



Full wwPDB EM Validation Report ⓘ

Nov 21, 2022 – 03:11 PM EST

PDB ID : 8ESQ
EMDB ID : EMD-24411
Title : Ytm1 associated nascent 60S ribosome State 2
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-14
Resolution : 2.80 Å (reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

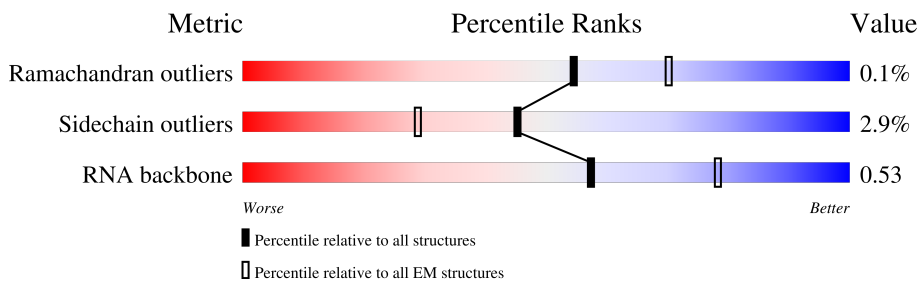
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.



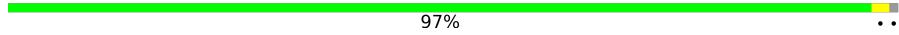


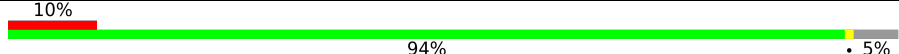
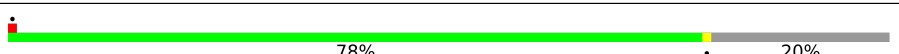
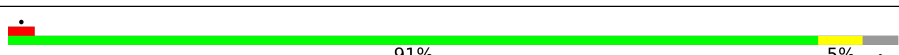
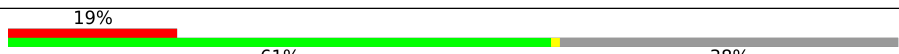
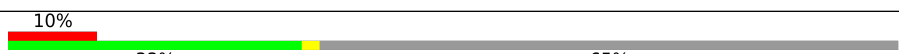
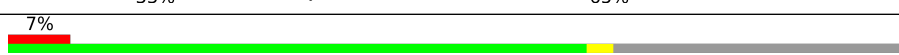

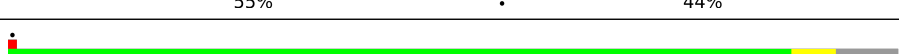
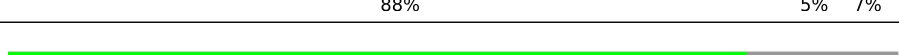

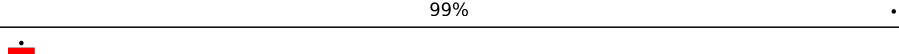
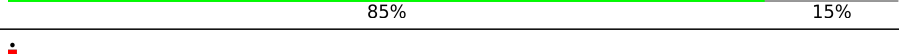




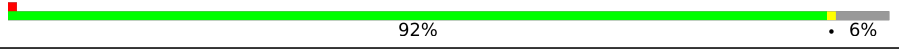
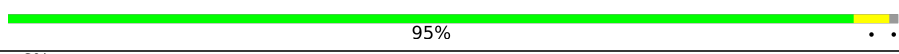
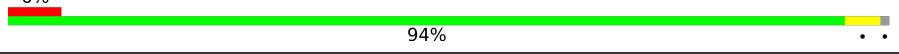

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 $\leq 5\%$. 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	7	707	
2	1	3497	
3	2	165	
4	3	302	
5	6	300	
6	8	51	
7	A	295	
8	B	388	

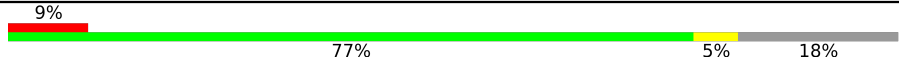

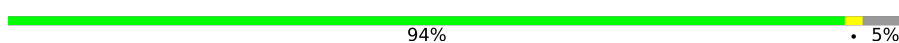
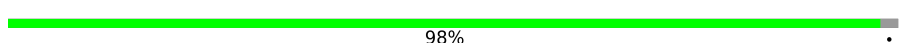
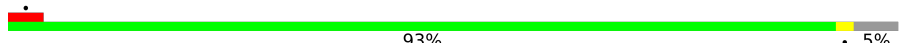
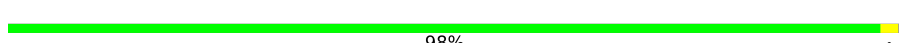


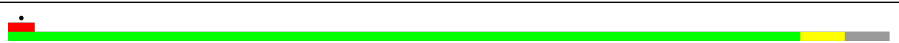

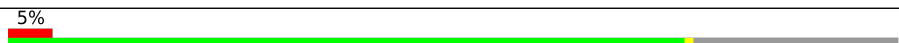


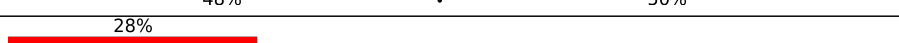
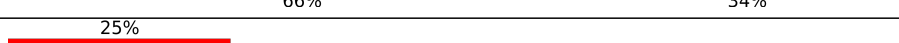
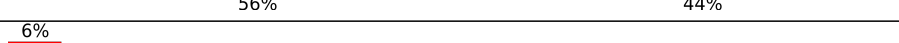
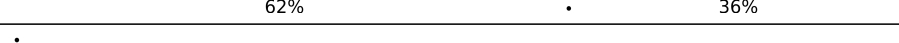
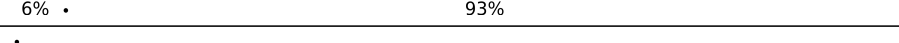
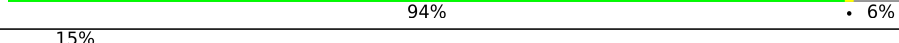






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Mol	Chain	Length	Quality of chain
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	I	747	
16	J	333	
17	K	373	
18	L	208	
19	M	134	
20	N	201	
21	O	197	
22	P	187	
23	Q	187	
24	R	193	
25	S	176	
26	U	117	
27	V	139	
28	W	241	
29	X	141	
30	Y	126	
31	Z	136	
32	a	148	
33	b	642	

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Mol	Chain	Length	Quality of chain
34	c	117	
35	d	113	
36	e	127	
37	f	108	
38	g	112	
39	h	122	
40	i	99	
41	j	91	
42	k	74	
43	l	180	
44	m	740	
45	n	607	
46	o	276	
47	p	440	
48	q	608	
49	r	260	
50	s	470	
51	t	249	
52	u	192	
53	v	209	
54	w	802	
55	x	306	
56	y	244	
57	z	117	
58	T	160	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 130409 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 Noc2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	7	245	1218	728	245	245	0	0

- Molecule 2 is a RNA chain called RNA (2231-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1	2230	47746	21325	8659	15532	2230	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1746	C	U	conflict	GB 157310483

- Molecule 3 is a RNA chain called RNA (150-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	2	150	3189	1427	564	1048	150	0	0

- Molecule 4 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	160	1336	845	257	228	6	0	0

- Molecule 5 is a RNA chain called RNA (81-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	6	81	1717	770	296	570	81	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	137	C	U	conflict	GB 157310483
6	146	G	U	conflict	GB 157310483

- Molecule 6 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	8	35	Total	C	N	O	0	0
			291	182	64	45		

- Molecule 7 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	211	Total	C	N	O	S	0	0
			1686	1079	301	299	7		

- Molecule 8 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	339	Total	C	N	O	S	0	0
			2687	1701	499	478	9		

- Molecule 9 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	359	Total	C	N	O	S	0	0
			2795	1765	536	491	3		

- Molecule 10 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	427	Total	C	N	O	S	0	0
			3396	2190	581	614	11		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	165	Total	C	N	O	S	0	0
			1283	822	237	221	3		

- Molecule 12 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	F	237	1925	1238	353	331	3	0	0

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	G	206	1615	1034	295	283	3	1	0

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	H	183	1451	914	266	265	6	0	0

- Molecule 15 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	I	460	3725	2412	620	682	11	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	607	LYS	LEU	conflict	UNP O94288

- Molecule 16 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	J	118	959	607	166	184	2	0	0

- Molecule 17 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	K	251	1973	1262	338	367	6	0	0

- Molecule 18 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	L	116	942	592	198	151	1	0	0

- Molecule 19 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	M	125	1007	644	191	168	4	0	0

- Molecule 20 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	N	166	1406	883	291	229	3	0	0

- Molecule 21 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	O	196	1557	999	297	257	4	0	0

- Molecule 22 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	P	159	1248	794	233	218	3	0	0

- Molecule 23 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Q	133	1032	650	199	182	1	0	0

- Molecule 24 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	R	114	949	596	195	153	5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	S	168	1408	909	263	231	5	0	0

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	U	98	791	513	137	141		0	0

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	V	132	991	625	182	176	8	0	0

- Molecule 28 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	W	215	1057	627	215	215		0	0

- Molecule 29 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	X	132	1044	664	194	185	1	0	0

- Molecule 30 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Y	125	998	622	201	173	2	0	0

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	Z	134	1072	693	199	178	2	0	0

- Molecule 32 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	80	Total	C	N	O	0	0
			634	404	116	114		

- Molecule 33 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	b	403	Total	C	N	O	0	0
			1999	1193	403	403		

- Molecule 34 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	96	Total	C	N	O	S	0	0
			720	457	125	134	4		

- Molecule 35 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	97	Total	C	N	O	S	0	0
			810	512	159	136	3		

- Molecule 36 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	121	Total	C	N	O	S	0	0
			971	608	198	160	5		

- Molecule 37 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	106	Total	C	N	O	S	0	0
			861	540	177	142	2		

- Molecule 39 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	h	121	Total	C	N	O	0	0
			999	629	194	176		

- Molecule 40 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	85	Total	C	N	O	S	0	0
			696	431	148	116	1		

- Molecule 41 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	71	Total	C	N	O	S	0	0
			563	346	121	90	6		

- Molecule 42 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	70	Total	C	N	O	S	0	0
			564	357	104	102	1		

- Molecule 43 is a protein called 60S ribosome subunit biogenesis protein nip7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	174	Total	C	N	O	S	0	0
			1418	906	254	250	8		

- Molecule 44 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	572	Total	C	N	O	S	0	0
			4536	2891	790	843	12		

- Molecule 45 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	433	Total	C	N	O	S	0	0
			3526	2268	608	638	12		

- Molecule 46 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	o	137	1138	732	213	187	6	0	0

- Molecule 47 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	p	290	1431	851	290	290		0	0

- Molecule 48 is a protein called 25S rRNA (cytosine-C(5))-methyltransferase nop2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	q	341	1684	1002	341	341		0	0

- Molecule 49 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	r	166	1357	850	259	243	5	0	0

- Molecule 50 is a protein called GTPase grn1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
50	s	32	269	163	63	43	0	0

- Molecule 51 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	t	235	1948	1242	367	334	5	0	0

- Molecule 52 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	u	114	944	598	190	147	9	0	0

- Molecule 53 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	161	Total	C	N	O	S	0	0
			1299	818	243	235	3		

- Molecule 54 is a protein called AdoMet-dependent rRNA methyltransferase spb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	504	Total	C	N	O	S	1	0
			4067	2573	723	753	18		

- Molecule 55 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	x	45	Total	C	N	O	S	0	0
			383	236	80	66	1		

- Molecule 56 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	y	225	Total	C	N	O	S	0	0
			1697	1058	293	341	5		

- Molecule 57 is a protein called UPF0642 protein C32H8.05.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	z	35	Total	C	N	O	0	0
			292	183	63	46		

- Molecule 58 is a protein called 60S ribosomal protein L21-A.

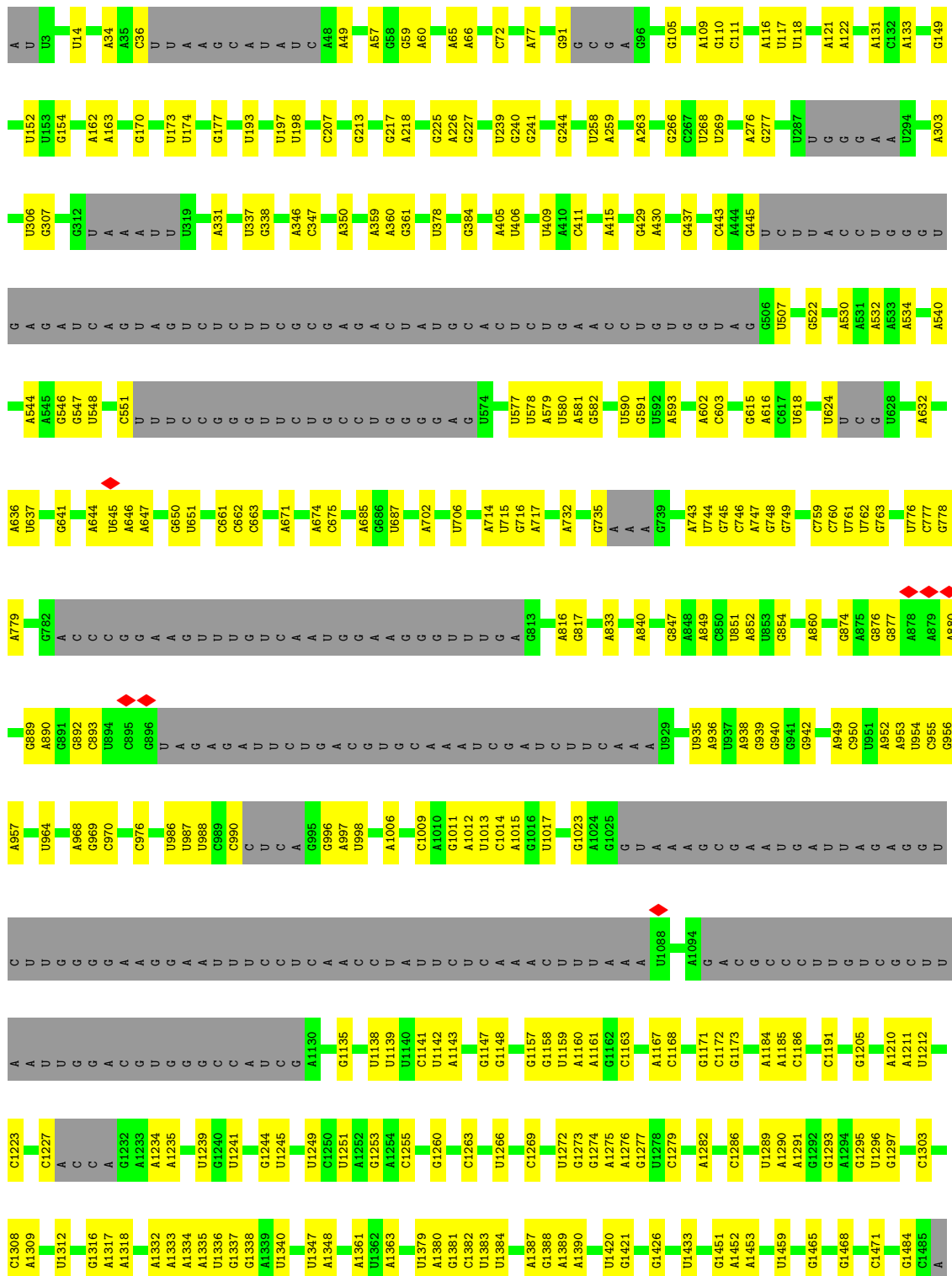
Mol	Chain	Residues	Atoms					AltConf	Trace
58	T	34	Total	C	N	O	S	0	0
			269	168	50	50	1		

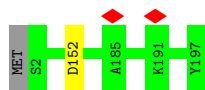
- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	j	1	Total	Zn	0
			1	1	

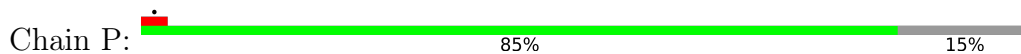
ALA	LEU
LYS	SER
ASP	ASP
ASP	TLE
GLU	LEU
LEU	ASP
ASP	ASP
SER	SER
GLU	GLU
GLU	ALA
GLU	GLU
ASP	ASP
TLE	TLE
ASP	ASP
GLU	GLU

● Molecule 2: RNA (2231-MER)

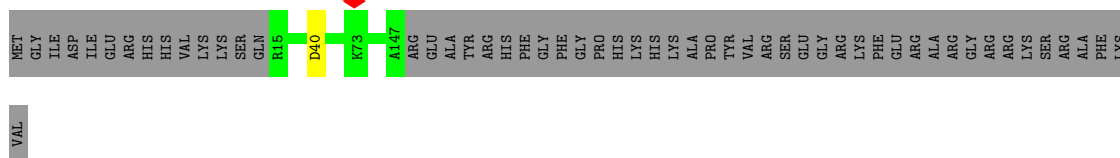




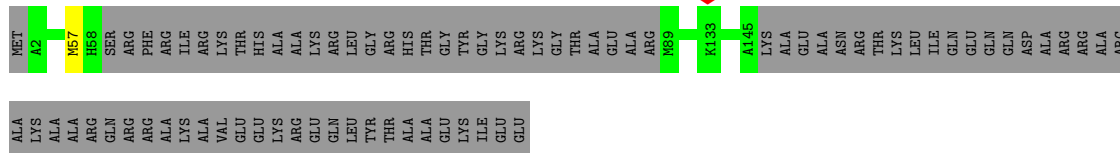
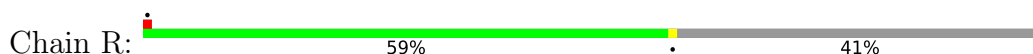
• Molecule 22: 60S ribosomal protein L17-A



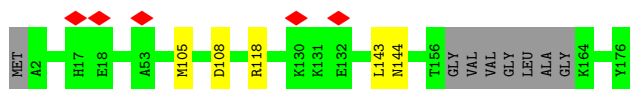
• Molecule 23: 60S ribosomal protein L18-A



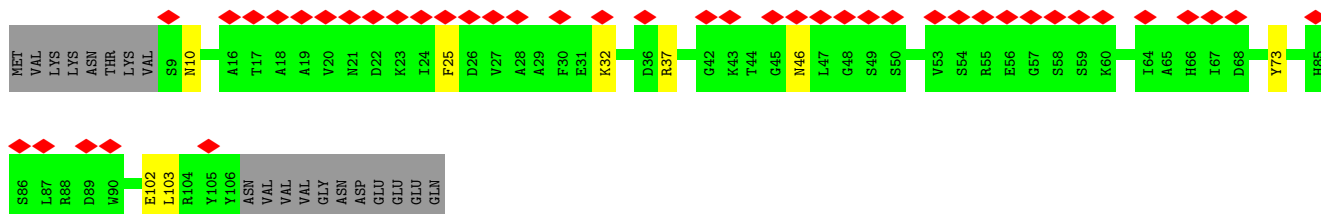
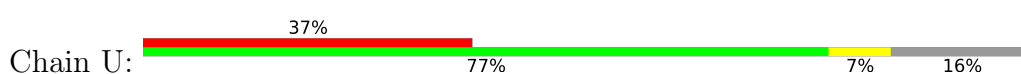
• Molecule 24: 60S ribosomal protein L19-A



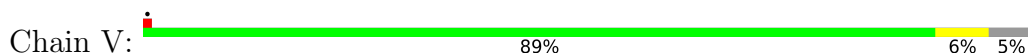
• Molecule 25: 60S ribosomal protein L20-A



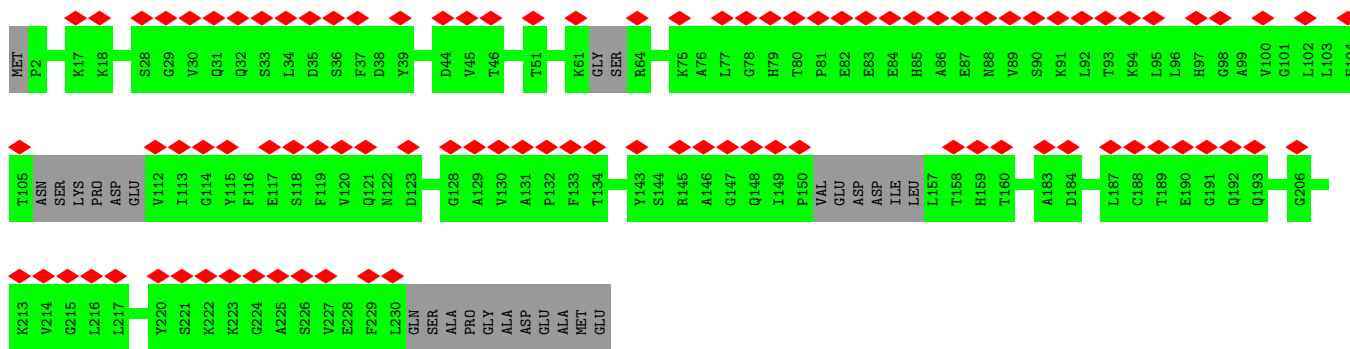
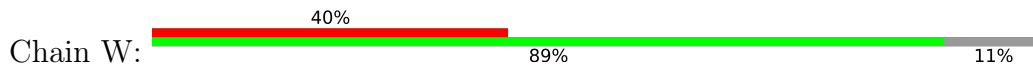
• Molecule 26: 60S ribosomal protein L22



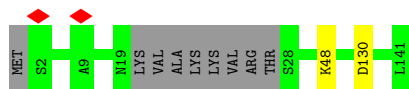
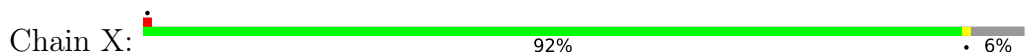
• Molecule 27: 60S ribosomal protein L23-A



• Molecule 28: Ribosome assembly factor mrt4



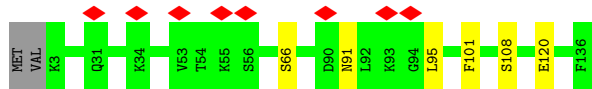
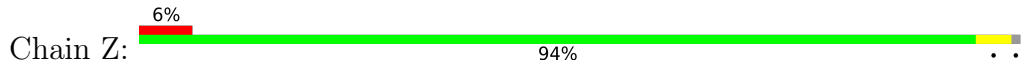
• Molecule 29: 60S ribosomal protein L25-A



• Molecule 30: 60S ribosomal protein L26

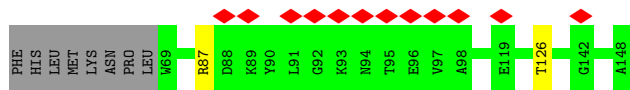


• Molecule 31: 60S ribosomal protein L27-A

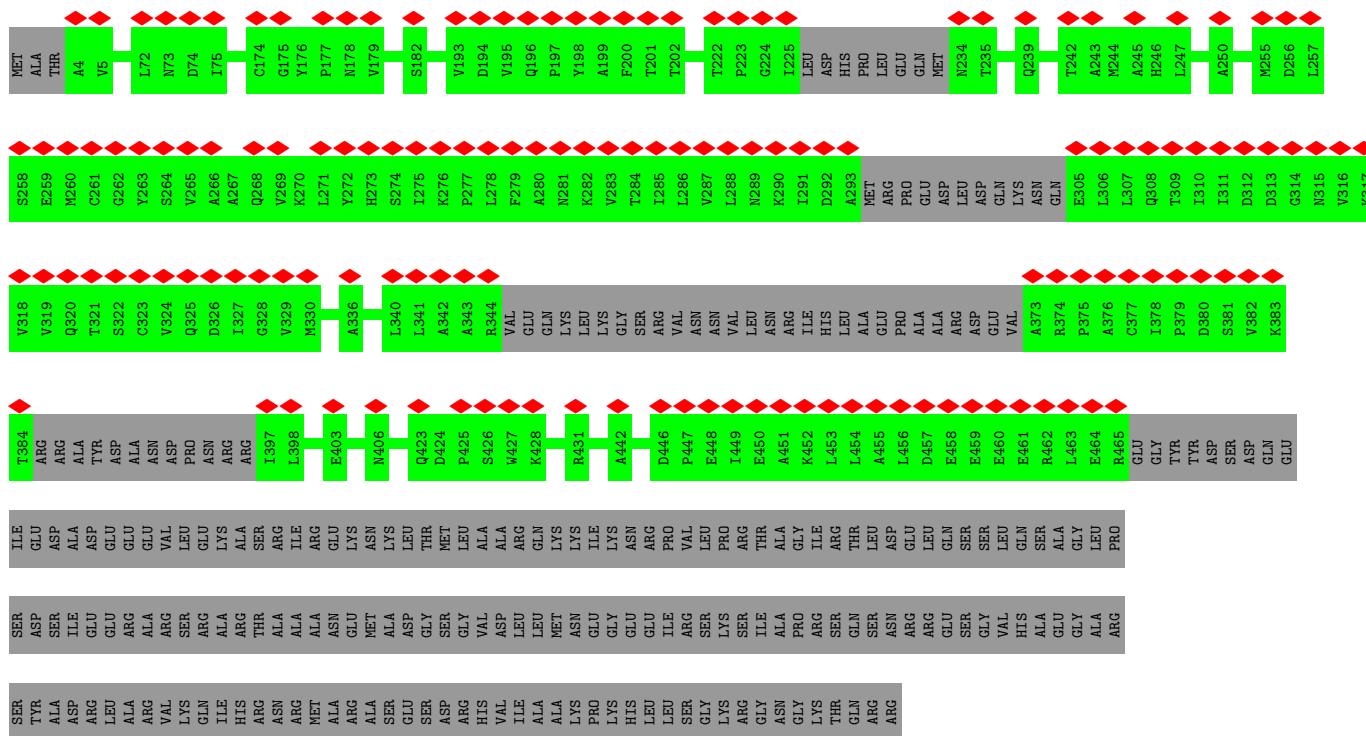


• Molecule 32: 60S ribosomal protein L28-A

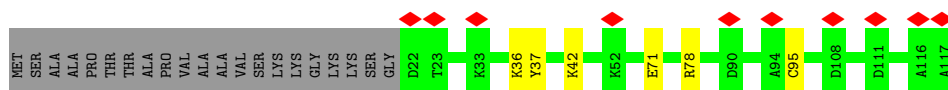
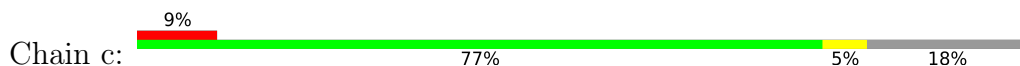




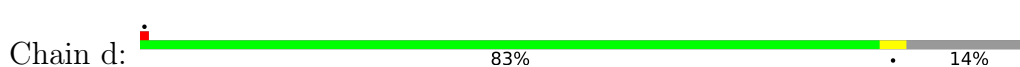
• Molecule 33: Probable nucleolar GTP-binding protein 1



• Molecule 34: 60S ribosomal protein L30-2



• Molecule 35: 60S ribosomal protein L31



• Molecule 36: 60S ribosomal protein L32-A





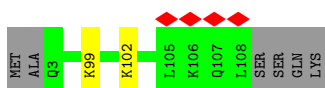
- Molecule 37: 60S ribosomal protein L33-B

Chain f: 98%



- Molecule 38: 60S ribosomal protein L34-A

Chain g: 93% 5%



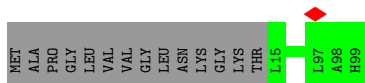
- Molecule 39: 60S ribosomal protein L35

Chain h: 98%



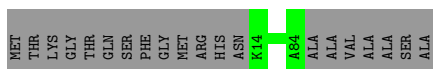
- Molecule 40: 60S ribosomal protein L36-B

Chain i: 86% 14%



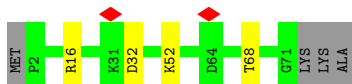
- Molecule 41: 60S ribosomal protein L37-B

Chain j: 78% 22%



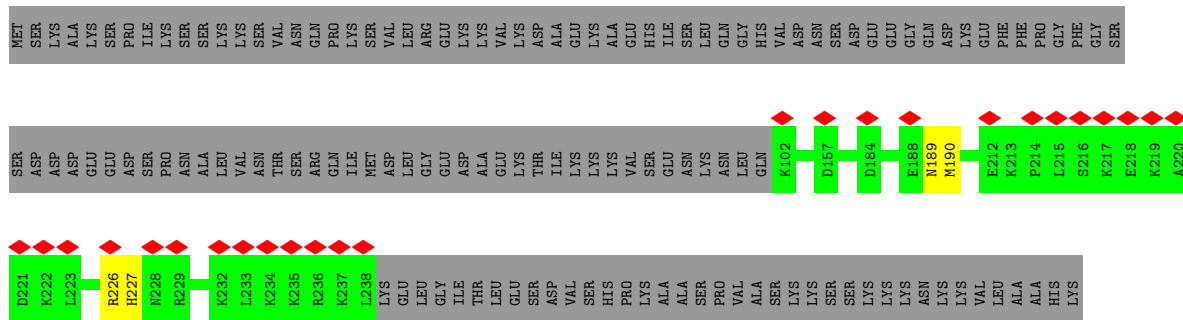
- Molecule 42: 60S ribosomal protein L38-1

Chain k: 89% 5% 5%

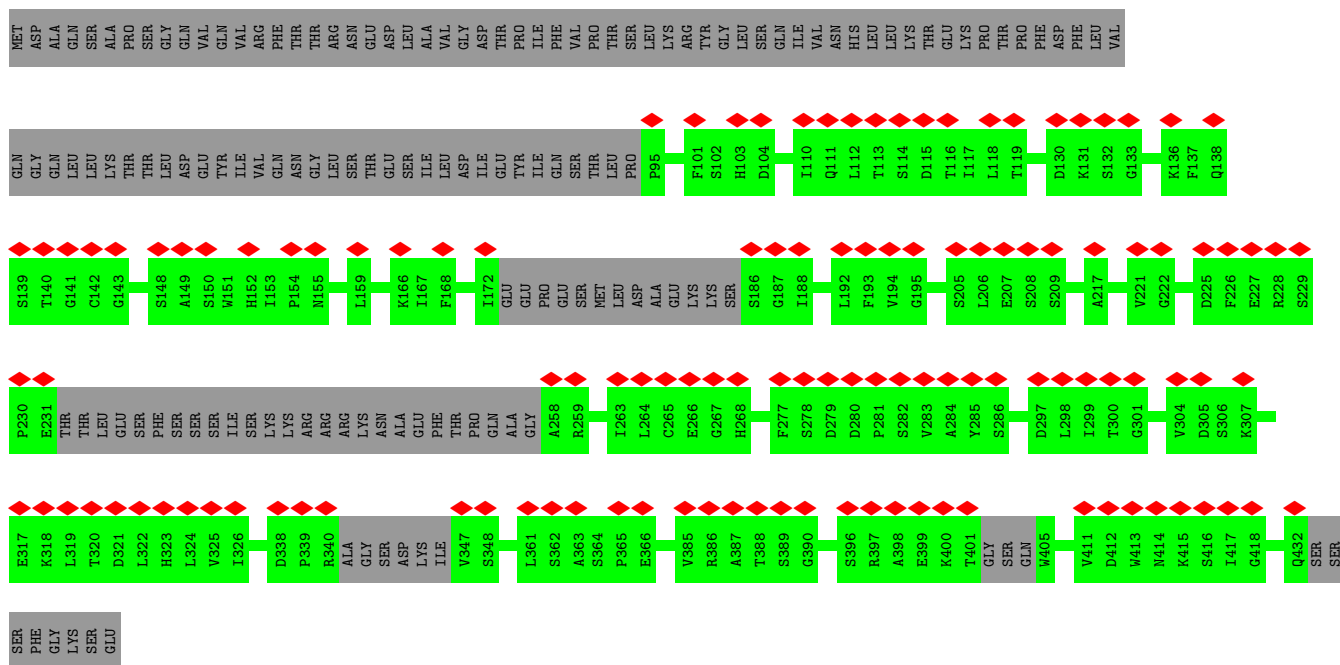


- Molecule 43: 60S ribosome subunit biogenesis protein nip7

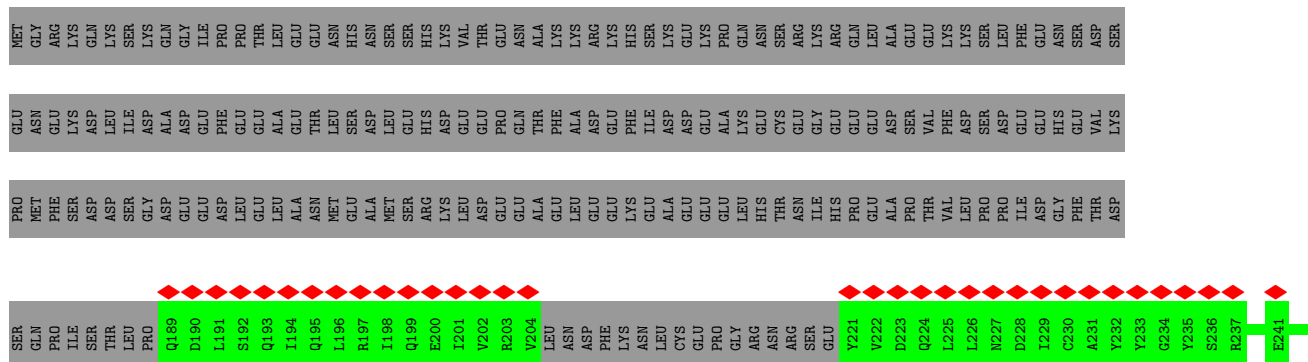
Chain l: 11% 88% 9%



• Molecule 47: Ribosome biogenesis protein ytm1



• Molecule 48: 25S rRNA (cytosine-C(5))-methyltransferase nop2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	172500	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.806	Depositor
Minimum map value	-0.343	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	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

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	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	7	0.23	0/1213	0.33	0/1686
2	1	0.33	0/53422	0.73	0/83211
3	2	0.44	0/3563	0.72	0/5543
4	3	0.25	0/1363	0.51	0/1832
5	6	0.24	0/1916	0.72	0/2973
6	8	0.28	0/298	0.62	0/399
7	A	0.27	0/1722	0.54	0/2325
8	B	0.25	0/2740	0.52	0/3680
9	C	0.29	0/2848	0.53	0/3842
10	D	0.26	0/3458	0.46	0/4662
11	E	0.28	0/1308	0.55	0/1763
12	F	0.28	0/1963	0.48	0/2632
13	G	0.30	0/1637	0.49	0/2203
14	H	0.27	0/1470	0.57	0/1982
15	I	0.24	0/3782	0.46	0/5087
16	J	0.28	0/972	0.51	0/1304
17	K	0.27	0/2008	0.52	0/2713
18	L	0.30	0/960	0.60	0/1288
19	M	0.27	0/1024	0.56	0/1375
20	N	0.33	0/1436	0.58	0/1920
21	O	0.27	0/1588	0.50	0/2128
22	P	0.26	0/1269	0.50	0/1699
23	Q	0.28	0/1043	0.55	0/1401
24	R	0.29	0/963	0.64	0/1284
25	S	0.26	0/1444	0.54	0/1939
26	U	0.27	0/805	0.63	0/1080
27	V	0.28	0/1007	0.60	0/1357
28	W	0.23	0/1053	0.43	0/1457
29	X	0.28	0/1060	0.53	0/1422
30	Y	0.27	0/1008	0.58	0/1341
31	Z	0.28	0/1095	0.56	0/1467
32	a	0.25	0/645	0.54	0/874

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.23	0/1994	0.38	0/2774
34	c	0.28	0/729	0.61	0/980
35	d	0.27	0/824	0.57	0/1106
36	e	0.28	0/985	0.55	0/1313
37	f	0.29	0/859	0.52	0/1152
38	g	0.26	0/873	0.58	0/1170
39	h	0.30	0/1008	0.53	0/1340
40	i	0.28	0/703	0.57	0/931
41	j	0.31	0/575	0.59	0/761
42	k	0.29	0/570	0.60	0/762
43	l	0.31	0/1452	0.65	0/1961
44	m	0.27	0/4655	0.51	0/6327
45	n	0.29	0/3607	0.50	0/4856
46	o	0.28	0/1163	0.51	0/1552
47	p	0.24	0/1426	0.44	0/1977
48	q	0.23	0/1682	0.40	0/2339
49	r	0.25	0/1373	0.56	0/1827
50	s	0.23	0/268	0.61	0/346
51	t	0.26	0/1979	0.52	0/2645
52	u	0.25	0/966	0.55	0/1292
53	v	0.28	0/1319	0.52	0/1769
54	w	0.25	0/4139	0.50	0/5567
55	x	0.22	0/384	0.51	0/505
56	y	0.25	0/1720	0.54	0/2345
57	z	0.29	0/297	0.45	0/388
58	T	0.25	0/276	0.52	0/375
All	All	0.30	0/137909	0.62	0/198229

There are no bond length outliers.

There are no bond angle outliers.

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

5.3.1 Protein backbone

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	Percentiles	
1	7	235/707 (33%)	234 (100%)	1 (0%)	0	100	100
4	3	158/302 (52%)	150 (95%)	8 (5%)	0	100	100
6	8	33/51 (65%)	31 (94%)	2 (6%)	0	100	100
7	A	209/295 (71%)	197 (94%)	12 (6%)	0	100	100
8	B	335/388 (86%)	323 (96%)	12 (4%)	0	100	100
9	C	357/363 (98%)	334 (94%)	23 (6%)	0	100	100
10	D	421/578 (73%)	412 (98%)	9 (2%)	0	100	100
11	E	163/195 (84%)	150 (92%)	13 (8%)	0	100	100
12	F	235/250 (94%)	227 (97%)	8 (3%)	0	100	100
13	G	203/259 (78%)	193 (95%)	8 (4%)	2 (1%)	15	44
14	H	181/190 (95%)	172 (95%)	8 (4%)	1 (1%)	25	56
15	I	447/747 (60%)	422 (94%)	23 (5%)	2 (0%)	34	66
16	J	116/333 (35%)	111 (96%)	5 (4%)	0	100	100
17	K	247/373 (66%)	227 (92%)	18 (7%)	2 (1%)	19	49
18	L	114/208 (55%)	110 (96%)	4 (4%)	0	100	100
19	M	123/134 (92%)	117 (95%)	6 (5%)	0	100	100
20	N	160/201 (80%)	158 (99%)	2 (1%)	0	100	100
21	O	194/197 (98%)	190 (98%)	4 (2%)	0	100	100
22	P	153/187 (82%)	147 (96%)	6 (4%)	0	100	100
23	Q	131/187 (70%)	127 (97%)	4 (3%)	0	100	100
24	R	110/193 (57%)	109 (99%)	1 (1%)	0	100	100
25	S	164/176 (93%)	156 (95%)	8 (5%)	0	100	100
26	U	96/117 (82%)	89 (93%)	7 (7%)	0	100	100
27	V	130/139 (94%)	126 (97%)	4 (3%)	0	100	100
28	W	207/241 (86%)	194 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	X	128/141 (91%)	125 (98%)	3 (2%)	0	100	100
30	Y	123/126 (98%)	119 (97%)	4 (3%)	0	100	100
31	Z	132/136 (97%)	128 (97%)	4 (3%)	0	100	100
32	a	78/148 (53%)	77 (99%)	1 (1%)	0	100	100
33	b	393/642 (61%)	382 (97%)	11 (3%)	0	100	100
34	c	94/117 (80%)	93 (99%)	1 (1%)	0	100	100
35	d	93/113 (82%)	91 (98%)	2 (2%)	0	100	100
36	e	119/127 (94%)	117 (98%)	2 (2%)	0	100	100
37	f	104/108 (96%)	96 (92%)	8 (8%)	0	100	100
38	g	104/112 (93%)	101 (97%)	3 (3%)	0	100	100
39	h	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
40	i	83/99 (84%)	83 (100%)	0	0	100	100
41	j	69/91 (76%)	67 (97%)	2 (3%)	0	100	100
42	k	68/74 (92%)	67 (98%)	1 (2%)	0	100	100
43	l	172/180 (96%)	163 (95%)	9 (5%)	0	100	100
44	m	558/740 (75%)	527 (94%)	30 (5%)	1 (0%)	47	78
45	n	427/607 (70%)	404 (95%)	23 (5%)	0	100	100
46	o	135/276 (49%)	130 (96%)	5 (4%)	0	100	100
47	p	280/440 (64%)	271 (97%)	9 (3%)	0	100	100
48	q	337/608 (55%)	332 (98%)	5 (2%)	0	100	100
49	r	158/260 (61%)	158 (100%)	0	0	100	100
50	s	30/470 (6%)	29 (97%)	1 (3%)	0	100	100
51	t	233/249 (94%)	220 (94%)	13 (6%)	0	100	100
52	u	112/192 (58%)	105 (94%)	7 (6%)	0	100	100
53	v	157/209 (75%)	150 (96%)	6 (4%)	1 (1%)	25	56
54	w	495/802 (62%)	476 (96%)	19 (4%)	0	100	100
55	x	41/306 (13%)	41 (100%)	0	0	100	100
56	y	223/244 (91%)	215 (96%)	8 (4%)	0	100	100
57	z	33/117 (28%)	31 (94%)	2 (6%)	0	100	100
58	T	30/160 (19%)	30 (100%)	0	0	100	100
All	All	10050/15027 (67%)	9651 (96%)	390 (4%)	9 (0%)	54	81

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	I	698	ILE
17	K	153	ILE
13	G	227[A]	ASP
13	G	227[B]	ASP
15	I	624	VAL
53	v	130	ILE
17	K	14	GLU
44	m	115	VAL
14	H	14	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain 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	Percentiles	
4	3	141/271 (52%)	131 (93%)	10 (7%)	14	39
6	8	31/47 (66%)	26 (84%)	5 (16%)	2	7
7	A	184/266 (69%)	181 (98%)	3 (2%)	62	88
8	B	285/326 (87%)	280 (98%)	5 (2%)	59	86
9	C	296/297 (100%)	290 (98%)	6 (2%)	55	84
10	D	371/505 (74%)	367 (99%)	4 (1%)	73	92
11	E	135/155 (87%)	130 (96%)	5 (4%)	34	68
12	F	199/210 (95%)	196 (98%)	3 (2%)	65	89
13	G	168/212 (79%)	166 (99%)	2 (1%)	71	92
14	H	164/170 (96%)	155 (94%)	9 (6%)	21	52
15	I	418/685 (61%)	412 (99%)	6 (1%)	67	90
16	J	104/288 (36%)	96 (92%)	8 (8%)	13	35
17	K	224/333 (67%)	216 (96%)	8 (4%)	35	69
18	L	97/167 (58%)	95 (98%)	2 (2%)	53	84
19	M	108/113 (96%)	101 (94%)	7 (6%)	17	44
20	N	146/176 (83%)	146 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	O	161/162 (99%)	160 (99%)	1 (1%)	86	96
22	P	128/149 (86%)	128 (100%)	0	100	100
23	Q	114/159 (72%)	113 (99%)	1 (1%)	78	94
24	R	102/162 (63%)	101 (99%)	1 (1%)	76	93
25	S	150/154 (97%)	145 (97%)	5 (3%)	38	72
26	U	85/103 (82%)	77 (91%)	8 (9%)	8	26
27	V	103/107 (96%)	95 (92%)	8 (8%)	12	35
29	X	114/122 (93%)	112 (98%)	2 (2%)	59	86
30	Y	110/111 (99%)	105 (96%)	5 (4%)	27	60
31	Z	113/115 (98%)	107 (95%)	6 (5%)	22	54
32	a	68/122 (56%)	66 (97%)	2 (3%)	42	76
34	c	77/91 (85%)	71 (92%)	6 (8%)	12	35
35	d	89/102 (87%)	86 (97%)	3 (3%)	37	71
36	e	103/107 (96%)	101 (98%)	2 (2%)	57	85
37	f	89/91 (98%)	89 (100%)	0	100	100
38	g	92/97 (95%)	90 (98%)	2 (2%)	52	83
39	h	106/107 (99%)	104 (98%)	2 (2%)	57	85
40	i	74/84 (88%)	74 (100%)	0	100	100
41	j	58/71 (82%)	58 (100%)	0	100	100
42	k	63/66 (96%)	59 (94%)	4 (6%)	18	46
43	l	152/158 (96%)	136 (90%)	16 (10%)	7	20
44	m	506/659 (77%)	496 (98%)	10 (2%)	55	84
45	n	379/532 (71%)	371 (98%)	8 (2%)	53	84
46	o	123/246 (50%)	119 (97%)	4 (3%)	38	72
49	r	146/224 (65%)	140 (96%)	6 (4%)	30	64
50	s	29/409 (7%)	25 (86%)	4 (14%)	3	11
51	t	211/223 (95%)	209 (99%)	2 (1%)	78	94
52	u	99/168 (59%)	91 (92%)	8 (8%)	11	33
53	v	138/181 (76%)	135 (98%)	3 (2%)	52	83
54	w	444/697 (64%)	435 (98%)	9 (2%)	55	84
55	x	42/273 (15%)	41 (98%)	1 (2%)	49	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	y	189/206 (92%)	183 (97%)	6 (3%)	39	73
57	z	31/107 (29%)	29 (94%)	2 (6%)	17	44
58	T	31/139 (22%)	27 (87%)	4 (13%)	4	13
All	All	7590/10725 (71%)	7366 (97%)	224 (3%)	45	75

All (224) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	3	23	GLU
4	3	35	THR
4	3	37	LEU
4	3	38	CYS
4	3	43	CYS
4	3	75	LYS
4	3	95	GLN
4	3	114	ARG
4	3	130	GLN
4	3	136	ILE
6	8	3	SER
6	8	8	ARG
6	8	27	ILE
6	8	28	ARG
6	8	30	ARG
7	A	81	ASP
7	A	136	ASN
7	A	170	GLN
8	B	17	LEU
8	B	19	ARG
8	B	20	LYS
8	B	132	LYS
8	B	137	TYR
9	C	22	LEU
9	C	56	GLU
9	C	275	LYS
9	C	330	LEU
9	C	343	ILE
9	C	347	LYS
10	D	150	MET
10	D	156	PHE
10	D	261	MET
10	D	298	ASN

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Mol	Chain	Res	Type
11	E	110	ASP
11	E	111	VAL
11	E	152	GLU
11	E	156	ASP
11	E	173	ASN
12	F	75	LYS
12	F	87	GLU
12	F	128	LYS
13	G	83	ASP
13	G	216	SER
14	H	13	ILE
14	H	15	LYS
14	H	78	MET
14	H	94	TYR
14	H	133	SER
14	H	135	SER
14	H	144	LEU
14	H	181	GLU
14	H	186	GLU
15	I	306	HIS
15	I	339	CYS
15	I	340	CYS
15	I	539	MET
15	I	664	MET
15	I	729	HIS
16	J	101	GLU
16	J	109	TYR
16	J	143	TYR
16	J	145	GLN
16	J	168	HIS
16	J	170	TYR
16	J	185	ARG
16	J	205	ARG
17	K	17	CYS
17	K	23	TYR
17	K	27	ARG
17	K	77	LYS
17	K	172	LYS
17	K	222	GLN
17	K	234	LYS
17	K	245	GLN
18	L	49	ARG

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Mol	Chain	Res	Type
18	L	110	GLN
19	M	34	HIS
19	M	71	SER
19	M	82	ASP
19	M	89	SER
19	M	109	ASP
19	M	114	MET
19	M	122	GLU
21	O	152	ASP
23	Q	40	ASP
24	R	57	MET
25	S	105	MET
25	S	108	ASP
25	S	118	ARG
25	S	143	LEU
25	S	144	ASN
26	U	10	ASN
26	U	25	PHE
26	U	32	LYS
26	U	37	ARG
26	U	46	ASN
26	U	73	TYR
26	U	102	GLU
26	U	103	LEU
27	V	15	MET
27	V	19	LEU
27	V	71	LEU
27	V	74	LYS
27	V	76	MET
27	V	83	GLN
27	V	100	ASN
27	V	134	ASN
29	X	48	LYS
29	X	130	ASP
30	Y	2	LYS
30	Y	50	ARG
30	Y	73	TYR
30	Y	83	ARG
30	Y	116	ASP
31	Z	66	SER
31	Z	91	ASN
31	Z	95	LEU

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Mol	Chain	Res	Type
31	Z	101	PHE
31	Z	108	SER
31	Z	120	GLU
32	a	87	ARG
32	a	126	THR
34	c	36	LYS
34	c	37	TYR
34	c	42	LYS
34	c	71	GLU
34	c	78	ARG
34	c	95	CYS
35	d	52	LYS
35	d	84	ARG
35	d	106	MET
36	e	5	ASN
36	e	49	MET
38	g	99	LYS
38	g	102	LYS
39	h	92	ARG
39	h	110	GLU
42	k	16	ARG
42	k	32	ASP
42	k	52	LYS
42	k	68	THR
43	l	12	PHE
43	l	14	GLU
43	l	29	ASP
43	l	42	ASP
43	l	64	MET
43	l	91	GLN
43	l	104	GLU
43	l	109	TYR
43	l	111	ASN
43	l	128	HIS
43	l	135	SER
43	l	136	MET
43	l	143	PHE
43	l	157	GLU
43	l	159	THR
43	l	164	PHE
44	m	120	TYR
44	m	131	ASN

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Mol	Chain	Res	Type
44	m	144	THR
44	m	306	TYR
44	m	383	LYS
44	m	413	MET
44	m	644	ASP
44	m	665	TYR
44	m	719	CYS
44	m	738	MET
45	n	379	LYS
45	n	411	GLN
45	n	460	TYR
45	n	555	LYS
45	n	558	LYS
45	n	563	MET
45	n	565	MET
45	n	570	ARG
46	o	189	ASN
46	o	190	MET
46	o	226	ARG
46	o	227	HIS
49	r	10	SER
49	r	68	HIS
49	r	174	MET
49	r	192	MET
49	r	210	GLN
49	r	225	SER
50	s	8	SER
50	s	11	ARG
50	s	20	GLU
50	s	32	ARG
51	t	163	ASN
51	t	195	TYR
52	u	7	TYR
52	u	25	ASP
52	u	84	ARG
52	u	92	ASN
52	u	94	MET
52	u	103	LYS
52	u	104	ARG
52	u	107	LEU
53	v	136	GLU
53	v	147	LYS

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Mol	Chain	Res	Type
53	v	181	SER
54	w	16	TRP
54	w	127	TRP
54	w	140	MET
54	w	142	MET
54	w	243[A]	GLU
54	w	243[B]	GLU
54	w	328	MET
54	w	689	MET
54	w	709	MET
55	x	24	ASP
56	y	38	PHE
56	y	52	THR
56	y	93	LYS
56	y	110	CYS
56	y	157	GLN
56	y	168	GLN
57	z	104	ARG
57	z	106	LYS
58	T	103	GLN
58	T	105	PHE
58	T	139	HIS
58	T	150	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
4	3	41	GLN
6	8	25	GLN
9	C	314	HIS
9	C	363	ASN
10	D	270	GLN
12	F	86	HIS
15	I	729	HIS
24	R	130	ASN
26	U	10	ASN
42	k	59	GLN
43	l	165	HIS
44	m	682	GLN
44	m	685	HIS
45	n	190	GLN
45	n	197	GLN

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Mol	Chain	Res	Type
45	n	408	HIS
46	o	211	HIS
49	r	246	ASN
52	u	24	ASN
56	y	66	ASN
56	y	157	GLN
57	z	107	ASN
58	T	103	GLN
58	T	146	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	1	2191/3497 (62%)	555 (25%)	21 (0%)
3	2	147/165 (89%)	27 (18%)	1 (0%)
5	6	77/300 (25%)	31 (40%)	0
All	All	2415/3962 (60%)	613 (25%)	22 (0%)

All (613) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	14	U
2	1	34	A
2	1	36	C
2	1	49	A
2	1	57	A
2	1	59	G
2	1	60	A
2	1	65	A
2	1	66	A
2	1	72	C
2	1	77	A
2	1	91	G
2	1	105	G
2	1	109	A
2	1	110	G
2	1	111	C
2	1	116	A
2	1	117	U
2	1	118	U
2	1	121	A

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Mol	Chain	Res	Type
2	1	122	A
2	1	131	A
2	1	133	A
2	1	149	G
2	1	152	U
2	1	154	G
2	1	162	A
2	1	163	A
2	1	170	G
2	1	173	U
2	1	174	U
2	1	177	G
2	1	193	U
2	1	197	U
2	1	198	U
2	1	207	C
2	1	213	G
2	1	217	G
2	1	218	A
2	1	225	G
2	1	226	A
2	1	227	G
2	1	239	U
2	1	240	G
2	1	241	G
2	1	244	G
2	1	258	U
2	1	259	A
2	1	263	A
2	1	266	G
2	1	268	U
2	1	269	U
2	1	276	A
2	1	277	G
2	1	303	A
2	1	306	U
2	1	307	G
2	1	331	A
2	1	337	U
2	1	338	G
2	1	346	A
2	1	347	C

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Mol	Chain	Res	Type
2	1	350	A
2	1	359	A
2	1	360	A
2	1	361	G
2	1	378	U
2	1	384	G
2	1	405	A
2	1	406	U
2	1	409	U
2	1	411	C
2	1	415	A
2	1	429	G
2	1	430	A
2	1	437	G
2	1	443	C
2	1	445	G
2	1	507	U
2	1	522	G
2	1	530	A
2	1	532	A
2	1	534	A
2	1	540	A
2	1	544	A
2	1	546	G
2	1	547	G
2	1	548	U
2	1	551	C
2	1	577	U
2	1	578	U
2	1	579	A
2	1	580	U
2	1	581	A
2	1	582	G
2	1	590	U
2	1	591	G
2	1	593	A
2	1	602	A
2	1	603	C
2	1	615	G
2	1	616	A
2	1	618	U
2	1	624	U

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Mol	Chain	Res	Type
2	1	632	A
2	1	636	A
2	1	637	U
2	1	641	G
2	1	644	A
2	1	645	U
2	1	646	A
2	1	647	A
2	1	650	G
2	1	651	U
2	1	661	C
2	1	662	C
2	1	663	C
2	1	671	A
2	1	674	A
2	1	675	C
2	1	685	A
2	1	687	U
2	1	702	A
2	1	706	U
2	1	714	A
2	1	715	U
2	1	716	G
2	1	717	A
2	1	732	A
2	1	735	G
2	1	743	A
2	1	744	U
2	1	745	G
2	1	746	C
2	1	747	A
2	1	748	G
2	1	749	G
2	1	760	C
2	1	761	U
2	1	762	U
2	1	763	G
2	1	776	U
2	1	777	C
2	1	778	G
2	1	779	A
2	1	816	A

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Mol	Chain	Res	Type
2	1	817	G
2	1	833	A
2	1	840	A
2	1	847	G
2	1	849	A
2	1	851	U
2	1	852	A
2	1	854	G
2	1	860	A
2	1	874	G
2	1	876	G
2	1	877	G
2	1	880	A
2	1	889	G
2	1	890	A
2	1	892	G
2	1	893	C
2	1	935	U
2	1	936	A
2	1	938	A
2	1	939	G
2	1	940	G
2	1	942	G
2	1	950	C
2	1	952	A
2	1	953	A
2	1	954	U
2	1	955	C
2	1	956	G
2	1	957	A
2	1	964	U
2	1	968	A
2	1	969	G
2	1	970	C
2	1	976	C
2	1	986	U
2	1	987	U
2	1	988	U
2	1	990	C
2	1	996	G
2	1	997	A
2	1	998	U

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Mol	Chain	Res	Type
2	1	1006	A
2	1	1009	C
2	1	1011	G
2	1	1012	A
2	1	1013	U
2	1	1014	C
2	1	1015	A
2	1	1017	U
2	1	1023	G
2	1	1135	G
2	1	1138	U
2	1	1139	U
2	1	1141	C
2	1	1142	U
2	1	1143	A
2	1	1147	G
2	1	1148	G
2	1	1157	G
2	1	1158	G
2	1	1159	U
2	1	1160	A
2	1	1161	A
2	1	1163	C
2	1	1167	A
2	1	1168	C
2	1	1171	G
2	1	1172	C
2	1	1173	G
2	1	1184	A
2	1	1185	A
2	1	1186	C
2	1	1191	C
2	1	1205	G
2	1	1210	A
2	1	1211	A
2	1	1212	U
2	1	1223	C
2	1	1227	C
2	1	1234	A
2	1	1235	A
2	1	1239	U
2	1	1241	U

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Mol	Chain	Res	Type
2	1	1244	G
2	1	1245	U
2	1	1249	U
2	1	1251	U
2	1	1253	G
2	1	1255	C
2	1	1260	G
2	1	1263	C
2	1	1266	U
2	1	1269	C
2	1	1272	U
2	1	1273	G
2	1	1274	G
2	1	1275	A
2	1	1276	A
2	1	1277	G
2	1	1279	C
2	1	1282	A
2	1	1286	C
2	1	1289	U
2	1	1290	A
2	1	1291	A
2	1	1293	G
2	1	1295	G
2	1	1296	U
2	1	1297	G
2	1	1303	C
2	1	1308	C
2	1	1309	A
2	1	1312	U
2	1	1316	G
2	1	1317	A
2	1	1318	A
2	1	1332	A
2	1	1333	A
2	1	1334	A
2	1	1335	A
2	1	1336	U
2	1	1337	G
2	1	1338	G
2	1	1340	U
2	1	1347	U

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Mol	Chain	Res	Type
2	1	1348	A
2	1	1361	A
2	1	1363	A
2	1	1379	U
2	1	1380	A
2	1	1381	G
2	1	1382	C
2	1	1383	U
2	1	1384	U
2	1	1387	A
2	1	1388	G
2	1	1389	A
2	1	1390	A
2	1	1420	U
2	1	1421	G
2	1	1426	G
2	1	1433	U
2	1	1451	G
2	1	1452	A
2	1	1453	A
2	1	1459	U
2	1	1465	G
2	1	1468	G
2	1	1471	C
2	1	1484	G
2	1	1502	A
2	1	1515	A
2	1	1517	G
2	1	1518	U
2	1	1519	G
2	1	1521	G
2	1	1528	U
2	1	1529	U
2	1	1537	A
2	1	1538	A
2	1	1539	C
2	1	1541	G
2	1	1542	C
2	1	1546	U
2	1	1548	G
2	1	1568	A
2	1	1570	G

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Mol	Chain	Res	Type
2	1	1588	A
2	1	1589	U
2	1	1590	G
2	1	1591	A
2	1	1594	G
2	1	1603	U
2	1	1604	U
2	1	1605	U
2	1	1607	U
2	1	1608	C
2	1	1622	A
2	1	1623	A
2	1	1624	A
2	1	1628	A
2	1	1640	A
2	1	1643	C
2	1	1654	A
2	1	1655	G
2	1	1663	C
2	1	1664	A
2	1	1665	A
2	1	1674	C
2	1	1677	A
2	1	1678	A
2	1	1686	U
2	1	1691	A
2	1	1709	G
2	1	1715	G
2	1	1718	C
2	1	1731	A
2	1	1736	A
2	1	1737	C
2	1	1753	A
2	1	1754	A
2	1	1764	U
2	1	1780	G
2	1	1782	U
2	1	1790	A
2	1	1791	G
2	1	1797	A
2	1	1798	G
2	1	1806	U

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Mol	Chain	Res	Type
2	1	1807	G
2	1	1811	A
2	1	1814	C
2	1	1816	G
2	1	1818	U
2	1	1819	G
2	1	1820	C
2	1	1821	G
2	1	1829	C
2	1	1833	C
2	1	1834	C
2	1	1835	U
2	1	1836	U
2	1	1838	A
2	1	1849	G
2	1	1852	G
2	1	1871	U
2	1	1872	G
2	1	1873	U
2	1	1874	U
2	1	1876	U
2	1	1917	U
2	1	1935	U
2	1	1936	A
2	1	1940	C
2	1	1941	A
2	1	1961	G
2	1	2423	G
2	1	2424	U
2	1	2451	A
2	1	2452	G
2	1	2455	U
2	1	2456	G
2	1	2458	G
2	1	2459	G
2	1	2461	A
2	1	2462	C
2	1	2463	G
2	1	2464	G
2	1	2465	G
2	1	2466	C
2	1	2473	A

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Mol	Chain	Res	Type
2	1	2476	U
2	1	2480	C
2	1	2481	G
2	1	2498	U
2	1	2499	U
2	1	2505	U
2	1	2506	G
2	1	2507	A
2	1	2521	U
2	1	2700	G
2	1	2701	G
2	1	2702	G
2	1	2706	U
2	1	2898	A
2	1	2902	U
2	1	2905	C
2	1	2906	A
2	1	2907	C
2	1	2908	A
2	1	2921	U
2	1	2925	G
2	1	2929	G
2	1	2931	C
2	1	2932	A
2	1	2946	A
2	1	2952	C
2	1	2953	U
2	1	2971	C
2	1	2972	G
2	1	2973	G
2	1	2978	U
2	1	2982	A
2	1	2984	C
2	1	2993	G
2	1	3009	G
2	1	3011	U
2	1	3014	A
2	1	3023	C
2	1	3024	C
2	1	3025	A
2	1	3030	U
2	1	3031	A

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Mol	Chain	Res	Type
2	1	3036	A
2	1	3037	C
2	1	3038	G
2	1	3040	G
2	1	3042	G
2	1	3044	U
2	1	3046	G
2	1	3057	U
2	1	3059	G
2	1	3060	U
2	1	3061	G
2	1	3062	A
2	1	3063	G
2	1	3064	A
2	1	3065	C
2	1	3071	A
2	1	3072	G
2	1	3073	U
2	1	3082	A
2	1	3085	G
2	1	3087	U
2	1	3093	G
2	1	3107	A
2	1	3108	A
2	1	3113	A
2	1	3117	A
2	1	3118	G
2	1	3119	U
2	1	3125	A
2	1	3126	G
2	1	3128	A
2	1	3151	A
2	1	3155	G
2	1	3168	A
2	1	3170	G
2	1	3172	C
2	1	3173	A
2	1	3174	A
2	1	3176	G
2	1	3182	G
2	1	3188	U
2	1	3189	C

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Mol	Chain	Res	Type
2	1	3192	C
2	1	3195	C
2	1	3198	G
2	1	3200	U
2	1	3218	A
2	1	3225	A
2	1	3226	A
2	1	3227	U
2	1	3237	A
2	1	3238	A
2	1	3239	A
2	1	3248	U
2	1	3272	U
2	1	3273	A
2	1	3275	A
2	1	3276	A
2	1	3282	G
2	1	3288	G
2	1	3301	C
2	1	3307	U
2	1	3309	U
2	1	3315	A
2	1	3316	G
2	1	3317	A
2	1	3318	A
2	1	3319	G
2	1	3327	A
2	1	3337	A
2	1	3338	A
2	1	3339	A
2	1	3343	A
2	1	3344	A
2	1	3345	G
2	1	3346	U
2	1	3349	U
2	1	3351	U
2	1	3353	U
2	1	3354	U
2	1	3357	C
2	1	3359	U
2	1	3360	G
2	1	3362	C

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Mol	Chain	Res	Type
2	1	3367	A
2	1	3368	A
2	1	3370	U
2	1	3372	C
2	1	3373	C
2	1	3374	A
2	1	3375	U
2	1	3404	G
2	1	3405	C
2	1	3414	U
2	1	3417	A
2	1	3418	U
2	1	3419	G
2	1	3420	U
2	1	3421	G
2	1	3424	A
2	1	3425	C
2	1	3430	U
2	1	3431	A
2	1	3435	U
2	1	3436	A
2	1	3469	U
2	1	3470	G
2	1	3476	A
2	1	3479	C
2	1	3483	U
2	1	3490	A
2	1	3491	A
2	1	3492	G
2	1	3493	A
2	1	3495	U
3	2	9	A
3	2	24	G
3	2	29	C
3	2	42	U
3	2	43	C
3	2	46	U
3	2	60	A
3	2	67	A
3	2	70	C
3	2	71	G
3	2	79	A

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Mol	Chain	Res	Type
3	2	87	A
3	2	98	U
3	2	103	G
3	2	112	A
3	2	114	C
3	2	115	G
3	2	124	G
3	2	132	G
3	2	133	U
3	2	134	U
3	2	136	U
3	2	137	A
3	2	156	G
3	2	159	U
3	2	160	G
3	2	162	C
5	6	2	C
5	6	5	U
5	6	6	C
5	6	8	U
5	6	9	C
5	6	47	U
5	6	56	A
5	6	57	A
5	6	60	U
5	6	82	A
5	6	83	A
5	6	86	U
5	6	89	U
5	6	92	G
5	6	93	A
5	6	94	A
5	6	96	U
5	6	97	C
5	6	99	A
5	6	101	U
5	6	102	G
5	6	105	G
5	6	106	A
5	6	108	A
5	6	178	U
5	6	181	C

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Mol	Chain	Res	Type
5	6	182	C
5	6	184	C
5	6	186	U
5	6	187	U
5	6	188	G

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	674	A
2	1	759	C
2	1	761	U
2	1	816	A
2	1	949	A
2	1	996	G
2	1	1159	U
2	1	1272	U
2	1	1333	A
2	1	1380	A
2	1	1389	A
2	1	1540	A
2	1	1806	U
2	1	1851	A
2	1	1916	G
2	1	3024	C
2	1	3070	U
2	1	3081	U
2	1	3217	U
2	1	3337	A
2	1	3367	A
3	2	131	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

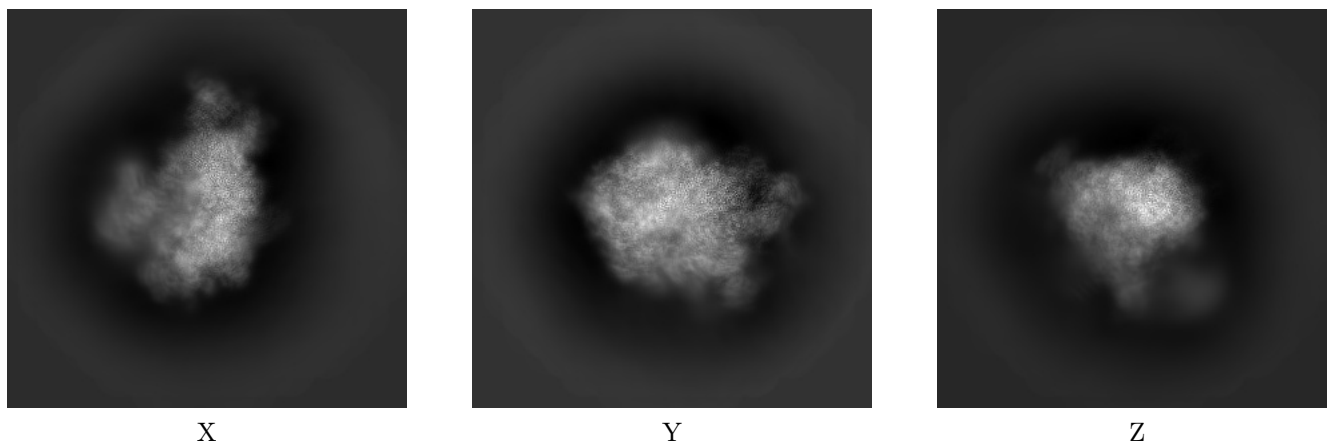
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24411. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

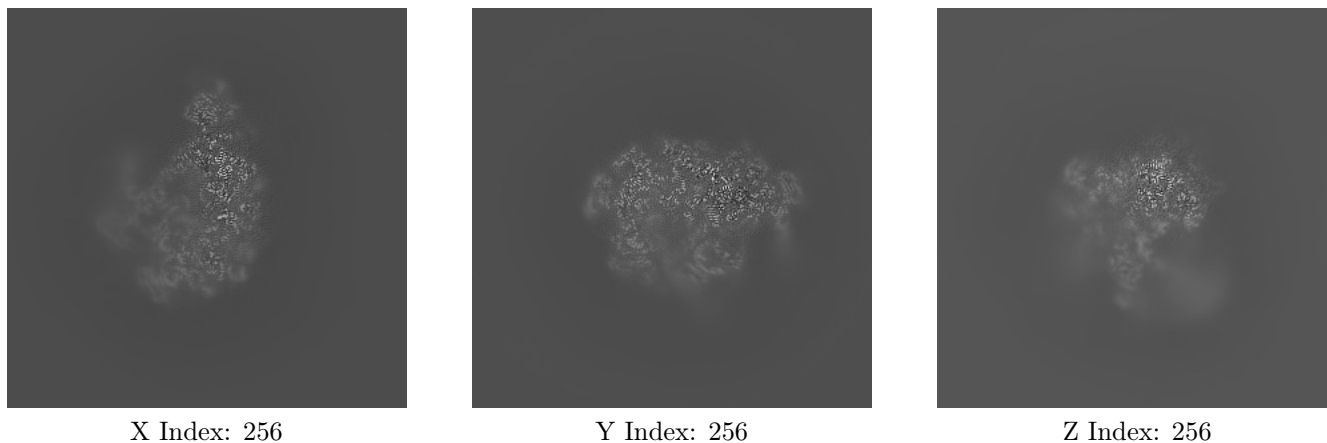
6.1.1 Primary map



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

6.2 Central slices [i](#)

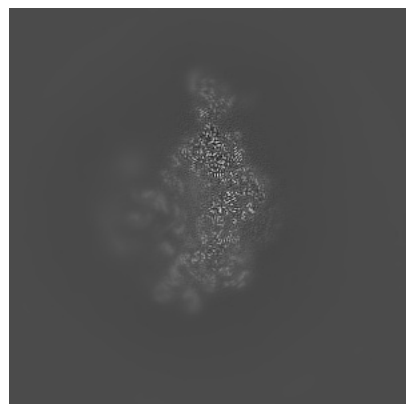
6.2.1 Primary map



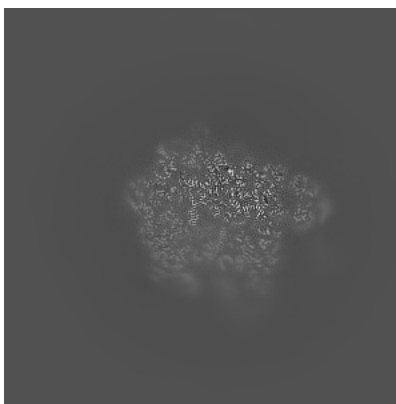
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

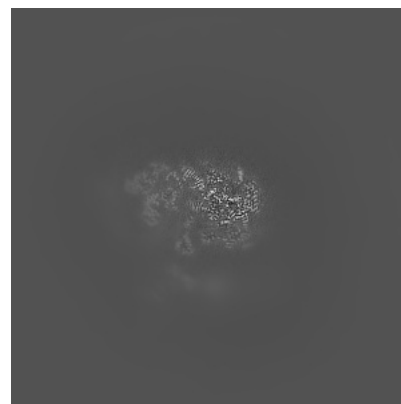
6.3.1 Primary map



X Index: 271



Y Index: 274



Z Index: 314

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

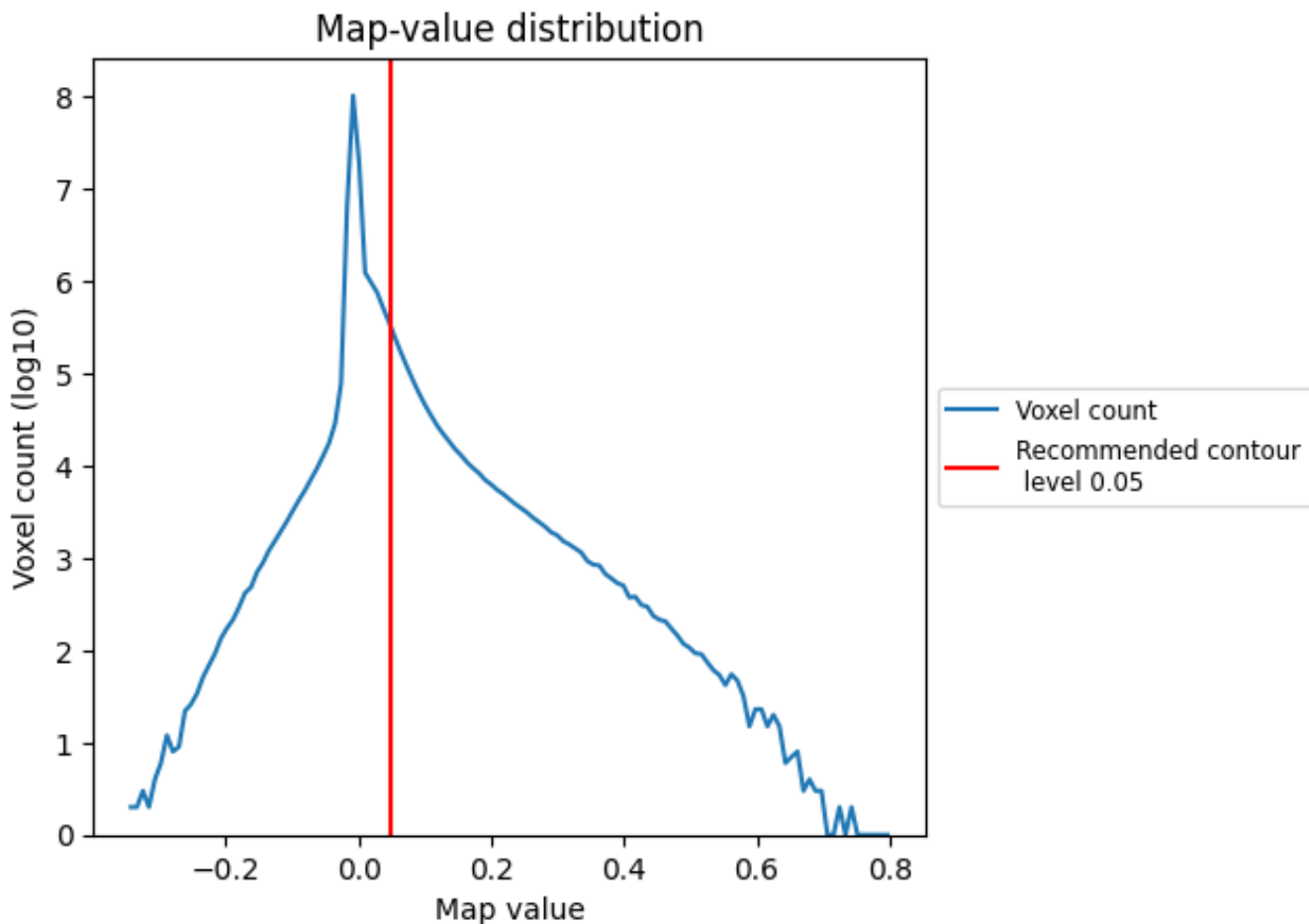
6.5 Mask visualisation

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

7 Map analysis [i](#)

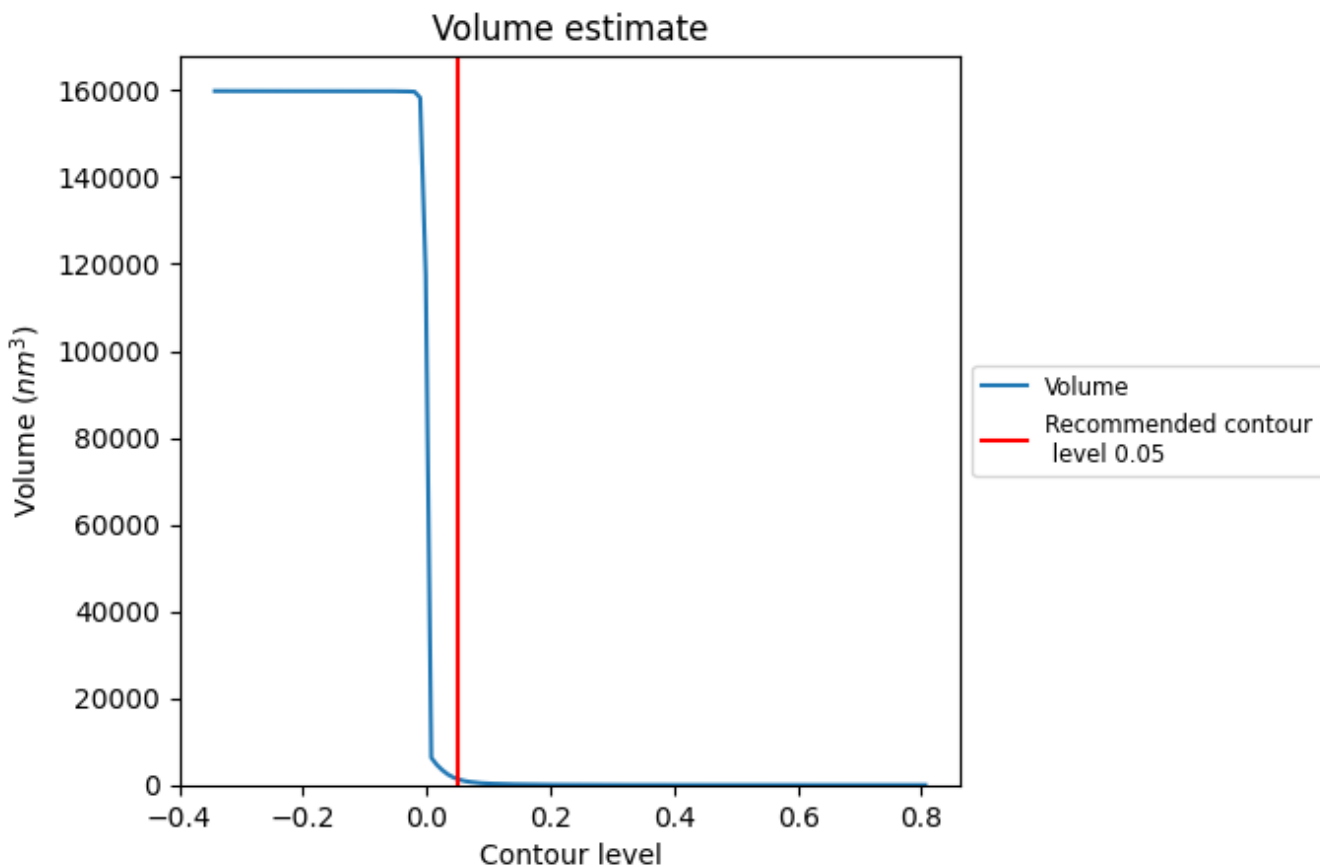
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

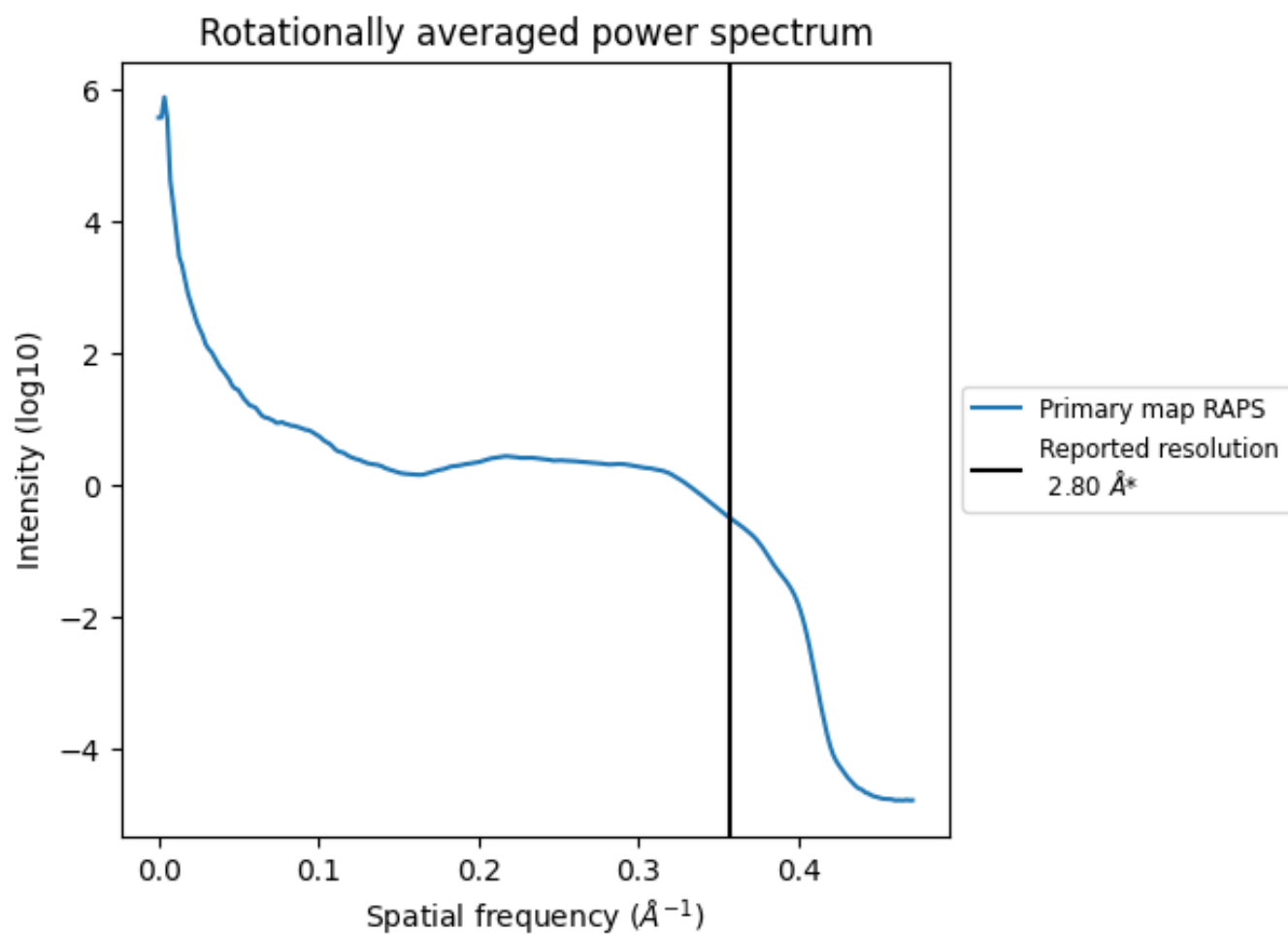
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1366 nm³; this corresponds to an approximate mass of 1234 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 0.357 \AA^{-1}

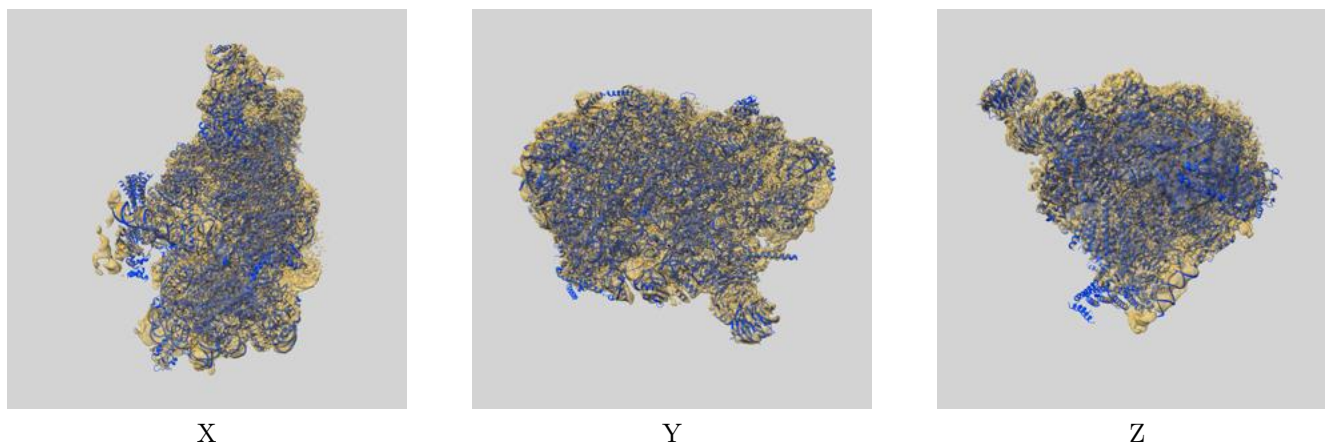
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

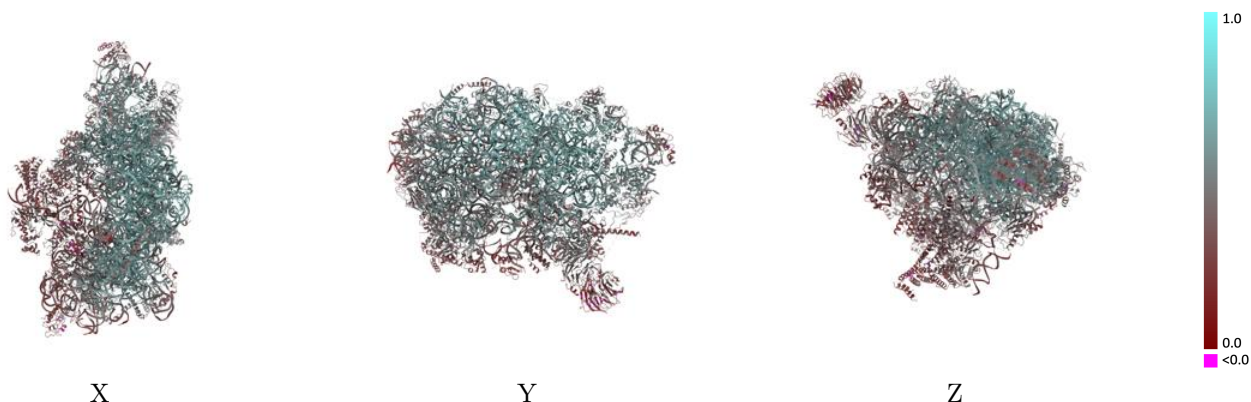
This section contains information regarding the fit between EMDB map EMD-24411 and PDB model 8ESQ. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



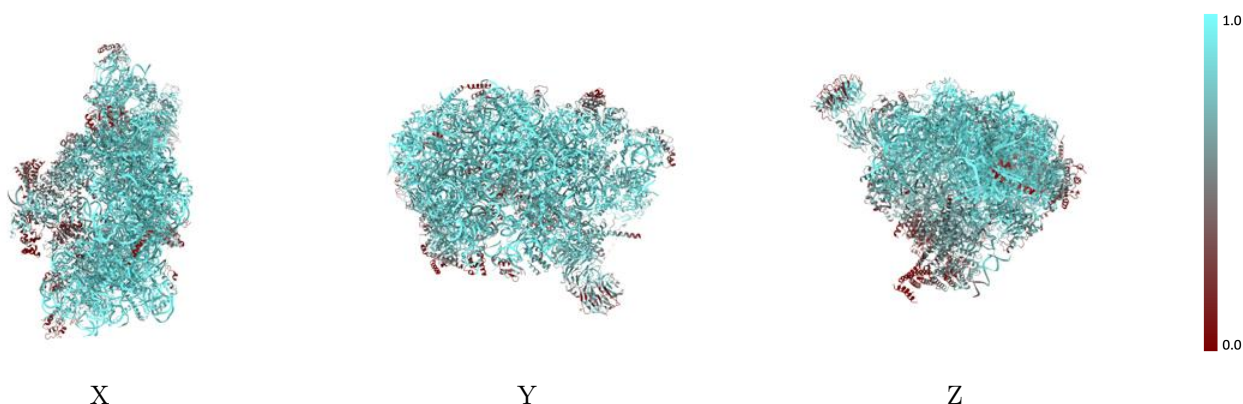
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



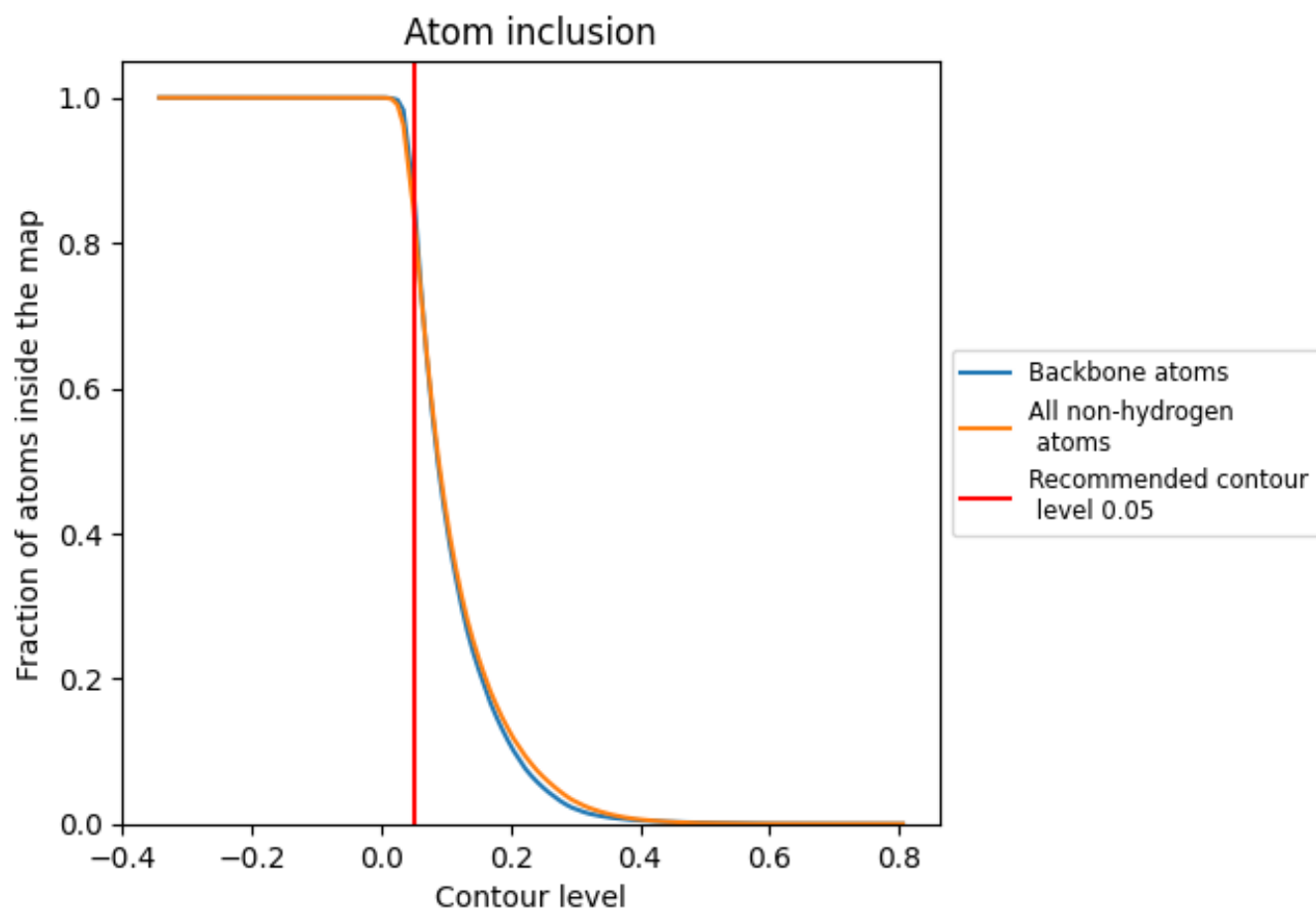
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

















































The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8453	 0.4890
1	 0.9673	 0.5130
2	 0.9893	 0.6270
3	 0.6620	 0.5250
6	 0.9447	 0.5020
7	 0.2233	 0.2600
8	 0.8679	 0.4260
A	 0.8411	 0.4450
B	 0.9272	 0.5150
C	 0.9717	 0.6220
D	 0.6478	 0.5090
E	 0.8219	 0.4660
F	 0.8430	 0.5430
G	 0.9498	 0.6220
H	 0.8767	 0.4450
I	 0.5248	 0.3430
J	 0.5652	 0.3300
K	 0.7437	 0.4620
L	 0.9789	 0.6500
M	 0.9591	 0.4900
N	 0.9963	 0.6690
O	 0.9564	 0.5490
P	 0.9132	 0.5590
Q	 0.9421	 0.5830
R	 0.8457	 0.4080
S	 0.8862	 0.4800
T	 0.5358	 0.2880
U	 0.4864	 0.2730
V	 0.8563	 0.4610
W	 0.4891	 0.3040
X	 0.9493	 0.5960
Y	 0.9615	 0.6190
Z	 0.8057	 0.4220
a	 0.7203	 0.5210
b	 0.5978	 0.3670



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Chain	Atom inclusion	Q-score
c	 0.7185	 0.3420
d	 0.9104	 0.5160
e	 0.9668	 0.6030
f	 0.9865	 0.6030
g	 0.9057	 0.5000
h	 0.9658	 0.6270
i	 0.9564	 0.6130
j	 0.9963	 0.6580
k	 0.7927	 0.4580
l	 0.6389	 0.3410
m	 0.7769	 0.4360
n	 0.8547	 0.5060
o	 0.7532	 0.5000
p	 0.5332	 0.2850
q	 0.4786	 0.3460
r	 0.7241	 0.3690
s	 0.6471	 0.3240
t	 0.8780	 0.5260
u	 0.6924	 0.3860
v	 0.9140	 0.5820
w	 0.3878	 0.3550
x	 0.5324	 0.4510
y	 0.7377	 0.3610
z	 0.6211	 0.3470