

wwPDB EM Validation Summary Report (i)

Oct 28, 2024 - 07:54 pm GMT

PDB ID	:	7NWG
EMDB ID	:	EMD-12631
Title	:	Mammalian pre-termination 80S ribosome with Hybrid P/E- and A/P-site
		tRNA's bound by Blasticidin S.
Authors	:	Powers, K.T.; Yadav, S.K.N.; Bufton, J.C.; Schaffitzel, C.
Deposited on	:	2021-03-16
Resolution	:	3.80 Å(reported)
Based on initial model	:	6HCJ

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.dev113
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7(2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 3.80 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.



Motria	Whole archive	EM structures		
wiethc	$(\# { m Entries})$	$(\# { m Entries})$		
Ramachandran outliers	207382	16835		
Sidechain outliers	206894	16415		
RNA backbone	6643	2191		

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	51	3788	56%	35%	5% •						
2	71	120	60%	32%	8%						
3	81	151	65%	30%	5%						
4	A2	1818	• 56%	35%	• •						
5	B2	295	73%	•	26%						
6	C2	264	80%	.	19%						
7	D2	259	85%		15%						
8	E2	281	81%		19%						



Mol	Chain	Length	Quality of chain	
9	F2	262	99%	·
10	G2	205	89%	• 10%
11	H2	262	85%	5% 10%
12	I2	190	96%	
13	J2	206	97%	•
14	K2	194	93%	• 5%
15	L2	151	• 61% · 36%	
16	M2	158	91%	9%
17	N2	123	19%	. 5%
18	Ω^2	1/0	•	• 578
10	D2	168	90%	•
20	02	145	/9% ·	19%
20		140	5%	17%
21	R2	157	87%	•• 10%
22	S2	145	90%	• 9%
23	Τ2	152	90%	5% 5%
24	U2	145	95%	• •
25	V2	130	9% 76% •	23%
26	W2	83	100%	
27	X2	139	91%	•• 7%
28	Y2	141	99%	·
29	Z2	146	84%	15%
30	a2	198	• <u> </u>	
31	b2	117	84%	• 14%
32	c2	84	98%	••
33	d2	69	<mark>6%</mark> 90%	10%



Mol	Chain	Length	Quality of chain	
34	e2	55	100%	
35	f2	133	41% 59%	
36	g2	68	12%	
37	h2	313	9%	•
38	A3	246	98%	·
39	B3	403	97%	••
40	C3	425	84% •	15%
41	D3	297	97%	••
42	E3	291	74% . 2	26%
43	F3	249	90%	• 10%
44	G3	241	89%	7% •
45	H3	190	98%	•
46	I3	214	95%	•
47	J3	181	91%	• 6%
48	L3	211	95%	
49	M3	218	61% · 37%	
50	N3	203	98%	•
51	O3	203	97%	•••
52	P3	199	•	23%
53	Q3	188	97%	••
54	R3	196	88%	• 8%
55	S3	176	98%	•
56	Τ3	159	98%	•
57	U3	128		23%
58	V3	131	99%	•



Mol	Chain	Length	Quality of chair	1	
59	X3	156	74%	•	24%
60	Y3	132	99%		
61	Z3	135	98%		••
62	a3	160	• 92%		8%
63	b3	245	41%	58%	
64	c3	115	• 80%		5% 15%
65	d3	107	• 99%		
66	e3	128	• 99%		
67	f3	109	• 99%		•
68	g3	126	6% 		10%
69	h3	122	98%		
70	i3	117	84%		• 13%
71	i3	97	89%		11%
72	k3	69	100%		
73	13	50	100%		
74	m3	128	/10/	50%	
75	n3	25	41/0		
76	03	149	710/		•
77	- 00 - n2	142	/1%	•	27%
70	po "?	109	81%		• 17%
70	rə	137	88%		• 9%
79	q3	(4	43% 33%	51%	5%
80	t3	318	58% • 35%	3	38%
81	u3	195	78%		22%
82	v3	18	33%	67%	
83	33	75	55%	459	%



Mol	Chain	Length	Quality of chain	
			37%	
84	w3	217	95%	5%
			7%	
85	1	15	93%	7%
86	W	134	47% 53%	



2 Entry composition (i)

There are 89 unique types of molecules in this entry. The entry contains 383415 atoms, of which 163452 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 28S Ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	51	3626	Total 116849	C 34571	H 39208	N 14211	O 25233	Р 3626	0	0

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

Mol	Chain	Residues			Aton	ıs			AltConf	Trace
2	71	120	Total 3853	C 1141	Н 1295	N 456	0 842	Р 119	0	0

• Molecule 3 is a RNA chain called 5.8S Ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	81	151	Total	С	Н	N	0	Р	0	0
			4835	1432	1627	564	1062	150	, i i i i i i i i i i i i i i i i i i i	, i i i i i i i i i i i i i i i i i i i

• Molecule 4 is a RNA chain called 18S Ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	A2	1740	Total 55909	C 16578	H 18768	N 6668	O 12156	Р 1739	0	0

• Molecule 5 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues			AltConf	Trace				
5	B2	217	Total 3418	C 1086	Н 1708	N 300	O 316	S 8	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B2	114	THR	ALA	conflict	UNP G1TLT8

• Molecule 6 is a protein called 40S ribosomal protein S3a.



Mol	Chain	Residues			Atom	.s			AltConf	Trace
6	C2	213	Total	C	H	N	0	S 14	0	0
			3532	1098	1803	309	308	14		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C2	236	GLY	SER	conflict	UNP G1SS70
C2	242	ALA	THR	conflict	UNP G1SS70

• Molecule 7 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues			AltConf	Trace				
7	D2	221	Total 3522	C 1111	Н 1806	N 295	0 301	S 9	0	0

• Molecule 8 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
8	E9	228	Total	С	Η	Ν	0	\mathbf{S}	0	0
0	ΓZ	220	3624	1125	1859	316	316	8	0	0

• Molecule 9 is a protein called S4.

Mol	Chain	Residues			AltConf	Trace				
9	F2	262	Total 4252	C 1324	Н 2176	N 386	O 358	S 8	0	0

• Molecule 10 is a protein called Ribosomal protein S5.

Mol	Chain	Residues			AltConf	Trace				
10	G2	185	Total 2993	C 921	Н 1522	N 277	O 266	${ m S} 7$	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G2	0	MET	-	initiating methionine	UNP G1TFM5

• Molecule 11 is a protein called 40S ribosomal protein S6.



Mol	Chain	Residues			AltConf	Trace				
11	H2	237	Total 4008	C 1200	Н 2085	N 387	O 329	${ m S} 7$	0	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H2	-12	LEU	-	expression tag	UNP A0A5K1UJS7
H2	-11	PHE	-	expression tag	UNP A0A5K1UJS7
H2	-10	ARG	-	expression tag	UNP A0A5K1UJS7
H2	-9	GLY	-	expression tag	UNP A0A5K1UJS7
H2	-8	ALA	-	expression tag	UNP A0A5K1UJS7
H2	-7	SER	-	expression tag	UNP A0A5K1UJS7
H2	-6	GLU	-	expression tag	UNP A0A5K1UJS7
H2	-5	ALA	-	expression tag	UNP A0A5K1UJS7
H2	-4	VAL	-	expression tag	UNP A0A5K1UJS7
H2	-3	GLY	-	expression tag	UNP A0A5K1UJS7
H2	-2	SER	-	expression tag	UNP A0A5K1UJS7
H2	-1	LEU	-	expression tag	UNP A0A5K1UJS7
H2	0	LYS	-	expression tag	UNP A0A5K1UJS7

• Molecule 12 is a protein called ribosomal protein eS7.

Mol	Chain	Residues			Atom	S			AltConf	Trace
12	I2	185	Total	C	H 1599	N 971	0	S 1	0	0
			3070	952	1582	2(1	204	T		

• Molecule 13 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
13	J2	206	Total 3457	C 1058	H 1771	N 332	0 291	${S \atop 5}$	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J2	47	ARG	GLY	variant	UNP G1TJW1

• Molecule 14 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues			Atom	S			AltConf	Trace
14	K9	185	Total	С	Η	Ν	0	\mathbf{S}	0	0
14	112	100	3165	969	1640	306	248	2	0	0



• Molecule 15 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	L2	96	Total 1646	C 530	Н 836	N 143	0 131	S 6	0	0

• Molecule 16 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues			AltConf	Trace				
16	M2	143	Total 2424	C 749	Н 1249	N 222	0 198	S 6	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M2	25	GLN	LEU	conflict	UNP G1TRM4
M2	29	SER	GLY	conflict	UNP G1TRM4

• Molecule 17 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues			Aton	ns			AltConf	Trace
17	N2	117	Total 1847	C 570	Н 939	N 161	O 169	S 8	0	0

• Molecule 18 is a protein called ribosomal protein uS15.

Mol	Chain	Residues			Atom	IS			AltConf	Trace
18	O2	149	Total 2491	C 770	H 1289	N 228	O 203	S 1	0	0

• Molecule 19 is a protein called uS11.

Mol	Chain	Residues			AltConf	Trace				
19	P2	136	Total 2055	C 621	Н 1039	N 199	0 190	S 6	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P2	-16	MET	-	initiating methionine	UNP G1T1F0
P2	-15	LYS	-	expression tag	UNP G1T1F0
P2	-14	ALA	-	expression tag	UNP G1T1F0
P2	-13	ARG	-	expression tag	UNP G1T1F0



Chain	Residue	Modelled	Actual	Comment	Reference
P2	-12	ALA	-	expression tag	UNP G1T1F0
P2	-11	LEU	-	expression tag	UNP G1T1F0
P2	-10	SER	-	expression tag	UNP G1T1F0
P2	-9	GLY	-	expression tag	UNP G1T1F0
P2	-8	SER	-	expression tag	UNP G1T1F0
P2	-7	GLY	-	expression tag	UNP G1T1F0
P2	-6	VAL	-	expression tag	UNP G1T1F0
P2	-5	ARG	-	expression tag	UNP G1T1F0

• Molecule 20 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
20	Q2	120	Total 2042	C 635	Н 1045	N 187	O 168	S 7	0	0

• Molecule 21 is a protein called Ribosomal protein S16.

Mol	Chain	Residues			AltConf	Trace				
21	R2	142	Total 2323	С 717	Н 1195	N 213	0 195	${ m S} { m 3}$	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R2	-8	VAL	GLU	conflict	UNP G1SGX4
R2	-7	GLU	ASP	conflict	UNP G1SGX4
R2	-6	LEU	ARG	conflict	UNP G1SGX4
R2	-5	VAL	HIS	conflict	UNP G1SGX4
R2	-4	LEU	SER	conflict	UNP G1SGX4
R2	-3	VAL	SER	conflict	UNP G1SGX4
R2	-2	LEU	ALA	conflict	UNP G1SGX4
R2	-1	GLY	ALA	conflict	UNP G1SGX4

• Molecule 22 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues			Atom		AltConf	Trace		
22	S2	132	Total 2189	C 670	Н 1121	N 199	0 195	${S \over 4}$	0	0

• Molecule 23 is a protein called 40S ribosomal protein uS13.



Mol	Chain	Residues			Atom	IS			AltConf	Trace
23	Τ2	144	Total 2439	C 746	Н 1249	N 241	O 202	S 1	0	0

• Molecule 24 is a protein called S19.

Mol	Chain	Residues			Atom	S			AltConf	Trace
24	U2	141	Total 2227	C 688	Н 1130	N 211	0 195	${ m S} { m 3}$	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U2	119	GLY	TRP	conflict	UNP G1TN62

• Molecule 25 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues			Aton	AltConf	Trace			
25	V2	100	Total 1657	C 498	Н 862	N 152	0 141	${S \atop 4}$	0	0

• Molecule 26 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues			AltConf	Trace				
26	W2	83	Total 1273	C 393	Н 637	N 117	0 121	${ m S}{ m 5}$	0	0

• Molecule 27 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues			AltConf	Trace				
27	X2	129	Total 2114	C 659	Н 1080	N 193	O 176	${ m S}{ m 6}$	0	0

• Molecule 28 is a protein called Ribosomal protein S23.

Mol	Chain	Residues			AltConf	Trace				
28	Y2	141	Total 2263	C 693	Н 1165	N 219	0 183	${ m S} { m 3}$	0	0

• Molecule 29 is a protein called 40S ribosomal protein S24.



Mol	Chain	Residues			Atom	IS			AltConf	Trace
29	Z2	124	Total 2094	C 640	Н 1083	N 198	O 168	${ m S}{ m 5}$	0	0

• Molecule 30 is a protein called ribosomal protein eS25.

Mol	Chain	Residues			AltConf	Trace				
30	a2	75	Total 1254	C 382	Н 656	N 111	0 104	S 1	0	0

• Molecule 31 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues			AltConf	Trace				
31	b2	101	Total 1678	$\begin{array}{c} \mathrm{C} \\ 507 \end{array}$	Н 864	N 170	O 132	${ m S}{ m 5}$	0	0

• Molecule 32 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues			AltConf	Trace				
32	c2	83	Total 1323	C 408	Н 672	N 121	0 115	S 7	0	0

• Molecule 33 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues		A	AltConf	Trace				
33	d2	62	Total 1002	C 297	Н 514	N 97	O 92	${ m S} { m 2}$	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d2	5	HIS	ARG	conflict	UNP G1TIB4

• Molecule 34 is a protein called uS14.

Mol	Chain	Residues		ŀ	AltConf	Trace				
34	e2	55	Total 911	C 286	Н 452	N 94	0 74	${ m S}{ m 5}$	0	0

• Molecule 35 is a protein called 40S ribosomal protein S30.



Mol	Chain	Residues		ŀ	Atom	S			AltConf	Trace
35	f2	55	Total 935	С 274	Н 492	N 97	0 71	S 1	0	0

• Molecule 36 is a protein called eS31.

Mol	Chain	Residues			AltConf	Trace				
36	g2	68	Total 1122	C 351	Н 567	N 103	0 94	S 7	0	0

• Molecule 37 is a protein called ribosomal protein RACK1.

Mol	Chain	Residues			AltConf	Trace				
37	h2	313	Total 4829	C 1535	Н 2393	N 424	O 465	S 12	0	0

• Molecule 38 is a protein called L8.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
38	A3	246	Total 3870	C 1183	Н 1983	N 387	0 311	S 6	0	0

• Molecule 39 is a protein called uL3.

Mol	Chain	Residues			AltConf	Trace				
39	B3	394	Total 6482	C 2020	Н 3310	N 597	O 542	S 13	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B3	1	MET	-	initiating methionine	UNP G1TL06

• Molecule 40 is a protein called uL4.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
40	C3	362	Total 5937	C 1812	Н 3054	N 577	O 480	S 14	0	0

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C3	379	VAL	-	expression tag	UNP G1SVW5



Continu	ied from pre	evious page			
Chain	Residue	Modelled	Actual	Comment	Reference
C3	380	LYS	-	expression tag	UNP G1SVW5
C3	381	LYS	-	expression tag	UNP G1SVW5
C3	382	PRO	-	expression tag	UNP G1SVW5
C3	383	ARG	-	expression tag	UNP G1SVW5
C3	384	ALA	-	expression tag	UNP G1SVW5
C3	385	VAL	-	expression tag	UNP G1SVW5
C3	386	GLY	-	expression tag	UNP G1SVW5
C3	387	ILE	-	expression tag	UNP G1SVW5
C3	388	LYS	-	expression tag	UNP G1SVW5
C3	389	GLN	-	expression tag	UNP G1SVW5
C3	390	LYS	-	expression tag	UNP G1SVW5
C3	391	LYS	-	expression tag	UNP G1SVW5
C3	392	LYS	-	expression tag	UNP G1SVW5
C3	393	PRO	-	expression tag	UNP G1SVW5
C3	394	VAL	-	expression tag	UNP G1SVW5
C3	395	VAL	-	expression tag	UNP G1SVW5
C3	396	GLY	-	expression tag	UNP G1SVW5
C3	397	ARG	-	expression tag	UNP G1SVW5
C3	398	LYS	-	expression tag	UNP G1SVW5
C3	399	ALA	-	expression tag	UNP G1SVW5
C3	400	ALA	-	expression tag	UNP G1SVW5
C3	401	ALA	-	expression tag	UNP G1SVW5
C3	402	ALA	-	expression tag	UNP G1SVW5
C3	403	LYS	-	expression tag	UNP G1SVW5
C3	404	LYS	-	expression tag	UNP G1SVW5
C3	405	PRO	-	expression tag	UNP G1SVW5
C3	406	ALA	-	expression tag	UNP G1SVW5
C3	407	ALA	-	expression tag	UNP G1SVW5
C3	408	ASP	-	expression tag	UNP G1SVW5
C3	409	LYS	-	expression tag	UNP G1SVW5
C3	410	LYS	-	expression tag	UNP G1SVW5
C3	411	ALA	-	expression tag	UNP G1SVW5
C3	412	ALA	-	expression tag	UNP G1SVW5
C3	413	ASP	-	expression tag	UNP G1SVW5
C3	414	LYS	-	expression tag	UNP G1SVW5
C3	415	ARG	-	expression tag	UNP G1SVW5
C3	416	ALA	-	expression tag	UNP G1SVW5
C3	417	GLY	-	expression tag	UNP G1SVW5
C3	418	PRO	-	expression tag	UNP G1SVW5
C3	419	GLU	-	expression tag	UNP G1SVW5
C3	420	ASP	-	expression tag	UNP G1SVW5
C3	421	LYS	-	expression tag	UNP G1SVW5

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Chain	Residue	Modelled	Actual	Comment	Reference
C3	422	LYS	-	expression tag	UNP G1SVW5
C3	423	PRO	-	expression tag	UNP G1SVW5
C3	424	ALA	-	expression tag	UNP G1SVW5
C3	425	ALA	-	expression tag	UNP G1SVW5

• Molecule 41 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues			AltConf	Trace				
41	D3	293	Total 4815	C 1512	Н 2424	N 438	O 427	S 14	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D3	1	MET	-	initiating methionine	UNP G1SYJ6

• Molecule 42 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues			AltConf	Trace				
42	E3	216	Total	С	Н	Ν	0	\mathbf{S}	0	0
12	Ц	210	3616	1115	1887	329	282	3	0	0

• Molecule 43 is a protein called uL30.

Mol	Chain	Residues			AltConf	Trace				
43	F3	225	Total 3870	C 1205	Н 1995	N 358	O 303	S 9	0	0

• Molecule 44 is a protein called L7a.

Mol	Chain	Residues		Atoms						Trace
44	G3	233	Total 3905	C 1199	Н 2026	N 361	0 315	${S \atop 4}$	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G3	244	GLY	CYS	conflict	UNP G1STW0

• Molecule 45 is a protein called L9.



Mol	Chain	Residues			AltConf	Trace				
45	H3	190	Total 3113	C 954	H 1597	N 284	O 272	S 6	0	0

• Molecule 46 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues			AltConf	Trace				
46	I3	205	Total 3376	C 1056	Н 1712	N 321	О 274	S 13	0	0

• Molecule 47 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues			AltConf	Trace				
47	J3	170	Total 2761	C 861	Н 1399	N 254	0 241	S 6	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J3	0	GLN	-	insertion	UNP G1TUB8
J3	1	ARG	-	insertion	UNP G1TUB8
J3	2	PRO	-	insertion	UNP G1TUB8

• Molecule 48 is a protein called L13.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
48	L3	207	Total 3455	C 1047	Н 1781	N 348	0 275	$\frac{S}{4}$	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L3	74	ARG	HIS	conflict	UNP G1TKB3
L3	190	ARG	HIS	conflict	UNP G1TKB3

• Molecule 49 is a protein called Ribosomal protein L14.

Mol	Chain	Residues			Atom	IS			AltConf	Trace
49	M3	138	Total 2348	C 727	H 1211	N 221	0 182	S 7	0	0

• Molecule 50 is a protein called Ribosomal protein L15.



Mol	Chain	Residues			Atom	5			AltConf	Trace
50	N3	203	$\begin{array}{c} \text{Total} \\ 3450 \end{array}$	C 1072	H 1749	N 359	O 266	$\frac{S}{4}$	0	0

• Molecule 51 is a protein called 60S RIBOSOMAL PROTEIN UL13.

Mol	Chain	Residues			Atoms							
51	O3	199	Total 3408	C 1051	Н 1778	N 319	O 255	${ m S}{ m 5}$	0	0		

• Molecule 52 is a protein called uL22.

Mol	Chain	Residues			Atom	.S			AltConf	Trace
52	P3	153	Total 2516	C 777	Н 1274	N 241	0 215	S 9	0	0

• Molecule 53 is a protein called L18.

Mol	Chain	Residues			AltConf	Trace				
53	Q3	187	Total 3149	C 946	Н 1634	N 315	O 250	$\frac{S}{4}$	0	0

• Molecule 54 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues			AltConf	Trace				
54	R3	180	Total 3172	C 933	Н 1664	N 328	O 238	S 9	0	0

• Molecule 55 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues			Aton	ns			AltConf	Trace
55	S3	176	Total	С	Η	Ν	Ο	\mathbf{S}	0	0
		110	2970	930	1508	285	236	11	0	0

• Molecule 56 is a protein called eL21.

Mol	Chain	Residues				AltConf	Trace			
56	Т3	159	Total 2664	C 823	Н 1366	N 252	0 217	S 6	0	0

• Molecule 57 is a protein called L22.



Mol	Chain	Residues			Aton	ns			AltConf	Trace
57	U3	99	Total	C 510	H	N 141	0	S 2	0	0
			1042	519	833	141	147	2		

• Molecule 58 is a protein called eL14.

Mol	Chain	Residues			AltConf	Trace				
58	V3	131	Total 2018	C 618	Н 1039	N 184	0 172	${ m S}{ m 5}$	0	0

• Molecule 59 is a protein called uL23.

Mol	Chain	Residues			AltConf	Trace				
59	X3	118	Total 2003	C 618	Н 1036	N 181	O 167	S 1	0	0

• Molecule 60 is a protein called Ribosomal protein L26.

Mol	Chain	Residues			Atom	IS			AltConf	Trace
60	Y3	132	Total 2291	C 692	Н 1189	N 223	0 184	${ m S} { m 3}$	0	0

• Molecule 61 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues			Atom	S			AltConf	Trace
61	Z3	135	Total 2289	С 714	Н 1182	N 208	0 182	${ m S} { m 3}$	0	0

• Molecule 62 is a protein called uL15.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
62	a3	147	Total 2372	C 734	Н 1210	N 239	0 185	${S \atop 4}$	0	0

• Molecule 63 is a protein called eL29.

Mol	Chain	Residues			AltConf	Trace				
63	b3	104	Total 1768	C 527	Н 920	N 189	0 129	${ m S} { m 3}$	0	0

There are 19 discrepancies between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference
b3	227	ALA	-	expression tag	UNP G1SGR6
b3	228	PRO	-	expression tag	UNP G1SGR6
b3	229	VAL	-	expression tag	UNP G1SGR6
b3	230	PRO	-	expression tag	UNP G1SGR6
b3	231	ALA	-	expression tag	UNP G1SGR6
b3	232	GLN	-	expression tag	UNP G1SGR6
b3	233	ALA	-	expression tag	UNP G1SGR6
b3	234	PRO	-	expression tag	UNP G1SGR6
b3	235	PRO	-	expression tag	UNP G1SGR6
b3	236	LYS	-	expression tag	UNP G1SGR6
b3	237	GLY	-	expression tag	UNP G1SGR6
b3	238	ALA	-	expression tag	UNP G1SGR6
b3	239	GLN	-	expression tag	UNP G1SGR6
b3	240	PRO	-	expression tag	UNP G1SGR6
b3	241	PRO	-	expression tag	UNP G1SGR6
b3	242	ALA	-	expression tag	UNP G1SGR6
b3	243	LYS	-	expression tag	UNP G1SGR6
b3	244	ALA	-	expression tag	UNP G1SGR6
b3	245	PRO	-	expression tag	UNP G1SGR6

• Molecule 64 is a protein called eL30.

Mol	Chain	Residues			AltConf	Trace				
64	c3	98	Total 1555	C 481	Н 794	N 134	0 140	S 6	0	0

• Molecule 65 is a protein called eL31.

Mol	Chain	Residues			AltConf	Trace				
65	d3	107	Total 1818	C 560	Н 930	N 171	0 155	$\frac{\mathrm{S}}{2}$	0	0

• Molecule 66 is a protein called eL32.

Mol	Chain	Residues			Atom	IS			AltConf	Trace
66	e3	128	Total 2200	C 667	H 1147	N 216	0 165	${ m S}{ m 5}$	0	0

• Molecule 67 is a protein called eL33.

Mol	Chain	Residues			Atom	ıs			AltConf	Trace
67	f3	109	Total 1788	C 555	Н 912	N 174	0 143	$\frac{S}{4}$	0	0



• Molecule 68 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues			Aton	ns			AltConf	Trace
68	g3	114	Total 1905	C 566	Н 999	N 187	0 147	${ m S}{ m 6}$	0	0

• Molecule 69 is a protein called uL29.

Mol	Chain	Residues			Atom	IS			AltConf	Trace
69	h3	122	Total 2160	C 640	Н 1147	N 204	O 168	S 1	0	0

• Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues			Aton	ıs			AltConf	Trace
70	i3	102	Total 1746	C 520	Н 916	N 176	O 129	${ m S}{ m 5}$	0	0

• Molecule 71 is a protein called Ribosomal protein L37.

Mol	Chain	Residues			Aton	ıs			AltConf	Trace
71	j3	86	Total 1442	C 434	Н 737	N 155	0 111	${ m S}{ m 5}$	0	0

• Molecule 72 is a protein called L38.

Mol	Chain	Residues		L	Atom	S			AltConf	Trace
72	k3	69	Total 1206	C 366	Н 637	N 103	O 99	S 1	0	0

• Molecule 73 is a protein called eL39.

Mol	Chain	Residues		A	Atoms	5			AltConf	Trace
73	13	50	Total 927	C 286	Н 480	N 96	O 64	S 1	0	0

• Molecule 74 is a protein called 60S RIBOSOMAL PROTEIN EL40.

Mol	Chain	Residues		ŀ	Atoms	s			AltConf	Trace
74	m3	52	Total 895	C 266	Н 466	N 90	O 67	S 6	0	0

• Molecule 75 is a protein called 60s ribosomal protein l41.



Mol	Chain	Residues		ŀ	Atom	s			AltConf	Trace
75	n3	25	Total 528	C 145	Н 289	N 64	O 27	${ m S} { m 3}$	0	0

• Molecule 76 is a protein called eL42.

Mol	Chain	Residues			Aton	ıs			AltConf	Trace
76	03	104	Total 1775	C 533	Н 924	N 174	0 138	S 6	0	0

• Molecule 77 is a protein called ribosomal protein eL43.

Mol	Chain	Residues			Aton	ıs			AltConf	Trace
77	p3	91	Total 1466	C 445	Н 758	N 136	O 120	${f S}{7}$	0	0

• Molecule 78 is a protein called eL28.

Mol	Chain	Residues			Atom	IS			AltConf	Trace
78	r3	124	Total 2045	C 616	Н 1051	N 205	0 167	S 6	0	0

• Molecule 79 is a RNA chain called A/P-Site tRNA.

Mol	Chain	Residues			Ator	\mathbf{ns}			AltConf	Trace
79	q3	74	Total 2381	C 705	Н 805	N 286	O 512	Р 73	0	0

• Molecule 80 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues			Atom	IS			AltConf	Trace
80	t3	196	Total 3071	C 959	Н 1564	N 263	0 276	${ m S} 9$	0	0

• Molecule 81 is a protein called uL12.

Mol	Chain	Residues			Atom	S			AltConf	Trace
81	u3	153	Total 2378	C 722	Н 1218	N 218	O 217	${ m S} { m 3}$	0	0

• Molecule 82 is a RNA chain called mRNA.



Mol	Chain	Residues			Atom	ıs			AltConf	Trace
82	v3	18	Total 573	C 171	Н 192	N 65	0 127	Р 18	0	0

• Molecule 83 is a RNA chain called P/E-Site tRNA.

Mol	Chain	Residues			Ator	ns			AltConf	Trace
83	33	75	Total 2403	C 712	H 809	N 281	O 527	Р 74	0	0

• Molecule 84 is a protein called Ribosomal protein.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
84	w3	217	Total 3595	C 1113	Н 1854	N 312	O 307	S 9	0	0

• Molecule 85 is a protein called Sec61Beta.

Mol	Chain	Residues		_	Atom	IS			AltConf	Trace
85	1	15	Total 242	C 82	Н 117	N 20	O 22	S 1	0	0

• Molecule 86 is a protein called 60S ribosomal protein L24-like protein.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
86	W	63	Total 1069	C 337	Н 541	N 103	O 85	${ m S} { m 3}$	0	0

• Molecule 87 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
87	51	193	Total Mg 193 193	0
87	71	6	Total Mg 6 6	0
87	81	7	Total Mg 7 7	0
87	A2	74	Total Mg 74 74	0
87	F2	1	Total Mg 1 1	0
87	K2	1	Total Mg 1 1	0



Mol	Chain	Residues	Atoms	AltConf
87	M2	1	Total Mg 1 1	0
87	b2	1	Total Mg 1 1	0
87	g2	1	Total Mg 1 1	0
87	B3	3	Total Mg 3 3	0
87	J3	1	Total Mg 1 1	0
87	N3	1	Total Mg 1 1	0
87	P3	2	Total Mg 2 2	0
87	R3	1	Total Mg 1 1	0
87	V3	2	Total Mg 2 2	0
87	a3	1	Total Mg 1 1	0
87	e3	1	Total Mg 1 1	0
87	g3	1	Total Mg 1 1	0
87	33	1	Total Mg 1 1	0

Continued from previous page...

• Molecule 88 is BLASTICIDIN S (three-letter code: BLS) (formula: $C_{17}H_{26}N_8O_5$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues		Ate	oms			AltConf
88	51	1	Total	С	Η	Ν	0	0
00	51	T	55	17	25	8	5	0

 $\bullet\,$ Molecule 89 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
89	A2	2	Total Zn 2 2	0
89	b2	1	Total Zn 1 1	0
89	g3	1	Total Zn 1 1	0
89	j3	1	Total Zn 1 1	0
89	m3	1	Total Zn 1 1	0
89	03	1	Total Zn 1 1	0
89	p3	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: 28S Ribosomal RNA





PROTEIN DATA BANK

C2583	G2584 C2585	G2586 A7587		G2590 A2591	A2601	G2602	C2603	A2611	G2620		U2628 U2628		U2631	G2638	G2645	C2646	G2649		C2653 C2654	C2655	U2656 G2657	G2658	U2661	G2662 G2663		C2669 C2670	G2673	000	A2678	G2679 C2680	00075	C2684 C2685	G2686	U2687 G2688	C2689	<mark>G2694</mark> A2695	
A2696 A2697	G2698 C2699	G2700	C2702	<mark>62703</mark> C2704		U2708	C2709	C2/10 G2711	G2712	C2713 G2714	G2715	C2716	C2719	G2724	A2725	G2726 C2727	U2728	C2729	C2731	G2732 C2733	U2734	G2735	U2740	A2743	A2744	U2747	C2749 C2749	G2750 G2751	G2752	66125	G2756	A2757 G2758	G2759	62760 U2761	G2762 U2763	A2764	U2767
C2768 U2769	C2770 G2771	c2772	C2775	G2778	C2779 C2780	<mark>G2781</mark>	C2785	C2786	A2/8/ U2788	A2789	02791 C2791	C2792	G2794 C2794	A2795	G2797 C2797	A2798	A2812		C2817 C2818		G2823	U2826	17970	A2832	A2835	G2842	U2843 A2844	A2845	01075	A2849 A2850	62851 G2851	(1)855 (1)855	C2856	A2857 A2858	G2859	A2864	
A2870	C2875	A2879	U2893	G2896	G2897	G2901	C	A C	A C	υ.	A D	Ä	A C	G3597	C3598	C3601	C3602 G3603	A3604	C3605 113606		C3612	G3615	01050	C3622 C3623	A3624	G3625 G3626	A3635	C3636	03037 G3638	A3646	05004	A3649	A3652	A3662	A3663 G3664	C3667	
C3673	G3674	U3679	G3681	A3682 C3683	G3684 C3685	G3686	A3687	U3690	G3691 A3692		03697 U3697		0.37.04	G3710	A3711	N3712 U3713	G3714	A3717	A3718	G3720	U3721	A3723	A 3724 G3725	A3726	A37.27 A37.28	U3729	A3737	G37 <u>44</u>	A3748		C3752 G3753		A3756 • • • • • • • • • • • • • • • • • • •	U3758	A3759 A3760	C3761 U3762	A3/63
U3764	A3766	U3768	C3769 U3770	C3771 U3772	U3773	P 114	G3777	G3780	C3781	A3783	A3784 A3785	U3786	G3787	C37 89	03790 137	U3798	A3799	G3804		G3810 G3811	C3812 A 3813	U3814	A3817	U3818	63819 63820	A3821 113822	(3823 13823	A3025 A3825	C3826	C3834	C3835 A3836	C3837	03839 G3839	U3840	A3845	C3858	
<mark>G3859</mark> A3860	C3863	C3864	C3866	C3869	A3876	A3877	C3878 G3879	G3880	63881	G3888	63889	<mark>C3893</mark>	G 3897	G3898	A3901	A3902	A3905	A3906	G3907 A3908	C3909	C3910 C3911		03916 63916	C3924		A3936 C3937	63939 63939		A3942 A3943	G3944 A3045	63946 63946	<u>A3949</u>	U3950	G3951	G3956 U3957	G3958 U3959	
A3960 G3961	A3962 A3963	U3964	A3966	<mark>G3969</mark>	G3970	G3973	G3974 C3975	C3976	C3977 A	р.	A D	Ä	A C	С	C P	A	G4034 G4035	G4036	C4037 C4038	G4039	C4040 C4041	G4042	04043 U4044	G4045	A4046 A4047	A4048 114049	A4050	C4052	A4053	A4056	C4059		C4064 G4065	U4066 114067	U4068	04069 U4070 114071	
C4072 A4073	C4074 114075	G4076	A4085	G4086 G4087	C4088 G4089	G4090	G4091 G4092	G4093	G4094 G4095	C4096	64097 A4098	G4099	C4100	C4101 A	U	A C	Å	G4107 G4108	G4109	C4110		U4113	C4114	G4115 C4116	U4117 11418	C4119	04120 G4121	G4122 C4123	G4124	C4125 C4126	A4127	64128 G4129	C4130	C4132	C4133 C4134	G4135 G4136	C4137 C4138
A C	A		A	G4146	C4149 G4150	G4151	G4152 C4153	0 1 7 7 7 7	64156 A4157	C4158	C4162	U4163	G4166	G4167	G4168 G4169	A4170	C4171 A4172	G4173	C4176	C4177	G4183	G4184	U4188	G4191	A4192	C4193	U4202 A4203	C4204	C0754	G4209	C4211 C4211	A4212	C4223	G4226	U4229	C4230 C4231	
U4232 A4233	A4234 G4235	G4236	A4239	G4240 C4241	G4249	G4250	A4251	G4254	A4255 A4256	A4257	C4258	C4261	C4262	U4265	G4266 G4267	A4268	A4271	G4272	A4273 A4274	G4275	C4278	A4279	A4280 A4281	A4282	C4288	G4291	G4297		04303 C4303	A4304	04306 U4306	C4314		C4318	A4323	G4328 G4329	
G4330 G4331	C4332 C4333	00000	DOD EV	C4345	C4349 C4350		64355	G4373	04374 C4375	A4376	64377 A4378	A4379	C4387		A4390 G4391	G4392	G4393 A4394	<mark>U4395</mark>	A4396	C4402	U4406	010	04419 04420	C4421 A4422		G4425	G4433	U4437	C4444	CA 448	44449 A4449	04450	C4453	U4459	U4460 C4461	A4464	
U4465 C4466	A4474	G4475		A4480 U4481	U4482 C4483	A4484	G4489		04493	G4499	04500	A4503	C4505 C4505	C4506	A4507	A4511	U4512 A4513		G4520	C4525	G4528		64538	G4545	A4548	G4549	C4560 C4561	C4562	00070	04569 C4570	A4571	U4572 04573	U4574	G4575 U4576	G4586	A4589	
C4592	C4593	A4599	A4602	A4607	U4632		04636 G4637	11 2 2 2 2 2	C4645	G4649	64650 A4651	G4652	C4653	A4656	04657 G4658	G4659	C4667	U4668	A4669 C4670	C4671	A4672 U4673		04677 U4677	44687		A4691	C4695 C4696		04703 04703	44707	A4707 A4708	04709	G4713	G4719	C4720 G4721	C4725	





















•		
ARG ALY VAL CLU CLU CLU CLU CLU CLU SER CLU SER CLU SER CLU SER CLU SER CLU SER CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	89 142 143 144 144 144 144 144 144 152 167 167 184 184 184 184 101	
• Molecule 22: 40S ribos	somal protein S17	
Chain S2:	90%	• 9%
MET LYS SER LYS LYS LYS CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	L108 9121 9122 6133 ALA ALA VAL	
• Molecule 23: 40S ribos	somal protein uS13	
Chain T2:	90%	<mark>5%</mark> 5%
MET 82 82 865 865 865 865 8104 8108 8109 81108 8121 8131	K137 1145 VAL SER LYS LYS LYS LYS	
• Molecule 24: S19		
Chain U2:	95%	• •
MET PR0 d3 d3 A61 F92 F92 F92 G109 Q126 A135	K143 LIYS HITS	
• Molecule 25: 40S ribos	somal protein S20	
Chain V2:	76%	• 23%
MET ALLA ARG SER GLN TYR GLN TYR CLLU LEU LEU LEU LEU LEU LEU LEU CLR GLY GLY	LYS ALA PRO PRO GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU	H92 D78 H92 Q100 T101 T102 S103 S103 E113 E113 A117 ASP ALA
• Molecule 26: 40S ribos	somal protein S21	
Chain W2:	100%	
M1 D40 663 865 F83 F83		
• Molecule 27: Ribosom	al protein S15a	
Chain X2:	91%	•• 7%
MET HIS ALA SER SER ALA LEU MET MET MET MET MET MET MET	2 <mark>19</mark> 0	
• Molecule 28: Ribosom	al protein S23	



Chain Y2:	99%	·
G2 K 60 R 142 R 142		
• Molecule 29: 4	0S ribosomal protein S24	
Chain Z2:	84%	15%
MET ASN ASP ASP ASP A12 A127 A127 A127 CI27	LIS CLU SER TRP TRP TRP TRP TRP TRP TRP TRP TRP TR	
• Molecule 30: r	ibosomal protein eS25	
Chain a2:	36% · 62%	
R41 D42 D51 D51 L58 V62 L91 L91 L91 L91	ALLA CLITS ASP LYSS LYSS LYSS LYSS LYSS LYSS LYSS LY	VAL ARG ASP LYS LEU ASN ASN VAL
LEU PHE ASP LYS ALA THR TYR CYS LEU CYS LEU	CLU CLU PRAC PRAC PRAC PRAC PRAC PRAC PRAC PRAC	VAL SER LYS HIS ARG ALA GLN VAL ILE
TYR THR ARG ASN THR LYS GLY GLY ASP ALA ALA	ALA GLU ALA ALA	
• Molecule 31: 4	0S ribosomal protein S26	
Chain b2:	84% •	14%
MET T2 R5 R5 R5 R87	P101 P102 P1102 P1102 P1102 VAL ALA ALA ALA ALA ALA ALA ALA	
• Molecule 32: 4	0S ribosomal protein S27	
Chain c2:	98%	
MET P2 K36 C58 G58 H84		
• Molecule 33: 4	0S ribosomal protein S28	
Chain d2:	90%	10%
MET ASP THR STR HIS HIS F34 F34 F34 M35		
• Molecule 34: u	1014	



Chain e2:		100%			
02 D56 6					
• Molecule 35: 4	40S ribosomal p	rotein S30			
Chain f2:	41%		59%		
MET GLN GLN LEU PHE VAL ARG ALA GLN GLN LEU HIS THR	LEU GLU GLU GLY GLY GLY GLU THR VAL ALA GLN GLN	LLE LYS ALA HIS VAL ALA SER LEU GLU GLU GLV GLY TLE ALA	GLU GLU ASP GLN VAL LEU LEU LEU LEU ALA GLY THR FIN	GLU GLU GLU GLU THR LEU GLY GLN	GLY VAL GLU
ALA LEU SER THR LEU CLU VAL ALA GLY MET LEU	GLY GLY LYS LYS VAL GLY GLY F121 F122 F122	K125			
• Molecule 36: 6	2S31				
Chain g2:		100%			
K83 K90 N91 K92 K92 A101 V102 L103	E110				
• Molecule 37: r	ribosomal protei	n RACK1			
Chain h2:	•	99%			
12 R8 H1 4 C20 C20 C20 C20 C20 C20 C20 C20 C20 C20	A34 R47 D48 E49 C455 C455 C455 C455 C455 C455 C455 C4	St 15 St 15 St 12 St 60 St 160 St 160 St 164	G1 69 K1 72 L1 73 S209 W219 D220	L221 D234 R245 V274 I275	S276 S279 K280 A290 A290 P294
V312 T313 T314					
• Molecule 38: I	18				
Chain A3:		98%		·	
62 R3 V45 A191 K192 R247					
• Molecule 39: 1	ıL3				
Chain B3:		97%		•••	
MET 82 82 K143 R261 R264 D329	DB95 DB95 ARC TILE ALA CLYS CLYS CLU CLYS CLU CLU ALA				
• Molecule 40: 1	JL4				


Chain C3:	84% · 15%	-
MET A2 D35 V79 M95	R113 117 117 117 117 117 117 117	ALA ALA ALA LYS
LYS PRO ALA ALA ASP LYS LYS ALA	AILA LYNS ARG GLY PRO PRO PRO AILA AILA AILA	
• Molecule	41: 60S ribosomal protein L5	
Chain D3:	• 97% ••	
MET GLY G26 G26 G137	1154 M208 12295 A 295 BEU SER	
• Molecule	42: 60S ribosomal protein L6	
Chain E3:	74% • 26%	
MET ALA GLY GLU GLU LYS ALA ALA	ALA LYS PRO ASP PRO ASP ASP ASP ASP ASP ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	LYS ARG GLU LYS
VAL L92 G100 GLY ASP ASN	d105 RX224 LEU ARG ARG CLU CLU CLU CLU CLU CLU CLU CLU	
• Molecule	43: uL30	
Chain F3:	90% · 10%	-
LEU PHE ALA ASN ASN TLE ARG GLU	LYS LYS LYS LYS LYS LEU LYS LYS LYS LYS LYS LYS LYS LYS LYS N23 ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG	
• Molecule	44: L7a	
Chain G3:	89% 7% ·	
LYS V80 197 198 198 T105	R106 F107 F107 V139 V139 V139 V157 V157 V159 V157 V139 C17 A176 V194 VAL VAL VAL P157 A176 A176 V194 V194 V194 V194 V194 V232 Y234 V235 Y234 V232 Y234 Y235 Y249 <td>E313 L314 A315 K317 I318</td>	E313 L314 A315 K317 I318
G319		
• Molecule	45: L9	
Chain H3 [.]	08%	





• Molecule 46: 60S ribosomal protein L10

Chain I3:	95%	·
MET R3 C2 SER SER SER ALA ALA ASP ASP ASP ASP ASP		
• Molecule 47: 60S	5 ribosomal protein L11	
Chain J3:	91% .	6%
MET ALA ALA ALA ARG GLN GLN GLN K8 CLU K8 CLU	140 5140 1175 1175 1175	
• Molecule 48: L13	3	
Chain L3:	95%	••
MET A2 R21 R21 R21 F63 A112 G137 A180	R183 A202 A203 A203 LYS LYS LYS	
• Molecule 49: Rib	posomal protein L14	
Chain M3:	61% · 37%	_
MET V2 L62 M111 M120 M139 S139 FR0 FR0	LYS LYS VAL VAL VAL ALA ALA ALA ALA ALA ALA ALA	ALA PRO GLN LYS ALA ALA
GLY GLN LYS ALA ALA GLN PRO PRO PRO FRO CLY GLN GLY	LYS PRO GLA CLYS CLYS CLYS PRO PRO LYS CLYS ALA ALA ALA	
• Molecule 50: Rib	posomal protein L15	
Chain N3:	98%	·
G2 W11 R12 P76 K77 G78 G78 S100 R204		
• Molecule 51: 60S	S RIBOSOMAL PROTEIN UL13	
Chain O3:	97%	••
MET ALA GLV GLV GS HI K170 K170 K170		
• Molecule 52: uL	22	
	WORLDWIDE PROTEIN DATA BANK	

Chain P3:	76%	• 23%
MET ARG ARG ARA ALA ALA VAL EER SER GLN ARG GLN ARG ARA ALA MET	V2 N101 E154 GLN TLE FR0 GLU GLU GLU CLU CLU CLU CLU CLU CLU CLU CLU CLU C	LYS LYS LYS LYS LYS LYS MET MET ARG GLU
• Molecule 53: L18		
Chain Q3:	97%	•••
MET 23 123 R33 R33 R33 R33 R33 R34 R134 N188 N188		
• Molecule 54: 60S rib	posomal protein L19	
Chain R3:	88%	• 8%
MET 82 82 89 89 193 193 193 1125	M130 V131 V131 V131 V134 M134 V135 V135 V135 C1U C1U C1U C1U C1U C1U C1U C1U C1U C1U	SAT
• Molecule 55: 60S rib	posomal protein L18a	
Chain S3:	98%	·
M1 45 7145 8166 8166 8176		
• Molecule 56: eL21		
Chain T3:	98%	•
12 8104 8107 1108 1160		
• Molecule 57: L22		
Chain U3:	75%	• 23%
MET ALA PRO PRO LYS LYS LYS LYS GLY GLY GLY CYS LYS LYS	17 17 143 143 143 143 15 651 651 651 116 116 610 610 610 610 610 610 610 610 610 610 610 610 610 610 610 610	7.12.4 1.12.4
• Molecule 58: eL14		
Chain V3:	99%	
810 611 118 A140		
• Molecule 59: uL23		

WORLDWIDE PROTEIN DATA BANK

Chain X3:	74% · 24%	
MET ALA PRO LYS ALA LYS LYS GLU	ALA ALA PRO PRO PRO PRO PRO PRO CVAL CVS CVAL CVS CVAL CVS CVAL CVS CVAL CVS CVAL CVS CVAL CVS CVAL CVS CVS CVS CVS CVS CVS CVS CVS CVS CVS	
• Molecule	60: Ribosomal protein L26	
Chain Y3:	99% •	
M1 K2 K132		
• Molecule	61: 60S ribosomal protein L27	
Chain Z3:	98% ···	
G2 S70 R84 Y85 F136		
• Molecule	62: uL15	
Chain a3:	92% 8%	
MET VAL ALA ALA LYS CYS GLN HIS	ARG GLY GLY FIA FIA FIA FIA FIA FIA	
• Molecule	63: eL29	
Chain b3:	• 41% • 58%	
MET A25 A69 T7 2	AT A A A A A A A A A A A A A A A A A A	ILE LYS ALA GLN GLN GLN
ALA GLN ILE LYS SER LYS GLY LYS	ULY ALA ALA ALA ALA ALA ALA ALA A	PRU LYS ALA GLN
ALA GLN LYS LYS PRO LYS ALA GLN	ALA CLIN LYS LYS LYS LYS ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	
• Molecule	64: eL30	
Chain c3:	80% 5% 15%	
MET VAL ALA ALA LYS LYS THR LYS	IVS 111 111 111 111 111 112 112 11	
• Molecule	65: eL31	
Chain d3:	99% .	
	WORLDWIDE PROTEIN DATA BANK	

• Molecule 66: eL32		
Chain e3:	99%	
A2 P42 L129		
\bullet Molecule 67: eL33		
Chain f3:	99%	•
82 N20 D37 1110		
• Molecule 68: 60S ribose	omal protein L34	
Chain g3:	90%	10%
LEU PRO RLY ARG CYS CYS CYS CLU GLU MET MET MET V106 K108 K108	A111 A112 S113 A14 ALA	
• Molecule 69: uL29		
Chain h3:	98%	·
A2 R66 E67 A123 A123		
• Molecule 70: 60S ribose	omal protein L36	
Chain i3:	84%	• 13%
MET GLY PHE ARG CLY GLY GLY ARG ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	M(1 L90 S91 A101 A103 A103 A103 A103	
• Molecule 71: Ribosoma	l protein L37	
Chain j3:	89%	11%
MET T2 ARG ALA ALA ALA SER SER SER SER SER		
• Molecule 72: L38		



Chain k3:
• Molecule 73: eL39
Chain 13: 100%
There are no outlier residues recorded for this chain.
• Molecule 74: 60S RIBOSOMAL PROTEIN EL40
Chain m3: 41% 59%
MET MET CILN CILN CILN CILN CILN CILN CILN CILN
ILE CLN GLN GLN GLN HIS CLEU LEU LEU LEU CLEU GLY GLY CLO
• Molecule 75: 60s ribosomal protein l41
Chain n3:
M1 R2 823 X25
• Molecule 76: eL42
Chain o3: 71% · 27%
MET VAL ALA ALA ALA ALA ALA ALA CUU CUU CUU CUU CUU CUU CUU CUU CUU CU
\bullet Molecule 77: ribosomal protein eL43
Chain p3: 81% • 17%
MET ARG ALA ALA ALA ALA ALA ALA ALA ALA ALA AL
• Molecule 78: eL28
Chain r3: • 9%
MET S92 S92 S92 S92 A110 A110 A125







Chain 33:	55%	45%	
G1 C2 C3 C4 C4 C4 C4 C4 C4 C5 C1 C2 C3 C3 C4 C4 C3 C3 C3 C3 C3 C3 C3 C3 C3 C3 C3 C3 C3	C11 C15 C16 C16 C16 C16 C16 C18 C28 C28 C28 C28 C28 C28 C32 C32 C32 C32 C32 C32 C32 C32 C32 C32	450 G82 053 053 055 055 457 457 457 456 456 055 055 055 055 055 055 055 055 070 071 071	
• Molecule 8	4: Ribosomal protein		
Chain w3:	37% 95%		5%
M1 82 86 86 87 13 73 73 73	L10	152 V53 S57 S57 F61 F63 F63 F63 F63 C66 C66 C66 C66 C66 C66 C66 C66 C71 C71	V80 V81 182 P83 P83 A89 A89 A89 A89 A89 A89 A89 A89
F110 L111 A112 A112 K117 K118 Q119 Q119	P121 R122 L124 L124 C125 C125 C127 C127 C128 R130 R131 C132 R133 R133 R133 R133 R133 R133 R133 R133 R133 R133 R133 R128 R	H1135 H1141 H141 H143 H143 H144 H144 V145 D149 D149 H155 T155	F1175 G158 K161 K161 A168 A168 A168 A168 A188 A188 A188 A188 A188 A188
S192 S192 L194 K195 N196 N197	1199 1200 1205 1205 1216 1216		
• Molecule 8	5: Sec61Beta		
Chain 1:	93%		7%
G54 T60 G65 V68			
• Molecule 8	6: 60S ribosomal protein L24-lil	ke protein	
Chain W:	47%	53%	
M1 063 SER GLU GLU GLU GLN LYS CLU	LYS THR THR ARG ARG ALA ALA CVAL LYS PHE GLN THR ALA ALA ALA ALA ALA ALA ALA ALA ALA	LIS ASN ASN GLN CLN CLU PRO FRO GLU CLN GLU GLN GLN GLN ALA ALA ALA	ALA LVS GLU ALA LVS LVS LVS GLN GLN

ALA SER LYS LYS LYS LYS ALA ALA ALA ALA ALA CYS GLU LYS GLU



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29879	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose $(e^-/\text{\AA}^2)$	41.9	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	79000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.172	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	405.0, 405.0, 405.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	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: ZN, MG, BLS

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

Mal	Chain	Bond lengths		Bond angles	
NIOI		RMSZ	# Z > 5	RMSZ	# Z > 5
1	51	1.13	47/86836~(0.1%)	1.56	873/135406~(0.6%)
2	71	1.03	1/2858~(0.0%)	1.31	19/4455~(0.4%)
3	81	1.43	6/3581~(0.2%)	1.32	23/5577~(0.4%)
4	A2	0.94	4/41517~(0.0%)	1.33	306/64674~(0.5%)
5	B2	0.58	0/1747	0.77	0/2374
6	C2	0.63	0/1756	0.78	0/2350
7	D2	0.69	0/1753	0.74	0/2369
8	E2	0.54	0/1793	0.72	0/2413
9	F2	0.55	0/2118	0.70	0/2849
10	G2	0.53	0/1492	0.77	0/2005
11	H2	0.51	0/1946	0.82	0/2590
12	I2	0.53	0/1510	0.77	0/2022
13	J2	0.56	0/1715	0.80	0/2287
14	K2	0.58	1/1550~(0.1%)	0.83	1/2069~(0.0%)
15	L2	0.54	0/834	0.79	0/1125
16	M2	0.68	0/1195	0.73	0/1597
17	N2	0.46	0/918	0.80	1/1233~(0.1%)
18	O2	0.65	0/1226	0.74	0/1649
19	P2	0.60	0/1029	0.74	0/1380
20	Q2	0.61	0/1017	0.80	1/1358~(0.1%)
21	R2	0.57	0/1146	0.76	0/1534
22	S2	0.53	0/1082	0.73	0/1452
23	T2	0.55	0/1208	0.79	0/1618
24	U2	0.56	0/1115	0.78	0/1493
25	V2	0.53	0/805	0.80	1/1081~(0.1%)
26	W2	0.56	0/643	0.73	0/860
27	X2	0.70	0/1051	0.78	1/1406~(0.1%)
28	Y2	0.71	0/1116	0.76	0/1490
29	Z2	0.53	0/1028	0.78	0/1366
30	a2	0.51	0/604	0.82	0/810
31	b2	0.67	0/828	0.74	0/1109
32	c2	0.54	0/665	0.68	0/891



Mol Chain		Bond lengths		Bond angles		
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5	
33	d2	0.51	0/490	0.84	0/656	
34	e2	0.64	0/470	0.72	0/623	
35	f2	0.50	0/447	0.78	0/587	
36	g2	0.49	0/567	0.80	0/753	
37	h2	0.47	0/2493	0.75	1/3394~(0.0%)	
38	A3	0.86	0/1925	0.79	0/2581	
39	B3	0.76	0/3240	0.73	0/4339	
40	C3	0.82	1/2937~(0.0%)	0.79	0/3946	
41	D3	0.67	0/2437	0.76	1/3264~(0.0%)	
42	E3	0.67	0/1762	0.77	0/2362	
43	F3	0.87	1/1911~(0.1%)	0.78	0/2549	
44	G3	1.57	1/1909~(0.1%)	0.90	5/2566~(0.2%)	
45	H3	0.70	0/1535	0.78	0/2063	
46	I3	0.76	0/1702	0.74	0/2272	
47	J3	0.70	1/1385~(0.1%)	0.78	0/1852	
48	L3	0.69	0/1705	0.76	0/2283	
49	M3	0.76	0/1158	0.81	0/1547	
50	N3	0.83	0/1746	0.78	0/2338	
51	O3	0.83	0/1662	0.76	0/2222	
52	P3	0.82	0/1268	0.75	0/1700	
53	Q3	0.84	0/1539	0.80	0/2054	
54	R3	0.69	0/1524	0.90	0/2013	
55	S3	0.81	1/1501~(0.1%)	0.75	0/2012	
56	Τ3	0.79	0/1326	0.74	0/1770	
57	U3	0.59	0/823	0.80	1/1104~(0.1%)	
58	V3	0.80	0/993	0.76	0/1332	
59	X3	0.73	0/984	0.76	0/1323	
60	Y3	0.78	0/1119	0.75	0/1488	
61	Z3	0.67	0/1130	0.77	0/1507	
62	a3	0.81	0/1191	0.73	0/1590	
63	b3	0.57	0/861	0.78	0/1138	
64	c3	0.68	0/771	0.77	1/1034~(0.1%)	
65	d3	0.71	0/903	0.73	0/1216	
66	e3	0.81	0/1071	0.78	0/1429	
67	f3	0.88	0/895	0.80	0/1198	
68	g3	0.72	0/916	0.82	0/1220	
69	h3	0.71	0/1021	0.76	0/1348	
70	i3	0.65	0/841	0.76	0/1112	
71	j3	0.85	0/720	0.78	0/952	
72	k3	0.62	0/575	0.82	0/761	
73	13	0.74	0/459	0.77	0/608	
74	m3	0.62	0/435	0.76	0/575	
75	n3	0.65	0/240	1.05	0/305	



		Bond lengths		Bond angles	
Mol	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
76	03	0.70	0/864	0.75	0/1140
77	p3	0.87	0/718	0.86	0/953
78	r3	0.80	2/1010~(0.2%)	0.78	0/1354
79	q3	0.69	0/1759	1.16	12/2733~(0.4%)
80	t3	0.38	0/1530	0.83	2/2064~(0.1%)
81	u3	0.39	0/1174	0.81	0/1582
82	v3	0.59	0/425	0.89	0/659
83	33	0.73	0/1780	1.11	6/2773~(0.2%)
84	w3	0.41	0/1769	0.85	2/2371~(0.1%)
85	1	0.42	0/129	0.63	0/173
86	W	0.71	0/541	0.54	0/720
All	All	0.94	66/235968~(0.0%)	1.26	1257/346400~(0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	51	0	14
2	71	0	1
3	81	0	1
4	A2	0	4
5	B2	0	1
8	E2	0	1
9	F2	0	1
10	G2	0	1
11	H2	0	7
12	I2	0	1
13	J2	0	4
15	L2	0	2
18	O2	0	3
20	Q2	0	2
21	R2	0	2
22	S2	0	1
23	T2	0	3
24	U2	0	1
27	X2	0	2
29	Z2	0	1
30	a2	0	1
37	h2	0	1
38	A3	0	1



Mol	Chain	#Chirality outliers	#Planarity outliers
39	B3	0	1
40	C3	0	4
42	E3	0	1
43	F3	0	1
44	G3	0	11
45	H3	0	2
47	J3	0	2
48	L3	0	3
49	M3	0	2
50	N3	0	5
51	O3	0	3
52	P3	0	1
53	Q3	0	2
54	R3	0	2
55	S3	0	2
56	Τ3	0	2
57	U3	0	2
59	X3	0	1
61	Z3	0	2
63	b3	0	2
64	c3	0	3
66	e3	0	1
67	f3	0	1
69	h3	0	2
70	i3	0	3
75	n3	0	1
76	03	0	1
77	p3	0	1
78	r3	0	1
80	t3	0	6
84	w3	0	2
All	All	0	129

The worst 5 of 66 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	G3	117	GLN	CB-CG	62.24	3.20	1.52
1	51	1966	С	N1-C6	41.23	1.61	1.37
3	81	151	G	C6-N1	29.84	1.60	1.39
3	81	151	G	N1-C2	25.61	1.58	1.37
3	81	151	G	N3-C4	22.98	1.51	1.35



Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	51	1966	С	C6-N1-C2	-187.56	45.27	120.30
1	51	1966	С	N1-C2-N3	-136.00	24.00	119.20
1	51	1966	С	N3-C4-C5	-65.39	95.74	121.90
1	51	1966	С	C4-C5-C6	-57.09	88.85	117.40
1	51	1966	С	C6-N1-C1'	29.32	155.99	120.80

The worst 5 of 1257 bond angle outliers are listed below:

There are no chirality outliers.

5 of 129 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	51	1106	A	Sidechain
1	51	221	С	Sidechain
1	51	41	С	Sidechain
1	51	497	G	Sidechain
1	51	727	С	Sidechain

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	\mathbf{ntiles}
5	B2	215/295~(73%)	189 (88%)	26 (12%)	0	100	100
6	C2	211/264~(80%)	192~(91%)	19 (9%)	0	100	100
7	D2	219/259~(85%)	205~(94%)	14 (6%)	0	100	100
8	E2	226/281~(80%)	209~(92%)	17 (8%)	0	100	100
9	F2	260/262~(99%)	232~(89%)	27~(10%)	1 (0%)	30	63
10	G2	181/205~(88%)	162 (90%)	18 (10%)	1 (1%)	22	55



α \cdots 1	C		
Continued	trom	previous	page
00111111000	J. 0110	proceedae	p ~ g ~

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
11	H2	235/262~(90%)	184 (78%)	47 (20%)	4 (2%)	$\overline{7}$	34
12	I2	181/190~(95%)	169 (93%)	12~(7%)	0	100	100
13	J2	204/206~(99%)	168 (82%)	33 (16%)	3 (2%)	8	37
14	K2	183/194~(94%)	157 (86%)	26 (14%)	0	100	100
15	L2	94/151~(62%)	86 (92%)	8 (8%)	0	100	100
16	M2	139/158~(88%)	129 (93%)	10 (7%)	0	100	100
17	N2	115/123~(94%)	96 (84%)	19 (16%)	0	100	100
18	O2	147/149~(99%)	136 (92%)	11 (8%)	0	100	100
19	P2	134/168~(80%)	122 (91%)	12 (9%)	0	100	100
20	Q2	118/145~(81%)	106 (90%)	11 (9%)	1 (1%)	16	49
21	R2	140/157~(89%)	126 (90%)	12 (9%)	2 (1%)	9	37
22	S2	130/145~(90%)	122 (94%)	8 (6%)	0	100	100
23	Τ2	142/152~(93%)	119 (84%)	22 (16%)	1 (1%)	19	52
24	U2	139/145~(96%)	125 (90%)	12 (9%)	2 (1%)	9	37
25	V2	98/130~(75%)	92 (94%)	6 (6%)	0	100	100
26	W2	81/83~(98%)	72 (89%)	9 (11%)	0	100	100
27	X2	127/139~(91%)	117 (92%)	10 (8%)	0	100	100
28	Y2	139/141~(99%)	126 (91%)	11 (8%)	2 (1%)	9	37
29	Z2	122/146~(84%)	109 (89%)	13 (11%)	0	100	100
30	a2	73/198~(37%)	65~(89%)	8 (11%)	0	100	100
31	b2	99/117~(85%)	89 (90%)	10 (10%)	0	100	100
32	c2	81/84~(96%)	76 (94%)	5~(6%)	0	100	100
33	d2	60/69~(87%)	58 (97%)	2(3%)	0	100	100
34	e2	53/55~(96%)	50 (94%)	3~(6%)	0	100	100
35	f2	53/133~(40%)	49 (92%)	4 (8%)	0	100	100
36	g2	66/68~(97%)	53~(80%)	13~(20%)	0	100	100
37	h2	$311/313$ ($\overline{99\%}$)	261 (84%)	50 (16%)	0	100	100
38	A3	$244/24\overline{6\ (99\%)}$	205 (84%)	36~(15%)	3 (1%)	11	40
39	B3	392/403~(97%)	354 (90%)	38 (10%)	0	100	100
40	C3	$360/425~(\overline{85\%})$	330 (92%)	$30 \ (8\%)$	0	100	100
41	D3	291/297~(98%)	257 (88%)	32 (11%)	2 (1%)	19	52



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
42	E3	208/291~(72%)	189 (91%)	19 (9%)	0	100	100
43	F3	223/249~(90%)	208~(93%)	15~(7%)	0	100	100
44	G3	227/241~(94%)	188 (83%)	35~(15%)	4 (2%)	7	34
45	H3	188/190~(99%)	175 (93%)	13 (7%)	0	100	100
46	I3	201/214~(94%)	178 (89%)	23~(11%)	0	100	100
47	J3	168/181~(93%)	150 (89%)	17 (10%)	1 (1%)	22	55
48	L3	205/211~(97%)	185 (90%)	18 (9%)	2 (1%)	13	44
49	M3	136/218~(62%)	123 (90%)	13 (10%)	0	100	100
50	N3	201/203~(99%)	179 (89%)	22 (11%)	0	100	100
51	O3	197/203~(97%)	182 (92%)	15 (8%)	0	100	100
52	P3	151/199~(76%)	143 (95%)	8 (5%)	0	100	100
53	Q3	185/188~(98%)	170 (92%)	15 (8%)	0	100	100
54	R3	178/196~(91%)	156 (88%)	19 (11%)	3 (2%)	7	34
55	S3	174/176~(99%)	157 (90%)	16 (9%)	1 (1%)	22	55
56	T3	157/159~(99%)	146 (93%)	11 (7%)	0	100	100
57	U3	97/128~(76%)	77 (79%)	20 (21%)	0	100	100
58	V3	129/131~(98%)	117 (91%)	12 (9%)	0	100	100
59	X3	116/156~(74%)	99~(85%)	15~(13%)	2 (2%)	7	34
60	Y3	130/132~(98%)	121 (93%)	9~(7%)	0	100	100
61	Z3	133/135~(98%)	113 (85%)	18 (14%)	2 (2%)	8	37
62	a3	145/160~(91%)	133 (92%)	12 (8%)	0	100	100
63	b3	100/245~(41%)	95~(95%)	5 (5%)	0	100	100
64	c3	96/115~(84%)	87 (91%)	8 (8%)	1 (1%)	13	44
65	d3	105/107~(98%)	93~(89%)	12 (11%)	0	100	100
66	e3	126/128~(98%)	116 (92%)	10 (8%)	0	100	100
67	f3	107/109 (98%)	94 (88%)	13(12%)	0	100	100
68	g3	112/126~(89%)	100 (89%)	12 (11%)	0	100	100
69	h3	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
70	i3	100/117~(86%)	93 (93%)	7 (7%)	0	100	100
71	j3	$84/97~(8\overline{7\%})$	74 (88%)	10 (12%)	0	100	100
72	k3	67/69~(97%)	54 (81%)	13 (19%)	0	100	100



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
73	13	48/50~(96%)	41 (85%)	7 (15%)	0	100 100
74	m3	50/128~(39%)	46 (92%)	4 (8%)	0	100 100
75	n3	23/25~(92%)	20 (87%)	2 (9%)	1 (4%)	2 20
76	03	102/142~(72%)	93~(91%)	9 (9%)	0	100 100
77	p3	89/109 (82%)	72 (81%)	16 (18%)	1 (1%)	12 42
78	r3	122/137~(89%)	111 (91%)	11 (9%)	0	100 100
80	t3	194/318~(61%)	152 (78%)	41 (21%)	1 (0%)	25 58
81	u3	151/195~(77%)	127 (84%)	24 (16%)	0	100 100
84	w3	215/217~(99%)	181 (84%)	31 (14%)	3 (1%)	9 37
85	1	13/15~(87%)	7 (54%)	5 (38%)	1 (8%)	1 11
86	W	61/134~(46%)	50 (82%)	11 (18%)	0	100 100
All	All	11697/13624~(86%)	10406 (89%)	1246 (11%)	45 (0%)	32 63

 $5~{\rm of}~45$ Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	H2	34	THR
13	J2	105	ASP
23	T2	137	LYS
28	Y2	61	GLN
54	R3	85	ALA

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
5	B2	180/245~(74%)	179~(99%)	1 (1%)	84	88
6	C2	194/229~(85%)	192 (99%)	2 (1%)	73	80
7	D2	187/208~(90%)	187 (100%)	0	100	100
8	E2	189/232~(82%)	189 (100%)	0	100	100
9	F2	224/224~(100%)	223 (100%)	1 (0%)	89	91



Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
10	G2	158/171~(92%)	158 (100%)	0	100	100
11	H2	207/227~(91%)	204 (99%)	3 (1%)	62	75
12	I2	165/170~(97%)	164 (99%)	1 (1%)	84	88
13	J2	178/178~(100%)	178 (100%)	0	100	100
14	K2	161/168~(96%)	159 (99%)	2 (1%)	67	77
15	L2	87/127~(68%)	85 (98%)	2 (2%)	45	63
16	M2	130/143~(91%)	130 (100%)	0	100	100
17	N2	99/104~(95%)	97~(98%)	2 (2%)	50	68
18	O2	130/130~(100%)	130 (100%)	0	100	100
19	P2	106/130~(82%)	103 (97%)	3 (3%)	38	59
20	Q2	109/130~(84%)	108 (99%)	1 (1%)	75	82
21	R2	117/129~(91%)	114 (97%)	3 (3%)	41	61
22	S2	119/131~(91%)	118 (99%)	1 (1%)	79	84
23	Τ2	125/132~(95%)	122 (98%)	3 (2%)	44	62
24	U2	111/115~(96%)	111 (100%)	0	100	100
25	V2	92/115~(80%)	92 (100%)	0	100	100
26	W2	67/67~(100%)	67 (100%)	0	100	100
27	X2	112/119~(94%)	111 (99%)	1 (1%)	75	82
28	Y2	113/113~(100%)	113 (100%)	0	100	100
29	Z2	107/126~(85%)	107 (100%)	0	100	100
30	a2	66/167~(40%)	63~(96%)	3 (4%)	23	47
31	b2	88/99~(89%)	85 (97%)	3 (3%)	32	55
32	c2	75/76~(99%)	74 (99%)	1 (1%)	65	76
33	d2	55/62~(89%)	55 (100%)	0	100	100
34	e2	48/48 (100%)	48 (100%)	0	100	100
35	f2	46/106 (43%)	46 (100%)	0	100	100
36	g2	61/61~(100%)	61 (100%)	0	100	100
37	h2	272/272~(100%)	270 (99%)	2 (1%)	81	86
38	A3	189/189~(100%)	187 (99%)	2 (1%)	70	79
39	B3	342/348~(98%)	338~(99%)	4 (1%)	67	77
40	C3	302/347~(87%)	300 (99%)	2 (1%)	81	86



Mol	Chain	Analysed	Rotameric	Outliers	ers Percent	
41	D3	247/250~(99%)	246 (100%)	1 (0%)	89	91
42	E3	190/251~(76%)	189 (100%)	1 (0%)	86	90
43	F3	196/218~(90%)	196 (100%)	0	100	100
44	G3	200/206~(97%)	198 (99%)	2 (1%)	73	80
45	H3	169/169~(100%)	167 (99%)	2 (1%)	67	77
46	I3	175/181~(97%)	174 (99%)	1 (1%)	84	88
47	J3	143/152~(94%)	142 (99%)	1 (1%)	81	86
48	L3	172/176~(98%)	171 (99%)	1 (1%)	84	88
49	M3	117/161~(73%)	115 (98%)	2 (2%)	56	72
50	N3	171/171~(100%)	171 (100%)	0	100	100
51	O3	171/173~(99%)	171 (100%)	0	100	100
52	P3	134/175~(77%)	134 (100%)	0	100	100
53	Q3	164/165~(99%)	162 (99%)	2 (1%)	67	77
54	R3	159/175~(91%)	157 (99%)	2 (1%)	65	76
55	S3	157/157~(100%)	157 (100%)	0	100	100
56	Т3	139/139~(100%)	138 (99%)	1 (1%)	81	86
57	U3	89/114 (78%)	89 (100%)	0	100	100
58	V3	101/101 (100%)	100 (99%)	1 (1%)	73	80
59	X3	106/134~(79%)	106 (100%)	0	100	100
60	Y3	123/123~(100%)	122 (99%)	1 (1%)	79	84
61	Z3	117/117~(100%)	117 (100%)	0	100	100
62	a3	119/127~(94%)	119 (100%)	0	100	100
63	b3	84/184~(46%)	83~(99%)	1 (1%)	67	77
64	c3	84/98~(86%)	83 (99%)	1 (1%)	67	77
65	d3	98/98~(100%)	97~(99%)	1 (1%)	73	80
66	e3	114/114 (100%)	114 (100%)	0	100	100
67	f3	88/88 (100%)	88 (100%)	0	100	100
68	g3	98/106~(92%)	98 (100%)	0	100	100
69	h3	109/109~(100%)	108 (99%)	1 (1%)	75	82
70	i3	86/96~(90%)	85 (99%)	1 (1%)	67	77
71	j3	73/80~(91%)	73 (100%)	0	100	100



Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
72	k3	64/64~(100%)	64 (100%)	0	100	100
73	13	47/47~(100%)	47 (100%)	0	100	100
74	m3	48/116~(41%)	48 (100%)	0	100	100
75	n3	24/24~(100%)	24 (100%)	0	100	100
76	03	92/121~(76%)	90~(98%)	2(2%)	47	64
77	p3	74/87~(85%)	73~(99%)	1 (1%)	62	75
78	r3	108/121~(89%)	108 (100%)	0	100	100
80	t3	164/258~(64%)	161 (98%)	3 (2%)	54	71
81	u3	126/163~(77%)	126 (100%)	0	100	100
84	w3	195/196~(100%)	192~(98%)	3(2%)	60	74
85	1	13/13~(100%)	13 (100%)	0	100	100
86	W	55/109~(50%)	55 (100%)	0	100	100
All	All	10214/11565~(88%)	10139 (99%)	75 (1%)	80	86

 $5~{\rm of}~75$ residues with a non-rotameric side chain are listed below:

Mol	Chain	\mathbf{Res}	Type
54	R3	173	ARG
80	t3	197	SER
58	V3	18	LEU
70	i3	23	LYS
23	Τ2	121	ARG

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 106 such side chains are listed below:

Mol	Chain	Res	Type
45	H3	79	ASN
54	R3	130	ASN
84	w3	40	ASN
47	J3	112	HIS
51	O3	50	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	51	3589/3788~(94%)	1190 (33%)	53~(1%)



Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	71	119/120~(99%)	43 (36%)	0
3	81	149/151~(98%)	45 (30%)	0
4	A2	1718/1818 (94%)	607~(35%)	31 (1%)
79	q3	70/74~(94%)	40 (57%)	0
82	v3	17/18~(94%)	12 (70%)	0
83	33	74/75~(98%)	29~(39%)	2(2%)
All	All	5736/6044~(94%)	1966~(34%)	86 (1%)

5 of 1966 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	51	4	G
1	51	7	С
1	51	8	U
1	51	14	С
1	51	18	С

5 of 86 RNA pucker outliers are listed below:

Mol	Chain	\mathbf{Res}	Type
4	A2	241	G
4	A2	870	А
4	A2	434	G
4	A2	688	U
4	A2	1253	А

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 308 ligands modelled in this entry, 307 are monoatomic - leaving 1 for Mogul analysis.

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).

Mol	Type	Chain	Dog	Link	Bo	ond leng	ths	В	ond ang	les
	туре	Ullalli	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
88	BLS	51	5294	-	28,31,31	0.83	0	28,43,43	1.72	4 (14%)

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
88	BLS	51	5294	-	-	9/21/38/38	0/2/2/2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
88	51	5294	BLS	O5'-C1'-C2'	-5.95	109.92	113.13
88	51	5294	BLS	C4-N3-C2	3.74	120.13	116.34
88	51	5294	BLS	C10-C11-N12	-3.21	106.98	112.15
88	51	5294	BLS	N4-C4-N3	2.34	120.19	116.49

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
88	51	5294	BLS	C4'-C5'-C6'-O4
88	51	5294	BLS	C4'-C5'-C6'-O3
88	51	5294	BLS	C11-C10-C9-C8
88	51	5294	BLS	C11-C10-C9-N9
88	51	5294	BLS	O7-C7-C8-C9

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is



within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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
4	A2	11
1	51	7
79	q3	3
3	81	1
44	G3	1

The worst 5 of 23 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	81	79:G	O3'	85:U	Р	13.18



	<i>J</i> 1	1 0				
Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	201:C	O3'	202:G	Р	8.18
1	q3	15:G	O3'	18:G	Р	7.28
1	A2	747:U	O3'	748:C	Р	6.91
1	51	1232:G	O3'	1233:G	Р	5.66



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-12631. 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: 150





Z Index: 150

6.2.2 Raw map



X Index: 150

Y Index: 150



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: 158





Z Index: 124

6.3.2 Raw map



X Index: 159

Y Index: 130



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



6.4.2 Raw map



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



6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 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) 6.6

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_12631_msk_1.map (i) 6.6.1



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 2614 nm^3 ; this corresponds to an approximate mass of 2362 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 0.263 $\mathrm{\AA^{-1}}$



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 0.263 $\mathrm{\AA^{-1}}$



8.2 Resolution estimates (i)

$\mathbf{Bosolution} \text{ ostimato } (\mathbf{\hat{\lambda}})$	Estimation criterion (FSC cut-off)			
Resolution estimate (A)	0.143	0.5	Half-bit	
Reported by author	3.80	-	-	
Author-provided FSC curve	3.81	4.89	3.92	
Unmasked-calculated*	4.52	8.24	4.78	

*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 4.52 differs from the reported value 3.8 by more than 10 %



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-12631 and PDB model 7NWG. Per-residue inclusion information can be found in section 3 on page 26.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.014 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 (0.014).



9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 87% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	$\mathbf{Q} extsf{-score}$
All	0.8740	0.4060
1	0.6860	0.3610
33	0.9050	0.3580
51	0.9180	0.4110
71	0.9300	0.4220
81	0.9390	0.4300
A2	0.8970	0.3760
A3	0.8880	0.4770
B2	0.8090	0.3910
B3	0.8830	0.4690
C2	0.8350	0.4220
C3	0.8890	0.4760
D2	0.8340	0.4300
D3	0.8580	0.4190
E2	0.7640	0.3760
E3	0.8800	0.4330
F2	0.8190	0.3980
F3	0.8730	0.4680
G2	0.7980	0.3780
G3	0.7890	0.3830
H2	0.7680	0.3290
H3	0.8580	0.4320
I2	0.7690	0.3580
I3	0.8790	0.4660
J2	0.7960	0.3770
J3	0.8660	0.4220
K2	0.7720	0.3610
L2	0.8250	0.3680
L3	0.8660	0.4520
M2	0.8550	0.4460
M3	0.8580	0.4290
N2	0.6400	0.2720
N3	0.9090	0.4930
O2	0.8440	0.4200
O3	0.8830	0.4770

Continued on next page...



Continued from previous page...

Chain	Atom inclusion	Q-score
P2	0.8090	0.4110
P3	0.8920	0.4810
Q2	0.8740	0.4130
Q3	0.8970	0.4880
R2	0.7920	0.3860
R3	0.8420	0.4200
S2	0.7750	0.3610
S3	0.8920	0.4630
T2	0.8460	0.3890
T3	0.8810	0.4690
U2	0.8240	0.3670
U3	0.8390	0.3840
V2	0.7200	0.3400
V3	0.8770	0.4820
W	0.9020	0.4820
W2	0.8100	0.3940
X2	0.8550	0.4380
X3	0.8610	0.4430
Y2	0.8610	0.4590
Y3	0.8970	0.4750
Z2	0.8180	0.3680
Z3	0.8390	0.4200
a2	0.7580	0.3490
a3	0.9060	0.4900
b2	0.8600	0.4570
b3	0.8060	0.4070
c2	0.7900	0.4040
c3	0.8320	0.4270
d2	0.7530	0.3530
d3	0.8500	0.4450
e2	0.8930	0.4270
e3	0.8770	0.4870
f2	0.8070	0.3960
f3	0.8880	0.4840
g2	0.7260	0.2860
g3	0.8510	0.4460
h2	0.7100	0.2930
h3	0.8810	0.4460
i3	0.8590	0.4390
j3	0.9200	0.5020
k3	0.7900	0.3770
13	0.9020	0.4820

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Chain	Atom inclusion	Q-score
m3	0.8970	0.4580
n3	0.8390	0.4600
03	0.8910	0.4680
p3	0.8480	0.4630
q3	0.8730	0.3480
r3	0.8920	0.4740
t3	0.4090	0.2180
u3	0.4240	0.2080
v3	0.8320	0.4020
w3	0.4850	0.2100

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