



wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 04:06 PM EST

PDB ID : 8EV3
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.

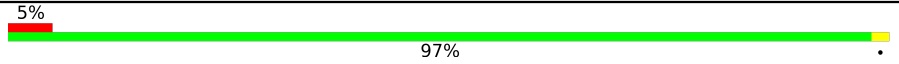
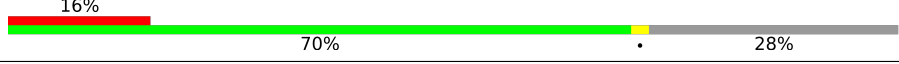
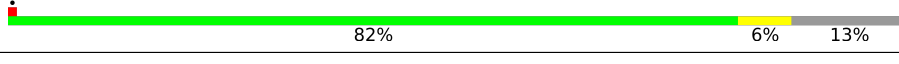
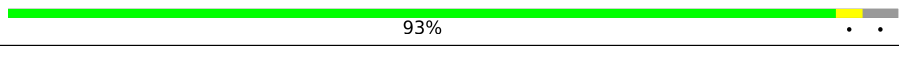

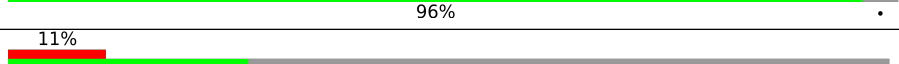
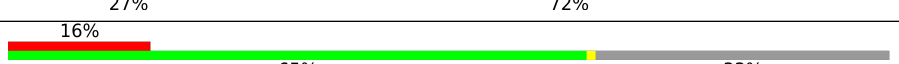
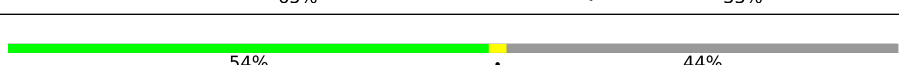
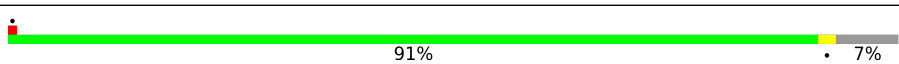

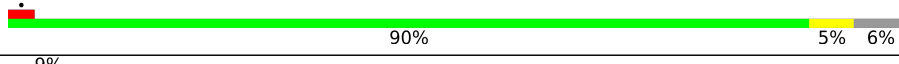
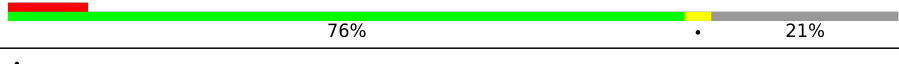
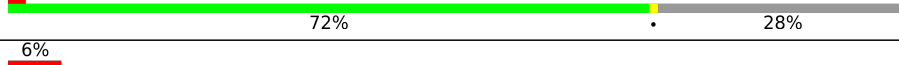

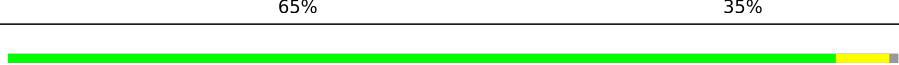
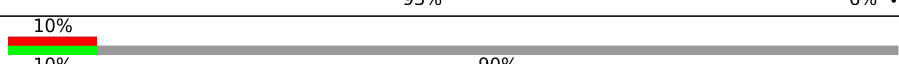
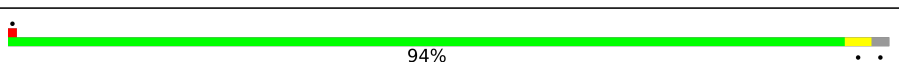
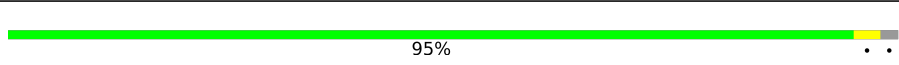
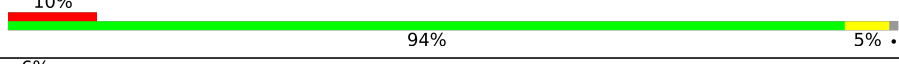
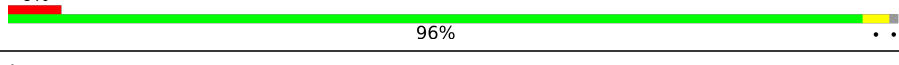

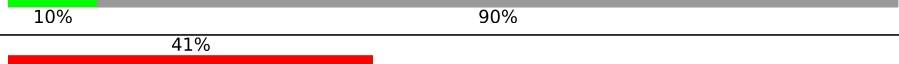



The types of validation reports are described at

<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.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

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Mol	Chain	Length	Quality of chain
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	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	
33	n	607	

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Mol	Chain	Length	Quality of chain
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	Total	C	N	O	S	0	0
			1999	1267	363	361	8		

- 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	Total	C	N	O	S	0	0
			2641	1676	488	468	9		

- 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	Total	C	N	O	S	0	0
			2810	1774	539	494	3		

- Molecule 10 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	D	416	Total	C	N	O	S	0	0
			3186	2057	544	574	11		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	F	240	Total	C	N	O	S	0	0
			1944	1250	356	335	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	G	164	Total	C	N	O	S	1	0
			1273	816	223	232	2		

- 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

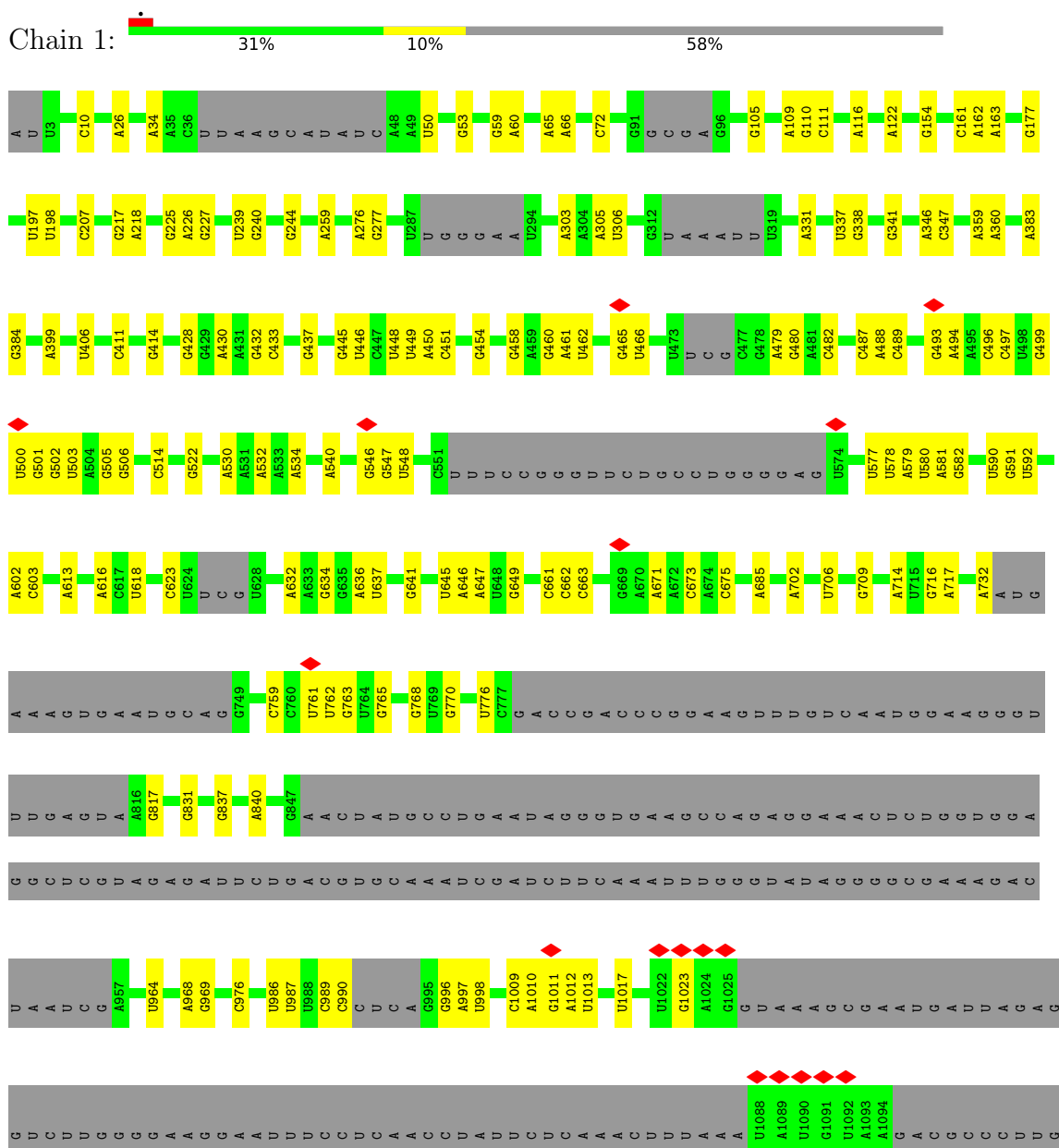
- Molecule 42 is ZINC ION (three-letter code: ZN) (formula: Zn).

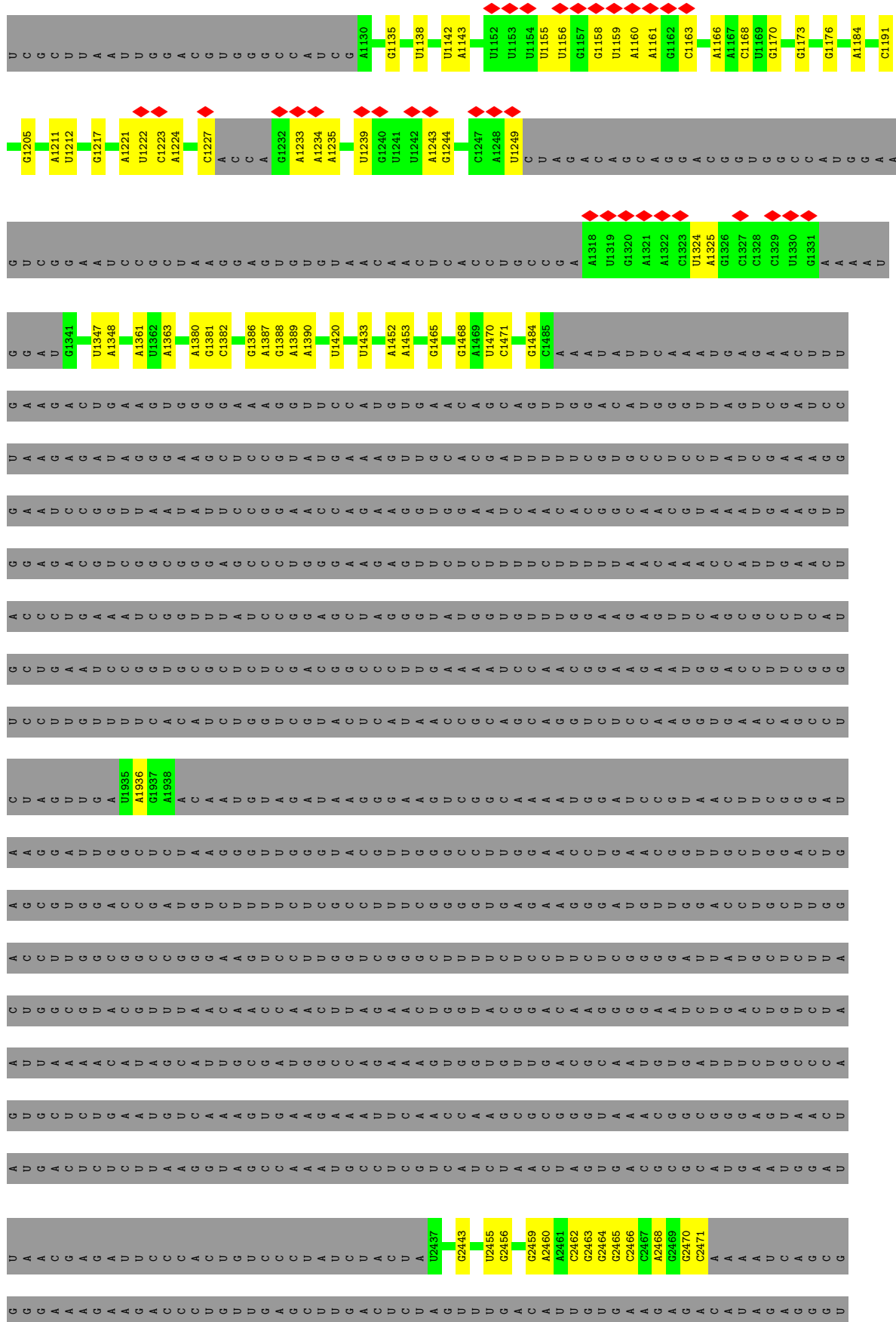
Mol	Chain	Residues	Atoms		AltConf
42	j	1	Total 1	Zn 1	0

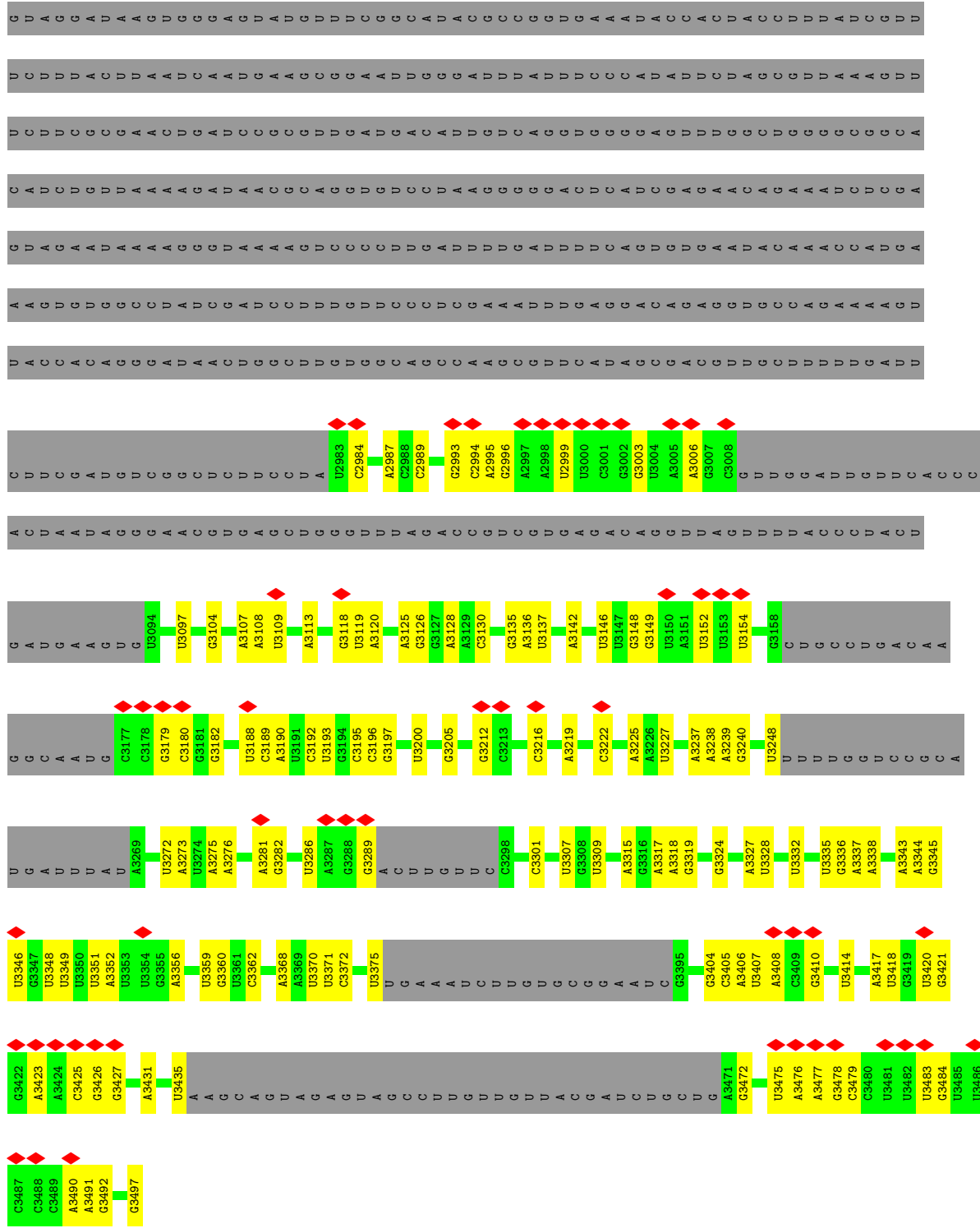
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

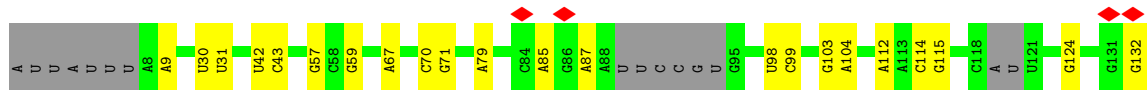
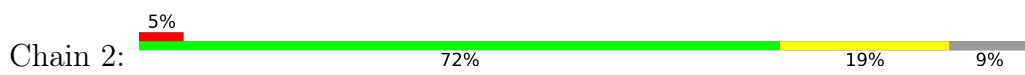
- Molecule 1: RNA (1452-MER)

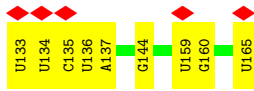




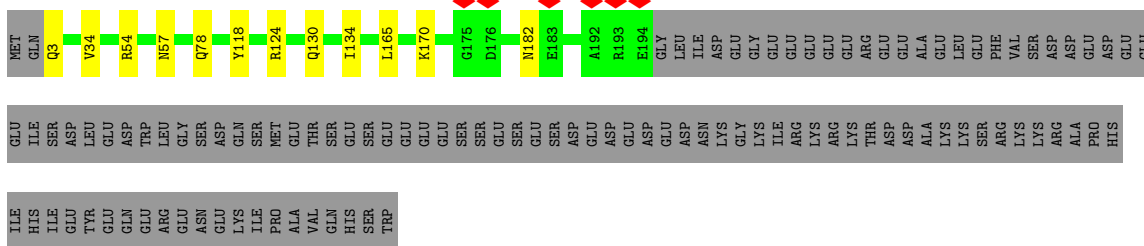


● Molecule 2: RNA (150-MER)





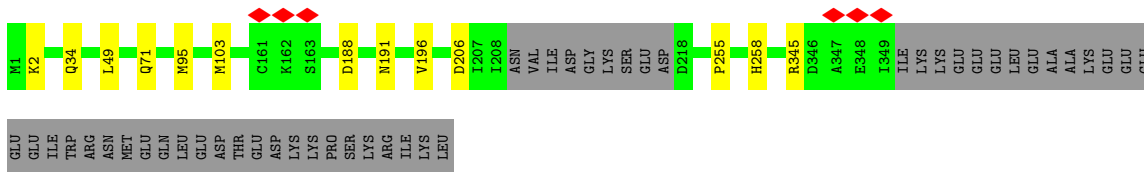
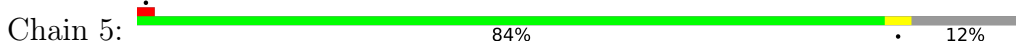
• Molecule 3: Protein mak16



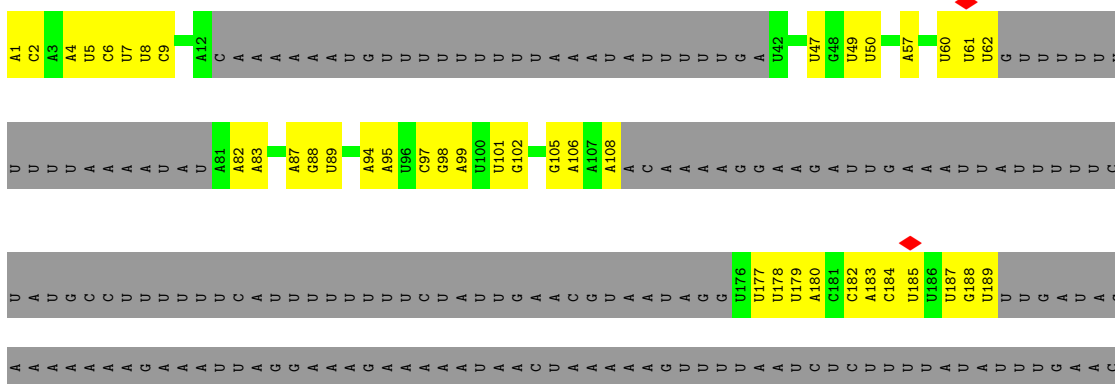
• Molecule 4: Ribosomal RNA-processing protein 1 homolog



• Molecule 5: Ribosome biogenesis protein nsa1

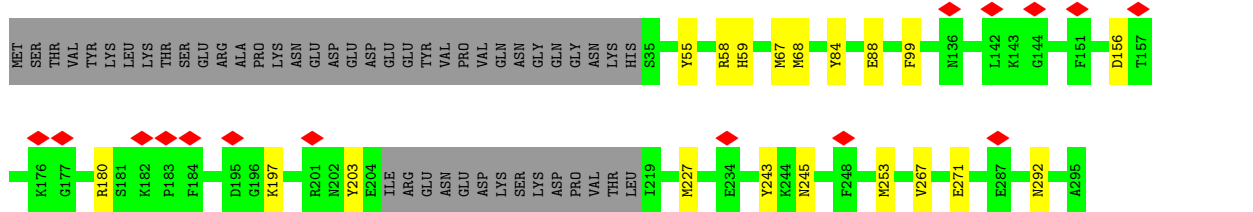
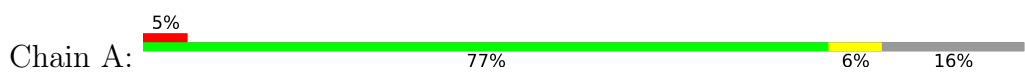


• Molecule 6: RNA (75-MER)

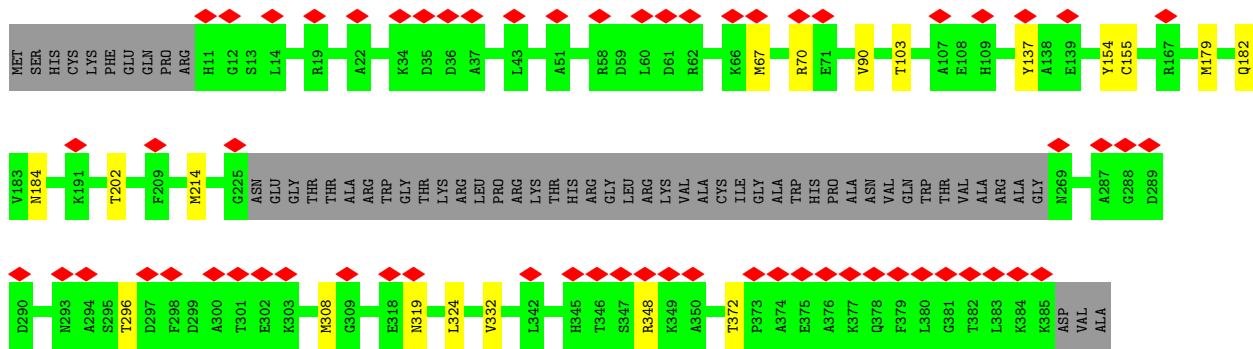
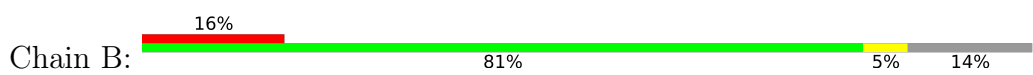


C U U V A A C C G A A A A A A G G U

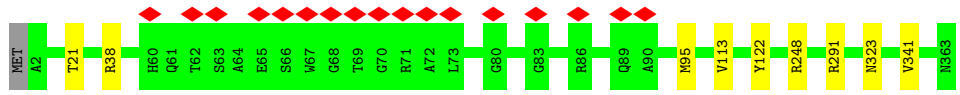
• Molecule 7: Ribosome biogenesis protein brx1



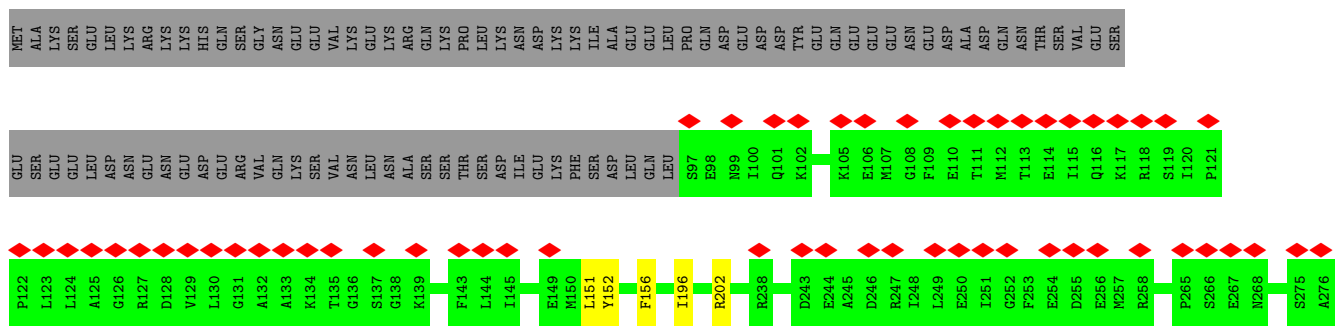
• Molecule 8: 60S ribosomal protein L3-A

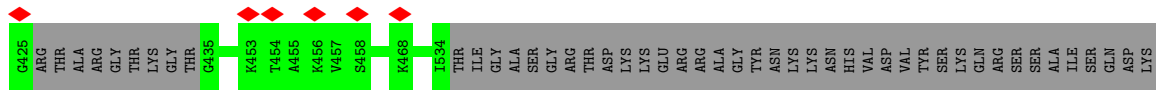
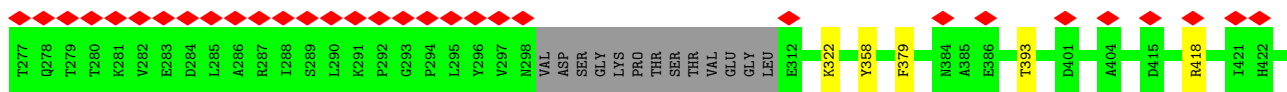


• Molecule 9: 60S ribosomal protein L4-B



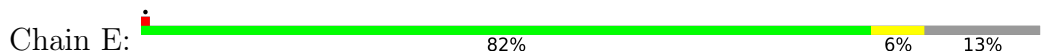
• Molecule 10: RNA helicase



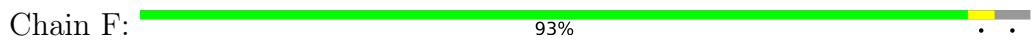


GLU
ARG
GLY
TRP
SER
ARG

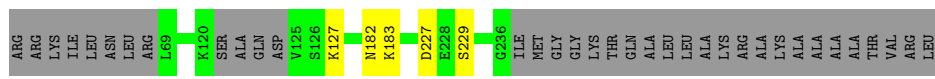
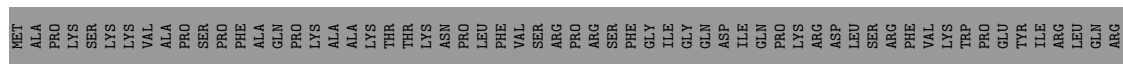
• Molecule 11: 60S ribosomal protein L6



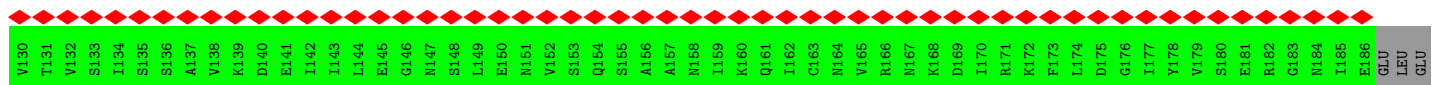
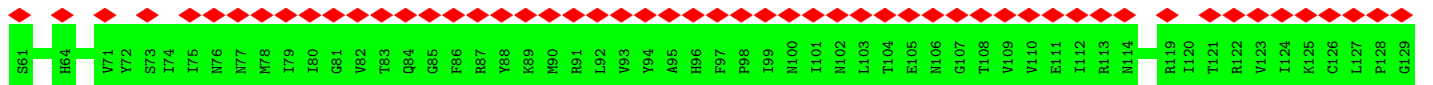
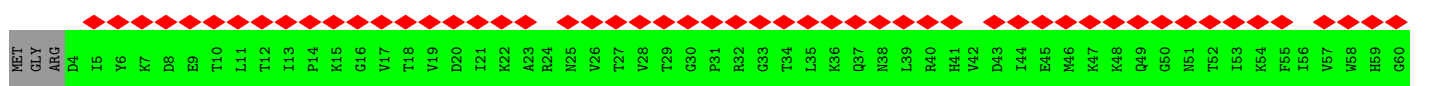
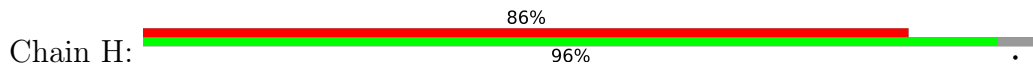
• Molecule 12: 60S ribosomal protein L7-B



• Molecule 13: 60S ribosomal protein L8



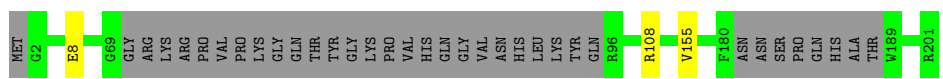
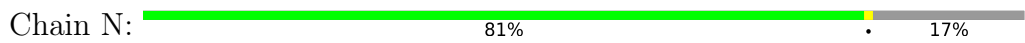
• Molecule 14: 60S ribosomal protein L9-A



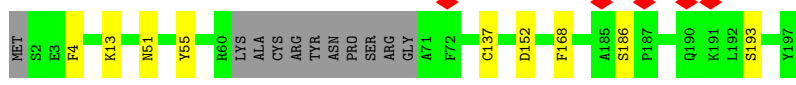
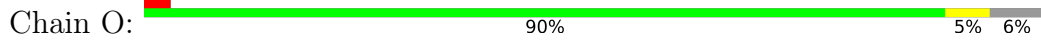
GLU



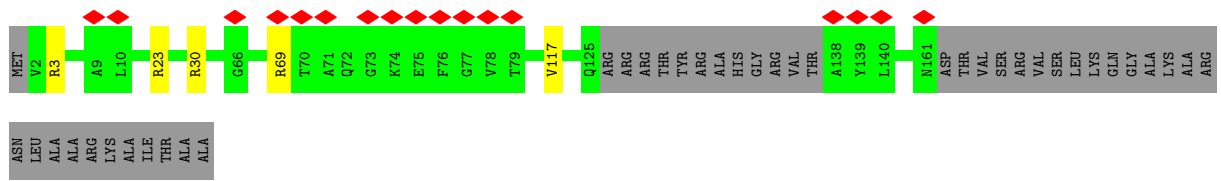
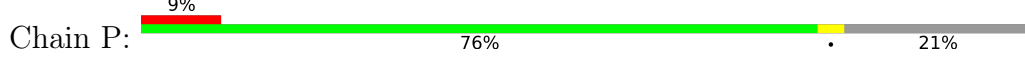
• Molecule 19: 60S ribosomal protein L15-A



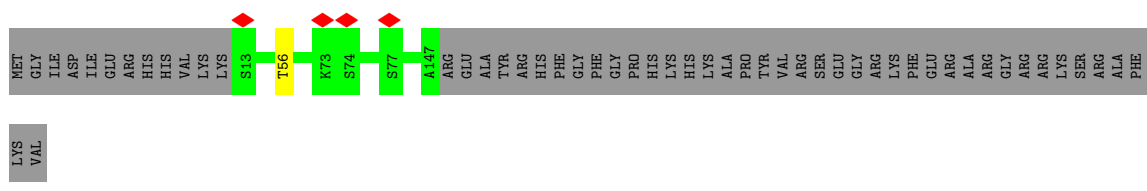
• Molecule 20: 60S ribosomal protein L16-B



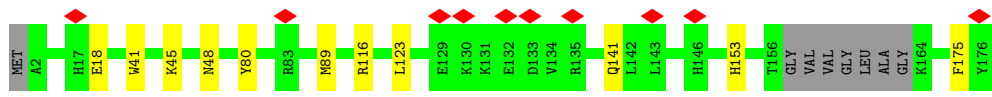
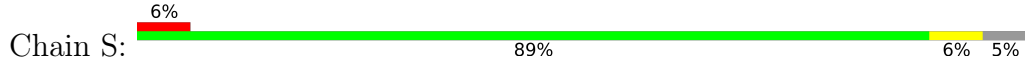
• Molecule 21: 60S ribosomal protein L17-A



• Molecule 22: 60S ribosomal protein L18-A

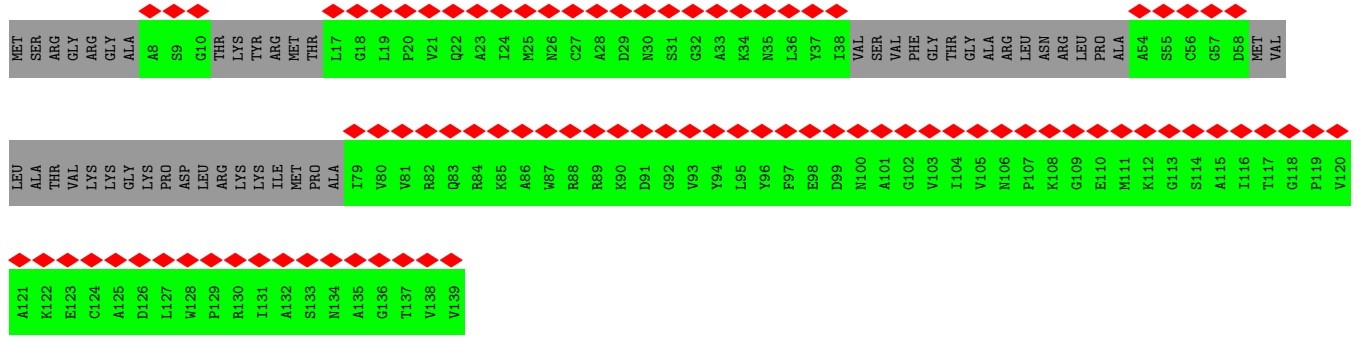


• Molecule 23: 60S ribosomal protein L20-A



• Molecule 24: 60S ribosomal protein L23-A





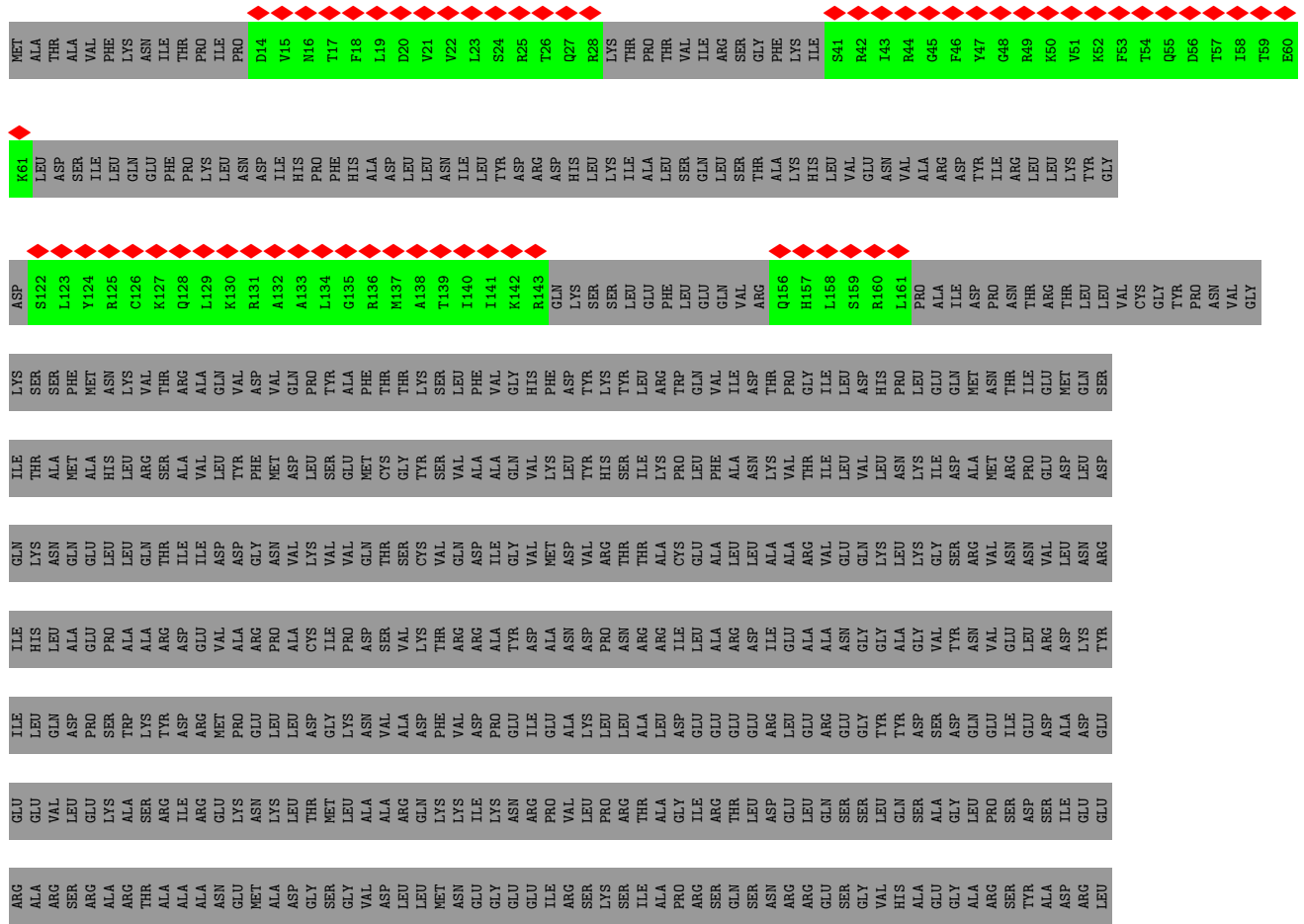
● Molecule 25: Ribosomal protein L26

Chain Y: 93% 6%



● Molecule 26: Probable nucleolar GTP-binding protein 1

Chain b: 10% 90%



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

- Molecule 27: 60S ribosomal protein L32-A

Chain e:  94%

MET
ALA
VAL
N5
D36
V79
R100
S125
E127

- Molecule 28: 60S ribosomal protein L33-B

Chain f:  95%

MET
PRO
A3
E40
R49
K58
I108

- Molecule 29: 60S ribosomal protein L35

Chain h:  10% 94% 5%

MET
A2
F6
Q11
M15
R31
Q32
Q33
K34
I35
A36
G37
G38
S39
G40
S41
K42
L43
K47
D52
E70
A122

- Molecule 30: 60S ribosomal protein L36-B

Chain i:  6% 96%

MET
A2
K11
G12
L15
K33
S90
R96
L97
A98
H99

- Molecule 31: 60S ribosomal protein L37-B

Chain j:  74% 22%

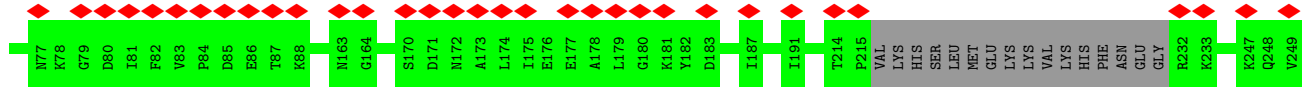
MET
THR
LYS
GLY
THR
GLN
SER
PHE
GLY
MET
ARG
HIS
ASN
K14
R25
Q30
R57
T58
K84
ALA
ALA
VAL
ALA
ALA
SER
ALA

- Molecule 32: Ribosome biogenesis protein erb1

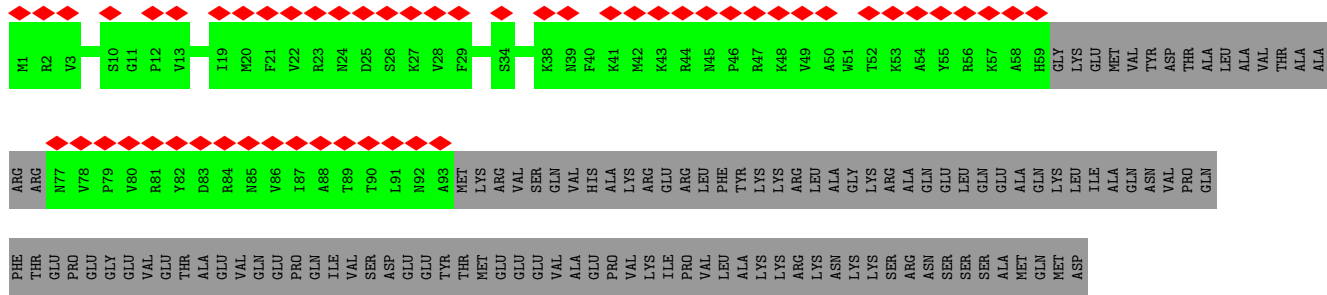
Chain m:  10% 90%

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

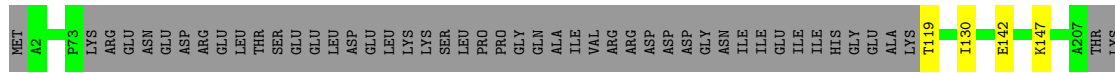
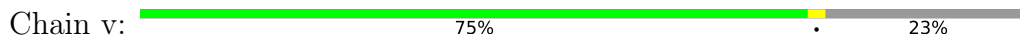
SER
LEU
THR
ALA
GLU
LEU
SER
GLU
GLU
GLU
GLU
GLY
TYR
SER
SER
SER
SER
GLY
ARG
SER
THR
PRO
GLU
LEU
SER
PRO
LYS
ASP
PHE
GLY
ASP
ALA
ASP
ASP
GLU
GLU
GLU
PHE
E101
E113
ASP
VAL
ALA
PRO
GLY
LEU
TYR
GLU
SER
TYR
ASP
VAL
ASP
ASN
GLU
LEU
TYR
ILE



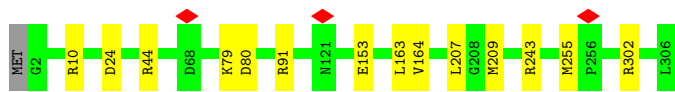
• Molecule 37: Ribosome biogenesis protein rlp24



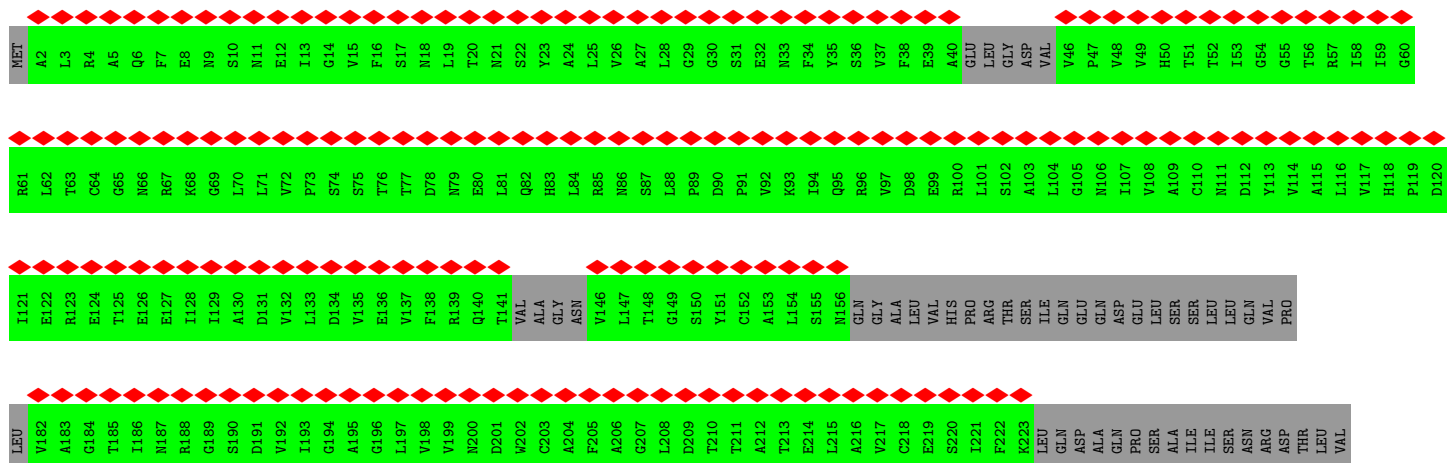
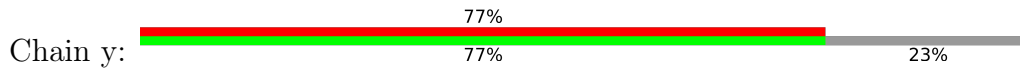
• Molecule 38: Nucleolar protein 16



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



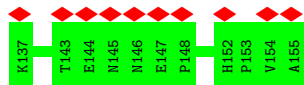
• Molecule 40: Eukaryotic translation initiation factor 6



GLU
SER
TYR
THR

• Molecule 41: RPL21

Chain T:  53% 100%



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 (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

5.1 Standard geometry

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	0.36	0/34768	0.71	0/54150
2	2	0.33	0/3563	0.70	0/5543
3	3	0.32	0/1627	0.50	0/2188
4	4	0.28	0/1823	0.49	0/2462
5	5	0.27	0/2739	0.51	0/3702
6	6	0.18	0/1770	0.70	0/2745
7	A	0.26	0/2038	0.53	0/2747
8	B	0.25	0/2694	0.54	0/3619
9	C	0.31	0/2863	0.51	0/3863
10	D	0.25	0/3245	0.44	0/4396
11	E	0.29	0/1356	0.54	0/1829
12	F	0.28	0/1982	0.48	0/2658
13	G	0.29	0/1291	0.44	0/1742
14	H	0.24	0/901	0.43	0/1252
15	J	0.23	0/458	0.37	0/639
16	K	0.25	0/1948	0.46	0/2640
17	L	0.31	0/960	0.59	0/1288
18	M	0.28	0/1024	0.56	0/1375
19	N	0.32	0/1436	0.56	0/1920
20	O	0.26	0/1506	0.47	0/2017
21	P	0.27	0/1187	0.47	0/1595
22	Q	0.28	0/1058	0.55	0/1421
23	S	0.25	0/1444	0.53	0/1939
24	V	0.24	0/442	0.41	0/605
25	Y	0.28	0/1008	0.58	0/1341
26	b	0.22	0/313	0.29	0/430
27	e	0.29	0/1009	0.55	0/1345
28	f	0.29	0/859	0.52	0/1152
29	h	0.28	0/1008	0.54	0/1340
30	i	0.27	0/791	0.53	0/1050
31	j	0.27	0/575	0.56	0/761
32	m	0.28	0/627	0.54	0/844

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	n	0.24	0/1788	0.39	0/2487
34	o	0.26	0/1049	0.51	0/1419
35	r	0.22	0/282	0.29	0/392
36	t	0.25	0/1009	0.46	0/1385
37	u	0.23	0/375	0.38	0/520
38	v	0.28	0/1319	0.51	0/1769
39	x	0.27	0/2562	0.52	0/3432
40	y	0.23	0/921	0.45	0/1274
41	T	0.24	0/151	0.42	0/207
All	All	0.31	0/89769	0.61	0/129483

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	D	410/578 (71%)	400 (98%)	10 (2%)	0	100	100
11	E	168/195 (86%)	154 (92%)	13 (8%)	1 (1%)	25	64
12	F	238/250 (95%)	229 (96%)	9 (4%)	0	100	100
13	G	161/259 (62%)	152 (94%)	7 (4%)	2 (1%)	13	48
14	H	181/190 (95%)	180 (99%)	1 (1%)	0	100	100
15	J	90/333 (27%)	86 (96%)	3 (3%)	1 (1%)	14	50
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
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%)	25	64
39	x	303/306 (99%)	297 (98%)	6 (2%)	0	100	100
40	y	180/244 (74%)	173 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	T	17/19 (90%)	16 (94%)	1 (6%)	0	100	100
All	All	6476/9976 (65%)	6239 (96%)	232 (4%)	5 (0%)	54	85

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%)	157 (93%)	12 (7%)	14	46
4	4	192/197 (98%)	185 (96%)	7 (4%)	35	70
5	5	301/345 (87%)	288 (96%)	13 (4%)	29	66
7	A	221/266 (83%)	202 (91%)	19 (9%)	10	37
8	B	282/326 (86%)	263 (93%)	19 (7%)	16	49
9	C	296/297 (100%)	287 (97%)	9 (3%)	41	75
10	D	332/505 (66%)	322 (97%)	10 (3%)	41	75
11	E	139/155 (90%)	129 (93%)	10 (7%)	14	45
12	F	201/210 (96%)	193 (96%)	8 (4%)	31	68
13	G	135/212 (64%)	131 (97%)	4 (3%)	41	75
16	K	210/333 (63%)	205 (98%)	5 (2%)	49	79
17	L	97/167 (58%)	93 (96%)	4 (4%)	30	67
18	M	108/113 (96%)	105 (97%)	3 (3%)	43	77
19	N	146/176 (83%)	143 (98%)	3 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	O	153/162 (94%)	144 (94%)	9 (6%)	19	54
21	P	120/149 (80%)	115 (96%)	5 (4%)	30	66
22	Q	116/159 (73%)	115 (99%)	1 (1%)	78	92
23	S	150/154 (97%)	139 (93%)	11 (7%)	14	44
25	Y	110/111 (99%)	102 (93%)	8 (7%)	14	44
27	e	106/107 (99%)	102 (96%)	4 (4%)	33	69
28	f	89/91 (98%)	86 (97%)	3 (3%)	37	72
29	h	106/107 (99%)	100 (94%)	6 (6%)	20	56
30	i	83/84 (99%)	80 (96%)	3 (4%)	35	70
31	j	58/71 (82%)	54 (93%)	4 (7%)	15	48
32	m	67/659 (10%)	64 (96%)	3 (4%)	27	64
34	o	93/246 (38%)	81 (87%)	12 (13%)	4	19
36	t	23/223 (10%)	17 (74%)	6 (26%)	0	2
38	v	138/181 (76%)	135 (98%)	3 (2%)	52	81
39	x	272/273 (100%)	258 (95%)	14 (5%)	24	60
41	T	17/17 (100%)	17 (100%)	0	100	100
All	All	4530/6367 (71%)	4312 (95%)	218 (5%)	29	62

5 of 218 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	K	191	PHE
23	S	45	LYS
36	t	67	GLU
17	L	134	LYS
20	O	137	CYS

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

Mol	Chain	Res	Type
21	P	80	GLN
21	P	97	ASN
29	h	25	GLN
22	Q	79	ASN
8	B	211	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1426/3497 (40%)	356 (24%)	16 (1%)
2	2	147/165 (89%)	31 (21%)	0
6	6	72/300 (24%)	40 (55%)	1 (1%)
All	All	1645/3962 (41%)	427 (25%)	17 (1%)

5 of 427 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 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

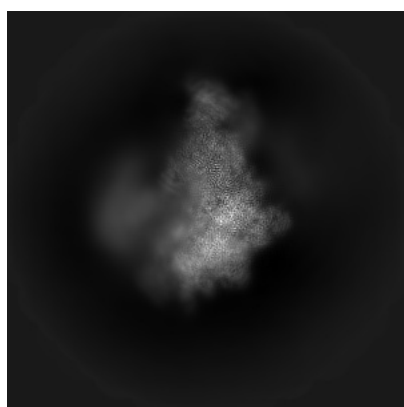
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24421. These allow visual inspection of the internal detail of the map and identification of artifacts.

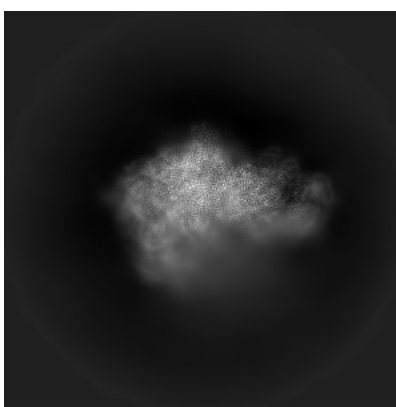
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

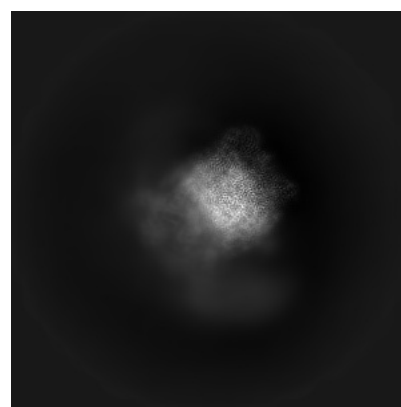
6.1.1 Primary map



X



Y

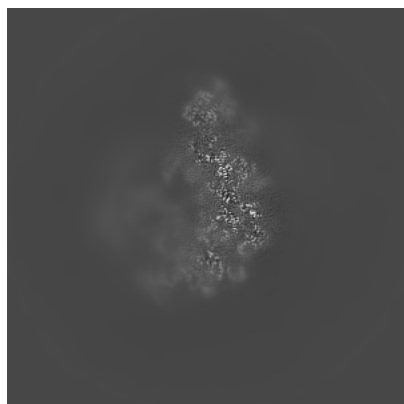


Z

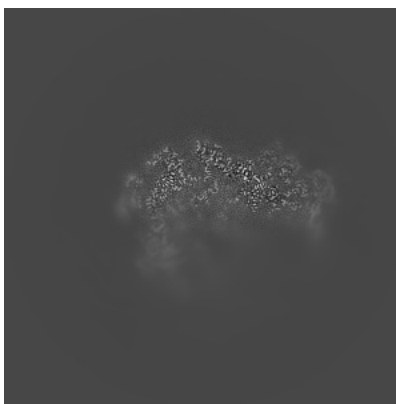
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

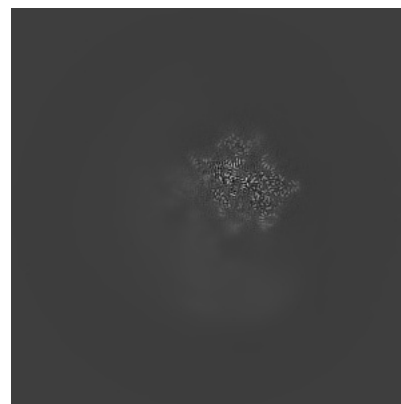
6.2.1 Primary map



X Index: 256



Y Index: 256

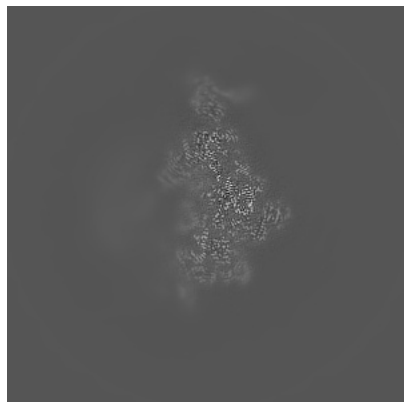


Z Index: 256

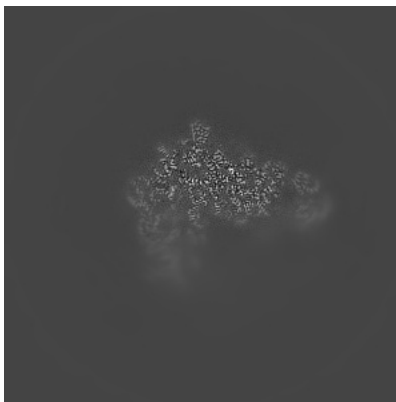
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

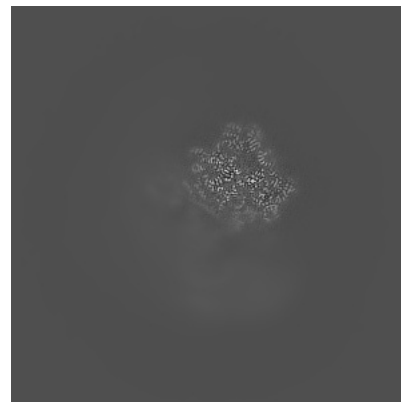
6.3.1 Primary map



X Index: 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.

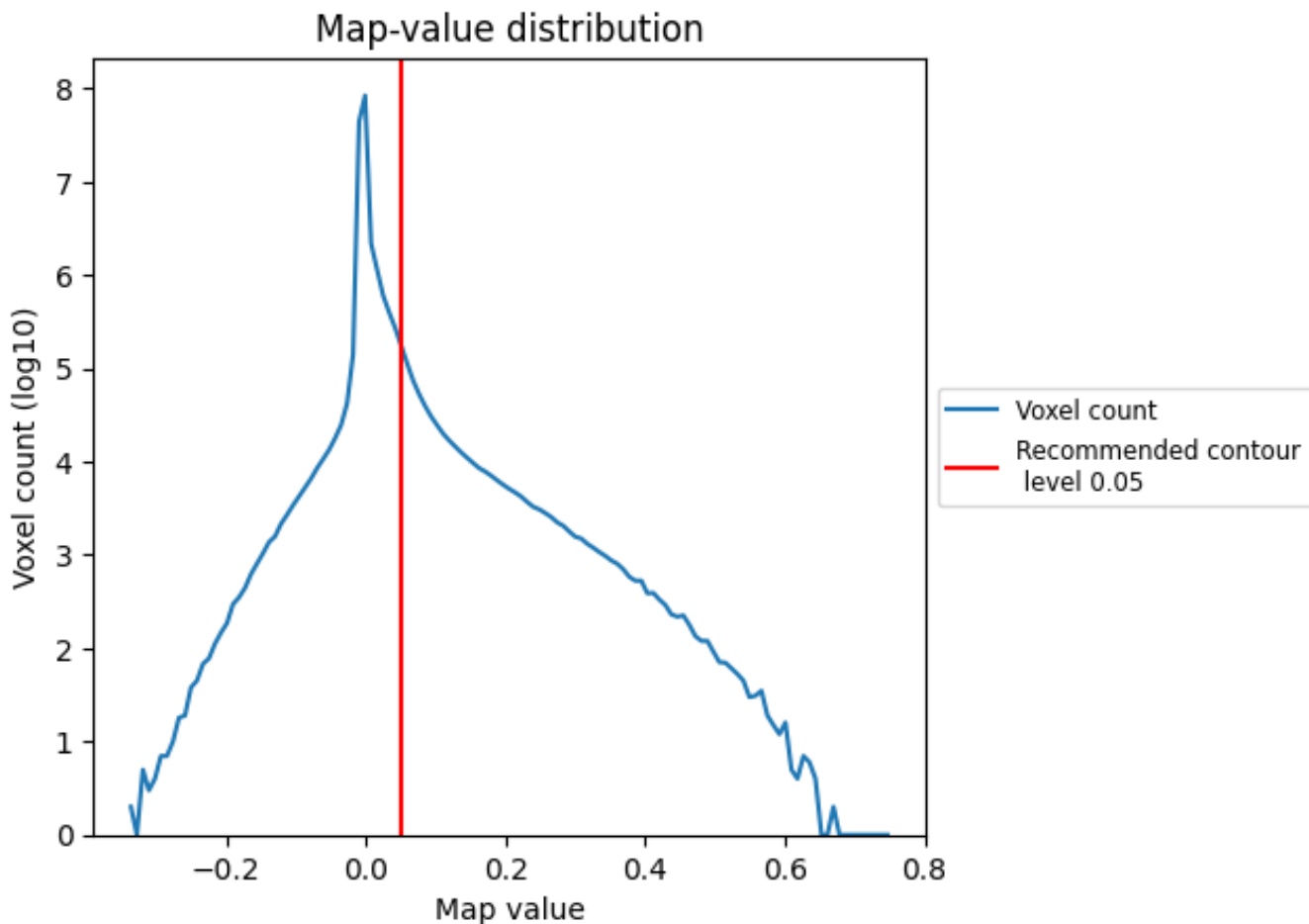
6.5 Mask visualisation

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

7 Map analysis [i](#)

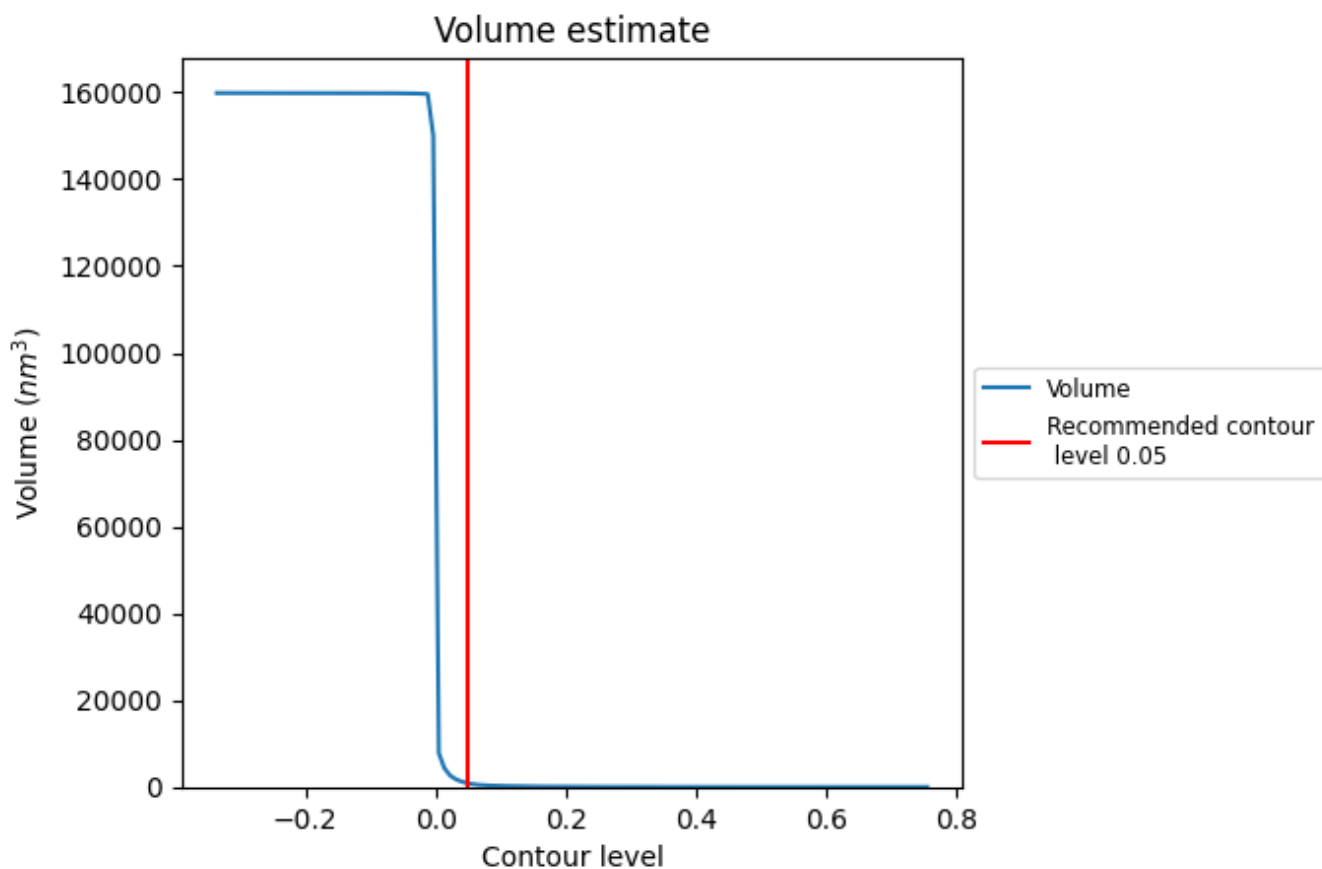
This section contains the results of statistical analysis of the map.

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.

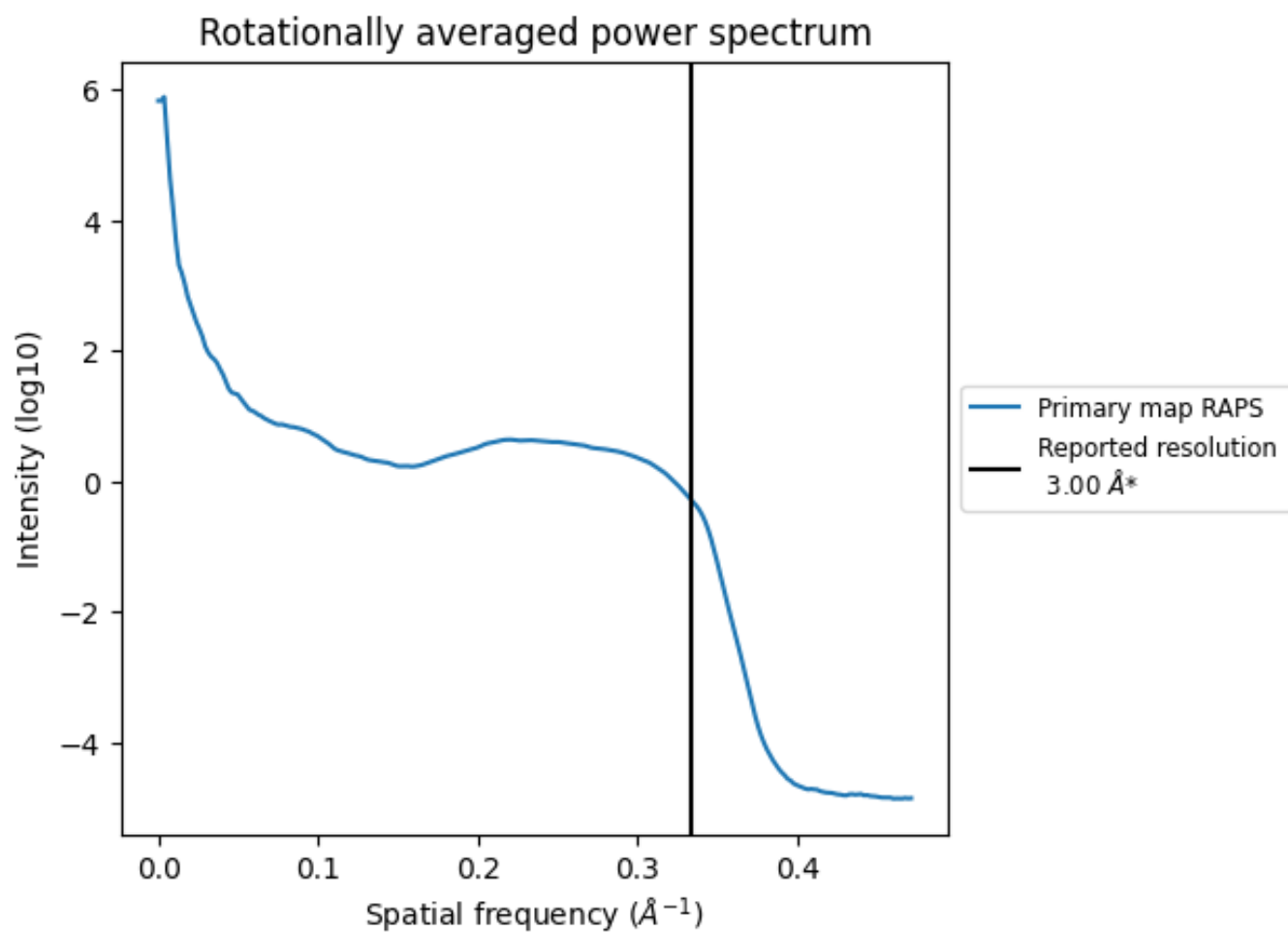
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 836 nm^3 ; 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

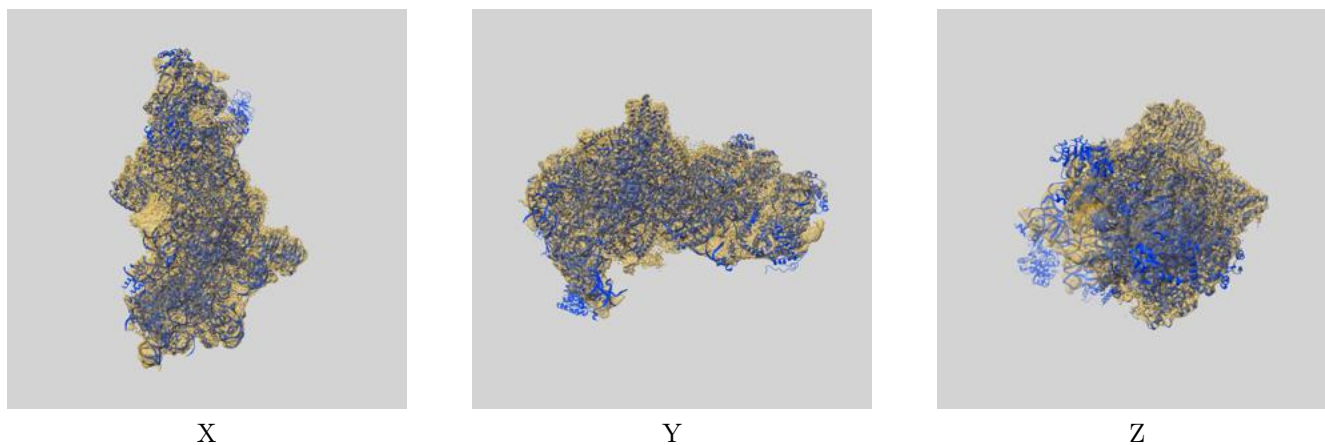
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

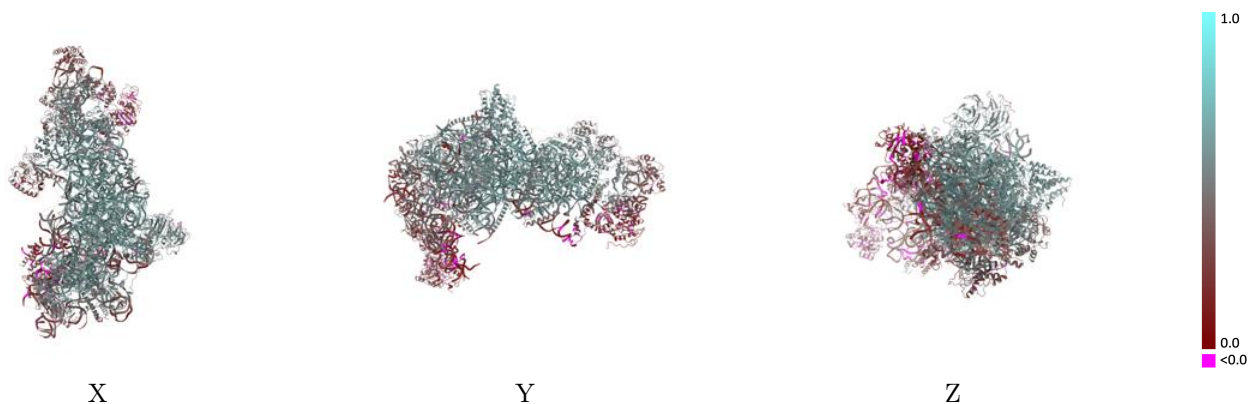
This section contains information regarding the fit between EMDB map EMD-24421 and PDB model 8EV3. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



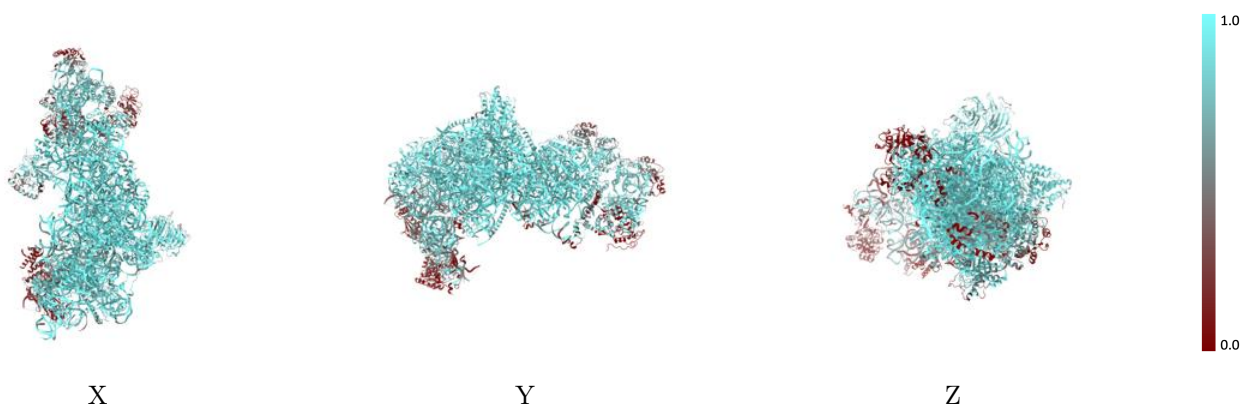
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



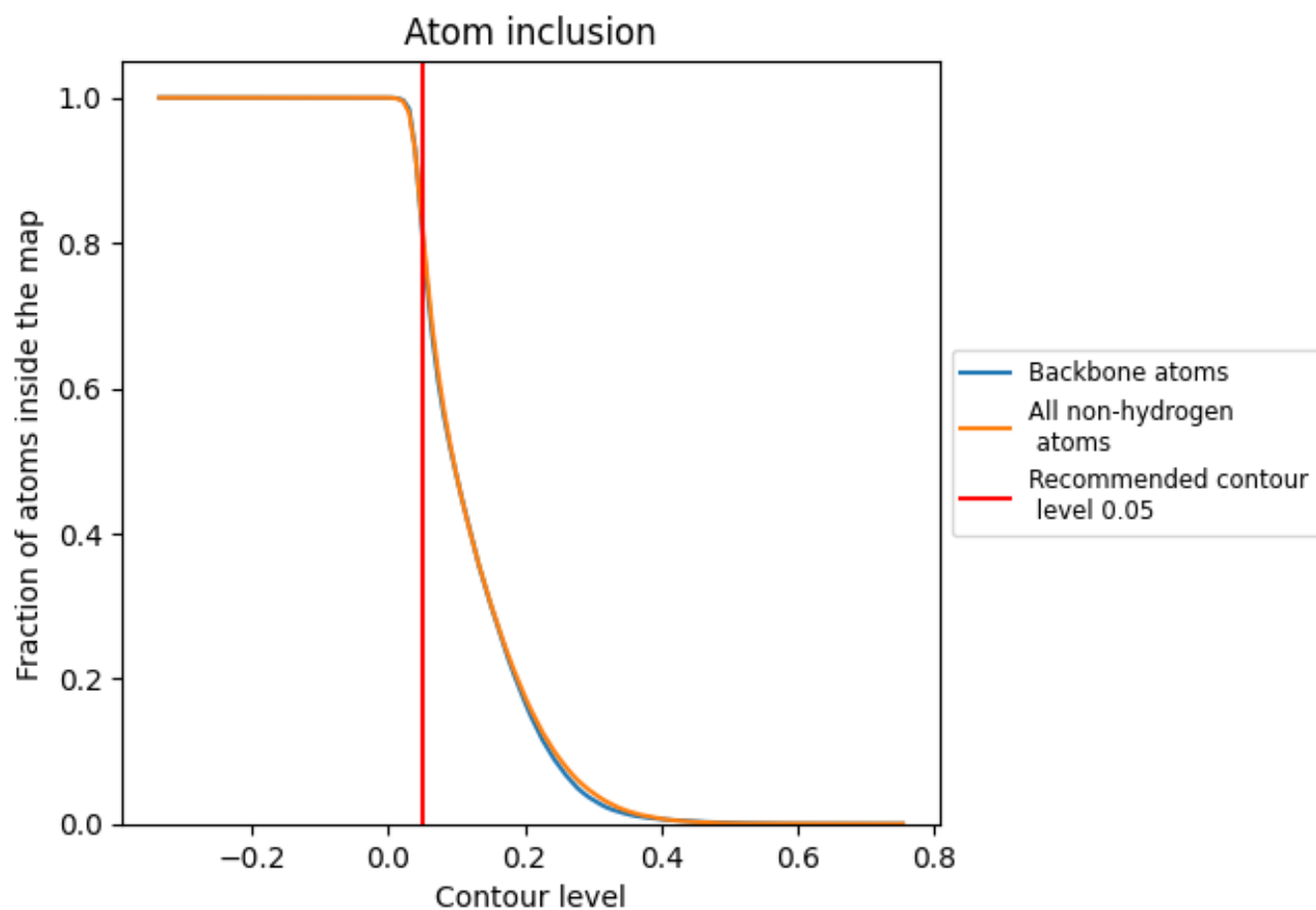
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.8777	 0.4450
2	 0.8887	 0.4570
3	 0.9399	 0.5940
4	 0.9174	 0.5770
5	 0.8803	 0.5330
6	 0.8399	 0.3210
A	 0.7852	 0.3930
B	 0.6338	 0.2630
C	 0.9281	 0.5840
D	 0.6539	 0.4890
E	 0.9135	 0.5290
F	 0.9415	 0.5710
G	 0.9463	 0.5840
H	 0.1330	 0.2830
J	 0.5425	 0.3010
K	 0.6147	 0.3940
L	 0.9800	 0.6290
M	 0.9314	 0.4890
N	 0.9888	 0.6200
O	 0.8987	 0.4840
P	 0.8329	 0.5180
Q	 0.9558	 0.5890
S	 0.8443	 0.4560
T	 0.3673	 0.3620
V	 0.0000	 0.1100
Y	 0.9751	 0.5990
b	 0.0000	 0.2500
e	 0.9833	 0.6170
f	 0.9939	 0.6020
h	 0.8261	 0.5190
i	 0.9242	 0.5510
j	 0.9426	 0.5820
m	 0.8600	 0.5230
n	 0.3199	 0.1710



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Chain	Atom inclusion	Q-score
o	 0.7271	 0.4300
r	 0.0141	 0.1790
t	 0.7815	 0.3250
u	 0.2440	 0.1920
v	 0.9313	 0.5680
x	 0.9110	 0.5640
y	 0.0011	 0.1830