wwPDB EM Validation Summary Report ⓘ

Nov 7, 2022 – 09:33 AM EST

PDB ID	:	6N8O
EMDB ID	:	EMD-0374
Title	:	Cryo-EM structure of Rpl10-inserted (RI) pre-60S ribosomal subunit
Authors	:	Zhou, Y.; Musalgaonkar, S.; Johnson, A.W.; Taylor, D.W.
Deposited on	:	2018-11-29
Resolution	:	3.50 Å(reported)
Based on initial model	:	5T62

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:

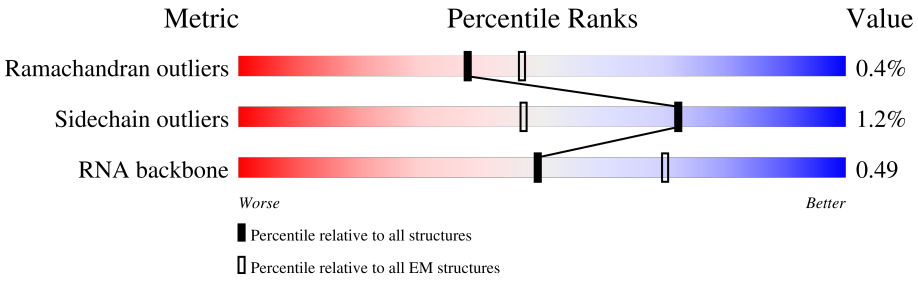
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.50 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 >=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 <=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	A	3396	74% 19% 6%
2	B	121	87% 13%
3	C	158	82% 18%
4	Y	364	7% 33% 65%
5	X	245	95%
6	L	165	54% 88% 11%
7	W	640	9% 55% 41%
8	V	518	11% 73% 24%

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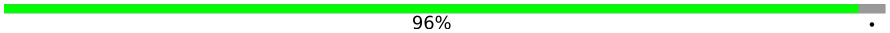
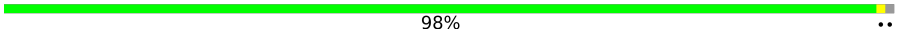
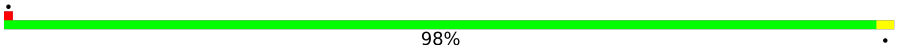
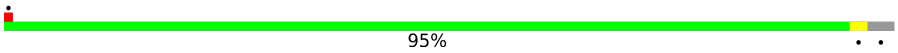
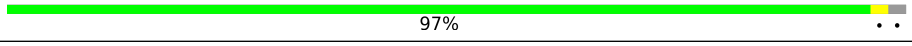
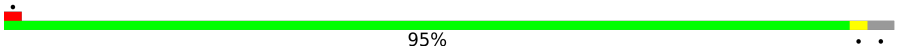
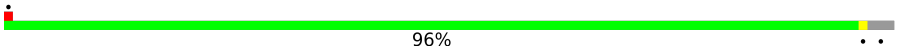
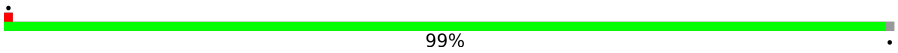
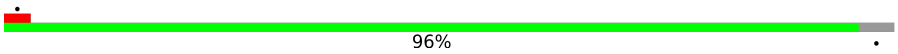
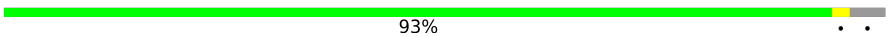
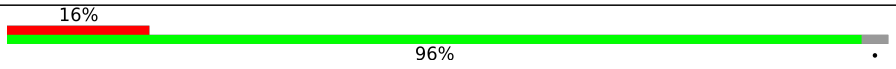
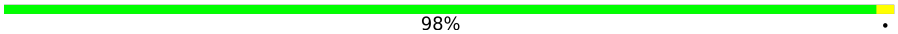
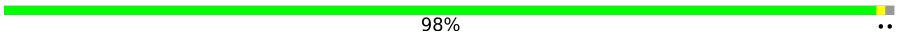
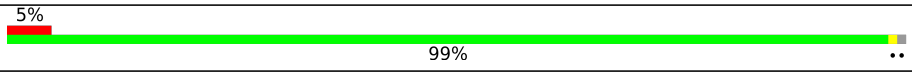
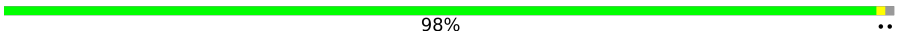
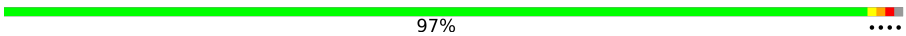
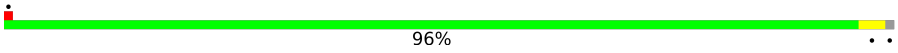
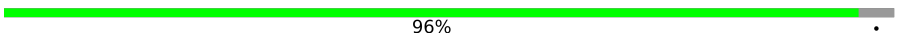
Mol	Chain	Length	Quality of chain
9	D	254	
10	E	387	
11	F	362	
12	G	297	
13	H	176	
14	I	244	
15	J	256	
16	K	191	
17	Z	221	
18	M	174	
19	N	199	
20	O	138	
21	Q	106	
22	R	92	
23	S	217	
24	a	204	
25	b	199	
26	c	184	
27	d	186	
28	e	189	
29	f	172	
30	g	160	
31	h	121	
32	i	137	
33	j	155	

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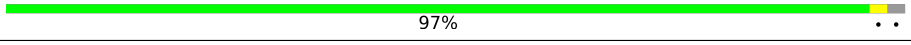
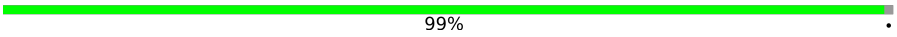
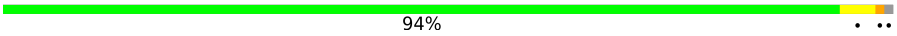
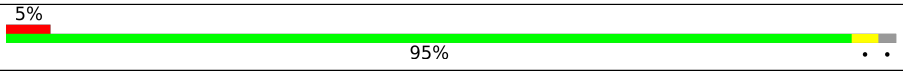
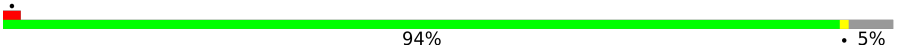
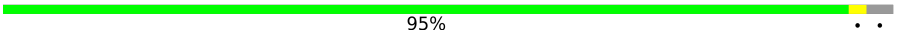
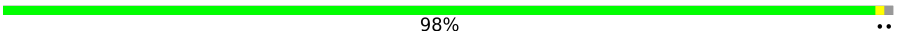
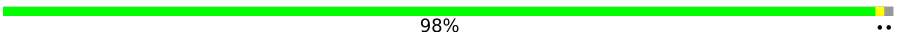
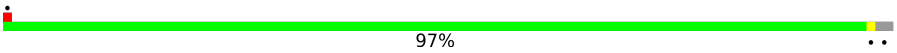
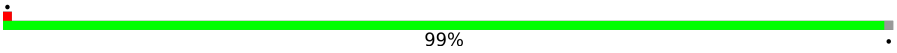
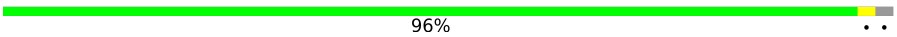
Mol	Chain	Length	Quality of chain
34	k	142	
35	l	127	
36	m	136	
37	n	149	
38	o	59	
39	p	105	
40	q	113	
41	r	130	
42	s	107	
43	t	121	
44	u	120	
45	v	100	
46	w	88	
47	x	78	
48	y	51	
49	z	128	

2 Entry composition (i)

There are 49 unique types of molecules in this entry. The entry contains 133453 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 Saccharomyces cerevisiae S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	3201	68470	30584	12346	22339	3201	0	0

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	121	2579	1152	461	845	121	0	0

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C	158	3353	1500	586	1109	158	0	0

- Molecule 4 is a protein called Tyrosine-protein phosphatase YVH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	Y	128	991	625	179	179	8	0	0

- Molecule 5 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	X	234	1710	1063	294	346	7	0	0

- Molecule 6 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	L	147	817	499	159	159	0	0

- Molecule 7 is a protein called Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	W	377	Total	C	N	O	S	0	0
			2976	1905	516	548	7		

- Molecule 8 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	392	Total	C	N	O	S	0	0
			3034	1930	523	561	20		

- Molecule 9 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

- Molecule 10 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	384	Total	C	N	O	S	0	0
			3059	1940	582	529	8		

- Molecule 11 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 12 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	289	Total	C	N	O	S	0	0
			2315	1464	403	446	2		

- Molecule 13 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	155	Total	C	N	O	S	0	0
			1217	785	220	211	1		

- Molecule 14 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	220	Total	C	N	O	S	0	0
			1770	1143	322	304	1		

- Molecule 15 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	227	Total	C	N	O	S	0	0
			1762	1128	315	316	3		

- Molecule 16 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 17 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Z	201	Total	C	N	O	S	0	0
			1648	1050	309	284	5		

- Molecule 18 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	168	Total	C	N	O	S	0	0
			1344	841	251	248	4		

- Molecule 19 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	N	193	Total	C	N	O	0	0
			1539	959	314	266		

- Molecule 20 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 21 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	102	Total	C	N	O	S	0	0
			819	514	166	134	5		

- Molecule 22 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	88	Total	C	N	O	S	0	0
			673	416	135	116	6		

- Molecule 23 is a protein called Ribosomal Protein uL1.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	S	210	Total	C	N	O	0	0
			1050	630	210	210		

- Molecule 24 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 25 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 26 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	c	183	Total	C	N	O	0	0
			1420	882	281	257		

- Molecule 27 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 28 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	e	151	Total	C	N	O	0	0
			1219	757	258	204		

- Molecule 29 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	f	170	Total	C	N	O	S	0	0
			1432	922	265	242	3		

- Molecule 30 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 31 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	h	97	Total	C	N	O	0	0
			766	496	126	144		

- Molecule 32 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	i	132	Total	C	N	O	S	0	0
			981	617	184	173	7		

- Molecule 33 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	j	61	Total	C	N	O	S	0	0
			509	328	100	80	1		

- Molecule 34 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	k	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 35 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	l	125	Total 984	C 620	N 191	O 173	0	0

- Molecule 36 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	m	135	Total 1092	C 710	N 202	O 180	0	0

- Molecule 37 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	148	Total 1173	C 749	N 231	O 190	S 3	0	0

- Molecule 38 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	o	58	Total 462	C 289	N 100	O 73	0	0

- Molecule 39 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	96	Total 737	C 476	N 123	O 137	S 1	0	0

- Molecule 40 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	107	Total 866	C 550	N 165	O 150	S 1	0	0

- Molecule 41 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	126	Total 1012	C 641	N 204	O 166	S 1	0	0

- Molecule 42 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 43 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	109	Total	C	N	O	S	0	0
			861	533	175	149	4		

- Molecule 44 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 45 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	98	Total	C	N	O	S	0	0
			753	471	150	130	2		

- Molecule 46 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	w	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 47 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	x	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 48 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 49 is a protein called Ubiquitin-60S ribosomal protein L40.

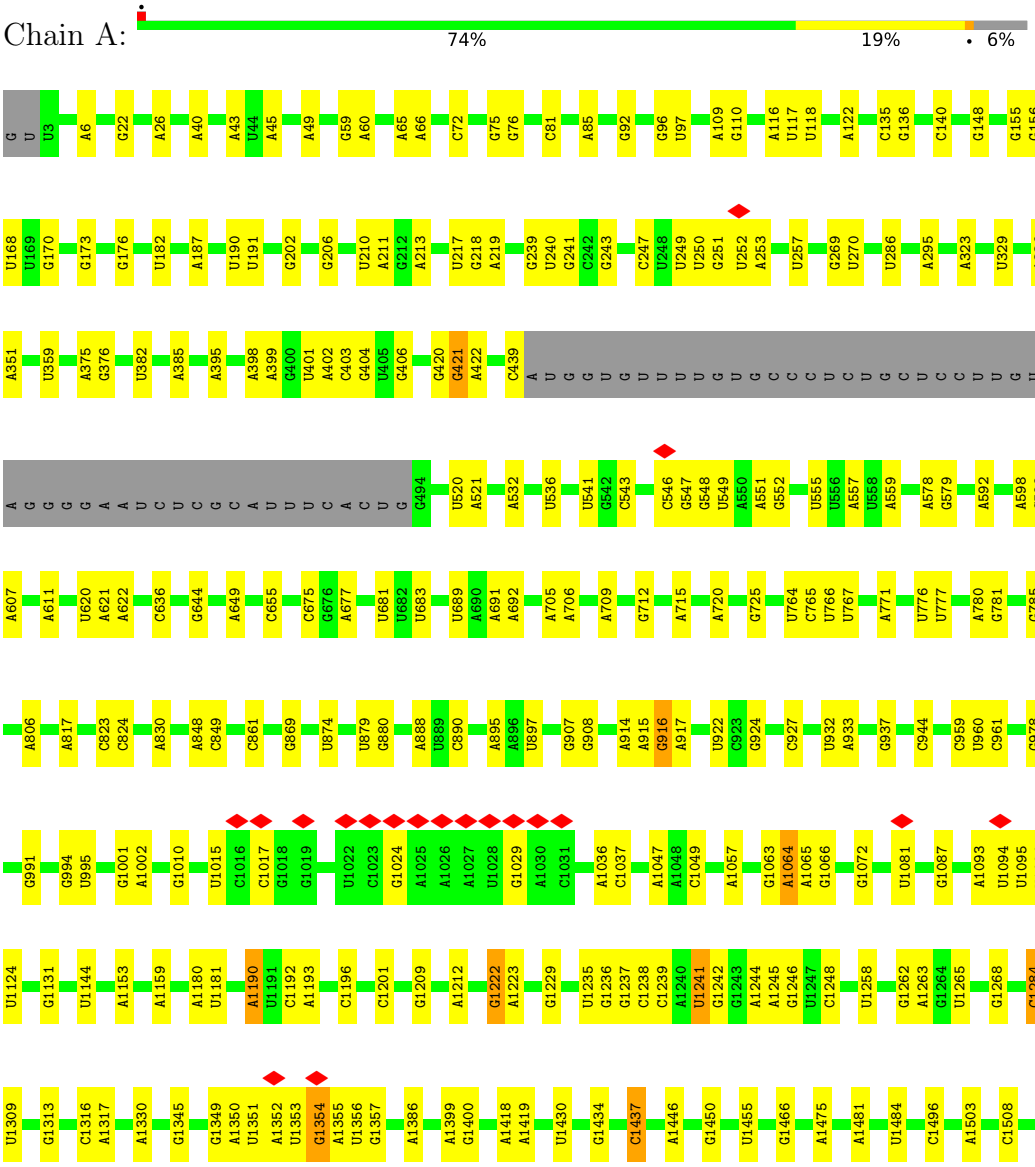
Mol	Chain	Residues	Atoms					AltConf	Trace
49	z	51	Total	C	N	O	S	0	0
			408	253	84	66	5		

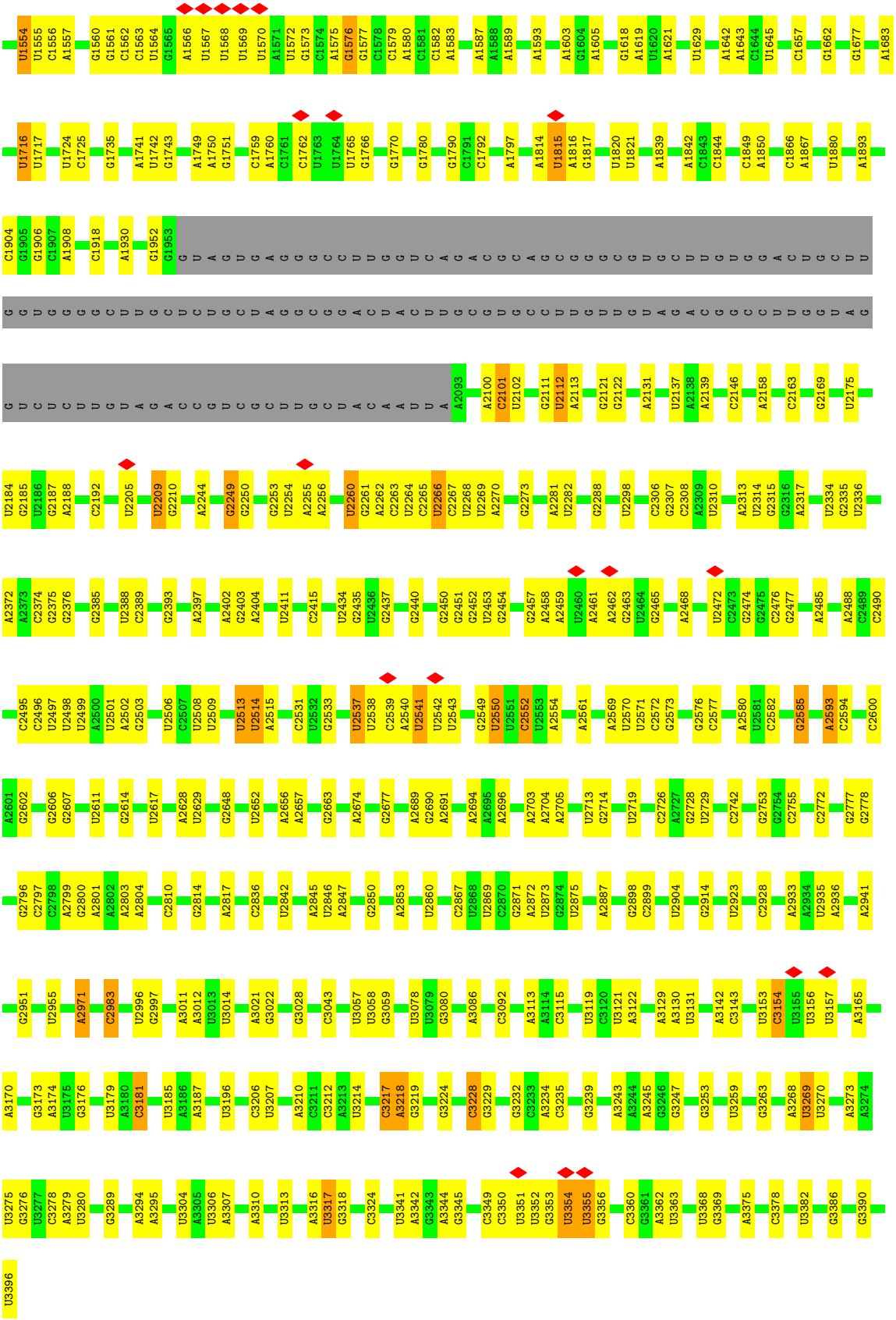
3 Residue-property plots (i)

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: Saccharomyces cerevisiae S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA

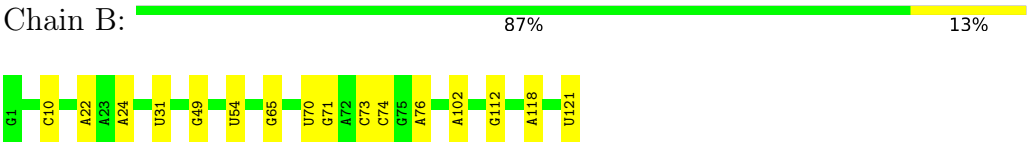
Chain A:





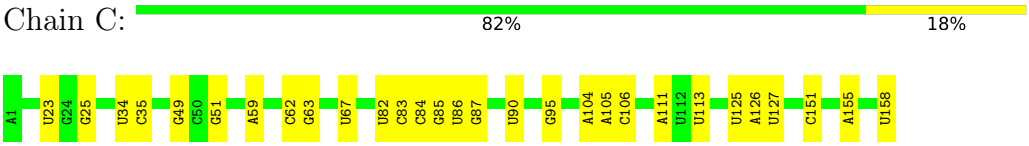
• Molecule 2: 5S rRNA

Chain B:



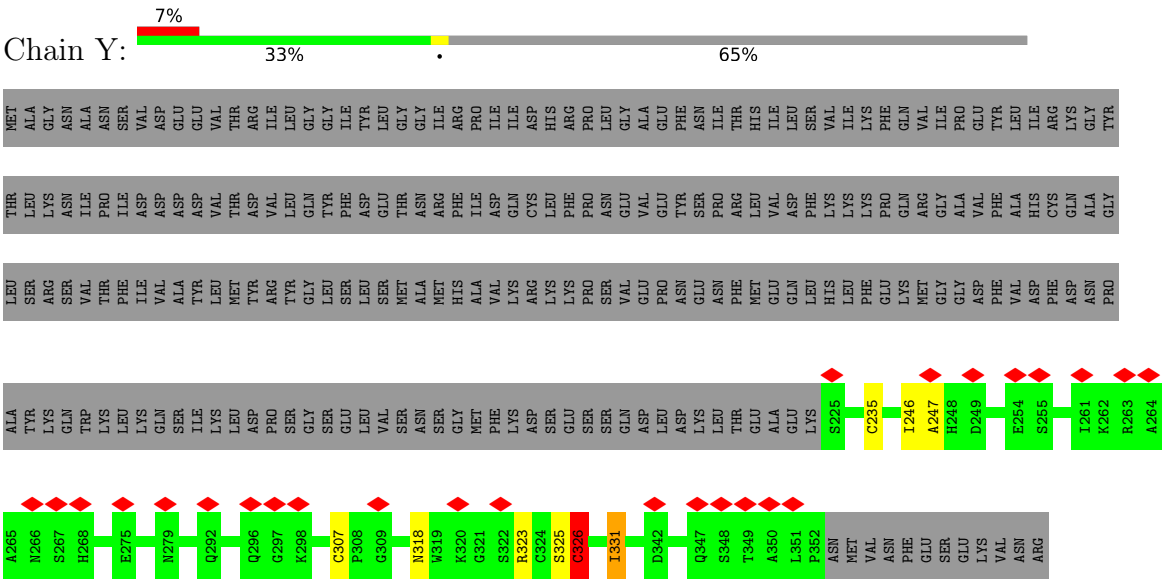
• Molecule 3: 5.8S rRNA

Chain C:



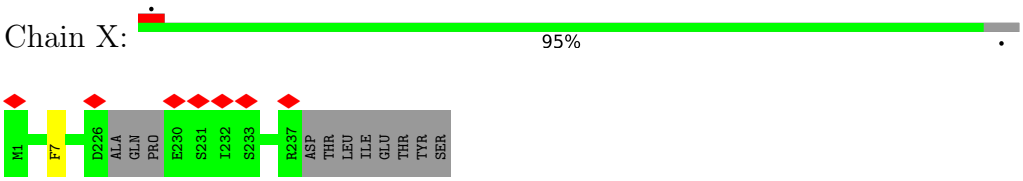
• Molecule 4: Tyrosine-protein phosphatase YVH1

Chain Y:



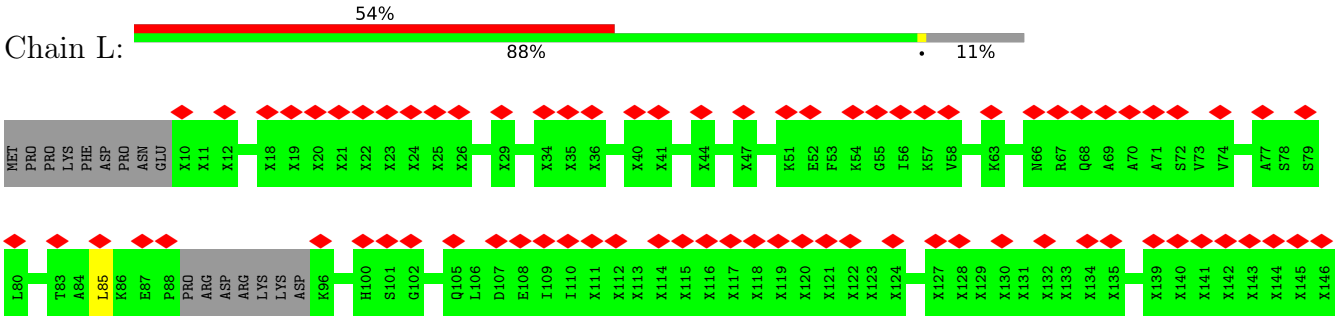
• Molecule 5: Eukaryotic translation initiation factor 6

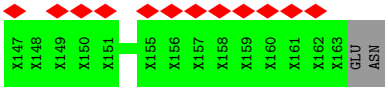
Chain X:



• Molecule 6: Ribosomal protein L12

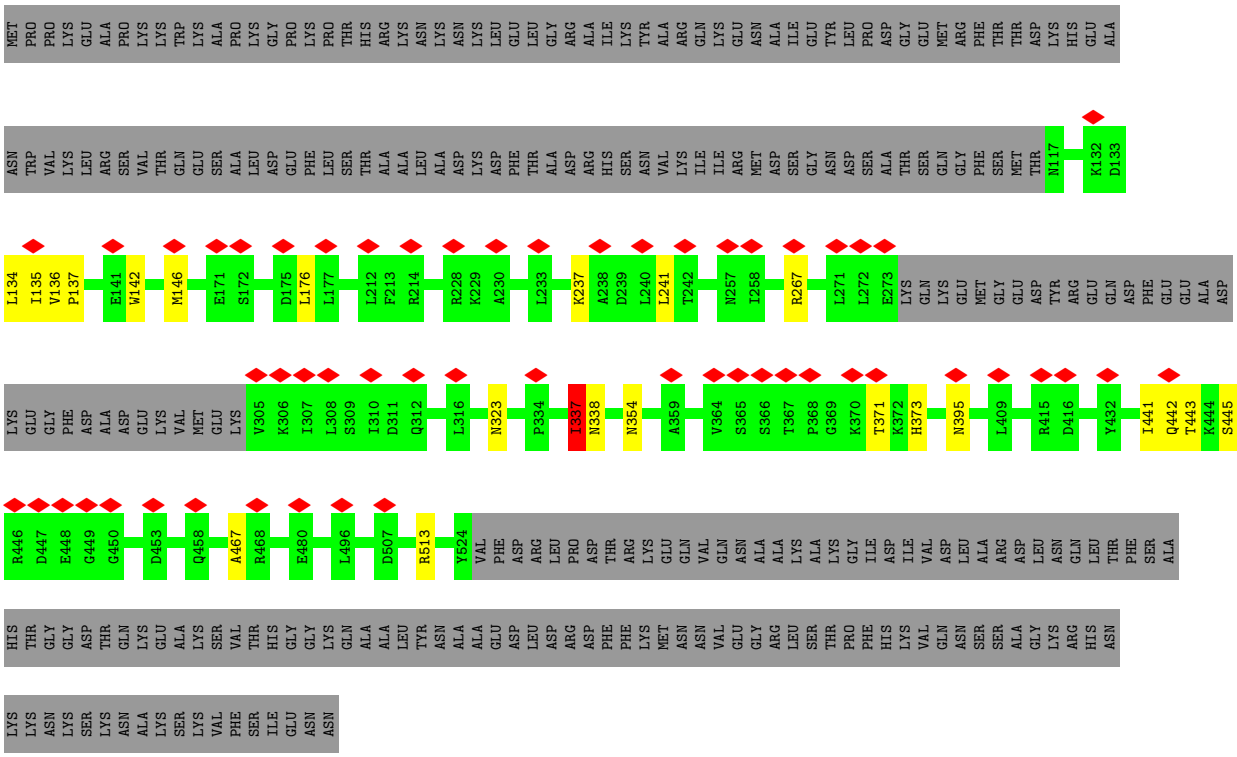
Chain L:





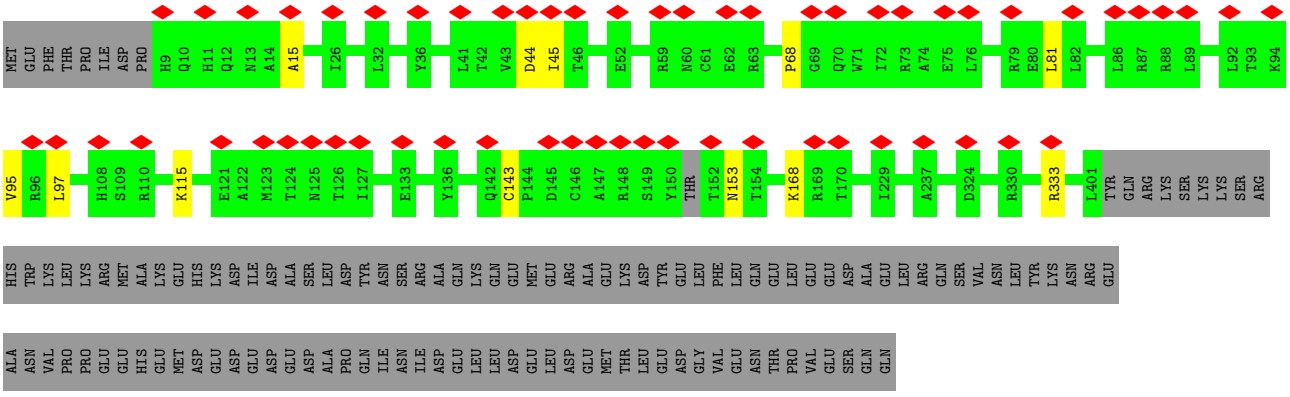
• Molecule 7: Large subunit GTPase 1

Chain W:



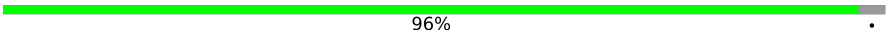
• Molecule 8: 60S ribosomal export protein NMD3

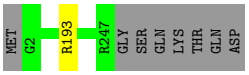
Chain V:



• Molecule 9: 60S ribosomal protein L2-A

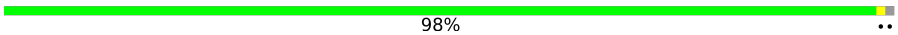
Chain D:

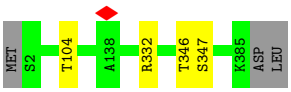




• Molecule 10: 60S ribosomal protein L3

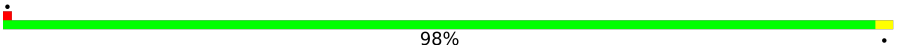
Chain E:

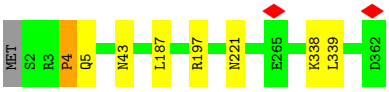




• Molecule 11: 60S ribosomal protein L4-A

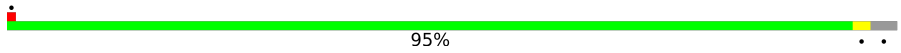
Chain F:

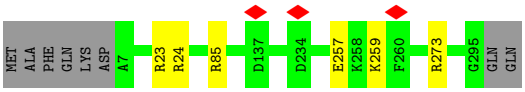




• Molecule 12: 60S ribosomal protein L5

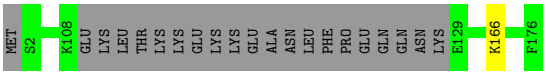
Chain G:





• Molecule 13: 60S ribosomal protein L6-A

Chain H:

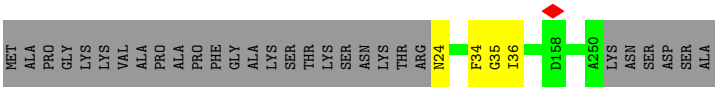


• Molecule 14: 60S ribosomal protein L7-A

Chain I:

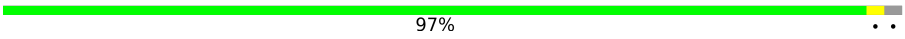
• Molecule 15: 60S ribosomal protein L8-A

Chain J:



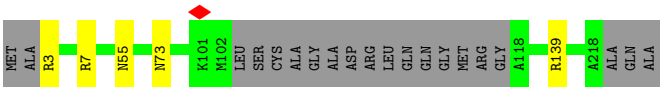
• Molecule 16: 60S ribosomal protein L9-A

Chain K:



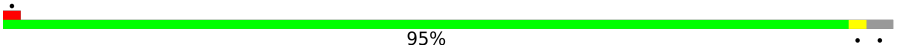
• Molecule 17: 60S ribosomal protein L10

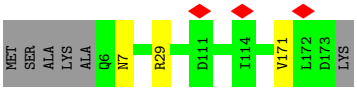
Chain Z:



• Molecule 18: 60S ribosomal protein L11-A

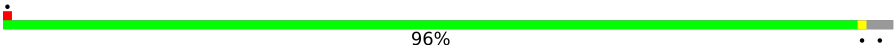
Chain M:

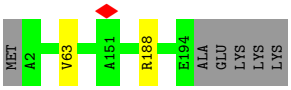




• Molecule 19: 60S ribosomal protein L13-A

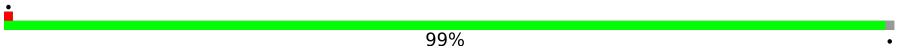
Chain N:

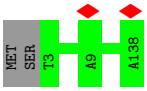




• Molecule 20: 60S ribosomal protein L14-A

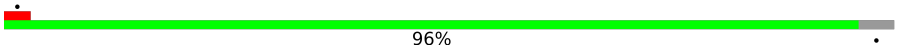
Chain O:

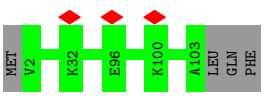




• Molecule 21: 60S ribosomal protein L42-A

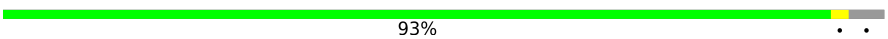
Chain Q:

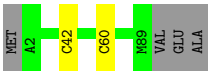




• Molecule 22: 60S ribosomal protein L43-A

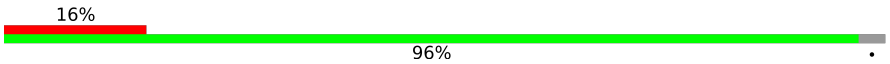
Chain R:

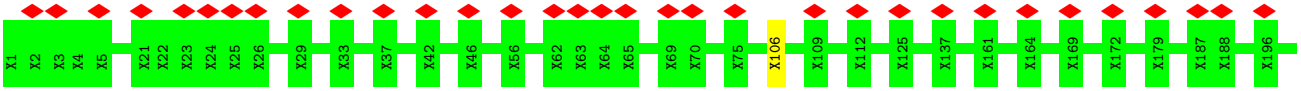


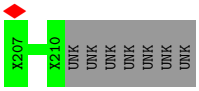


• Molecule 23: Ribosomal Protein uL1

Chain S:

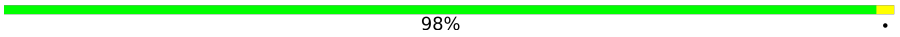


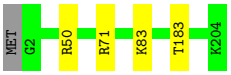




• Molecule 24: 60S ribosomal protein L15-A

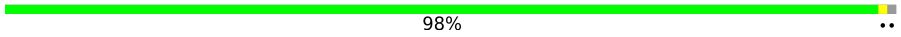
Chain a:

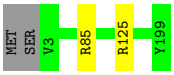




• Molecule 25: 60S ribosomal protein L16-A

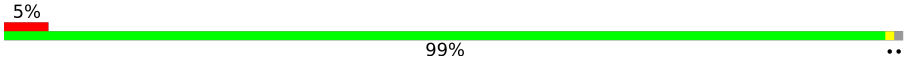
Chain b:

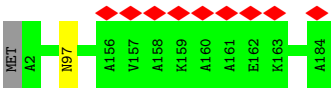




• Molecule 26: 60S ribosomal protein L17-A

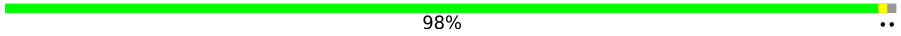
Chain c:





• Molecule 27: 60S ribosomal protein L18-A

Chain d:

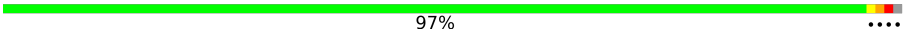


• Molecule 28: 60S ribosomal protein L19-A

Chain e:

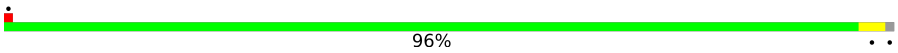
• Molecule 29: 60S ribosomal protein L20-A

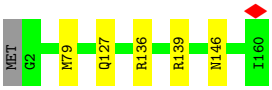
Chain f:



• Molecule 30: 60S ribosomal protein L21-A

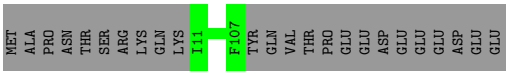
Chain g:





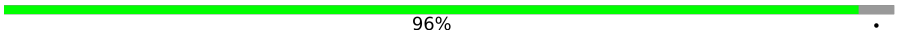
• Molecule 31: 60S ribosomal protein L22-A

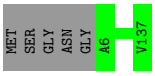
Chain h:



• Molecule 32: 60S ribosomal protein L23-A

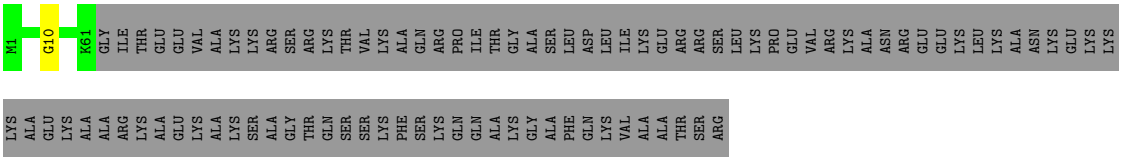
Chain i:





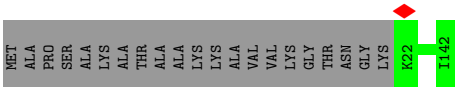
• Molecule 33: 60S ribosomal protein L24-A

Chain j:



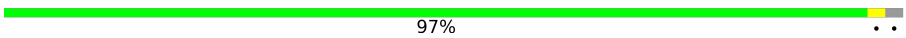
• Molecule 34: 60S ribosomal protein L25

Chain k:



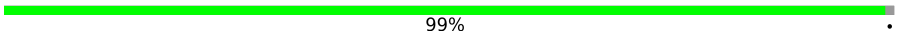
• Molecule 35: 60S ribosomal protein L26-A

Chain l:



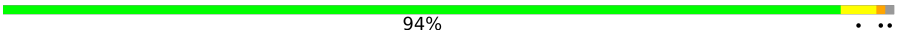
• Molecule 36: 60S ribosomal protein L27-A

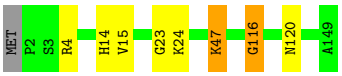
Chain m:



• Molecule 37: 60S ribosomal protein L28

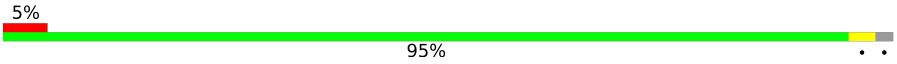
Chain n:

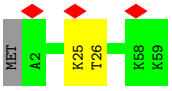




• Molecule 38: 60S ribosomal protein L29

Chain o:



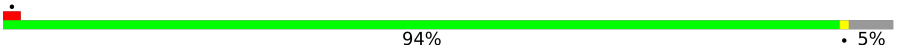


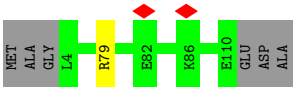
• Molecule 39: 60S ribosomal protein L30

Chain p:

• Molecule 40: 60S ribosomal protein L31-A

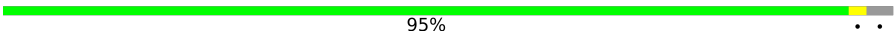
Chain q:





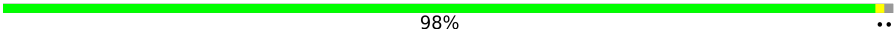
• Molecule 41: 60S ribosomal protein L32

Chain r:



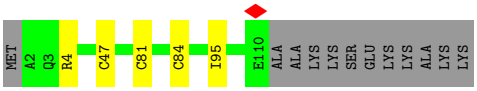
• Molecule 42: 60S ribosomal protein L33-A

Chain s:



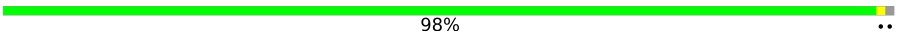
• Molecule 43: 60S ribosomal protein L34-A

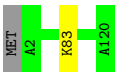
Chain t:



• Molecule 44: 60S ribosomal protein L35-A

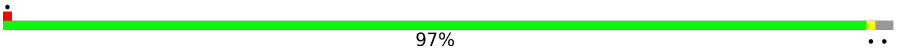
Chain u:

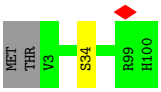




• Molecule 45: 60S ribosomal protein L36-A

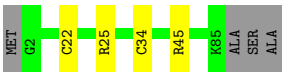
Chain v:





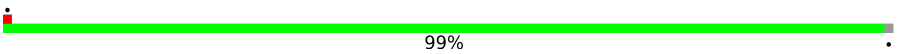
• Molecule 46: 60S ribosomal protein L37-A

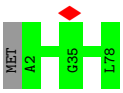
Chain w:



• Molecule 47: 60S ribosomal protein L38

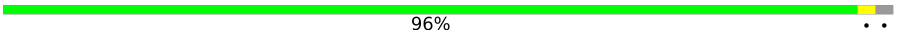
Chain x:

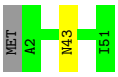




• Molecule 48: 60S ribosomal protein L39

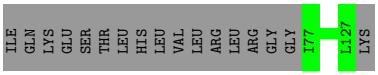
Chain y:





• Molecule 49: Ubiquitin-60S ribosomal protein L40

Chain z:


ILE
GLN
LYS
GLU
SER
THR
LEU
HIS
LEU
VAL
LEU
ARG
LEU
ARG
GLY
GLY
I77
L127
LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	112292	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.161	Depositor
Minimum map value	-0.089	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

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	A	0.75	0/76644	0.94	118/119497 (0.1%)
2	B	0.67	0/2883	0.87	0/4491
3	C	0.76	0/3746	0.92	0/5832
4	Y	0.37	0/1016	0.85	2/1368 (0.1%)
5	X	0.34	0/1729	0.55	0/2355
6	L	0.32	0/359	0.73	1/489 (0.2%)
7	W	0.33	0/3039	0.70	1/4124 (0.0%)
8	V	0.36	0/3093	0.64	2/4203 (0.0%)
9	D	0.43	0/1908	0.57	0/2564
10	E	0.44	0/3130	0.58	0/4206
11	F	0.39	0/2800	0.59	1/3790 (0.0%)
12	G	0.37	0/2364	0.57	1/3190 (0.0%)
13	H	0.38	0/1236	0.56	0/1661
14	I	0.39	0/1807	0.55	0/2432
15	J	0.38	0/1794	0.58	0/2425
16	K	0.40	0/1514	0.57	1/2039 (0.0%)
17	Z	0.36	0/1684	0.51	0/2259
18	M	0.31	0/1365	0.60	0/1831
19	N	0.39	0/1564	0.59	0/2102
20	O	0.37	0/1068	0.52	0/1438
21	Q	0.38	0/831	0.56	0/1097
22	R	0.43	0/680	0.59	0/905
24	a	0.46	0/1757	0.56	0/2354
25	b	0.41	0/1585	0.52	0/2128
26	c	0.42	0/1443	0.59	0/1944
27	d	0.38	0/1465	0.55	0/1965
28	e	0.40	0/1236	0.57	1/1650 (0.1%)
29	f	0.42	0/1468	0.58	1/1973 (0.1%)
30	g	0.40	0/1300	0.54	0/1743
31	h	0.38	0/781	0.54	0/1058
32	i	0.41	0/996	0.54	0/1340
33	j	0.37	0/521	0.50	0/691
34	k	0.42	0/979	0.59	0/1321
35	l	0.35	0/995	0.56	1/1329 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
36	m	0.39	0/1118	0.58	0/1497
37	n	0.41	0/1204	0.65	3/1612 (0.2%)
38	o	0.34	0/473	0.61	0/629
39	p	0.38	0/745	0.55	0/1001
40	q	0.43	0/880	0.55	0/1182
41	r	0.38	0/1033	0.54	0/1383
42	s	0.46	0/868	0.54	0/1168
43	t	0.45	0/871	0.66	2/1164 (0.2%)
44	u	0.36	0/978	0.55	0/1301
45	v	0.34	0/759	0.57	0/1009
46	w	0.45	0/680	0.61	0/901
47	x	0.34	0/614	0.53	0/822
48	y	0.39	0/443	0.59	0/588
49	z	0.36	0/414	0.50	0/551
All	All	0.63	0/141860	0.82	135/208602 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	Y	0	3
5	X	0	1
7	W	0	10
8	V	0	2
10	E	0	1
11	F	0	2
14	I	0	2
15	J	0	2
16	K	0	1
18	M	0	2
23	S	0	1
29	f	0	2
37	n	0	3
38	o	0	1
44	u	0	1
All	All	0	34

There are no bond length outliers.

The worst 5 of 135 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	3217	C	N1-C2-O2	11.39	125.73	118.90
1	A	3217	C	C2-N1-C1'	10.59	130.45	118.80
43	t	81	CYS	CA-CB-SG	10.48	132.87	114.00
1	A	3217	C	N3-C2-O2	-9.21	115.45	121.90
1	A	2550	U	C2-N1-C1'	8.35	127.72	117.70

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	W	134	LEU	Peptide
5	X	7	PHE	Peptide
4	Y	325	SER	Peptide
4	Y	326	CYS	Peptide
4	Y	331	ILE	Peptide

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
4	Y	126/364 (35%)	99 (79%)	23 (18%)	4 (3%)	4 29
5	X	230/245 (94%)	222 (96%)	8 (4%)	0	100 100
6	L	53/165 (32%)	48 (91%)	5 (9%)	0	100 100
7	W	373/640 (58%)	313 (84%)	53 (14%)	7 (2%)	8 40
8	V	388/518 (75%)	332 (86%)	52 (13%)	4 (1%)	15 54
9	D	244/254 (96%)	227 (93%)	17 (7%)	0	100 100
10	E	382/387 (99%)	357 (94%)	24 (6%)	1 (0%)	41 75

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	F	359/362 (99%)	328 (91%)	28 (8%)	3 (1%)	19	58
12	G	287/297 (97%)	266 (93%)	20 (7%)	1 (0%)	41	75
13	H	151/176 (86%)	144 (95%)	7 (5%)	0	100	100
14	I	218/244 (89%)	204 (94%)	13 (6%)	1 (0%)	29	68
15	J	225/256 (88%)	215 (96%)	9 (4%)	1 (0%)	34	72
16	K	186/191 (97%)	173 (93%)	13 (7%)	0	100	100
17	Z	197/221 (89%)	187 (95%)	10 (5%)	0	100	100
18	M	166/174 (95%)	153 (92%)	13 (8%)	0	100	100
19	N	191/199 (96%)	170 (89%)	20 (10%)	1 (0%)	29	68
20	O	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
21	Q	100/106 (94%)	93 (93%)	7 (7%)	0	100	100
22	R	86/92 (94%)	80 (93%)	6 (7%)	0	100	100
24	a	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
25	b	195/199 (98%)	187 (96%)	8 (4%)	0	100	100
26	c	181/184 (98%)	167 (92%)	14 (8%)	0	100	100
27	d	183/186 (98%)	174 (95%)	9 (5%)	0	100	100
28	e	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
29	f	168/172 (98%)	156 (93%)	10 (6%)	2 (1%)	13	50
30	g	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
31	h	95/121 (78%)	89 (94%)	6 (6%)	0	100	100
32	i	130/137 (95%)	127 (98%)	3 (2%)	0	100	100
33	j	59/155 (38%)	56 (95%)	2 (3%)	1 (2%)	9	42
34	k	119/142 (84%)	110 (92%)	9 (8%)	0	100	100
35	l	123/127 (97%)	121 (98%)	2 (2%)	0	100	100
36	m	133/136 (98%)	119 (90%)	14 (10%)	0	100	100
37	n	146/149 (98%)	129 (88%)	14 (10%)	3 (2%)	7	38
38	o	56/59 (95%)	51 (91%)	4 (7%)	1 (2%)	8	41
39	p	94/105 (90%)	90 (96%)	4 (4%)	0	100	100
40	q	105/113 (93%)	96 (91%)	9 (9%)	0	100	100
41	r	124/130 (95%)	120 (97%)	4 (3%)	0	100	100
42	s	104/107 (97%)	99 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
43	t	107/121 (88%)	101 (94%)	6 (6%)	0	100 100
44	u	117/120 (98%)	113 (97%)	4 (3%)	0	100 100
45	v	96/100 (96%)	86 (90%)	9 (9%)	1 (1%)	15 54
46	w	82/88 (93%)	72 (88%)	10 (12%)	0	100 100
47	x	75/78 (96%)	73 (97%)	2 (3%)	0	100 100
48	y	48/51 (94%)	45 (94%)	3 (6%)	0	100 100
49	z	49/128 (38%)	47 (96%)	2 (4%)	0	100 100
All	All	7192/8490 (85%)	6643 (92%)	518 (7%)	31 (0%)	38 72

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	W	135	ILE
8	V	95	VAL
8	V	97	LEU
11	F	339	LEU
12	G	259	LYS

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
4	Y	110/323 (34%)	107 (97%)	3 (3%)	44 73
5	X	186/211 (88%)	186 (100%)	0	100 100
6	L	30/65 (46%)	30 (100%)	0	100 100
7	W	317/555 (57%)	310 (98%)	7 (2%)	52 78
8	V	332/467 (71%)	328 (99%)	4 (1%)	71 87
9	D	189/196 (96%)	188 (100%)	1 (0%)	88 94
10	E	317/323 (98%)	315 (99%)	2 (1%)	86 94
11	F	288/289 (100%)	285 (99%)	3 (1%)	76 88
12	G	238/245 (97%)	234 (98%)	4 (2%)	60 82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
13	H	131/153 (86%)	130 (99%)	1 (1%)	81 91
14	I	185/205 (90%)	183 (99%)	2 (1%)	73 88
15	J	182/208 (88%)	181 (100%)	1 (0%)	88 94
16	K	168/171 (98%)	167 (99%)	1 (1%)	86 94
17	Z	175/187 (94%)	170 (97%)	5 (3%)	42 71
18	M	146/150 (97%)	145 (99%)	1 (1%)	84 93
19	N	153/159 (96%)	152 (99%)	1 (1%)	84 93
20	O	107/109 (98%)	107 (100%)	0	100 100
21	Q	87/91 (96%)	87 (100%)	0	100 100
22	R	69/72 (96%)	67 (97%)	2 (3%)	42 71
24	a	175/176 (99%)	171 (98%)	4 (2%)	50 77
25	b	160/162 (99%)	158 (99%)	2 (1%)	69 86
26	c	140/146 (96%)	139 (99%)	1 (1%)	84 93
27	d	150/151 (99%)	148 (99%)	2 (1%)	69 86
28	e	125/154 (81%)	125 (100%)	0	100 100
29	f	155/156 (99%)	152 (98%)	3 (2%)	57 80
30	g	136/137 (99%)	131 (96%)	5 (4%)	34 65
31	h	84/107 (78%)	84 (100%)	0	100 100
32	i	102/105 (97%)	102 (100%)	0	100 100
33	j	54/129 (42%)	54 (100%)	0	100 100
34	k	104/118 (88%)	104 (100%)	0	100 100
35	l	108/110 (98%)	107 (99%)	1 (1%)	78 90
36	m	115/116 (99%)	115 (100%)	0	100 100
37	n	118/119 (99%)	116 (98%)	2 (2%)	60 82
38	o	46/47 (98%)	46 (100%)	0	100 100
39	p	81/88 (92%)	80 (99%)	1 (1%)	71 87
40	q	92/97 (95%)	91 (99%)	1 (1%)	73 88
41	r	108/111 (97%)	105 (97%)	3 (3%)	43 72
42	s	90/91 (99%)	89 (99%)	1 (1%)	73 88
43	t	94/103 (91%)	91 (97%)	3 (3%)	39 69
44	u	104/105 (99%)	104 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
45	v	78/82 (95%)	78 (100%)	0	100 100
46	w	69/71 (97%)	65 (94%)	4 (6%)	20 53
47	x	67/69 (97%)	67 (100%)	0	100 100
48	y	45/46 (98%)	44 (98%)	1 (2%)	52 78
49	z	46/116 (40%)	46 (100%)	0	100 100
All	All	6056/7091 (85%)	5984 (99%)	72 (1%)	72 87

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

Mol	Chain	Res	Type
37	n	120	ASN
48	y	43	ASN
40	q	79	ARG
43	t	47	CYS
13	H	166	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
18	M	109	HIS
32	i	98	ASN
19	N	25	HIS
25	b	55	HIS
37	n	74	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3198/3396 (94%)	642 (20%)	33 (1%)
2	B	120/121 (99%)	16 (13%)	0
3	C	157/158 (99%)	28 (17%)	1 (0%)
All	All	3475/3675 (94%)	686 (19%)	34 (0%)

5 of 686 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	A
1	A	22	G

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Mol	Chain	Res	Type
1	A	26	A
1	A	40	A
1	A	43	A

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	3218	A
1	A	3228	C
1	A	3353	G
1	A	1576	G
1	A	1554	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)

There are no ligands in this entry.

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.

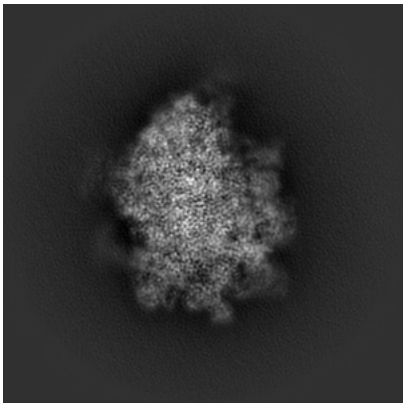
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-0374. These allow visual inspection of the internal detail of the map and identification of artifacts.

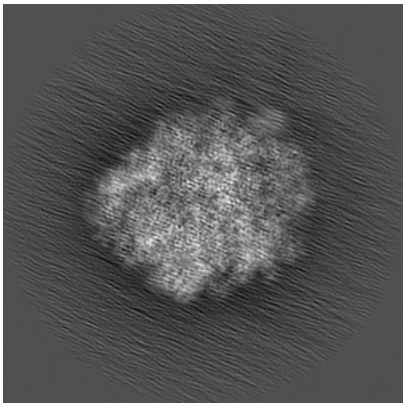
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

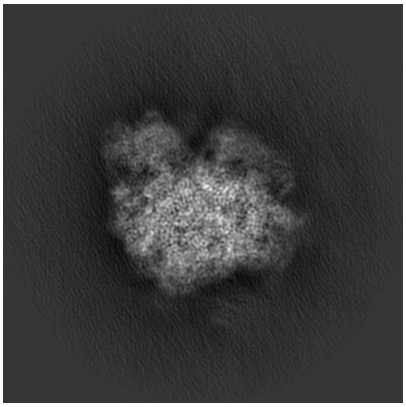
6.1.1 Primary map



X



Y

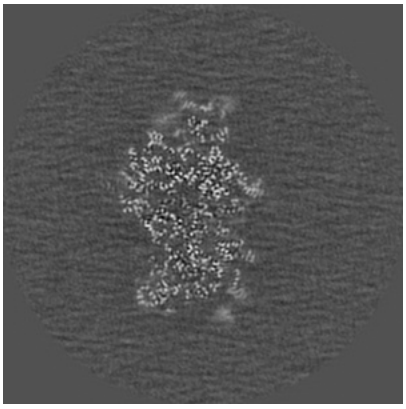


Z

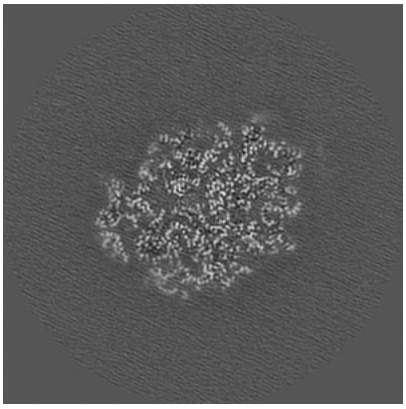
The images above show the map projected in three orthogonal directions.

6.2 Central slices

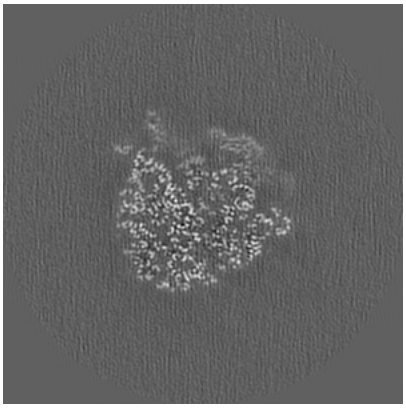
6.2.1 Primary map



X Index: 192



Y Index: 192

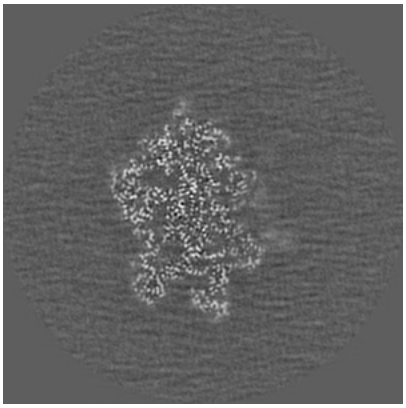


Z Index: 192

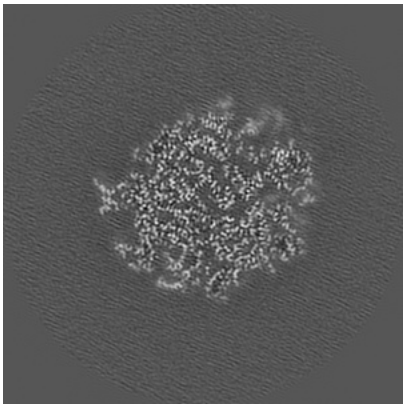
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

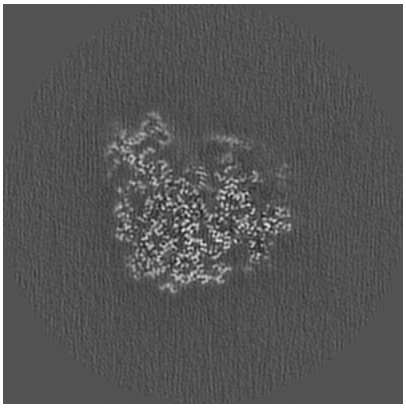
6.3.1 Primary map



X Index: 172



Y Index: 177



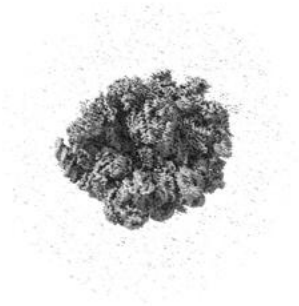
Z Index: 185

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

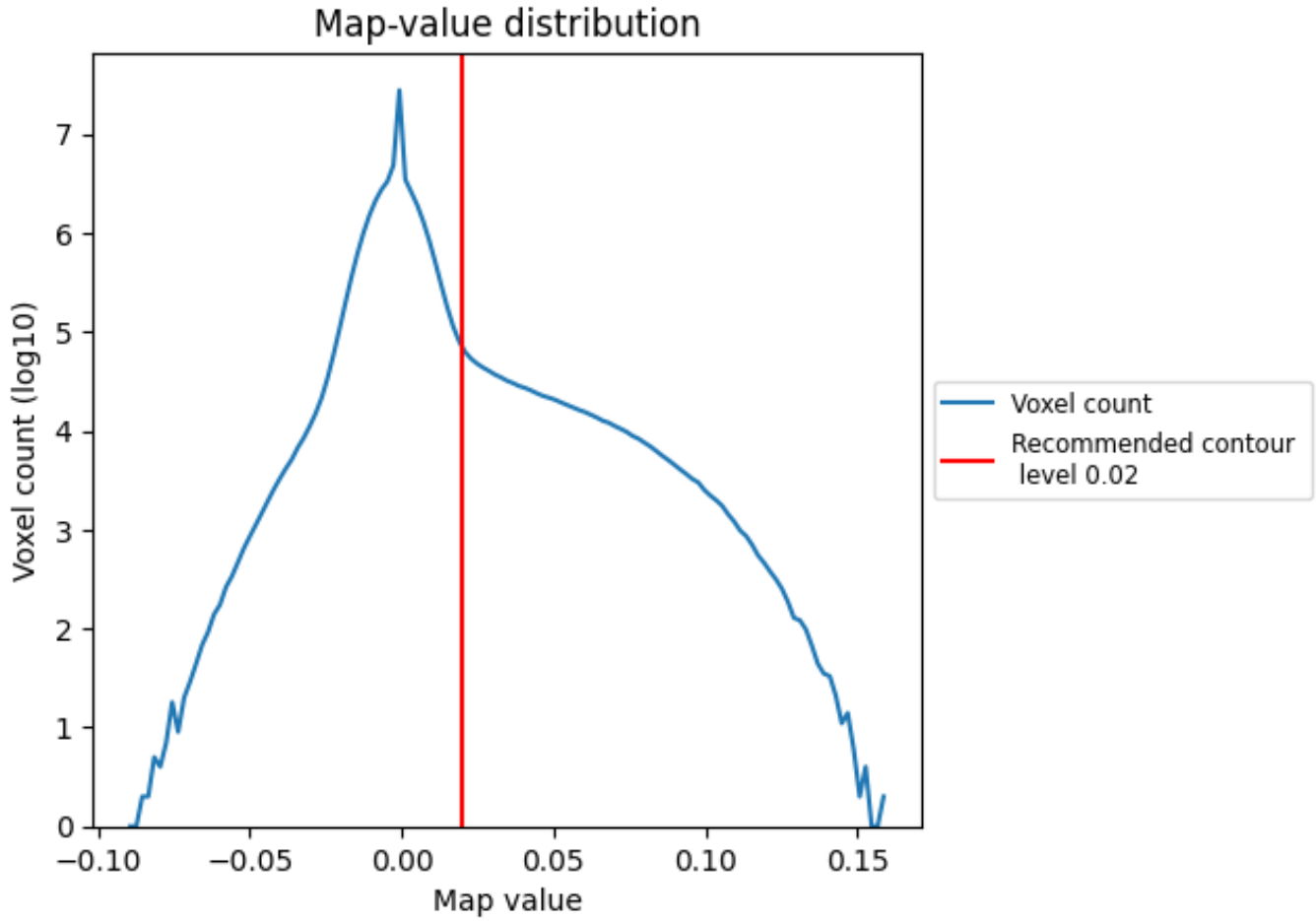
6.5 Mask visualisation (i)

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

7 Map analysis

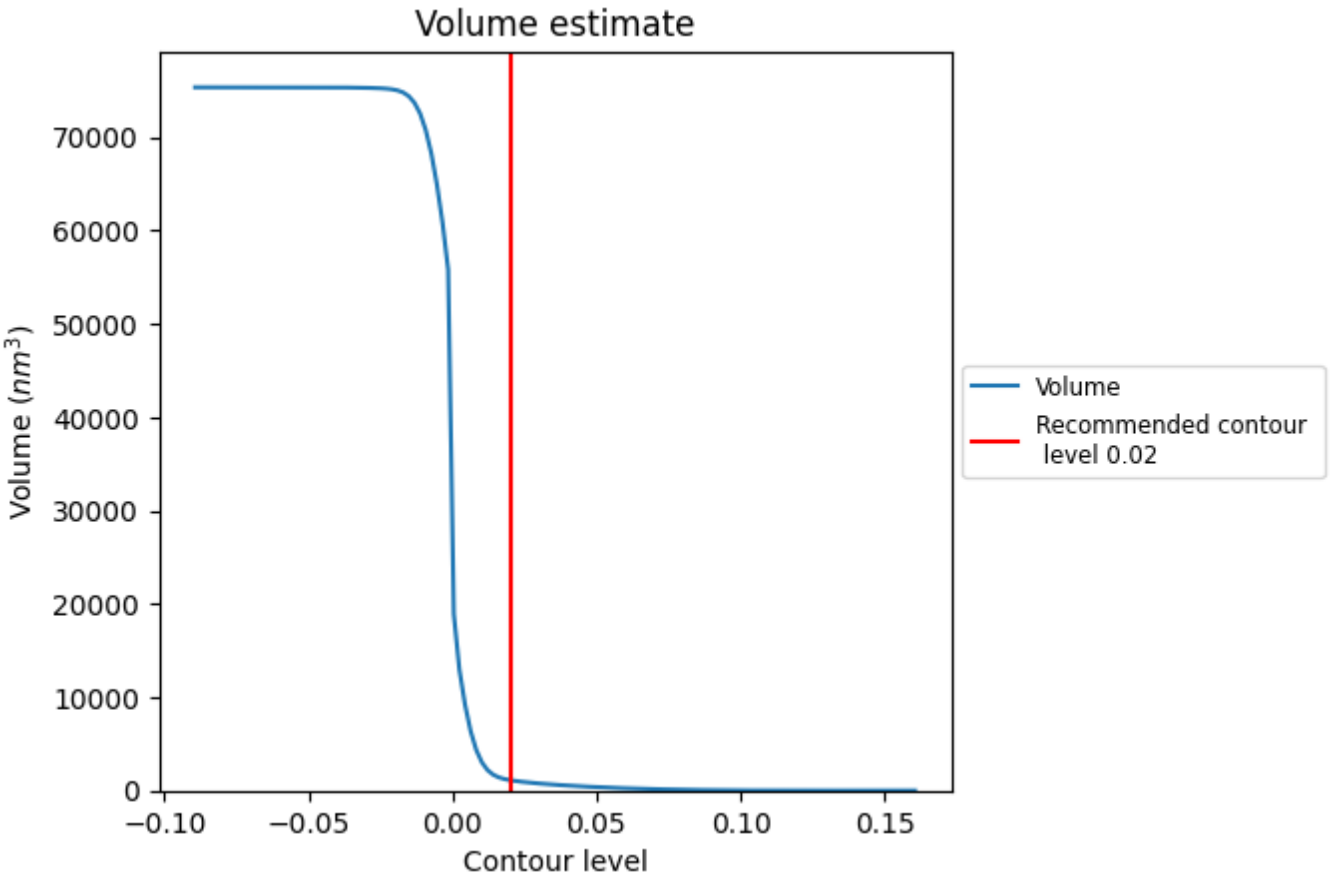
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

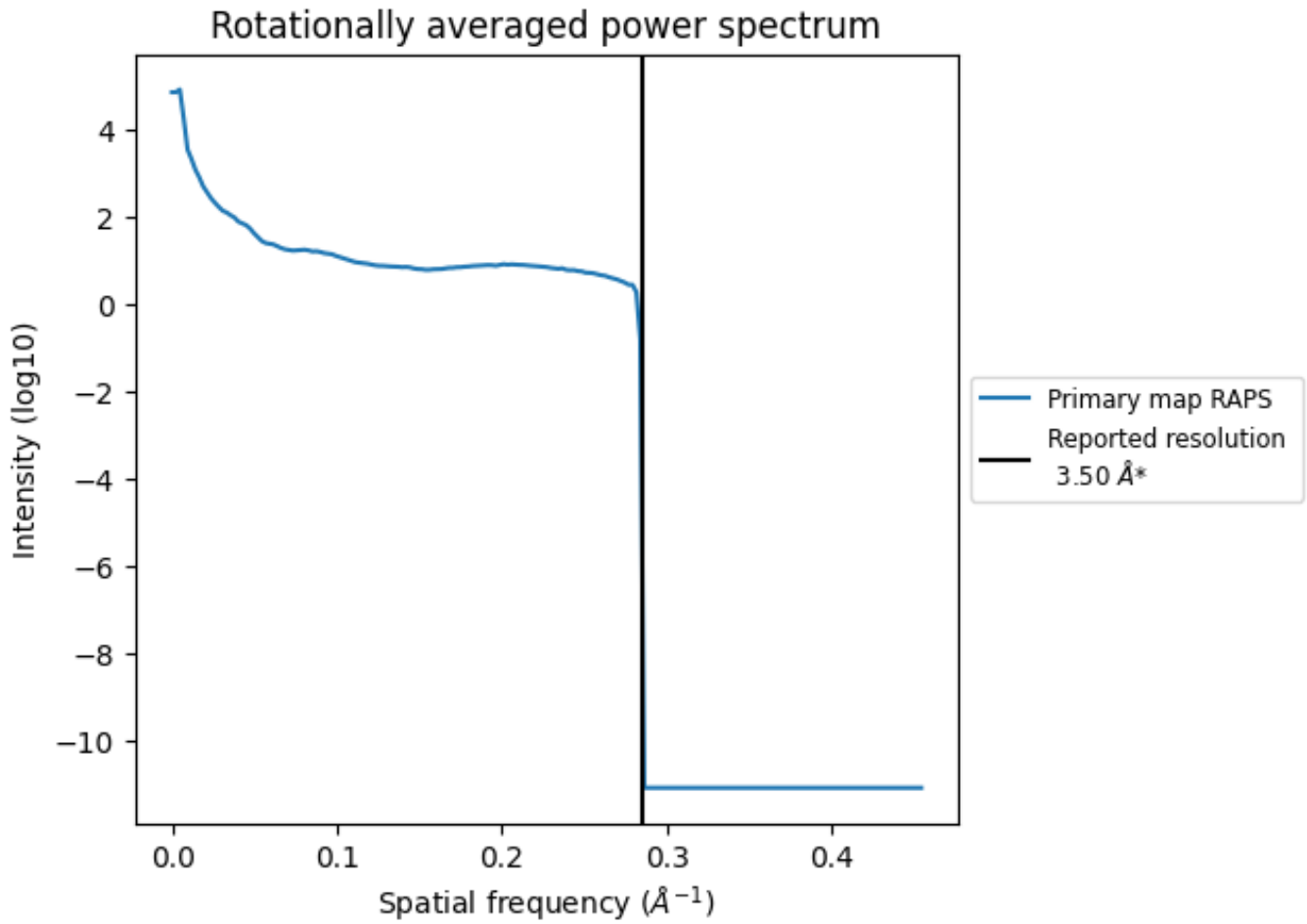
7.2 Volume estimate (i)



The volume at the recommended contour level is 1114 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)

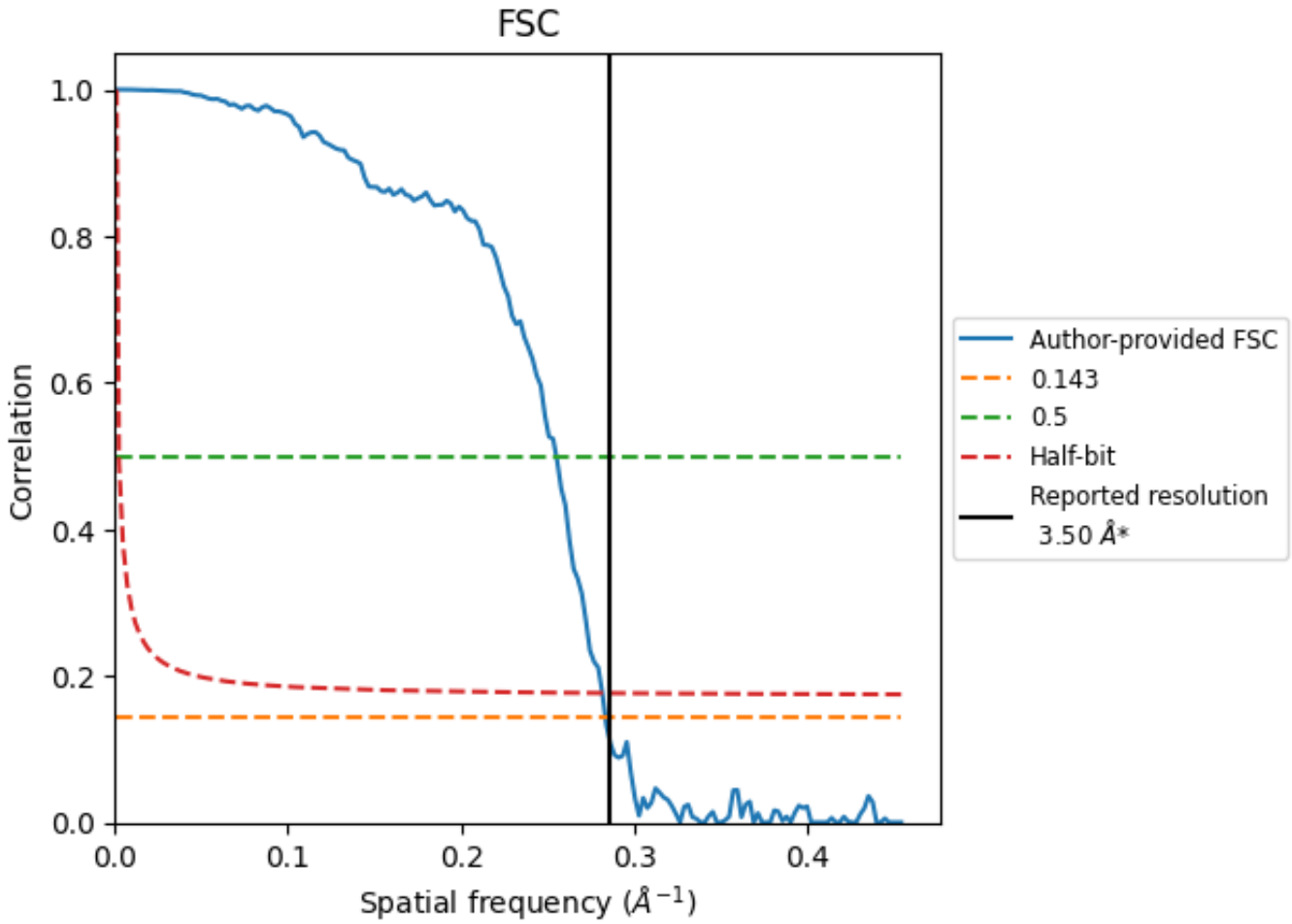


*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

8.2 Resolution estimates (i)

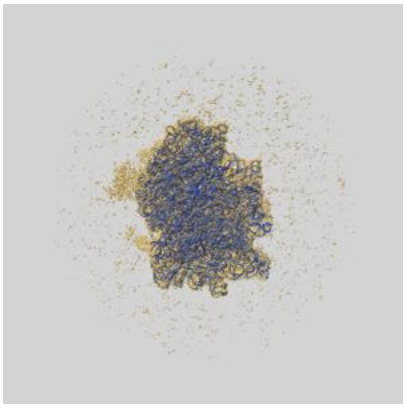
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.53	3.92	3.55
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

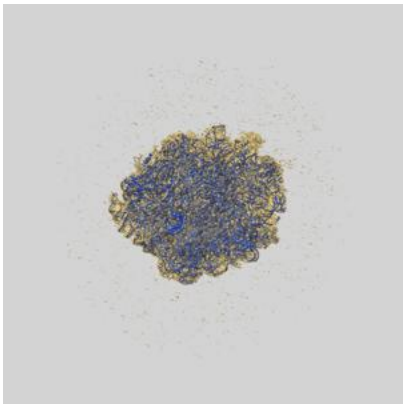
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-0374 and PDB model 6N8O. Per-residue inclusion information can be found in section 3 on page 13.

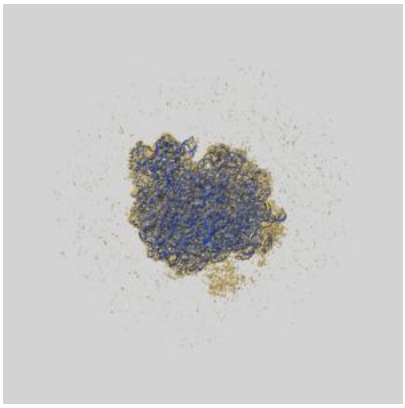
9.1 Map-model overlay



X



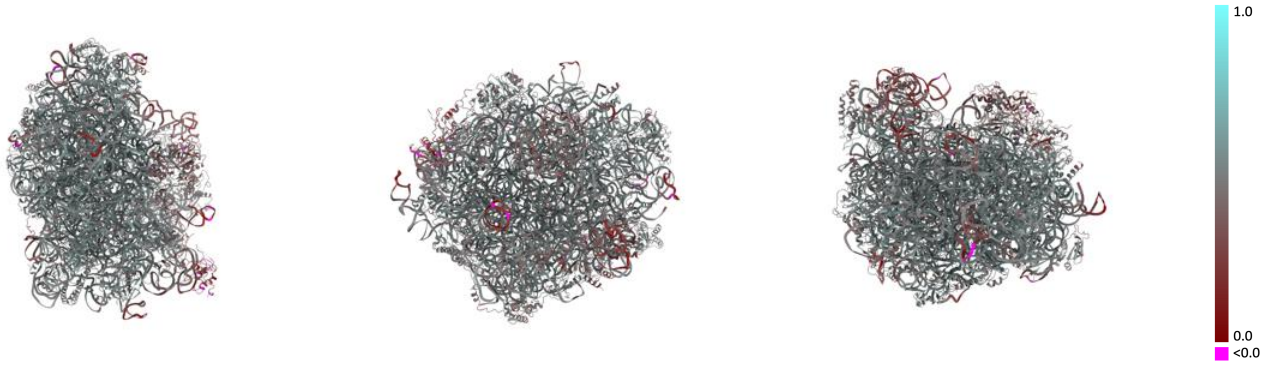
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02 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.

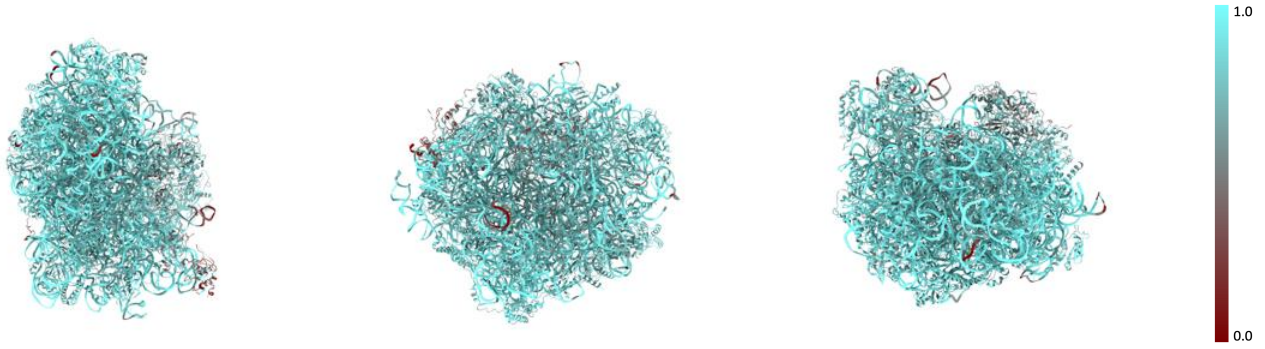
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

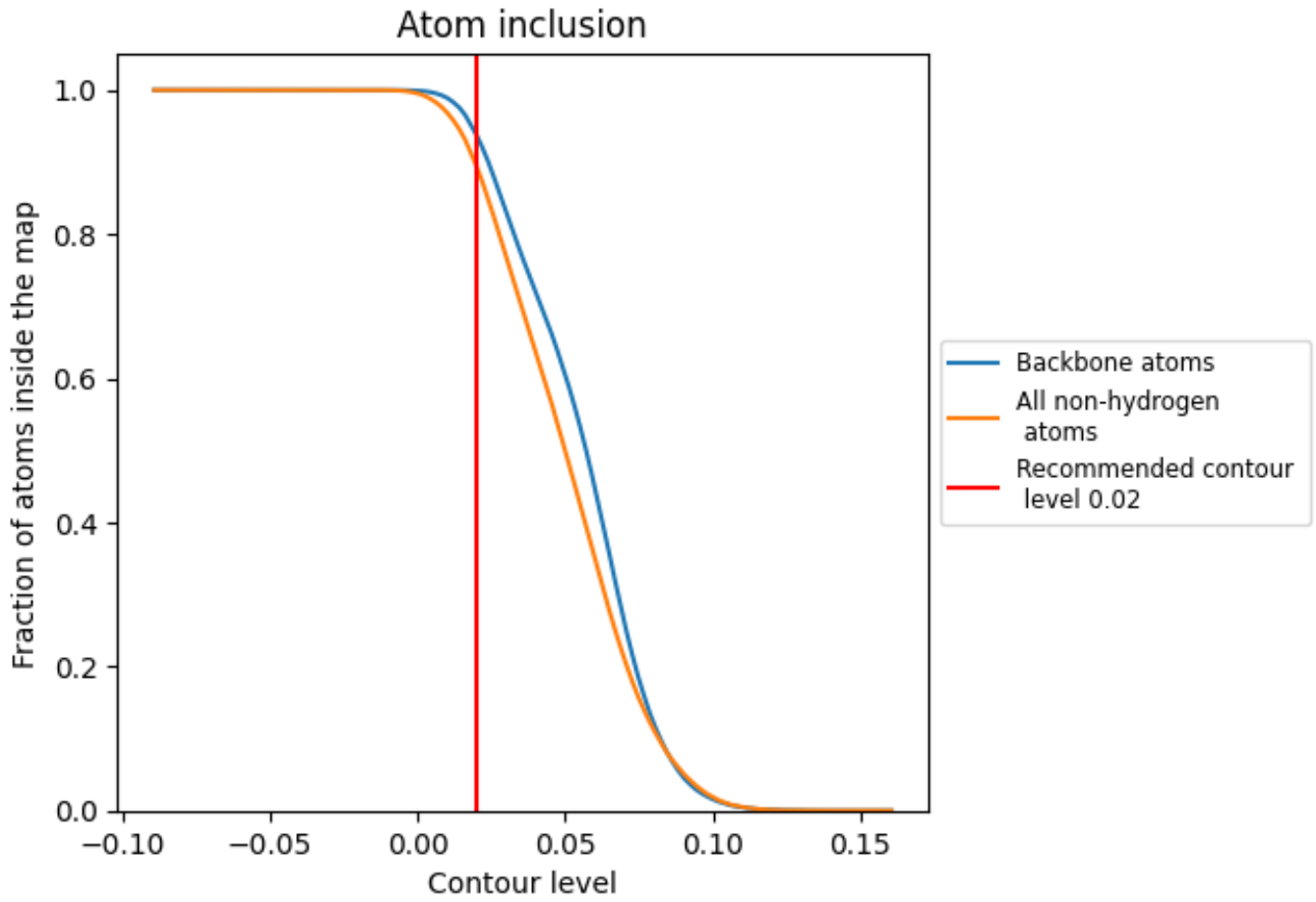
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 89% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8937	0.4930
A	0.9462	0.4950
B	0.9713	0.4980
C	0.9606	0.5030
D	0.8815	0.5360
E	0.8833	0.5230
F	0.8615	0.5110
G	0.8504	0.4670
H	0.8490	0.5020
I	0.8634	0.5040
J	0.8699	0.4960
K	0.8655	0.5120
L	0.3828	0.2450
M	0.8009	0.4380
N	0.8604	0.4980
O	0.8762	0.5080
Q	0.8225	0.5140
R	0.8781	0.5250
S	0.7524	0.3650
V	0.6645	0.4270
W	0.6448	0.3660
X	0.7912	0.4810
Y	0.5988	0.4140
Z	0.8222	0.4930
a	0.8858	0.5340
b	0.8679	0.5220
c	0.8474	0.5140
d	0.8573	0.5180
e	0.8789	0.5190
f	0.8618	0.5140
g	0.8556	0.5140
h	0.8499	0.4830
i	0.8297	0.5330
j	0.8580	0.5130
k	0.8567	0.5050

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Chain	Atom inclusion	Q-score
l	0.8579	0.5100
m	0.8814	0.5010
n	0.8870	0.5330
o	0.8252	0.4920
p	0.8510	0.4870
q	0.8440	0.5070
r	0.8529	0.5270
s	0.8831	0.5370
t	0.8413	0.5310
u	0.8865	0.5130
v	0.8450	0.4930
w	0.9061	0.5420
x	0.8034	0.4790
y	0.8627	0.5300
z	0.8579	0.5200