100	100
16	р	86/90~(96%)	81 (94%)	5 (6%)	0	100	100
17	q	78/87~(90%)	71 (91%)	7 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
18	r	62/79~(78%)	56~(90%)	5 (8%)	1 (2%)	9	36
19	S	79/92~(86%)	69~(87%)	10 (13%)	0	100	100
20	t	79/84~(94%)	76~(96%)	3 (4%)	0	100	100
25	С	271/277~(98%)	257 (95%)	14 (5%)	0	100	100
26	D	204/209~(98%)	193 (95%)	11 (5%)	0	100	100
27	Е	203/207~(98%)	193 (95%)	10 (5%)	0	100	100
28	F	163/179~(91%)	151 (93%)	12 (7%)	0	100	100
29	G	158/178~(89%)	149 (94%)	9 (6%)	0	100	100
30	L	141/145~(97%)	135 (96%)	6 (4%)	0	100	100
31	М	120/122~(98%)	113 (94%)	7 (6%)	0	100	100
32	N	143/146~(98%)	131 (92%)	12 (8%)	0	100	100
33	Ο	132/144~(92%)	127 (96%)	5 (4%)	0	100	100
34	Р	118/135~(87%)	108 (92%)	10 (8%)	0	100	100
35	Q	110/119~(92%)	104 (94%)	6 (6%)	0	100	100
36	R	111/114 (97%)	106 (96%)	5 (4%)	0	100	100
37	S	115/119~(97%)	111 (96%)	4 (4%)	0	100	100
38	Т	99/102~(97%)	94 (95%)	5 (5%)	0	100	100
39	U	109/118 (92%)	106 (97%)	3 (3%)	0	100	100
40	V	90/94~(96%)	83 (92%)	7 (8%)	0	100	100
41	W	100/103~(97%)	90 (90%)	10 (10%)	0	100	100
42	Y	73/96~(76%)	65~(89%)	8 (11%)	0	100	100
43	Z	57/62~(92%)	49 (86%)	8 (14%)	0	100	100
44	1	57/63~(90%)	54 (95%)	2 (4%)	1 (2%)	8	35
45	2	54/59~(92%)	52 (96%)	2 (4%)	0	100	100
46	3	74/81~(91%)	58 (78%)	16 (22%)	0	100	100
47	4	51/57~(90%)	46 (90%)	5 (10%)	0	100	100
48	5	46/49~(94%)	41 (89%)	5 (11%)	0	100	100
49	6	41/44~(93%)	40 (98%)	1 (2%)	0	100	100
50	7	62/66~(94%)	56 (90%)	6 (10%)	0	100	100
51	8	34/37~(92%)	32 (94%)	2 (6%)	0	100	100
All	All	5173/5545~(93%)	4802 (93%)	368 (7%)	3 (0%)	54	81



All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	b	128	VAL
18	r	14	VAL
44	1	11	THR

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
2	b	31/214~(14%)	31 (100%)	0	100	100
3	с	112/177~(63%)	111 (99%)	1 (1%)	78	87
4	d	124/170~(73%)	124 (100%)	0	100	100
5	е	108/131~(82%)	108 (100%)	0	100	100
6	f	49/85~(58%)	49 (100%)	0	100	100
7	g	90/130~(69%)	90 (100%)	0	100	100
8	h	86/110~(78%)	86 (100%)	0	100	100
9	i	85/102~(83%)	85 (100%)	0	100	100
10	j	71/93~(76%)	71 (100%)	0	100	100
11	k	44/100~(44%)	44 (100%)	0	100	100
12	1	83/118~(70%)	83 (100%)	0	100	100
13	m	64/102~(63%)	64 (100%)	0	100	100
14	n	46/52~(88%)	44 (96%)	2~(4%)	29	59
15	О	54/81~(67%)	54 (100%)	0	100	100
16	р	60/80~(75%)	59~(98%)	1 (2%)	60	78
17	q	45/78~(58%)	44 (98%)	1 (2%)	52	74
18	r	39/67~(58%)	39 (100%)	0	100	100
19	S	$2\overline{4}/78~(31\%)$	24 (100%)	0	100	100
20	t	31/66~(47%)	31 (100%)	0	100	100
25	С	209/225~(93%)	209 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
26	D	159/171~(93%)	159 (100%)	0	100 100
27	Ε	156/174~(90%)	156 (100%)	0	100 100
28	F	100/155~(64%)	100 (100%)	0	100 100
29	G	90/147~(61%)	90 (100%)	0	100 100
30	L	109/121 (90%)	109 (100%)	0	100 100
31	М	98/101~(97%)	98 (100%)	0	100 100
32	Ν	93/115~(81%)	93 (100%)	0	100 100
33	Ο	98/113~(87%)	98 (100%)	0	100 100
34	Р	94/111~(85%)	94 (100%)	0	100 100
35	Q	40/97~(41%)	40 (100%)	0	100 100
36	R	83/99~(84%)	83 (100%)	0	100 100
37	S	92/97~(95%)	92 (100%)	0	100 100
38	Т	76/82~(93%)	76 (100%)	0	100 100
39	U	89/97~(92%)	89 (100%)	0	100 100
40	V	76/84~(90%)	76 (100%)	0	100 100
41	W	76/88~(86%)	76 (100%)	0	100 100
42	Y	54/76~(71%)	54 (100%)	0	100 100
43	Ζ	44/53~(83%)	44 (100%)	0	100 100
44	1	47/55~(86%)	47 (100%)	0	100 100
45	2	49/52~(94%)	48 (98%)	1 (2%)	55 76
46	3	45/73~(62%)	45 (100%)	0	100 100
47	4	47/50~(94%)	47 (100%)	0	100 100
48	5	41/48~(85%)	41 (100%)	0	100 100
49	6	$\overline{38/39}\ (97\%)$	38 (100%)	0	100 100
50	7	52/56~(93%)	52 (100%)	0	100 100
51	8	35/35~(100%)	35 (100%)	0	100 100
All	All	3436/4648~(74%)	3430 (100%)	6 (0%)	93 97

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	р	71	ARG
17	q	39	ARG
	<i>a</i>	7	

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Mol	Chain	Res	Type
45	2	57	LYS
14	n	25	GLU
3	с	39	ARG

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such side chains are listed below:

Mol	Chain	Res	Type
36	R	102	ASN
47	4	23	GLN
37	S	52	GLN
41	W	67	ASN
17	q	74	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1512/1550~(97%)	261~(17%)	0
21	Х	71/76~(93%)	25~(35%)	0
22	W	5/21~(23%)	1 (20%)	0
23	А	2900/2932~(98%)	507~(17%)	31 (1%)
24	В	113/116~(97%)	13~(11%)	0
All	All	4601/4695~(97%)	807 (17%)	31~(0%)

5 of 807 RNA backbone outliers are listed below:

Mol	Chain	\mathbf{Res}	Type
1	a	8	А
1	a	9	G
1	a	31	G
1	a	32	А
1	a	39	G

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	А	979	U
23	А	2472	А
23	А	1248	А
23	А	2809	А
23	А	1595	G



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

7 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mal	Turne	Chain	Dog	Tink	Bo	ond leng	$_{\rm sths}$	B	ond ang	gles
INIOI	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
21	PSU	х	55	21	18,21,22	1.34	2 (11%)	22,30,33	1.88	4 (18%)
21	4SU	х	8	21	18,21,22	1.80	4 (22%)	26,30,33	2.34	5 (19%)
21	PSU	х	32	21	$18,\!21,\!22$	1.36	3 (16%)	22,30,33	1.87	4 (18%)
21	PSU	х	39	21	$18,\!21,\!22$	1.32	2 (11%)	22,30,33	1.97	4 (18%)
21	5MU	х	54	21	$19,\!22,\!23$	1.32	4 (21%)	28,32,35	2.30	10 (35%)
21	MIA	x	37	21	24,31,32	2.20	3 (12%)	26,44,47	2.52	9 (34%)
21	7MG	х	46	21	22,26,27	1.30	3 (13%)	29,39,42	2.63	8 (27%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	PSU	х	55	21	-	2/7/25/26	0/2/2/2
21	4SU	х	8	21	-	2/7/25/26	0/2/2/2
21	PSU	Х	32	21	-	0/7/25/26	0/2/2/2
21	PSU	Х	39	21	-	1/7/25/26	0/2/2/2
21	5MU	Х	54	21	-	0/7/25/26	0/2/2/2
21	MIA	х	37	21	-	3/11/33/34	0/3/3/3
21	7MG	х	46	21	-	4/7/37/38	0/3/3/3

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	Х	37	MIA	C13-C14	7.08	1.52	1.32
21	Х	37	MIA	C2-S10	-6.91	1.69	1.75
21	Х	8	4SU	C4-S4	-4.77	1.59	1.68
21	Х	8	4SU	C4-N3	-3.29	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	Х	55	PSU	C6-C5	3.20	1.39	1.35

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms		$Observed(^{o})$	$Ideal(^{o})$
21	Х	46	7MG	N9-C4-N3	9.32	139.41	125.47
21	Х	37	MIA	C12-C13-C14	-7.79	111.98	127.14
21	Х	8	4SU	C4-N3-C2	-7.11	120.43	127.34
21	Х	8	4SU	C5-C4-N3	6.42	120.64	114.69
21	Х	39	PSU	N1-C2-N3	6.03	121.96	115.13

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
21	Х	37	MIA	C12-C13-C14-C15
21	Х	8	4SU	O4'-C4'-C5'-O5'
21	Х	46	7MG	O4'-C1'-N9-C8
21	Х	46	7MG	O4'-C1'-N9-C4
21	Х	8	4SU	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 103 ligands modelled in this entry, 103 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-42561. 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.

Orthogonal projections (i) 6.1

6.1.1Primary map



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

6.2Central slices (i)

6.2.1Primary map



X Index: 256

Y Index: 256

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: 254

Y Index: 234

Z Index: 296

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 3.2. 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 1168 nm^3 ; this corresponds to an approximate mass of 1055 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 0.303 ${\rm \AA^{-1}}$



8 Fourier-Shell correlation (i)

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



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-42561 and PDB model 8UU6. 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 3.2 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 (3.2).



9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.



9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (3.2) and Q-score for the entire model and for each chain.

\mathbf{Chain}	Atom inclusion	$\mathbf{Q} extsf{-score}$
All	0.9030	0.4890
1	0.8740	0.4880
2	0.8650	0.5280
3	0.4180	0.3130
4	0.8540	0.5110
5	0.8500	0.5350
6	0.8990	0.5620
7	0.9190	0.5670
8	0.8220	0.5480
А	0.9230	0.4900
В	0.9350	0.4280
С	0.8570	0.5560
D	0.8820	0.5520
Е	0.8670	0.5280
F	0.5630	0.3370
G	0.8240	0.4470
L	0.9150	0.5550
М	0.7640	0.5390
Ν	0.8800	0.5330
0	0.8500	0.5280
Р	0.8810	0.5350
Q	0.8440	0.4580
R	0.8500	0.5430
S	0.9050	0.5490
Т	0.9020	0.5490
U	0.8780	0.5470
V	0.8390	0.5230
W	0.8370	0.5090
Y	0.8930	0.5530
Z	0.8880	0.5500
a	0.9330	0.4730
b	0.8320	0.4720
с	0.8820	0.5100
d	0.8990	0.4840
е	0.8560	0.5140

0.0 <0.0

1.0

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Chain	Atom inclusion	Q-score
f	0.8610	0.4800
g	0.8880	0.4840
h	0.9190	0.5170
i	0.9560	0.5090
j	0.9230	0.4930
k	0.8670	0.4890
1	0.8810	0.5290
m	0.8900	0.4940
n	0.9580	0.5400
0	0.8230	0.5070
р	0.9200	0.5090
q	0.9150	0.5070
r	0.9180	0.5100
S	0.7900	0.5220
t	0.9080	0.4810
W	0.8250	0.4920
X	0.6190	0.3410

