



## wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 03:54 PM EST

PDB ID : 8ESR  
EMDB ID : EMD-24422  
Title : Ytm1 associated nascent 60S ribosome (-fkbp39) State 2  
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.  
Deposited on : 2022-10-14  
Resolution : 3.20 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

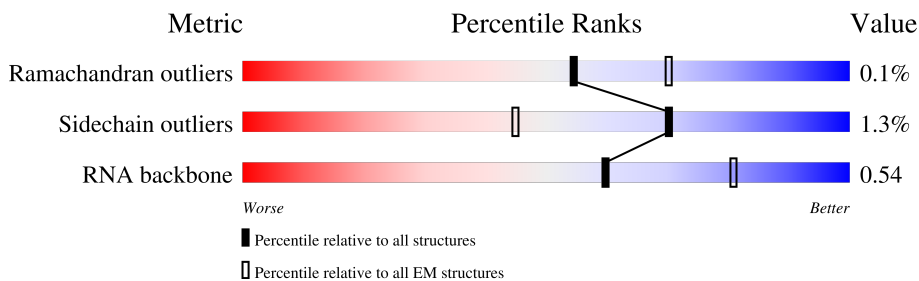
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



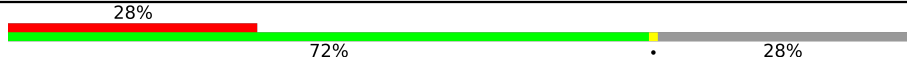
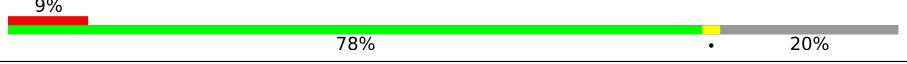
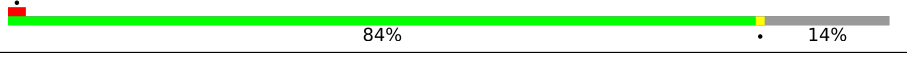

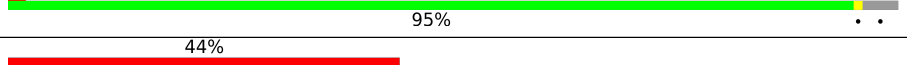

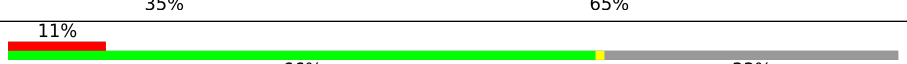
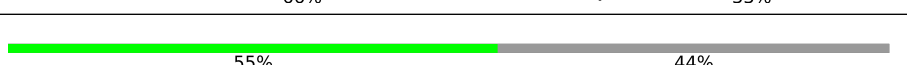
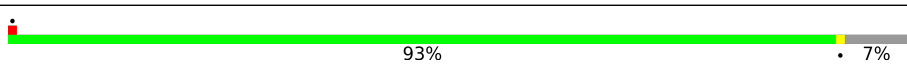

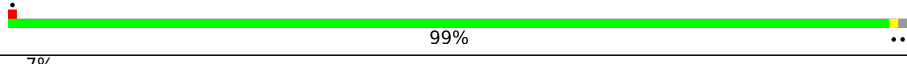
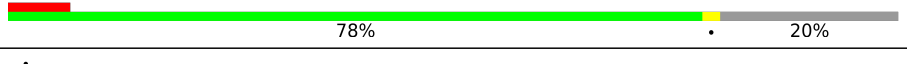
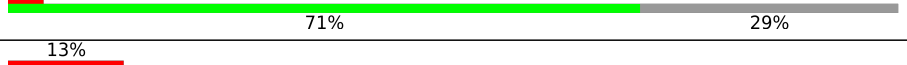

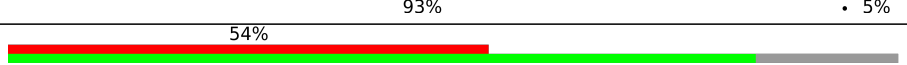

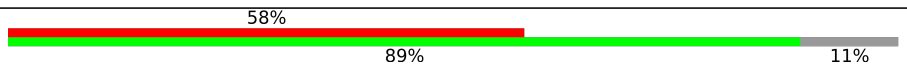
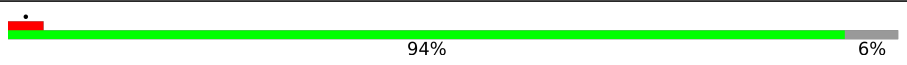
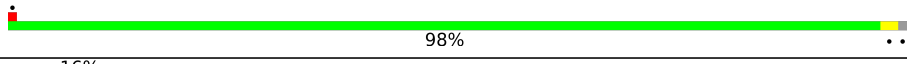
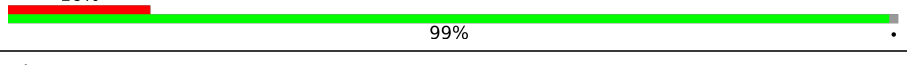





Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	6	300	
4	7	707	
5	8	51	
6	A	295	
7	B	388	
8	C	363	

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Mol	Chain	Length	Quality of chain
9	D	578	
10	E	195	
11	F	250	
12	G	259	
13	H	190	
14	I	747	
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	R	193	
24	S	176	
25	U	117	
26	V	139	
27	W	241	
28	X	141	
29	Y	126	
30	Z	136	
31	a	148	
32	b	642	
33	c	117	

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Mol	Chain	Length	Quality of chain
34	d	113	84% 15%
35	e	127	93% 6%
36	f	108	98%
37	g	112	87% 13%
38	h	122	99%
39	i	99	86% 14%
40	j	91	78% 22%
41	k	74	92% 5%
42	l	180	97%
43	m	740	76% 23%
44	n	607	70% 29%
45	o	276	49% 50%
46	p	440	62% 38%
47	q	608	43% 57%
48	r	260	63% 37%
49	s	470	95%
50	t	249	93% 6%
51	u	192	51% 47%
52	v	209	75% 23%
53	w	802	78%
54	y	244	91% 9%
55	z	117	70%
56	T	160	89%

## 2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 116762 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 (2142-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2143	45883	20493	8324	14923	2143	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1741	C	U	conflict	GB 157310483

- 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 RNA chain called RNA (79-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	6	79	1674	751	288	556	79	0	0

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 4 is a protein called Noc2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	7	110	548	328	110	110	0	0

- Molecule 5 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	8	22	187	119	40	28	0	0

- Molecule 6 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A	204	1652	1057	295	293	7	0	0

- Molecule 7 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	B	335	2662	1687	492	474	9	0	0

- Molecule 8 is a protein called 60S ribosomal protein L4-B.

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

- Molecule 9 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	D	418	3320	2140	570	599	11	0	0

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	E	156	1213	777	226	207	3	0	0

- Molecule 11 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	F	214	1745	1124	320	298	3	0	0

- Molecule 12 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	G	206	1607	1030	294	280	3	0	0

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 14 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	I	409	2032	1214	409	409	0	0

There is a discrepancy between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	J	115	574	344	115	115	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	250	1964	1256	336	366	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	165	1392	872	289	228	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	196	1557	999	297	257	4	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	149	1168	742	216	207	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	133	1032	650	199	182	1	0	0

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	R	112	729	445	148	133	3	0	0

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	S	167	1401	905	262	229	5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L22.



Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	U	98	484	288	98	98	0	0

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 27 is a protein called Ribosome assembly factor mrt4.

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

- Molecule 28 is a protein called 60S ribosomal protein L25-A.

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

- Molecule 29 is a protein called 60S ribosomal protein L26.

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

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	Z	134	662	393	134	135	0	0

- Molecule 31 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
31	a	97	762	483	145	134	0	0

- Molecule 32 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	b	359	Total	C	N	O	0	0
			1780	1062	359	359		

- Molecule 33 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	c	94	Total	C	N	O	0	0
			462	274	94	94		

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	96	Total	C	N	O	S	0	0
			801	507	158	133	3		

- Molecule 35 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	119	Total	C	N	O	S	0	0
			953	597	193	158	5		

- Molecule 36 is a protein called 60S ribosomal protein L33-B.

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

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	g	97	Total	C	N	O	0	0
			478	284	97	97		

- Molecule 38 is a protein called 60S ribosomal protein L35.

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

- Molecule 39 is a protein called 60S ribosomal protein L36-B.

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

- Molecule 40 is a protein called 60S ribosomal protein L37-B.

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

- Molecule 41 is a protein called 60S ribosomal protein L38-1.

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

- Molecule 42 is a protein called 60S ribosome subunit biogenesis protein nip7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	l	174	860	512	174	174	0	0

- Molecule 43 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	m	572	4526	2883	790	842	11	0	0

- Molecule 44 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	n	432	3517	2262	606	637	12	0	0

- Molecule 45 is a protein called Uncharacterized RNA-binding protein C1827.05c.

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

- Molecule 46 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
46	p	275	1357	807	275	275	0	0

- Molecule 47 is a protein called 25S rRNA (cytosine-C(5))-methyltransferase nop2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
47	q	260	1282	762	260	260	0	0

- Molecule 48 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	r	165	1081	653	223	204	1	0	0

- Molecule 49 is a protein called GTPase grn1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
49	s	23	193	117	44	32	0	0

- Molecule 50 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 51 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	u	101	714	448	143	116	7	0	0

- Molecule 52 is a protein called Nucleolar protein 16.

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

- Molecule 53 is a protein called AdoMet-dependent rRNA methyltransferase spb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	w	180	1462	910	276	270	6	0	0

- Molecule 54 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
54	y	223	1097	651	223	223	0	0

- Molecule 55 is a protein called UPF0642 protein C32H8.05.

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

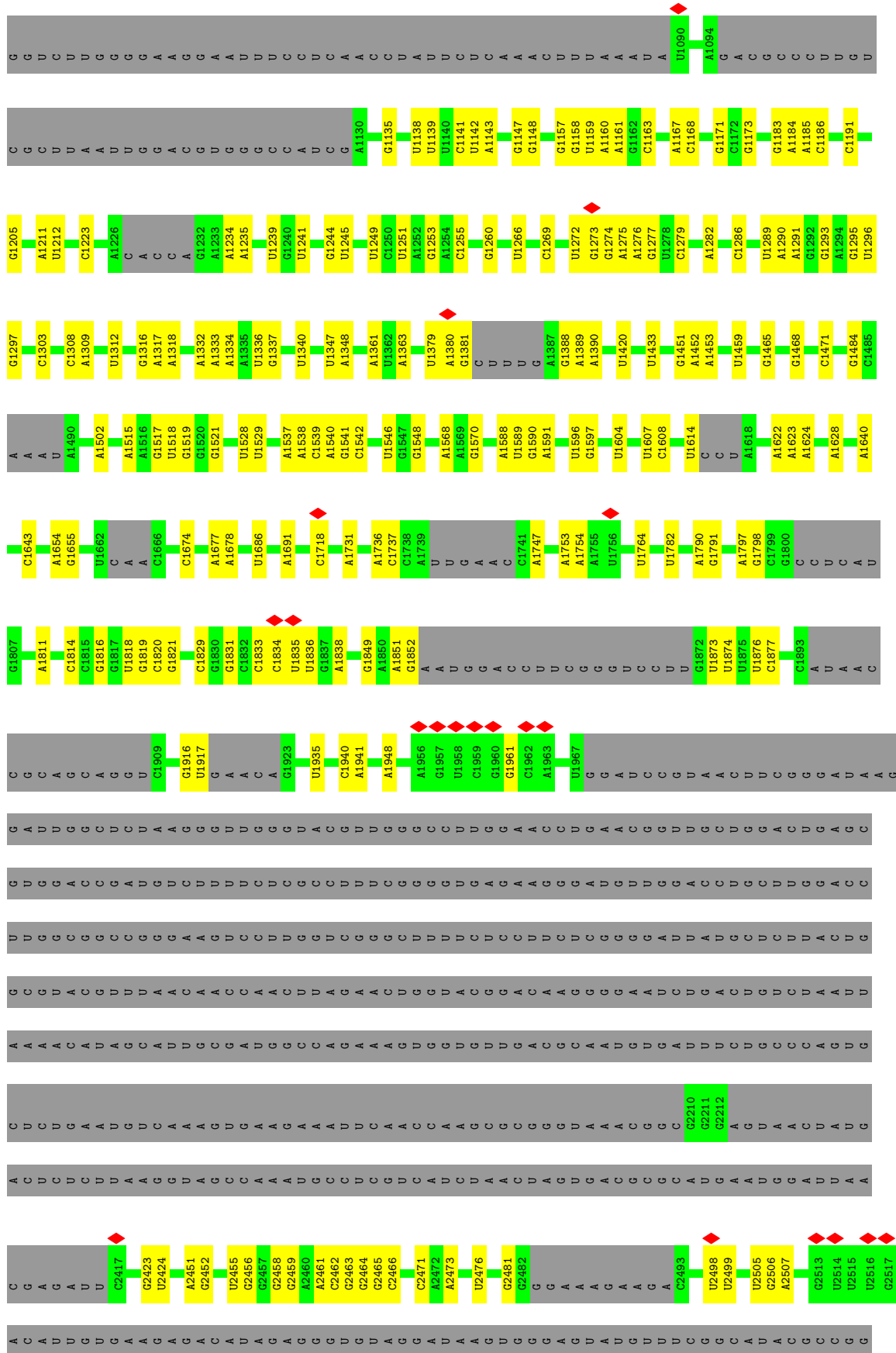
- Molecule 56 is a protein called 60S ribosomal protein L21-A.

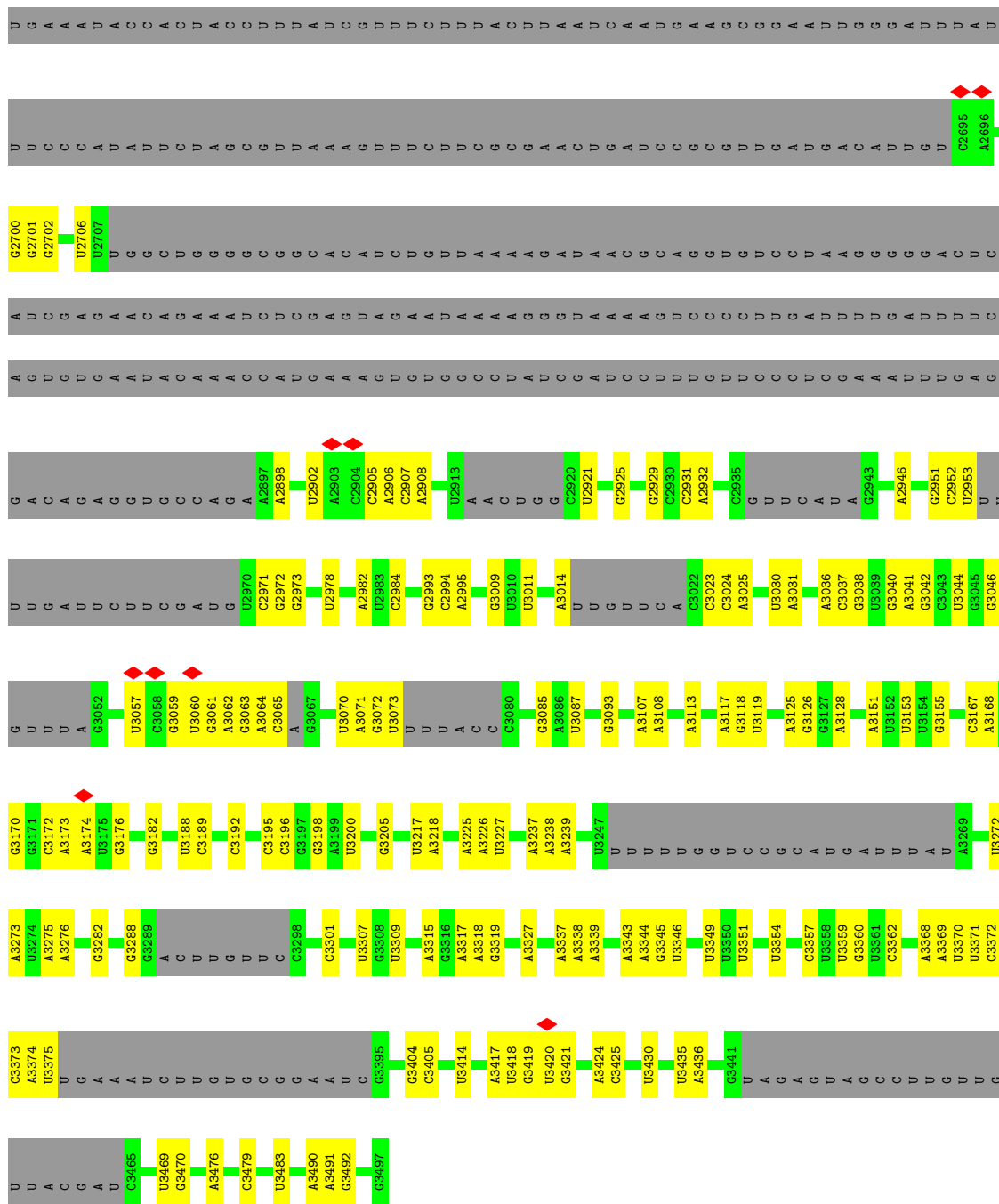
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
56	T	18	138	87	24	27	0	0

- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

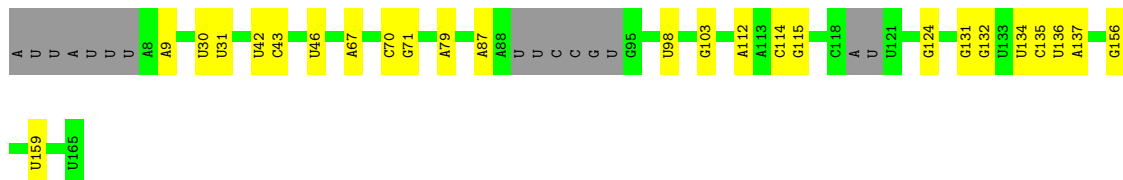
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
57	j	1	1	1	0







● Molecule 2: RNA (150-MER)



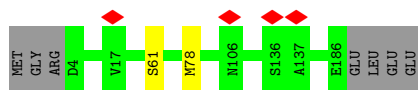
● Molecule 3: RNA (79-MER)



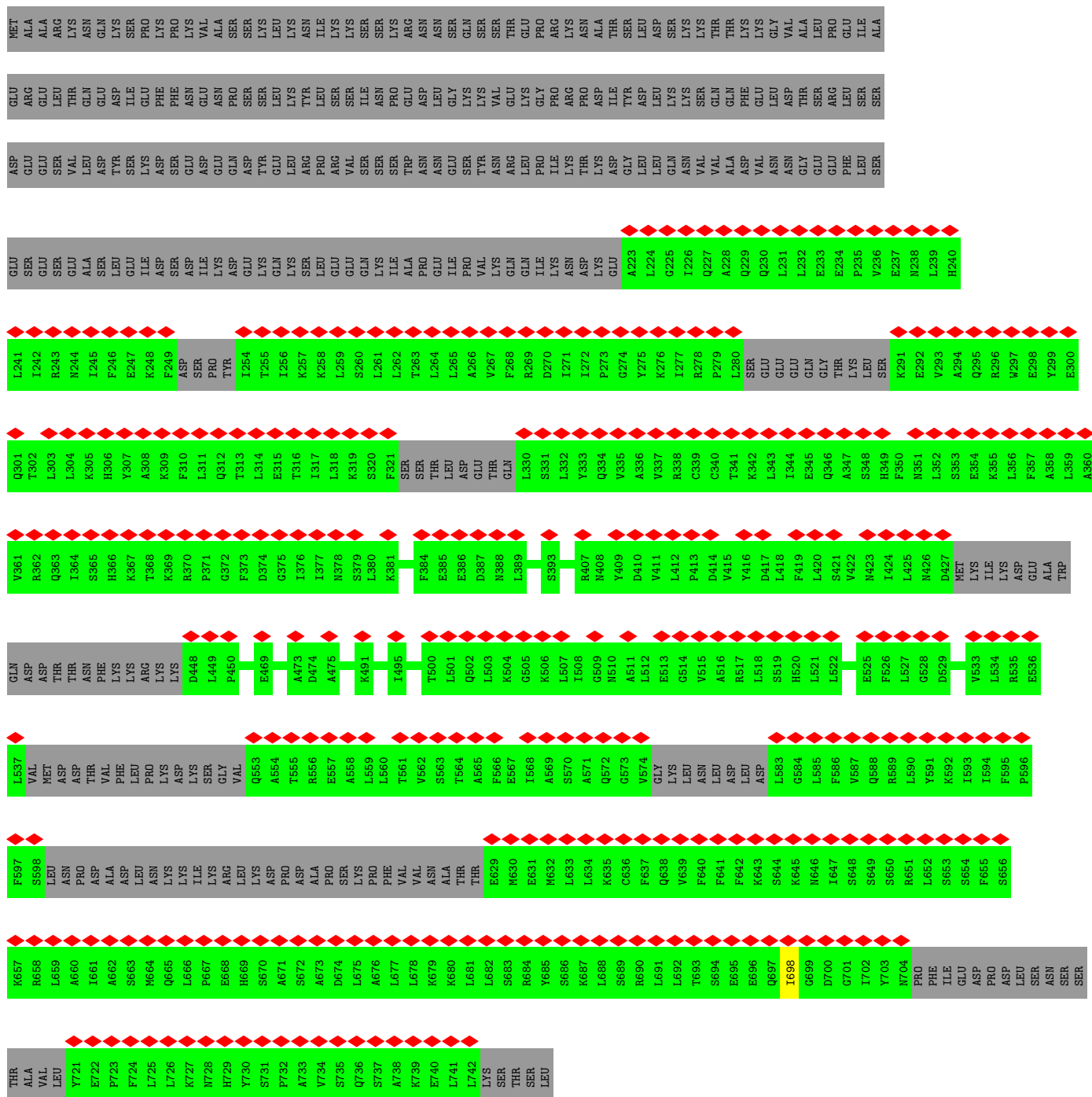
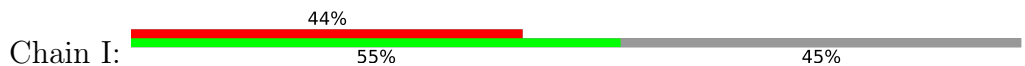






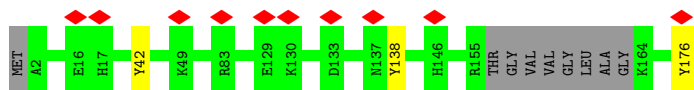
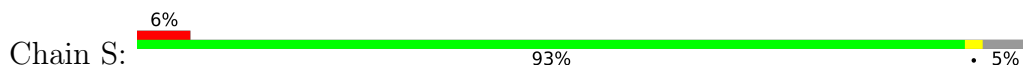


● Molecule 14: Nucleolar complex-associated protein 3

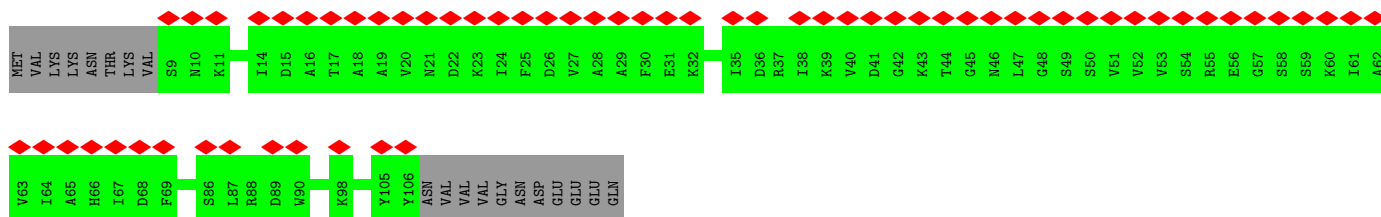
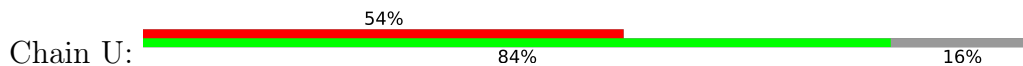




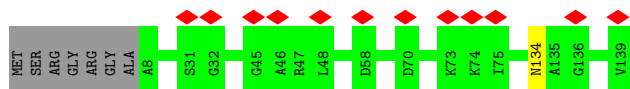
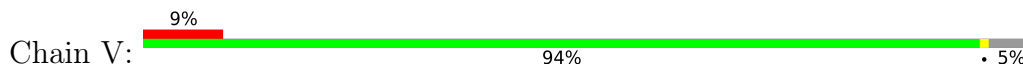




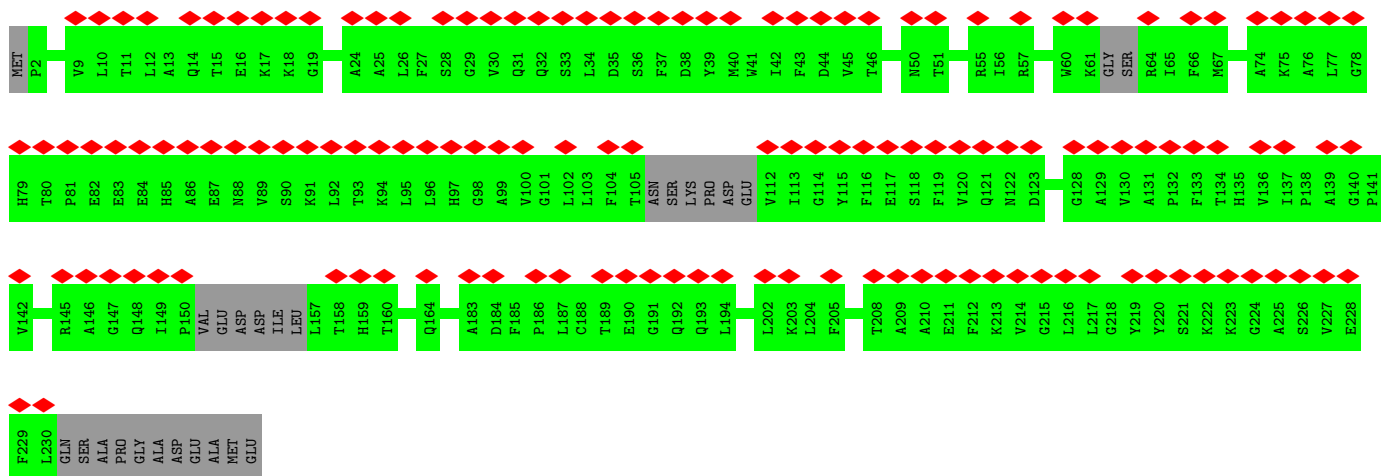
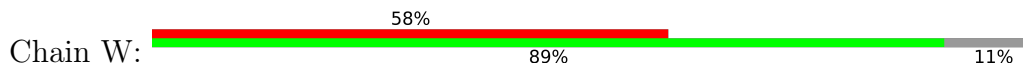
• Molecule 25: 60S ribosomal protein L22



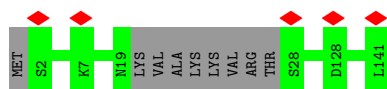
• Molecule 26: 60S ribosomal protein L23-A



• Molecule 27: Ribosome assembly factor mrt4



• Molecule 28: 60S ribosomal protein L25-A



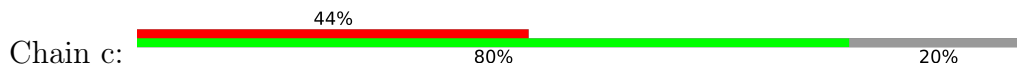




ARG  
ALA  
THR  
ARG  
ALA  
ALA  
ASN  
GLU  
MET  
ASP  
GLY  
SER  
GLY  
VAL  
ASP  
LEU  
LEU  
MET  
ASN  
GLY  
GLY  
LYS  
LYS  
ILE  
ALA  
PRO  
ARG  
GLN  
SER  
ASN  
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GLU  
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GLY  
ALA  
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SER  
TYR  
ASP  
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ALA  
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SER  
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HIS  
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LEU  
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SER  
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GLY  
THR  
GLN  
ARG  
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ARG

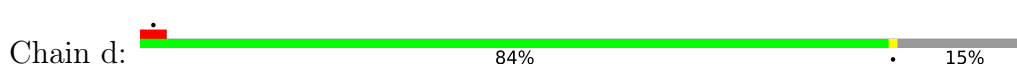
• Molecule 33: 60S ribosomal protein L30-2



MET SER ALA ALA PRO THR THR PRO PRO VAL VAL VAL VAL SER LYS LYS GLY LYS LYS SER SER GLY D22 T23 T24 M25 S26 K27 L28 A29 L30 T31 M32 K33 S34 G35 K36 Y37 G51 K52 A53 A60 M61 P64 A74 S77 R78 S85 G86 M87 N88 I89 D90 L91 G92

T93 A94 C95 G96 K97 L98 F99 R100 A105 V106 I107 D108 A109 G110 D111 S112 D113 I114 L115 A116 A117

• Molecule 34: 60S ribosomal protein L31



MET ALA THR LYS SER ALA ILE Q11 D86 GLU ASP LYS L92 D100 V101 A102 V111 GLU GLU

• Molecule 35: 60S ribosomal protein L32-A



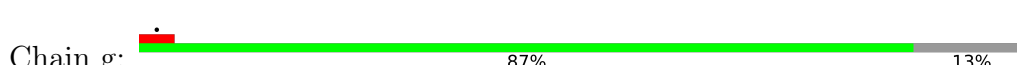
MET ALA THR LYS SER ALA ILE Q11 D86 GLU ASP LYS L92 D100 V101 A102 V111 GLU GLU

• Molecule 36: 60S ribosomal protein L33-B



MET PRO A3 I108

• Molecule 37: 60S ribosomal protein L34-A

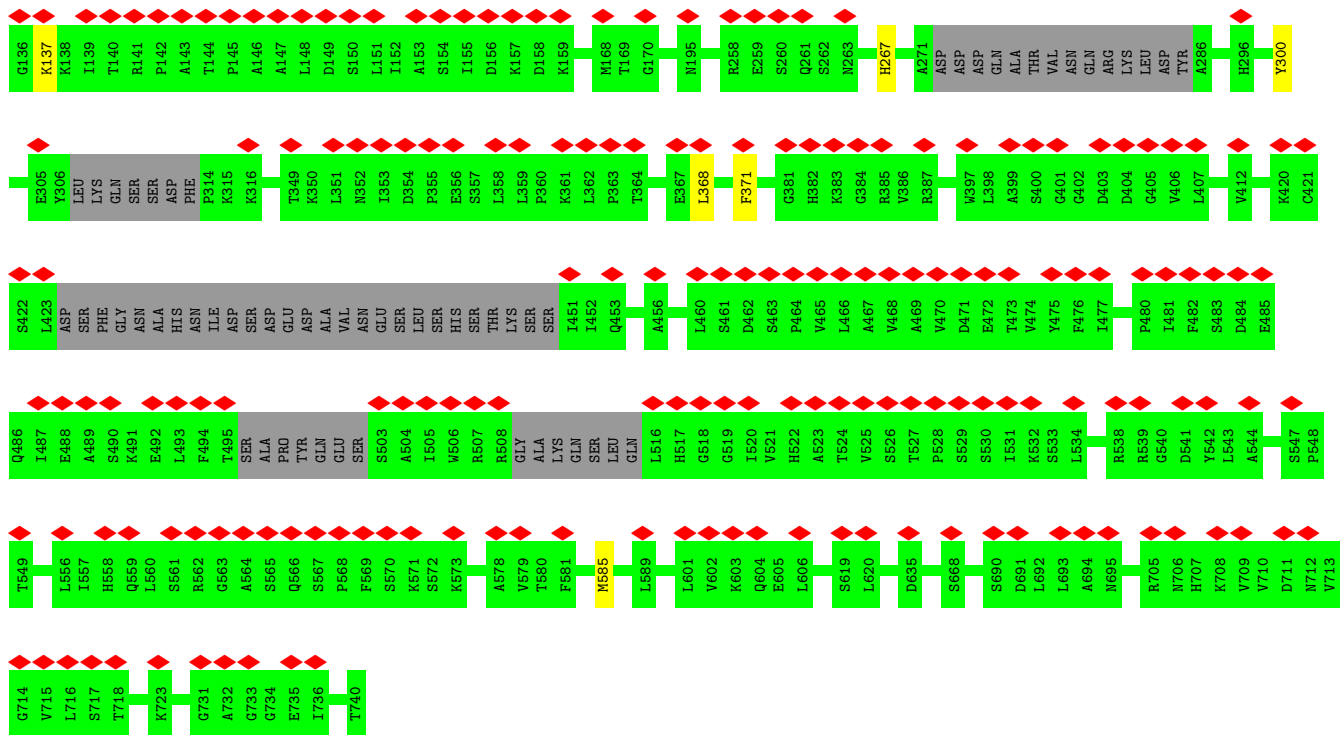


MET ALA GLN ARG THR TYR ARG ARG ARG L11 K104 L105 K106 Q107 LEU SER SER GLN LYS

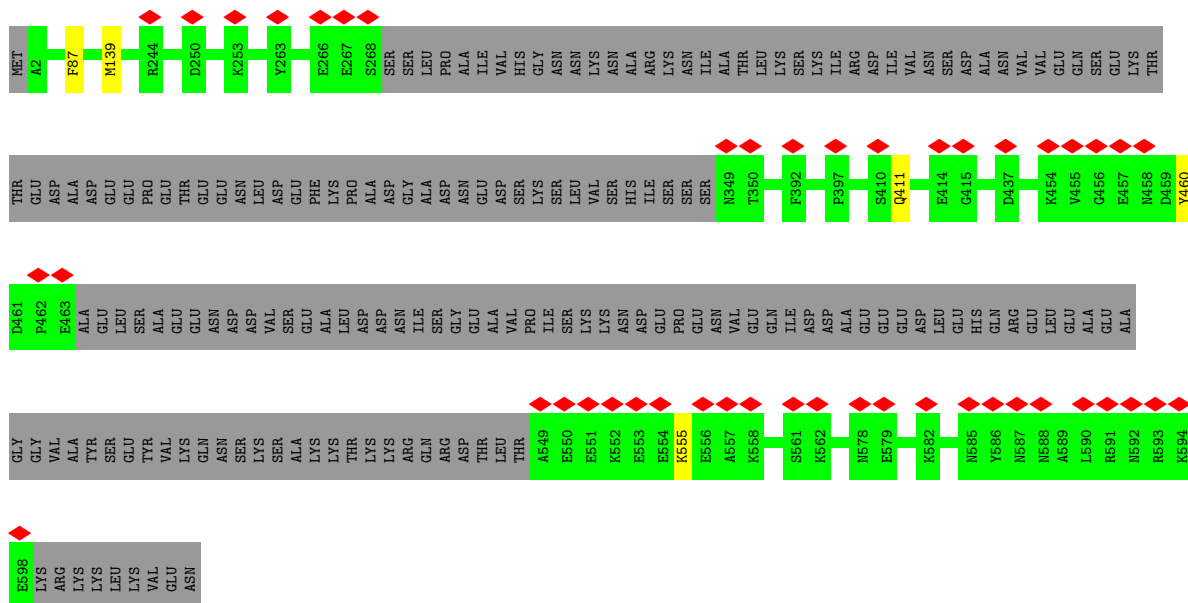
• Molecule 38: 60S ribosomal protein L35



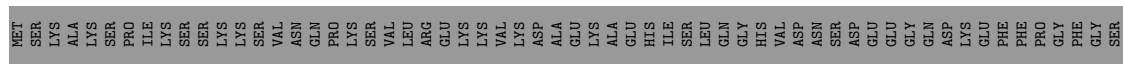


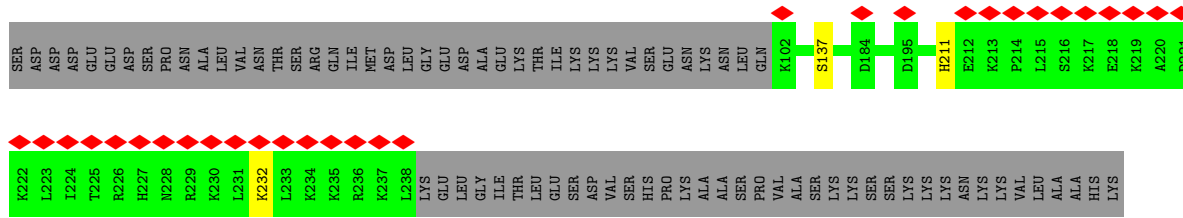


• Molecule 44: Pescadillo homolog

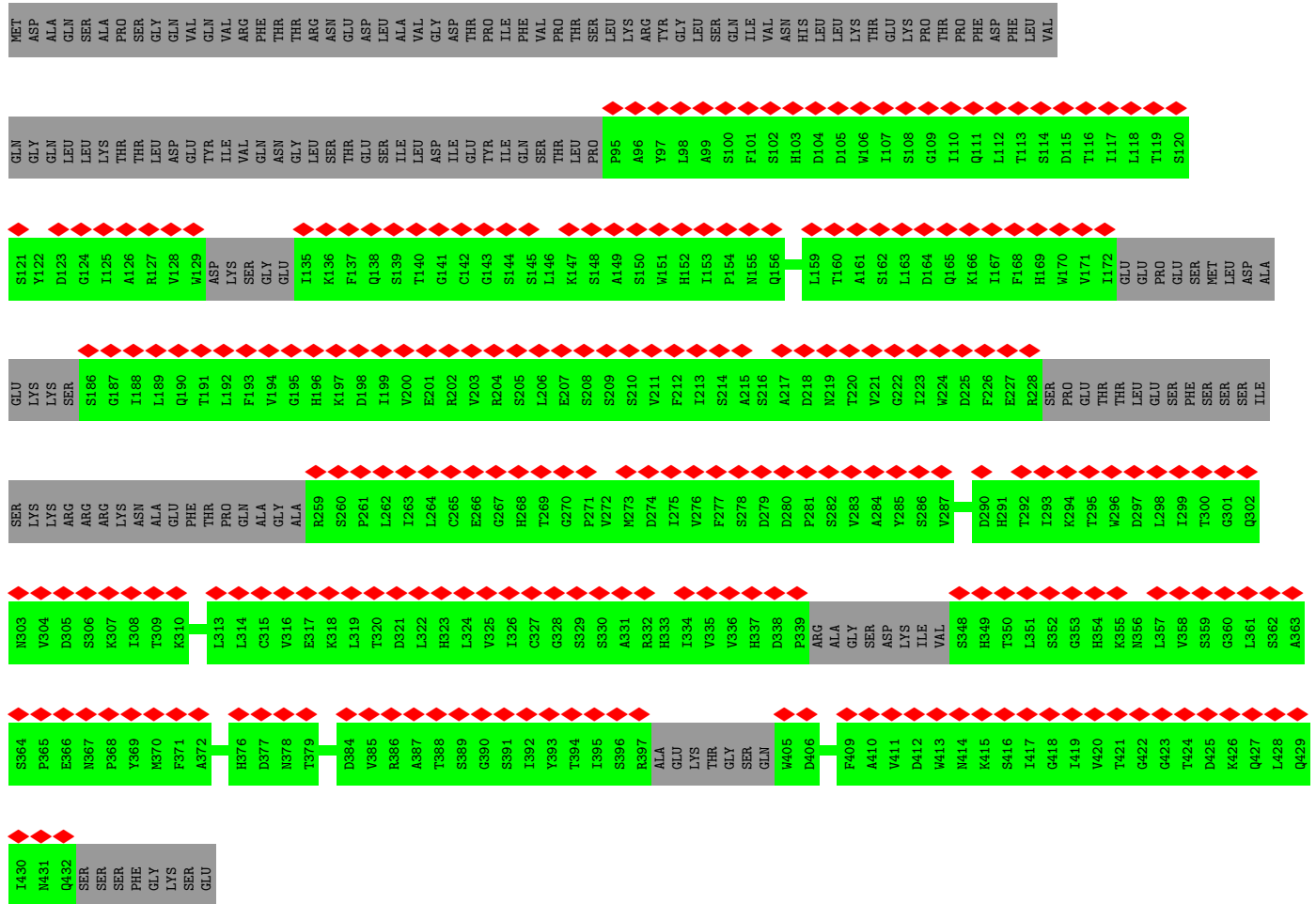


• Molecule 45: Uncharacterized RNA-binding protein C1827.05c

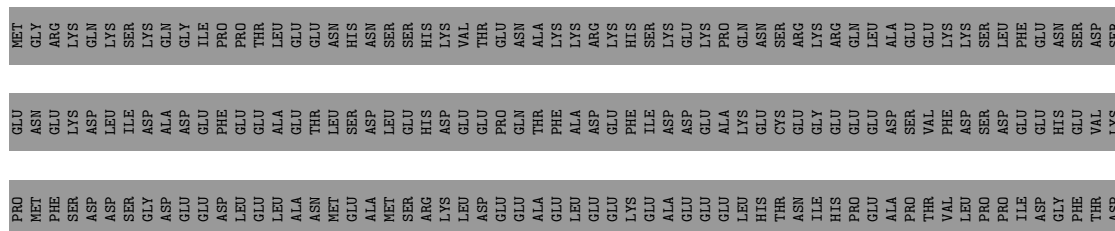
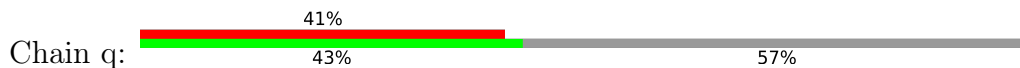




• Molecule 46: Ribosome biogenesis protein ytml



• Molecule 47: 25S rRNA (cytosine-C(5))-methyltransferase nop2













## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	109000	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	0.568	Depositor
Minimum map value	-0.215	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	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	0.19	0/51332	0.72	0/79942
2	2	0.23	0/3563	0.72	0/5543
3	6	0.18	0/1868	0.71	0/2898
4	7	0.23	0/544	0.33	0/754
5	8	0.25	0/191	0.49	0/254
6	A	0.25	0/1686	0.52	0/2272
7	B	0.24	0/2715	0.52	0/3647
8	C	0.25	0/2848	0.50	0/3842
9	D	0.25	0/3381	0.46	0/4559
10	E	0.26	0/1235	0.53	0/1663
11	F	0.25	0/1781	0.48	0/2389
12	G	0.26	0/1629	0.49	0/2192
13	H	0.26	0/1470	0.54	0/1982
14	I	0.23	0/2023	0.34	0/2810
15	J	0.23	0/573	0.34	0/800
16	K	0.26	0/1999	0.50	0/2702
17	L	0.26	0/960	0.57	0/1288
18	M	0.23	0/1024	0.49	0/1375
19	N	0.26	0/1420	0.56	0/1897
20	O	0.25	0/1588	0.49	0/2128
21	P	0.26	0/1188	0.51	0/1590
22	Q	0.24	0/1043	0.54	0/1401
23	R	0.24	0/732	0.47	0/992
24	S	0.25	0/1437	0.54	0/1929
25	U	0.23	0/483	0.42	0/671
26	V	0.26	0/1007	0.58	0/1357
27	W	0.23	0/1053	0.43	0/1457
28	X	0.26	0/1060	0.50	0/1422
29	Y	0.25	0/1008	0.56	0/1341
30	Z	0.24	0/661	0.40	0/917
31	a	0.25	0/775	0.58	1/1047 (0.1%)
32	b	0.23	0/1776	0.37	0/2471

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	c	0.24	0/461	0.39	0/639
34	d	0.25	0/815	0.58	0/1094
35	e	0.26	0/967	0.55	0/1289
36	f	0.25	0/859	0.52	0/1152
37	g	0.24	0/477	0.41	0/662
38	h	0.25	0/1008	0.50	0/1340
39	i	0.24	0/703	0.55	0/931
40	j	0.26	0/575	0.57	0/761
41	k	0.27	0/570	0.56	0/762
42	l	0.24	0/859	0.43	0/1195
43	m	0.24	0/4644	0.50	0/6313
44	n	0.25	0/3598	0.46	0/4845
45	o	0.26	0/1163	0.56	0/1552
46	p	0.24	0/1351	0.44	0/1871
47	q	0.24	0/1280	0.42	0/1778
48	r	0.30	0/1086	0.57	0/1457
49	s	0.23	0/192	0.60	0/248
50	t	0.24	0/1979	0.51	0/2645
51	u	0.29	0/729	0.56	0/981
52	v	0.25	0/1319	0.49	0/1769
53	w	0.25	0/1478	0.52	0/1967
54	y	0.24	0/1096	0.45	0/1522
55	z	0.25	0/297	0.49	0/388
56	T	0.25	0/142	0.46	0/196
All	All	0.22	0/123701	0.62	1/178889 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	67	PRO	N-CA-CB	5.88	110.36	103.30

There are no chirality outliers.

There are no planarity outliers.

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

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	7	102/707 (14%)	101 (99%)	1 (1%)	0	100	100
5	8	20/51 (39%)	20 (100%)	0	0	100	100
6	A	200/295 (68%)	194 (97%)	6 (3%)	0	100	100
7	B	331/388 (85%)	318 (96%)	13 (4%)	0	100	100
8	C	357/363 (98%)	342 (96%)	15 (4%)	0	100	100
9	D	412/578 (71%)	401 (97%)	11 (3%)	0	100	100
10	E	152/195 (78%)	142 (93%)	10 (7%)	0	100	100
11	F	212/250 (85%)	205 (97%)	7 (3%)	0	100	100
12	G	202/259 (78%)	196 (97%)	4 (2%)	2 (1%)	15	54
13	H	181/190 (95%)	173 (96%)	8 (4%)	0	100	100
14	I	391/747 (52%)	382 (98%)	8 (2%)	1 (0%)	41	74
15	J	113/333 (34%)	112 (99%)	1 (1%)	0	100	100
16	K	246/373 (66%)	232 (94%)	13 (5%)	1 (0%)	34	69
17	L	114/208 (55%)	112 (98%)	2 (2%)	0	100	100
18	M	123/134 (92%)	117 (95%)	6 (5%)	0	100	100
19	N	159/201 (79%)	158 (99%)	1 (1%)	0	100	100
20	O	194/197 (98%)	188 (97%)	6 (3%)	0	100	100
21	P	143/187 (76%)	139 (97%)	4 (3%)	0	100	100
22	Q	131/187 (70%)	127 (97%)	4 (3%)	0	100	100
23	R	108/193 (56%)	107 (99%)	1 (1%)	0	100	100
24	S	163/176 (93%)	154 (94%)	9 (6%)	0	100	100
25	U	96/117 (82%)	93 (97%)	3 (3%)	0	100	100
26	V	130/139 (94%)	126 (97%)	4 (3%)	0	100	100
27	W	207/241 (86%)	196 (95%)	11 (5%)	0	100	100
28	X	128/141 (91%)	124 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	Y	123/126 (98%)	117 (95%)	6 (5%)	0	100	100
30	Z	132/136 (97%)	130 (98%)	2 (2%)	0	100	100
31	a	93/148 (63%)	92 (99%)	1 (1%)	0	100	100
32	b	351/642 (55%)	346 (99%)	5 (1%)	0	100	100
33	c	92/117 (79%)	92 (100%)	0	0	100	100
34	d	92/113 (81%)	91 (99%)	1 (1%)	0	100	100
35	e	117/127 (92%)	114 (97%)	3 (3%)	0	100	100
36	f	104/108 (96%)	99 (95%)	5 (5%)	0	100	100
37	g	95/112 (85%)	92 (97%)	3 (3%)	0	100	100
38	h	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
39	i	83/99 (84%)	83 (100%)	0	0	100	100
40	j	69/91 (76%)	68 (99%)	1 (1%)	0	100	100
41	k	68/74 (92%)	66 (97%)	2 (3%)	0	100	100
42	l	172/180 (96%)	170 (99%)	2 (1%)	0	100	100
43	m	558/740 (75%)	529 (95%)	28 (5%)	1 (0%)	47	79
44	n	426/607 (70%)	415 (97%)	11 (3%)	0	100	100
45	o	135/276 (49%)	129 (96%)	6 (4%)	0	100	100
46	p	263/440 (60%)	257 (98%)	6 (2%)	0	100	100
47	q	256/608 (42%)	252 (98%)	4 (2%)	0	100	100
48	r	157/260 (60%)	157 (100%)	0	0	100	100
49	s	21/470 (4%)	18 (86%)	3 (14%)	0	100	100
50	t	233/249 (94%)	221 (95%)	12 (5%)	0	100	100
51	u	97/192 (50%)	94 (97%)	3 (3%)	0	100	100
52	v	157/209 (75%)	151 (96%)	5 (3%)	1 (1%)	25	64
53	w	174/802 (22%)	170 (98%)	4 (2%)	0	100	100
54	y	221/244 (91%)	218 (99%)	3 (1%)	0	100	100
55	z	33/117 (28%)	31 (94%)	1 (3%)	1 (3%)	4	28
56	T	16/160 (10%)	16 (100%)	0	0	100	100
All	All	9072/14419 (63%)	8795 (97%)	270 (3%)	7 (0%)	54	83

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
52	v	130	ILE
12	G	227	ASP
16	K	153	ILE
12	G	182	ASN
55	z	104	ARG

### 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	
5	8	19/47 (40%)	19 (100%)	0	100	100
6	A	184/266 (69%)	182 (99%)	2 (1%)	73	88
7	B	284/326 (87%)	279 (98%)	5 (2%)	59	82
8	C	296/297 (100%)	293 (99%)	3 (1%)	76	90
9	D	362/505 (72%)	359 (99%)	3 (1%)	81	93
10	E	128/155 (83%)	125 (98%)	3 (2%)	50	78
11	F	180/210 (86%)	177 (98%)	3 (2%)	60	83
12	G	167/212 (79%)	167 (100%)	0	100	100
13	H	164/170 (96%)	162 (99%)	2 (1%)	71	88
16	K	223/333 (67%)	219 (98%)	4 (2%)	59	82
17	L	97/167 (58%)	96 (99%)	1 (1%)	76	90
18	M	108/113 (96%)	107 (99%)	1 (1%)	78	91
19	N	145/176 (82%)	145 (100%)	0	100	100
20	O	161/162 (99%)	160 (99%)	1 (1%)	86	94
21	P	121/149 (81%)	118 (98%)	3 (2%)	47	77
22	Q	114/159 (72%)	114 (100%)	0	100	100
23	R	51/162 (32%)	50 (98%)	1 (2%)	55	80
24	S	149/154 (97%)	146 (98%)	3 (2%)	55	80
26	V	103/107 (96%)	102 (99%)	1 (1%)	76	90
28	X	114/122 (93%)	114 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	Y	110/111 (99%)	108 (98%)	2 (2%)	59	82
31	a	81/122 (66%)	80 (99%)	1 (1%)	71	88
34	d	88/102 (86%)	87 (99%)	1 (1%)	73	88
35	e	101/107 (94%)	100 (99%)	1 (1%)	76	90
36	f	89/91 (98%)	89 (100%)	0	100	100
38	h	106/107 (99%)	106 (100%)	0	100	100
39	i	74/84 (88%)	74 (100%)	0	100	100
40	j	58/71 (82%)	58 (100%)	0	100	100
41	k	63/66 (96%)	61 (97%)	2 (3%)	39	71
43	m	504/659 (76%)	497 (99%)	7 (1%)	67	86
44	n	378/532 (71%)	373 (99%)	5 (1%)	69	87
45	o	123/246 (50%)	120 (98%)	3 (2%)	49	77
48	r	63/224 (28%)	61 (97%)	2 (3%)	39	71
49	s	21/409 (5%)	21 (100%)	0	100	100
50	t	211/223 (95%)	208 (99%)	3 (1%)	67	86
51	u	55/168 (33%)	52 (94%)	3 (6%)	21	57
52	v	138/181 (76%)	135 (98%)	3 (2%)	52	79
53	w	158/697 (23%)	158 (100%)	0	100	100
55	z	31/107 (29%)	29 (94%)	2 (6%)	17	51
56	T	16/139 (12%)	15 (94%)	1 (6%)	18	52
All	All	5638/8438 (67%)	5566 (99%)	72 (1%)	70	87

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	o	232	LYS
56	T	140	PHE
48	r	60	GLN
51	u	42	MET
16	K	234	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
41	k	59	GLN
44	n	190	GLN
45	o	187	HIS
44	n	408	HIS
9	D	367	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2100/3497 (60%)	496 (23%)	21 (1%)
2	2	147/165 (89%)	24 (16%)	1 (0%)
3	6	75/300 (25%)	32 (42%)	0
All	All	2322/3962 (58%)	552 (23%)	22 (0%)

5 of 552 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	6	A
1	1	26	A
1	1	34	A
1	1	36	C
1	1	49	A

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2951	G
1	1	3041	A
1	1	3024	C
1	1	3070	U
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 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](#)

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	3315:A	O3'	3316:G	P	3.15

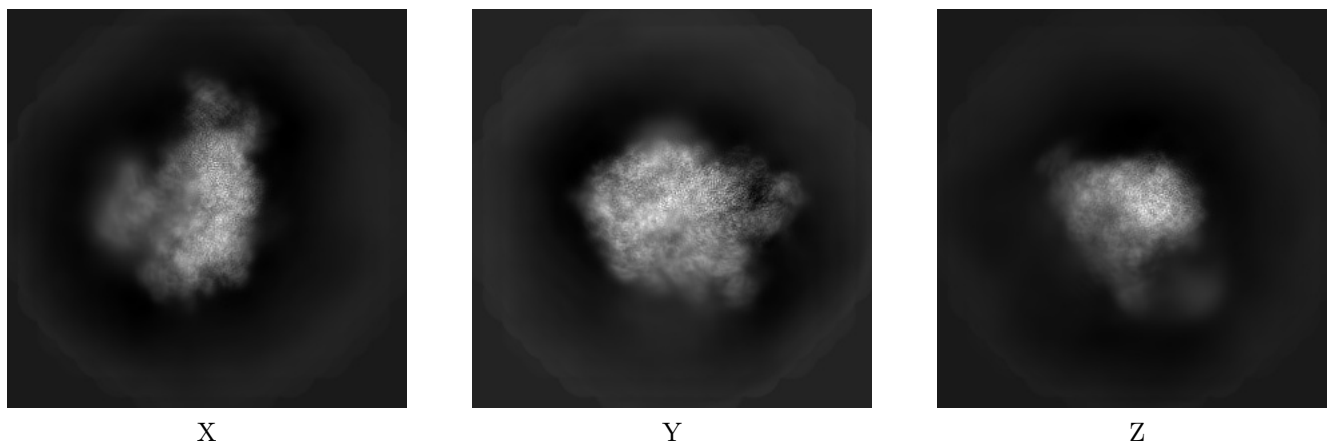
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24422. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

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

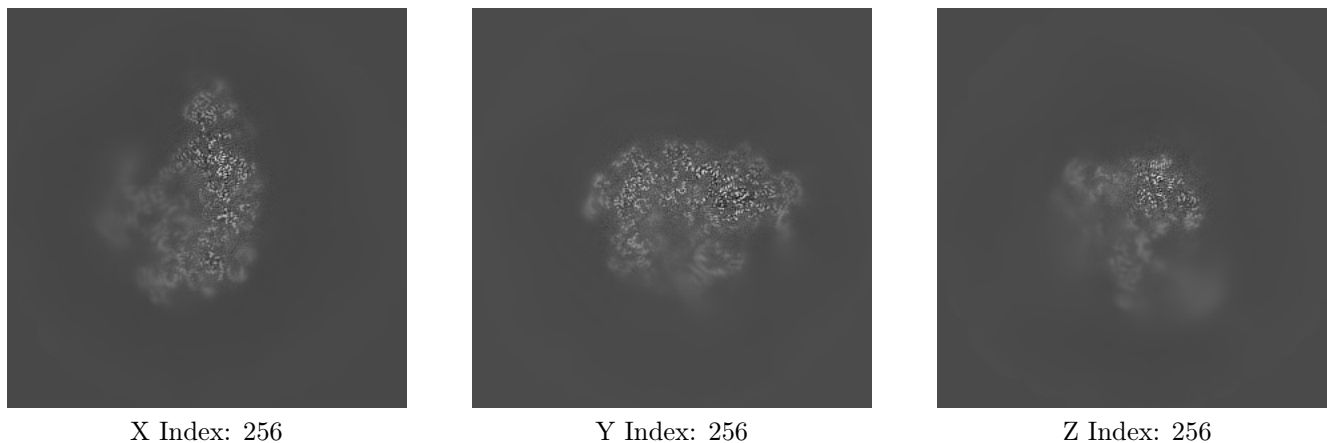
#### 6.1.1 Primary map



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

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

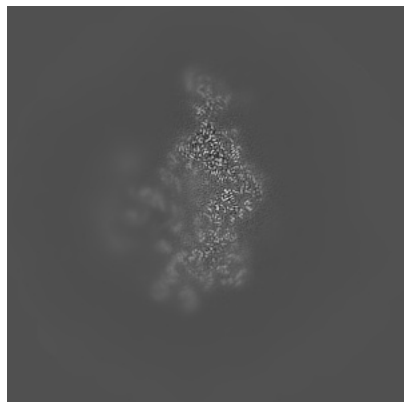
#### 6.2.1 Primary map



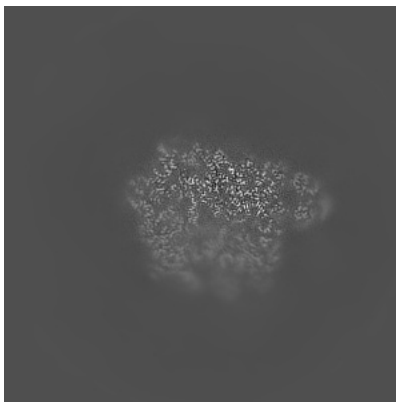
The images above show central slices of the map in three orthogonal directions.

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

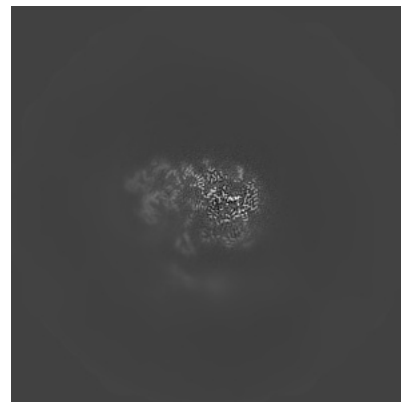
### 6.3.1 Primary map



X Index: 271



Y Index: 273



Z Index: 314

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

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

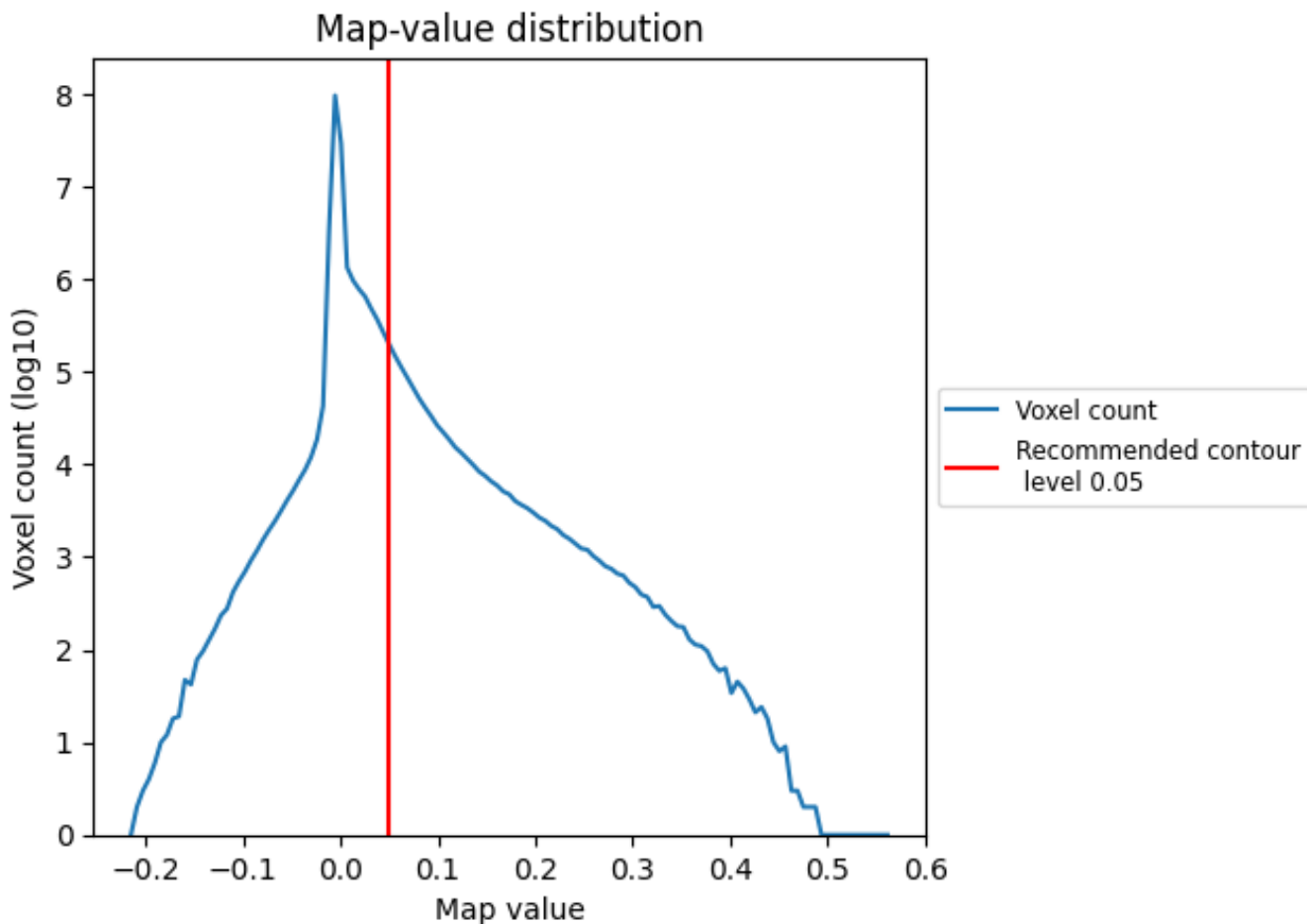
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

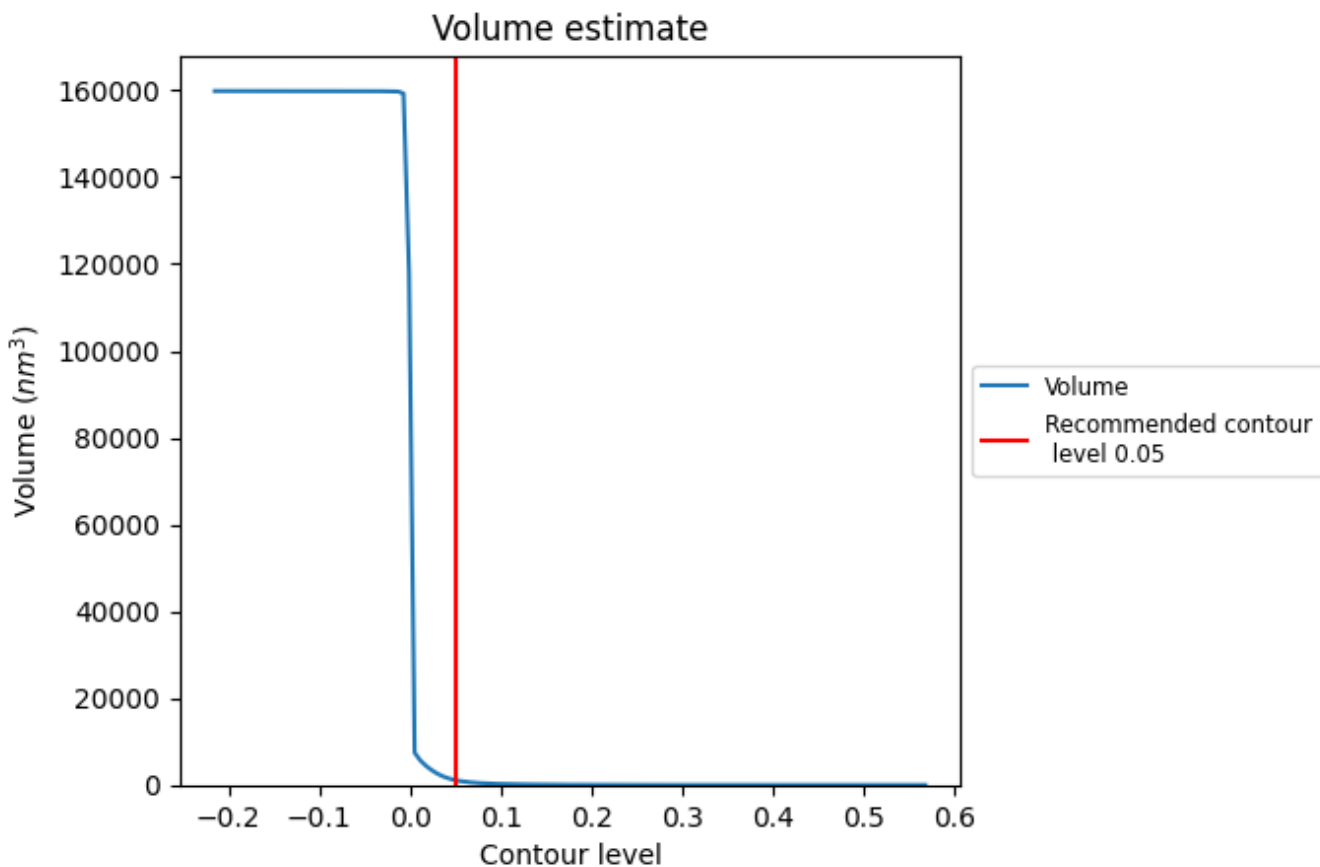
This section contains the results of statistical analysis of the map.

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



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

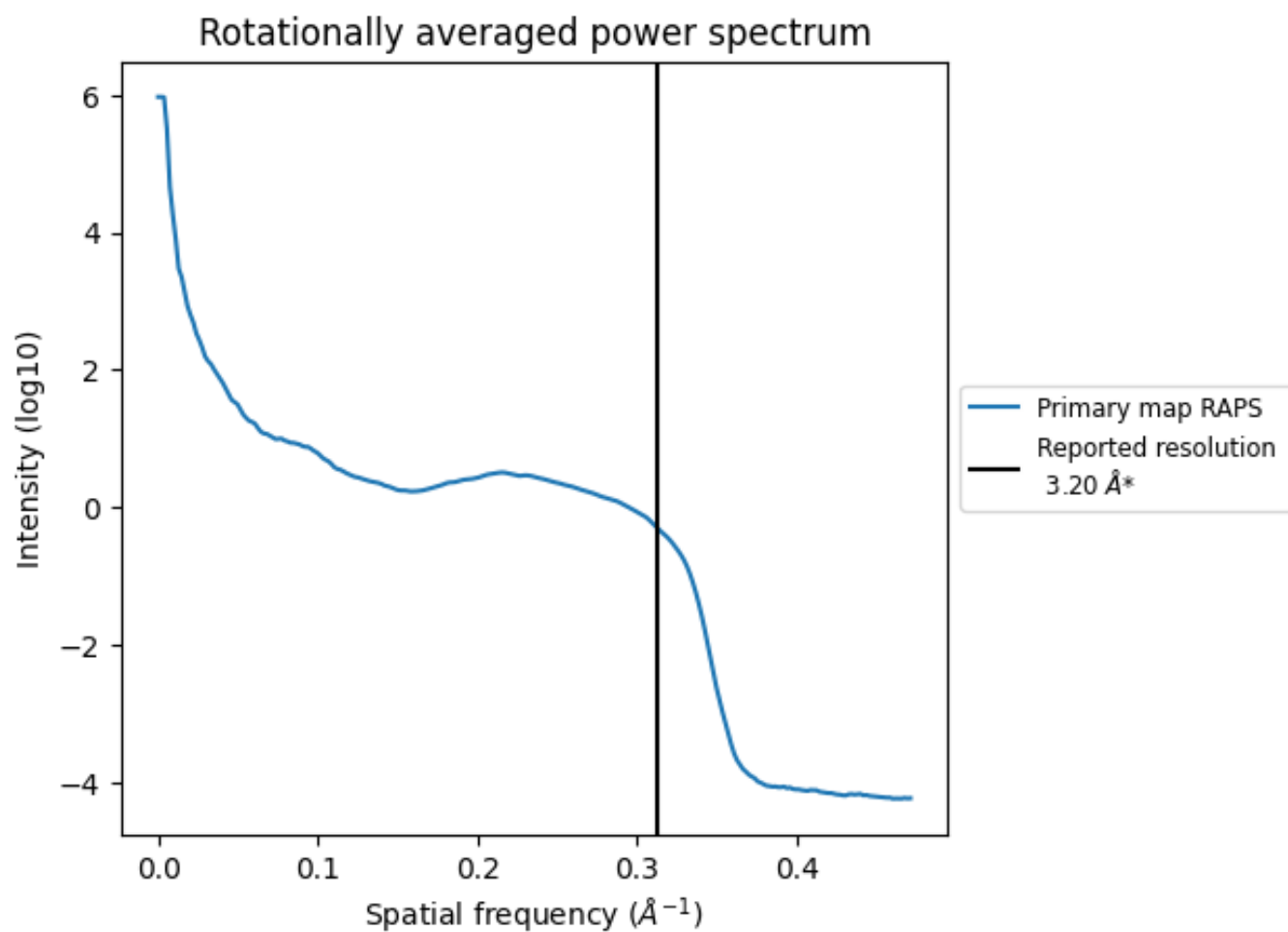
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1113  $\text{nm}^3$ ; this corresponds to an approximate mass of 1006 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  $0.312 \text{\AA}^{-1}$

## 8 Fourier-Shell correlation

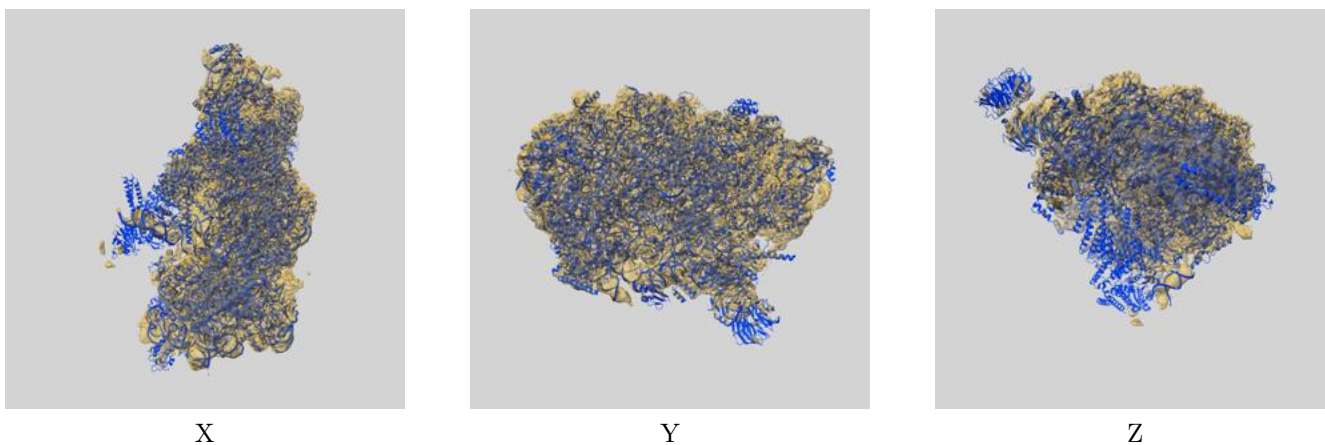
This section was not generated. No FSC curve or half-maps provided.



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

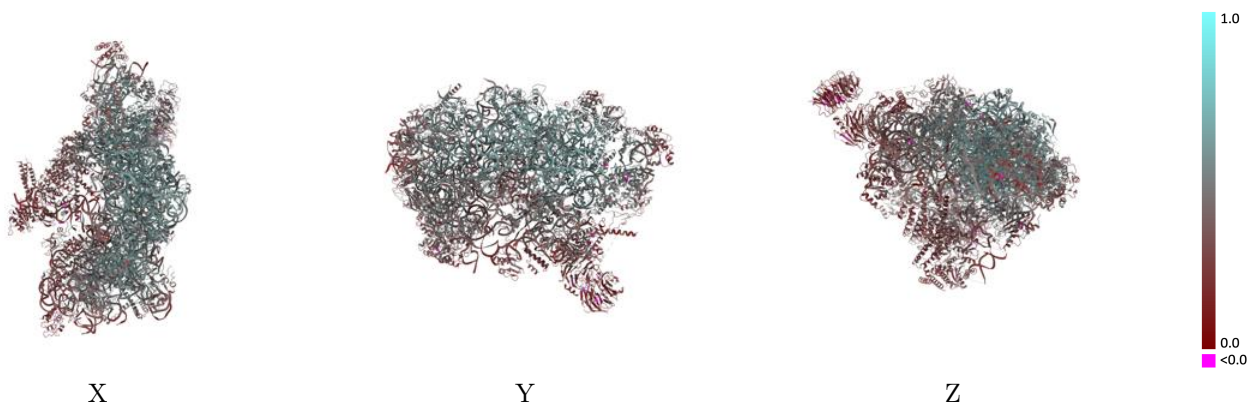
This section contains information regarding the fit between EMDB map EMD-24422 and PDB model 8ESR. Per-residue inclusion information can be found in section 3 on page 14.

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



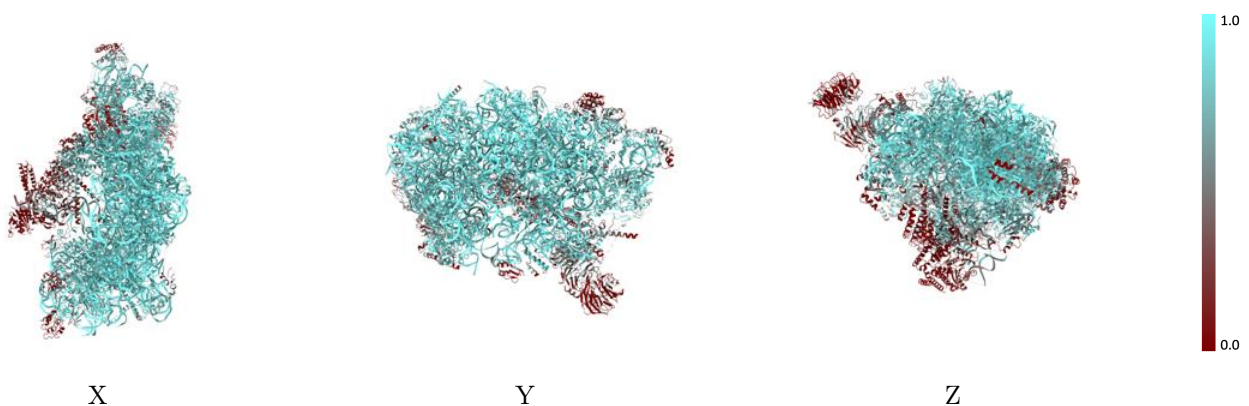
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



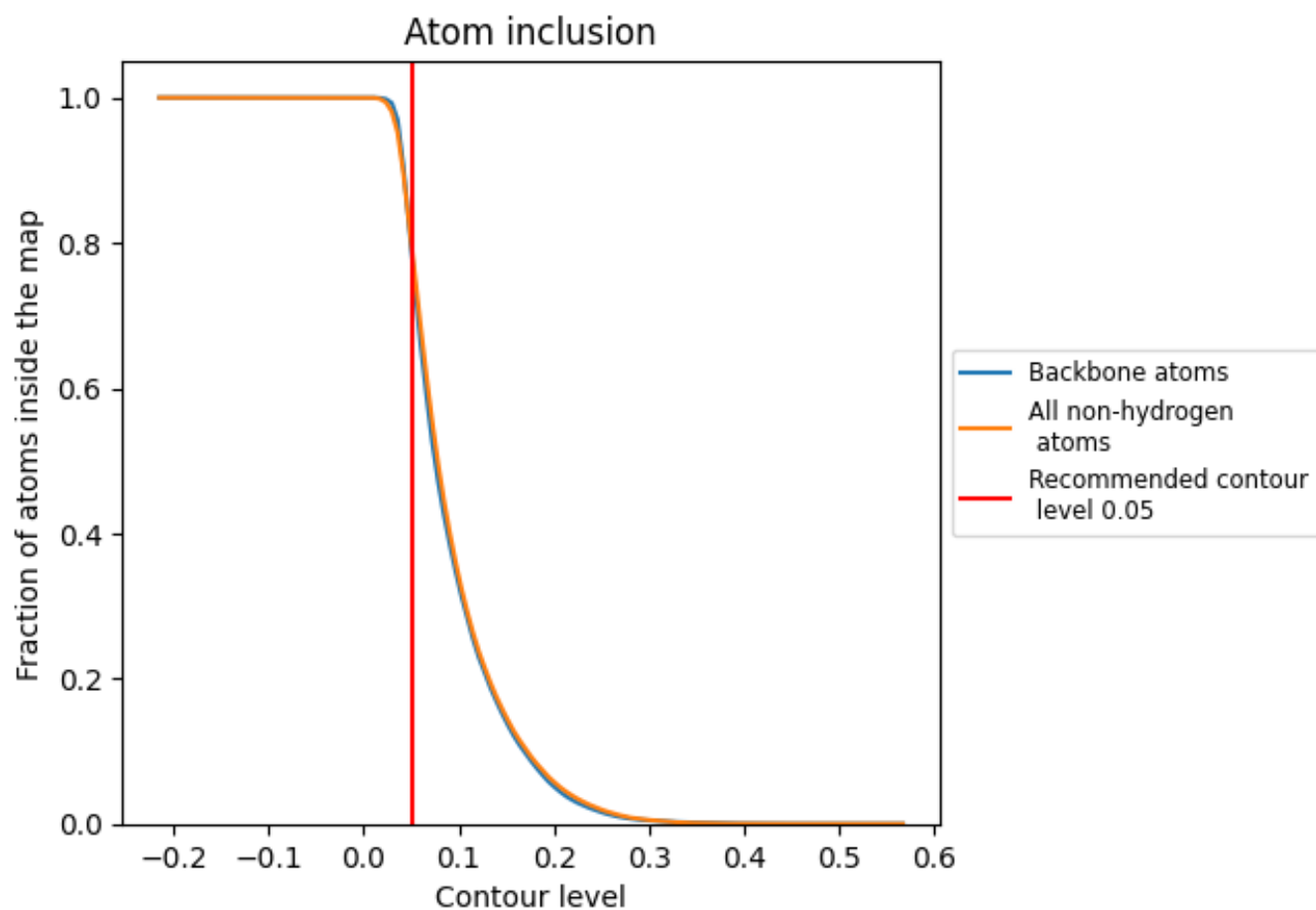
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 80% 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	 0.7998	 0.4400
1	 0.9349	 0.4440
2	 0.9790	 0.5630
6	 0.8865	 0.4240
7	 0.0000	 0.2620
8	 0.7333	 0.4100
A	 0.6941	 0.3800
B	 0.8776	 0.4640
C	 0.9424	 0.5670
D	 0.4979	 0.4460
E	 0.7718	 0.4590
F	 0.8942	 0.5070
G	 0.8964	 0.5620
H	 0.7999	 0.4020
I	 0.1924	 0.3030
J	 0.4617	 0.3280
K	 0.6686	 0.4160
L	 0.9744	 0.5950
M	 0.8690	 0.4500
N	 0.9902	 0.6090
O	 0.9050	 0.4940
P	 0.8412	 0.5050
Q	 0.8852	 0.5220
R	 0.7291	 0.3660
S	 0.8118	 0.4390
T	 0.4493	 0.3560
U	 0.3223	 0.2920
V	 0.6939	 0.3970
W	 0.3377	 0.2720
X	 0.8907	 0.5290
Y	 0.9252	 0.5570
Z	 0.7462	 0.3650
a	 0.8011	 0.5060
b	 0.5360	 0.3310
c	 0.4329	 0.2760



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Chain	Atom inclusion	Q-score
d	 0.8044	 0.4260
e	 0.9347	 0.5520
f	 0.9620	 0.5560
g	 0.8870	 0.4270
h	 0.9151	 0.5640
i	 0.9158	 0.5410
j	 0.9852	 0.5950
k	 0.6582	 0.3760
l	 0.2779	 0.2860
m	 0.5501	 0.3440
n	 0.7587	 0.4360
o	 0.6793	 0.4390
p	 0.0877	 0.2130
q	 0.0468	 0.2600
r	 0.6304	 0.3590
s	 0.7268	 0.3880
t	 0.8068	 0.4680
u	 0.6997	 0.3320
v	 0.8524	 0.5330
w	 0.5592	 0.3930
y	 0.7912	 0.3600
z	 0.3930	 0.2780