



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 06:45 PM UTC

PDB ID : 8EV3 / pdb_00008ev3
EMDB ID : EMD-24421
Title : Ytm1 associated 60S nascent ribosome (-Fkbp39) State 1B
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

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:

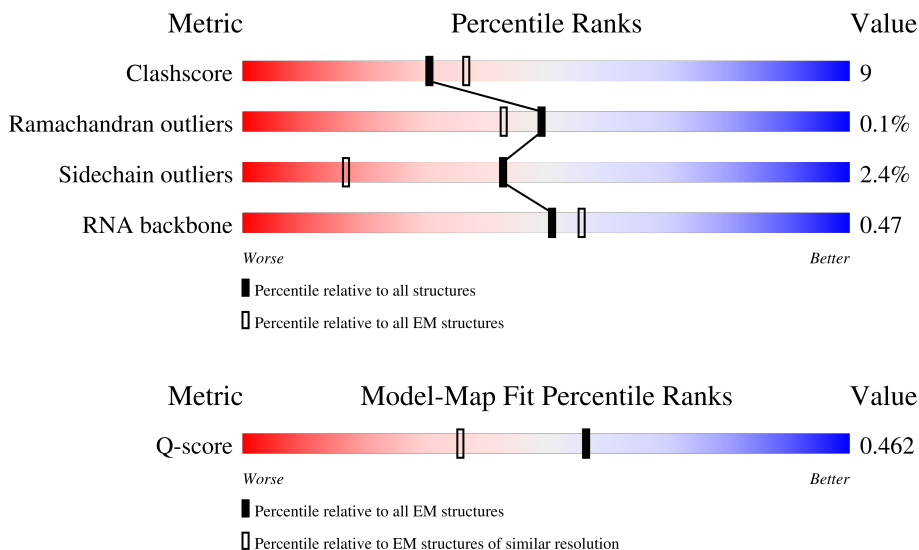
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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.






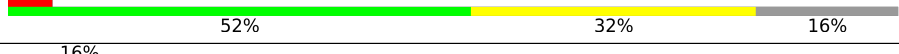



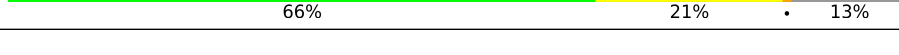
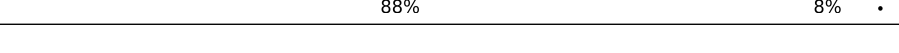

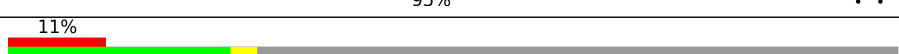

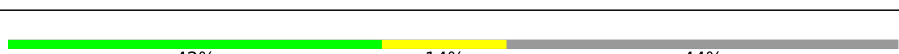
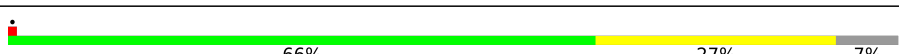
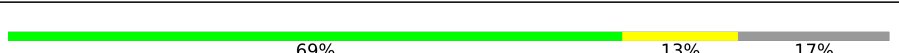




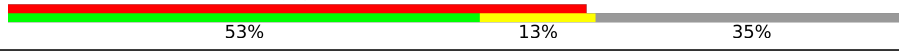





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	1	3497	
2	2	165	
3	3	302	

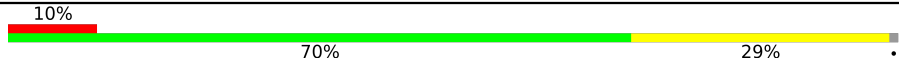

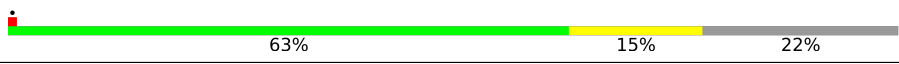
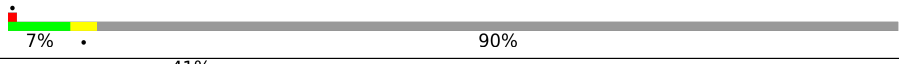

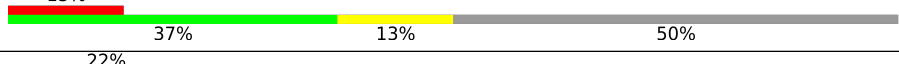







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Mol	Chain	Length	Quality of chain
4	4	217	
5	5	387	
6	6	300	
7	A	295	
8	B	388	
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	J	333	
16	K	373	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	S	176	
24	V	139	
25	Y	126	
26	b	642	
27	e	127	
28	f	108	

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Mol	Chain	Length	Quality of chain
29	h	122	
30	i	99	
31	j	91	
32	m	740	
33	n	607	
34	o	276	
35	r	260	
36	t	249	
37	u	192	
38	v	209	
39	x	306	
40	y	244	
41	T	19	

2 Entry composition

There are 42 unique types of molecules in this entry. The entry contains 84746 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 (1452-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1452	31076	13882	5623	10119	1452	0	0

- Molecule 2 is a RNA chain called RNA (150-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	150	3189	1427	564	1048	150	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	211	1776	1156	303	309	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 (75-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	6	75	1587	712	270	530	75	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	247	1999	1267	363	361	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	362	2810	1774	539	494	3	0	0

- Molecule 10 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	D	416	3186	2057	544	574	11	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	183	902	536	183	183	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	92	459	275	92	92	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	K	249	1914	1224	328	356	6	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	186	1478	952	279	244	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	148	Total	C	N	O	S	0	0
			1164	743	210	208	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	135	Total	C	N	O	S	0	0
			1047	658	202	186	1		

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	91	Total	C	N	O	0	0
			446	263	91	92		

- Molecule 25 is a protein called Ribosomal protein L26.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
26	b	64	Total	C	N	O	0	0
			317	189	64	64		

- 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
			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	121	999	629	194	176		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	75	615	379	112	124	0	0

- Molecule 33 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	n	362	1791	1067	362	362	0	0

- Molecule 34 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	o	137	1026	655	189	176	6	0	0

- Molecule 35 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
35	r	57	283	169	57	57	0	0

- Molecule 36 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
36	t	183	1008	602	209	197	0	0

- Molecule 37 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	u	76	377	225	76	76	0	0

- Molecule 38 is a protein called Nucleolar protein 16.

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

- Molecule 39 is a protein called Brix domain-containing protein C4F8.04.

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

- Molecule 40 is a protein called Eukaryotic translation initiation factor 6.

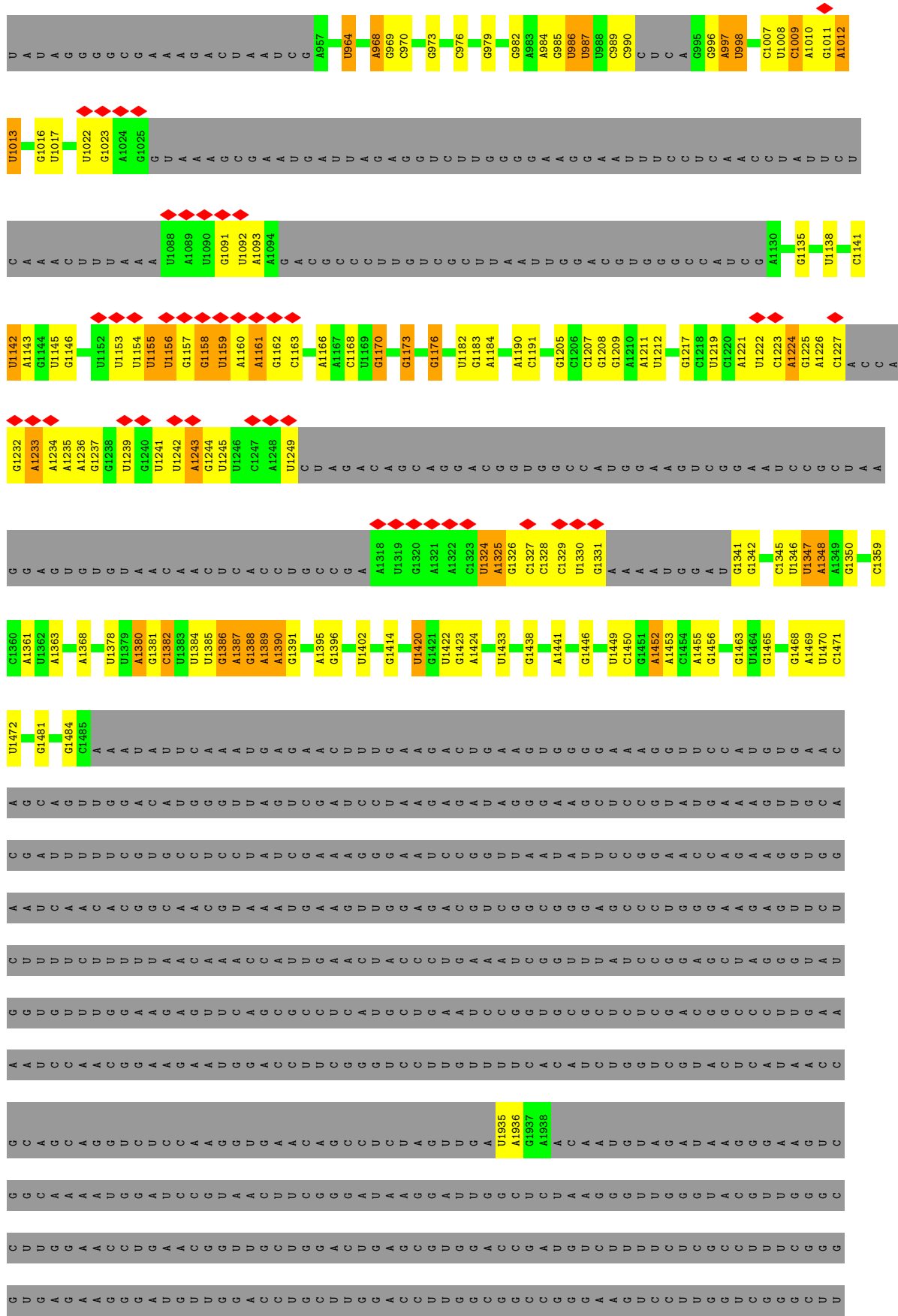
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	y	188	925	549	188	188	0	0

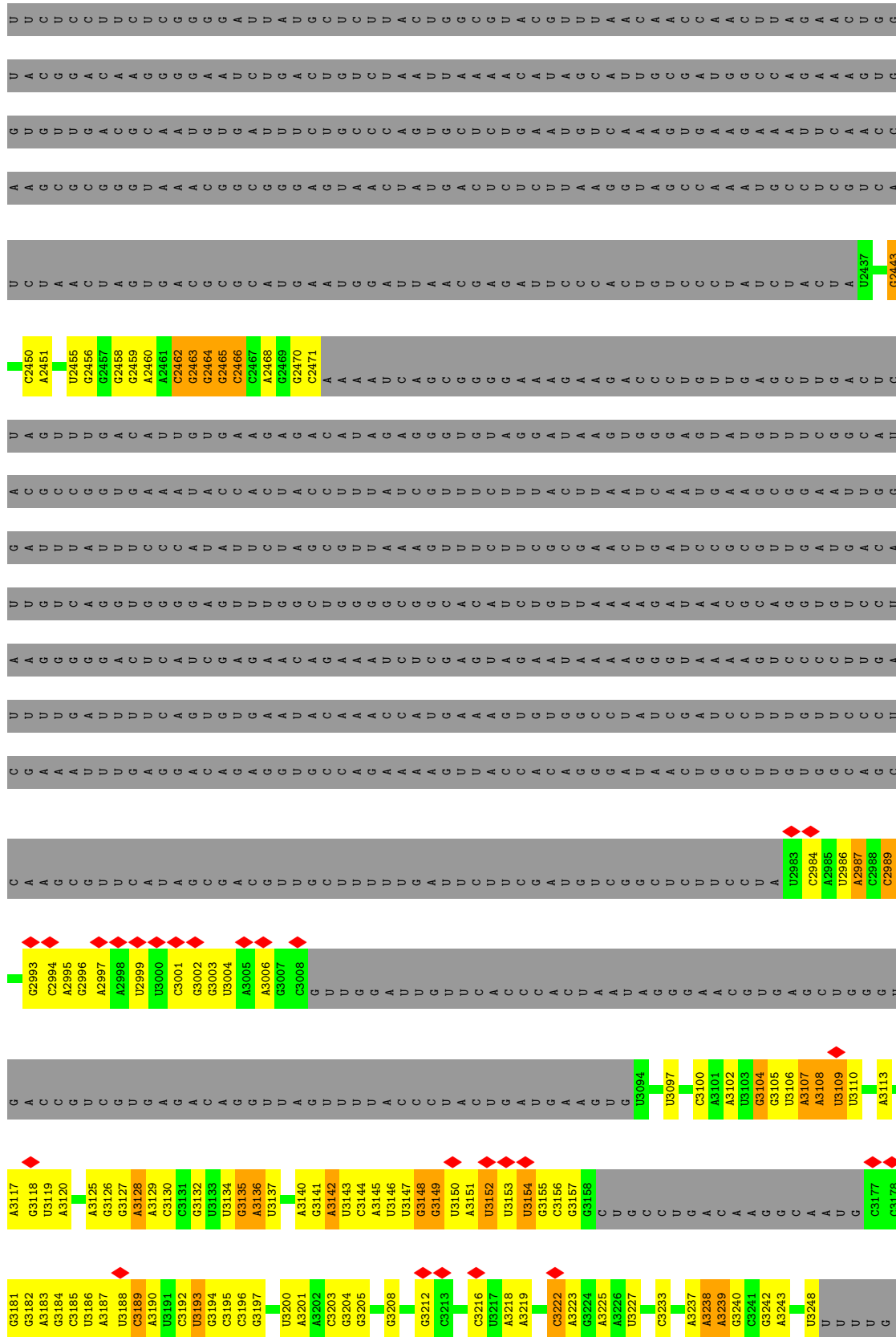
- Molecule 41 is a protein called RPL21.

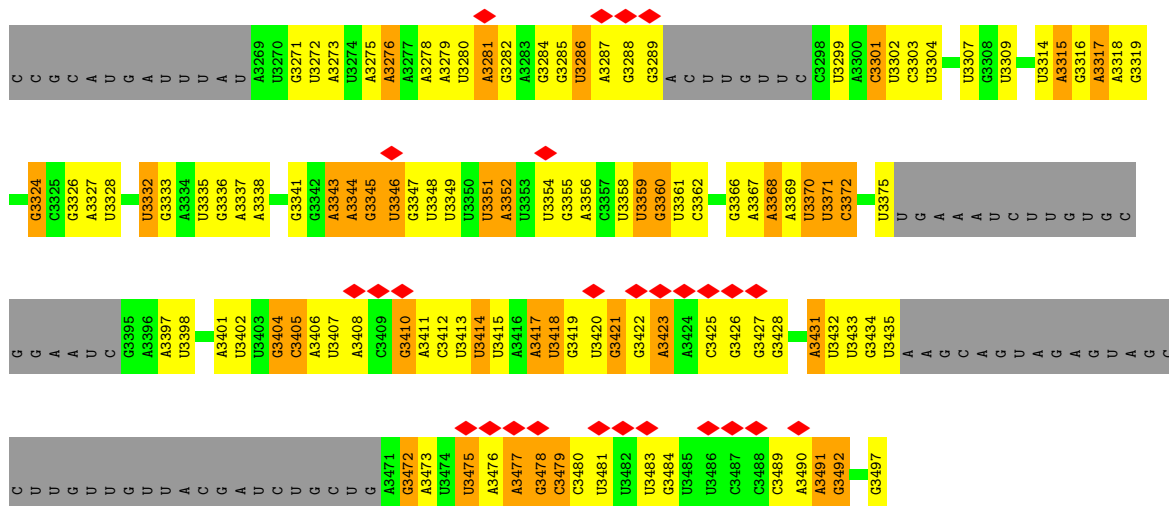
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
41	T	19	147	93	26	28	0	0

- Molecule 42 is ZINC ION (CCD ID: ZN) (formula: Zn).

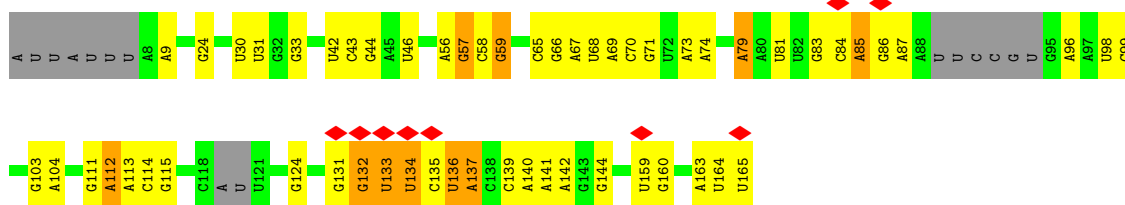
Mol	Chain	Residues	Atoms		AltConf
42	j	1	Total 1	Zn 1	0



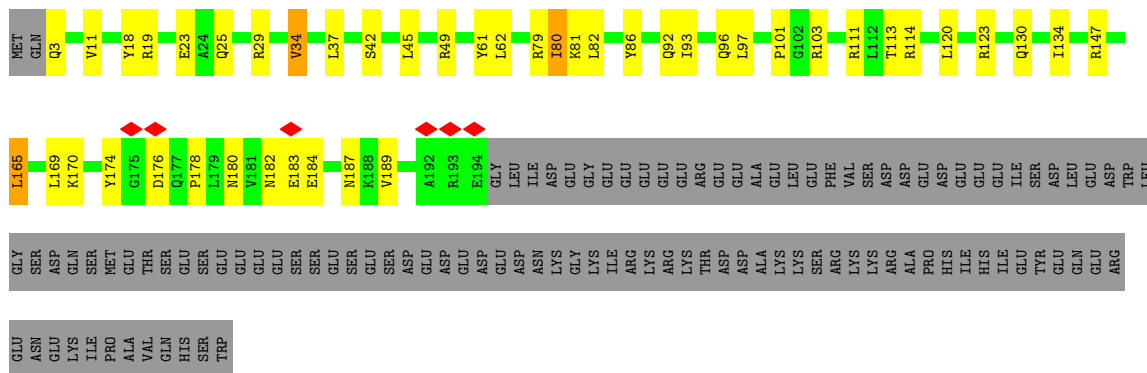




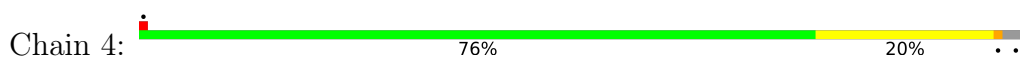
• Molecule 2: RNA (150-MER)

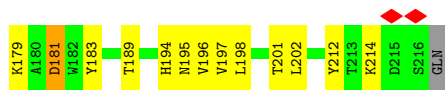


• Molecule 3: Protein mak16

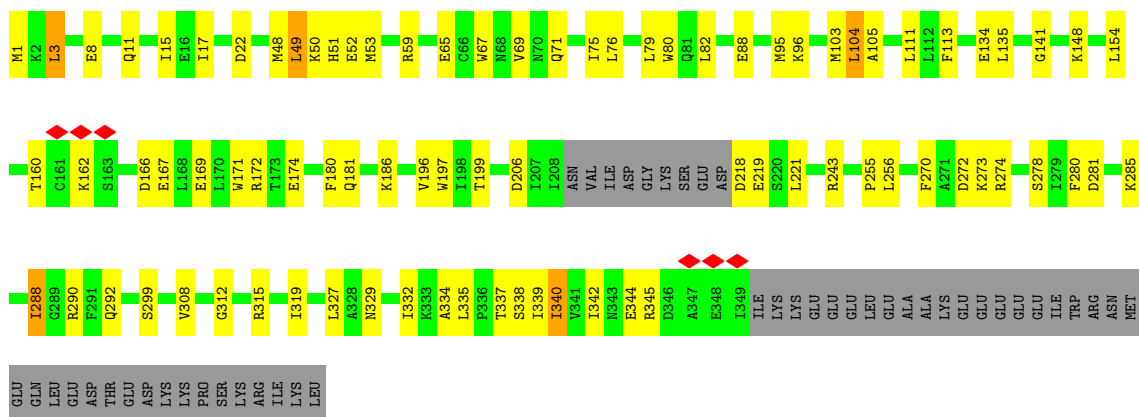


• Molecule 4: Ribosomal RNA-processing protein 1 homolog

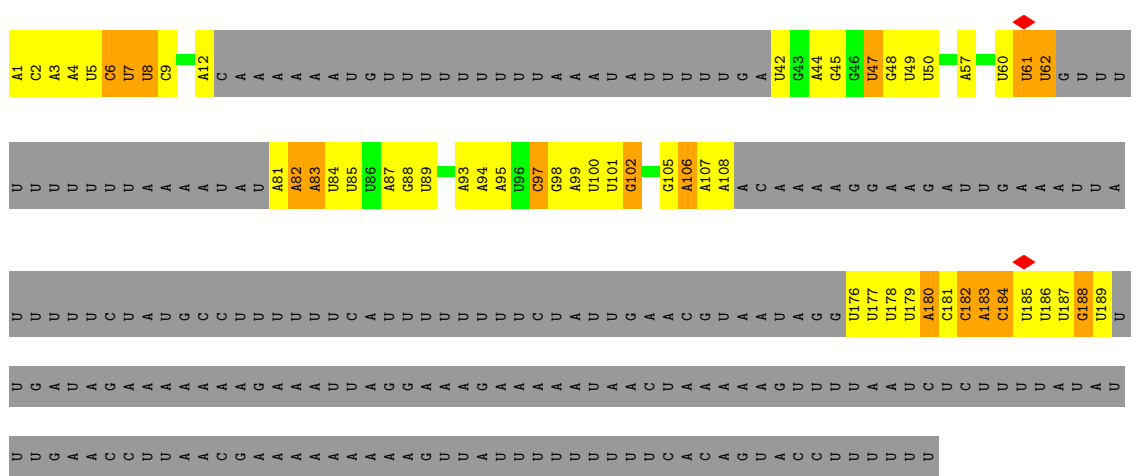




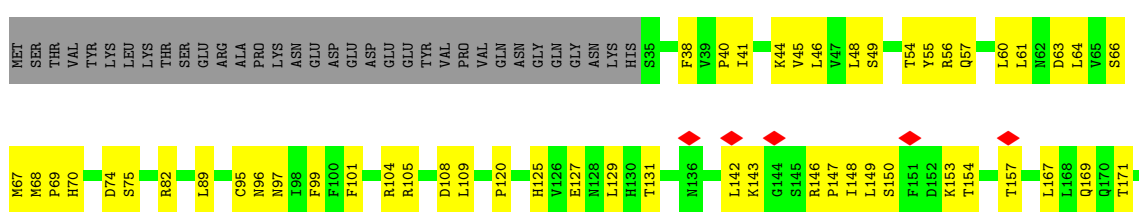
• Molecule 5: Ribosome biogenesis protein nsa1

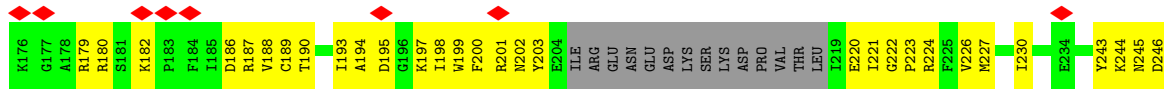


• Molecule 6: RNA (75-MER)

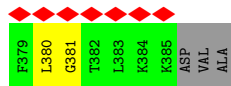
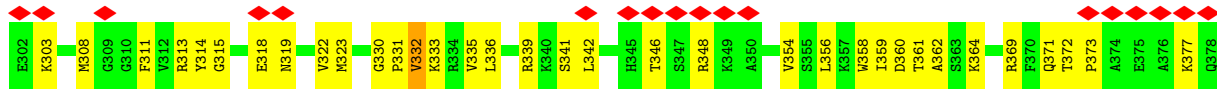
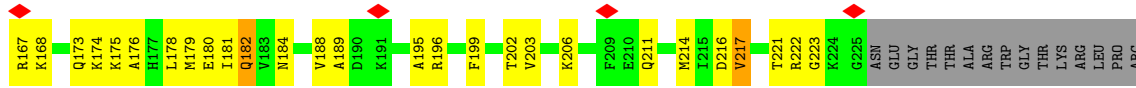


• Molecule 7: Ribosome biogenesis protein brx1

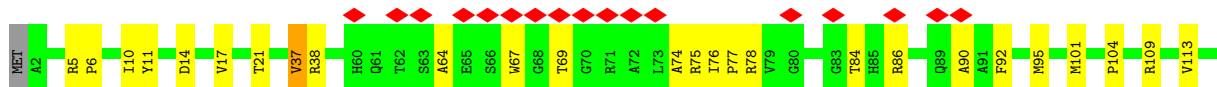
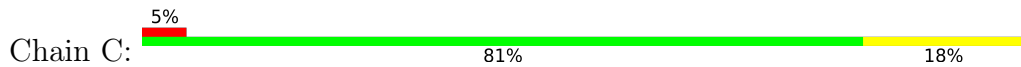




• Molecule 8: 60S ribosomal protein L3-A

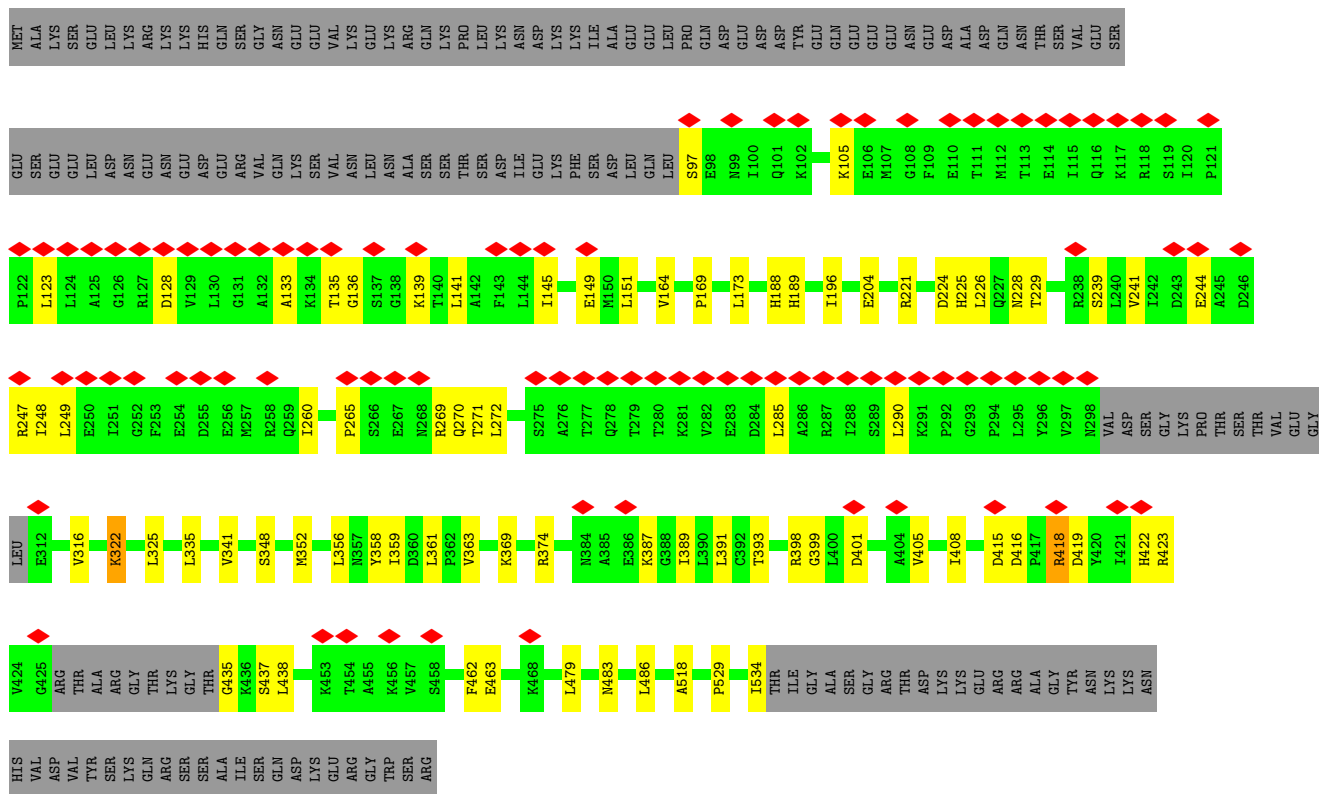


• Molecule 9: 60S ribosomal protein L4-B

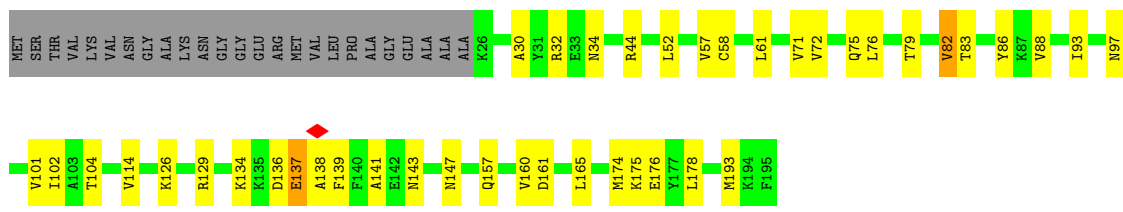


• Molecule 10: RNA helicase

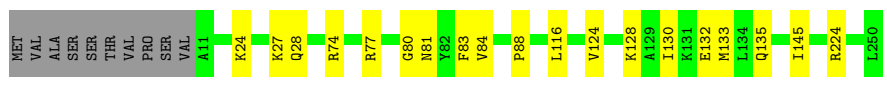
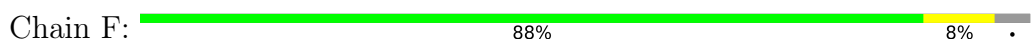




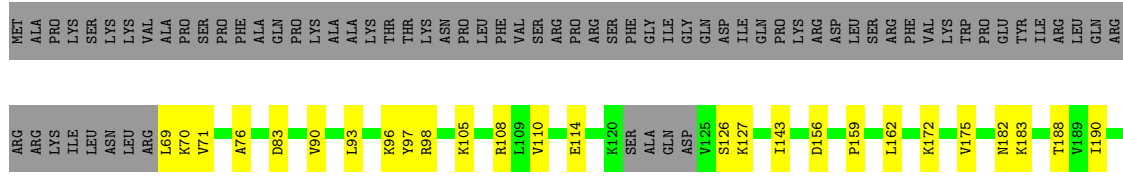
• Molecule 11: 60S ribosomal protein L6

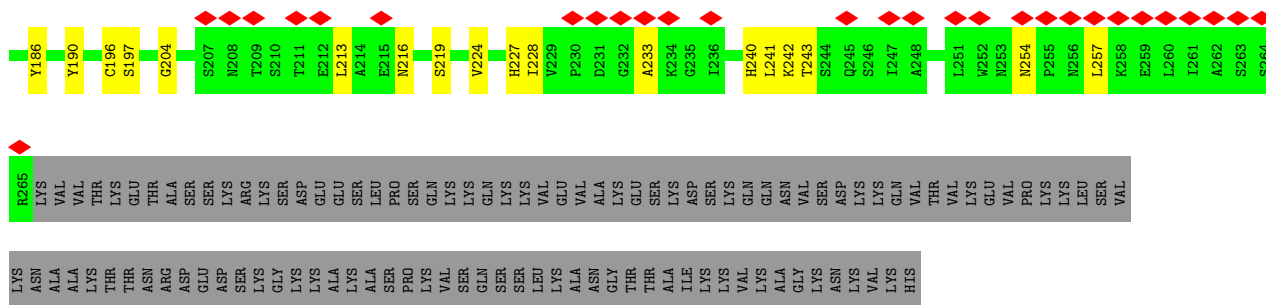


• Molecule 12: 60S ribosomal protein L7-B

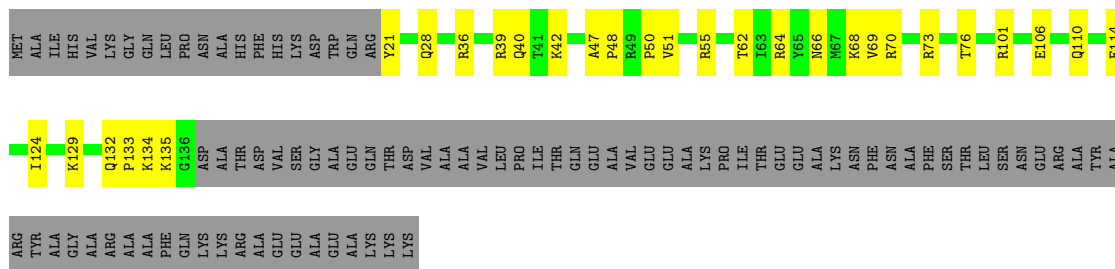


• Molecule 13: 60S ribosomal protein L8

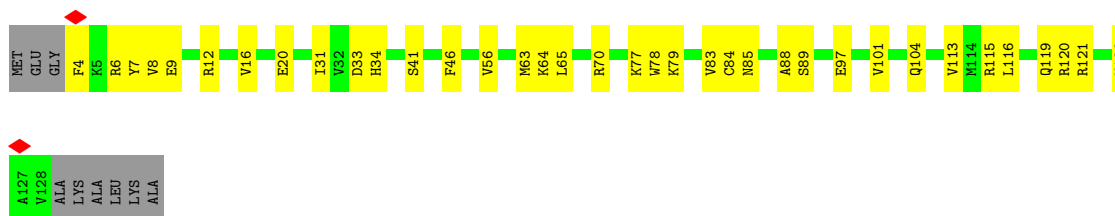




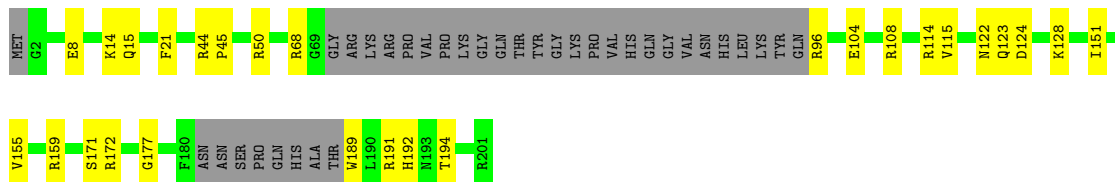
• Molecule 17: 60S ribosomal protein L13



• Molecule 18: 60S ribosomal protein L14

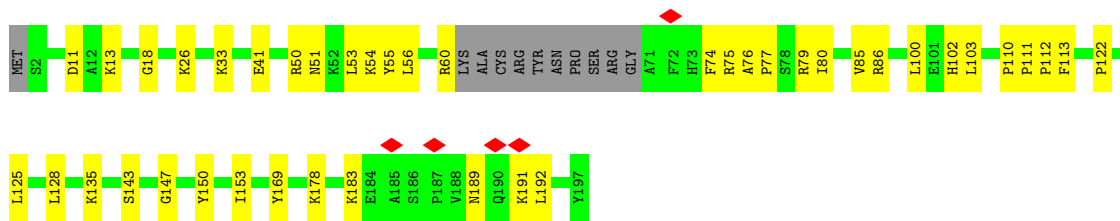


• Molecule 19: 60S ribosomal protein L15-A

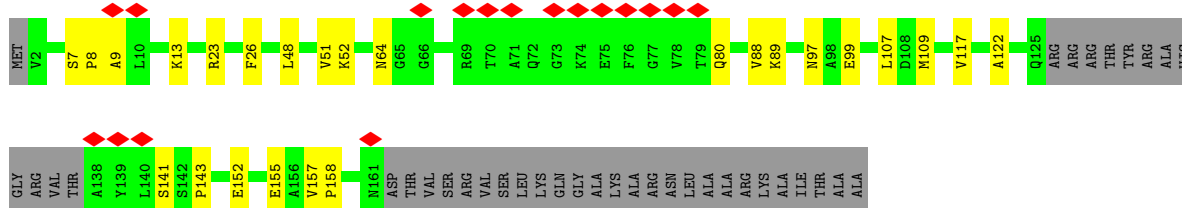


• Molecule 20: 60S ribosomal protein L16-B

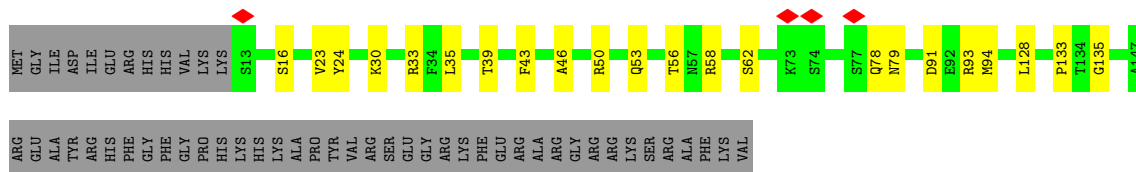




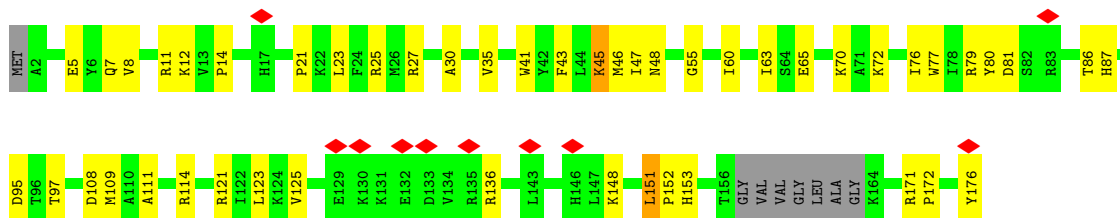
• Molecule 21: 60S ribosomal protein L17-A



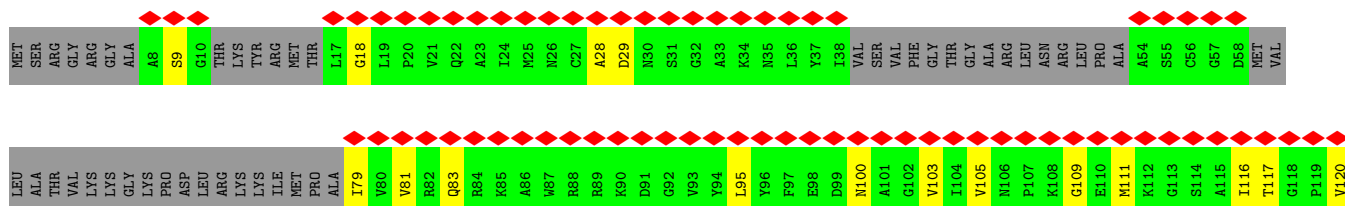
• Molecule 22: 60S ribosomal protein L18-A

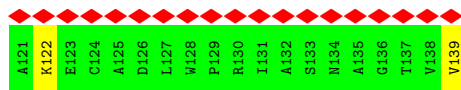


• Molecule 23: 60S ribosomal protein L20-A

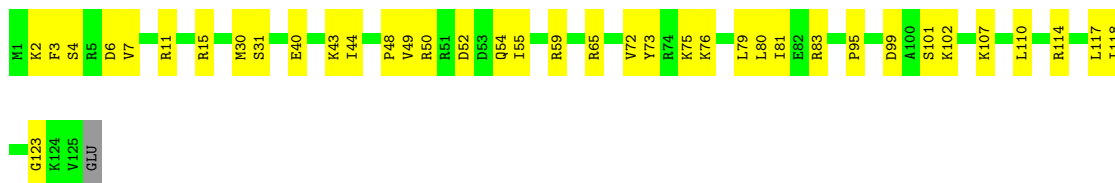


• Molecule 24: 60S ribosomal protein L23-A

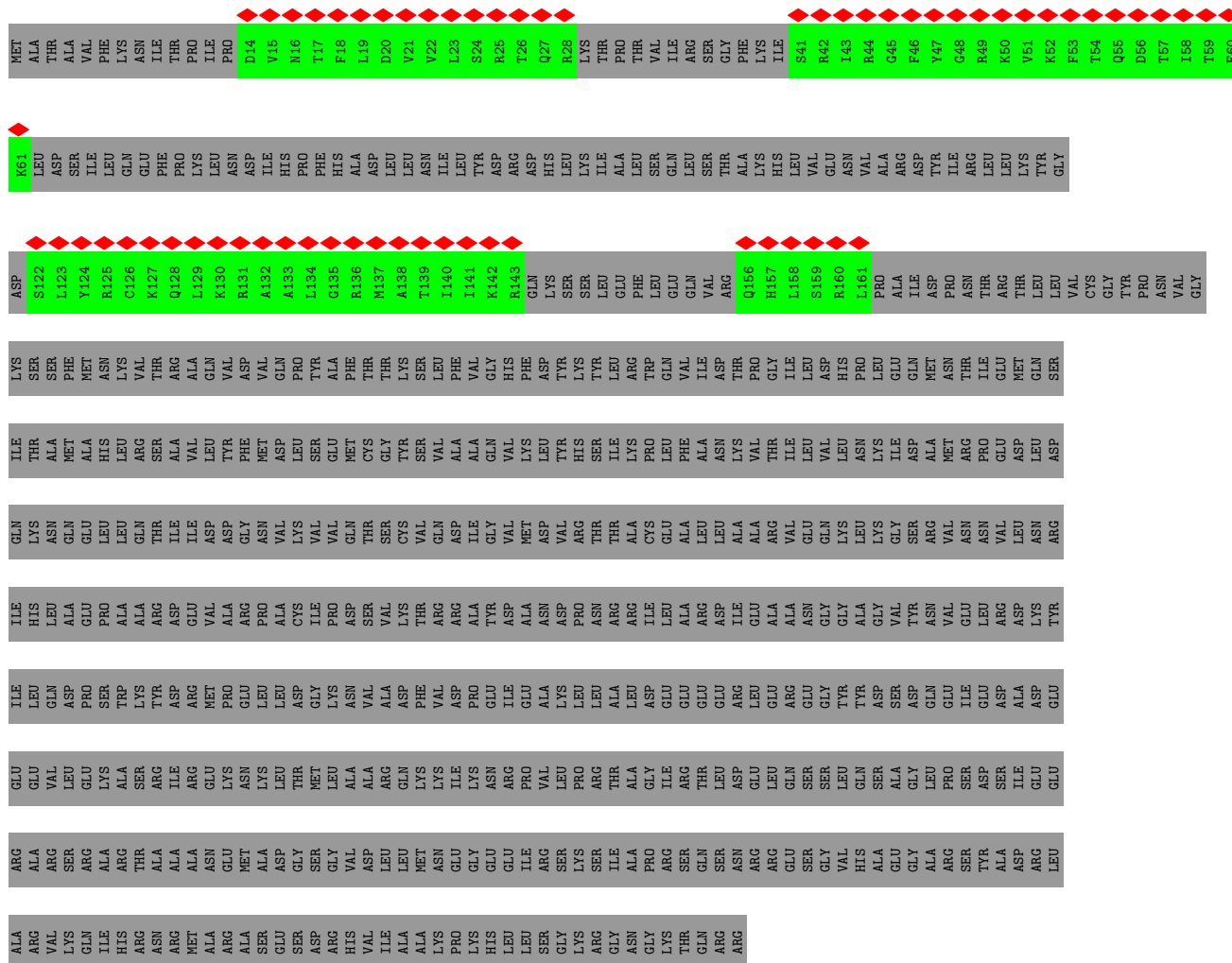




● Molecule 25: Ribosomal protein L26



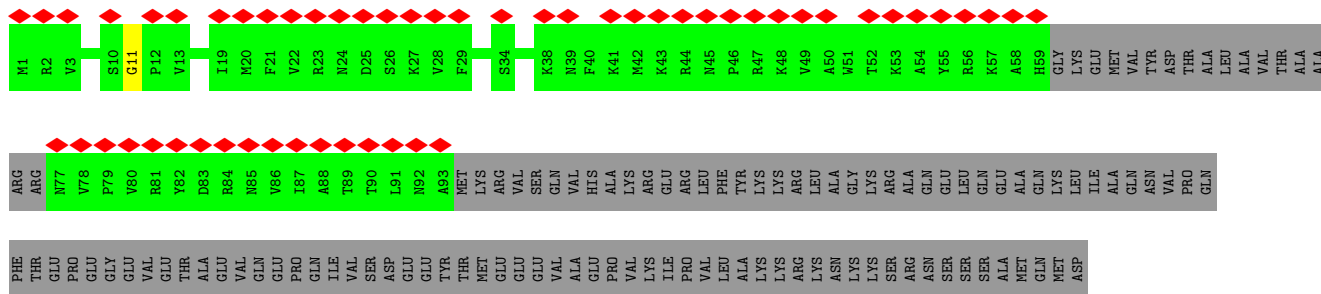
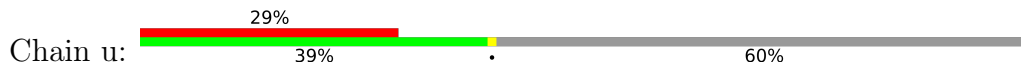
● Molecule 26: Probable nucleolar GTP-binding protein 1



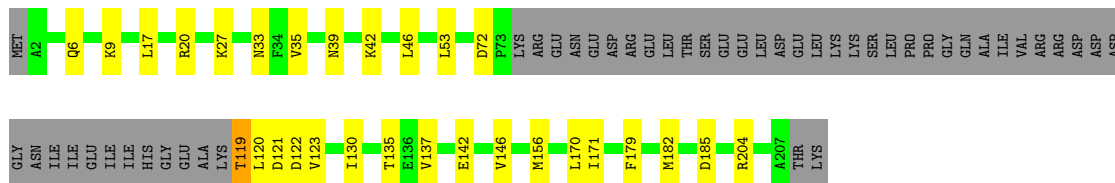
● Molecule 27: 60S ribosomal protein L32-A



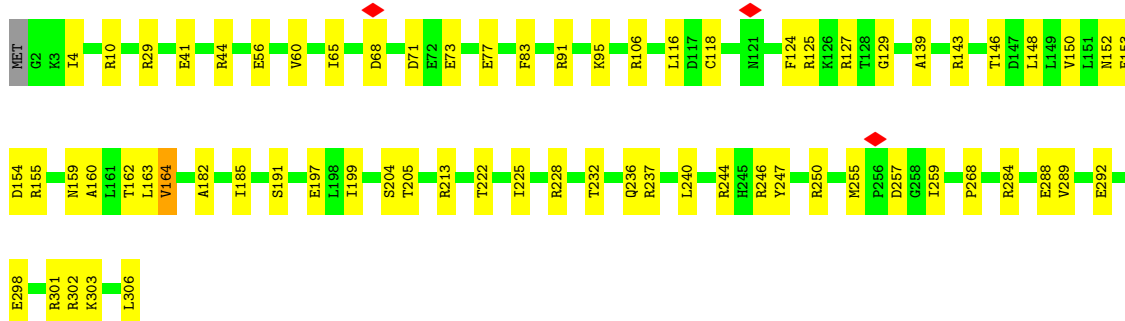
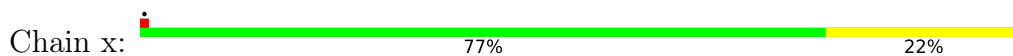
• Molecule 37: Ribosome biogenesis protein rlp24



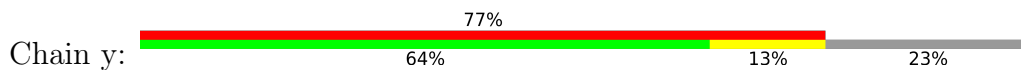
• Molecule 38: Nucleolar protein 16

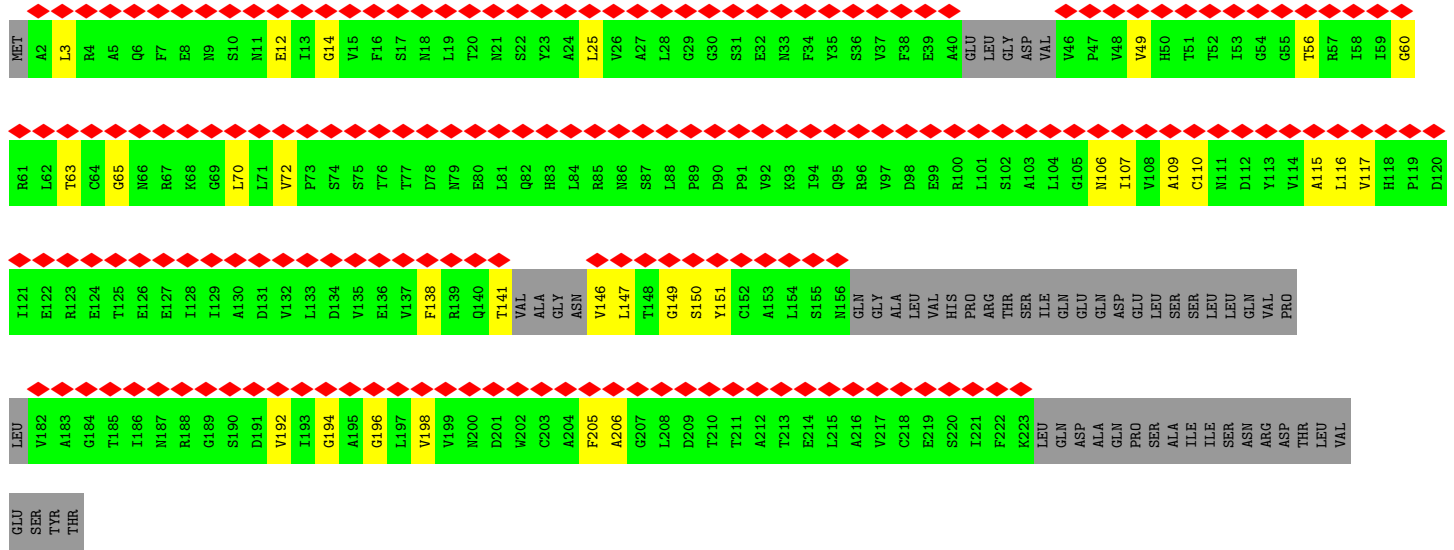


• Molecule 39: Brix domain-containing protein C4F8.04

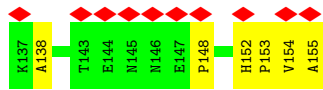


• Molecule 40: Eukaryotic translation initiation factor 6





• Molecule 41: RPL21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	250000	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	0.756	Depositor
Minimum map value	-0.337	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	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	1	0.18	1/34768 (0.0%)	0.23	0/54150
2	2	0.16	0/3563	0.21	0/5543
3	3	0.23	0/1627	0.30	0/2188
4	4	0.17	0/1823	0.29	0/2462
5	5	0.15	0/2739	0.33	0/3702
6	6	0.09	0/1770	0.19	0/2745
7	A	0.13	0/2038	0.34	0/2747
8	B	0.12	0/2694	0.34	0/3619
9	C	0.21	0/2863	0.30	0/3863
10	D	0.10	0/3245	0.23	0/4396
11	E	0.15	0/1356	0.34	0/1829
12	F	0.16	0/1982	0.26	0/2658
13	G	0.18	0/1291	0.27	0/1742
14	H	0.06	0/901	0.20	0/1252
15	J	0.11	0/458	0.32	0/639
16	K	0.10	0/1948	0.26	0/2640
17	L	0.22	0/960	0.31	0/1288
18	M	0.15	0/1024	0.38	0/1375
19	N	0.20	0/1436	0.26	0/1920
20	O	0.11	0/1506	0.24	0/2017
21	P	0.13	0/1187	0.27	0/1595
22	Q	0.19	0/1058	0.30	0/1421
23	S	0.13	0/1444	0.30	0/1939
24	V	0.10	0/442	0.25	0/605
25	Y	0.18	0/1008	0.31	0/1341
26	b	0.04	0/313	0.13	0/430
27	e	0.19	0/1009	0.24	0/1345
28	f	0.17	0/859	0.27	0/1152
29	h	0.17	0/1008	0.35	0/1340
30	i	0.15	0/791	0.24	0/1050
31	j	0.12	0/575	0.27	0/761
32	m	0.16	0/627	0.39	0/844

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	n	0.05	0/1788	0.17	0/2487
34	o	0.14	0/1049	0.35	0/1419
35	r	0.05	0/282	0.15	0/392
36	t	0.08	0/1009	0.22	0/1385
37	u	0.05	0/375	0.17	0/520
38	v	0.17	0/1319	0.29	0/1769
39	x	0.15	0/2562	0.27	0/3432
40	y	0.09	0/921	0.28	0/1274
41	T	0.09	0/151	0.26	0/207
All	All	0.16	1/89769 (0.0%)	0.26	0/129483

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	500	U	C1'-N1	5.28	1.55	1.47

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	31076	0	15637	396	0
2	2	3189	0	1613	37	0
3	3	1596	0	1645	35	0
4	4	1776	0	1793	28	0
5	5	2686	0	2745	58	0
6	6	1587	0	800	37	0
7	A	1999	0	2025	77	0
8	B	2641	0	2727	134	0
9	C	2810	0	2933	47	0
10	D	3186	0	3200	49	0
11	E	1328	0	1408	30	0
12	F	1944	0	2035	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	G	1273	0	1348	25	0
14	H	902	0	392	1	0
15	J	459	0	208	10	0
16	K	1914	0	1950	44	0
17	L	942	0	1012	23	0
18	M	1007	0	1072	28	0
19	N	1406	0	1441	19	0
20	O	1478	0	1572	34	0
21	P	1164	0	1183	19	0
22	Q	1047	0	1142	14	0
23	S	1408	0	1462	47	0
24	V	446	0	220	12	0
25	Y	998	0	1090	27	0
26	b	317	0	136	0	0
27	e	995	0	1059	19	0
28	f	839	0	866	8	0
29	h	999	0	1092	27	0
30	i	783	0	863	20	0
31	j	563	0	578	12	0
32	m	615	0	589	19	0
33	n	1791	0	805	4	0
34	o	1026	0	940	34	0
35	r	283	0	133	0	0
36	t	1008	0	571	7	0
37	u	377	0	167	1	0
38	v	1299	0	1347	23	0
39	x	2516	0	2524	47	0
40	y	925	0	430	17	0
41	T	147	0	140	7	0
42	j	1	0	0	0	0
All	All	84746	0	64893	1234	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 9.

The worst 5 of 1234 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)
2:2:132:G:H1	2:2:137:A:H61	1.11	0.94
9:C:101:MET:HE2	9:C:104:PRO:HA	1.54	0.88
1:1:3148:G:H1	1:1:3186:U:H3	1.20	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:84:THR:HG22	9:C:86:ARG:H	1.44	0.82
16:K:65:ASN:HA	34:o:208:ARG:HH12	1.45	0.82

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%)	184 (97%)	6 (3%)	0	100	100
4	4	209/217 (96%)	205 (98%)	4 (2%)	0	100	100
5	5	336/387 (87%)	311 (93%)	25 (7%)	0	100	100
7	A	243/295 (82%)	231 (95%)	12 (5%)	0	100	100
8	B	328/388 (84%)	318 (97%)	10 (3%)	0	100	100
9	C	360/363 (99%)	342 (95%)	18 (5%)	0	100	100
10	D	410/578 (71%)	400 (98%)	10 (2%)	0	100	100
11	E	168/195 (86%)	154 (92%)	13 (8%)	1 (1%)	21	56
12	F	238/250 (95%)	229 (96%)	9 (4%)	0	100	100
13	G	161/259 (62%)	152 (94%)	7 (4%)	2 (1%)	10	40
14	H	181/190 (95%)	180 (99%)	1 (1%)	0	100	100
15	J	90/333 (27%)	86 (96%)	3 (3%)	1 (1%)	11	43
16	K	245/373 (66%)	231 (94%)	14 (6%)	0	100	100
17	L	114/208 (55%)	110 (96%)	4 (4%)	0	100	100
18	M	123/134 (92%)	118 (96%)	5 (4%)	0	100	100
19	N	160/201 (80%)	158 (99%)	2 (1%)	0	100	100
20	O	182/197 (92%)	180 (99%)	2 (1%)	0	100	100
21	P	144/187 (77%)	136 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	Q	133/187 (71%)	123 (92%)	10 (8%)	0	100	100
23	S	164/176 (93%)	156 (95%)	8 (5%)	0	100	100
24	V	83/139 (60%)	78 (94%)	5 (6%)	0	100	100
25	Y	123/126 (98%)	118 (96%)	5 (4%)	0	100	100
26	b	56/642 (9%)	56 (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
29	h	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
30	i	96/99 (97%)	93 (97%)	3 (3%)	0	100	100
31	j	69/91 (76%)	66 (96%)	3 (4%)	0	100	100
32	m	71/740 (10%)	69 (97%)	2 (3%)	0	100	100
33	n	356/607 (59%)	352 (99%)	4 (1%)	0	100	100
34	o	135/276 (49%)	129 (96%)	6 (4%)	0	100	100
35	r	55/260 (21%)	54 (98%)	1 (2%)	0	100	100
36	t	179/249 (72%)	172 (96%)	7 (4%)	0	100	100
37	u	72/192 (38%)	72 (100%)	0	0	100	100
38	v	157/209 (75%)	153 (98%)	3 (2%)	1 (1%)	21	56
39	x	303/306 (99%)	297 (98%)	6 (2%)	0	100	100
40	y	180/244 (74%)	173 (96%)	7 (4%)	0	100	100
41	T	17/19 (90%)	16 (94%)	1 (6%)	0	100	100
All	All	6476/9976 (65%)	6239 (96%)	232 (4%)	5 (0%)	49	80

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	G	227[A]	ASP
13	G	227[B]	ASP
38	v	130	ILE
11	E	137	GLU
15	J	162	VAL

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%)	162 (96%)	7 (4%)	27	61
4	4	192/197 (98%)	185 (96%)	7 (4%)	31	65
5	5	301/345 (87%)	292 (97%)	9 (3%)	36	69
7	A	221/266 (83%)	214 (97%)	7 (3%)	34	67
8	B	282/326 (86%)	272 (96%)	10 (4%)	32	65
9	C	296/297 (100%)	287 (97%)	9 (3%)	36	69
10	D	332/505 (66%)	326 (98%)	6 (2%)	51	77
11	E	139/155 (90%)	134 (96%)	5 (4%)	31	65
12	F	201/210 (96%)	198 (98%)	3 (2%)	57	80
13	G	135/212 (64%)	133 (98%)	2 (2%)	57	80
16	K	210/333 (63%)	207 (99%)	3 (1%)	59	80
17	L	97/167 (58%)	94 (97%)	3 (3%)	35	68
18	M	108/113 (96%)	107 (99%)	1 (1%)	70	85
19	N	146/176 (83%)	143 (98%)	3 (2%)	47	75
20	O	153/162 (94%)	152 (99%)	1 (1%)	76	86
21	P	120/149 (80%)	119 (99%)	1 (1%)	73	86
22	Q	116/159 (73%)	113 (97%)	3 (3%)	40	72
23	S	150/154 (97%)	148 (99%)	2 (1%)	61	81
25	Y	110/111 (99%)	109 (99%)	1 (1%)	70	85
27	e	106/107 (99%)	104 (98%)	2 (2%)	50	76
28	f	89/91 (98%)	86 (97%)	3 (3%)	32	66
29	h	106/107 (99%)	104 (98%)	2 (2%)	50	76
30	i	83/84 (99%)	80 (96%)	3 (4%)	31	65
31	j	58/71 (82%)	57 (98%)	1 (2%)	53	78
32	m	67/659 (10%)	63 (94%)	4 (6%)	17	50
34	o	93/246 (38%)	91 (98%)	2 (2%)	45	74
36	t	23/223 (10%)	22 (96%)	1 (4%)	26	60
38	v	138/181 (76%)	134 (97%)	4 (3%)	37	70
39	x	272/273 (100%)	267 (98%)	5 (2%)	51	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	T	17/17 (100%)	17 (100%)	0	100	100
All	All	4530/6367 (71%)	4420 (98%)	110 (2%)	43	73

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	E	114	VAL
18	M	113	VAL
39	x	292	GLU
34	o	199	LYS
11	E	193	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
20	O	176	GLN
27	e	5	ASN
20	O	190	GLN
23	S	48	ASN
31	j	48	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1427/3497 (40%)	357 (25%)	16 (1%)
2	2	147/165 (89%)	31 (21%)	0
6	6	72/300 (24%)	40 (55%)	1 (1%)
All	All	1646/3962 (41%)	428 (26%)	17 (1%)

5 of 428 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	C
1	1	26	A
1	1	34	A
1	1	50	U
1	1	53	G

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1389	A
6	6	1	A
1	1	496	C
1	1	500	U
1	1	761	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 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](#)

There are no chain breaks in this entry.

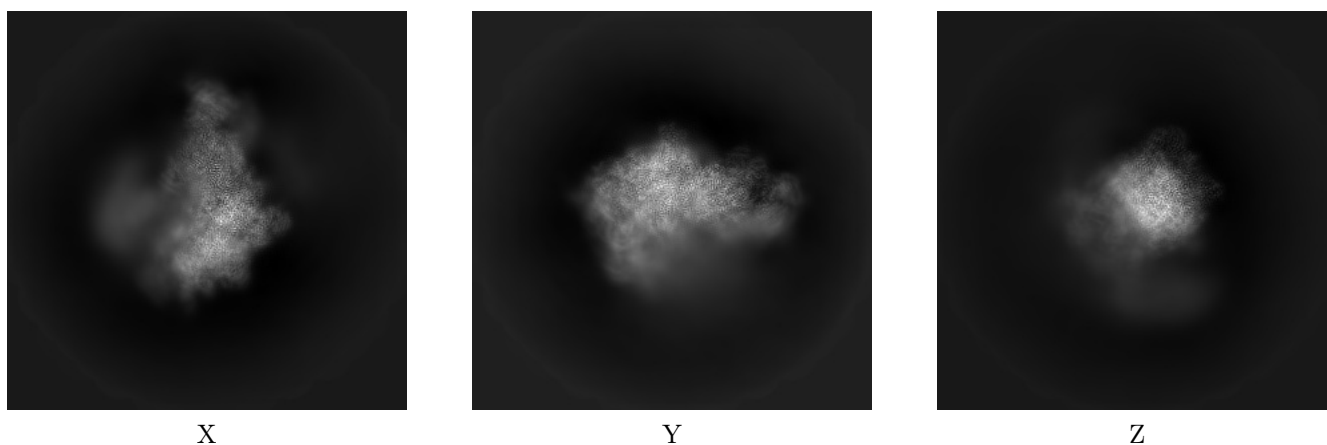
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24421. 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](#)

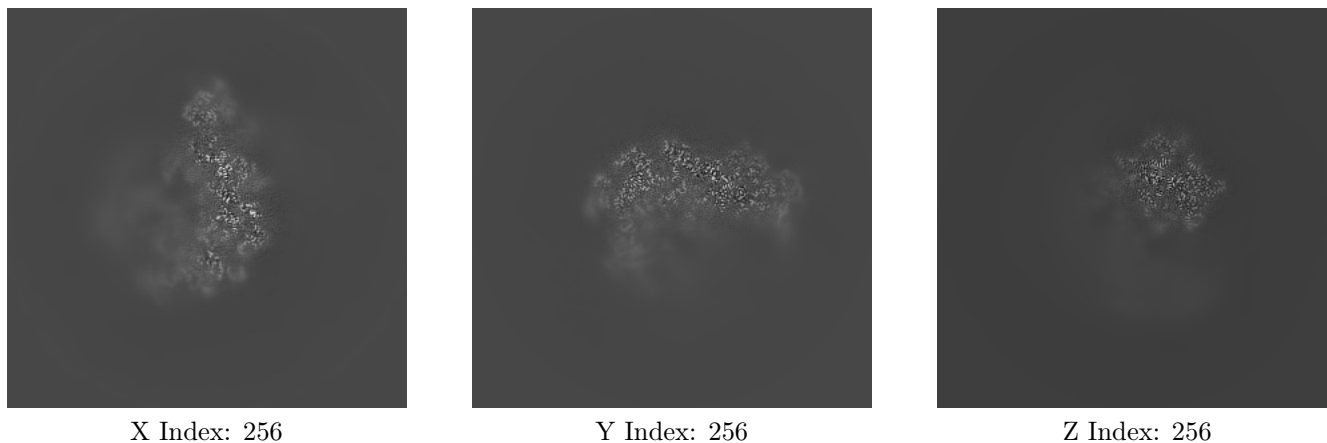
6.1.1 Primary map



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

6.2 Central slices [i](#)

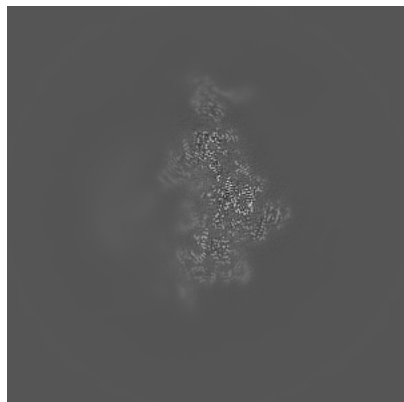
6.2.1 Primary map



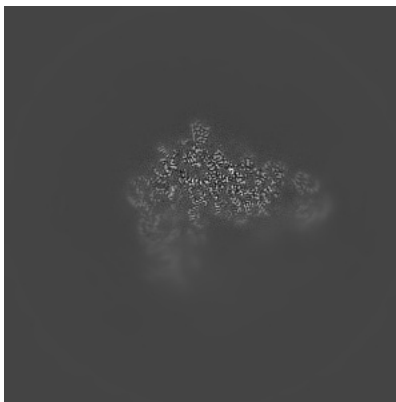
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

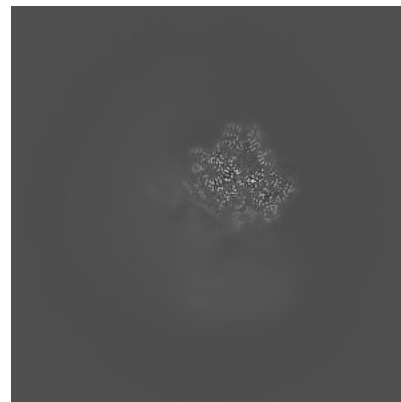
6.3.1 Primary map



X Index: 282



Y Index: 274

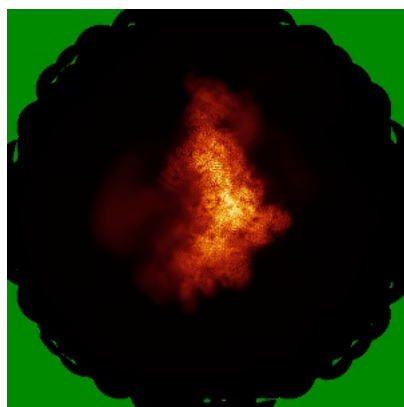


Z Index: 249

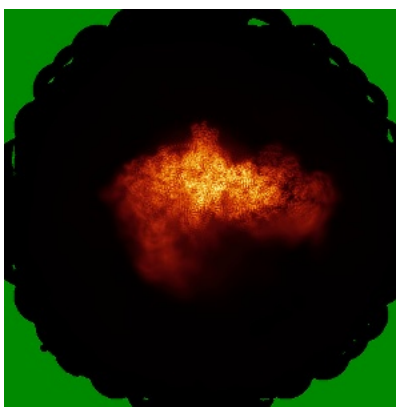
The images above show the largest variance slices of the map in three orthogonal directions.

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

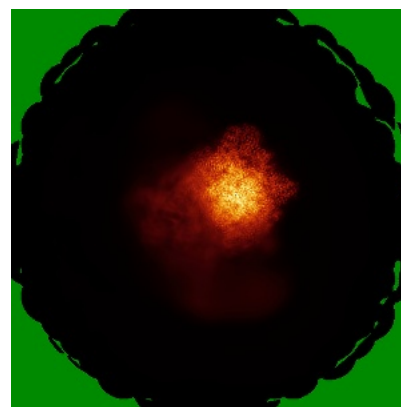
6.4.1 Primary map



X



Y

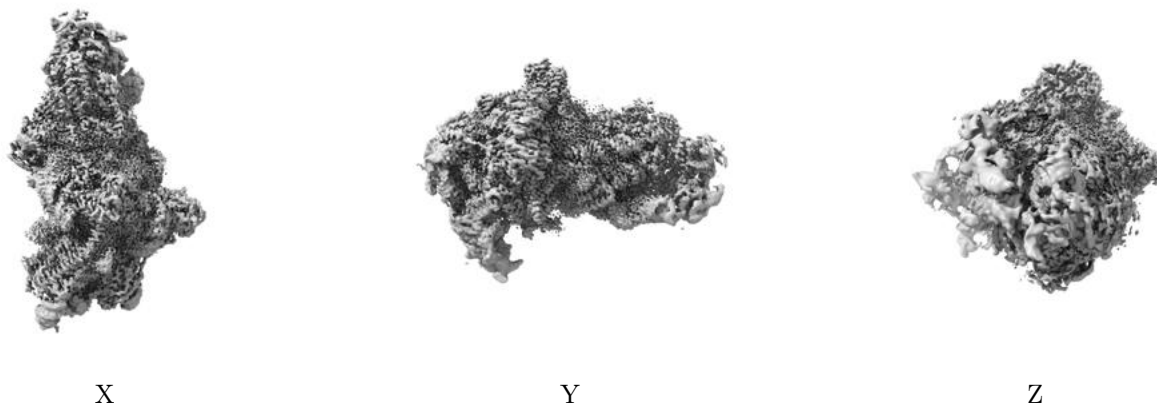


Z

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.

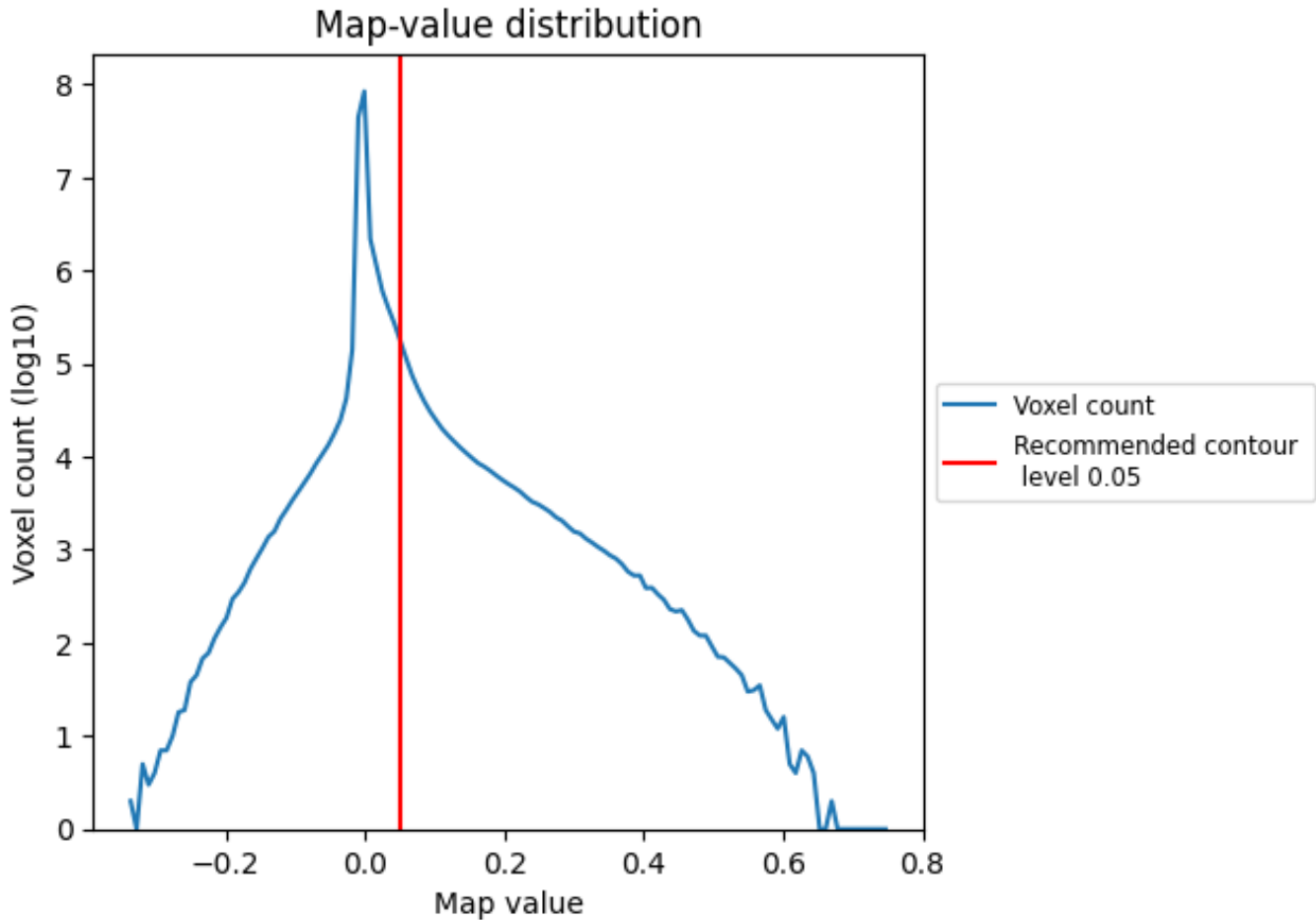
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

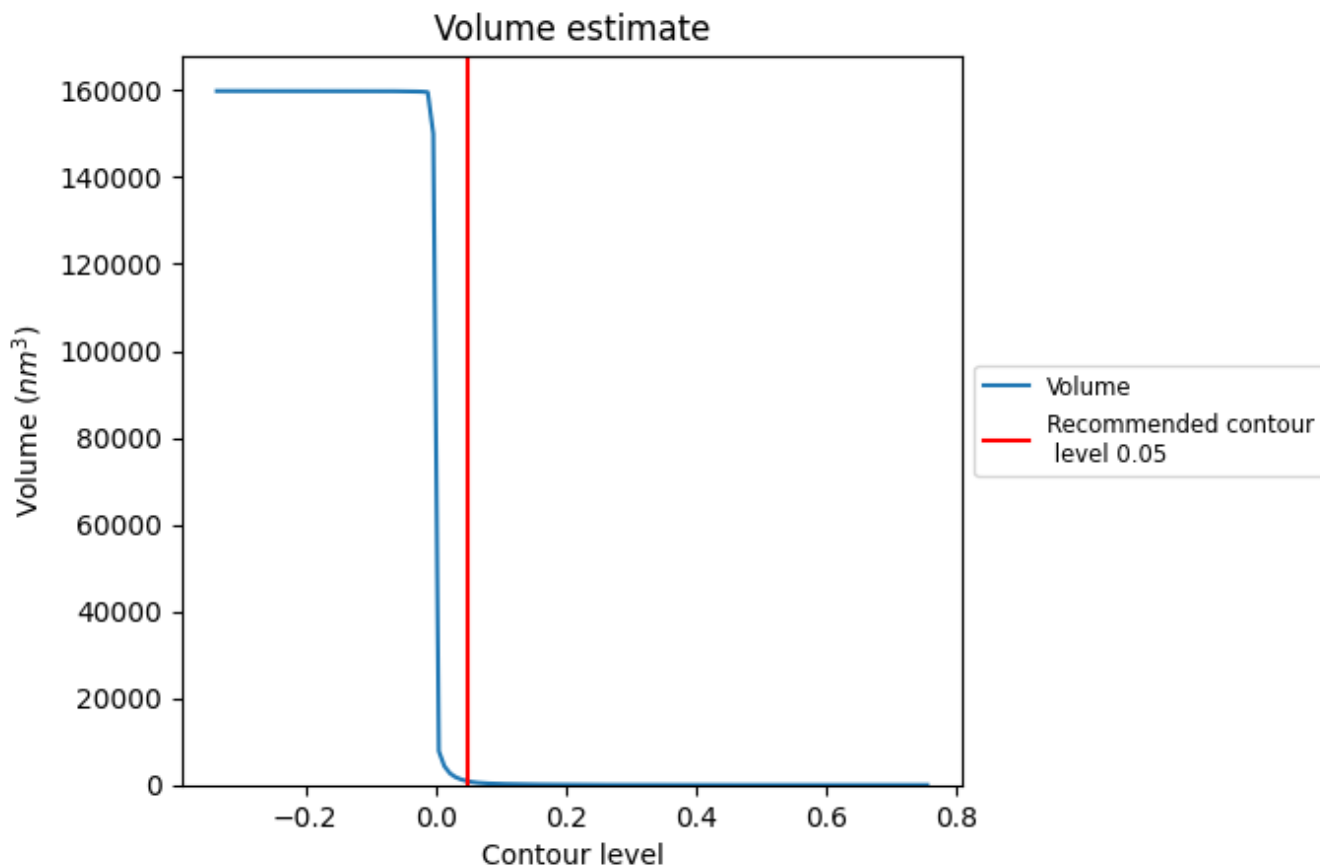
This section contains the results of statistical analysis of the map.

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.

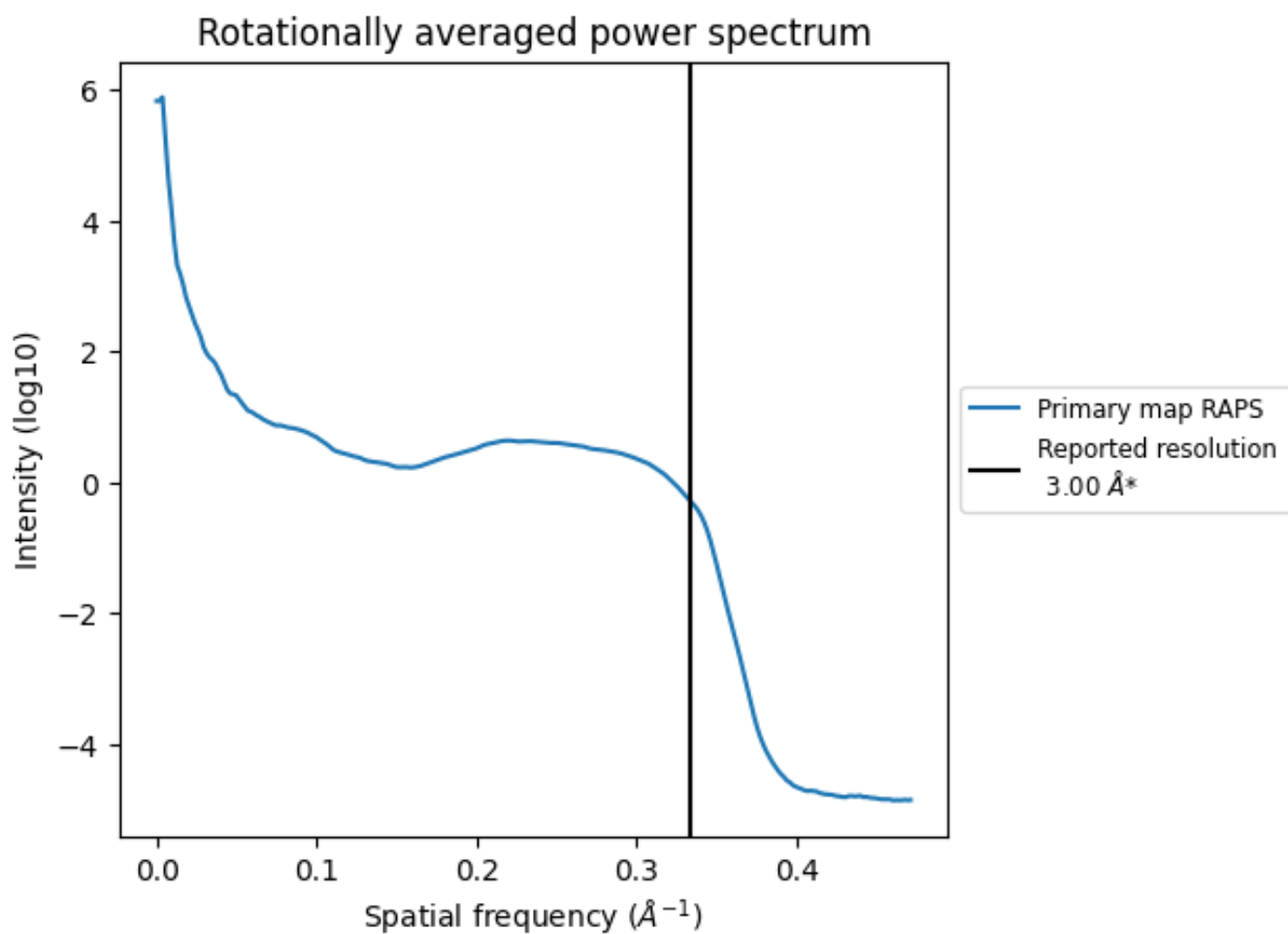
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 836 nm³; this corresponds to an approximate mass of 756 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 Å⁻¹

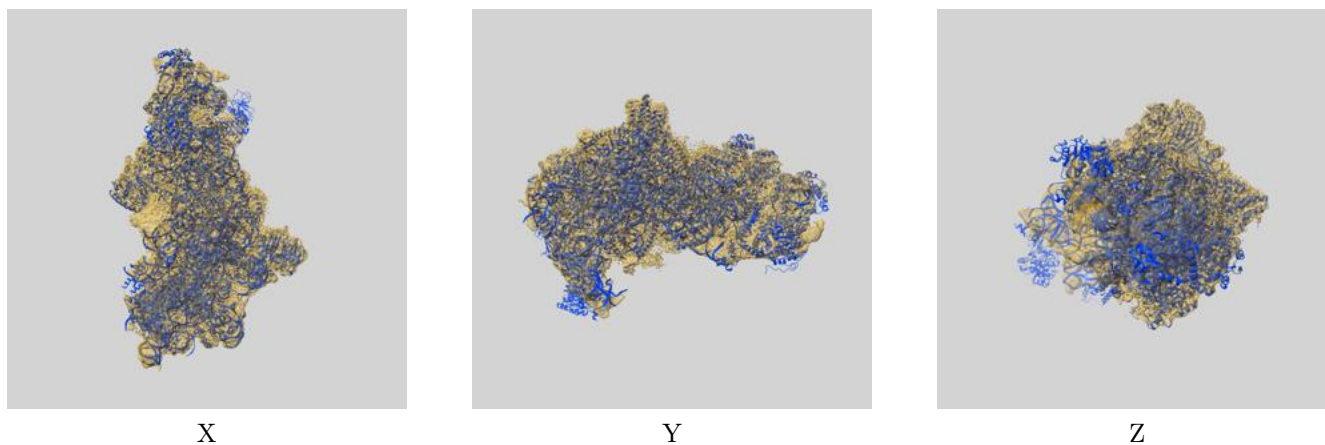
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

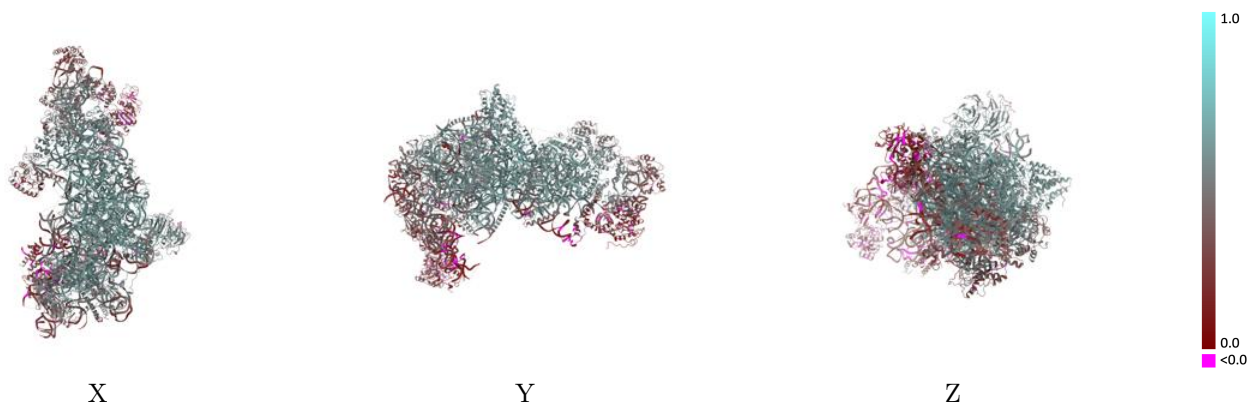
This section contains information regarding the fit between EMDB map EMD-24421 and PDB model 8EV3. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



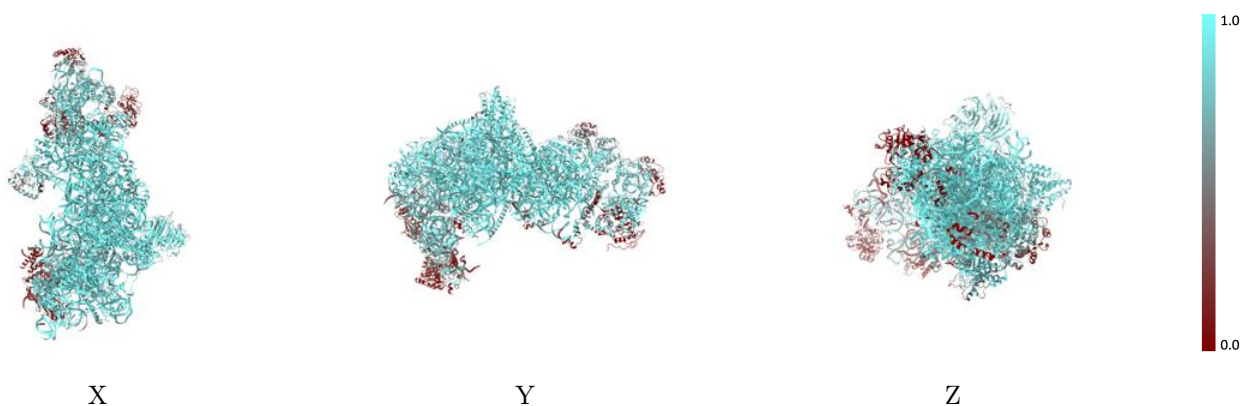
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



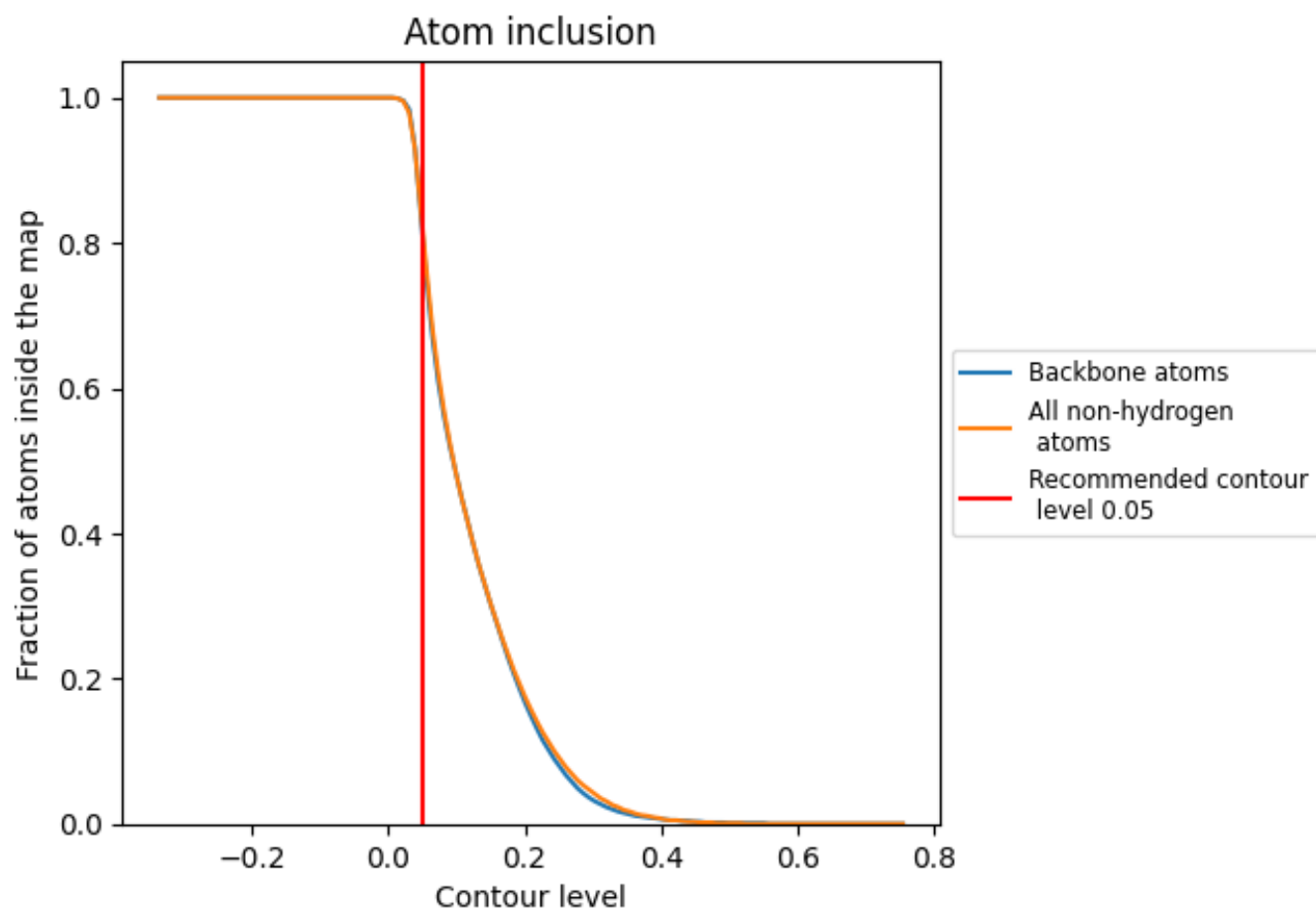
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 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	 0.8200	 0.4620
1	 0.8780	 0.4450
2	 0.8890	 0.4570
3	 0.9400	 0.5940
4	 0.9170	 0.5770
5	 0.8800	 0.5330
6	 0.8400	 0.3210
A	 0.7850	 0.3930
B	 0.6340	 0.2630
C	 0.9280	 0.5840
D	 0.6540	 0.4890
E	 0.9130	 0.5290
F	 0.9420	 0.5710
G	 0.9460	 0.5840
H	 0.1330	 0.2830
J	 0.5420	 0.3010
K	 0.6150	 0.3940
L	 0.9800	 0.6290
M	 0.9310	 0.4890
N	 0.9890	 0.6200
O	 0.8990	 0.4840
P	 0.8330	 0.5180
Q	 0.9560	 0.5890
S	 0.8440	 0.4560
T	 0.3670	 0.3620
V	 0.0000	 0.1100
Y	 0.9750	 0.5990
b	 0.0000	 0.2500
e	 0.9830	 0.6170
f	 0.9940	 0.6020
h	 0.8260	 0.5190
i	 0.9240	 0.5510
j	 0.9430	 0.5830
m	 0.8600	 0.5230
n	 0.3200	 0.1710



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Chain	Atom inclusion	Q-score
o	 0.7270	 0.4300
r	 0.0140	 0.1790
t	 0.7810	 0.3250
u	 0.2440	 0.1920
v	 0.9310	 0.5680
x	 0.9110	 0.5640
y	 0.0010	 0.1830