



wwPDB EM Validation Summary Report ⓘ

Apr 2, 2025 – 12:47 am BST

PDB ID : 6ENU / pdb_00006enu
EMDB ID : EMD-3903
Title : Polyproline-stalled ribosome in the presence of elongation-factor P (EF-P)
Authors : Huter, P.; Arenz, S.; Wilson, D.N.
Deposited on : 2017-10-06
Resolution : 3.10 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.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

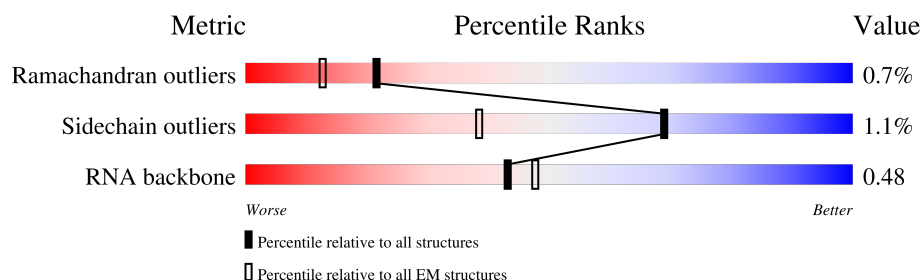
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	a	1539	<div> <div>7%</div> <div>75%</div> <div>23%</div> <div>.</div> </div>
2	b	218	<div> <div>70%</div> <div>97%</div> <div>.</div> </div>
3	c	206	<div> <div>13%</div> <div>99%</div> <div>.</div> </div>
4	d	205	<div> <div>30%</div> <div>98%</div> <div>.</div> </div>
5	e	157	<div> <div>10%</div> <div>97%</div> <div>..</div> </div>
6	f	100	<div> <div>31%</div> <div>97%</div> <div>.</div> </div>
7	g	151	<div> <div>31%</div> <div>99%</div> <div>.</div> </div>
8	h	129	<div> <div>9%</div> <div>98%</div> <div>.</div> </div>

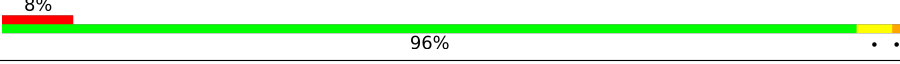
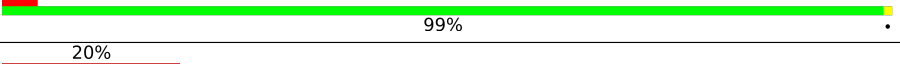
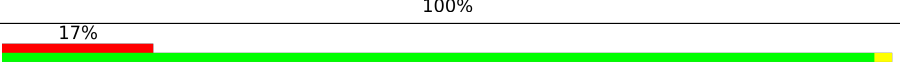
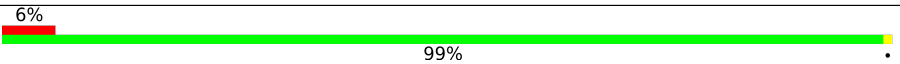
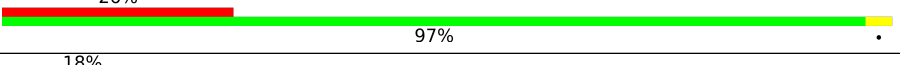
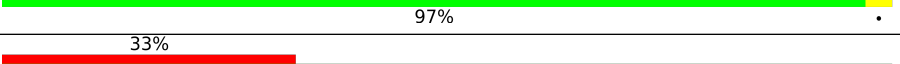
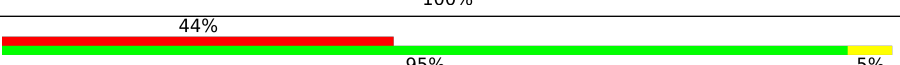
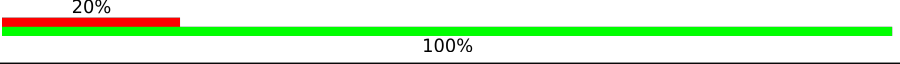
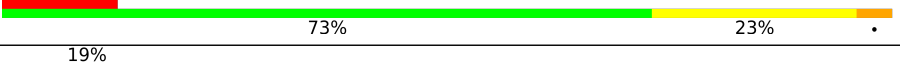
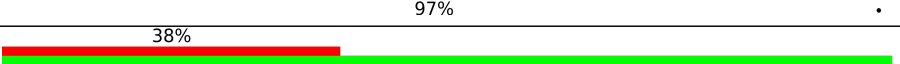
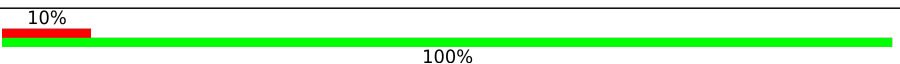
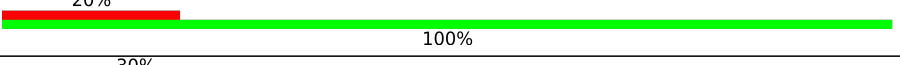
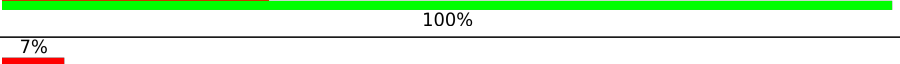
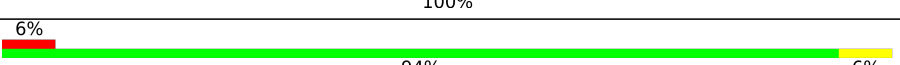
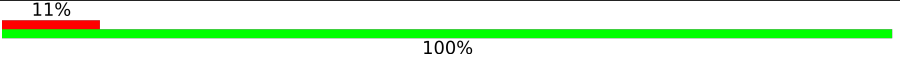
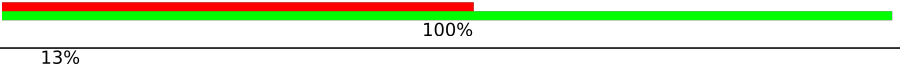
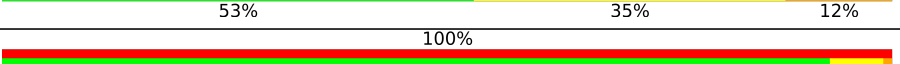
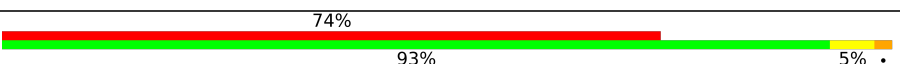





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Mol	Chain	Length	Quality of chain
9	i	127	23% 96% .
10	j	98	38% 99% .
11	k	116	26% 98% .
12	l	123	16% 96% .
13	m	114	20% 97% ..
14	n	101	16% 100%
15	o	88	17% 99% .
16	p	82	23% 99% .
17	q	80	31% 94% 6%
18	r	65	15% 100%
19	s	79	22% 99% .
20	t	85	16% 100%
21	u	65	80% 98% .
22	v	6	50% 50%
23	A	2903	9% 74% 22% ..
24	B	120	6% 78% 20% .
25	C	271	7% 99% .
26	D	209	12% 99% .
27	E	201	25% 100%
28	F	177	31% 98% .
29	G	176	41% 97% .
30	H	149	85% 100%
31	J	142	8% 99% .
32	K	122	13% 100%
33	L	143	17% 99% .

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Mol	Chain	Length	Quality of chain
34	M	136	
35	N	120	
36	O	116	
37	P	114	
38	Q	117	
39	R	103	
40	S	110	
41	T	93	
42	U	102	
43	V	94	
44	W	78	
45	X	77	
46	Y	63	
47	Z	58	
48	0	56	
49	1	50	
50	2	46	
51	3	64	
52	4	38	
53	6	66	
54	x	77	
55	7	224	
56	w	188	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 146475 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1539	Total	C	N	O	P	0	0
			33016	14725	6052	10700	1539		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP P0AG59

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	r	65	Total	C	N	O	0	0
			504	317	96	91		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	65	Total	C	N	O	S	0	0
			495	307	100	87	1		

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	v	6	Total	C	N	O	P	0	0
			126	56	22	42	6		

- Molecule 23 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A	2871	Total	C	N	O	P	0	0
			61641	27498	11350	19922	2871		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	747	C	U	conflict	GB 802133627
A	1847	G	A	conflict	GB 802133627
A	2069	A	G	conflict	GB 802133627
A	2104	U	C	conflict	GB 802133627

- Molecule 24 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	120	A	U	conflict	GB 1213441078

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 31 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 32 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 34 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 35 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 36 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 37 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 38 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 39 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 40 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 41 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 42 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	U	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 43 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	W	78	Total	C	N	O	S	0	0
			592	365	119	107	1		

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 47 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 50 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 53 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 54 is a RNA chain called Proline tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	77	Total	C	N	O	P	0	0
			1646	733	295	541	77		

- Molecule 55 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	224	Total	C	N	O	S	0	0
			1663	1039	303	315	6		

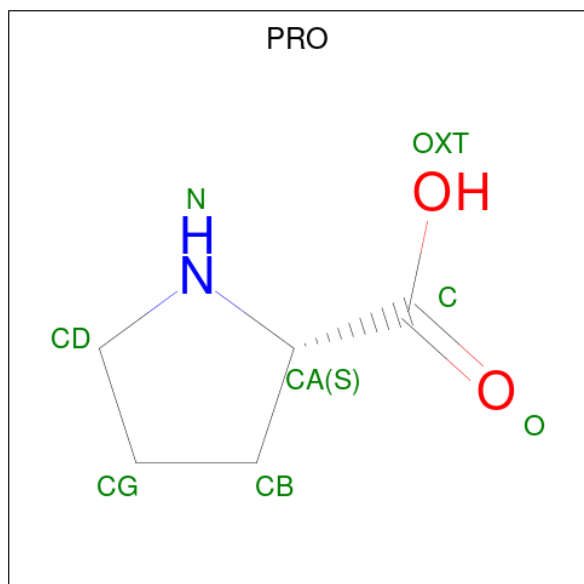
- Molecule 56 is a protein called Elongation factor P.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	w	188	Total	C	N	O	S	0	0
			1461	928	242	286	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	34	KEO	LYS	engineered mutation	UNP P0A6N4

- Molecule 57 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$).

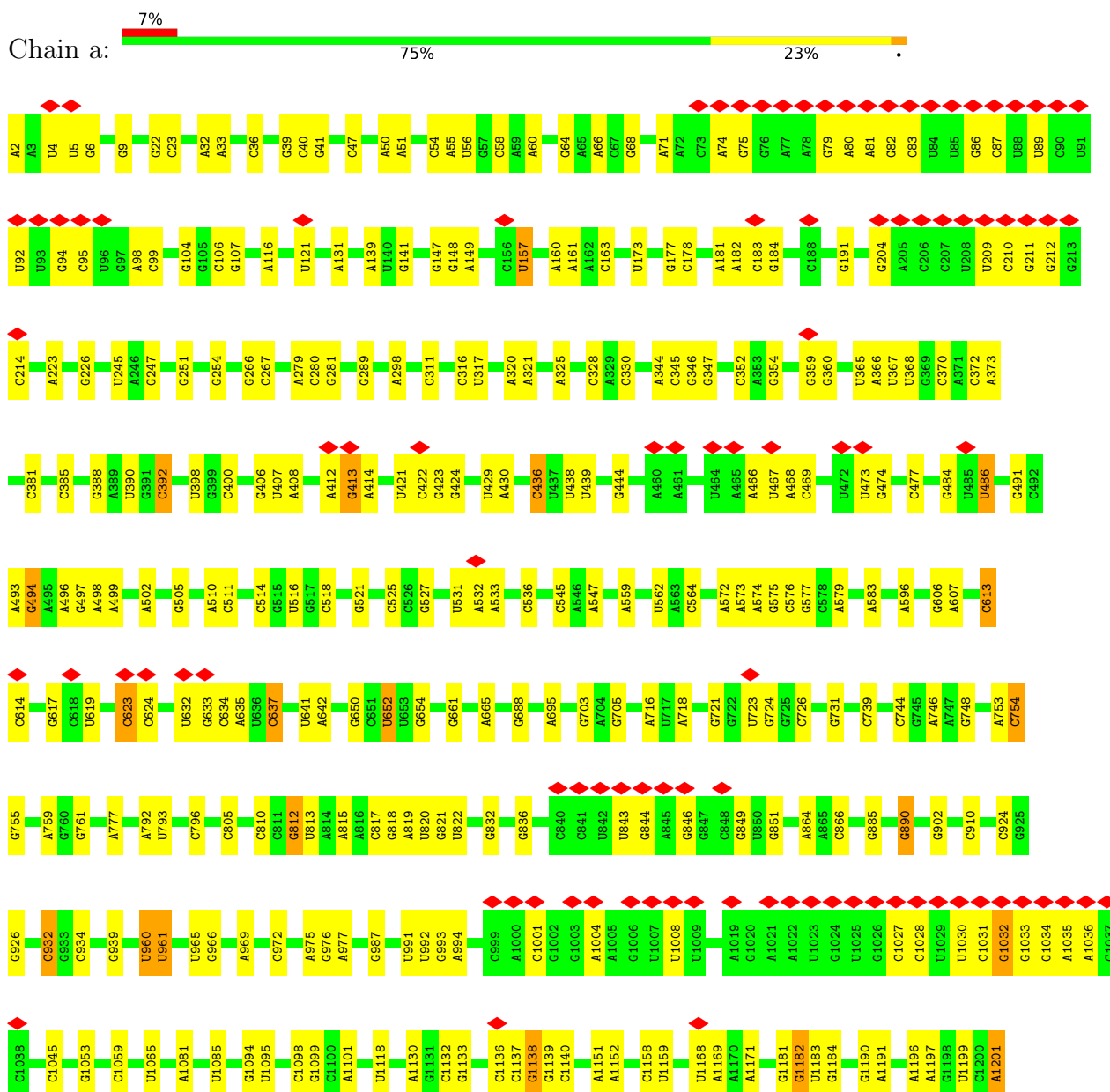


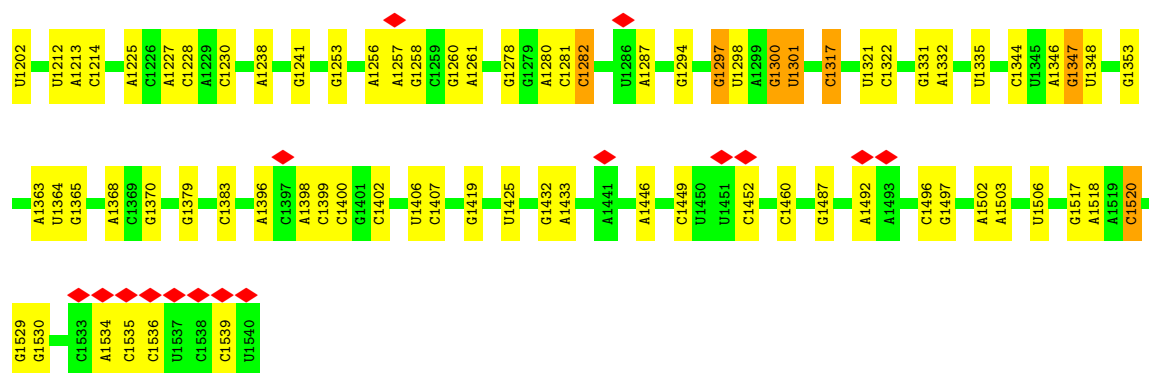
Mol	Chain	Residues	Atoms				AltConf
57	A	1	Total	C	N	O	0
			7	5	1	1	
57	x	1	Total	C	N	O	0
			7	5	1	1	

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: 16S ribosomal RNA

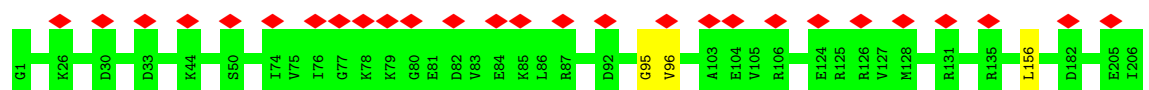




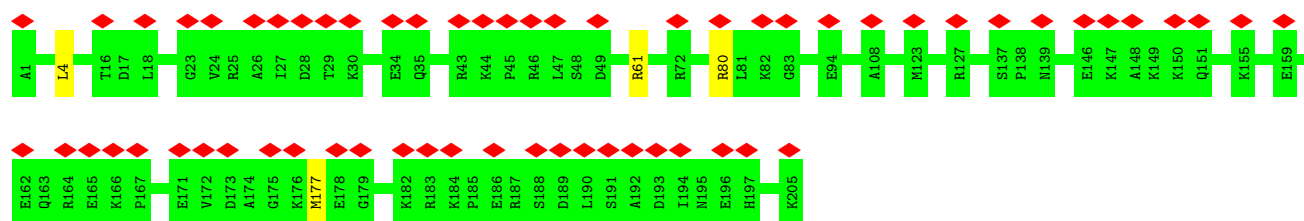
• Molecule 2: 30S ribosomal protein S2



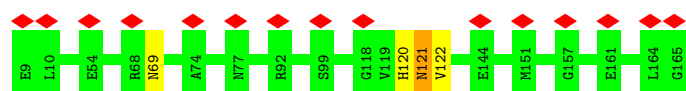
• Molecule 3: 30S ribosomal protein S3



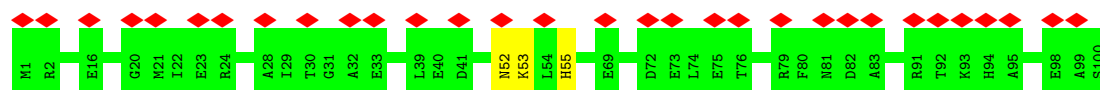
• Molecule 4: 30S ribosomal protein S4



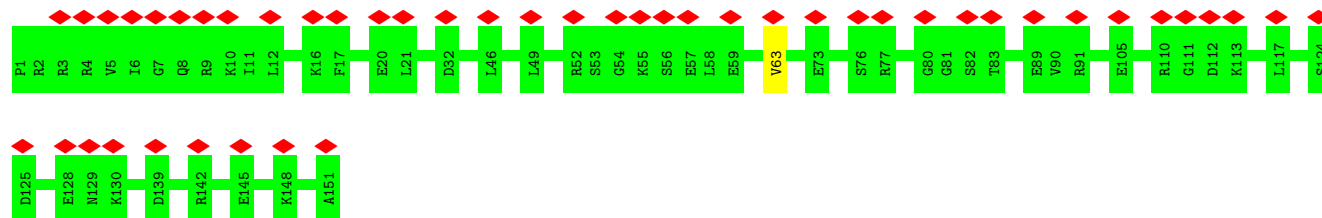
• Molecule 5: 30S ribosomal protein S5



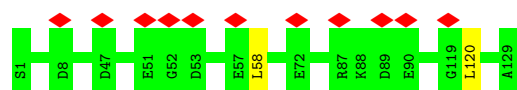
- Molecule 6: 30S ribosomal protein S6



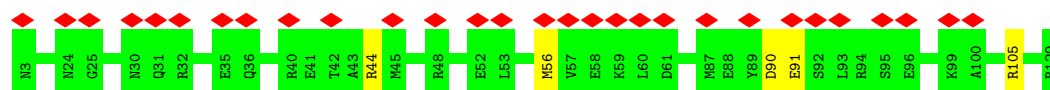
- Molecule 7: 30S ribosomal protein S7



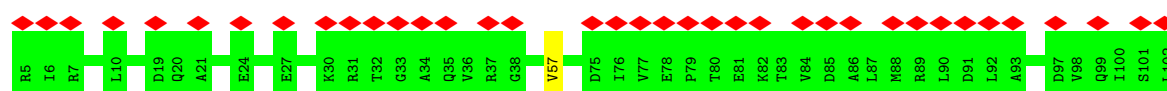
- Molecule 8: 30S ribosomal protein S8



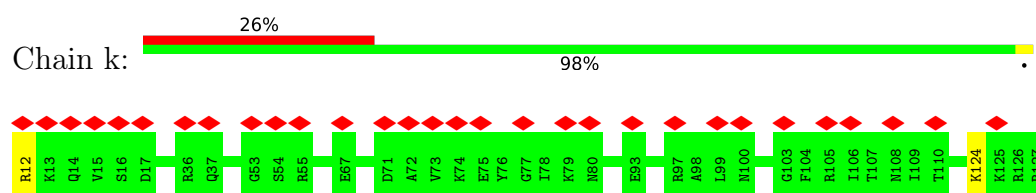
- Molecule 9: 30S ribosomal protein S9



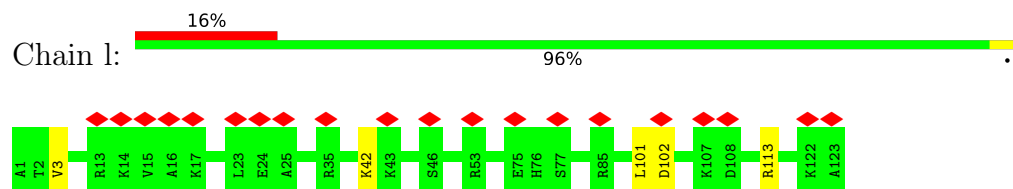
- Molecule 10: 30S ribosomal protein S10



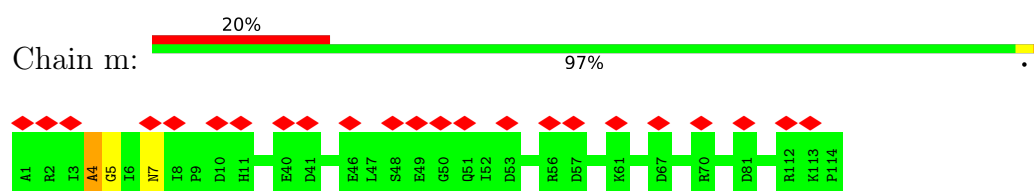
- Molecule 11: 30S ribosomal protein S11



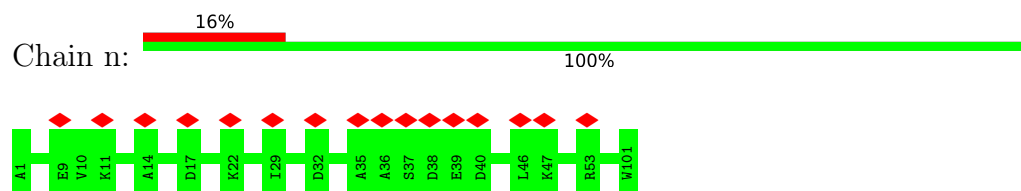
- Molecule 12: 30S ribosomal protein S12



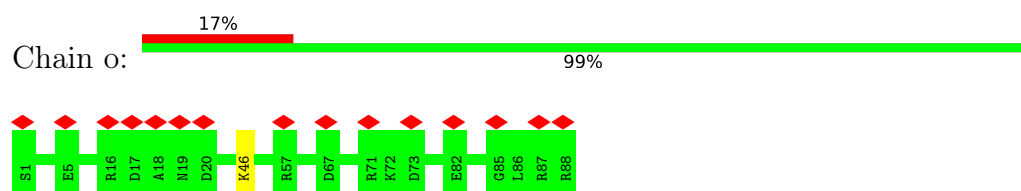
- Molecule 13: 30S ribosomal protein S13



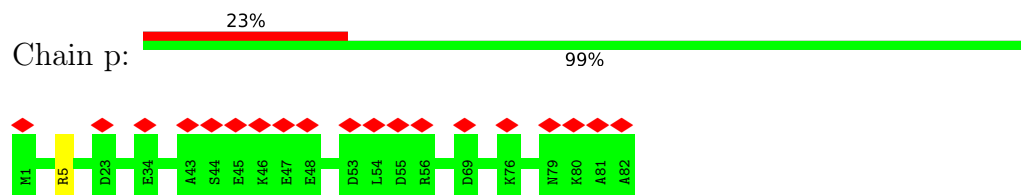
- Molecule 14: 30S ribosomal protein S14



- Molecule 15: 30S ribosomal protein S15

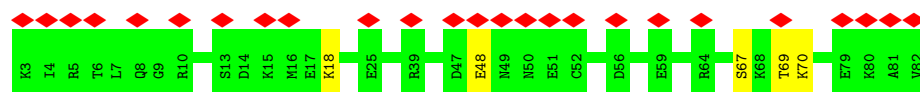


- Molecule 16: 30S ribosomal protein S16

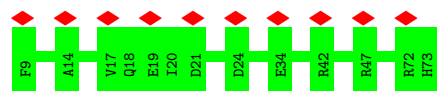


- Molecule 17: 30S ribosomal protein S17

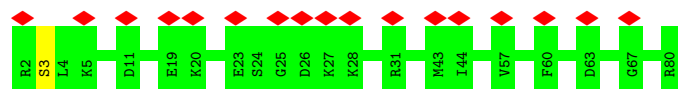




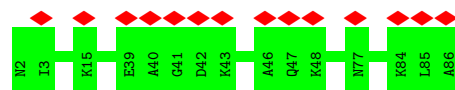
- Molecule 18: 30S ribosomal protein S18



- Molecule 19: 30S ribosomal protein S19



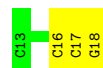
- Molecule 20: 30S ribosomal protein S20



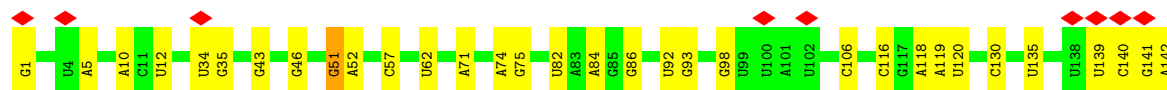
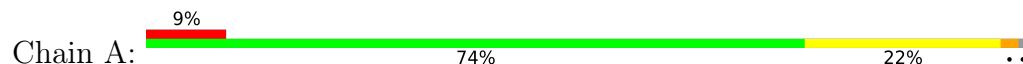
- Molecule 21: 30S ribosomal protein S21

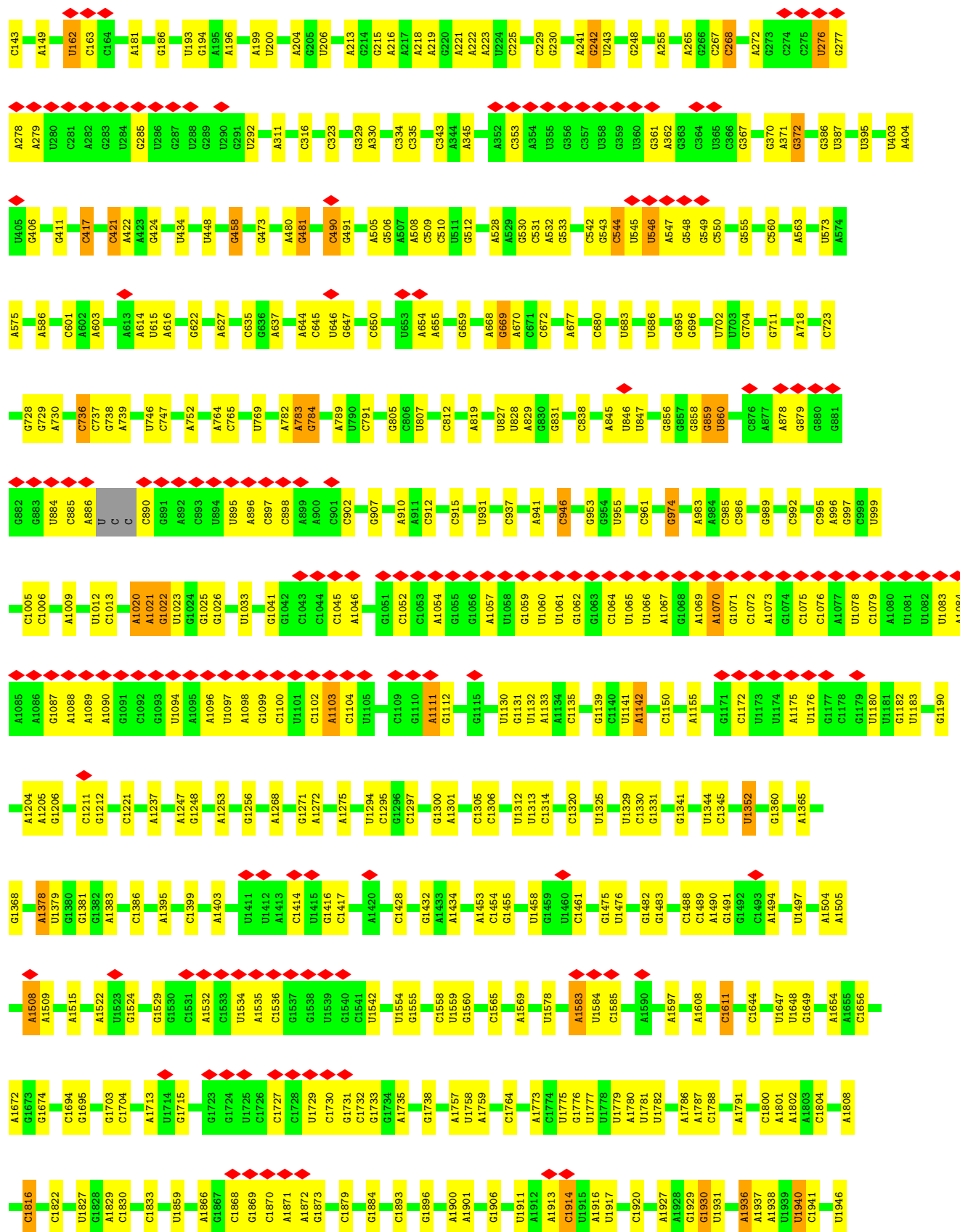


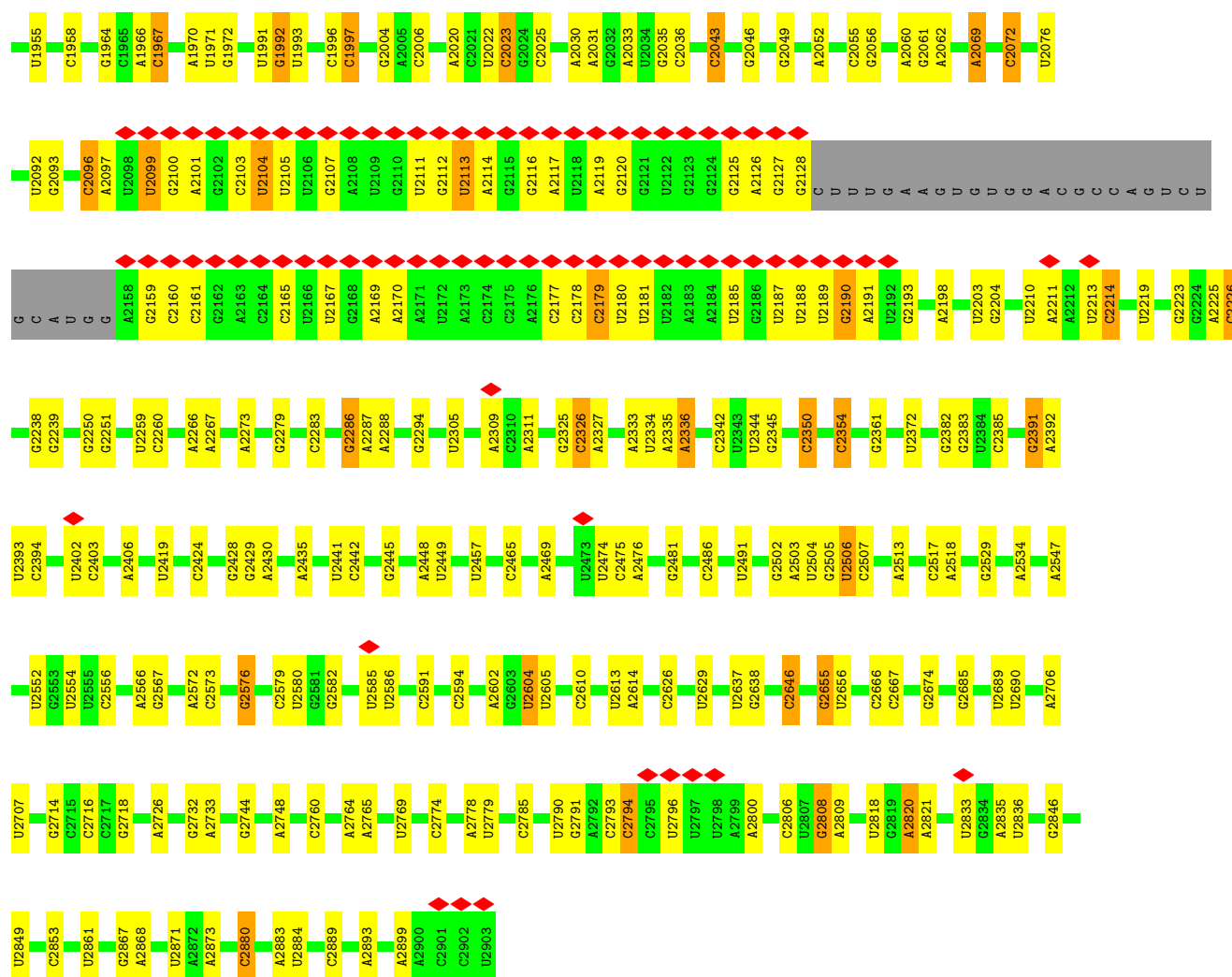
- Molecule 22: mRNA



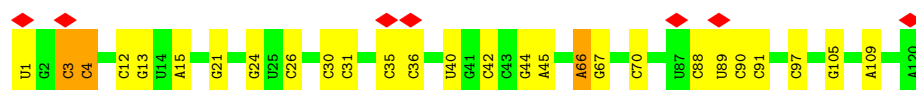
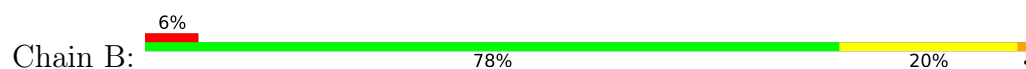
- Molecule 23: 23S Ribosomal RNA



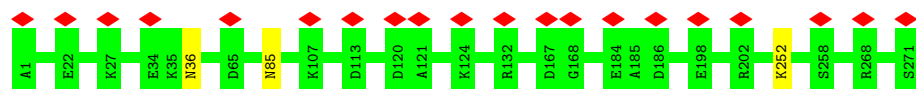




• Molecule 24: 5S Ribosomal RNA

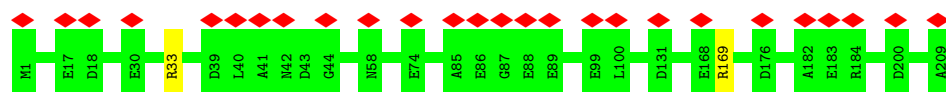


• Molecule 25: 50S ribosomal protein L2

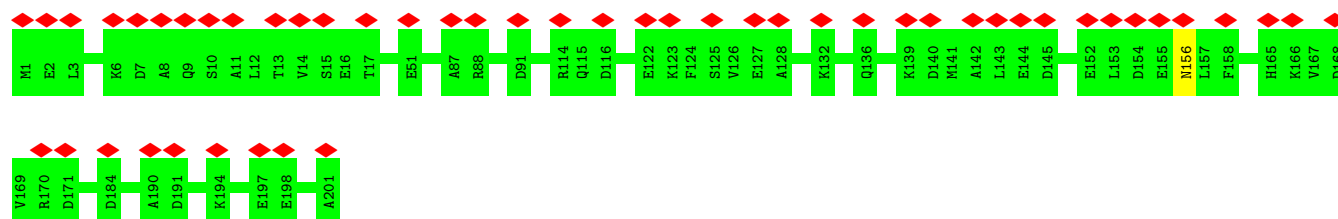


• Molecule 26: 50S ribosomal protein L3

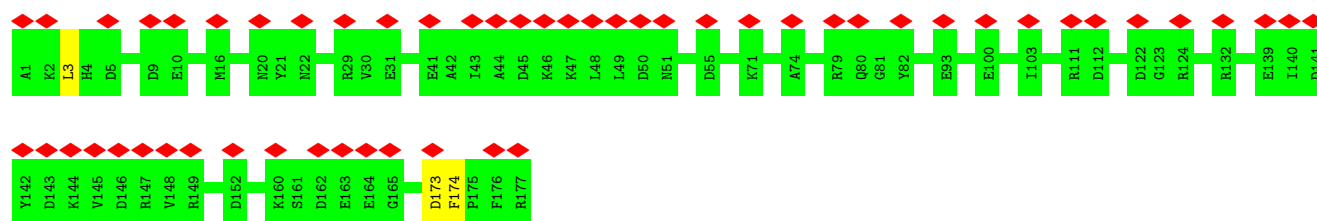




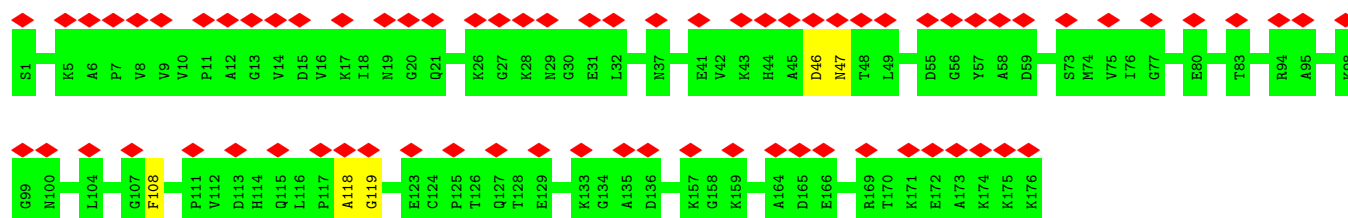
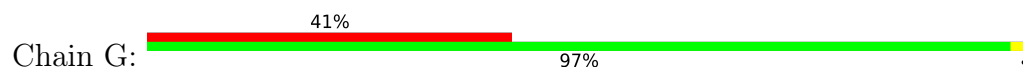
- Molecule 27: 50S ribosomal protein L4



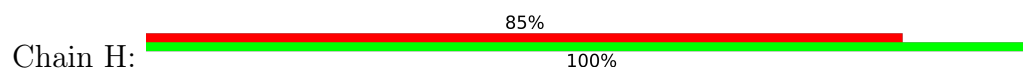
- Molecule 28: 50S ribosomal protein L5

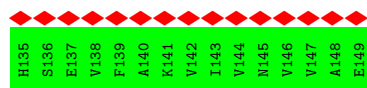


- Molecule 29: 50S ribosomal protein L6

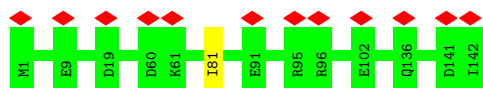


- Molecule 30: 50S ribosomal protein L9

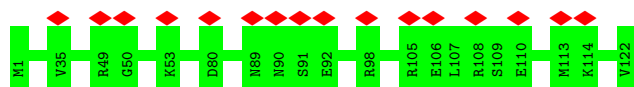




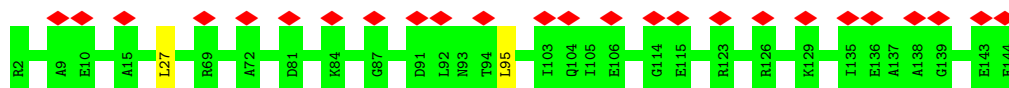
- Molecule 31: 50S ribosomal protein L13



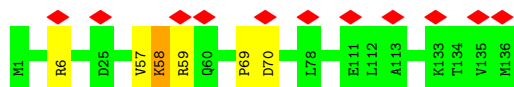
- Molecule 32: 50S ribosomal protein L14



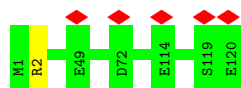
- Molecule 33: 50S ribosomal protein L15



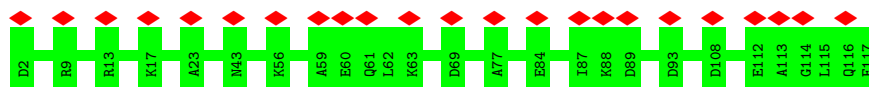
- Molecule 34: 50S ribosomal protein L16



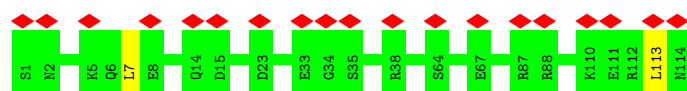
- Molecule 35: 50S ribosomal protein L17



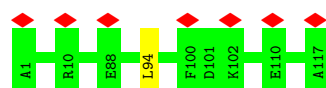
- Molecule 36: 50S ribosomal protein L18



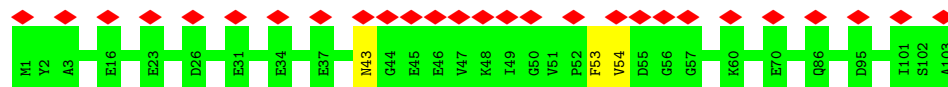
- Molecule 37: 50S ribosomal protein L19



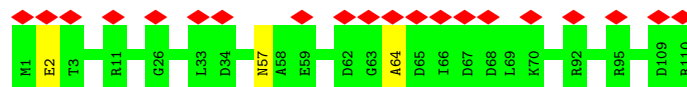
- Molecule 38: 50S ribosomal protein L20



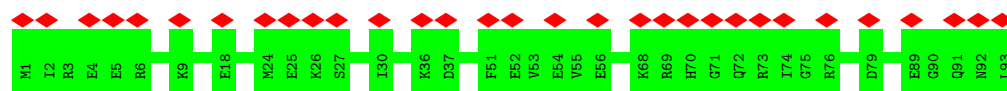
- Molecule 39: 50S ribosomal protein L21



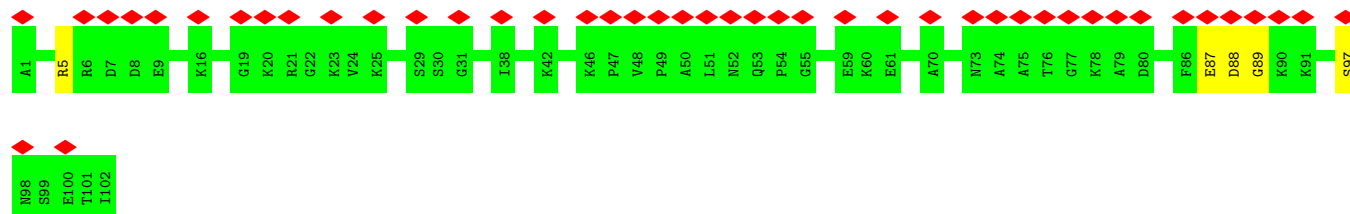
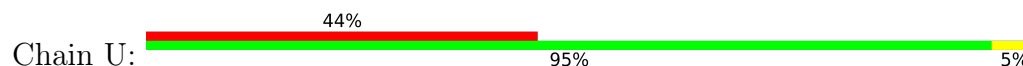
- Molecule 40: 50S ribosomal protein L22



- Molecule 41: 50S ribosomal protein L23

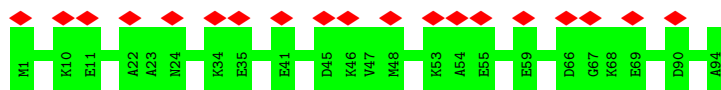


- Molecule 42: 50S ribosomal protein L24

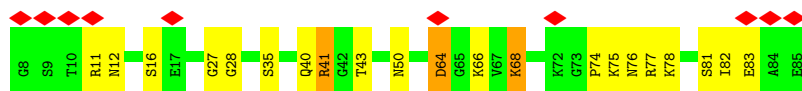
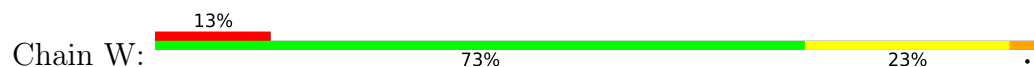


- Molecule 43: 50S ribosomal protein L25

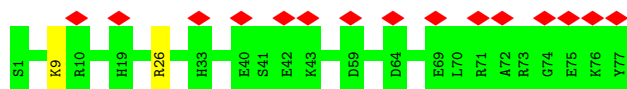




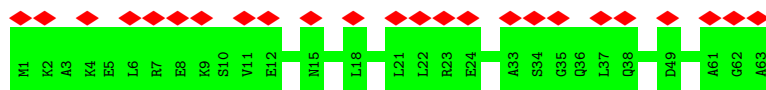
- Molecule 44: 50S ribosomal protein L27



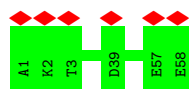
- Molecule 45: 50S ribosomal protein L28



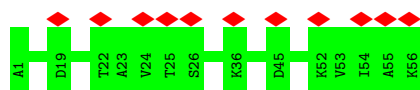
- Molecule 46: 50S ribosomal protein L29



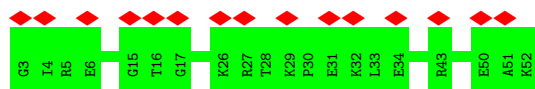
- Molecule 47: 50S ribosomal protein L30



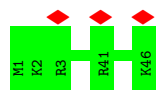
- Molecule 48: 50S ribosomal protein L32



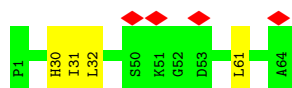
- Molecule 49: 50S ribosomal protein L33



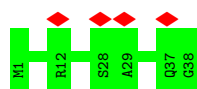
- Molecule 50: 50S ribosomal protein L34



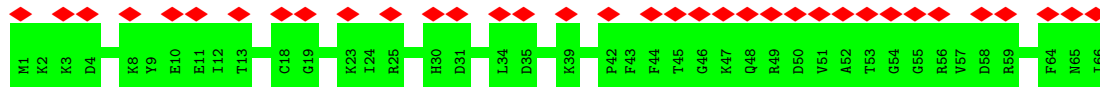
- Molecule 51: 50S ribosomal protein L35



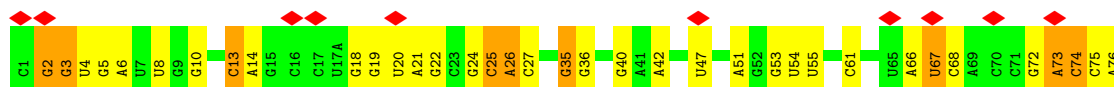
- Molecule 52: 50S ribosomal protein L36



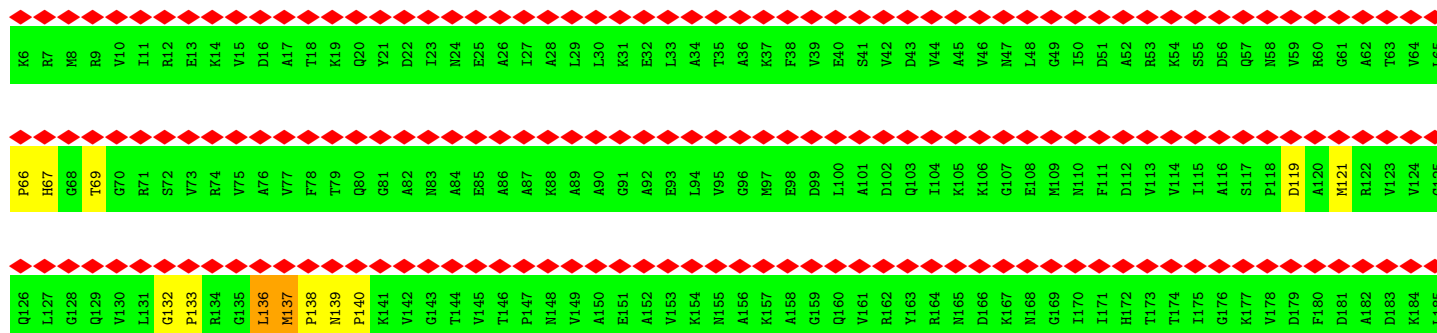
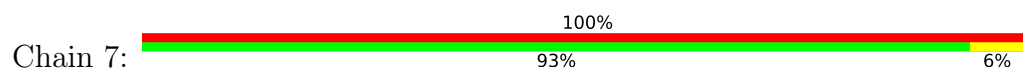
- Molecule 53: 50S ribosomal protein L31

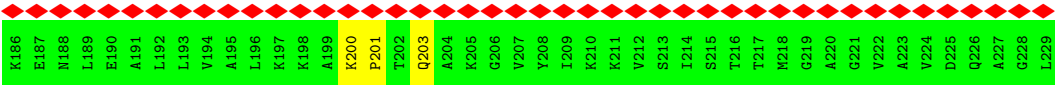


- Molecule 54: Proline tRNA

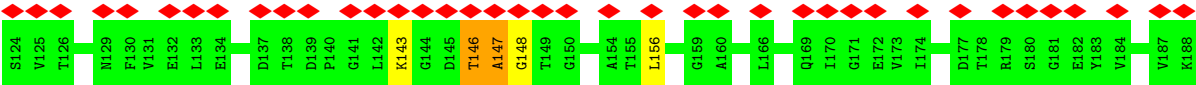
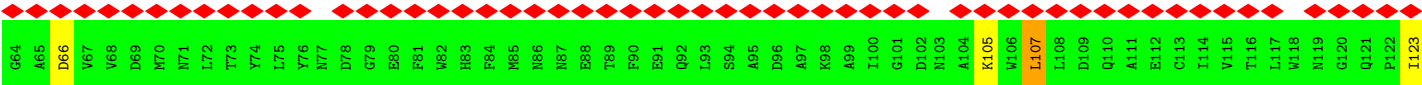
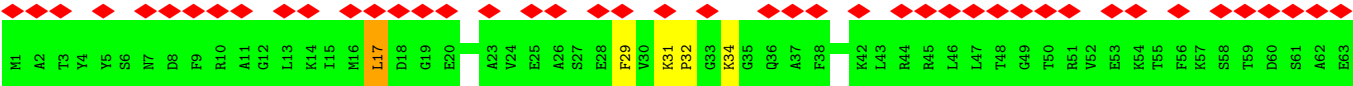
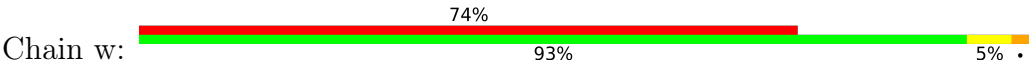


- Molecule 55: 50S ribosomal protein L1





• Molecule 56: Elongation factor P



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63665	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.669	Depositor
Minimum map value	-0.326	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.108	Depositor
Map size (\AA)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: KEO

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	0.81	2/36967 (0.0%)	1.07	146/57666 (0.3%)
2	b	0.34	0/1735	0.61	0/2338
3	c	0.40	0/1651	0.61	0/2225
4	d	0.40	0/1665	0.69	1/2227 (0.0%)
5	e	0.46	0/1154	0.70	1/1554 (0.1%)
6	f	0.40	0/835	0.67	0/1128
7	g	0.36	0/1195	0.64	0/1602
8	h	0.43	0/989	0.67	1/1326 (0.1%)
9	i	0.41	0/1034	0.67	0/1375
10	j	0.38	0/796	0.71	0/1077
11	k	0.40	0/885	0.65	0/1195
12	l	0.47	0/969	0.69	0/1300
13	m	0.37	0/892	0.70	0/1193
14	n	0.40	0/811	0.62	0/1081
15	o	0.36	0/722	0.60	0/964
16	p	0.46	0/659	0.66	0/884
17	q	0.41	0/657	0.65	0/881
18	r	0.41	0/511	0.62	0/689
19	s	0.42	0/652	0.63	0/877
20	t	0.35	0/671	0.57	0/888
21	u	0.37	0/500	0.71	0/668
22	v	0.78	0/139	1.14	1/214 (0.5%)
23	A	0.83	3/69039 (0.0%)	1.07	268/107701 (0.2%)
24	B	0.72	1/2876 (0.0%)	1.08	13/4483 (0.3%)
25	C	0.49	0/2121	0.65	0/2852
26	D	0.44	0/1586	0.62	0/2134
27	E	0.39	0/1571	0.57	0/2113
28	F	0.40	0/1434	0.62	1/1926 (0.1%)
29	G	0.35	0/1343	0.57	0/1816
30	H	0.30	0/1122	0.58	0/1515
31	J	0.41	0/1152	0.57	0/1551
32	K	0.46	0/947	0.64	0/1268

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	L	0.40	0/1054	0.69	1/1403 (0.1%)
34	M	0.44	0/1093	0.66	1/1460 (0.1%)
35	N	0.39	0/973	0.66	0/1301
36	O	0.39	0/902	0.59	0/1209
37	P	0.43	0/929	0.64	2/1242 (0.2%)
38	Q	0.47	0/960	0.61	1/1278 (0.1%)
39	R	0.41	0/829	0.64	0/1107
40	S	0.41	0/864	0.65	0/1156
41	T	0.36	0/744	0.60	0/994
42	U	0.36	0/787	0.60	0/1051
43	V	0.38	0/766	0.59	0/1025
44	W	0.58	0/599	0.82	0/792
45	X	0.46	1/635 (0.2%)	0.57	0/848
46	Y	0.32	0/510	0.55	0/677
47	Z	0.36	0/453	0.63	0/605
48	0	0.43	0/450	0.57	0/599
49	1	0.40	0/416	0.58	0/554
50	2	0.46	0/380	0.61	0/498
51	3	0.45	0/513	0.76	1/676 (0.1%)
52	4	0.45	0/303	0.66	0/397
53	6	0.31	0/531	0.57	0/709
54	x	0.72	1/1839 (0.1%)	1.34	26/2866 (0.9%)
55	7	0.28	0/1678	0.74	3/2262 (0.1%)
56	w	0.41	1/1470 (0.1%)	0.78	4/1992 (0.2%)
All	All	0.72	9/158958 (0.0%)	0.98	471/237412 (0.2%)

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
2	b	0	3
3	c	0	2
5	e	0	1
6	f	0	1
7	g	0	1
9	i	0	1
11	k	0	1
12	l	0	2
13	m	0	1
17	q	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
19	s	0	1
21	u	0	1
28	F	0	2
29	G	0	2
31	J	0	1
34	M	0	2
39	R	0	1
42	U	0	4
51	3	0	1
55	7	0	1
56	w	0	3
All	All	0	35

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	x	74	C	O3'-P	-11.19	1.47	1.61
1	a	2	A	OP3-P	-10.69	1.48	1.61
23	A	1	G	OP3-P	-10.60	1.48	1.61
24	B	1	U	OP3-P	-10.53	1.48	1.61
23	A	528	A	N9-C4	-6.63	1.33	1.37

The worst 5 of 471 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	7	132	GLY	C-N-CD	-15.98	85.44	120.60
55	7	139	ASN	C-N-CD	-15.65	86.17	120.60
54	x	74	C	OP1-P-OP2	14.87	141.90	119.60
54	x	73	A	OP1-P-O3'	-14.14	74.09	105.20
54	x	73	A	OP2-P-O3'	-13.31	75.92	105.20

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	b	15	PHE	Peptide
2	b	18	GLN	Peptide
2	b	30	ILE	Peptide
3	c	95	GLY	Peptide
3	c	96	VAL	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	
2	b	216/218 (99%)	191 (88%)	25 (12%)	0	100	100
3	c	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
4	d	203/205 (99%)	176 (87%)	27 (13%)	0	100	100
5	e	155/157 (99%)	132 (85%)	21 (14%)	2 (1%)	10	36
6	f	98/100 (98%)	82 (84%)	14 (14%)	2 (2%)	6	26
7	g	149/151 (99%)	130 (87%)	19 (13%)	0	100	100
8	h	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
9	i	125/127 (98%)	101 (81%)	22 (18%)	2 (2%)	8	31
10	j	96/98 (98%)	83 (86%)	12 (12%)	1 (1%)	13	42
11	k	114/116 (98%)	96 (84%)	18 (16%)	0	100	100
12	l	121/123 (98%)	90 (74%)	29 (24%)	2 (2%)	7	30
13	m	112/114 (98%)	97 (87%)	13 (12%)	2 (2%)	7	29
14	n	99/101 (98%)	86 (87%)	13 (13%)	0	100	100
15	o	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	11	38
16	p	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
17	q	78/80 (98%)	65 (83%)	12 (15%)	1 (1%)	10	36
18	r	63/65 (97%)	56 (89%)	7 (11%)	0	100	100
19	s	77/79 (98%)	72 (94%)	5 (6%)	0	100	100
20	t	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
21	u	63/65 (97%)	47 (75%)	16 (25%)	0	100	100
25	C	269/271 (99%)	250 (93%)	19 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	D	207/209 (99%)	191 (92%)	16 (8%)	0	100	100
27	E	199/201 (99%)	180 (90%)	19 (10%)	0	100	100
28	F	175/177 (99%)	157 (90%)	18 (10%)	0	100	100
29	G	174/176 (99%)	155 (89%)	16 (9%)	3 (2%)	7	30
30	H	147/149 (99%)	127 (86%)	20 (14%)	0	100	100
31	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
32	K	120/122 (98%)	107 (89%)	13 (11%)	0	100	100
33	L	141/143 (99%)	120 (85%)	21 (15%)	0	100	100
34	M	134/136 (98%)	125 (93%)	6 (4%)	3 (2%)	5	24
35	N	118/120 (98%)	104 (88%)	14 (12%)	0	100	100
36	O	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
37	P	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
38	Q	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
39	R	101/103 (98%)	87 (86%)	13 (13%)	1 (1%)	13	42
40	S	108/110 (98%)	99 (92%)	7 (6%)	2 (2%)	6	27
41	T	91/93 (98%)	78 (86%)	13 (14%)	0	100	100
42	U	100/102 (98%)	83 (83%)	16 (16%)	1 (1%)	13	42
43	V	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
44	W	76/78 (97%)	55 (72%)	13 (17%)	8 (10%)	0	2
45	X	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
46	Y	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
47	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
48	0	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
49	1	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
50	2	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
51	3	62/64 (97%)	54 (87%)	6 (10%)	2 (3%)	3	18
52	4	36/38 (95%)	30 (83%)	6 (17%)	0	100	100
53	6	64/66 (97%)	54 (84%)	10 (16%)	0	100	100
55	7	222/224 (99%)	181 (82%)	34 (15%)	7 (3%)	3	18
56	w	185/188 (98%)	153 (83%)	28 (15%)	4 (2%)	5	24
All	All	5989/6092 (98%)	5301 (88%)	644 (11%)	44 (1%)	21	51

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	f	53	LYS
17	q	70	LYS
29	G	47	ASN
42	U	89	GLY
44	W	27	GLY

5.3.2 Protein sidechains ⓘ

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	
2	b	180/180 (100%)	176 (98%)	4 (2%)	47	71
3	c	170/170 (100%)	169 (99%)	1 (1%)	84	91
4	d	172/172 (100%)	169 (98%)	3 (2%)	56	78
5	e	114/119 (96%)	113 (99%)	1 (1%)	75	88
6	f	87/87 (100%)	87 (100%)	0	100	100
7	g	124/124 (100%)	124 (100%)	0	100	100
8	h	104/104 (100%)	103 (99%)	1 (1%)	73	86
9	i	105/105 (100%)	103 (98%)	2 (2%)	52	75
10	j	86/86 (100%)	86 (100%)	0	100	100
11	k	89/89 (100%)	88 (99%)	1 (1%)	70	84
12	l	103/103 (100%)	102 (99%)	1 (1%)	73	86
13	m	92/92 (100%)	91 (99%)	1 (1%)	70	84
14	n	79/83 (95%)	79 (100%)	0	100	100
15	o	76/76 (100%)	76 (100%)	0	100	100
16	p	65/65 (100%)	64 (98%)	1 (2%)	60	80
17	q	74/74 (100%)	73 (99%)	1 (1%)	62	81
18	r	48/56 (86%)	48 (100%)	0	100	100
19	s	70/70 (100%)	70 (100%)	0	100	100
20	t	65/65 (100%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	u	44/55 (80%)	44 (100%)	0	100	100
25	C	216/216 (100%)	213 (99%)	3 (1%)	62	81
26	D	164/164 (100%)	162 (99%)	2 (1%)	67	83
27	E	165/165 (100%)	164 (99%)	1 (1%)	84	91
28	F	148/148 (100%)	148 (100%)	0	100	100
29	G	137/137 (100%)	137 (100%)	0	100	100
30	H	114/114 (100%)	114 (100%)	0	100	100
31	J	116/116 (100%)	116 (100%)	0	100	100
32	K	103/103 (100%)	103 (100%)	0	100	100
33	L	102/102 (100%)	101 (99%)	1 (1%)	73	86
34	M	109/109 (100%)	108 (99%)	1 (1%)	75	88
35	N	100/100 (100%)	99 (99%)	1 (1%)	73	86
36	O	86/86 (100%)	86 (100%)	0	100	100
37	P	99/99 (100%)	99 (100%)	0	100	100
38	Q	89/89 (100%)	89 (100%)	0	100	100
39	R	84/84 (100%)	83 (99%)	1 (1%)	67	83
40	S	93/93 (100%)	92 (99%)	1 (1%)	70	84
41	T	80/80 (100%)	80 (100%)	0	100	100
42	U	83/83 (100%)	83 (100%)	0	100	100
43	V	78/78 (100%)	78 (100%)	0	100	100
44	W	59/59 (100%)	43 (73%)	16 (27%)	0	1
45	X	67/67 (100%)	66 (98%)	1 (2%)	60	80
46	Y	55/55 (100%)	55 (100%)	0	100	100
47	Z	48/48 (100%)	48 (100%)	0	100	100
48	0	47/47 (100%)	47 (100%)	0	100	100
49	1	45/45 (100%)	45 (100%)	0	100	100
50	2	38/38 (100%)	38 (100%)	0	100	100
51	3	51/51 (100%)	51 (100%)	0	100	100
52	4	34/34 (100%)	34 (100%)	0	100	100
53	6	59/59 (100%)	59 (100%)	0	100	100
55	7	173/173 (100%)	167 (96%)	6 (4%)	31	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
56	w	154/154 (100%)	149 (97%)	5 (3%)	34 63
All	All	4943/4971 (99%)	4887 (99%)	56 (1%)	69 84

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	W	11	ARG
56	w	143	LYS
44	W	64	ASP
56	w	107	LEU
55	7	200	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
29	G	63	GLN
39	R	91	GLN
29	G	138	GLN
31	J	58	ASN
41	T	15	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1538/1539 (99%)	331 (21%)	0
22	v	5/6 (83%)	2 (40%)	0
23	A	2868/2903 (98%)	605 (21%)	27 (0%)
24	B	119/120 (99%)	21 (17%)	1 (0%)
54	x	76/77 (98%)	32 (42%)	0
All	All	4606/4645 (99%)	991 (21%)	28 (0%)

5 of 991 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	4	U
1	a	5	U
1	a	6	G
1	a	9	G
1	a	22	G

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	A	1331	G
24	B	66	A
23	A	1432	G
23	A	2391	G
23	A	1399	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
56	KEO	w	34	-	16,18,19	1.50	2 (12%)	14,21,23	1.47	3 (21%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	KEO	w	34	-	-	10/19/20/22	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	w	34	KEO	C05-NZ	5.12	1.45	1.33
56	w	34	KEO	O02-C05	-2.28	1.18	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	34	KEO	C06-C05-NZ	2.93	120.02	115.97
56	w	34	KEO	CE-NZ-C05	-2.85	117.55	122.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	34	KEO	CB-CG-CD	-2.42	107.31	112.51

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	w	34	KEO	O-C-CA-CB
56	w	34	KEO	N-CA-CB-CG
56	w	34	KEO	C-CA-CB-CG
56	w	34	KEO	CA-CB-CG-O01
56	w	34	KEO	C05-C06-C07-C08

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
57	PRO	A	3001	-	5,7,8	0.54	0	7,8,10	1.23	1 (14%)
57	PRO	x	101	-	5,7,8	0.60	0	7,8,10	1.27	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	PRO	A	3001	-	-	0/0/9/11	0/1/1/1
57	PRO	x	101	-	-	0/0/9/11	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
57	A	3001	PRO	O-C-CA	-2.31	118.73	124.78
57	x	101	PRO	O-C-CA	-2.22	118.97	124.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

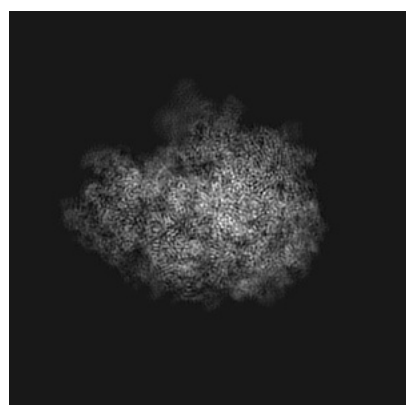
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3903. These allow visual inspection of the internal detail of the map and identification of artifacts.

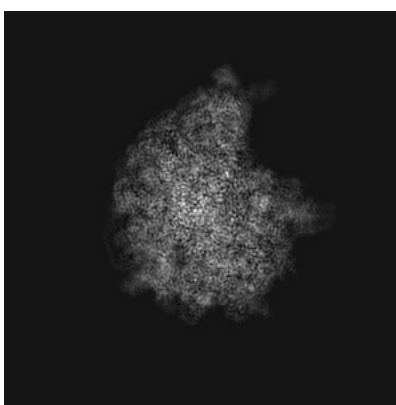
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

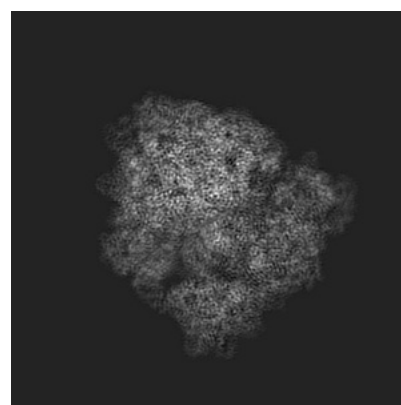
6.1.1 Primary map



X



Y

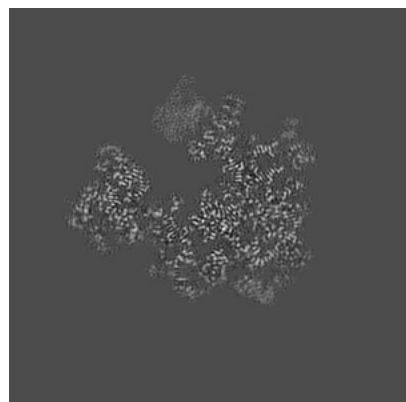


Z

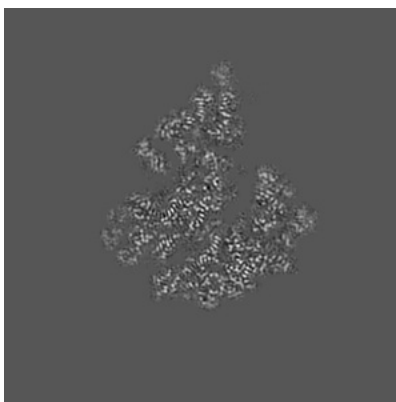
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

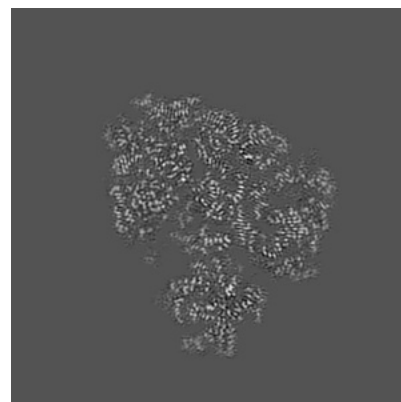
6.2.1 Primary map



X Index: 180



Y Index: 180

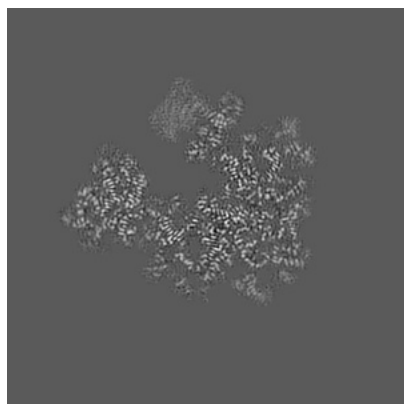


Z Index: 180

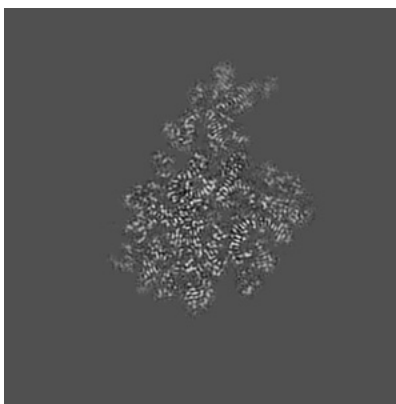
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

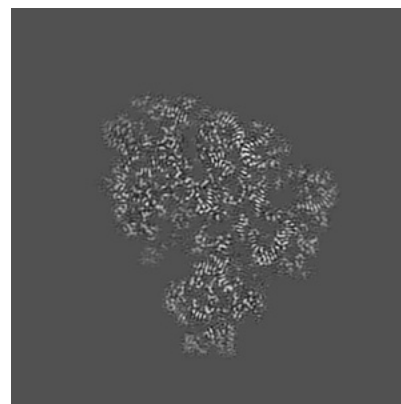
6.3.1 Primary map



X Index: 177



Y Index: 191

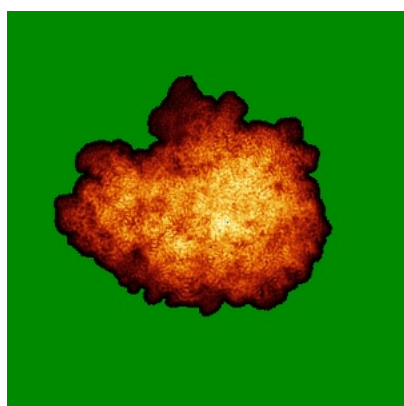


Z Index: 177

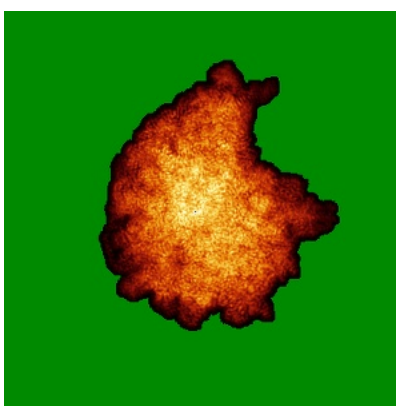
The images above show the largest variance slices of the map in three orthogonal directions.

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

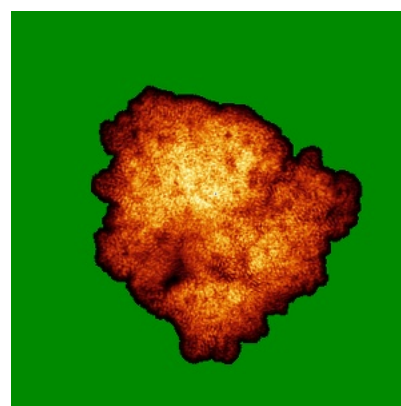
6.4.1 Primary map



X



Y

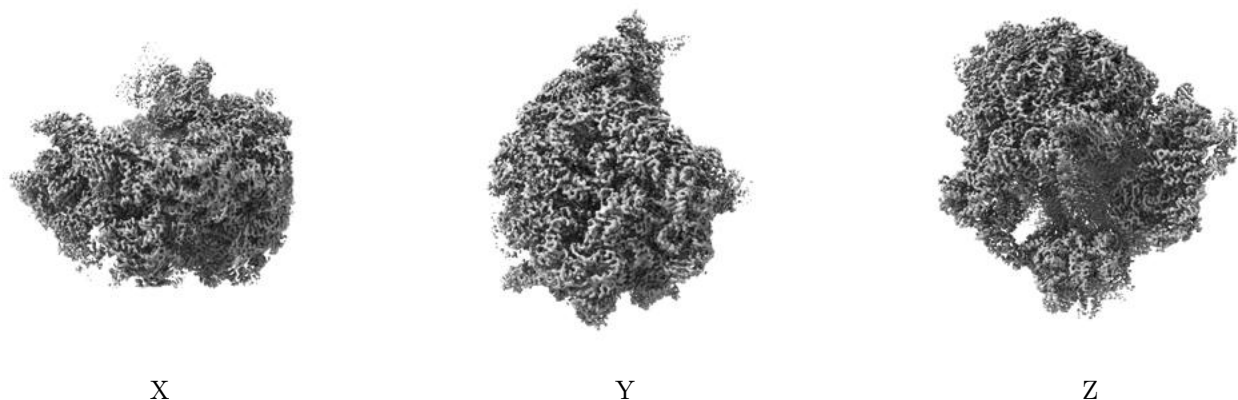


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.108. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

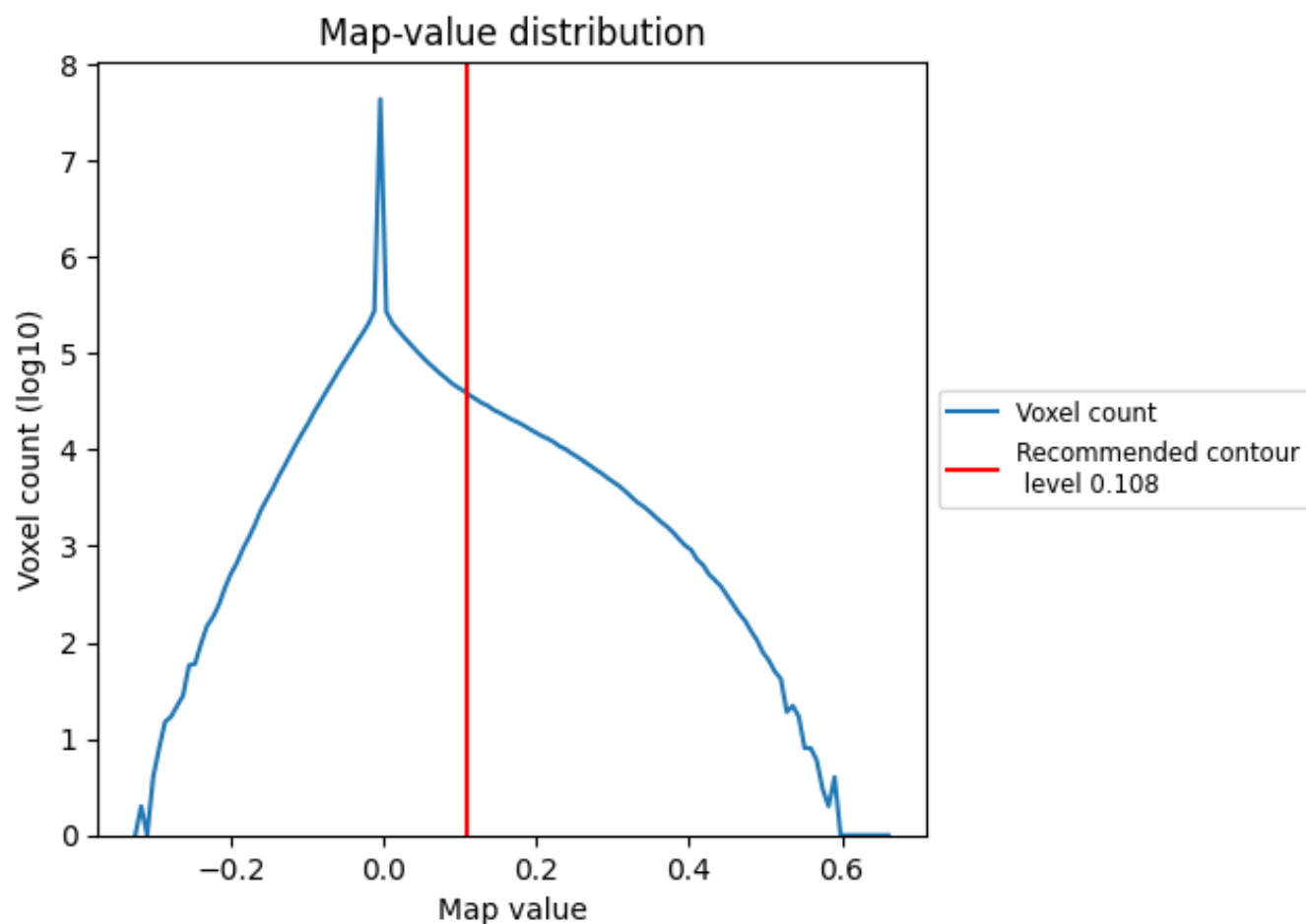
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

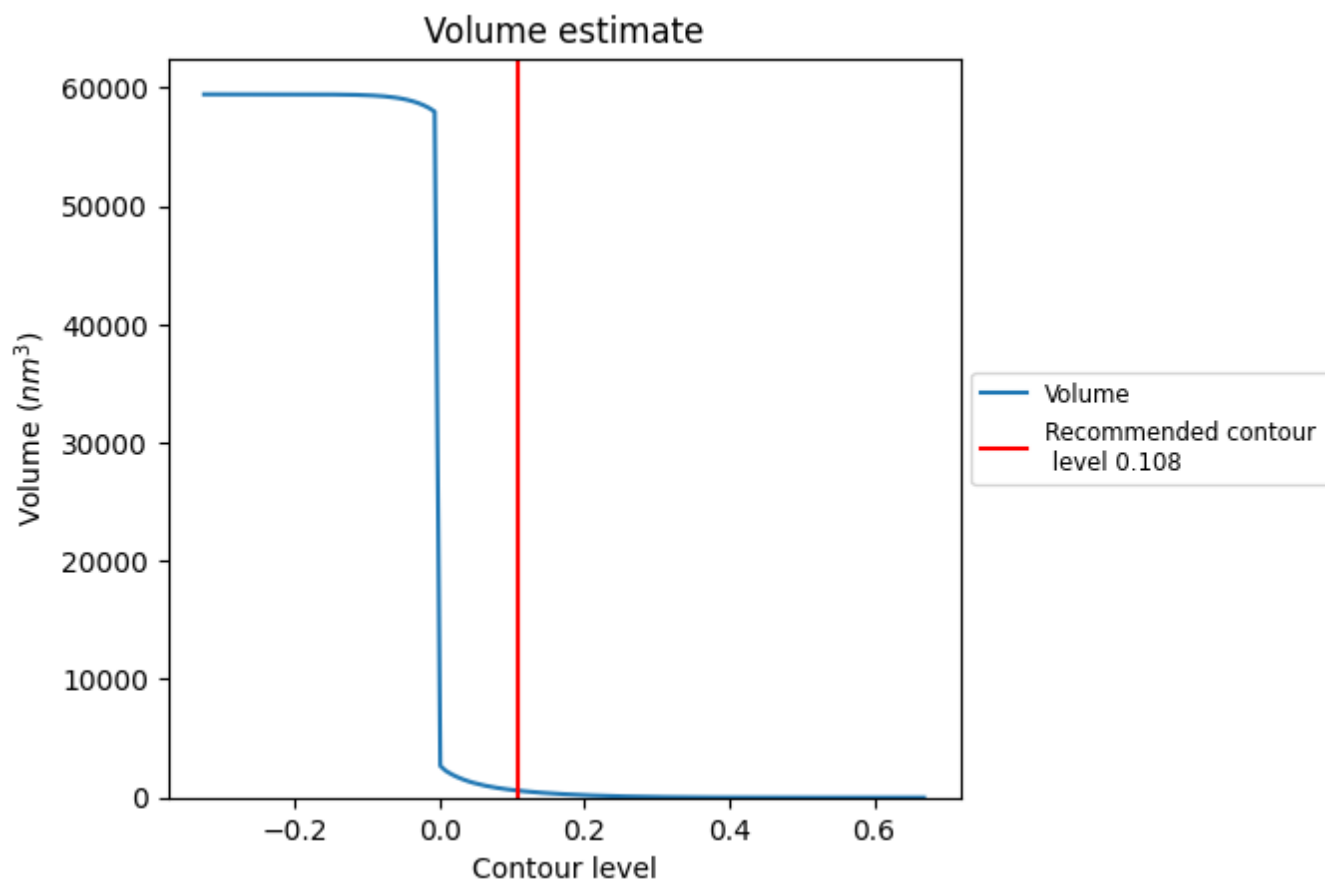
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

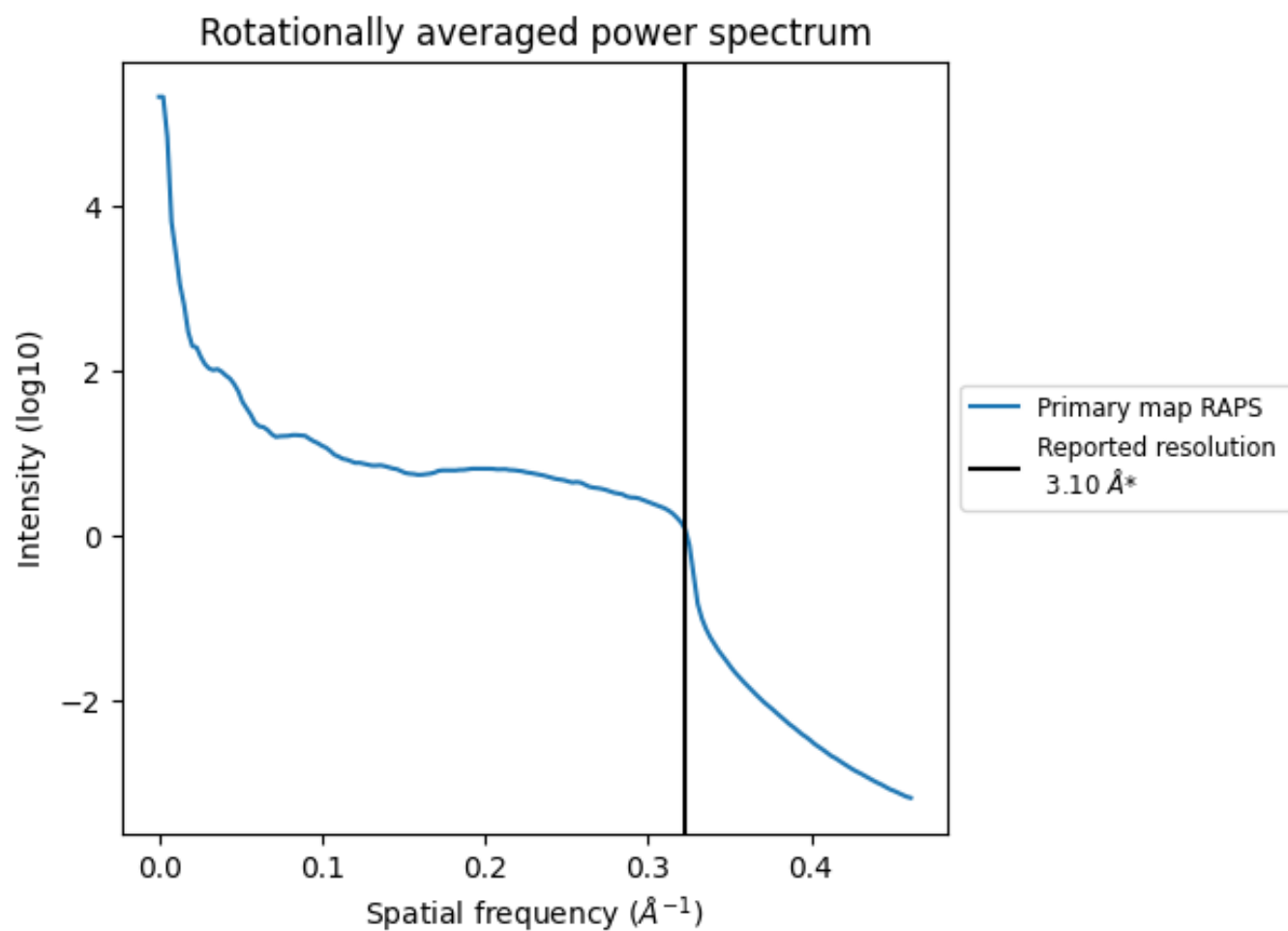
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 588 nm³; this corresponds to an approximate mass of 532 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

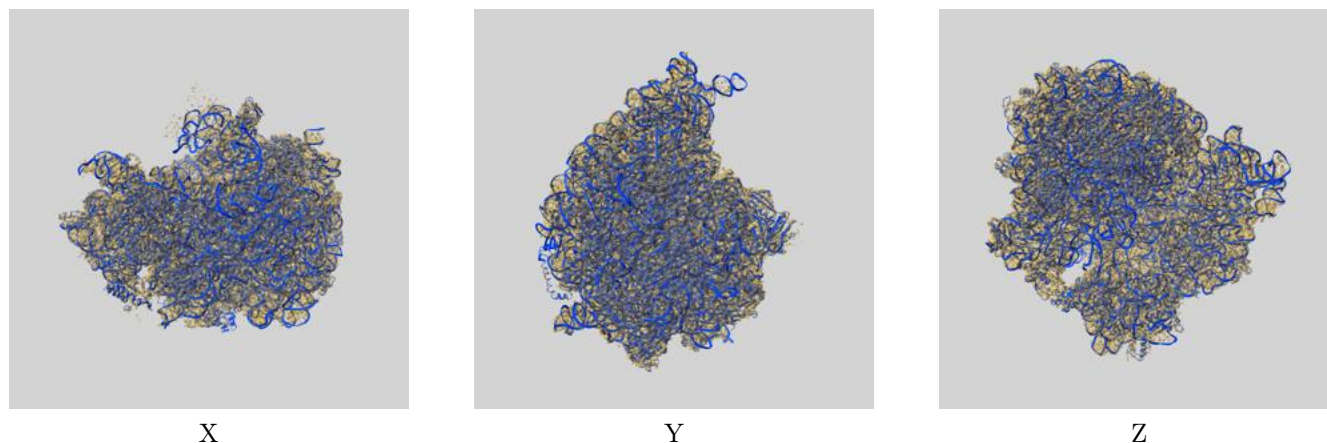
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

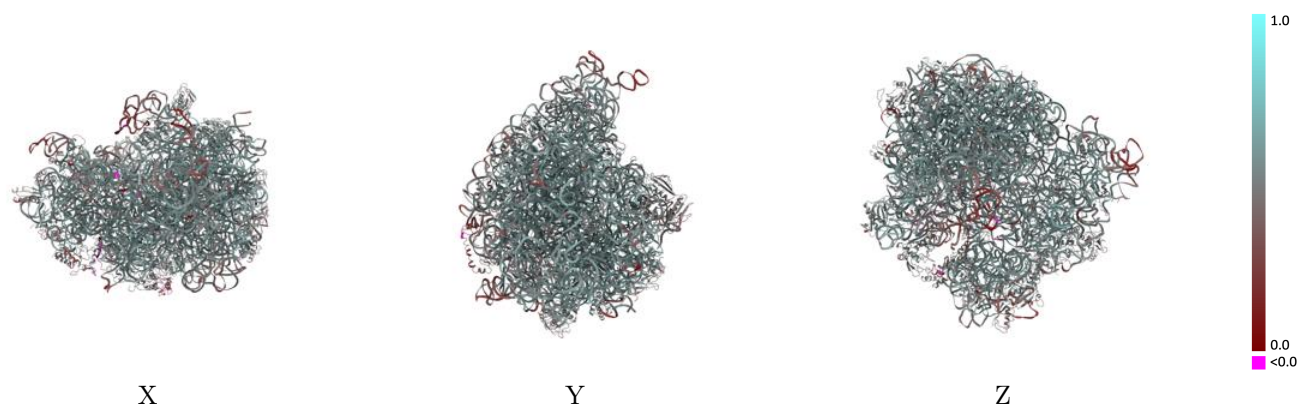
This section contains information regarding the fit between EMDB map EMD-3903 and PDB model 6ENU. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



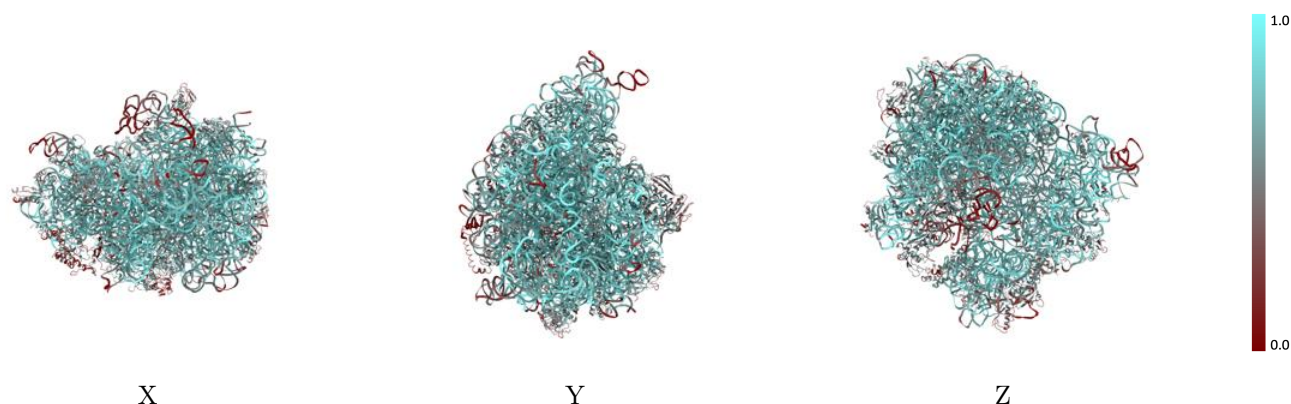
The images above show the 3D surface view of the map at the recommended contour level 0.108 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



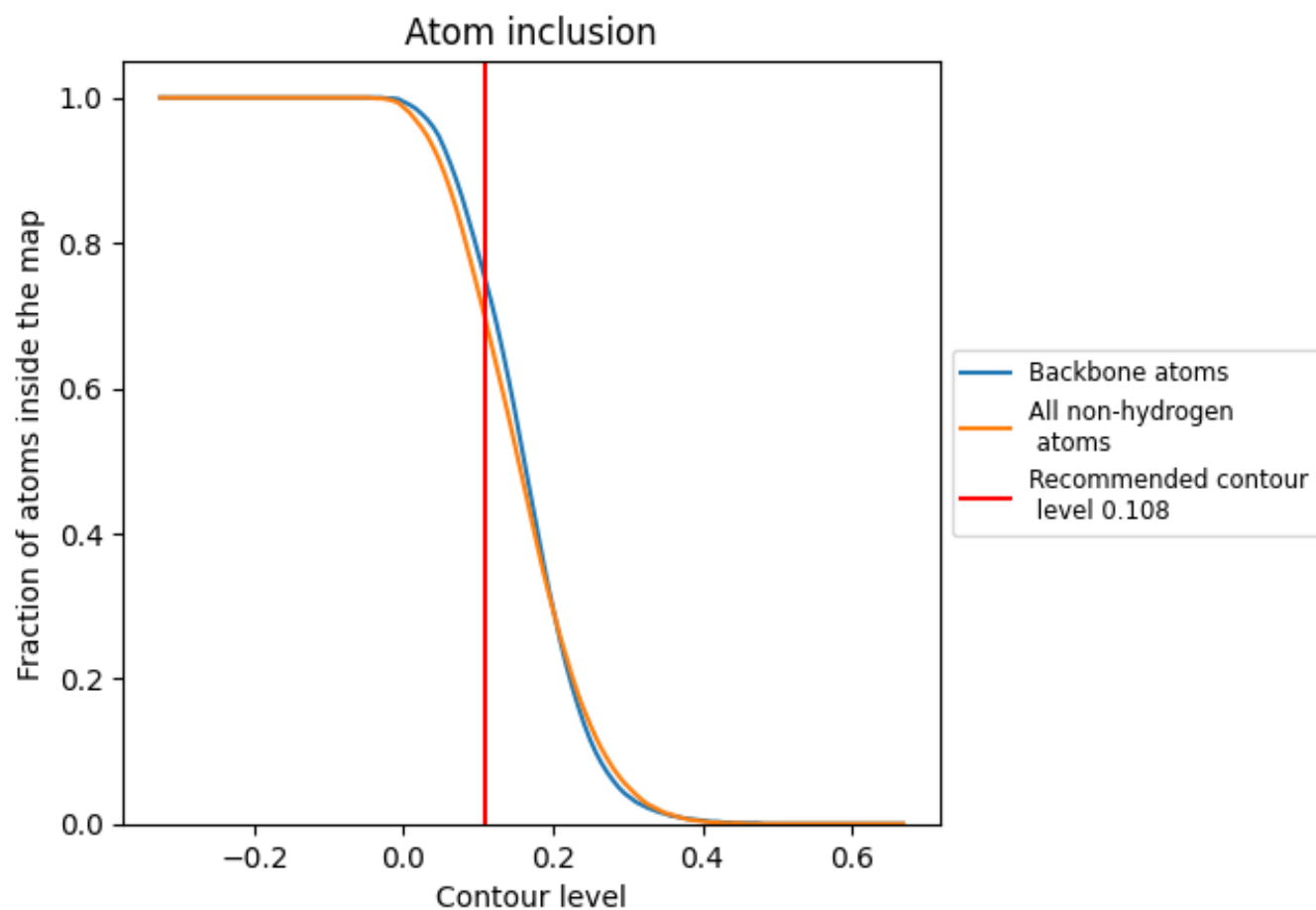
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.108).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 70% 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 (0.108) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7010	 0.5240
0	 0.6450	 0.5110
1	 0.5410	 0.5120
2	 0.7100	 0.5260
3	 0.6950	 0.5630
4	 0.6510	 0.5380
6	 0.3640	 0.4000
7	 0.0150	 0.2330
A	 0.7810	 0.5460
B	 0.7640	 0.5450
C	 0.6680	 0.5470
D	 0.6610	 0.5420
E	 0.5520	 0.5010
F	 0.5080	 0.4750
G	 0.4290	 0.4500
H	 0.1510	 0.2990
J	 0.6700	 0.5310
K	 0.6360	 0.5190
L	 0.6050	 0.5170
M	 0.6530	 0.5410
N	 0.6920	 0.5360
O	 0.6010	 0.5110
P	 0.5910	 0.5220
Q	 0.6950	 0.5470
R	 0.5660	 0.5040
S	 0.5960	 0.5150
T	 0.4940	 0.4830
U	 0.4300	 0.4670
V	 0.5800	 0.5120
W	 0.7010	 0.5680
X	 0.5910	 0.5160
Y	 0.4590	 0.4430
Z	 0.6270	 0.5260
a	 0.7860	 0.5430
b	 0.2910	 0.4060



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Chain	Atom inclusion	Q-score
c	 0.6280	 0.5090
d	 0.5190	 0.4650
e	 0.6420	 0.5080
f	 0.5000	 0.4660
g	 0.5050	 0.4770
h	 0.6490	 0.5250
i	 0.5490	 0.4680
j	 0.4990	 0.4560
k	 0.5230	 0.4900
l	 0.6220	 0.5050
m	 0.5700	 0.4820
n	 0.6340	 0.4950
o	 0.5900	 0.4970
p	 0.5690	 0.4690
q	 0.5220	 0.4810
r	 0.5960	 0.5030
s	 0.5730	 0.4790
t	 0.5830	 0.4880
u	 0.2580	 0.3250
v	 0.7780	 0.5620
w	 0.2770	 0.4440
x	 0.6410	 0.5170