



## wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:32 AM UTC

PDB ID : 8EUP / pdb\_00008eup  
EMDB ID : EMD-24410  
Title : Ytm1 associated 60S nascent ribosome State 1A  
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.  
Deposited on : 2022-10-19  
Resolution : 3.10 Å (reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

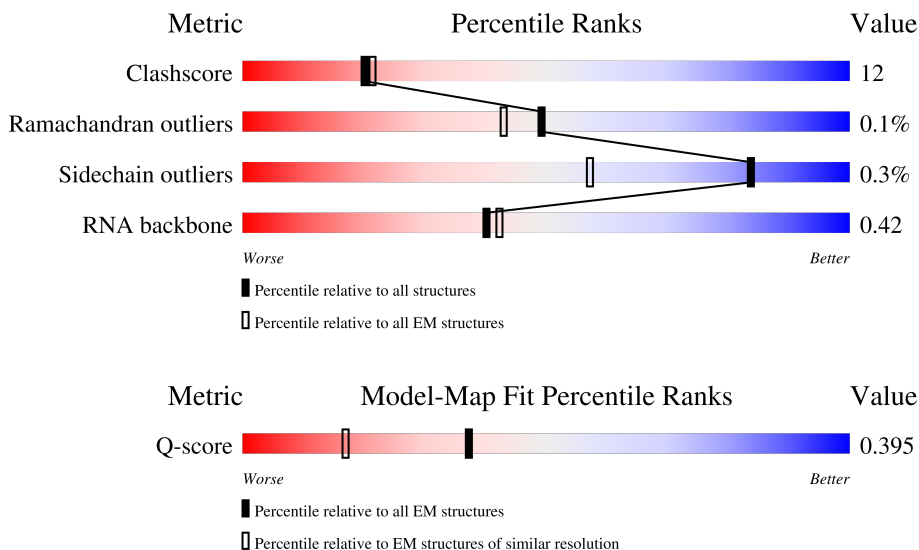
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 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 3.10 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 ( 2.60 - 3.60 )

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	1	3497	
2	2	165	
3	3	302	

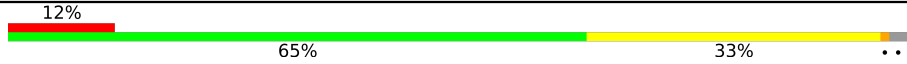
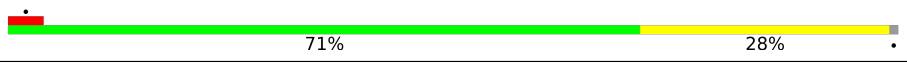

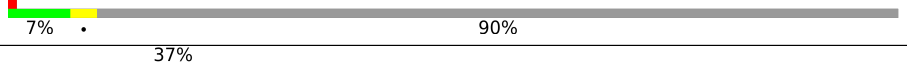



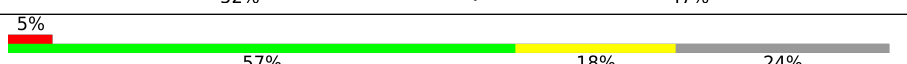
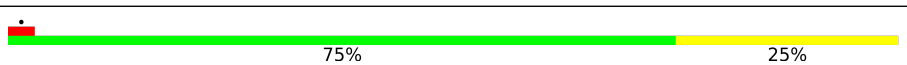
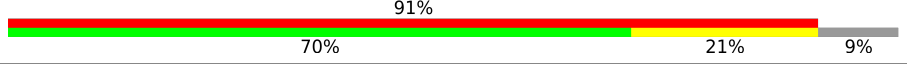


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Mol	Chain	Length	Quality of chain
4	4	217	71% 24% 5%
5	5	387	58% 29% 13%
6	6	300	11% 5% 82%
7	A	295	14% 54% 32% 14%
8	B	388	23% 78% 19%
9	C	363	60% 30% 10%
10	D	578	38% 51% 19% 31%
11	E	195	52% 34% 13%
12	F	250	74% 21% 5%
13	G	259	42% 20% 37%
14	H	190	81% 88% 8%
15	J	333	21% 27% 72%
16	K	373	47% 64% 34%
17	L	208	33% 23% 44%
18	M	134	89% 8%
19	N	201	55% 27% 17%
20	O	197	6% 64% 27% 8%
21	P	187	50% 20% 30%
22	Q	187	57% 14% 28%
23	S	176	9% 74% 22% 5%
24	V	139	89% 65% 26% 9%
25	Y	126	67% 32% 1%
26	b	642	23% 23% 76%
27	e	127	63% 35% 2%
28	f	108	67% 31% 2%

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Mol	Chain	Length	Quality of chain
29	h	122	
30	i	99	
31	j	91	
32	m	740	
33	o	276	
34	r	260	
35	t	249	
36	u	192	
37	v	209	
38	x	306	
39	y	244	
40	T	160	

## 2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 78722 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA (1422-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1422	30438	13596	5508	9912	1422	0	0

- Molecule 2 is a RNA chain called RNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	146	3109	1391	555	1017	146	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	194	1613	1020	307	279	7	0	0

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	4	207	1746	1138	298	302	8	0	0

- Molecule 5 is a protein called Ribosome biogenesis protein nsal.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	338	2669	1705	466	487	11	0	0

- Molecule 6 is a RNA chain called RNA (55-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	6	55	1167	524	204	384	55	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	A	253	2049	1299	372	370	8	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	B	315	1552	922	315	315	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	C	328	2568	1629	486	450	3	0	0

- Molecule 10 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	D	400	3055	1966	532	548	9	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	E	170	1328	854	243	228	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	F	239	1939	1247	355	334	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	163	1277	818	224	233	2	2	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	H	175	862	512	175	175	0	0

- Molecule 15 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	J	94	469	281	94	94	0	0

- Molecule 16 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	K	247	1225	731	247	247	0	0

- Molecule 17 is a protein called 60S ribosomal protein L13.

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

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	M	123	609	363	123	123	0	0

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	O	181	1437	925	271	238	3	0	0

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	P	130	1037	663	187	184	3	0	0

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Q	134	1041	655	201	184	1	0	0

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
24	V	126	619	366	126	127	0	0

- Molecule 25 is a protein called Ribosomal protein L26.

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

- Molecule 26 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	b	151	749	447	151	151	0	0

- Molecule 27 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	e	124	995	621	202	167	5	0	0

- Molecule 28 is a protein called 60S ribosomal protein L33-B.

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

- Molecule 29 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	h	120	993	626	193	174		0	0

- Molecule 30 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	i	98	783	487	164	131	1	0	0

- Molecule 31 is a protein called 60S ribosomal protein L37-B.

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

- Molecule 32 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	m	73	595	368	107	120	0	0

- Molecule 33 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	o	136	673	401	136	136	0	0

- Molecule 34 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	r	56	278	166	56	56	0	0

- Molecule 35 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	t	23	Total	C	N	O	0	0
			167	105	32	30		

- Molecule 36 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	u	102	Total	C	N	O	0	0
			506	302	102	102		

- Molecule 37 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	v	158	Total	C	N	O	S	0	0
			1276	804	240	229	3		

- Molecule 38 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	x	306	Total	C	N	O	S	0	0
			2524	1583	464	468	9		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	y	222	Total	C	N	O	0	0
			1092	648	222	222		

- Molecule 40 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	T	18	Total	C	N	O	0	0
			125	80	23	22		

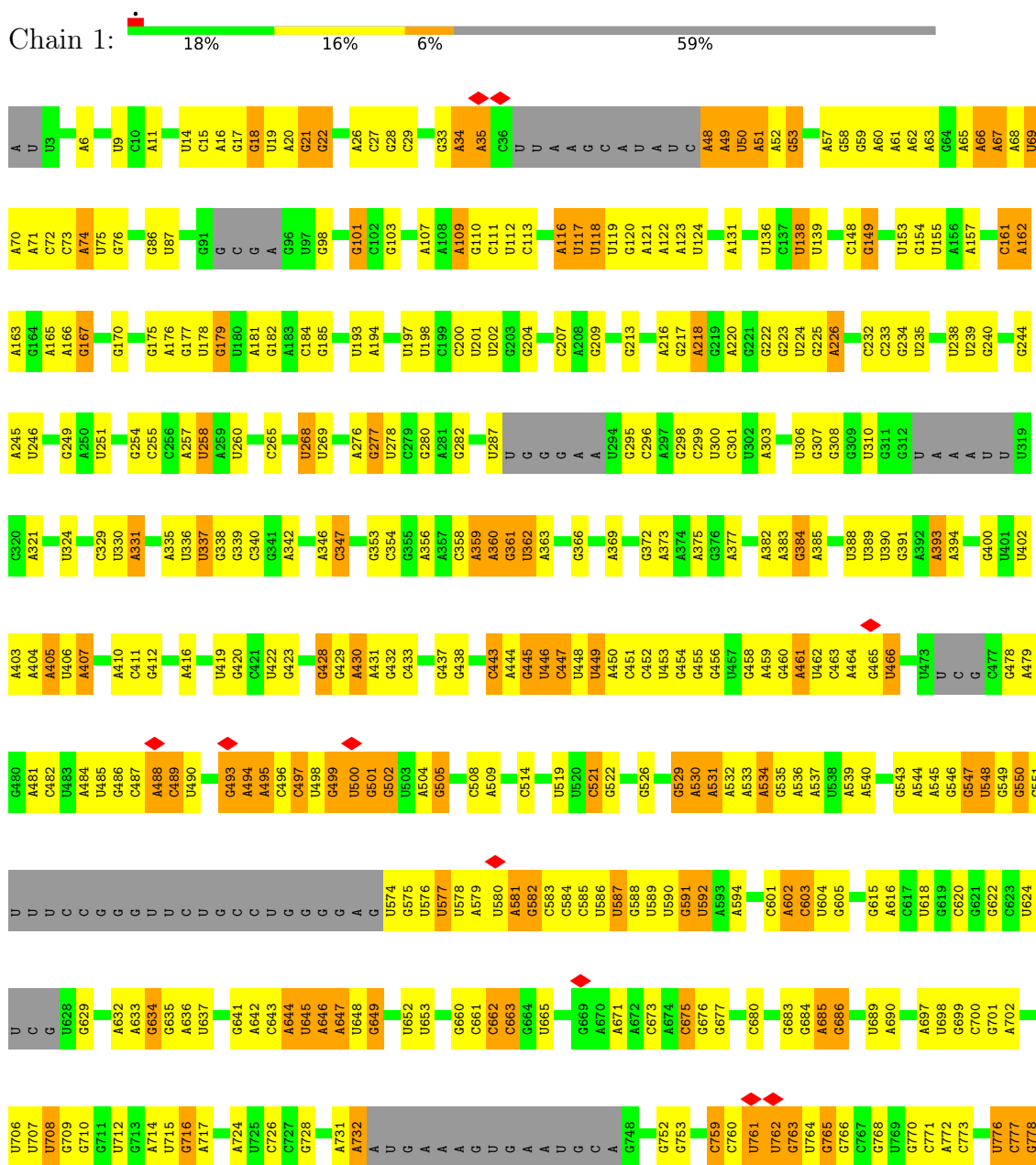
- Molecule 41 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

### 3 Residue-property plots

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: RNA (1422-MER)





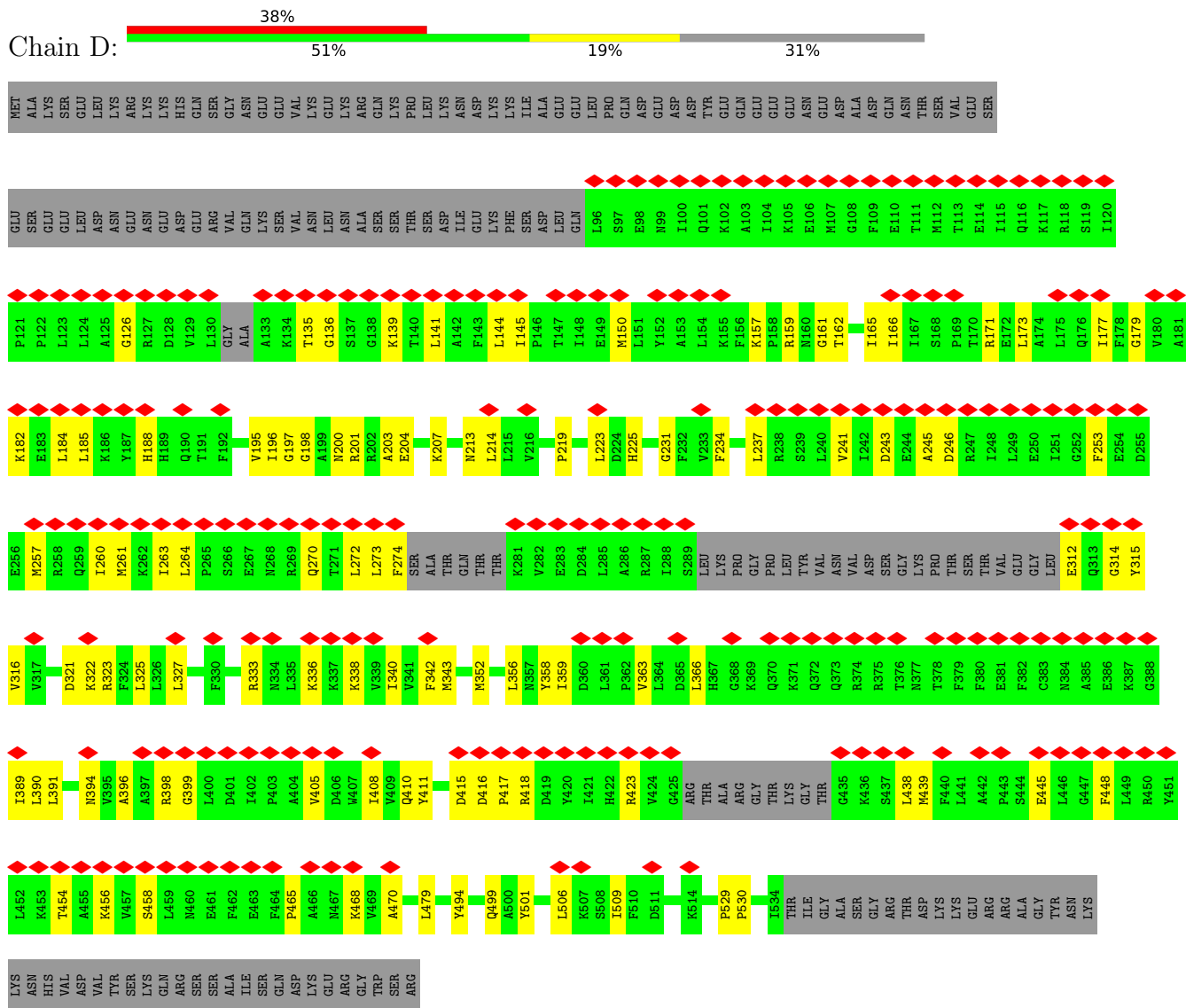




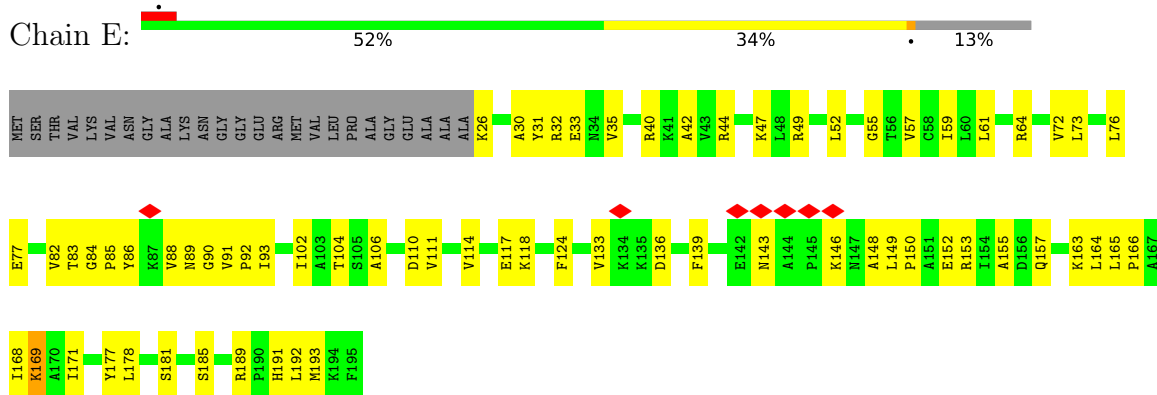




• Molecule 10: RNA helicase



• Molecule 11: 60S ribosomal protein L6

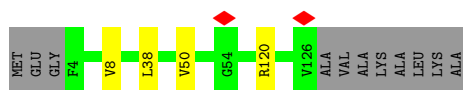
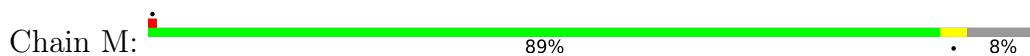


• Molecule 12: 60S ribosomal protein L7-B

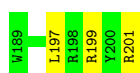
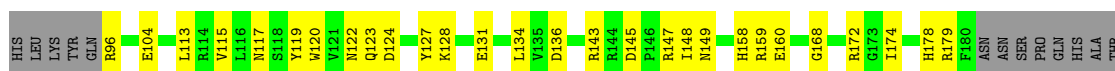
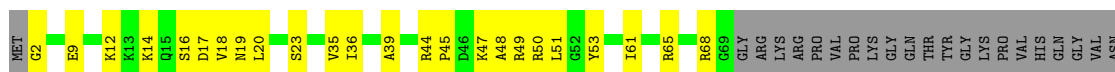




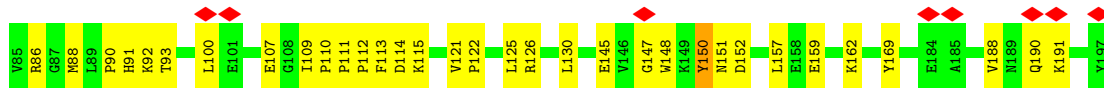
• Molecule 18: 60S ribosomal protein L14



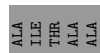
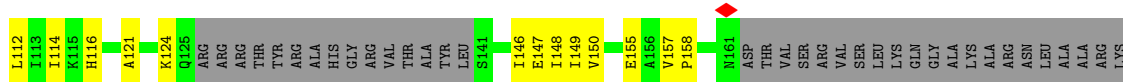
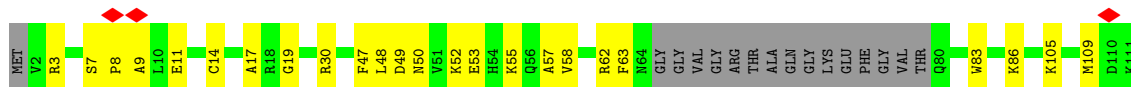
• Molecule 19: 60S ribosomal protein L15-A



• Molecule 20: 60S ribosomal protein L16-B

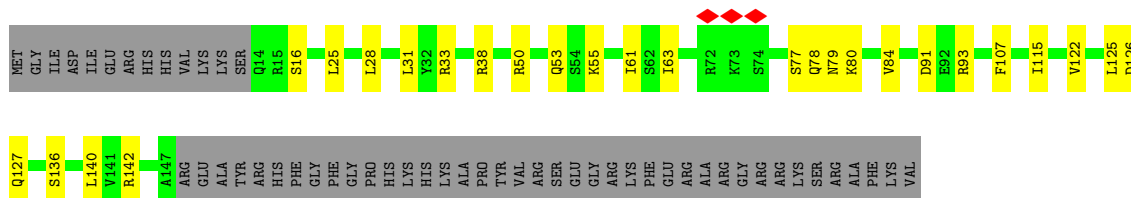


• Molecule 21: 60S ribosomal protein L17-A

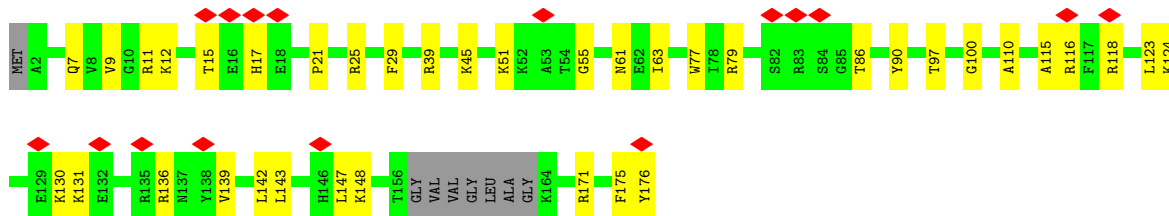
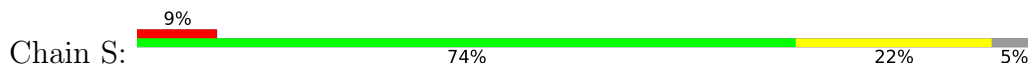


• Molecule 22: 60S ribosomal protein L18-A

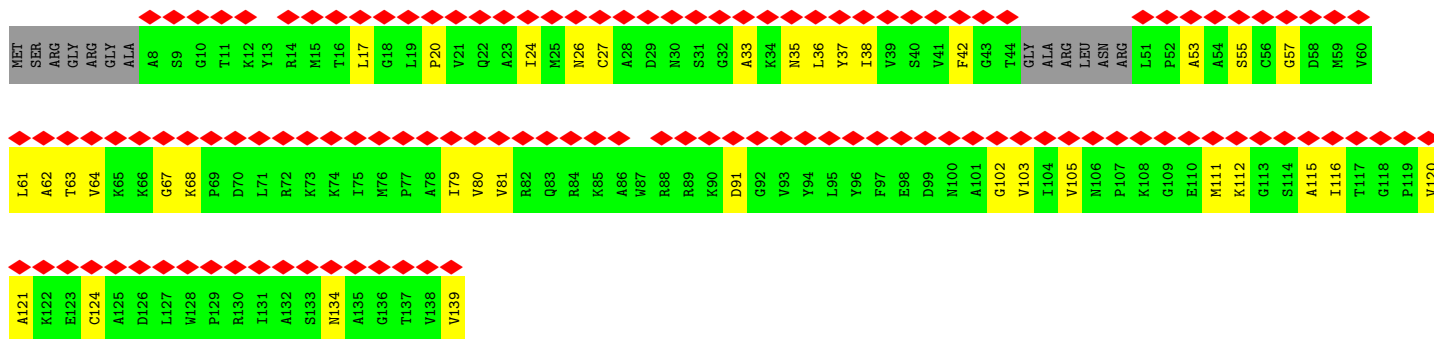
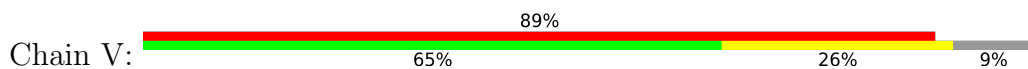




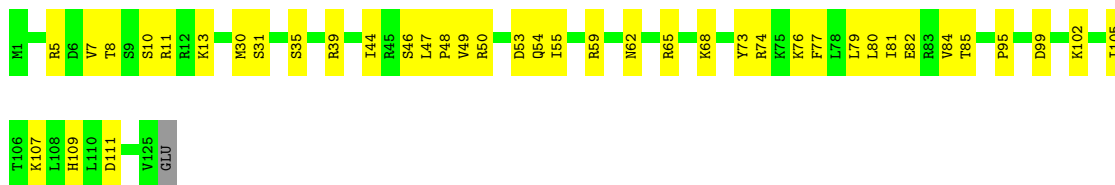
• Molecule 23: 60S ribosomal protein L20-A



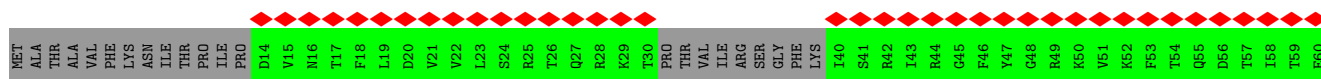
• Molecule 24: 60S ribosomal protein L23-A



• Molecule 25: Ribosomal protein L26



• Molecule 26: Probable nucleolar GTP-binding protein 1

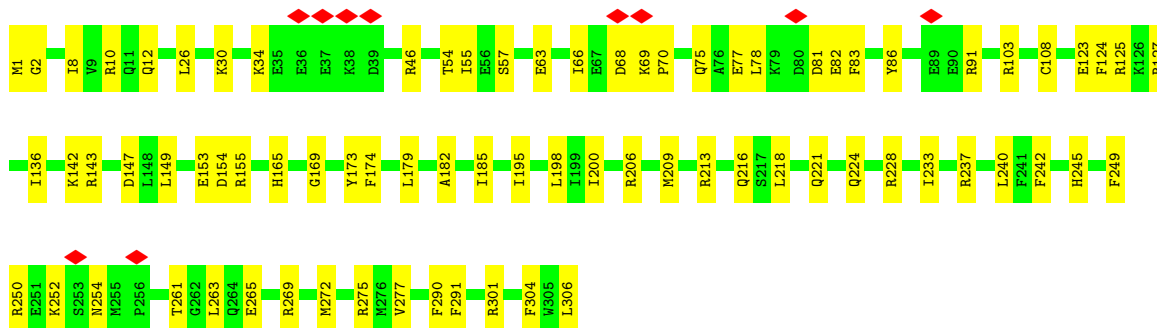




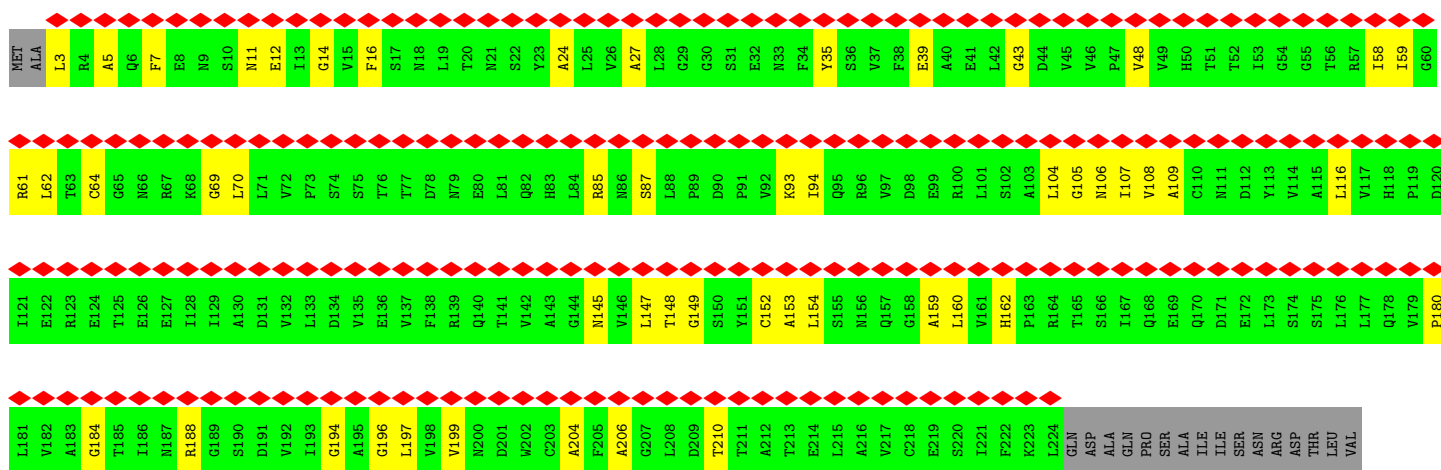






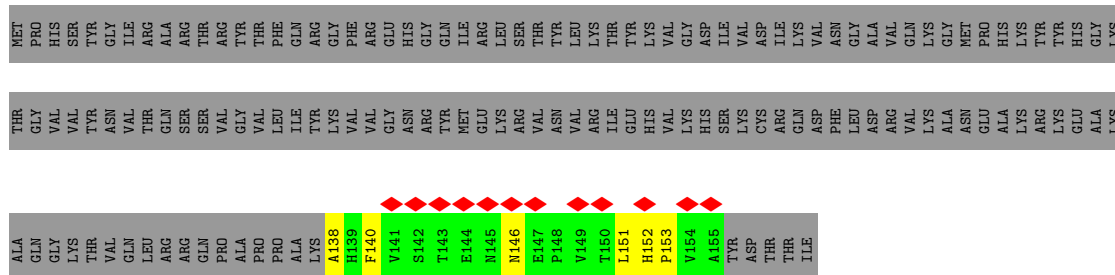


• Molecule 39: Eukaryotic translation initiation factor 6



GLU  
SER  
TYR  
THR

• Molecule 40: 60S ribosomal protein L21-A



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	71000	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	0.590	Depositor
Minimum map value	-0.339	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	1	0.24	0/34054	0.28	0/53038
2	2	0.23	0/3474	0.25	0/5403
3	3	0.32	0/1644	0.35	0/2210
4	4	0.23	0/1792	0.37	1/2421 (0.0%)
5	5	0.18	0/2722	0.34	0/3679
6	6	0.07	0/1303	0.13	0/2021
7	A	0.13	0/2088	0.31	0/2815
8	B	0.06	0/1550	0.20	0/2153
9	C	0.32	0/2614	0.41	1/3526 (0.0%)
10	D	0.14	0/3108	0.30	0/4197
11	E	0.20	0/1356	0.42	0/1829
12	F	0.20	0/1977	0.28	0/2651
13	G	0.22	0/1295	0.33	0/1748
14	H	0.06	0/860	0.21	0/1193
15	J	0.10	0/468	0.26	0/653
16	K	0.06	0/1223	0.20	0/1703
17	L	0.35	0/960	0.39	0/1288
18	M	0.09	0/608	0.28	0/846
19	N	0.32	0/1436	0.36	0/1920
20	O	0.11	0/1464	0.25	0/1961
21	P	0.16	0/1057	0.30	0/1419
22	Q	0.28	0/1052	0.36	0/1413
23	S	0.12	0/1444	0.31	0/1939
24	V	0.14	0/617	0.34	0/852
25	Y	0.23	0/1008	0.35	0/1341
26	b	0.09	0/745	0.26	0/1033
27	e	0.31	0/1009	0.36	0/1345
28	f	0.21	0/859	0.31	0/1152
29	h	0.23	0/1002	0.40	0/1333
30	i	0.21	0/791	0.33	0/1050
31	j	0.19	0/575	0.35	0/761
32	m	0.18	0/607	0.31	0/818

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	o	0.09	0/672	0.23	0/935
34	r	0.07	0/277	0.20	0/385
35	t	0.10	0/169	0.23	0/228
36	u	0.06	0/504	0.19	0/700
37	v	0.22	0/1296	0.36	0/1737
38	x	0.19	0/2570	0.34	0/3442
39	y	0.14	0/1091	0.42	0/1515
40	T	0.11	0/129	0.32	0/179
All	All	0.22	0/83470	0.30	2/120832 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	331	ASN	CB-CA-C	-5.81	104.61	110.65
4	4	46	LYS	N-CA-C	-5.50	105.19	111.07

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	30438	0	15314	545	0
2	2	3109	0	1573	49	0
3	3	1613	0	1665	57	0
4	4	1746	0	1763	41	0
5	5	2669	0	2728	84	0
6	6	1167	0	589	10	0
7	A	2049	0	2082	71	0
8	B	1552	0	708	11	0
9	C	2568	0	2702	103	0
10	D	3055	0	3009	75	0
11	E	1328	0	1408	56	0
12	F	1939	0	2030	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	G	1277	0	1350	47	0
14	H	862	0	372	4	0
15	J	469	0	212	3	0
16	K	1225	0	539	6	0
17	L	942	0	1012	57	0
18	M	609	0	278	3	0
19	N	1406	0	1441	48	0
20	O	1437	0	1529	48	0
21	P	1037	0	1056	32	0
22	Q	1041	0	1137	24	0
23	S	1408	0	1462	35	0
24	V	619	0	300	26	0
25	Y	998	0	1090	33	0
26	b	749	0	326	4	0
27	e	995	0	1059	34	0
28	f	839	0	866	26	0
29	h	993	0	1087	38	0
30	i	783	0	863	30	0
31	j	563	0	578	19	0
32	m	595	0	570	19	0
33	o	673	0	293	7	0
34	r	278	0	131	0	0
35	t	167	0	133	2	0
36	u	506	0	226	1	0
37	v	1276	0	1325	37	0
38	x	2524	0	2536	58	0
39	y	1092	0	505	30	0
40	T	125	0	108	6	0
41	j	1	0	0	0	0
All	All	78722	0	57955	1513	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 1513 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3285:G:H1	1:1:3302:U:H3	1.14	0.95
1:1:1155:U:H3	1:1:1165:G:H1	1.11	0.94
31:j:22:CYS:HB3	31:j:37:CYS:SG	2.11	0.91
19:N:115:VAL:HG11	19:N:160:GLU:HB3	1.54	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:710:G:H21	37:v:65:GLY:H	1.24	0.86

There are no symmetry-related clashes.

## 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	Percentiles	
3	3	192/302 (64%)	185 (96%)	7 (4%)	0	100	100
4	4	205/217 (94%)	198 (97%)	7 (3%)	0	100	100
5	5	334/387 (86%)	297 (89%)	37 (11%)	0	100	100
7	A	249/295 (84%)	235 (94%)	12 (5%)	2 (1%)	16	47
8	B	311/388 (80%)	306 (98%)	5 (2%)	0	100	100
9	C	324/363 (89%)	295 (91%)	29 (9%)	0	100	100
10	D	390/578 (68%)	380 (97%)	10 (3%)	0	100	100
11	E	168/195 (86%)	152 (90%)	16 (10%)	0	100	100
12	F	237/250 (95%)	223 (94%)	12 (5%)	2 (1%)	16	47
13	G	161/259 (62%)	144 (89%)	15 (9%)	2 (1%)	10	37
14	H	171/190 (90%)	170 (99%)	1 (1%)	0	100	100
15	J	92/333 (28%)	86 (94%)	5 (5%)	1 (1%)	11	39
16	K	243/373 (65%)	236 (97%)	6 (2%)	1 (0%)	30	61
17	L	114/208 (55%)	107 (94%)	7 (6%)	0	100	100
18	M	121/134 (90%)	118 (98%)	3 (2%)	0	100	100
19	N	160/201 (80%)	153 (96%)	7 (4%)	0	100	100
20	O	177/197 (90%)	175 (99%)	2 (1%)	0	100	100
21	P	124/187 (66%)	112 (90%)	12 (10%)	0	100	100
22	Q	132/187 (71%)	123 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	S	164/176 (93%)	155 (94%)	9 (6%)	0	100	100
24	V	122/139 (88%)	112 (92%)	10 (8%)	0	100	100
25	Y	123/126 (98%)	116 (94%)	7 (6%)	0	100	100
26	b	143/642 (22%)	139 (97%)	3 (2%)	1 (1%)	18	49
27	e	122/127 (96%)	112 (92%)	10 (8%)	0	100	100
28	f	104/108 (96%)	97 (93%)	7 (7%)	0	100	100
29	h	118/122 (97%)	115 (98%)	3 (2%)	0	100	100
30	i	96/99 (97%)	88 (92%)	8 (8%)	0	100	100
31	j	69/91 (76%)	64 (93%)	5 (7%)	0	100	100
32	m	69/740 (9%)	66 (96%)	3 (4%)	0	100	100
33	o	134/276 (49%)	128 (96%)	6 (4%)	0	100	100
34	r	54/260 (21%)	53 (98%)	1 (2%)	0	100	100
35	t	21/249 (8%)	21 (100%)	0	0	100	100
36	u	98/192 (51%)	96 (98%)	2 (2%)	0	100	100
37	v	154/209 (74%)	144 (94%)	9 (6%)	1 (1%)	21	52
38	x	304/306 (99%)	288 (95%)	16 (5%)	0	100	100
39	y	220/244 (90%)	201 (91%)	19 (9%)	0	100	100
40	T	16/160 (10%)	16 (100%)	0	0	100	100
All	All	6036/9510 (64%)	5706 (94%)	320 (5%)	10 (0%)	49	73

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	A	249	VAL
15	J	126	PRO
37	v	130	ILE
7	A	248	PHE
16	K	153	ILE

### 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	
3	3	171/271 (63%)	170 (99%)	1 (1%)	78	83
4	4	188/197 (95%)	187 (100%)	1 (0%)	81	85
5	5	299/345 (87%)	298 (100%)	1 (0%)	86	87
7	A	227/266 (85%)	227 (100%)	0	100	100
9	C	275/297 (93%)	275 (100%)	0	100	100
10	D	306/505 (61%)	305 (100%)	1 (0%)	86	87
11	E	139/155 (90%)	138 (99%)	1 (1%)	76	82
12	F	201/210 (96%)	200 (100%)	1 (0%)	81	85
13	G	136/212 (64%)	136 (100%)	0	100	100
17	L	97/167 (58%)	97 (100%)	0	100	100
19	N	146/176 (83%)	146 (100%)	0	100	100
20	O	149/162 (92%)	148 (99%)	1 (1%)	76	82
21	P	109/149 (73%)	109 (100%)	0	100	100
22	Q	115/159 (72%)	115 (100%)	0	100	100
23	S	150/154 (97%)	150 (100%)	0	100	100
25	Y	110/111 (99%)	110 (100%)	0	100	100
27	e	106/107 (99%)	104 (98%)	2 (2%)	50	73
28	f	89/91 (98%)	89 (100%)	0	100	100
29	h	106/107 (99%)	105 (99%)	1 (1%)	70	80
30	i	83/84 (99%)	83 (100%)	0	100	100
31	j	58/71 (82%)	58 (100%)	0	100	100
32	m	65/659 (10%)	65 (100%)	0	100	100
35	t	12/223 (5%)	12 (100%)	0	100	100
37	v	135/181 (75%)	134 (99%)	1 (1%)	76	82
38	x	273/273 (100%)	272 (100%)	1 (0%)	84	86
40	T	12/139 (9%)	11 (92%)	1 (8%)	10	35
All	All	3757/5471 (69%)	3744 (100%)	13 (0%)	84	87

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	e	125	SER

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Mol	Chain	Res	Type
27	e	127	GLU
40	T	151	LEU
37	v	123	VAL
38	x	154	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
35	t	60	ASN
37	v	10	GLN
38	x	216	GLN
10	D	200	ASN
10	D	188	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1398/3497 (39%)	420 (30%)	11 (0%)
2	2	142/165 (86%)	31 (21%)	0
6	6	52/300 (17%)	16 (30%)	0
All	All	1592/3962 (40%)	467 (29%)	11 (0%)

5 of 467 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	9	U
1	1	11	A
1	1	16	A
1	1	18	G
1	1	21	G

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1380	A
1	1	1389	A
1	1	3407	U
1	1	3337	A
1	1	996	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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 [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
1	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	505:G	O3'	506:G	P	6.68

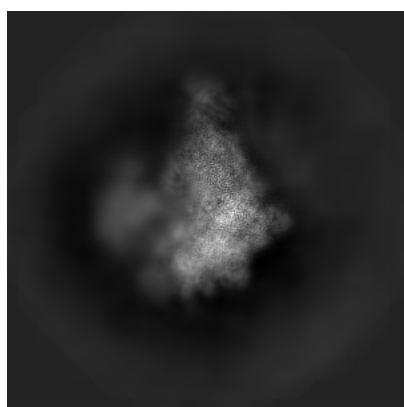
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24410. These allow visual inspection of the internal detail of the map and identification of artifacts.

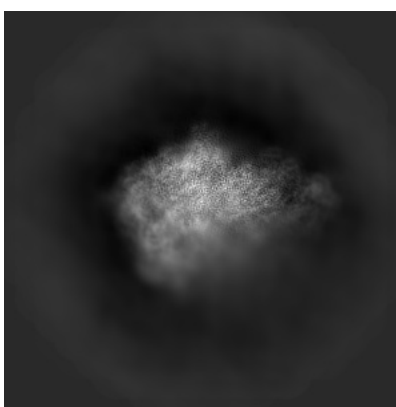
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

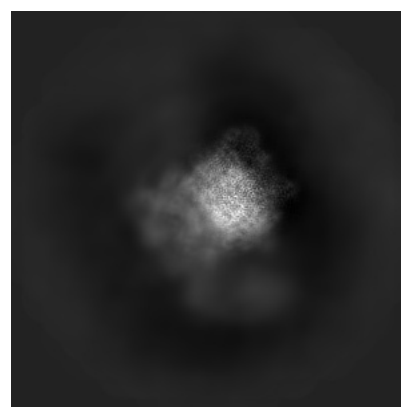
#### 6.1.1 Primary map



X



Y

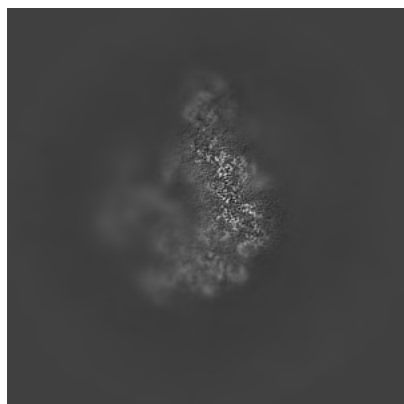


Z

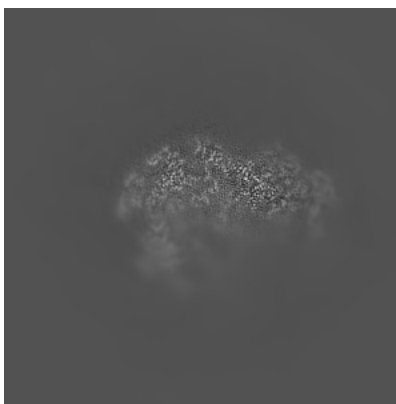
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

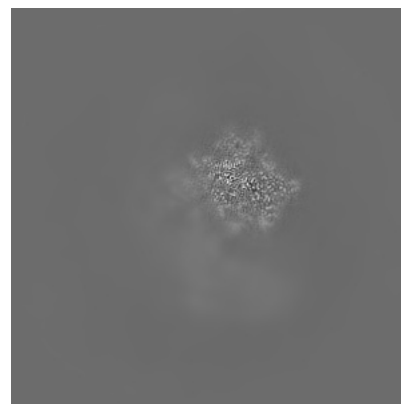
#### 6.2.1 Primary map



X Index: 256



Y Index: 256

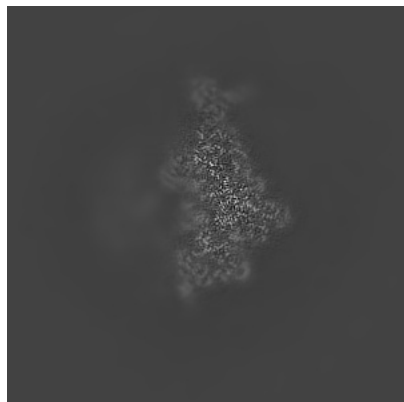


Z Index: 256

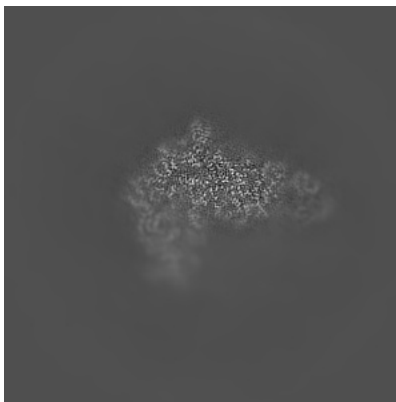
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

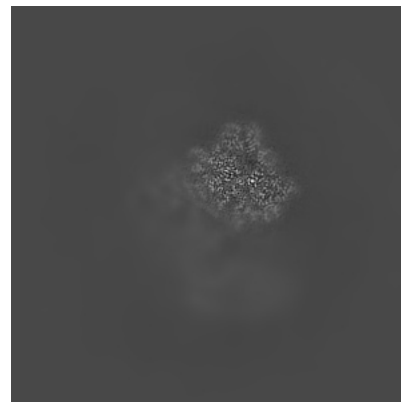
### 6.3.1 Primary map



X Index: 286



Y Index: 274

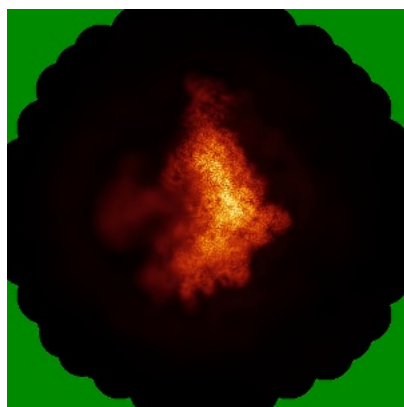


Z Index: 249

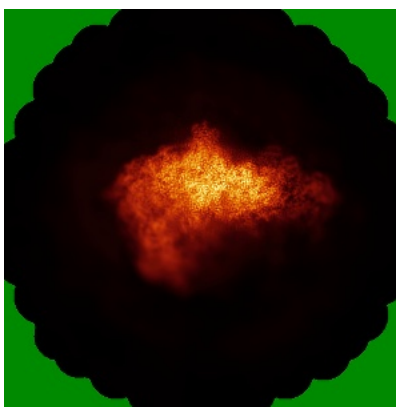
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

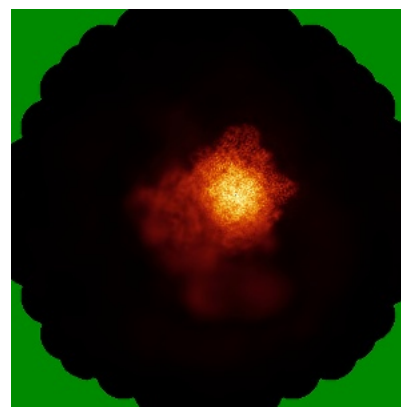
### 6.4.1 Primary map



X



Y

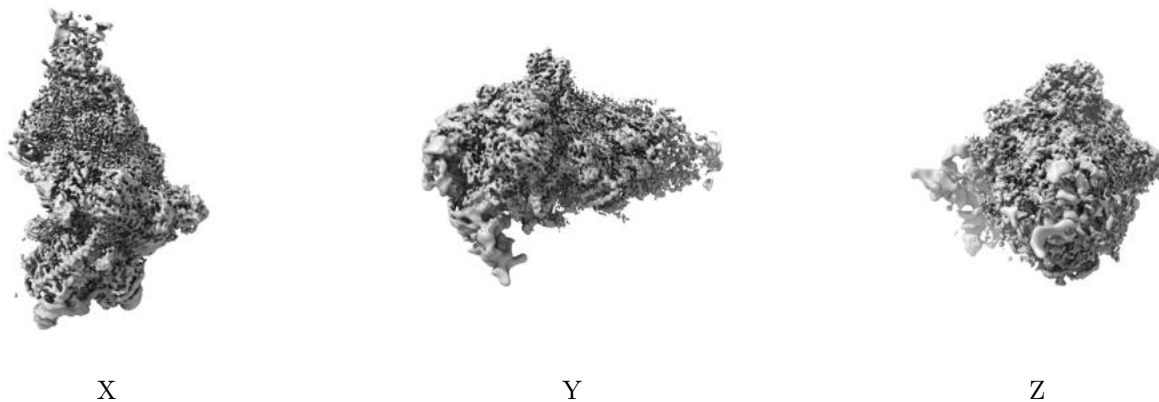


Z

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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

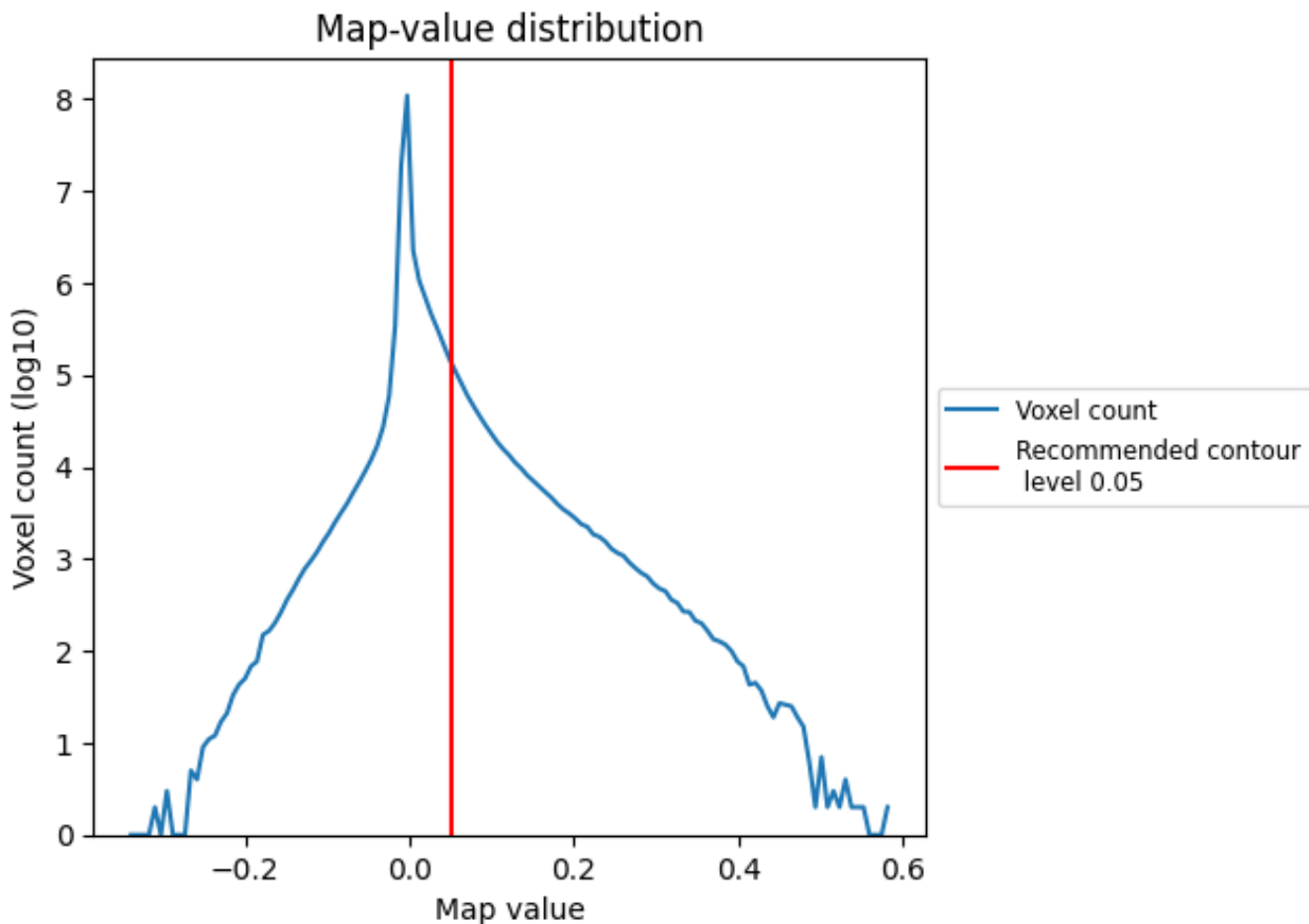
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

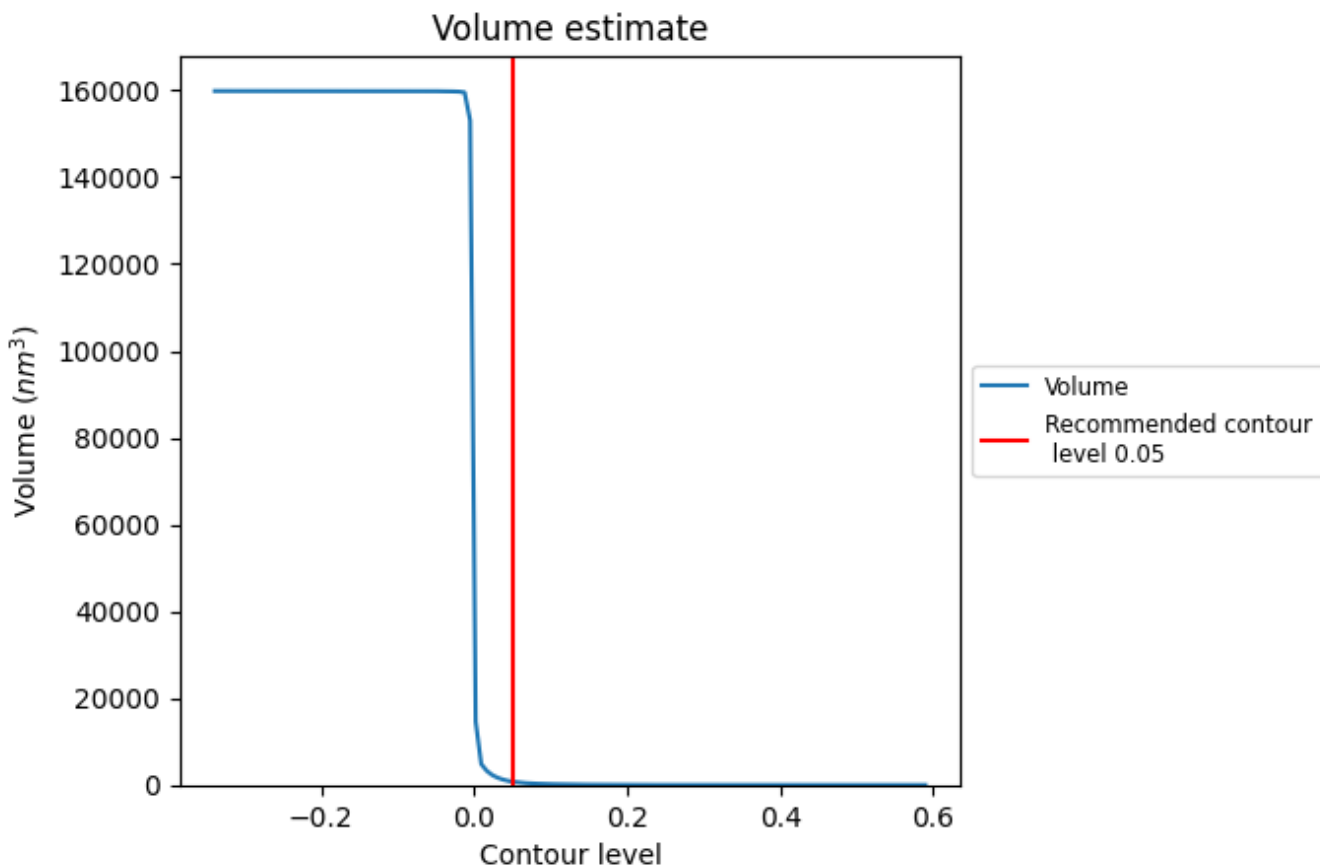
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

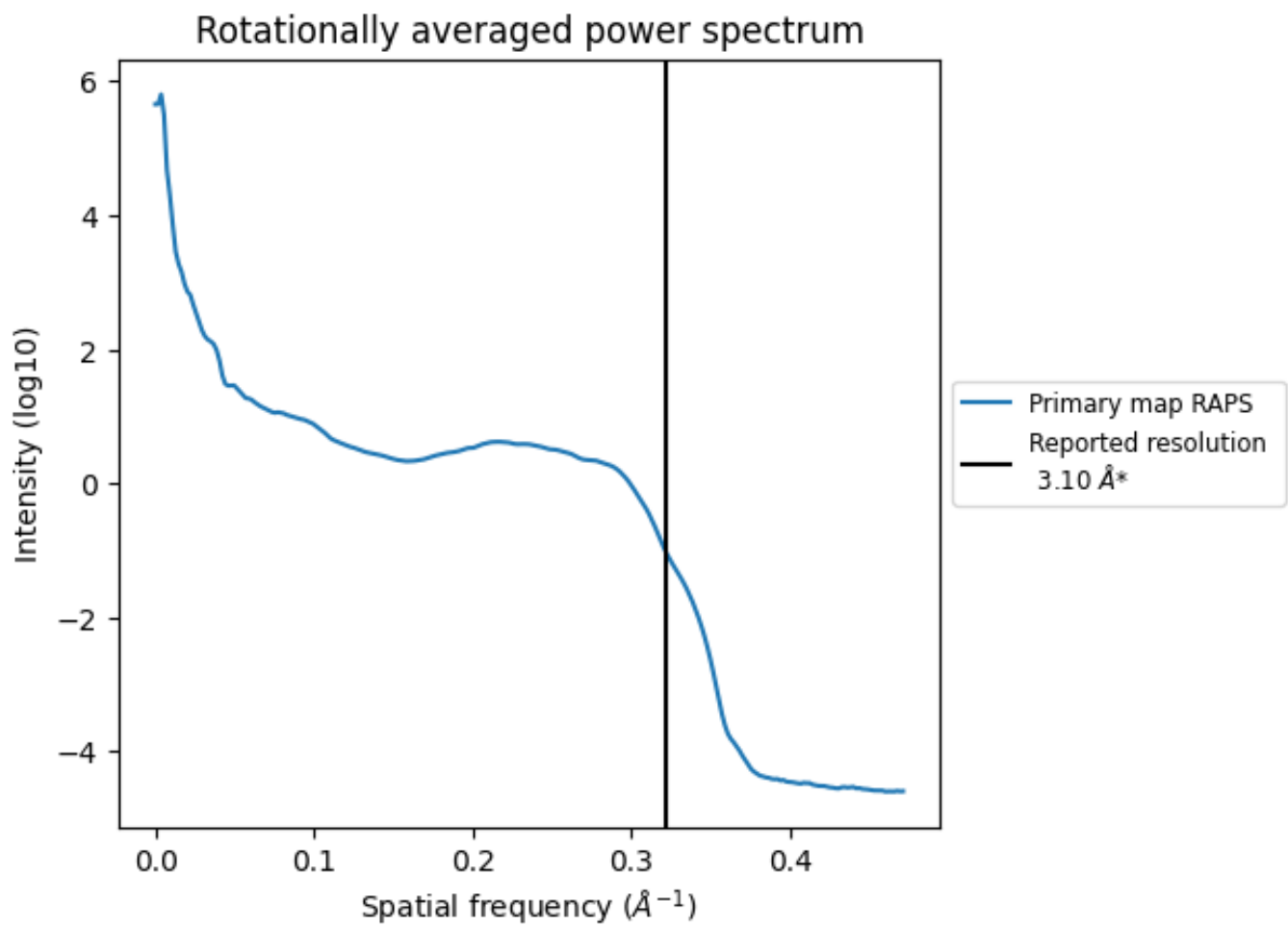
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is  $765 \text{ nm}^3$ ; this corresponds to an approximate mass of 691 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 0.323 Å<sup>-1</sup>

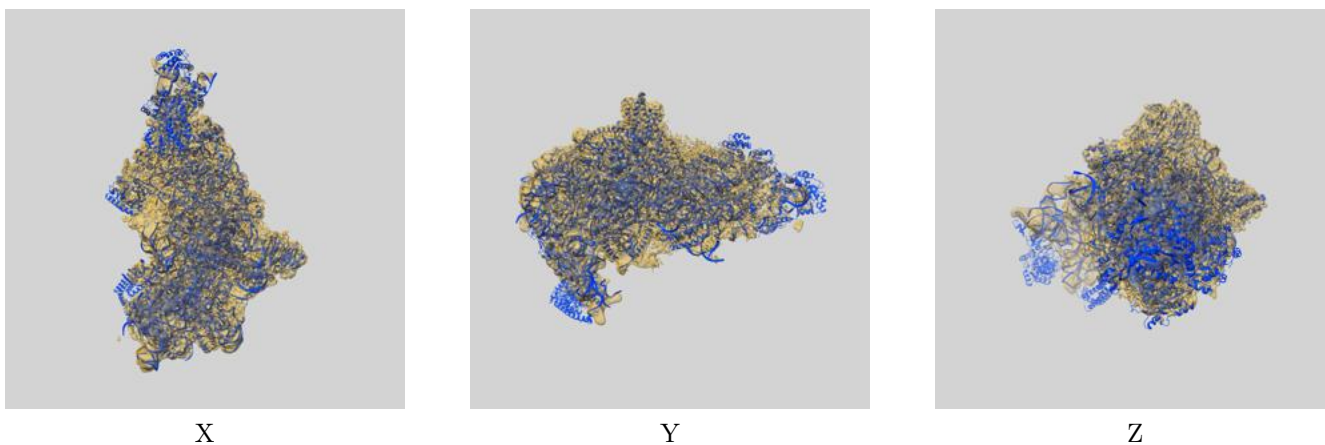
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

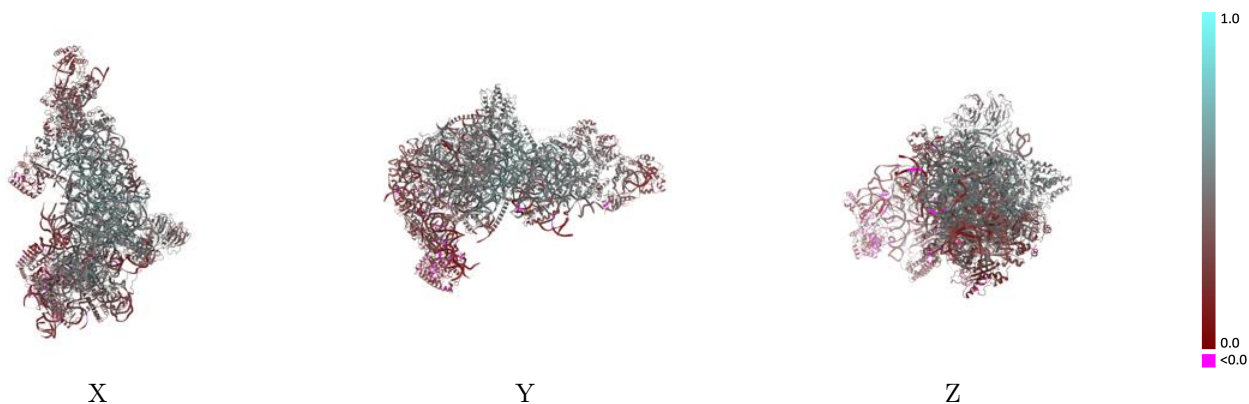
This section contains information regarding the fit between EMDB map EMD-24410 and PDB model 8EUP. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlay [i](#)



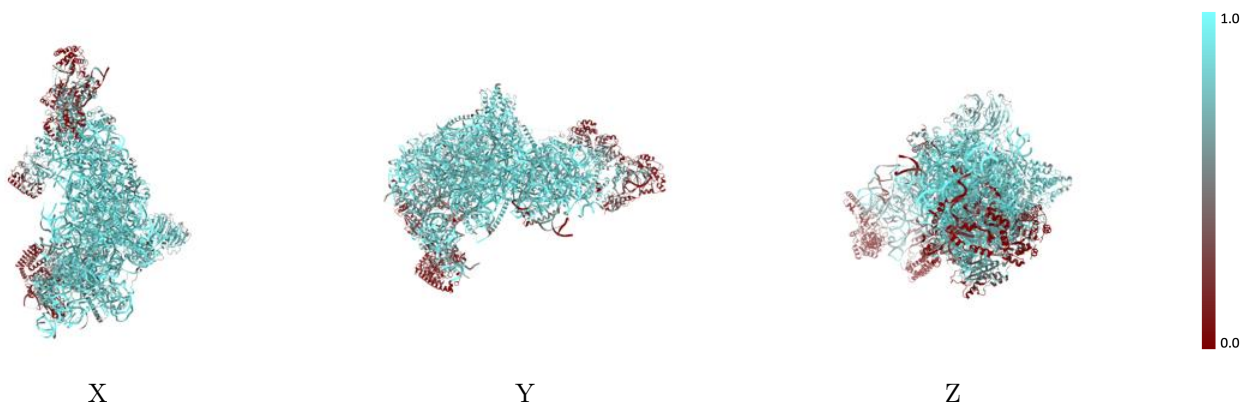
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



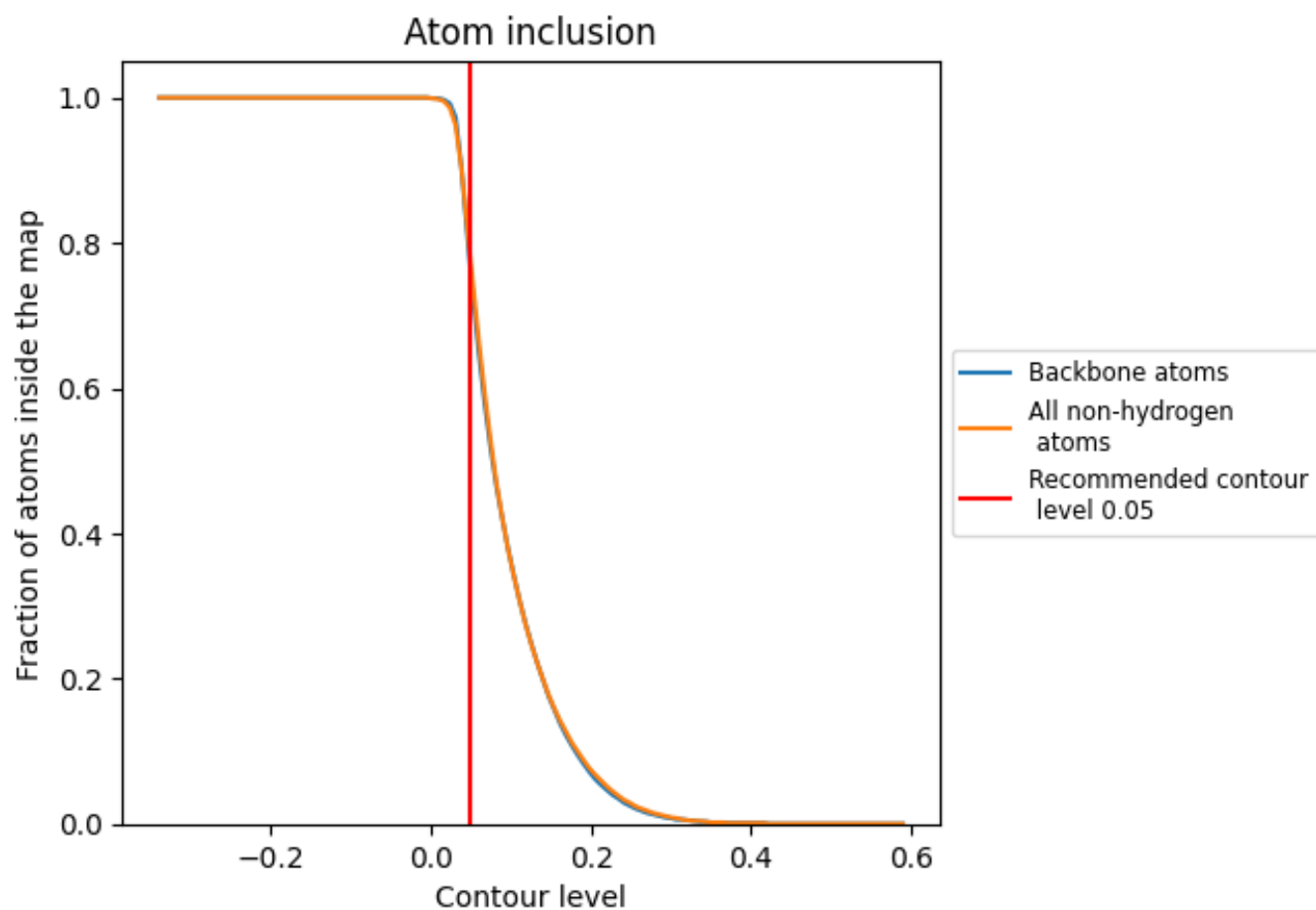
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 75% of all backbone atoms, 77% 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	 0.7700	 0.3950
1	 0.8880	 0.3820
2	 0.8200	 0.3820
3	 0.8760	 0.5110
4	 0.8410	 0.4880
5	 0.7830	 0.4390
6	 0.3820	 0.2380
A	 0.6610	 0.3020
B	 0.6580	 0.2340
C	 0.9210	 0.5340
D	 0.4050	 0.3710
E	 0.8230	 0.4210
F	 0.8600	 0.4750
G	 0.8810	 0.4930
H	 0.1430	 0.2360
J	 0.2520	 0.2300
K	 0.2720	 0.3170
L	 0.9540	 0.5490
M	 0.9520	 0.3990
N	 0.9590	 0.5460
O	 0.7290	 0.3420
P	 0.8560	 0.4510
Q	 0.9000	 0.5080
S	 0.7220	 0.3540
T	 0.2400	 0.3360
V	 0.0290	 0.1220
Y	 0.9100	 0.5150
b	 0.0070	 0.1780
e	 0.9470	 0.5390
f	 0.9290	 0.5070
h	 0.7600	 0.4280
i	 0.8840	 0.4760
j	 0.8940	 0.5020
m	 0.7880	 0.4440
o	 0.2660	 0.3230



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Chain	Atom inclusion	Q-score
r	 0.0110	 0.2110
t	 0.1790	 0.3170
u	 0.1420	 0.1310
v	 0.8220	 0.4710
x	 0.8360	 0.4730
y	 0.0010	 0.1050