

wwPDB EM Validation Summary Report (i)

Apr 16, 2024 - 06:46 am BST

PDB ID	:	7PWO
EMDB ID	:	EMD-13683
Title	:	Cryo-EM structure of Giardia lamblia ribosome at 2.75 A resolution
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Deposited on	:	2021-10-07
Resolution	:	2.75 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:

EMDB validation analysis	:	0.0.1. dev 92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	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 2.75 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 >=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 <=5%

Mol	Chain	Length	Quality of chain	
1	T1	139	76% •	22%
2	N1	154	98%	
3	J1	189	87%	• 12%
4	D1	217	83%	16%
5	X1	143	99%	
6	S1	154	84%	• 14%
7	Q1	158	79%	21%
8	C1	242	88%	12%
9	B1	248	87%	• 12%



Mol	Chain	Length	Quality of chain	
10	b1	124	63% · 36%	,)
11	a1	109	89%	11%
12	V1	89	92%	8%
13	R1	137	72%	28%
14	K1	134	62% 38%	
15	I1	174	94%	6%
16	e1	69	54% 46%	
17	H1	190	85%	• 15%
18	n1	41	59% 41%	
19	c1	64	84%	• 14%
20	01	145	87%	13%
21	W1	130	99%	
22	E1	268	96%	
23	 L1	199	80%	. 9%
24	II1	126	50%	
21	1	2707	600/ 200/	100/
20	2	120	09% 20%	• 10%
20	42	120	80%	17% ••
21	42	159	/1% 2	/% ••
20	A2 D9	201	100%	
29	D2	379	100%	
30	02	310	99%	
31	D2	297	89%	10%
32	F2	235	91%	9%
33	G2	225	80%	19%
34	H2	185	99%	••



Mol	Chain	Length	Quality of chain	
35	I2	210	95%	5%
36	J2	173	94%	• 5%
37	L2	234	81%	19%
38	M2	131	97%	••
39	N2	204	100%	
40	02	197	00%	
40	D2	164	35%	
41	12	104	94%	6%
42	Q2	179	99%	•
43	R2	196	88%	• 10%
44	S2	173	99%	•
45	Τ2	159	96%	• •
46	U2	171	58% 42%	
47	V2	142	97%	••
48	X2	141	82%	18%
49	Y2	135	99%	
50	Z2	135	96%	
51	a2	149	99%	
52	h2	62	00%	10%
52	62	100	5076	10 %
- JJ - E 4	10	103	92%	8%
54	d2	100	89%	11%
55	e2	136	93%	7%
56	f2	123	99%	·
57	g2	120	82%	18%
58	h2	124	97%	•
59	i2	90	94%	6%



Mol	Chain	Length	Quality of chain						
60	j2	89	98%	·					
61	k2	77	86%	14%					
62	12	51	96%	• •					
63	m2	127	39% • 6	0%					
64	o2	106	89%	11%					
65	p2	94	94%	· ·					
66	w2	14	29% 57%	14%					
67	W2	102	64%	36%					
68	Е	3	33% 67%						
69	d1	137	34% • 65%						
70	F1	190	78%	6% 15%					
71	Y1	132	67%	31%					
72	G1	248	73%	. 24%					
73	2	1452	64%	25% . 7%					
74	A1	245	79%	21%					



2 Entry composition (i)

There are 76 unique types of molecules in this entry. The entry contains 163704 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called Ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	T1	108	Total 795	$\begin{array}{c} \mathrm{C} \\ 503 \end{array}$	N 148	0 142	${ m S} { m 2}$	0	0

• Molecule 2 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace	
2	N1	152	Total	С	Ν	0	\mathbf{S}	Ο	0
	111	102	1192	759	227	201	5		0

• Molecule 3 is a protein called Ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J1	166	Total 1322	C 827	N 257	0 232	S 6	0	0

• Molecule 4 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D1	182	Total 1402	C 890	N 254	0 244	S 14	0	0

• Molecule 5 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms				AltConf	Trace	
5	X1	149	Total	С	Ν	Ο	\mathbf{S}	0	0
5	111	1-12	1104	697	219	184	4	0	0

• Molecule 6 is a protein called Ribosomal protein S18.

Mol	Chain	Residues		At	\mathbf{oms}		AltConf	Trace	
6	S1	133	Total 1055	C 651	N 210	0 188	S 6	0	0



• Molecule 7 is a protein called Ribosomal protein S16.

Mol	Chain	Residues		At	oms			AltConf	Trace
7	Q1	125	Total 960	C 603	N 190	0 164	${ m S} { m 3}$	0	0

• Molecule 8 is a protein called Ribosomal protein S2.

Mol	Chain	Residues		Ate	oms			AltConf	Trace
8	C1	212	Total 1641	C 1043	N 298	O 296	$\frac{S}{4}$	0	0

• Molecule 9 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues		At		AltConf	Trace		
9	B1	218	Total 1758	C 1113	N 323	O 309	S 13	0	0

• Molecule 10 is a protein called Ribosomal protein S27.

Mol	Chain	Residues		At	oms		AltConf	Trace	
10	b1	79	Total 614	C 389	N 105	0 114	S 6	0	0

• Molecule 11 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues		At	oms			AltConf	Trace
11	al	97	Total 785	C 484	N 162	0 131	S 8	0	0

• Molecule 12 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues		At	\mathbf{oms}		AltConf	Trace	
12	V1	82	Total 605	C 377	N 112	O 110	S 6	0	0

• Molecule 13 is a protein called Ribosomal protein S17.

Mol	Chain	Residues		At	oms			AltConf	Trace
13	R1	99	Total 767	C 476	N 141	0 147	${ m S} { m 3}$	0	0

• Molecule 14 is a protein called Ribosomal protein S10B.



Mol	Chain	Residues		At	oms			AltConf	Trace
14	K1	83	Total 689	C 446	N 116	O 123	$\frac{S}{4}$	0	0

• Molecule 15 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues		At	oms		AltConf	Trace	
15	I1	163	Total 1282	C 804	N 246	O 229	${ m S} { m 3}$	0	0

• Molecule 16 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace		
16	e1	37	Total 291	C 185	N 59	O 46	S 1	0	0

• Molecule 17 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues		At	oms			AltConf	Trace
17	H1	162	Total 1195	C 773	N 210	O 207	${ m S}{ m 5}$	0	0

• Molecule 18 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
18	n1	24	Total 217	C 134	N 55	O 25	${ m S} { m 3}$	0	0

• Molecule 19 is a protein called Ribosomal protein S28.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
10	<u>e1</u>	55	Total	С	N	0	S	0	0
19	CI	- 55	439	269	89	80	1	0	0

• Molecule 20 is a protein called Ribosomal protein S14.

Mol	Chain	Residues		At	oms	AltConf	Trace		
20	01	126	Total 935	C 572	N 189	0 170	$\frac{S}{4}$	0	0

• Molecule 21 is a protein called Ribosomal protein S15A.



Mol	Chain	Residues		At	oms			AltConf	Trace
21	W1	129	Total 1031	$\begin{array}{c} \mathrm{C} \\ 659 \end{array}$	N 192	O 177	${ m S} { m 3}$	0	0

• Molecule 22 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues		At	AltConf	Trace			
22	E1	258	Total 2062	C 1320	N 378	O 352	S 12	0	0

• Molecule 23 is a protein called SSU ribosomal protein S17P.

Mol	Chain	Residues		At	oms	AltConf	Trace		
23	L1	181	Total 1487	C 936	N 296	0 248	${f S}{7}$	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L1	12	SER	GLY	conflict	UNP V6TVJ7

• Molecule 24 is a protein called Ribosomal protein S20.

Mol	Chain	Residues		At	oms	AltConf	Trace		
24	U1	74	Total 609	C 394	N 111	O 102	${ m S} { m 2}$	0	0

• Molecule 25 is a RNA chain called rRNA 28S.

Mol	Chain	Residues		1	Atoms			AltConf	Trace
25	1	2448	Total 52571	C 23373	N 9743	O 17007	Р 2448	0	0

• Molecule 26 is a RNA chain called rRNA 5S.

Mol	Chain	Residues		\mathbf{A}^{\dagger}	AltConf	Trace			
26	3	117	Total 2501	C 1116	N 458	0 810	Р 117	0	0

• Molecule 27 is a RNA chain called rRNA 5.8S.



Mol	Chain	Residues		\mathbf{A}	Atoms						
27	42	138	Total 2958	C 1315	N 553	O 952	Р 138	0	0		

• Molecule 28 is a protein called Ribosomal protein L2.

Mol	Chain	Residues		At	oms			AltConf	Trace
28	A2	250	Total 1873	C 1157	N 383	O 320	S 13	0	0

• Molecule 29 is a protein called Ribosomal protein L3.

Mol	Chain	Residues		At	AltConf	Trace			
29	B2	378	Total 2987	C 1886	N 566	0 514	S 21	0	0

• Molecule 30 is a protein called Ribosomal protein L4.

Mol	Chain	Residues		At	oms			AltConf	Trace
30	C2	314	Total 2446	C 1539	N 474	0 424	S 9	0	0

• Molecule 31 is a protein called Ribosomal protein L5.

Mol	Chain	Residues		At	AltConf	Trace			
31	D2	266	Total 2115	C 1341	N 391	O 375	S 8	0	0

• Molecule 32 is a protein called Ribosomal protein L7.

Mol	Chain	Residues		At	oms			AltConf	Trace
32	F2	214	Total 1730	C 1100	N 315	O 310	${f S}{5}$	0	0

• Molecule 33 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues		At	oms			AltConf	Trace
33	G2	182	Total 1446	C 921	N 264	O 255	S 6	0	0

• Molecule 34 is a protein called Ribosomal protein L6.



Mol	Chain	Residues		\mathbf{A}^{\dagger}	toms			AltConf	Trace
34	H2	184	Total 1442	C 912	N 263	O 257	S 10	0	0

• Molecule 35 is a protein called Ribosomal protein L10.

Mol	Chain	Residues		Ate	AltConf	Trace			
35	I2	200	Total 1621	C 1019	N 321	0 273	S 8	0	0

• Molecule 36 is a protein called Ribosomal protein L11.

Mol	Chain	Residues		At	oms	AltConf	Trace		
36	J2	164	Total 1305	C 821	N 246	0 233	${ m S}{ m 5}$	0	0

• Molecule 37 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues		At	oms			AltConf	Trace
37	L2	189	Total 1512	C 942	N 309	O 255	S 6	0	0

• Molecule 38 is a protein called Ribosomal protein L14.

Mol	Chain	Residues		At	oms			AltConf	Trace
38	M2	128	Total 990	C 626	N 178	0 181	${S \atop 5}$	0	0

• Molecule 39 is a protein called Ribosomal protein L15.

Mol	Chain	Residues		At	oms			AltConf	Trace
39	N2	204	Total 1712	C 1083	N 358	O 265	S 6	0	0

• Molecule 40 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues		\mathbf{A}^{\dagger}	toms			AltConf	Trace
40	O2	195	Total 1587	C 997	N 310	0 267	S 13	0	0

• Molecule 41 is a protein called Ribosomal protein L17.



Mol	Chain	Residues		At	oms			AltConf	Trace
41	P2	154	Total 1235	C 781	N 239	0 211	$\frac{S}{4}$	0	0

• Molecule 42 is a protein called Ribosomal protein L18.

Mol	Chain	Residues		At	oms	AltConf	Trace		
42	Q2	178	Total 1402	C 871	N 279	0 243	S 9	0	0

• Molecule 43 is a protein called Ribosomal protein L19.

Mol	Chain	Residues		At	oms	AltConf	Trace		
43	R2	177	Total 1463	C 902	N 313	0 243	${f S}{5}$	0	0

• Molecule 44 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues		At	oms			AltConf	Trace
44	S2	173	Total 1418	C 895	N 274	0 240	S 9	0	0

• Molecule 45 is a protein called Ribosomal protein L21.

Mol	Chain	Residues		At	oms	AltConf	Trace		
45	Τ2	153	Total 1226	C 766	N 252	0 201	S 7	0	0

• Molecule 46 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues		At	oms			AltConf	Trace
46	U2	100	Total 820	C 524	N 141	0 153	${ m S} { m 2}$	0	0

• Molecule 47 is a protein called Ribosomal protein L23.

Mol	Chain	Residues		At	oms	AltConf	Trace		
47	V2	139	Total 1063	C 668	N 207	0 183	${S \atop 5}$	0	0

• Molecule 48 is a protein called Ribosomal protein L23A.



Mol	Chain	Residues		At	oms			AltConf	Trace
48	X2	116	Total 936	C 601	N 169	O 163	${ m S} { m 3}$	0	0

• Molecule 49 is a protein called Ribosomal protein L26.

Mol	Chain	Residues		At	oms	AltConf	Trace		
49	Y2	133	Total 1076	C 665	N 219	0 184	S 8	0	0

• Molecule 50 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues		At	oms			AltConf	Trace
50	Z2	129	Total 980	C 623	N 179	0 173	${ m S}{ m 5}$	0	0

• Molecule 51 is a protein called Ribosomal protein L27a.

Mol	Chain	Residues		At	oms	AltConf	Trace		
51	a2	148	Total 1201	C 759	N 240	O 199	${ m S} { m 3}$	0	0

• Molecule 52 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues		Ate	oms			AltConf	Trace
52	b2	56	Total 463	C 280	N 104	0 77	${S \over 2}$	0	0

• Molecule 53 is a protein called Ribosomal protein L30.

Mol	Chain	Residues		At	AltConf	Trace			
53	c2	100	Total 750	C 470	N 132	0 144	$\frac{S}{4}$	0	0

• Molecule 54 is a protein called Ribosomal protein L31B.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
54	d2	94	Total 752	C 482	N 149	O 121	0	0

• Molecule 55 is a protein called Ribosomal protein L32.



Mol	Chain	Residues		At	oms	AltConf	Trace		
55	e2	126	Total 1039	C 661	N 207	0 165	S 6	0	0

• Molecule 56 is a protein called Ribosomal protein L35a.

Mol	Chain	Residues		At	oms	AltConf	Trace		
56	f2	123	Total 974	C 619	N 180	0 171	$\frac{S}{4}$	0	0

• Molecule 57 is a protein called Ribosomal protein L34.

Mol	Chain	Residues		At	oms	AltConf	Trace		
57	g2	99	Total 798	C 493	N 167	0 134	$\frac{S}{4}$	0	0

• Molecule 58 is a protein called Ribosomal protein L35.

Mol	Chain	Residues		At	oms			AltConf	Trace
58	h2	120	Total 960	C 610	N 185	O 160	${ m S}{ m 5}$	0	0

• Molecule 59 is a protein called Ribosomal protein L36-1.

Mol	Chain	Residues		At	oms	AltConf	Trace		
59	i2	85	Total 691	C 438	N 138	0 111	$\frac{S}{4}$	0	0

• Molecule 60 is a protein called Ribosomal protein L37.

Mol	Chain	Residues		At	AltConf	Trace			
60	j2	87	Total 692	C 423	N 146	0 116	${f S}{7}$	0	0

• Molecule 61 is a protein called Ribosomal L38e.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
61	k2	66	Total 504	C 320	N 86	0 94	$\begin{array}{c} \mathrm{S} \\ 4 \end{array}$	0	0

• Molecule 62 is a protein called Ribosomal protein L39.



Mol	Chain	Residues		Aton	ns	AltConf	Trace	
62	12	50	Total 434	C 278	N 91	O 65	0	0

• Molecule 63 is a protein called Ubiquitin/Ribosomal protein L40e.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
63	m2	51	Total 421	C 257	N 88	O 69	${f S}{7}$	0	0

• Molecule 64 is a protein called Ribosomal protein L44.

Mol	Chain	Residues		At	oms	AltConf	Trace		
64	02	94	Total 762	С 474	N 157	O 126	${f S}{5}$	0	0

• Molecule 65 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms				AltConf	Trace	
65	p2	91	Total 708	C 436	N 144	0 122	${ m S}{ m 6}$	0	0

• Molecule 66 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms			AltConf	Trace		
66	w2	14	Total 299	C 133	N 56	O 96	Р 14	0	0

• Molecule 67 is a protein called Ribosomal protein L24A.

Mol	Chain	Residues	Atoms			AltConf	Trace		
67	W2	65	Total 540	C 343	N 110	O 85	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 68 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms			AltConf	Trace		
68	Е	3	Total 62	C 28	N 11	O 20	Р 3	0	0

• Molecule 69 is a protein called Ribosomal protein S29A.



Mol	Chain	Residues	Atoms			AltConf	Trace		
69	d1	48	Total 392	C 250	N 72	O 65	${ m S}{ m 5}$	0	0

• Molecule 70 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms			AltConf	Trace		
70	F1	161	Total 1246	С 771	N 240	0 227	S 8	0	0

• Molecule 71 is a protein called Ribosomal protein S24.

Mol	Chain	Residues	Atoms			AltConf	Trace		
71	Y1	91	Total 713	С 454	N 126	0 127	S 6	0	0

• Molecule 72 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace	
72	G1	189	Total 1453	C 914	N 280	0 249	S 10	0	0

• Molecule 73 is a RNA chain called rRNA 18S.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	2	1355	Total 29096	C 12946	N 5388	O 9407	Р 1355	0	0

• Molecule 74 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms			AltConf	Trace		
74	A1	194	Total	С	Ν	0	S	0	0
		101	1546	998	269	271	8	Ŭ	Ŭ

• Molecule 75 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
75	N1	3	Total K 3 3	0
75	X1	1	Total K 1 1	0
75	S1	2	Total K 2 2	0



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Mol	Chain	Residues	Atoms	AltConf
75	b1	2	Total K 2 2	0
75	a1	1	Total K 1 1	0
75	I1	2	Total K 2 2	0
75	01	5	Total K 5 5	0
75	W1	1	Total K 1 1	0
75	E1	4	Total K 4 4	0
75	L1	4	Total K 4 4	0
75	U1	1	Total K 1 1	0
75	1	181	Total K 181 181	0
75	3	1	Total K 1 1	0
75	42	2	Total K 2 2	0
75	A2	4	Total K 4 4	0
75	B2	3	Total K 3 3	0
75	C2	4	Total K 4 4	0
75	I2	1	Total K 1 1	0
75	L2	1	Total K 1 1	0
75	N2	2	Total K 2 2	0
75	V2	1	Total K 1 1	0
75	a2	2	Total K 2 2	0
75	e2	1	Total K 1 1	0
75	j2	1	Total K 1 1	0



Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf
75	o2	1	Total K 1 1	0
75	G1	1	Total K 1 1	0
75	2	222	Total K 222 222	0
75	A1	1	Total K 1 1	0

• Molecule 76 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
76	N1	1	Total Mg 1 1	0
76	E1	1	Total Mg 1 1	0
76	L1	1	Total Mg 1 1	0
76	1	71	TotalMg7171	0
76	42	1	Total Mg 1 1	0
76	C2	1	Total Mg 1 1	0
76	F2	1	Total Mg 1 1	0
76	P2	1	Total Mg 1 1	0
76	V2	1	Total Mg 1 1	0
76	b2	1	Total Mg 1 1	0
76	o2	1	Total Mg 1 1	0
76	G1	1	Total Mg 1 1	0
76	2	19	Total Mg 19 19	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. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.



 \bullet Molecule 1: Ribosomal protein S19e



MET THR THR VAL VAL VAL VAL VAL VAL VAL VAL VAL VAL	
• Molecule 7: Ribosomal protein S16	
Chain Q1: 79%	21%
MET ALA ALA ALA ASN ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	
• Molecule 8: Ribosomal protein S2	
Chain C1: 88%	12%
MET ALLA GLN GLN ALLA ALLA PRO PRO GLU GLU GLU GLU GLU GLU GLU GLU ALA ALA ALA ALA ALA ALA	
\bullet Molecule 9: 40S ribosomal protein S3a	
Chain B1: 87%	12%
MET ALA GLY GLY GLY GLY CLYS LLYS LLYS LLYS CLN M18 GLN M18 GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN	
• Molecule 10: Ribosomal protein S27	
Chain b1: 63% · 36%	
MET THR THR PRO PRO PRO PRO PRO PRO PRO PRO PRO PR	
\bullet Molecule 11: 40S ribosomal protein S26	
Chain a1: 89%	11%
HI PRO PRO ARIC ARIC ASR ASR GLN CLYS CLYS	
• Molecule 12: 40S ribosomal protein S21	
Chain V1: 92%	8%
MET SER ASP ASP ASP ISP LEU	
• Molecule 13: Ribosomal protein S17	
Chain R1: 72% · 28	%



MET 02 02 036 036 036 036 036 038 038 04 14 14 14 14 14 14 14 14 14 14 14 14 14	
• Molecule 14: Ribosomal protein S10B	
Chain K1: 62% 38%	
M1 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2	LYS
\bullet Molecule 15: 40S ribosomal protein S8	
Chain I1: 94% 6%	
MET C2 VAL VAL LYS LYS CLYS GLY GLY GLY GLY	
\bullet Molecule 16: 40S ribosomal protein S30	
Chain e1: 54% 46%	
MET ALA ALA ALA ALA ALA ALA ALA ALA CLY CLY CLY CLY CLY CLY CLY CLY CLY CLY	
\bullet Molecule 17: 40S ribosomal protein S7	
Chain H1: 85% · 15%	-
MET THR THR PRIC ALA ALA ALA ALA CLU CVS LVS LVS LVS LVS CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	
\bullet Molecule 18: Ribosomal protein eL41	
Chain n1: 59% 41%	
MET ASN CLUX CLYS CLYS CLYS CLYS ASN CLYS S2 CLYS CLYS	
• Molecule 19: Ribosomal protein S28	
Chain c1: 84% · 14%	
MET PRO BEE REC REC REC REC REC REC REC REC REC R	
• Molecule 20: Ribosomal protein S14	
Chain O1: 87% 13%	



MET SER LYS SER VAL LYS VAL TYR TYR AALA AALA AALA AASN ASN ASN SER SER SER

• Molecule 21: Ribosomal protein S15A

Chain W1: 99% MET • Molecule 22: 40S ribosomal protein S4 Chain E1: 96% LYS ARG GLY GLY GLY ALA SER TYR CLU • Molecule 23: SSU ribosomal protein S17P Chain L1: 89% 9% • Molecule 24: Ribosomal protein S20 Chain U1: 59% 41% ALA ALA PHE GLY ILE SER GLY PRO CYS CYS CYS GLY GLY GLY ASP ASP ASP ASP ILE LILE SER LEU SER LYS SER THR VAL GLU GLU PRO ASP ASN GLU • Molecule 25: rRNA 28S Chain 1: 69% 20% 10% 0000 0 0 0 0 0 0 0









MET GLY W2 W2 K70 K267 PR0	ARG ARG ARA ARA ARA ARA ARA ARA CLU CLYS ARA ARA ARA ARA ARA ARA ARA ARA ARA AR	
• Molecule	32: Ribosomal protein L7	
Chain F2:	91%	9%
MET PRO TLE PRO GLU CLU LEU LEU	HIYS HIYS CVAL ARG ALA ALA ALA ALA 1235 1235 1235	
• Molecule	33: 60S ribosomal protein L7a	
Chain G2:	80%	19%
MET SER LYS VAL SER GLY SER ASP	LIVE LIVE LIVE LALA ARK ARK ARK ARK CLEU ARK ARK ARK ARK ARK ARK ARK ARK ARK ARK	
• Molecule	34: Ribosomal protein L6	
Chain H2:	99%	
MET P2 E159 Q185		
• Molecule	35: Ribosomal protein L10	
Chain I2:	95%	5%
MET G2 L103 SER CYS ALA GLY	ARA ARG LI11 LYS LYS LEU	
• Molecule	36: Ribosomal protein L11	
Chain J2:	94%	• 5%
MET SER GLU SER N7 N7	0.17 0.17 0.17 0.11 0.11 0.11 7 8.119 8.119 8.119 8.113	
• Molecule	37: 60S ribosomal protein L13	
Chain L2:	81%	19%
MET ALA SER TYR ALA ALA SER PHE ILE	LEU ARG HILE HILE HILE HILE HILE ARIN ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	LYS
• Molecule	38: Ribosomal protein L14	
Chain M2:	97%	





• Molecule 39: Ribosomal protein L15

Chain N2: 100% • Molecule 40: Ribosomal protein L13a Chain O2: 99% GLY TYR • Molecule 41: Ribosomal protein L17 Chain P2: 94% 6% ASP VAL GLU GLU LYS ALA ALA ALA ALA LEU LEU CLN • Molecule 42: Ribosomal protein L18 Chain Q2: 99% MET • Molecule 43: Ribosomal protein L19 Chain R2: 88% 10% • Molecule 44: 60S ribosomal protein L18a Chain S2: 99% • Molecule 45: Ribosomal protein L21 Chain T2: 96% . .





 \bullet Molecule 46: Ribosomal protein eL22

Chain U	2:	58%	42%	
MET GLV GLV GLN TRP ILE	PLEO PLEO PRO ASP ASP CLN TLE ASN ASN ASP ASP ASP	HIS ARG LBU GLN ALA ALA ARG VAL SER SER SER SER ASN LFU ASN	SER ASN TYR AIA TYR TYR TYR TYR PRO SER SER SER SER ARG CLU SER CLYS CLYS CLYS CLYS CLYS CLYS CLYS CLYS	415 Y115
THR ILE GLU ASP ASP	ALA ALA ALA ALA ASP ASP GLU			
• Molecu	lle 47: Ribosomal pr	otein L23		
Chain V	2:	97%		
MET ALA SER K4 K14	H142			
• Molecu	lle 48: Ribosomal pr	otein L23A		
Chain X	2:	82%	18%	
MET SER GLU LYS ALA GLN	ALLA LYS LYS ALA ALA GLN GLN CYS ALA HIE HIE CUU	ALA LIYS LIYS LIJE R124 A139		
• Molecu	lle 49: Ribosomal pr	rotein L26		
Chain Y	2:	99%		
M1 1133 GLY LYS				
• Molecu	lle 50: 60S ribosoma	l protein L27		
Chain Z	2:	96%		
MET 82 854 MET SER	ADF GLU AGO A135			
• Molecu	lle 51: Ribosomal pr	rotein L27a		
Chain a2	::	99%		
MET P2 P149				

• Molecule 52: 60S ribosomal protein L29



Chain b2:	90%	10%
MET A2 B57 ASN LEU LYS GLU GLU		
• Molecule 53:	Ribosomal protein L30	
Chain c2:	92%	8%
MET SER THR LYS VAL ALA ALA S106 S106 ILE	d TT J	
• Molecule 54:	Ribosomal protein L31B	
Chain d2:	89%	11%
MET G2 G7 4 ASP ASP ASP ASP ASP CLU HIS LYS F80	SER ASP GLU GLU GLU	
• Molecule 55:	Ribosomal protein L32	
Chain e2:	93%	7%
MET ALA ALA GLY GLU MET MET 16 16 L131 ARG LYS CIU	C TEO	
• Molecule 56:	Ribosomal protein L35a	
Chain f2:	99%	·
MI F9 E123		
• Molecule 57:	Ribosomal protein L34	
Chain g2:	82%	18%
MET A2 R100 R100 GLU ALA ALA ALA ALA ALA	LLA THR THR LLA CLN THR ALA ALA ALA ALA ALA ALA ALA ALA LYS	
• Molecule 58:	Ribosomal protein L35	
Chain h2:	97%	
MET P2 T37 ALA GLY PRO V41 V124		

• Molecule 59: Ribosomal protein L36-1



Chain i2:	94%	6%
MET P2 E22 GLU ARG LYS LYS N89 N89		
• Molecule 60:	Ribosomal protein L37	
Chain j2:	98%	·
MET S2 A88 LYS		
• Molecule 61:	Ribosomal L38e	
Chain k2:	86%	14%
MET P2 C27 SER LYS GLY ARG CLU CLU CLU	K35 NT4 ASP SER GLU	
• Molecule 62:	Ribosomal protein L39	
Chain 12:	96%	
MET T2 R46 L51		
• Molecule 63:	Ubiquitin/Ribosomal protein L40e	
Chain m2:	39% • 60%	
MET GLN LEU LEU VAL ARG SER LEU LEU ARG	VAL VAL THR THR SER ALA ALA ARP ARPRO CLEU VAL THR SER ARC CLEU VAL TTR SER ARC CLV VAL CLEU VAL CLEU VAL ARC CLV VAL ARC CLV VAL ARC CLU VAL ARC ARC ARC ARC ARC ARC ARC ARC ARC ARC	LIAN LEU ASP ALA LYS LYS LEU CLY ASP TYR
ILE GLY GLV SER SER VAL LEU LEU VAL	ARG PHE GLY GLY GLY A127 A127	
• Molecule 64:	Ribosomal protein L44	
Chain o2:	89%	11%
MET V2 G95 LYS LYS SER LYS GLY	SER VAL PHE	
• Molecule 65:	Ribosomal protein L37a	
Chain p2:	94%	• •
MET A2 K3 K3 K3 K3 C60 R3 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1		



• Molecule 66:	E-site tRNA		
Chain w2:	29%	57%	14%
A1 62 68 689 669 670 671 773 773	A76		
• Molecule 67:	Ribosomal protein L2	24A	
Chain W2:	64%		36%
MET VS LYS ALA ALA ALA ALA ALA ALA ALA ALA ARG VAL	ARC LYS ALA ARL VAL VAL SER ARG ARG ARG ARG ARG ARG ASP SER SER SER SER	LYS LEU GLU GLU GLU GLU CLS SER LYS SER TYR SER ARG VAL	
• Molecule 68:	P-site tRNA		
Chain E:	33%	67%	
C74 C75 A76			
• Molecule 69:	Ribosomal protein S2	29A	
Chain d1:	34% •	65%	
MET ARG SER ALA LEU ALA CLY VAL ALA	ASP ASC ASP ARG ALY ARG PHE ALA ALA ALA ALA ALA ALA ASP VAL ASP VAL	VAL ASP ASP ASP ASP ASP ASP GLV GLV ARG GLV HIS CLU CLEU CLEU	ARG LYS LEU ASN ARG ARS ARS ALA ALA ALA ALA ASP ASP ASP ASP ASP ASP ASP ASP ASP AS
HIS PRO SER THR ILE PHE TRP PRO GLU	ASP ASN ASN ASN ASN ALK ASN ALA SLY CLY SC CLY SC CLY SER MET	BB9 C123 HIS	
• Molecule 70:	Ribosomal protein S5)	
Chain F1:	78	%	6% 15%
MET SER SER LEU CLU VAL ALA ALA LLA PHE ASN LYS TPD	PRO LEU VAL THR ASP CTN ASP CTN ASP CTN CTN CTN CTN CTN CTN CTN CTN CTN CTN	L68 M67 K71 K71 K71 K71 L12 L12 L12 L12 L12 L12 L12 L12	GLY GLY ALI VAL VAL V125 A126 A126 A126 A126 A126 A126 A126 A126
• Molecule 71:	Ribosomal protein S2	24	
Chain Y1:	67%	•	31%
MET PRO E3 E34 E37 GLN GLN	LEU LYS VAA ALA ALA ALA ALA ALA ALA PB0 PR0 PR0 PR0 PR0 VAL VAL VAL	GLN LEU LYS ASN LEU LEU ASN ASN ASN ANG ANG LEU LEU LEU LYS CYS THR	CLU LYS ALA THR THR THR LBU CLY LYS LYS
• Molecule 72:	40S ribosomal protein	n S6	
Chain G1:	73%		• 24%
MET PRO LYS GLY GLY FS FS FS FS FS FS FS FS FS FS FS FS FS	ASP PHE ARG LIVS CIN CIN CIN CIN CIN CIN CIN CIN CIN CVS	THR F56 965 977 1103 C106 P110 P110	A122 A172 ASP ASP ASP ASP ASP PRO PRO PRO PRO PRO C179 A170 A170 A170 A170 A170 A170 A170 A170
		WORLDWIDE PROTEIN DATA BANK	

• Molecule 73: rRNA 18S



 \bullet Molecule 74: 40S ribosomal protein SA



Chain A1:	79%	21%
MET THR CLU CLU CLU CLU CLU CLU CLU CLU CLU LLU L	R138 1210 1210 1116	PHE SER ALA ALA GLY GLY ASN LEU PHE ASP PHE ASP CLU TYR



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	91058	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 $(e^-/\text{\AA}^2)$	1	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 $(6k \ge 4k)$	Depositor



5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: M7A, 4AC, 7MG, OMU, C4J, OMC, MG, K, OMG, 5MC, MA6, A2M, 4OC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bo	ond lengths	I	Bond angles
		RMSZ	# Z > 5	RMSZ	# Z > 5
1	T1	0.33	0/812	0.56	0/1098
2	N1	0.35	0/1215	0.59	1/1634~(0.1%)
3	J1	0.34	0/1340	0.63	0/1796
4	D1	0.37	0/1422	0.60	1/1909~(0.1%)
5	X1	0.34	0/1119	0.63	0/1498
6	S1	0.33	0/1070	0.68	0/1435
7	Q1	0.35	0/968	0.64	0/1295
8	C1	0.36	0/1674	0.59	0/2259
9	B1	0.36	0/1793	0.61	1/2419~(0.0%)
10	b1	0.38	0/628	0.78	1/852~(0.1%)
11	a1	0.34	0/797	0.54	0/1072
12	V1	0.41	0/613	0.61	0/823
13	R1	0.38	0/773	0.61	0/1037
14	K1	0.34	0/707	0.64	0/957
15	I1	0.33	0/1302	0.59	0/1746
16	e1	0.31	0/294	0.53	0/392
17	H1	0.34	0/1211	0.55	0/1640
18	n1	0.36	0/219	0.64	0/280
19	c1	0.47	0/439	0.63	0/585
20	01	0.34	0/947	0.59	0/1273
21	W1	0.37	0/1048	0.59	0/1412
22	E1	0.33	0/2108	0.60	1/2845~(0.0%)
23	L1	0.35	0/1520	0.63	1/2037~(0.0%)
24	U1	0.35	0/619	0.64	0/833
25	1	0.78	0/58145	1.10	239/90686~(0.3%)
26	3	0.61	0/2797	1.00	7/4359~(0.2%)
27	42	0.75	0/3277	1.03	4/5109~(0.1%)
28	A2	0.39	0/1906	0.63	0/2561
29	B2	0.38	0/3058	0.59	0/4129
30	C2	0.40	0/2498	0.61	0/3388
31	D2	0.35	0/2157	0.56	0/2899
32	F2	0.39	0/1760	0.59	0/2374



N/L_1	Chain	Bond lengths		Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
33	G2	0.37	0/1472	0.59	0/1989	
34	H2	0.37	0/1469	0.61	1/1985~(0.1%)	
35	I2	0.36	0/1657	0.61	0/2219	
36	J2	0.35	0/1325	0.59	0/1776	
37	L2	0.38	0/1533	0.59	0/2052	
38	M2	0.36	0/1002	0.59	0/1349	
39	N2	0.40	0/1755	0.62	0/2353	
40	O2	0.41	0/1618	0.58	0/2169	
41	P2	0.40	0/1261	0.63	0/1688	
42	Q2	0.34	0/1425	0.59	0/1907	
43	R2	0.60	0/1478	0.64	0/1954	
44	S2	0.38	0/1452	0.57	0/1955	
45	T2	0.37	0/1251	0.59	1/1682~(0.1%)	
46	U2	0.41	0/836	0.59	0/1124	
47	V2	0.35	0/1083	0.58	0/1458	
48	X2	0.35	0/956	0.60	0/1293	
49	Y2	0.36	0/1091	0.61	0/1454	
50	Z2	0.37	0/997	0.54	0/1352	
51	a2	0.40	0/1231	0.60	0/1647	
52	b2	0.34	0/471	0.56	0/624	
53	c2	0.33	0/758	0.64	0/1025	
54	d2	0.36	0/764	0.62	0/1026	
55	e2	0.39	0/1063	0.56	0/1418	
56	f2	0.37	0/994	0.61	1/1338~(0.1%)	
57	g2	0.34	0/813	0.54	0/1092	
58	h2	0.36	0/971	0.61	0/1295	
59	i2	0.36	0/700	0.55	0/927	
60	j2	0.38	0/708	0.59	0/941	
61	k2	0.33	0/507	0.57	0/679	
62	12	0.34	0/445	0.64	0/594	
63	m2	0.34	0/426	0.56	0/568	
64	o2	0.40	0/773	0.62	0/1023	
65	p2	0.39	0/717	0.71	1/956~(0.1%)	
66	w2	0.93	1/332~(0.3%)	1.40	7/511~(1.4%)	
67	W2	0.37	0/551	0.58	0/738	
68	Ε	0.43	0/68	1.11	1/103~(1.0%)	
69	d1	0.45	0/400	0.60	0/532	
70	F1	0.65	0/1264	0.63	0/1697	
71	Y1	0.45	0/724	0.67	0/971	
72	G1	0.42	0/1466	0.67	0/1956	
73	2	0.62	0/32117	1.10	172/50066~(0.3%)	
74	A1	0.31	0/1580	0.50	0/2149	
All	All	0.60	1/173740 (0.0%)	0.93	$440/2542\overline{67}\ (0.2\%)$	



Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
66	w2	1	A	OP3-P	-10.48	1.48	1.61

All (1) bond length outliers are listed below:

The worst 5 of 440 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
73	2	155	C	P-O3'-C3'	-10.72	106.83	119.70
73	2	595	G	P-O3'-C3'	-10.62	106.96	119.70
73	2	138	G	P-O3'-C3'	-10.38	107.24	119.70
73	2	606	G	P-O3'-C3'	-10.24	107.41	119.70
10	b1	96	PHE	C-N-CA	10.16	147.09	121.70

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	entiles
1	T1	102/139~(73%)	97~(95%)	5 (5%)	0	100	100
2	N1	150/154~(97%)	142 (95%)	8 (5%)	0	100	100
3	J1	164/189~(87%)	153~(93%)	11 (7%)	0	100	100
4	D1	174/217~(80%)	163 (94%)	11 (6%)	0	100	100
5	X1	140/143~(98%)	130 (93%)	10 (7%)	0	100	100
6	S1	131/154~(85%)	113 (86%)	18 (14%)	0	100	100
7	Q1	119/158~(75%)	108 (91%)	11 (9%)	0	100	100



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
8	C1	210/242~(87%)	195~(93%)	15 (7%)	0	100	100
9	B1	216/248~(87%)	207 (96%)	9 (4%)	0	100	100
10	b1	77/124~(62%)	71~(92%)	6 (8%)	0	100	100
11	al	95/109~(87%)	90~(95%)	5 (5%)	0	100	100
12	V1	80/89~(90%)	72 (90%)	8 (10%)	0	100	100
13	R1	93/137~(68%)	87 (94%)	6 (6%)	0	100	100
14	K1	79/134~(59%)	70 (89%)	9 (11%)	0	100	100
15	I1	159/174~(91%)	147 (92%)	12 (8%)	0	100	100
16	e1	31/69~(45%)	29 (94%)	2 (6%)	0	100	100
17	H1	148/190~(78%)	133 (90%)	15 (10%)	0	100	100
18	n1	22/41~(54%)	22 (100%)	0	0	100	100
19	c1	51/64~(80%)	47 (92%)	4 (8%)	0	100	100
20	01	124/145~(86%)	121 (98%)	3 (2%)	0	100	100
21	W1	127/130~(98%)	117 (92%)	10 (8%)	0	100	100
22	E1	256/268~(96%)	234 (91%)	22 (9%)	0	100	100
23	L1	179/199~(90%)	169 (94%)	10 (6%)	0	100	100
24	U1	68/126~(54%)	63~(93%)	5 (7%)	0	100	100
28	A2	248/251~(99%)	237~(96%)	11 (4%)	0	100	100
29	B2	376/379~(99%)	357~(95%)	19 (5%)	0	100	100
30	C2	312/316~(99%)	295~(95%)	17 (5%)	0	100	100
31	D2	264/297~(89%)	247 (94%)	17 (6%)	0	100	100
32	F2	212/235~(90%)	209 (99%)	3 (1%)	0	100	100
33	G2	178/225~(79%)	173 (97%)	5 (3%)	0	100	100
34	H2	182/185~(98%)	172 (94%)	10 (6%)	0	100	100
35	I2	196/210~(93%)	187 (95%)	9 (5%)	0	100	100
36	J2	158/173~(91%)	144 (91%)	14 (9%)	0	100	100
37	L2	$\overline{185/234}$ (79%)	183 (99%)	2 (1%)	0	100	100
38	M2	126/131~(96%)	115 (91%)	11 (9%)	0	100	100
39	N2	$\overline{202/204} \ (99\%)$	192 (95%)	10 (5%)	0	100	100
40	O2	193/197~(98%)	186 (96%)	7 (4%)	0	100	100
41	P2	$\overline{152/164}~(93\%)$	143 (94%)	9 (6%)	0	100	100



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
42	Q2	176/179~(98%)	169~(96%)	7 (4%)	0	100	100
43	R2	175/196~(89%)	166~(95%)	9~(5%)	0	100	100
44	S2	171/173~(99%)	165~(96%)	6 (4%)	0	100	100
45	Τ2	149/159~(94%)	145~(97%)	4 (3%)	0	100	100
46	U2	98/171~(57%)	90~(92%)	8 (8%)	0	100	100
47	V2	137/142~(96%)	133 (97%)	4 (3%)	0	100	100
48	X2	114/141 (81%)	109 (96%)	5 (4%)	0	100	100
49	Y2	131/135~(97%)	126 (96%)	5 (4%)	0	100	100
50	Z2	125/135~(93%)	115 (92%)	10 (8%)	0	100	100
51	a2	146/149~(98%)	136 (93%)	10 (7%)	0	100	100
52	b2	54/62~(87%)	54 (100%)	0	0	100	100
53	c2	98/109~(90%)	97~(99%)	1 (1%)	0	100	100
54	d2	90/106~(85%)	81 (90%)	9 (10%)	0	100	100
55	e2	124/136~(91%)	119 (96%)	5 (4%)	0	100	100
56	f2	121/123~(98%)	114 (94%)	7 (6%)	0	100	100
57	g2	97/120 (81%)	94 (97%)	3 (3%)	0	100	100
58	h2	116/124 (94%)	114 (98%)	2 (2%)	0	100	100
59	i2	81/90 (90%)	76 (94%)	5 (6%)	0	100	100
60	j2	85/89~(96%)	83 (98%)	2 (2%)	0	100	100
61	k2	62/77~(80%)	60 (97%)	2 (3%)	0	100	100
62	12	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
63	m2	49/127~(39%)	46 (94%)	3 (6%)	0	100	100
64	02	92/106~(87%)	90~(98%)	2 (2%)	0	100	100
65	p2	89/94 (95%)	85 (96%)	4 (4%)	0	100	100
67	W2	63/102~(62%)	59 (94%)	4 (6%)	0	100	100
69	d1	46/137 (34%)	40 (87%)	6 (13%)	0	100	100
70	F1	157/190~(83%)	127 (81%)	27 (17%)	3 (2%)	8	14
71	Y1	87/132~(66%)	76 (87%)	10 (12%)	1 (1%)	14	25
72	G1	177/248 (71%)	134 (76%)	37 (21%)	6 (3%)	3	5
74	A1	192/245~(78%)	185 (96%)	7 (4%)	0	100	100
All	All	9329/10892 (86%)	8754 (94%)	565 (6%)	10 (0%)	54	75



5 of 10 Ramachandran outliers are listed below:

Mol	Chain	\mathbf{Res}	Type
72	G1	103	ILE
72	G1	114	ALA
72	G1	106	CYS
70	F1	34	PHE
72	G1	65	GLN

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	entiles
1	T1	78/115~(68%)	76~(97%)	2(3%)	46	66
2	N1	123/130~(95%)	123 (100%)	0	100	100
3	J1	141/164~(86%)	140 (99%)	1 (1%)	84	89
4	D1	142/182~(78%)	142 (100%)	0	100	100
5	X1	113/114~(99%)	113 (100%)	0	100	100
6	S1	112/131~(86%)	109 (97%)	3(3%)	44	65
7	Q1	101/130 (78%)	101 (100%)	0	100	100
8	C1	176/201~(88%)	176 (100%)	0	100	100
9	B1	196/220 (89%)	195 (100%)	1 (0%)	88	92
10	b1	70/112~(62%)	70 (100%)	0	100	100
11	a1	90/103~(87%)	90 (100%)	0	100	100
12	V1	62/72~(86%)	62 (100%)	0	100	100
13	R1	81/123~(66%)	80 (99%)	1 (1%)	71	82
14	K1	73/119~(61%)	73~(100%)	0	100	100
15	I1	138/148~(93%)	138 (100%)	0	100	100
16	e1	30/58~(52%)	30 (100%)	0	100	100
17	H1	116/170~(68%)	115~(99%)	1 (1%)	78	87
18	n1	$2\overline{1/38}~(55\%)$	21 (100%)	0	100	100
19	c1	49/57~(86%)	48 (98%)	1 (2%)	55	72



Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
20	O1	91/113~(80%)	91 (100%)	0	100	100
21	W1	114/115~(99%)	114 (100%)	0	100	100
22	E1	225/232~(97%)	225~(100%)	0	100	100
23	L1	155/173~(90%)	153~(99%)	2(1%)	69	81
24	U1	68/110~(62%)	68 (100%)	0	100	100
28	A2	189/192~(98%)	189 (100%)	0	100	100
29	B2	312/313~(100%)	312 (100%)	0	100	100
30	C2	261/263~(99%)	260 (100%)	1 (0%)	91	93
31	D2	210/242~(87%)	209 (100%)	1 (0%)	88	92
32	F2	184/204~(90%)	183 (100%)	1 (0%)	88	92
33	G2	159/198~(80%)	158 (99%)	1 (1%)	86	90
34	H2	160/164~(98%)	160 (100%)	0	100	100
35	I2	166/177~(94%)	166 (100%)	0	100	100
36	J2	137/149~(92%)	136 (99%)	1 (1%)	84	89
37	L2	159/197~(81%)	159 (100%)	0	100	100
38	M2	103/111~(93%)	102 (99%)	1 (1%)	76	85
39	N2	174/175~(99%)	173 (99%)	1 (1%)	86	90
40	O2	164/165~(99%)	164 (100%)	0	100	100
41	P2	130/139~(94%)	130 (100%)	0	100	100
42	Q2	154/155~(99%)	154 (100%)	0	100	100
43	R2	149/167~(89%)	144 (97%)	5 (3%)	37	58
44	S2	147/154~(96%)	146 (99%)	1 (1%)	84	89
45	Τ2	126/133~(95%)	126 (100%)	0	100	100
46	U2	87/153~(57%)	87 (100%)	0	100	100
47	V2	112/114~(98%)	111 (99%)	1 (1%)	78	87
48	X2	104/123~(85%)	104 (100%)	0	100	100
49	Y2	114/115~(99%)	114 (100%)	0	100	100
50	Z2	101/119~(85%)	101 (100%)	0	100	100
51	a2	126/127~(99%)	126 (100%)	0	100	100
52	b2	51/57~(90%)	51 (100%)	0	100	100
53	c2	84/92~(91%)	84 (100%)	0	100	100



Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles	;
54	d2	78/92~(85%)	78~(100%)	0	100	100	
55	e2	112/120~(93%)	112 (100%)	0	100	100	
56	f2	102/103~(99%)	102~(100%)	0	100	100	
57	g2	87/100~(87%)	87~(100%)	0	100	100	
58	h2	102/107~(95%)	102 (100%)	0	100	100	
59	i2	72/78~(92%)	72~(100%)	0	100	100	
60	j2	70/74~(95%)	70 (100%)	0	100	100	
61	k2	56/68~(82%)	56 (100%)	0	100	100	
62	12	46/48~(96%)	45~(98%)	1 (2%)	52	70	
63	m2	46/110~(42%)	45~(98%)	1 (2%)	52	70	
64	o2	81/93~(87%)	81 (100%)	0	100	100	
65	p2	71/73~(97%)	69~(97%)	2(3%)	43	63	
67	W2	58/92~(63%)	58 (100%)	0	100	100	
69	d1	41/116~(35%)	40 (98%)	1 (2%)	49	68	
70	F1	132/157~(84%)	123~(93%)	9~(7%)	16	28	
71	Y1	77/113~(68%)	75~(97%)	2(3%)	46	66	
72	G1	153/213~(72%)	152 (99%)	1 (1%)	84	89	
74	A1	168/217 (77%)	167 (99%)	1 (1%)	86	90	
All	All	$798\overline{0}/9302~(86\%)$	7936 (99%)	44 (1%)	86	90	

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
65	p2	3	LYS
70	F1	67	ARG
65	p2	80	ARG
70	F1	57	ARG
70	F1	125	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
30	C2	210	ASN
35	I2	51	HIS
70	F1	189	ASN



Continued from previous page...

Mol	Chain	Res	Type
33	G2	62	ASN
42	Q2	87	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	1	2419/2707~(89%)	410 (16%)	24~(0%)
26	3	116/120~(96%)	16 (13%)	2(1%)
27	42	136/139~(97%)	35~(25%)	2(1%)
66	w2	12/14~(85%)	4 (33%)	0
68	Е	2/3~(66%)	1 (50%)	0
73	2	1329/1452~(91%)	304 (22%)	17 (1%)
All	All	4014/4435~(90%)	770 (19%)	45 (1%)

5 of 770 RNA backbone outliers are listed below:

Mol	Chain	\mathbf{Res}	Type
25	1	5	G
25	1	21	G
25	1	39	А
25	1	42	А
25	1	48	G

5 of 45 RNA pucker outliers are listed below:

Mol	Chain	\mathbf{Res}	Type
73	2	8	U
73	2	600	G
73	2	204	G
73	2	589	G
73	2	835	А

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

40 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



Mal	Trune	Chain	Dec	Tinle	Bond lengths		Bond angles			
NIOI	Type	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
73	OMC	2	104	73	19,22,23	0.85	0	26,31,34	0.99	1 (3%)
25	OMG	1	1520	25	18,26,27	1.02	1 (5%)	19,38,41	1.20	<mark>3 (15%)</mark>
25	OMG	1	1882	25,75	18,26,27	1.02	1 (5%)	19,38,41	1.37	3 (15%)
73	MA6	2	1435	73	18,26,27	1.02	1 (5%)	19,38,41	<mark>3.68</mark>	2 (10%)
73	7MG	2	1261	73	22,26,27	<mark>3.75</mark>	10 (45%)	29,39,42	2.09	9 (31%)
25	OMG	1	1204	25	18,26,27	2.34	7 (38%)	19,38,41	1.86	7 (36%)
25	OMG	1	1775	25	18,26,27	2.30	8 (44%)	19,38,41	1.46	3 (15%)
25	OMG	1	2074	25	18,26,27	2.30	7 (38%)	19,38,41	1.41	3(15%)
25	A2M	1	1768	25	18,25,26	<mark>3.64</mark>	8 (44%)	18,36,39	<mark>3.47</mark>	<mark>6 (33%)</mark>
25	OMU	1	1897	25,75	19,22,23	2.90	7 (36%)	26,31,34	1.77	4 (15%)
25	OMC	1	2380	25	19,22,23	2.82	8 (42%)	26,31,34	0.89	1 (3%)
73	A2M	2	87	73,75	18,25,26	<mark>3.66</mark>	7 (38%)	18,36,39	3.28	4 (22%)
73	OMU	2	1314	73	19,22,23	2.90	8 (42%)	26,31,34	1.74	5 (19%)
27	OMG	42	133	27,25	18,26,27	2.34	8 (44%)	19,38,41	1.36	4 (21%)
25	A2M	1	396	25,75	18,25,26	0.95	1 (5%)	18,36,39	1.27	2 (11%)
73	M7A	2	1390	73	20,25,26	0.42	0	28,37,40	0.69	1 (3%)
25	A2M	1	393	25	18,25,26	3.56	8 (44%)	18,36,39	3.24	4 (22%)
25	OMC	1	1824	25	19,22,23	0.79	0	26,31,34	1.19	1 (3%)
73	A2M	2	348	76,73	18,25,26	<mark>3.62</mark>	8 (44%)	18,36,39	<mark>3.39</mark>	3 (16%)
25	OMG	1	313	25	18,26,27	2.33	8 (44%)	19,38,41	1.51	3 (15%)
25	OMG	1	2237	25,75	18,26,27	1.05	1 (5%)	19,38,41	1.06	2 (10%)
73	OMG	2	371	73	18,26,27	1.08	1 (5%)	19,38,41	1.35	3 (15%)
25	OMU	1	1896	25,75	19,22,23	2.89	8 (42%)	26,31,34	1.75	5 (19%)
25	OMU	1	49	25,75	19,22,23	2.94	7 (36%)	26,31,34	1.71	6 (23%)
25	A2M	1	523	25	18,25,26	<mark>3.54</mark>	8 (44%)	18,36,39	<mark>3.47</mark>	4 (22%)
25	OMG	1	624	25,75	18,26,27	2.33	7 (38%)	19,38,41	1.70	5 (26%)
73	4AC	2	1426	73,75	21,24,25	4.44	16 (76%)	29,34,37	1.37	3 (10%)
73	MA6	2	1434	73	18,26,27	1.04	1 (5%)	19,38,41	3.44	2 (10%)
25	OMC	1	1684	25,75	19,22,23	2.75	7 (36%)	26,31,34	0.97	1 (3%)
73	OMG	2	1035	73,75	18,26,27	2.44	8 (44%)	19,38,41	1.64	4 (21%)
25	OMU	1	1908	25	19,22,23	4.24	15 (78%)	26,31,34	1.92	7 (26%)
73	OMG	2	868	73	18,26,27	2.35	8 (44%)	19,38,41	1.40	2 (10%)
25	5MC	1	1765	25	18,22,23	3.26	7 (38%)	26,32,35	1.10	3 (11%)

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	Mol Type Chain B		Dec	Tink	B	ond leng	\mathbf{gths}	Bond angles		
IVIOI	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	OMG	1	1121	25	18,26,27	1.04	1 (5%)	19,38,41	1.45	3 (15%)
25	5MC	1	2292	25,75	18,22,23	<mark>3.36</mark>	7 (38%)	26,32,35	1.29	3 (11%)
73	OMG	2	1011	73	18,26,27	1.00	1 (5%)	19,38,41	1.18	3 (15%)
73	C4J	2	933	73	24,29,30	<mark>3.35</mark>	9 (37%)	29,42,45	1.35	4 (13%)
25	OMG	1	386	25	18,26,27	0.98	1 (5%)	19,38,41	1.12	3 (15%)
25	OMG	1	2042	25,68	18,26,27	2.33	8 (44%)	19,38,41	1.41	3 (15%)
73	4OC	2	1325	73	20,23,24	3.04	8 (40%)	26,32,35	0.96	1 (3%)

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
73	OMC	2	104	73	-	1/9/27/28	0/2/2/2
25	OMG	1	1520	25	-	1/5/27/28	0/3/3/3
25	OMG	1	1882	25,75	-	0/5/27/28	0/3/3/3
73	MA6	2	1435	73	-	3/7/29/30	0/3/3/3
73	7MG	2	1261	73	-	0/7/37/38	0/3/3/3
25	OMG	1	1204	25	-	0/5/27/28	0/3/3/3
25	OMG	1	1775	25	-	2/5/27/28	0/3/3/3
25	OMG	1	2074	25	-	1/5/27/28	0/3/3/3
25	A2M	1	1768	25	-	2/5/27/28	0/3/3/3
25	OMU	1	1897	25,75	-	0/9/27/28	0/2/2/2
25	OMC	1	2380	25	-	0/9/27/28	0/2/2/2
73	A2M	2	87	73,75	-	3/5/27/28	0/3/3/3
73	OMU	2	1314	73	-	0/9/27/28	0/2/2/2
27	OMG	42	133	27,25	-	0/5/27/28	0/3/3/3
25	A2M	1	396	25,75	-	1/5/27/28	0/3/3/3
73	M7A	2	1390	73	-	2/7/37/38	0/3/3/3
25	A2M	1	393	25	-	0/5/27/28	0/3/3/3
25	OMC	1	1824	25	-	1/9/27/28	0/2/2/2
73	A2M	2	348	76,73	-	0/5/27/28	0/3/3/3
25	OMG	1	313	25	-	2/5/27/28	0/3/3/3
25	OMG	1	2237	25,75	-	0/5/27/28	0/3/3/3
73	OMG	2	371	73	-	1/5/27/28	0/3/3/3
25	OMU	1	1896	25,75	-	0/9/27/28	0/2/2/2
25	OMU	1	49	25,75	-	1/9/27/28	0/2/2/2
25	A2M	1	523	25	-	1/5/27/28	0/3/3/3
25	OMG	1	624	25,75	_	1/5/27/28	0/3/3/3



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
73	4AC	2	1426	73,75	-	2/11/29/30	0/2/2/2
73	MA6	2	1434	73	-	0/7/29/30	0/3/3/3
25	OMC	1	1684	25,75	-	4/9/27/28	0/2/2/2
73	OMG	2	1035	73,75	-	1/5/27/28	0/3/3/3
25	OMU	1	1908	25	-	2/9/27/28	0/2/2/2
73	OMG	2	868	73	-	3/5/27/28	0/3/3/3
25	5MC	1	1765	25	-	0/7/25/26	0/2/2/2
25	OMG	1	1121	25	-	2/5/27/28	0/3/3/3
25	5MC	1	2292	25,75	-	4/7/25/26	0/2/2/2
73	OMG	2	1011	73	-	1/5/27/28	0/3/3/3
73	C4J	2	933	73	-	6/16/34/35	0/2/2/2
25	OMG	1	386	25	-	0/5/27/28	0/3/3/3
25	OMG	1	2042	25,68	-	0/5/27/28	0/3/3/3
73	4OC	2	1325	73	-	0/9/29/30	0/2/2/2

The worst 5 of 235 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\operatorname{Ideal}(\operatorname{\AA})$
73	2	933	C4J	C6-C5	12.11	1.52	1.34
25	1	1908	OMU	C3'-C2'	-10.39	1.29	1.52
25	1	2292	5MC	C6-C5	8.97	1.49	1.34
25	1	523	A2M	C3'-C4'	-8.76	1.30	1.53
73	2	87	A2M	C3'-C4'	-8.73	1.30	1.53

The worst 5 of 136 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
73	2	1435	MA6	N1-C6-N6	-14.68	101.61	117.06
73	2	1434	MA6	N1-C6-N6	-13.78	102.55	117.06
25	1	523	A2M	C5-C6-N6	10.88	136.88	120.35
73	2	348	A2M	C5-C6-N6	10.56	136.40	120.35
73	2	87	A2M	C5-C6-N6	10.32	136.03	120.35

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	1	49	OMU	C1'-C2'-O2'-CM2
25	1	313	OMG	O4'-C4'-C5'-O5'
25	1	396	A2M	C1'-C2'-O2'-CM'



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Mol	Chain	Res	Type	Atoms
25	1	523	A2M	C1'-C2'-O2'-CM'
25	1	624	OMG	C1'-C2'-O2'-CM2

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 556 ligands modelled in this entry, 556 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
66	w2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	w2	5:G	O3'	68:C	Р	17.08



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-13683. 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)

This section was not generated.

6.2 Central slices (i)

This section was not generated.

6.3 Largest variance slices (i)

This section was not generated.

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

This section was not generated.

6.5 Orthogonal surface views (i)

This section was not generated.

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)

This section was not generated.

7.2 Volume estimate versus contour level (i)

This section was not generated.

7.3 Rotationally averaged power spectrum (i)

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



8 Fourier-Shell correlation (i)

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



9 Map-model fit (i)

This section was not generated.

