



## wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 04:02 PM EST

PDB ID : 8EUY  
EMDB ID : EMD-24420  
Title : Ytm1 associated nascent 60S ribosome (-fkbp39) State 1A  
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.  
Deposited on : 2022-10-19  
Resolution : 3.00 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:

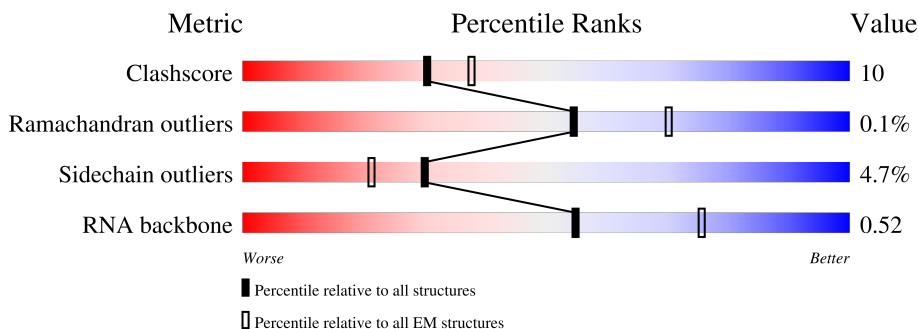
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 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 3.00 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.



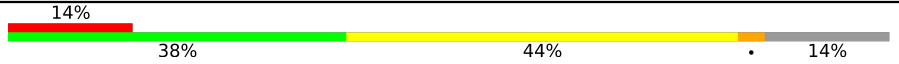







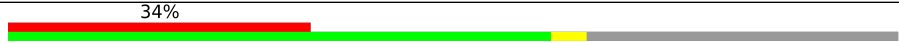



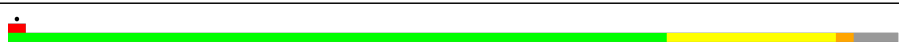




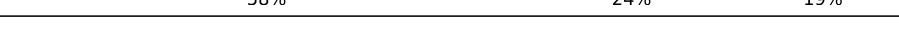

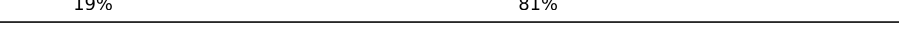
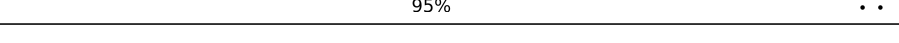
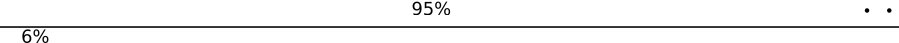
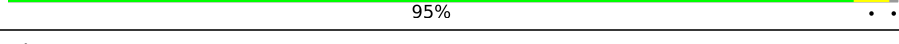


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	3497	
2	2	165	
3	3	302	
4	4	217	
5	5	387	
6	6	300	
7	A	295	



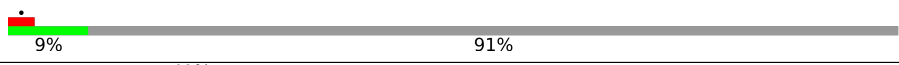
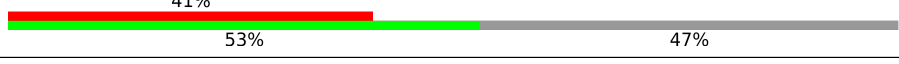
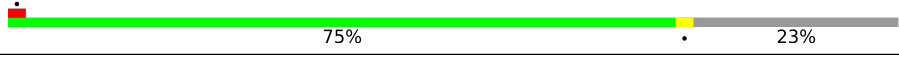
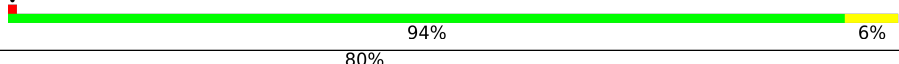


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Mol	Chain	Length	Quality of chain
8	B	388	
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	J	333	
16	K	373	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	S	176	
24	V	139	
25	Y	126	
26	b	642	
27	e	127	
28	f	108	
29	h	122	
30	i	99	
31	j	91	
32	m	740	

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Mol	Chain	Length	Quality of chain
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 [i](#)

There are 41 unique types of molecules in this entry. The entry contains 80249 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 (1095-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1433	30681	13703	5554	9991	1433	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	3196	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (148-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	130	2762	1236	487	909	130	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	192	1596	1010	304	276	6	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	210	1770	1153	302	307	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	340	2686	1716	468	491	11	0	0

- Molecule 6 is a RNA chain called RNA (93-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	6	56	1160	522	171	411	56	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	254	2057	1303	374	372	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	B	332	2641	1676	488	468	9	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	329	2572	1631	487	451	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	D	406	3001	1931	519	542	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	240	1944	1250	356	335	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	164	1273	816	223	232	2	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	H	155	764	454	155	155	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	89	444	266	89	89	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	243	1205	719	243	243	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	S		
18	M	125	1007	644	191	168	4	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	187	1487	958	281	245	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	145	1139	725	207	204	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	135	1047	658	202	186	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	1402	906	260	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	113	554	327	113	114	0	0

- Molecule 25 is a protein called 60S 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	120	594	354	120	120	0	0

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



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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	i	98	Total	C	N	O	S	0	0
			768	478	159	130	1		

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
32	m	92	Total	C	N	O	0	0
			725	447	128	150		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	129	Total	C	N	O	S	0	0
			992	636	180	170	6		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	r	50	249	149	50	50	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
35	t	23	216	132	49	35	0	0

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

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

- Molecule 37 is a protein called Nucleolar protein 16.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	x	305	2516	1578	463	467	8	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
39	y	198	974	578	198	198	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	T	19	147	93	26	28	0	0

- Molecule 41 is ZINC ION (three-letter code: ZN) (formula: Zn).

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
41	j	1	Total 1	Zn 1	0



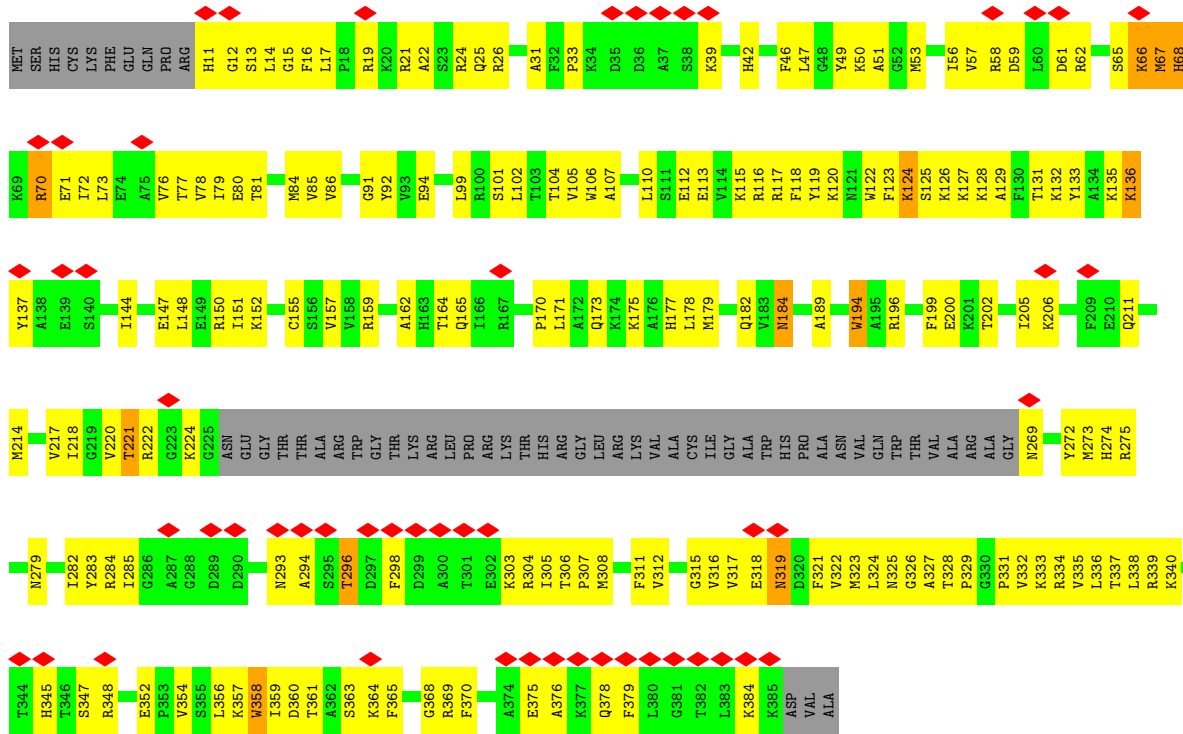




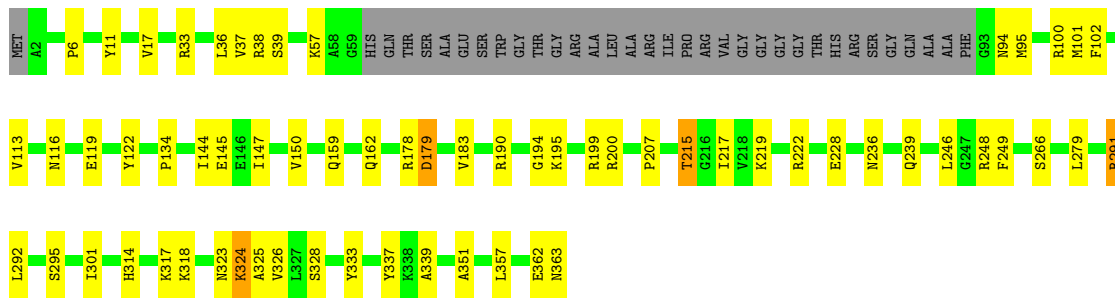




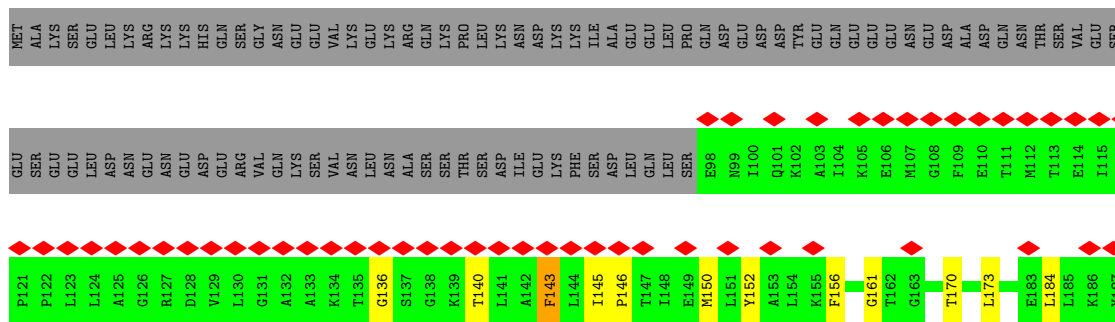


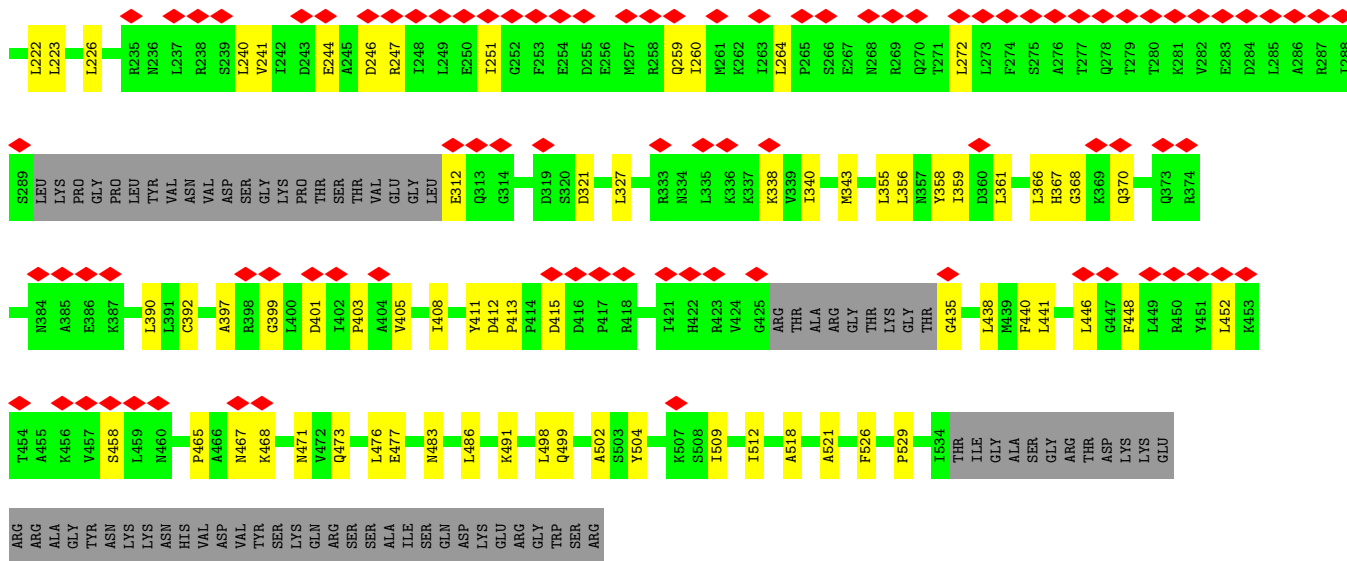


• Molecule 9: 60S ribosomal protein L4-B

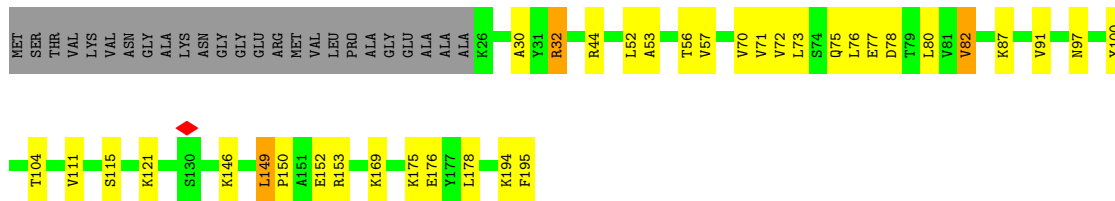


• Molecule 10: ATP-dependent RNA helicase has1

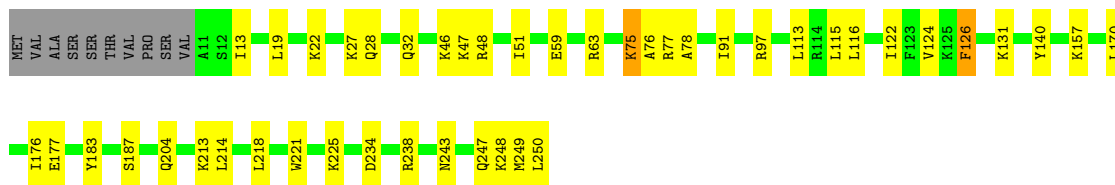
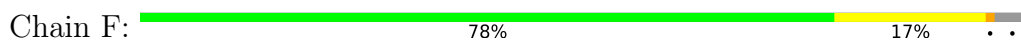




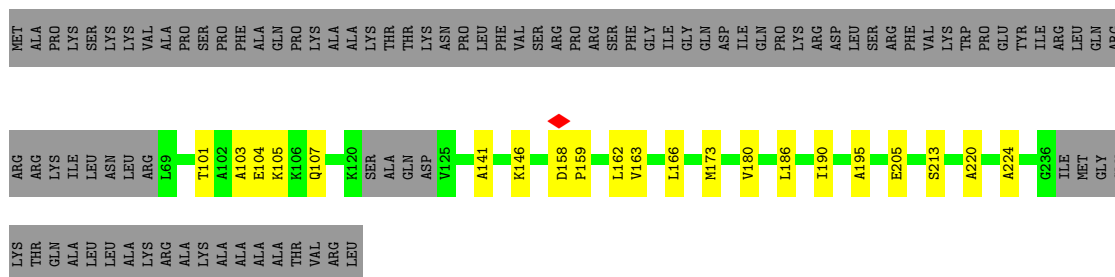
• Molecule 11: 60S ribosomal protein L6



• Molecule 12: 60S ribosomal protein L7-B

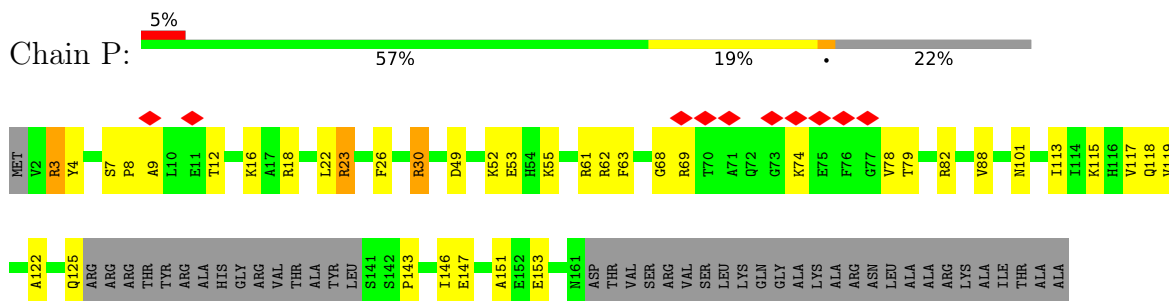


• Molecule 13: 60S ribosomal protein L8

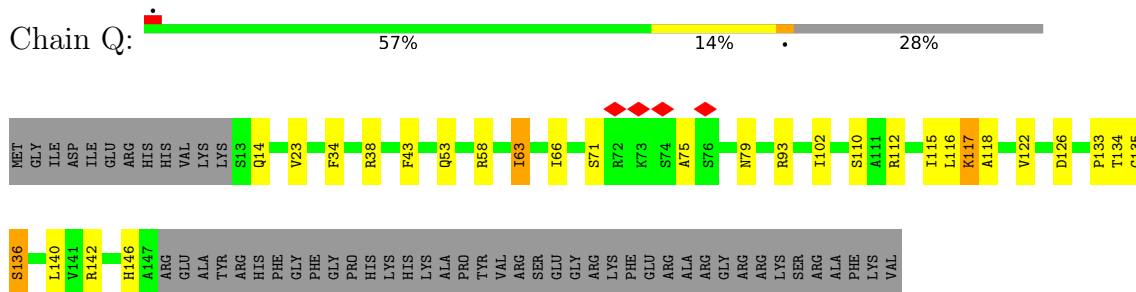




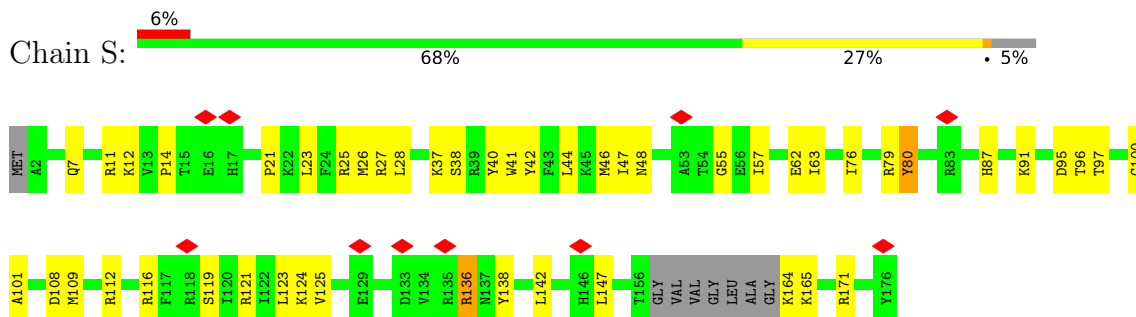




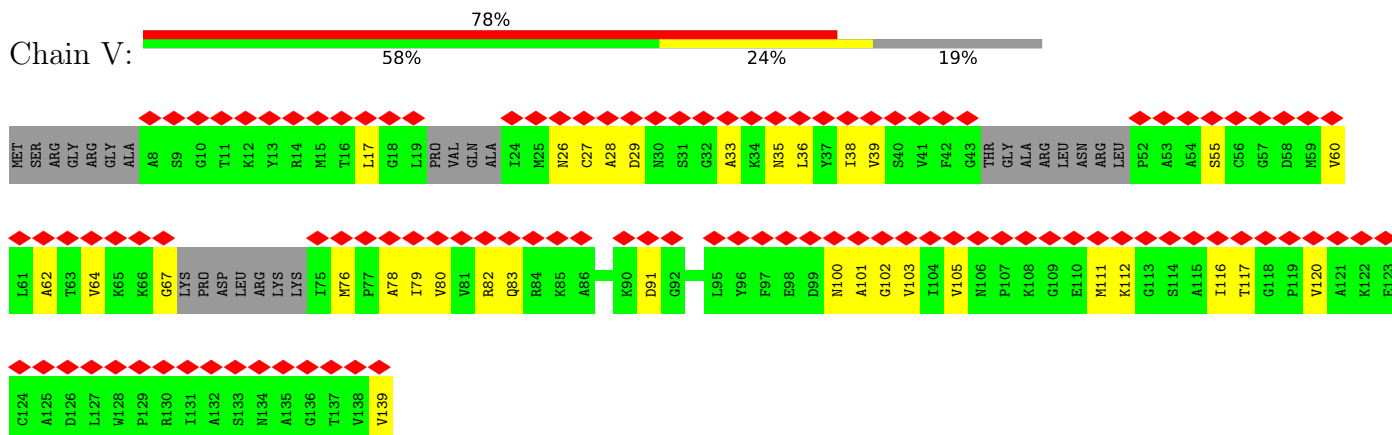
• Molecule 22: 60S ribosomal protein L18-A



• Molecule 23: 60S ribosomal protein L20-A



• Molecule 24: 60S ribosomal protein L23-A

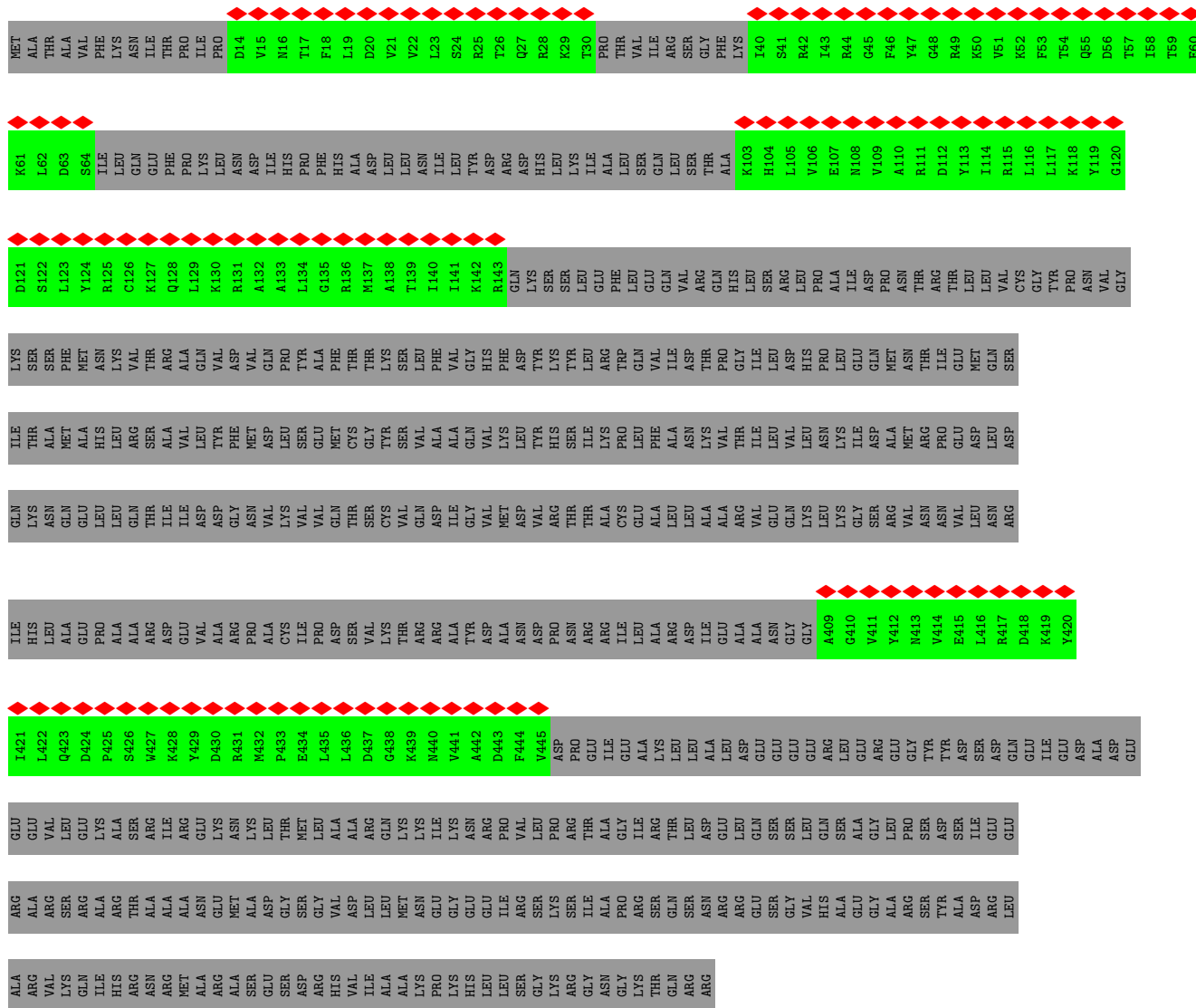


• Molecule 25: 60S ribosomal protein L26





• Molecule 26: Probable nucleolar GTP-binding protein 1



• Molecule 27: 60S ribosomal protein L32-A



• Molecule 28: 60S ribosomal protein L33-B













## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	220000	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	0.774	Depositor
Minimum map value	-0.343	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.05	Depositor
Map size ( $\text{\AA}$ )	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 ( $\text{\AA}$ )	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	1	0.35	0/34328	0.72	0/53470
2	2	0.34	0/3084	0.72	0/4794
3	3	0.31	0/1627	0.49	0/2188
4	4	0.28	0/1817	0.47	0/2454
5	5	0.26	0/2739	0.51	0/3702
6	6	0.23	0/1287	0.66	0/1990
7	A	0.25	0/2096	0.49	0/2826
8	B	0.31	0/2694	0.59	0/3619
9	C	0.30	0/2618	0.51	0/3531
10	D	0.25	0/3052	0.46	0/4138
11	E	0.29	0/1356	0.52	0/1829
12	F	0.27	0/1982	0.48	0/2658
13	G	0.28	0/1291	0.45	0/1742
14	H	0.24	0/761	0.43	0/1054
15	J	0.23	0/443	0.36	0/618
16	K	0.24	0/1203	0.41	0/1675
17	L	0.31	0/960	0.59	0/1288
18	M	0.26	0/1024	0.54	0/1375
19	N	0.31	0/1436	0.56	0/1920
20	O	0.27	0/1515	0.49	0/2028
21	P	0.27	0/1161	0.47	0/1559
22	Q	0.28	0/1058	0.55	0/1421
23	S	0.26	0/1438	0.54	0/1932
24	V	0.24	0/550	0.40	0/755
25	Y	0.29	0/1008	0.60	0/1341
26	b	0.23	0/590	0.33	0/816
27	e	0.30	0/1009	0.55	0/1345
28	f	0.31	0/859	0.54	0/1152
29	h	0.29	0/1008	0.54	0/1340
30	i	0.27	0/775	0.53	0/1030
31	j	0.26	0/575	0.55	0/761
32	m	0.26	0/738	0.48	0/997

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	o	0.32	0/1014	0.66	0/1366
34	r	0.23	0/247	0.36	0/342
35	t	0.30	0/218	0.62	0/287
36	u	0.23	0/504	0.36	0/700
37	v	0.26	0/1319	0.49	0/1769
38	x	0.27	0/2562	0.51	0/3432
39	y	0.24	0/971	0.43	0/1345
40	T	0.23	0/151	0.42	0/207
All	All	0.31	0/85068	0.62	0/122796

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](#)

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	30681	0	15431	331	0
2	2	2762	0	1399	24	0
3	3	1596	0	1645	22	0
4	4	1770	0	1788	36	0
5	5	2686	0	2745	47	0
6	6	1160	0	586	95	0
7	A	2057	0	2088	52	0
8	B	2641	0	2727	197	0
9	C	2572	0	2705	49	0
10	D	3001	0	2897	49	0
11	E	1328	0	1408	26	0
12	F	1944	0	2035	29	0
13	G	1273	0	1348	11	0
14	H	764	0	330	18	0
15	J	444	0	202	6	0
16	K	1205	0	528	9	0
17	L	942	0	1012	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	M	1007	0	1072	30	0
19	N	1406	0	1441	25	0
20	O	1487	0	1585	32	0
21	P	1139	0	1158	27	0
22	Q	1047	0	1142	20	0
23	S	1402	0	1451	35	0
24	V	554	0	272	20	0
25	Y	998	0	1090	18	0
26	b	594	0	258	0	0
27	e	995	0	1059	0	0
28	f	839	0	866	0	0
29	h	999	0	1092	0	0
30	i	768	0	835	0	0
31	j	563	0	578	0	0
32	m	725	0	660	0	0
33	o	992	0	939	0	0
34	r	249	0	117	0	0
35	t	216	0	219	0	0
36	u	506	0	226	0	0
37	v	1299	0	1347	0	0
38	x	2516	0	2524	0	0
39	y	974	0	448	0	0
40	T	147	0	140	9	0
41	j	1	0	0	0	0
All	All	80249	0	61393	1081	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 10.

The worst 5 of 1081 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)
8:B:331:PRO:HD2	8:B:334:ARG:HE	1.30	0.95
8:B:58:ARG:HB2	8:B:356:LEU:HD22	1.49	0.93
1:1:543:G:H1	1:1:582:G:H22	1.15	0.92
8:B:211:GLN:HB2	8:B:285:ILE:HG13	1.50	0.92
6:6:59:A:H3'	6:6:60:A:H8	1.32	0.92

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	190/302 (63%)	183 (96%)	7 (4%)	0	100	100
4	4	208/217 (96%)	203 (98%)	5 (2%)	0	100	100
5	5	336/387 (87%)	314 (94%)	22 (6%)	0	100	100
7	A	250/295 (85%)	238 (95%)	10 (4%)	2 (1%)	19	57
8	B	328/388 (84%)	311 (95%)	16 (5%)	1 (0%)	41	76
9	C	325/363 (90%)	308 (95%)	17 (5%)	0	100	100
10	D	400/578 (69%)	391 (98%)	9 (2%)	0	100	100
11	E	168/195 (86%)	155 (92%)	13 (8%)	0	100	100
12	F	238/250 (95%)	231 (97%)	7 (3%)	0	100	100
13	G	161/259 (62%)	156 (97%)	5 (3%)	0	100	100
14	H	149/190 (78%)	141 (95%)	8 (5%)	0	100	100
15	J	87/333 (26%)	87 (100%)	0	0	100	100
16	K	239/373 (64%)	229 (96%)	9 (4%)	1 (0%)	34	72
17	L	114/208 (55%)	112 (98%)	2 (2%)	0	100	100
18	M	123/134 (92%)	120 (98%)	3 (2%)	0	100	100
19	N	160/201 (80%)	158 (99%)	2 (1%)	0	100	100
20	O	183/197 (93%)	180 (98%)	3 (2%)	0	100	100
21	P	141/187 (75%)	135 (96%)	6 (4%)	0	100	100
22	Q	133/187 (71%)	127 (96%)	6 (4%)	0	100	100
23	S	164/176 (93%)	154 (94%)	10 (6%)	0	100	100
24	V	105/139 (76%)	99 (94%)	6 (6%)	0	100	100
25	Y	123/126 (98%)	119 (97%)	4 (3%)	0	100	100
26	b	112/642 (17%)	112 (100%)	0	0	100	100
27	e	122/127 (96%)	120 (98%)	2 (2%)	0	100	100
28	f	104/108 (96%)	100 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	h	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
30	i	96/99 (97%)	92 (96%)	3 (3%)	1 (1%)	15	53
31	j	69/91 (76%)	67 (97%)	2 (3%)	0	100	100
32	m	86/740 (12%)	80 (93%)	6 (7%)	0	100	100
33	o	125/276 (45%)	116 (93%)	7 (6%)	2 (2%)	9	40
34	r	46/260 (18%)	46 (100%)	0	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	157/209 (75%)	151 (96%)	5 (3%)	1 (1%)	25	64
38	x	303/306 (99%)	300 (99%)	3 (1%)	0	100	100
39	y	192/244 (79%)	180 (94%)	12 (6%)	0	100	100
40	T	17/160 (11%)	17 (100%)	0	0	100	100
All	All	5992/9510 (63%)	5765 (96%)	219 (4%)	8 (0%)	54	85

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	K	153	ILE
7	A	118	ASN
7	A	248	PHE
33	o	197	PRO
37	v	130	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	169/271 (62%)	163 (96%)	6 (4%)	35	70
4	4	191/197 (97%)	183 (96%)	8 (4%)	30	66
5	5	301/345 (87%)	284 (94%)	17 (6%)	21	56
7	A	228/266 (86%)	215 (94%)	13 (6%)	20	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	B	282/326 (86%)	268 (95%)	14 (5%)	24	60
9	C	275/297 (93%)	267 (97%)	8 (3%)	42	76
10	D	288/505 (57%)	277 (96%)	11 (4%)	33	69
11	E	139/155 (90%)	135 (97%)	4 (3%)	42	76
12	F	201/210 (96%)	195 (97%)	6 (3%)	41	75
13	G	135/212 (64%)	133 (98%)	2 (2%)	65	87
17	L	97/167 (58%)	91 (94%)	6 (6%)	18	52
18	M	108/113 (96%)	100 (93%)	8 (7%)	13	44
19	N	146/176 (83%)	141 (97%)	5 (3%)	37	72
20	O	154/162 (95%)	147 (96%)	7 (4%)	27	64
21	P	118/149 (79%)	111 (94%)	7 (6%)	19	54
22	Q	116/159 (73%)	109 (94%)	7 (6%)	19	53
23	S	149/154 (97%)	140 (94%)	9 (6%)	19	53
25	Y	110/111 (99%)	104 (94%)	6 (6%)	21	57
27	e	106/107 (99%)	103 (97%)	3 (3%)	43	77
28	f	89/91 (98%)	86 (97%)	3 (3%)	37	72
29	h	106/107 (99%)	101 (95%)	5 (5%)	26	63
30	i	79/84 (94%)	71 (90%)	8 (10%)	7	29
31	j	58/71 (82%)	55 (95%)	3 (5%)	23	59
32	m	76/659 (12%)	74 (97%)	2 (3%)	46	78
33	o	95/246 (39%)	84 (88%)	11 (12%)	5	23
35	t	22/223 (10%)	21 (96%)	1 (4%)	27	64
37	v	138/181 (76%)	135 (98%)	3 (2%)	52	81
38	x	272/273 (100%)	255 (94%)	17 (6%)	18	51
40	T	17/139 (12%)	17 (100%)	0	100	100
All	All	4265/6156 (69%)	4065 (95%)	200 (5%)	30	63

5 of 200 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	P	3	ARG
25	Y	114	ARG
38	x	302	ARG

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Mol	Chain	Res	Type
21	P	49	ASP
23	S	38	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
29	h	11	GLN
29	h	15	ASN
33	o	189	ASN
29	h	19	GLN
18	M	125	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1408/3497 (40%)	354 (25%)	23 (1%)
2	2	126/165 (76%)	25 (19%)	0
6	6	54/300 (18%)	36 (66%)	3 (5%)
All	All	1588/3962 (40%)	415 (26%)	26 (1%)

5 of 415 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	11	A
1	1	14	U
1	1	26	A
1	1	28	G
1	1	32	U

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1159	U
1	1	3189	C
6	6	71	U
1	1	1389	A
1	1	3217	U

## 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 [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](#)

There are no chain breaks in this entry.

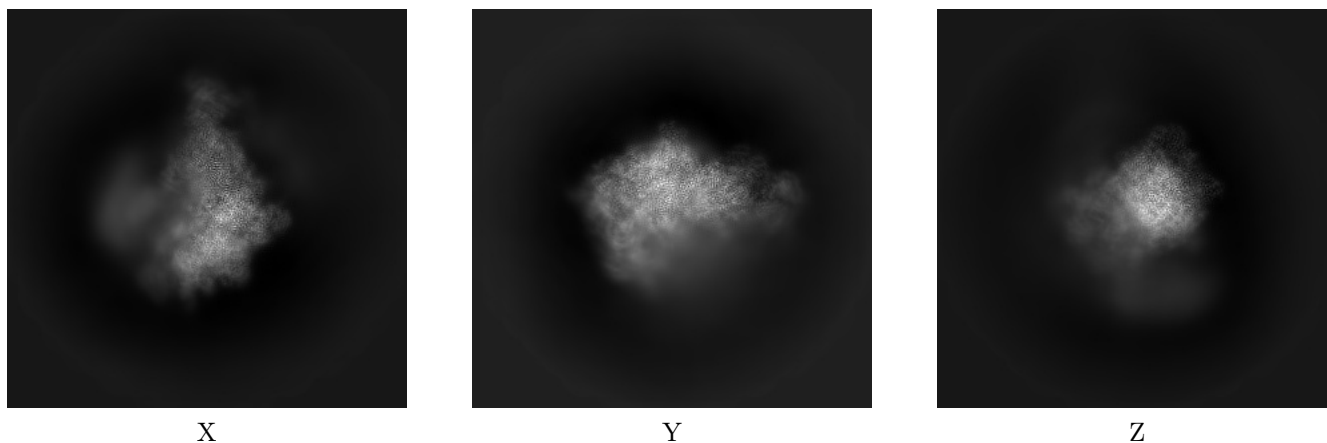
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24420. 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](#)

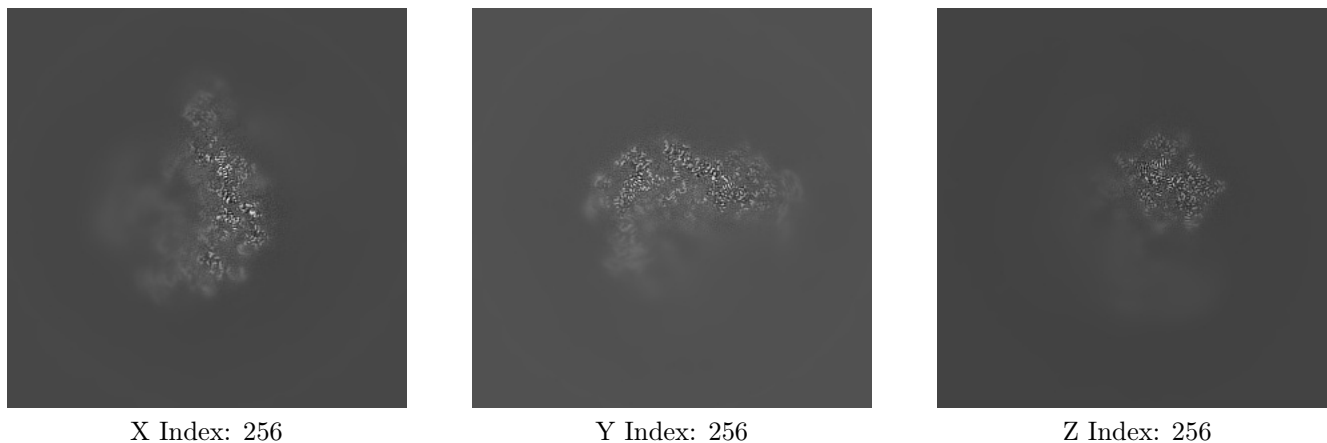
#### 6.1.1 Primary map



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

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

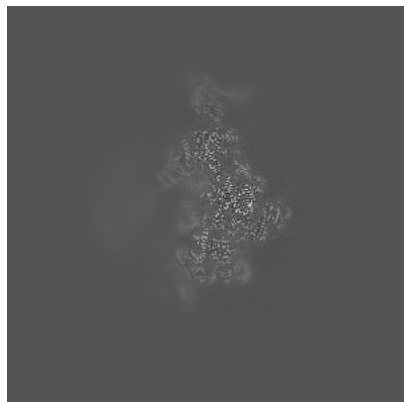
#### 6.2.1 Primary map



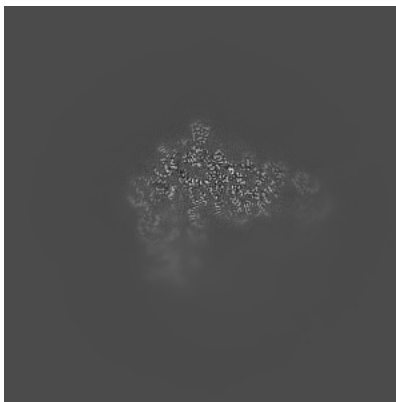
The images above show central slices of the map in three orthogonal directions.

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

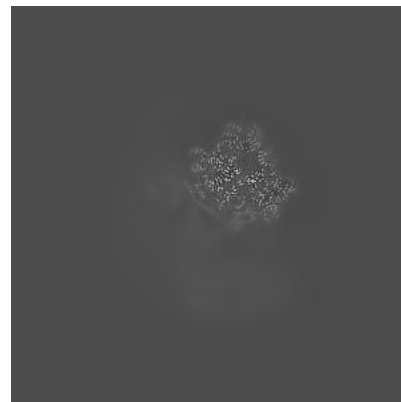
### 6.3.1 Primary map



X Index: 282



Y Index: 274



Z Index: 249

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.

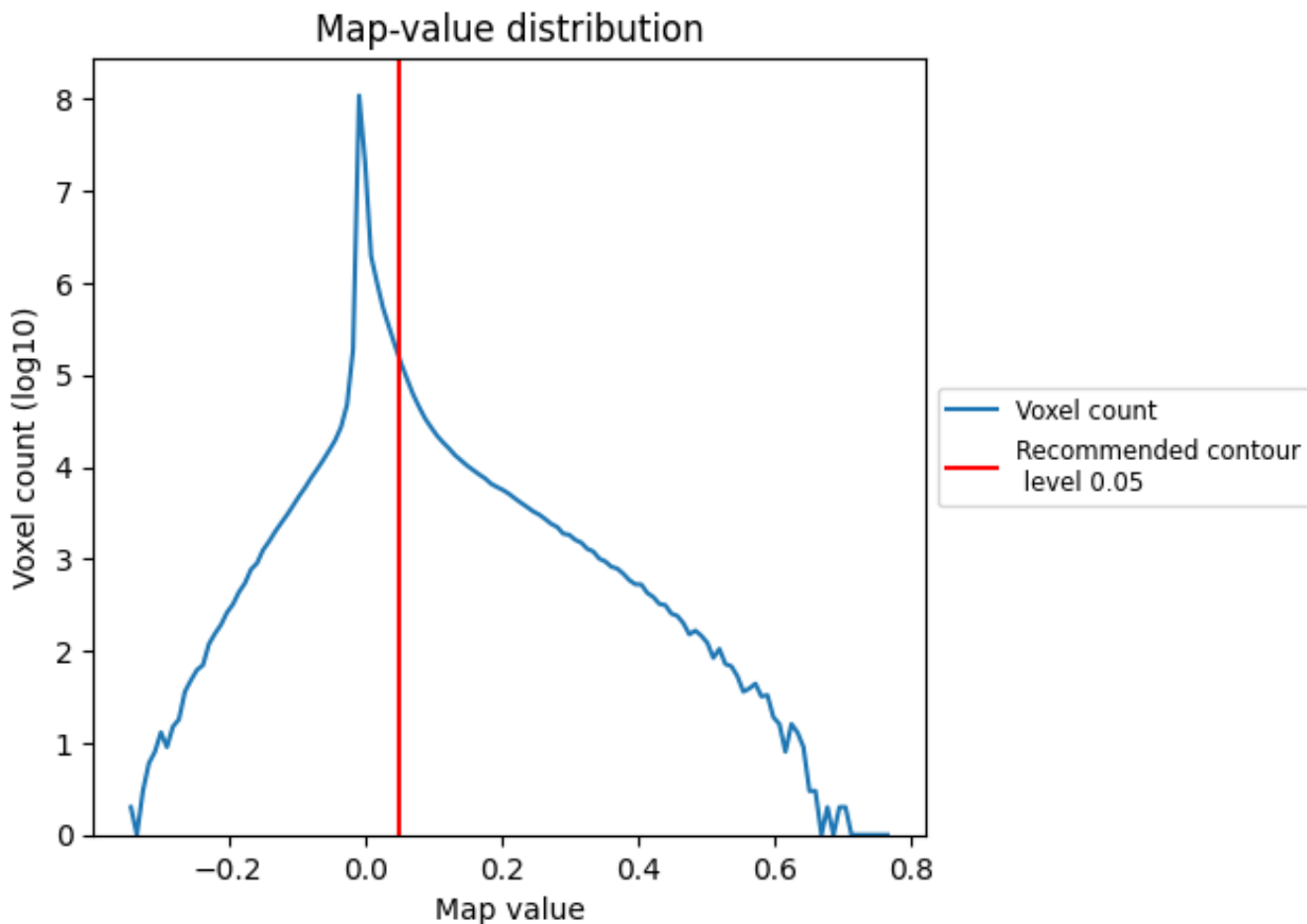
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

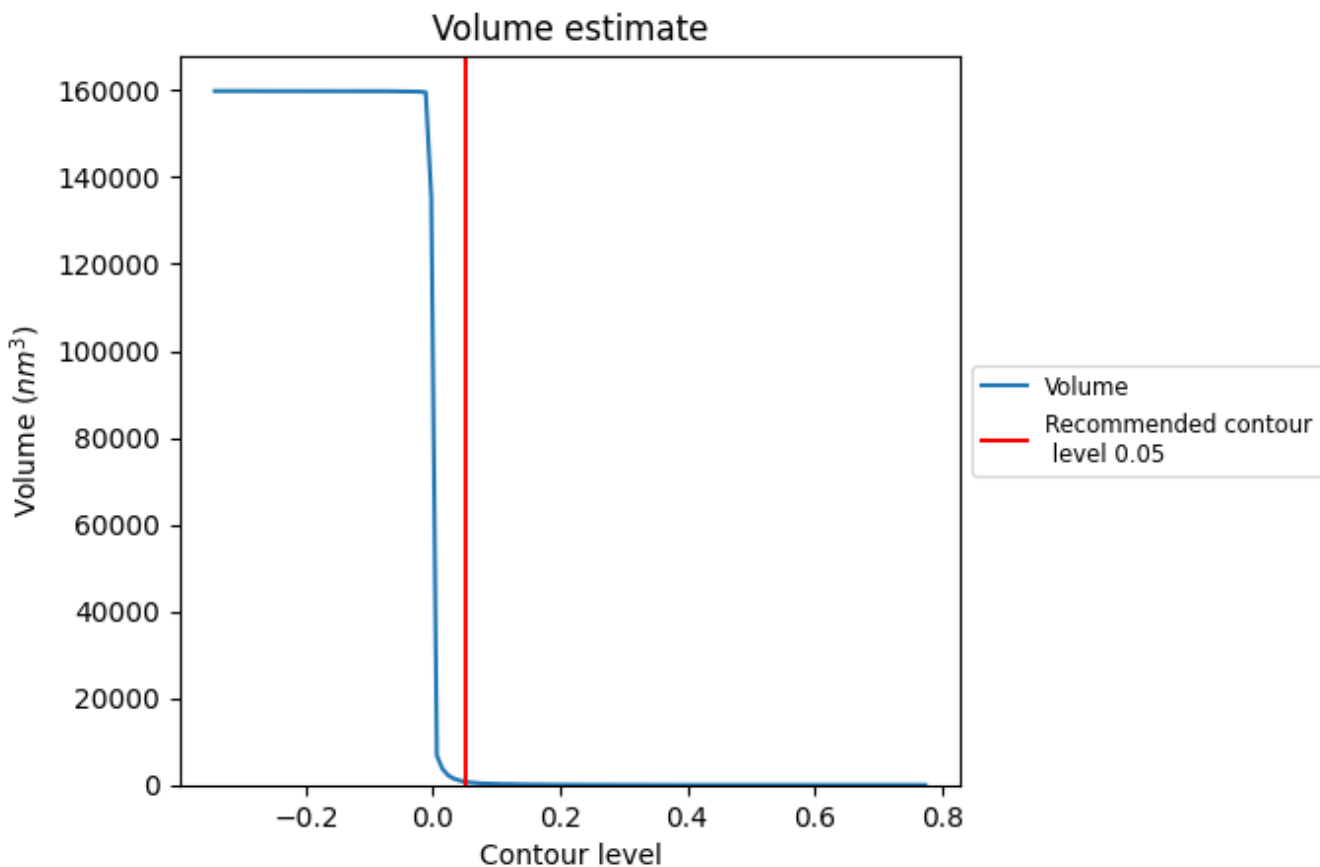
This section contains the results of statistical analysis of the map.

### 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 [\(i\)](#)

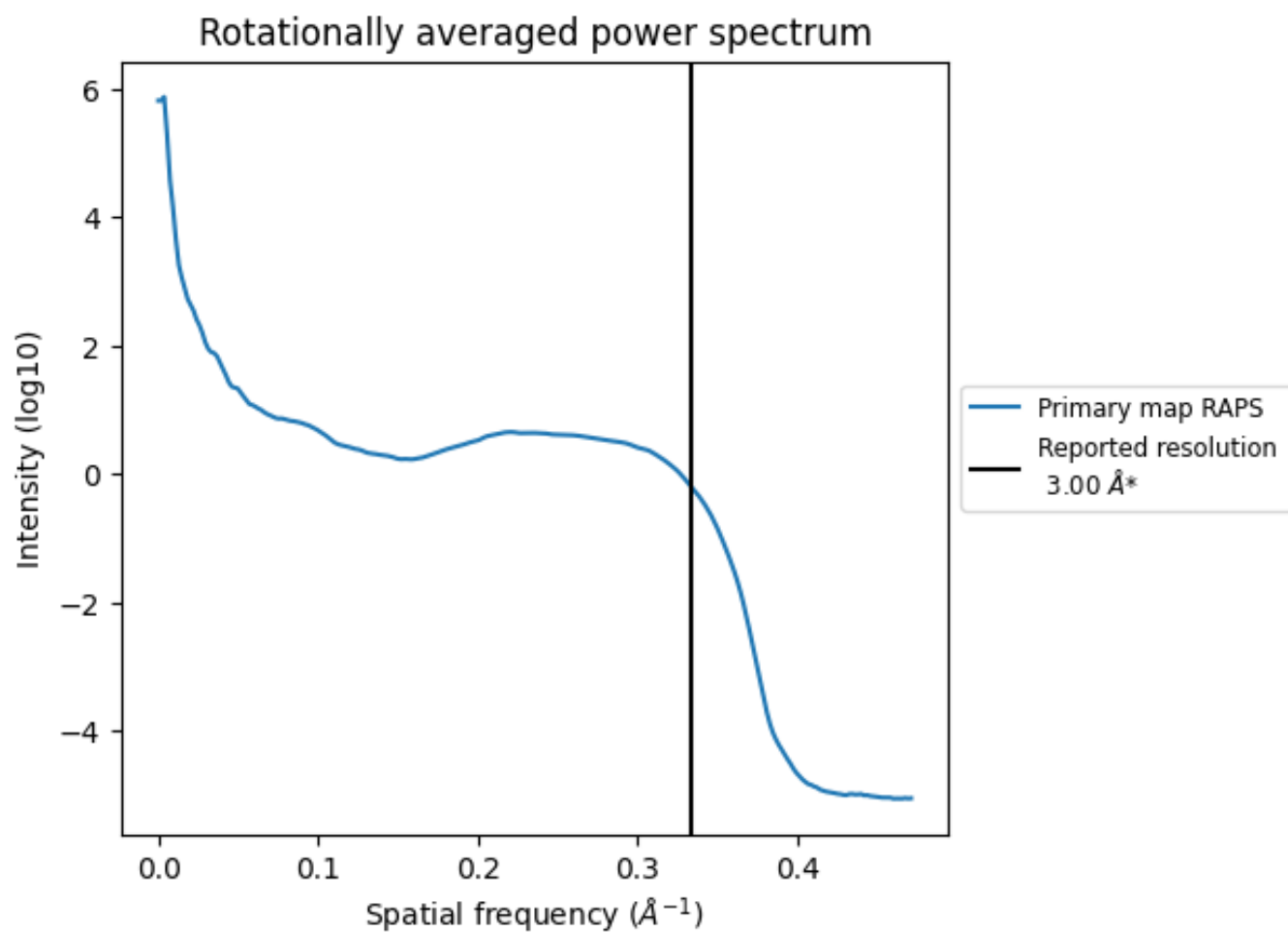


The volume at the recommended contour level is 754  $\text{nm}^3$ ; this corresponds to an approximate mass of 681 kDa.

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  $0.333 \text{ \AA}^{-1}$

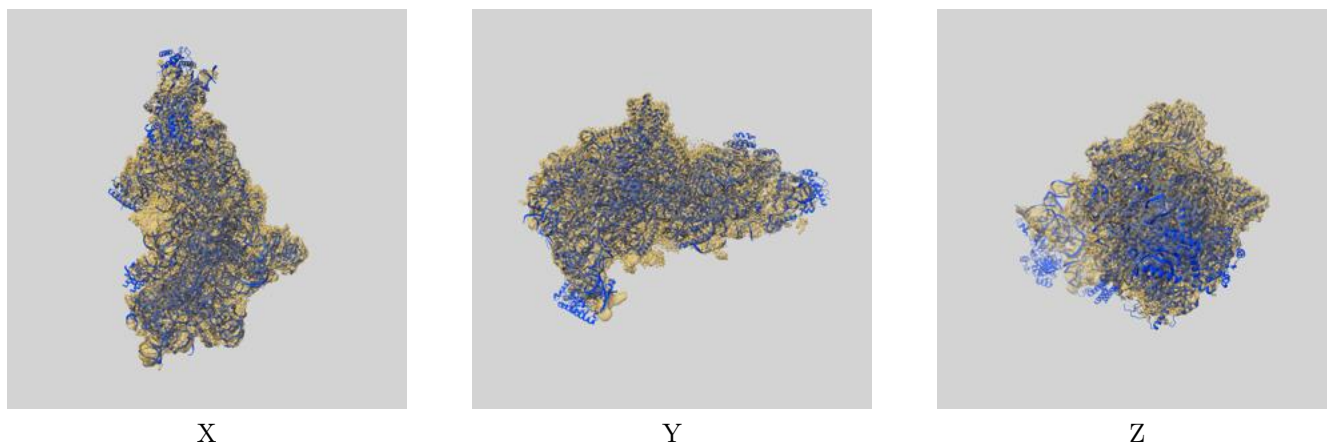
## 8 Fourier-Shell correlation

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

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

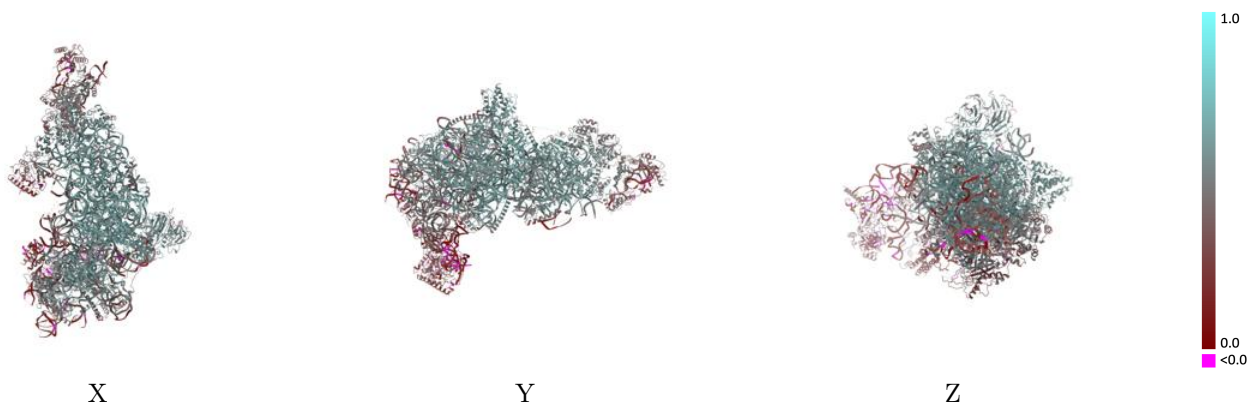
This section contains information regarding the fit between EMDB map EMD-24420 and PDB model 8EUY. Per-residue inclusion information can be found in section 3 on page 12.

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



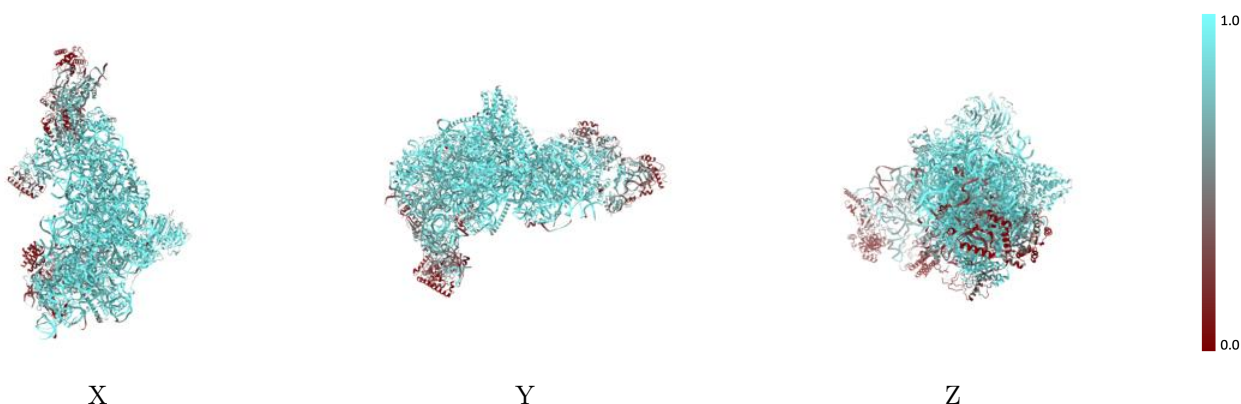
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



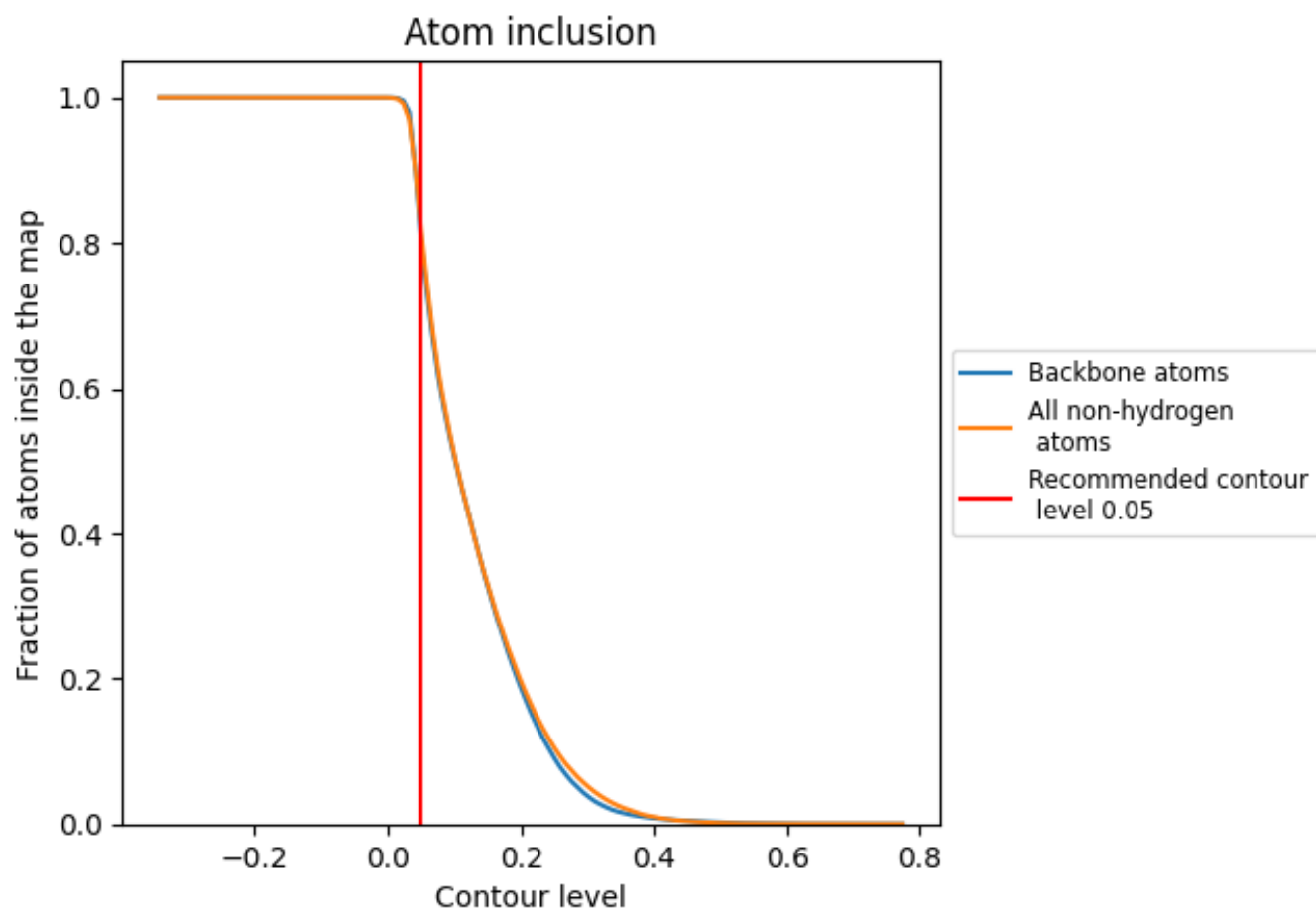
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 81% of all backbone atoms, 82% 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	 0.8219	 0.4810
1	 0.8913	 0.4590
2	 0.9305	 0.5240
3	 0.9483	 0.6070
4	 0.9351	 0.5900
5	 0.8959	 0.5460
6	 0.4690	 0.1990
A	 0.7334	 0.3900
B	 0.6590	 0.2860
C	 0.9785	 0.6230
D	 0.5451	 0.4790
E	 0.9143	 0.5420
F	 0.9442	 0.5790
G	 0.9391	 0.5790
H	 0.2277	 0.3100
J	 0.3739	 0.2880
K	 0.4266	 0.3990
L	 0.9756	 0.6280
M	 0.9222	 0.5050
N	 0.9873	 0.6140
O	 0.9007	 0.4930
P	 0.8758	 0.5360
Q	 0.9587	 0.5920
S	 0.8351	 0.4790
T	 0.3741	 0.3860
V	 0.0668	 0.1860
Y	 0.9751	 0.6070
b	 0.0101	 0.2360
e	 0.9844	 0.6280
f	 0.9840	 0.6140
h	 0.8530	 0.5270
i	 0.9405	 0.5740
j	 0.9519	 0.5980
m	 0.7234	 0.4810
o	 0.4578	 0.3660



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Chain	Atom inclusion	Q-score
r	 0.0602	 0.2490
t	 0.5124	 0.4230
u	 0.2332	 0.2230
v	 0.8934	 0.5610
x	 0.9298	 0.5810
y	 0.0185	 0.2290