



wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 02:21 AM EDT

PDB ID : 6PJ6 / pdb_00006pj6
EMDB ID : EMD-20353
Title : High resolution cryo-EM structure of E.coli 50S
Authors : Stojkovic, V.; Myasnikov, A.; Frost, A.; Fujimori, D.G.
Deposited on : 2019-06-27
Resolution : 2.20 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

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:

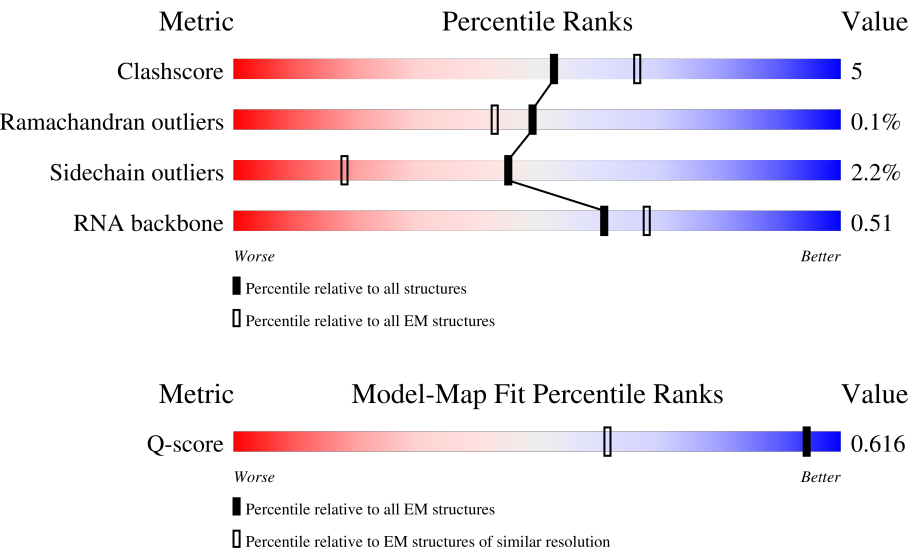
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 2.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3184 (1.71 - 2.70)

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	I	2904	
2	J	118	
3	K	271	

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Mol	Chain	Length	Quality of chain
4	L	209	
5	M	201	
6	N	177	
7	O	176	
8	P	149	
9	Q	134	
10	R	142	
11	S	122	
12	T	144	
13	U	136	
14	V	120	
15	W	117	
16	X	114	
17	Y	117	
18	Z	103	
19	a	110	
20	b	93	
21	c	102	
22	d	94	
23	e	75	
24	f	77	
25	g	62	
26	h	58	
27	i	56	
28	j	50	

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Mol	Chain	Length	Quality of chain
29	k	46	78% 20%
30	l	64	84% 14%
31	m	38	8% 79% 18%

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 154828 atoms, of which 59910 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 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	I	2898	Total	C	H	N	O	P	0	0
			93536	27768	31307	11448	20115	2898		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	J	118	Total	C	H	N	O	P	0	0
			3810	1126	1281	464	821	118		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	K	271	Total	C	H	N	O	S	1	0
			4261	1294	2167	427	366	7		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	L	209	Total	C	H	N	O	S	0	0
			3175	979	1610	288	294	4		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	M	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	N	177	Total	C	H	N	O	S	0	0
			2855	899	1444	249	257	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	O	176	Total	C	H	N	O	S	0	0
			2694	832	1371	243	246	2		

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	P	149	Total	C	H	N	O	S	0	0
			2258	699	1148	197	213	1		

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	Q	134	Total	C	H	N	O	S	0	0
			2007	619	1028	169	185	6		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	R	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	S	122	Total	C	H	N	O	S	0	0
			1950	587	1012	180	165	6		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	T	144	Total	C	H	N	O	S	0	0
			2169	654	1116	207	190	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	U	136	Total	C	H	N	O	S	0	0
			2229	686	1154	205	178	6		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	120	Total	C	H	N	O	S	
			1960	593	1000	196	166	5	
								0	0

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	116	Total	C	H	N	O		
			1815	552	923	178	162		
								0	0

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	114	Total	C	H	N	O	S	
			1879	574	962	179	163	1	
									0

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	117	Total	C	H	N	O		
			1967	604	1020	192	151		
								0	0

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	103	Total	C	H	N	O	S	
			1582	516	766	153	145	2	
									0

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	a	110	Total	C	H	N	O	S	
			1779	532	922	166	156	3	
									0

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	b	93	Total	C	H	N	O	S	
			1546	466	807	139	132	2	
									0

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	c	102	Total	C	H	N	O	0	0
			1611	492	831	146	142		

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	d	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	e	75	Total	C	H	N	O	S	0	0
			1156	356	581	116	102	1		

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	f	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace	
25	g	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace	
26	h	58	Total	C	H	N	O	S	0	0
			937	281	488	87	79	2		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
27	i	56	Total	C	H	N	O	S	0	0
			902	269	458	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	j	50	Total	C	H	N	O	0	0
			849	263	440	75	71		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace	
29	k	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	l	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace	
31	m	38	Total	C	H	N	O	S	0	0
			642	185	340	65	48	4		

- Molecule 32 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
32	I	182	Total	Mg	0
			182	182	
32	J	1	Total	Mg	0
			1	1	
32	K	1	Total	Mg	0
			1	1	
32	L	1	Total	Mg	0
			1	1	

- Molecule 33 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
33	K	1	Total	Na	0
			1	1	

- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
34	m	1	Total 1	Zn 1	0

- Molecule 35 is water.

Mol	Chain	Residues	Atoms		AltConf
35	I	3347	Total 3347	O 3347	0
35	J	62	Total 62	O 62	0
35	K	59	Total 59	O 59	0
35	L	41	Total 41	O 41	0
35	M	42	Total 42	O 42	0
35	N	14	Total 14	O 14	0
35	O	13	Total 13	O 13	0
35	P	6	Total 6	O 6	0
35	Q	10	Total 10	O 10	0
35	R	17	Total 17	O 17	0
35	S	7	Total 7	O 7	0
35	T	33	Total 33	O 33	0
35	U	13	Total 13	O 13	0
35	V	23	Total 23	O 23	0
35	W	11	Total 11	O 11	0
35	X	14	Total 14	O 14	0
35	Y	33	Total 33	O 33	0
35	Z	16	Total 16	O 16	0
35	a	18	Total 18	O 18	0

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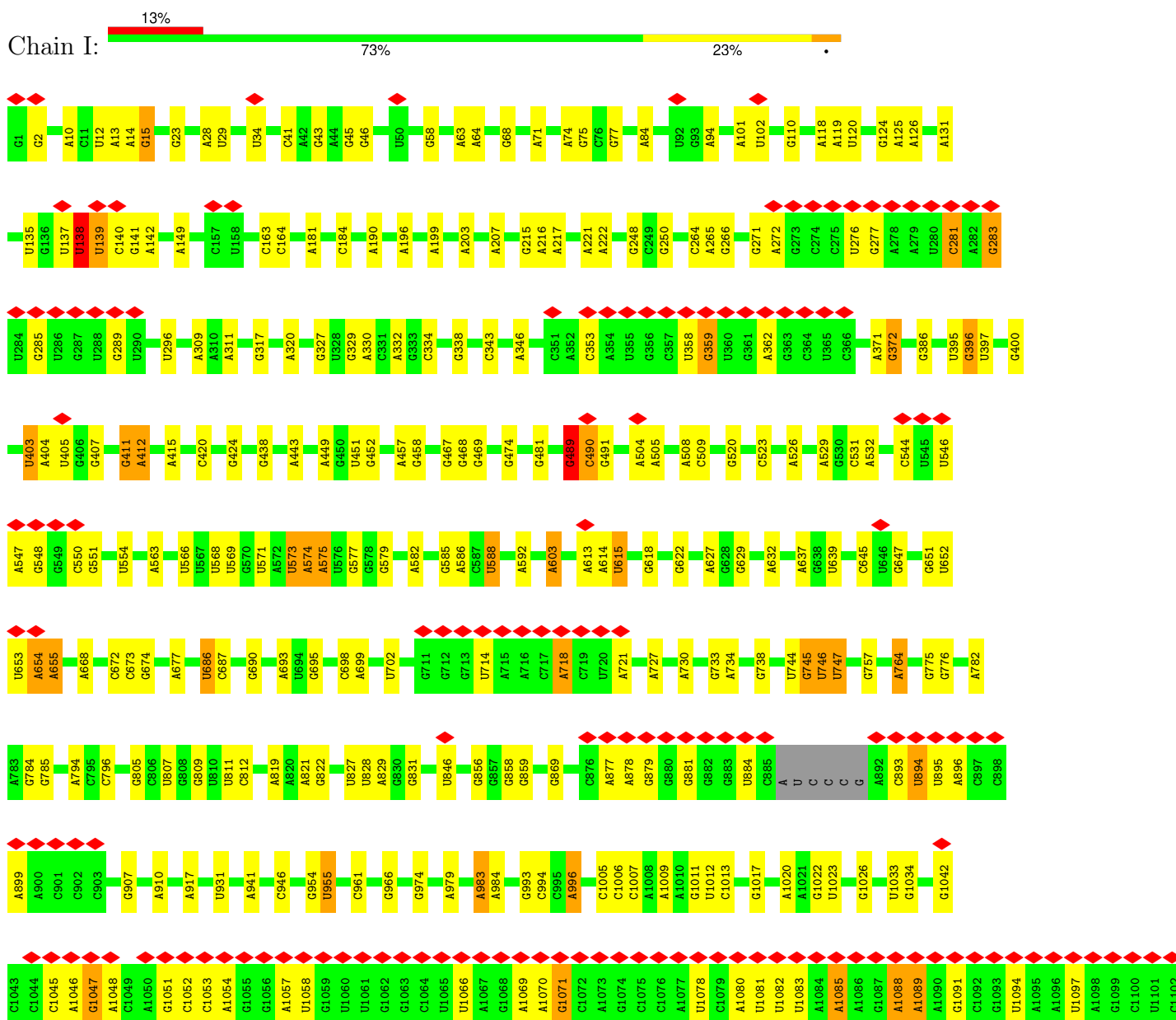
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Mol	Chain	Residues	Atoms		AltConf
35	b	15	Total 15	O 15	0
35	c	7	Total 7	O 7	0
35	d	9	Total 9	O 9	0
35	e	13	Total 13	O 13	0
35	f	9	Total 9	O 9	0
35	g	6	Total 6	O 6	0
35	h	4	Total 4	O 4	0
35	i	12	Total 12	O 12	0
35	j	9	Total 9	O 9	0
35	k	11	Total 11	O 11	0
35	l	19	Total 19	O 19	0
35	m	4	Total 4	O 4	0

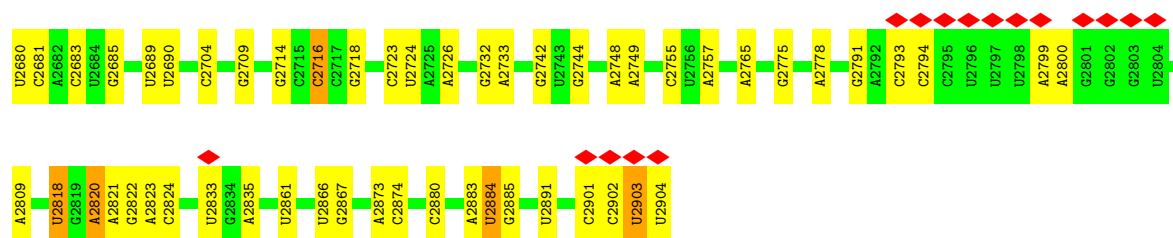
3 Residue-property plots

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

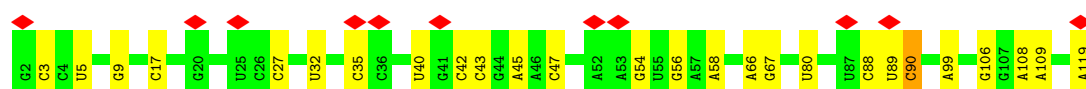
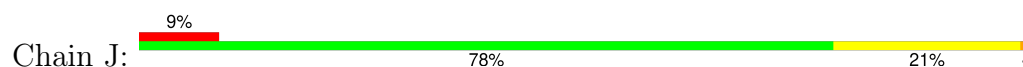
• Molecule 1: 23S rRNA



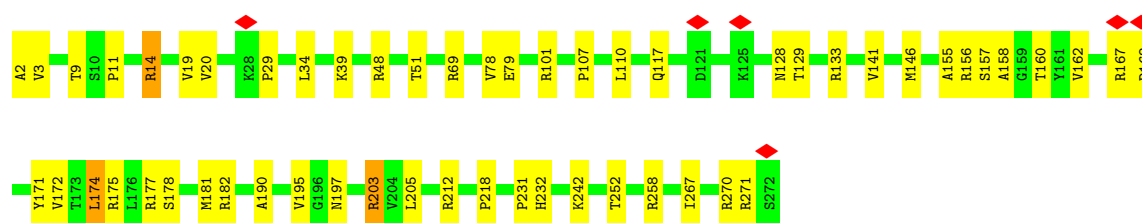
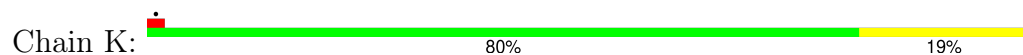




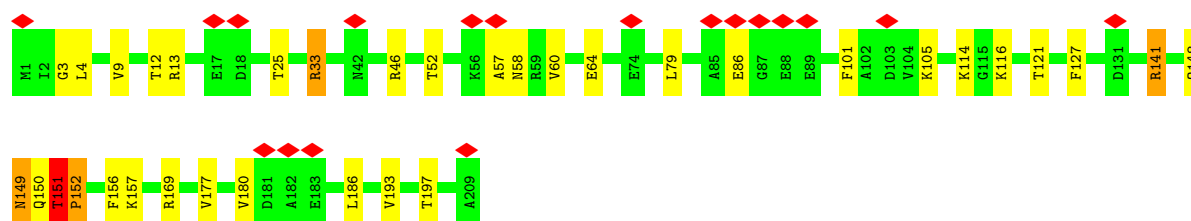
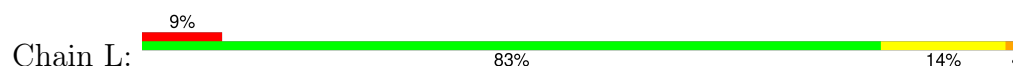
• Molecule 2: 5S rRNA



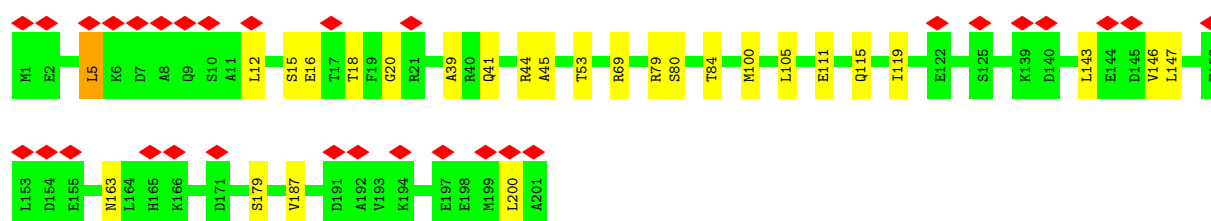
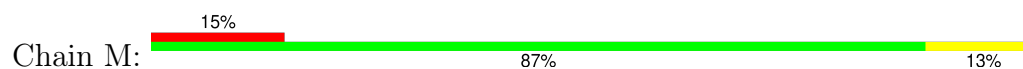
• Molecule 3: 50S ribosomal protein L2



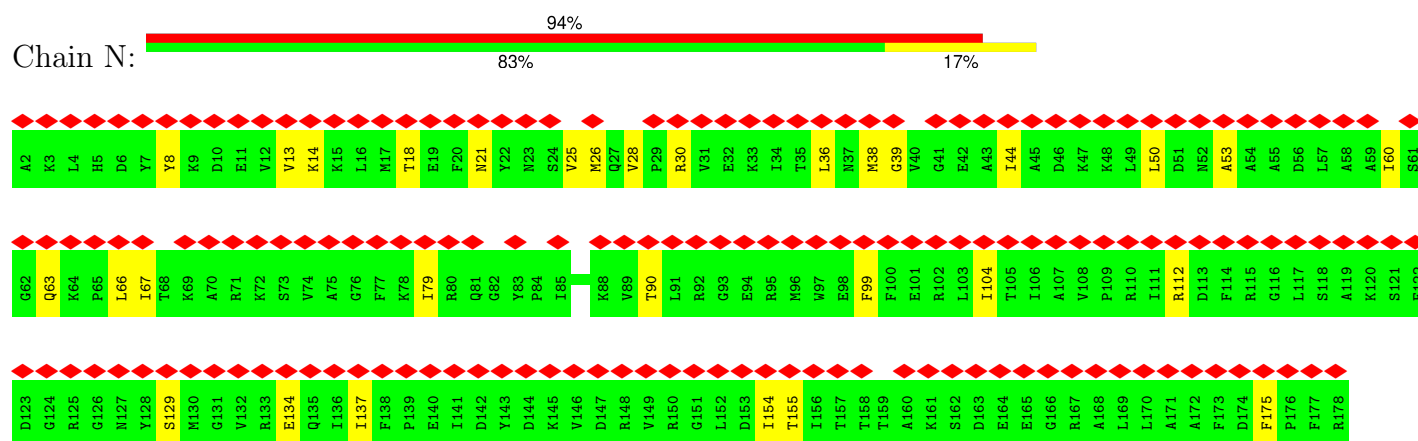
• Molecule 4: 50S ribosomal protein L3



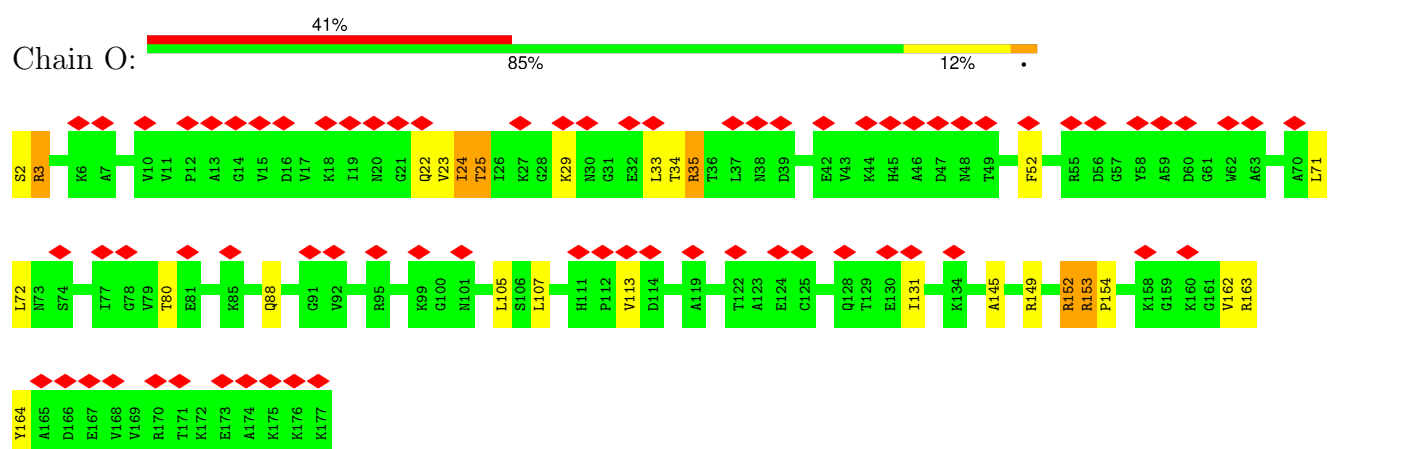
• Molecule 5: 50S ribosomal protein L4



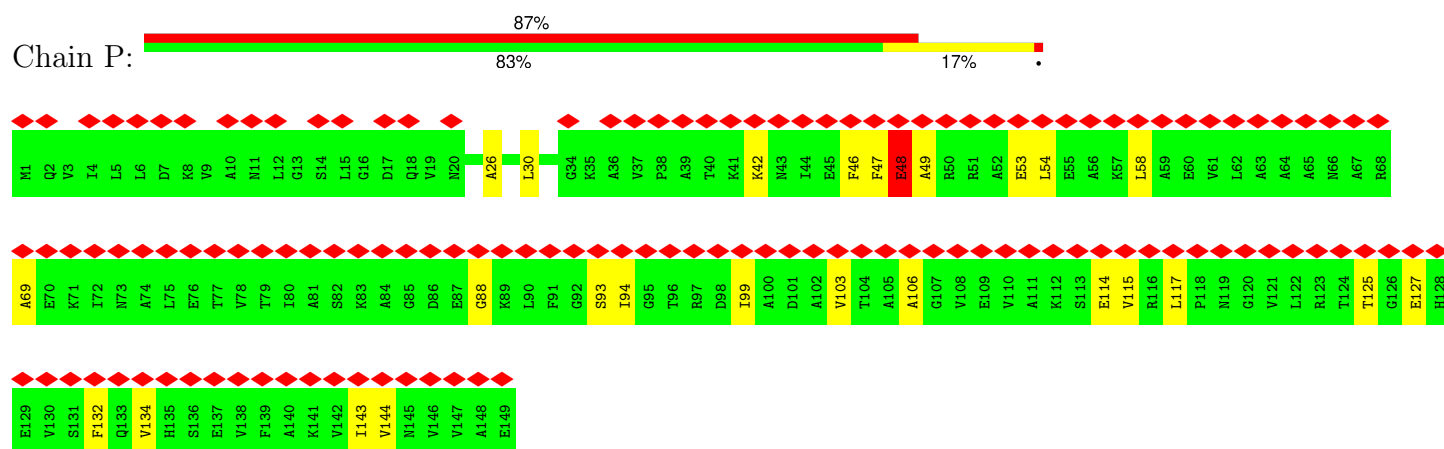
• Molecule 6: 50S ribosomal protein L5



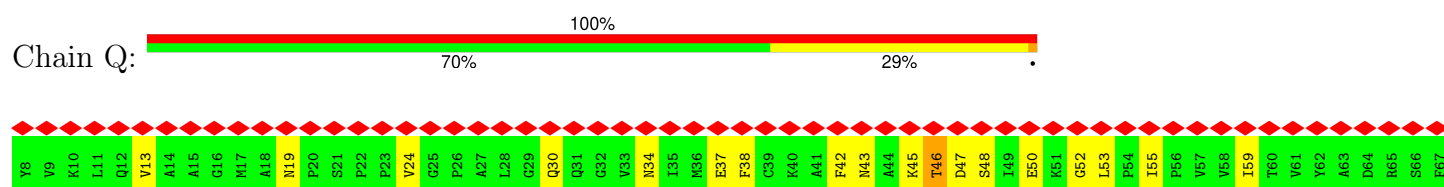
• Molecule 7: 50S ribosomal protein L6

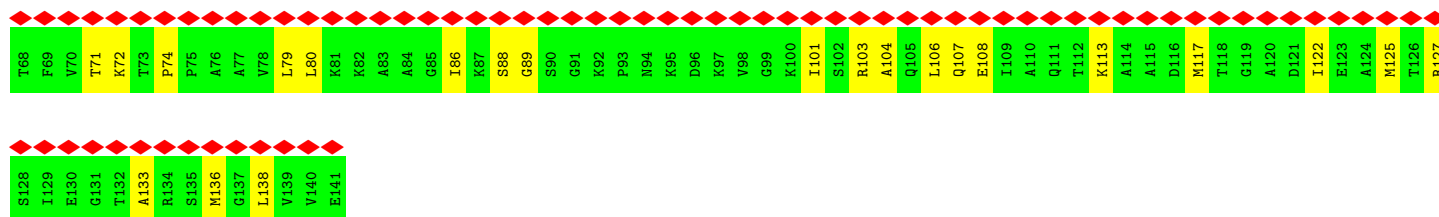


• Molecule 8: 50S ribosomal protein L9



• Molecule 9: 50S ribosomal protein L11





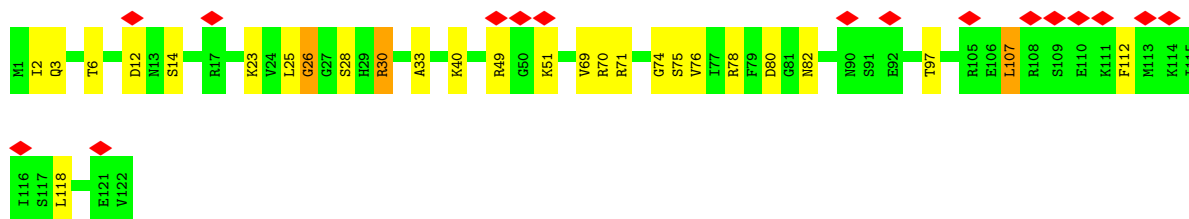
- Molecule 10: 50S ribosomal protein L13

Chain R: 86% 11%



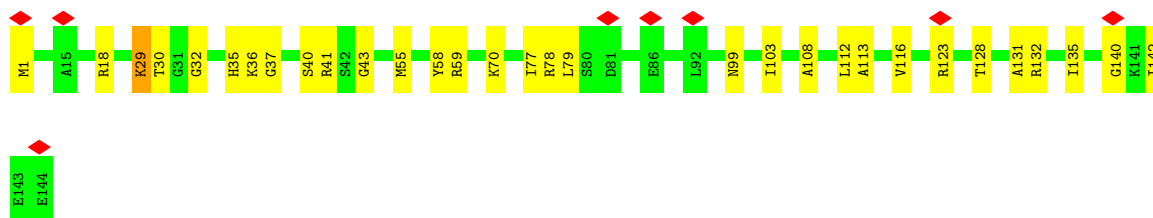
- Molecule 11: 50S ribosomal protein L14

Chain S: 13% 78% 20%



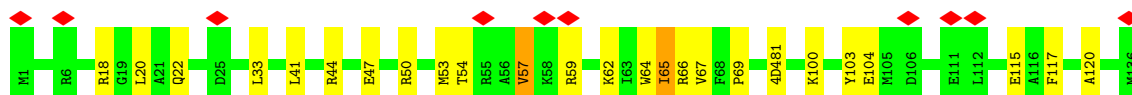
- Molecule 12: 50S ribosomal protein L15

Chain T: 6% 78% 21%



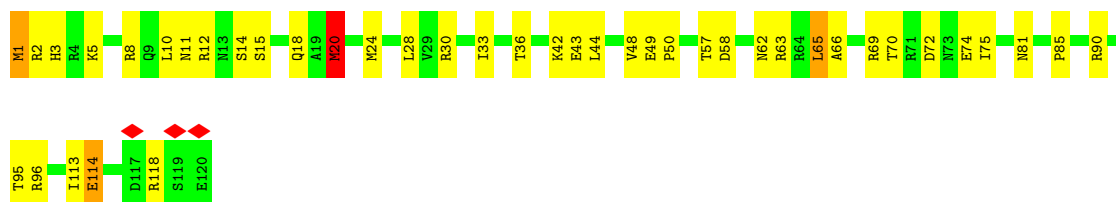
- Molecule 13: 50S ribosomal protein L16

Chain U: 7% 82% 17%

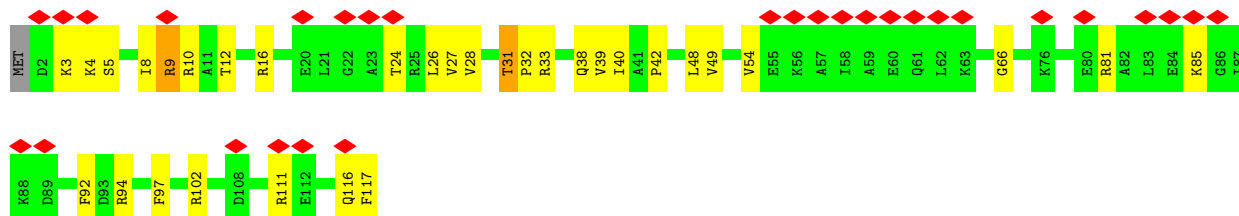


- Molecule 14: 50S ribosomal protein L17

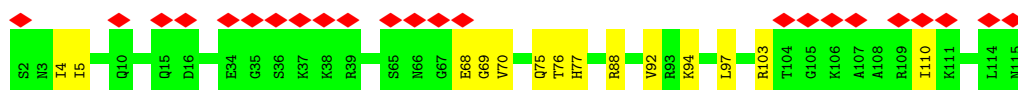
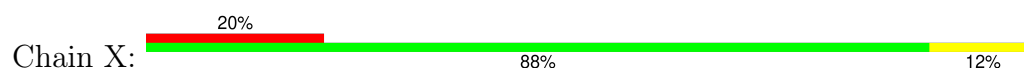
Chain V: 65% 32%



- Molecule 15: 50S ribosomal protein L18



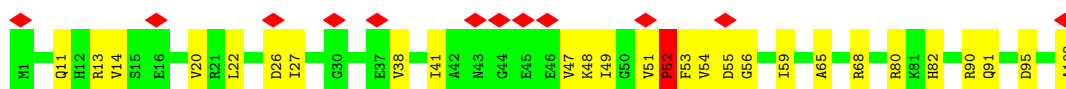
- Molecule 16: 50S ribosomal protein L19



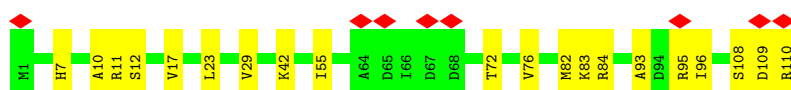
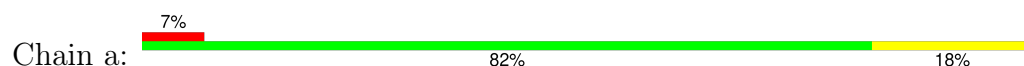
- Molecule 17: 50S ribosomal protein L20



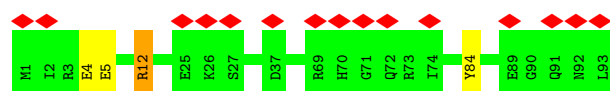
- Molecule 18: 50S ribosomal protein L21



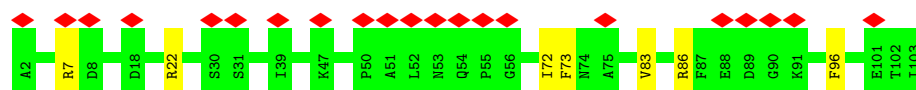
- Molecule 19: 50S ribosomal protein L22



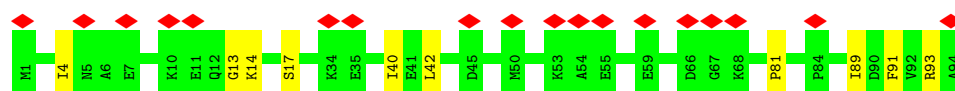
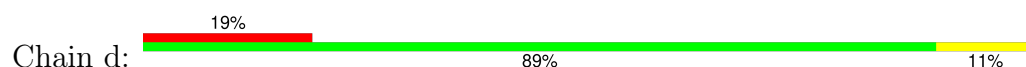
- Molecule 20: 50S ribosomal protein L23



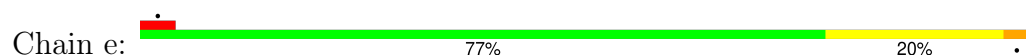
- Molecule 21: 50S ribosomal protein L24



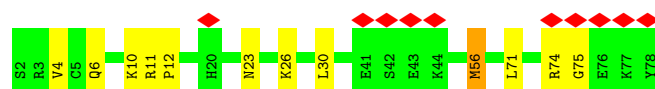
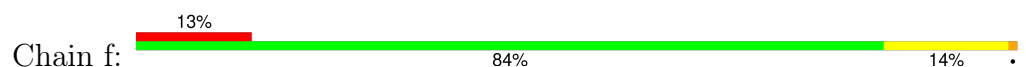
- Molecule 22: 50S ribosomal protein L25



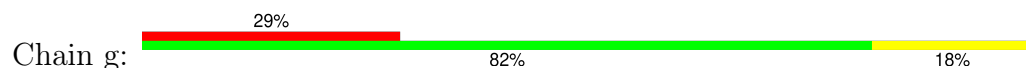
- Molecule 23: 50S ribosomal protein L27



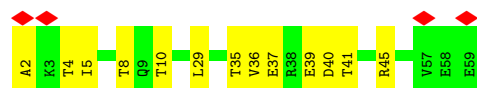
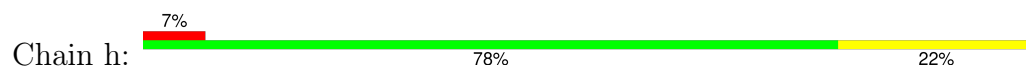
- Molecule 24: 50S ribosomal protein L28



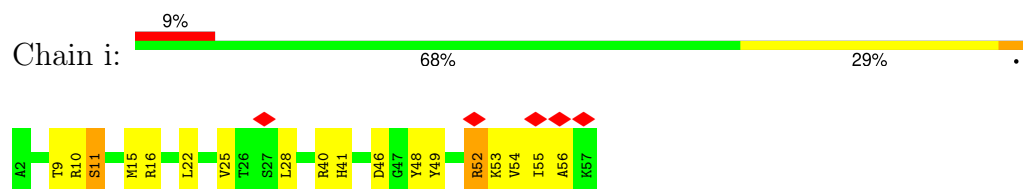
- Molecule 25: 50S ribosomal protein L29



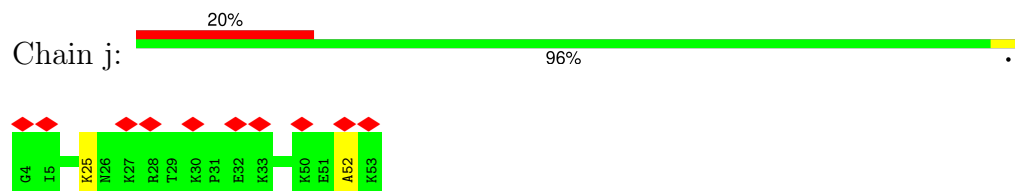
- Molecule 26: 50S ribosomal protein L30



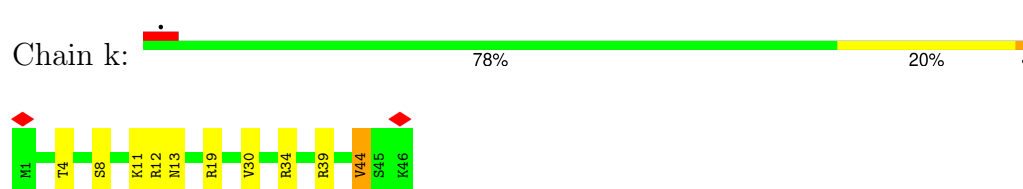
• Molecule 27: 50S ribosomal protein L32



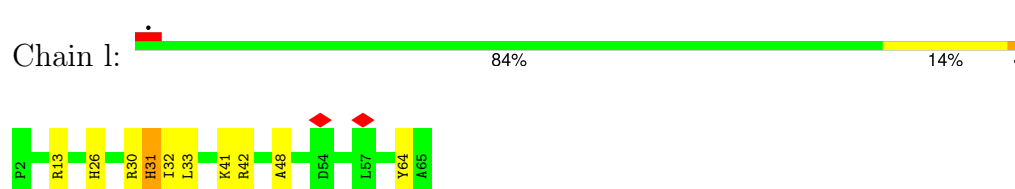
• Molecule 28: 50S ribosomal protein L33



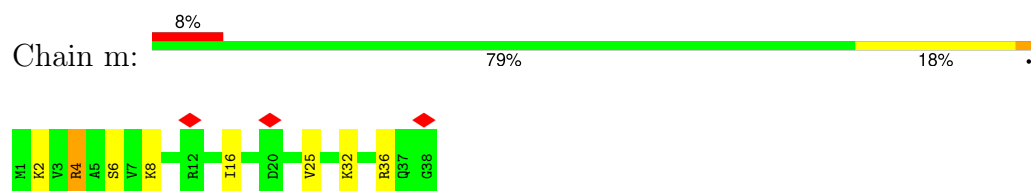
• Molecule 29: 50S ribosomal protein L34



• Molecule 30: 50S ribosomal protein L35



• Molecule 31: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	141549	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	60827	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	66.611	Depositor
Minimum map value	-32.287	Depositor
Average map value	-0.035	Depositor
Map value standard deviation	2.434	Depositor
Recommended contour level	10	Depositor
Map size ($\text{\AA}$)	420.864, 420.864, 420.864	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.822, 0.822, 0.822	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 2MG, NA, 4D4, 5MU, OMC, H2U, 1MG, 5MC, G7M, ZN, 2MA, 3TD, OMG, 6MZ, OMU, PSU

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	I	0.52	0/69121	0.45	9/107828 (0.0%)
2	J	0.42	0/2828	0.40	0/4410
3	K	0.81	2/2133 (0.1%)	0.92	2/2866 (0.1%)
4	L	0.85	2/1586 (0.1%)	0.93	5/2134 (0.2%)
5	M	0.76	1/1571 (0.1%)	0.90	1/2113 (0.0%)
6	N	0.34	0/1435	0.65	0/1926
7	O	0.53	1/1343 (0.1%)	0.83	2/1816 (0.1%)
8	P	0.43	0/1121	0.77	4/1515 (0.3%)
9	Q	0.34	0/993	0.71	0/1341
10	R	0.77	1/1152 (0.1%)	0.98	3/1551 (0.2%)
11	S	0.77	0/947	0.99	3/1268 (0.2%)
12	T	0.97	2/1062 (0.2%)	1.08	1/1413 (0.1%)
13	U	0.81	1/1081 (0.1%)	1.05	0/1443
14	V	1.06	2/973 (0.2%)	1.35	3/1301 (0.2%)
15	W	0.59	0/902	0.87	1/1209 (0.1%)
16	X	0.63	0/929	0.74	0/1242
17	Y	0.99	3/960 (0.3%)	1.30	9/1278 (0.7%)
18	Z	0.71	0/829	0.90	3/1107 (0.3%)
19	a	0.64	0/864	0.75	0/1156
20	b	0.56	0/745	0.67	0/994
21	c	0.52	0/788	0.75	0/1051
22	d	0.52	0/766	0.58	0/1025
23	e	0.86	1/582 (0.2%)	0.86	0/769
24	f	0.84	0/635	0.93	0/848
25	g	0.53	0/502	0.72	0/667
26	h	0.72	0/453	0.84	0/605
27	i	0.88	1/450 (0.2%)	1.21	2/599 (0.3%)
28	j	0.55	0/416	0.62	0/554
29	k	1.00	0/380	1.44	0/498
30	l	0.86	0/513	1.02	0/676
31	m	0.74	0/303	0.77	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.58	17/98363 (0.0%)	0.59	48/147600 (0.0%)

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
3	K	0	1
8	P	0	1
9	Q	0	2
All	All	0	4

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	218	PRO	C-O	-6.85	1.15	1.23
12	T	18	ARG	C-O	-6.52	1.16	1.24
17	Y	92	ARG	C-O	-5.84	1.17	1.24
27	i	11	SER	C-O	-5.81	1.17	1.24
17	Y	56	GLN	C-O	-5.80	1.17	1.24

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	2606	C	C4'-C3'-O3'	10.75	129.12	113.00
1	I	2606	C	C1'-C2'-O2'	-9.89	93.56	108.40
1	I	2607	G	C1'-C2'-O2'	-9.00	94.90	108.40
1	I	2607	G	N9-C1'-C2'	-8.14	99.80	112.00
18	Z	52	PRO	CA-N-CD	-7.91	100.93	112.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	K	203[B]	ARG	Mainchain
8	P	114	GLU	Peptide
9	Q	19	ASN	Peptide
9	Q	46	THR	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	62229	31307	31319	378	0
2	J	2529	1281	1281	10	0
3	K	2094	2167	2166	46	0
4	L	1565	1610	1616	46	0
5	M	1552	1619	1619	23	0
6	N	1411	1444	1444	18	0
7	O	1323	1371	1371	19	0
8	P	1110	1148	1148	15	0
9	Q	979	1028	1028	27	0
10	R	1129	1162	1162	20	0
11	S	938	1012	1012	24	0
12	T	1053	1116	1129	22	0
13	U	1075	1154	1155	21	0
14	V	960	1000	1000	42	0
15	W	892	923	923	29	0
16	X	917	962	962	13	0
17	Y	947	1020	1019	28	0
18	Z	816	766	839	30	0
19	a	857	922	922	16	0
20	b	739	807	807	4	0
21	c	780	831	831	5	0
22	d	753	780	780	9	0
23	e	575	581	592	12	0
24	f	625	652	652	10	0
25	g	501	531	531	8	0
26	h	449	488	488	12	0
27	i	444	458	458	18	0
28	j	409	440	440	1	0
29	k	377	418	418	14	0
30	l	504	572	572	10	0
31	m	302	340	340	7	0
32	I	182	0	0	0	0
32	J	1	0	0	0	0
32	K	1	0	0	0	0
32	L	1	0	0	0	0
33	K	1	0	0	0	0
34	m	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	I	3347	0	0	151	0
35	J	62	0	0	2	0
35	K	59	0	0	2	0
35	L	41	0	0	0	0
35	M	42	0	0	1	0
35	N	14	0	0	2	0
35	O	13	0	0	0	0
35	P	6	0	0	0	0
35	Q	10	0	0	2	0
35	R	17	0	0	0	0
35	S	7	0	0	0	0
35	T	33	0	0	3	0
35	U	13	0	0	0	0
35	V	23	0	0	0	0
35	W	11	0	0	0	0
35	X	14	0	0	1	0
35	Y	33	0	0	1	0
35	Z	16	0	0	0	0
35	a	18	0	0	0	0
35	b	15	0	0	0	0
35	c	7	0	0	0	0
35	d	9	0	0	0	0
35	e	13	0	0	1	0
35	f	9	0	0	1	0
35	g	6	0	0	0	0
35	h	4	0	0	0	0
35	i	12	0	0	0	0
35	j	9	0	0	0	0
35	k	11	0	0	0	0
35	l	19	0	0	2	0
35	m	4	0	0	0	0
All	All	94918	59910	60024	773	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 773 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:O:35:ARG:NH1	7:O:71:LEU:HD13	1.45	1.32
11:S:80:ASP:OD2	16:X:69:GLY:HA3	1.16	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:2572:A:OP2	4:L:149:ASN:O	1.59	1.20
26:h:5:ILE:HD12	26:h:45:ARG:NH1	1.62	1.16
1:I:2571:U:O2'	4:L:151:THR:CG2	1.93	1.15

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	K	270/271 (100%)	254 (94%)	16 (6%)	0	100	100
4	L	207/209 (99%)	195 (94%)	11 (5%)	1 (0%)	24	27
5	M	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
6	N	175/177 (99%)	152 (87%)	23 (13%)	0	100	100
7	O	174/176 (99%)	162 (93%)	12 (7%)	0	100	100
8	P	147/149 (99%)	126 (86%)	21 (14%)	0	100	100
9	Q	132/134 (98%)	110 (83%)	22 (17%)	0	100	100
10	R	140/142 (99%)	140 (100%)	0	0	100	100
11	S	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
12	T	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
13	U	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
14	V	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
15	W	114/117 (97%)	105 (92%)	9 (8%)	0	100	100
16	X	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
17	Y	115/117 (98%)	115 (100%)	0	0	100	100
18	Z	101/103 (98%)	96 (95%)	4 (4%)	1 (1%)	12	11
19	a	108/110 (98%)	102 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	b	91/93 (98%)	87 (96%)	4 (4%)	0	100	100
21	c	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
22	d	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
23	e	73/75 (97%)	73 (100%)	0	0	100	100
24	f	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
25	g	60/62 (97%)	55 (92%)	5 (8%)	0	100	100
26	h	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
27	i	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
28	j	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
29	k	44/46 (96%)	44 (100%)	0	0	100	100
30	l	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
31	m	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
All	All	3298/3357 (98%)	3112 (94%)	184 (6%)	2 (0%)	49	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	Z	52	PRO
4	L	151	THR

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	
3	K	217/216 (100%)	214 (99%)	3 (1%)	59	75
4	L	164/164 (100%)	158 (96%)	6 (4%)	30	41
5	M	165/165 (100%)	162 (98%)	3 (2%)	51	68
6	N	148/148 (100%)	146 (99%)	2 (1%)	59	75
7	O	137/137 (100%)	130 (95%)	7 (5%)	21	27
8	P	114/114 (100%)	113 (99%)	1 (1%)	70	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Q	104/104 (100%)	104 (100%)	0	100	100
10	R	116/116 (100%)	113 (97%)	3 (3%)	40	55
11	S	103/103 (100%)	100 (97%)	3 (3%)	37	51
12	T	103/103 (100%)	99 (96%)	4 (4%)	28	39
13	U	108/108 (100%)	104 (96%)	4 (4%)	30	41
14	V	100/100 (100%)	93 (93%)	7 (7%)	14	16
15	W	86/87 (99%)	84 (98%)	2 (2%)	44	59
16	X	99/99 (100%)	99 (100%)	0	100	100
17	Y	89/89 (100%)	87 (98%)	2 (2%)	45	61
18	Z	84/84 (100%)	83 (99%)	1 (1%)	63	78
19	a	93/93 (100%)	93 (100%)	0	100	100
20	b	80/80 (100%)	78 (98%)	2 (2%)	42	56
21	c	83/83 (100%)	81 (98%)	2 (2%)	43	58
22	d	78/78 (100%)	78 (100%)	0	100	100
23	e	57/57 (100%)	55 (96%)	2 (4%)	32	43
24	f	67/67 (100%)	66 (98%)	1 (2%)	57	73
25	g	54/54 (100%)	54 (100%)	0	100	100
26	h	48/48 (100%)	47 (98%)	1 (2%)	47	63
27	i	47/47 (100%)	46 (98%)	1 (2%)	47	63
28	j	45/45 (100%)	45 (100%)	0	100	100
29	k	38/38 (100%)	37 (97%)	1 (3%)	40	55
30	l	51/51 (100%)	50 (98%)	1 (2%)	48	64
31	m	34/34 (100%)	33 (97%)	1 (3%)	37	51
All	All	2712/2712 (100%)	2652 (98%)	60 (2%)	45	61

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	T	40	SER
26	h	10	THR
13	U	67	VAL
24	f	56	MET
31	m	4	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
14	V	11	ASN
15	W	104	GLN
28	j	19	HIS
14	V	31	HIS
17	Y	52	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	I	2896/2904 (99%)	454 (15%)	23 (0%)
2	J	117/118 (99%)	14 (11%)	0
All	All	3013/3022 (99%)	468 (15%)	23 (0%)

5 of 468 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	I	2	G
1	I	10	A
1	I	12	U
1	I	14	A
1	I	15	G

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	I	2162	G
1	I	2430	A
1	I	2425	A
1	I	2447	G
1	I	784	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

25 non-standard protein/DNA/RNA residues 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
1	OMC	I	2498	1,32	19,22,23	2.71	7 (36%)	25,31,34	0.67	0
1	PSU	I	2604	1	18,21,22	2.66	9 (50%)	21,30,33	2.84	6 (28%)
1	5MU	I	747	1	19,22,23	4.61	7 (36%)	27,32,35	3.59	9 (33%)
1	PSU	I	2580	1	18,21,22	1.87	6 (33%)	21,30,33	1.81	5 (23%)
1	5MC	I	1962	1	19,22,23	3.30	8 (42%)	26,32,35	1.17	2 (7%)
1	PSU	I	2605	1	18,21,22	3.01	10 (55%)	21,30,33	2.70	7 (33%)
1	PSU	I	2457	1	18,21,22	1.67	4 (22%)	21,30,33	2.05	3 (14%)
1	6MZ	I	1618	1	22,25,26	2.44	6 (27%)	29,36,39	3.18	12 (41%)
1	PSU	I	2504	1,32	18,21,22	1.71	5 (27%)	21,30,33	1.78	4 (19%)
1	G7M	I	2069	1	23,26,27	2.56	7 (30%)	34,39,42	1.93	10 (29%)
1	OMG	I	2251	1	23,26,27	2.24	8 (34%)	32,38,41	1.70	7 (21%)
1	PSU	I	746	1	18,21,22	1.66	6 (33%)	21,30,33	1.84	4 (19%)
1	6MZ	I	2030	1	22,25,26	2.61	6 (27%)	29,36,39	3.12	11 (37%)
1	PSU	I	1911	1	18,21,22	1.40	3 (16%)	21,30,33	2.35	3 (14%)
1	PSU	I	955	1	18,21,22	1.66	5 (27%)	21,30,33	1.90	4 (19%)
13	4D4	U	81	13	9,11,12	2.70	3 (33%)	7,13,15	1.23	0
1	2MG	I	2445	1	23,26,27	2.67	8 (34%)	33,38,41	1.93	8 (24%)
1	H2U	I	2449	1	18,21,22	1.58	3 (16%)	19,30,33	0.63	0
1	2MA	I	2503	1	22,25,26	3.65	11 (50%)	32,37,40	2.19	8 (25%)
1	2MG	I	1835	1	23,26,27	2.69	8 (34%)	33,38,41	2.00	7 (21%)
1	OMU	I	2552	1	19,22,23	2.89	8 (42%)	25,31,34	1.78	5 (20%)
1	1MG	I	745	1	23,26,27	2.95	8 (34%)	33,39,42	2.20	9 (27%)
1	5MU	I	1939	1	19,22,23	4.77	7 (36%)	27,32,35	3.59	9 (33%)
1	3TD	I	1915	1	19,22,23	4.28	7 (36%)	23,32,35	1.65	2 (8%)
1	PSU	I	1917	1	18,21,22	1.46	3 (16%)	21,30,33	2.02	4 (19%)

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
1	OMC	I	2498	1,32	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	I	2604	1	-	0/7/25/26	0/2/2/2
1	5MU	I	747	1	-	0/7/25/26	0/2/2/2
1	PSU	I	2580	1	-	0/7/25/26	0/2/2/2
1	5MC	I	1962	1	-	0/7/25/26	0/2/2/2
1	PSU	I	2605	1	-	2/7/25/26	0/2/2/2
1	PSU	I	2457	1	-	0/7/25/26	0/2/2/2
1	6MZ	I	1618	1	-	1/9/27/28	0/3/3/3
1	PSU	I	2504	1,32	-	2/7/25/26	0/2/2/2
1	G7M	I	2069	1	-	1/7/25/26	0/3/3/3
1	OMG	I	2251	1	-	0/9/27/28	0/3/3/3
1	PSU	I	746	1	-	1/7/25/26	0/2/2/2
1	6MZ	I	2030	1	-	2/9/27/28	0/3/3/3
1	PSU	I	1911	1	-	2/7/25/26	0/2/2/2
1	PSU	I	955	1	-	0/7/25/26	0/2/2/2
13	4D4	U	81	13	-	2/11/12/14	-
1	2MG	I	2445	1	-	2/9/27/28	0/3/3/3
1	H2U	I	2449	1	-	0/7/38/39	0/2/2/2
1	2MA	I	2503	1	-	1/7/25/26	0/3/3/3
1	2MG	I	1835	1	-	0/9/27/28	0/3/3/3
1	OMU	I	2552	1	-	0/9/27/28	0/2/2/2
1	1MG	I	745	1	-	0/7/25/26	0/3/3/3
1	5MU	I	1939	1	-	0/7/25/26	0/2/2/2
1	3TD	I	1915	1	-	3/7/25/26	0/2/2/2
1	PSU	I	1917	1	-	2/7/25/26	0/2/2/2

The worst 5 of 163 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	1915	3TD	C6-C5	12.97	1.49	1.35
1	I	1939	5MU	C2-N1	10.81	1.55	1.38
1	I	2503	2MA	C4-N3	10.51	1.47	1.34
1	I	747	5MU	C2-N1	10.38	1.54	1.38
1	I	1939	5MU	C6-N1	10.17	1.55	1.38

The worst 5 of 139 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	1939	5MU	C5-C4-N3	11.97	125.73	115.32
1	I	747	5MU	C5-C4-N3	11.37	125.20	115.32
1	I	747	5MU	C5-C6-N1	-8.82	113.73	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	2604	PSU	N1-C2-N3	8.61	124.25	115.17
1	I	1939	5MU	C5-C6-N1	-8.56	114.02	123.31

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	I	1911	PSU	O4'-C4'-C5'-O5'
1	I	1915	3TD	O4'-C4'-C5'-O5'
1	I	2504	PSU	O4'-C4'-C5'-O5'
1	I	1915	3TD	C3'-C4'-C5'-O5'
1	I	1917	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	I	2498	OMC	1	0
1	I	2605	PSU	2	0
1	I	2030	6MZ	1	0
1	I	955	PSU	1	0
1	I	2445	2MG	1	0
1	I	2503	2MA	1	0
1	I	745	1MG	1	0
1	I	1939	5MU	1	0
1	I	1917	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 187 ligands modelled in this entry, 187 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

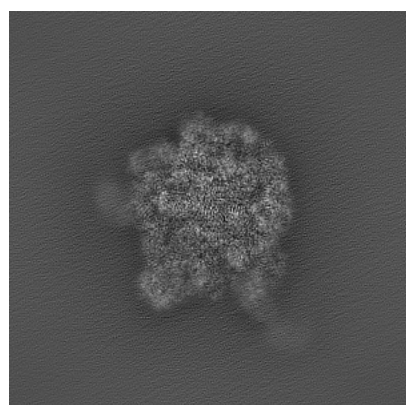
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20353. These allow visual inspection of the internal detail of the map and identification of artifacts.

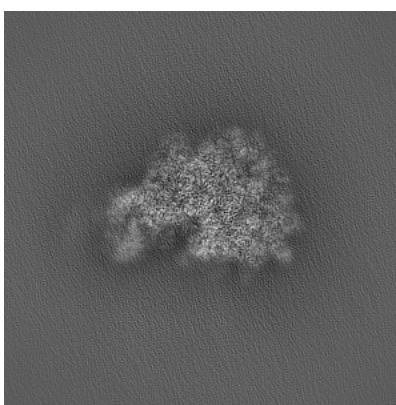
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

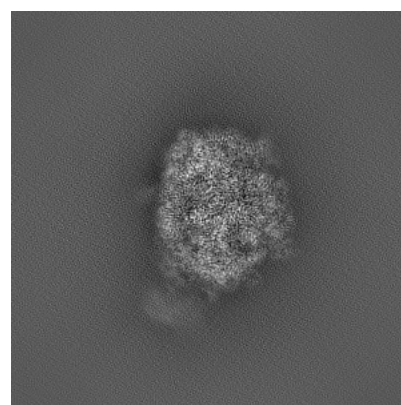
6.1.1 Primary map



X



Y

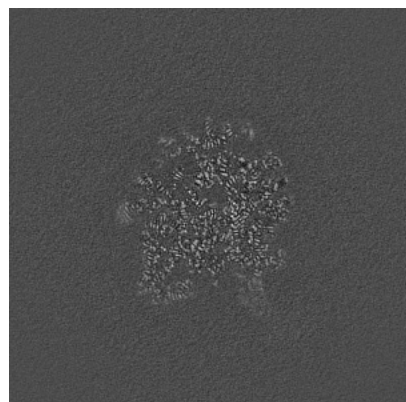


Z

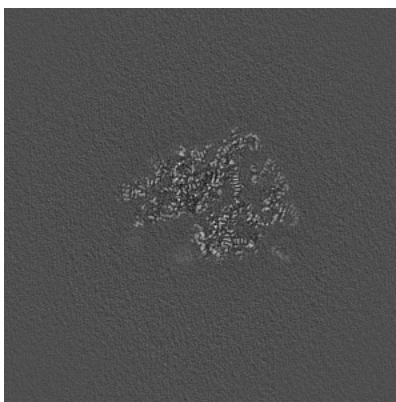
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

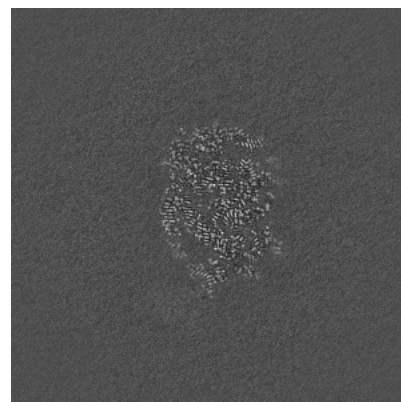
6.2.1 Primary map



X Index: 256



Y Index: 256

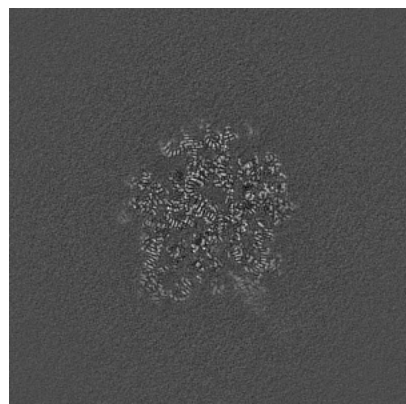


Z Index: 256

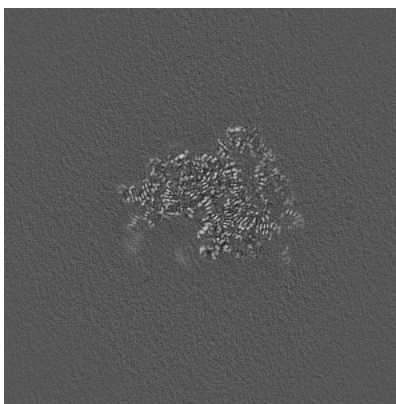
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

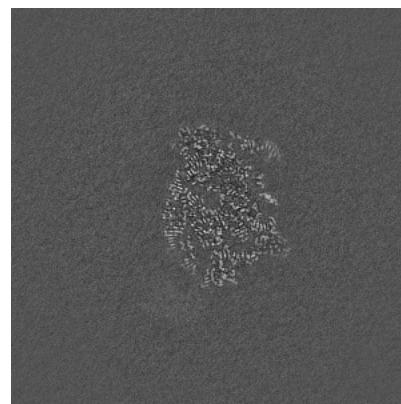
6.3.1 Primary map



X Index: 261



Y Index: 247

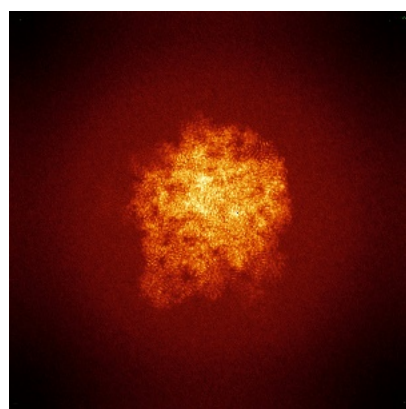


Z Index: 266

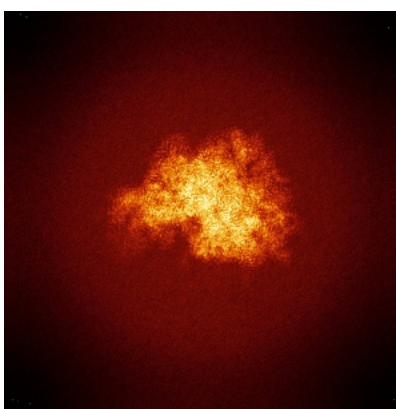
The images above show the largest variance slices of the map in three orthogonal directions.

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

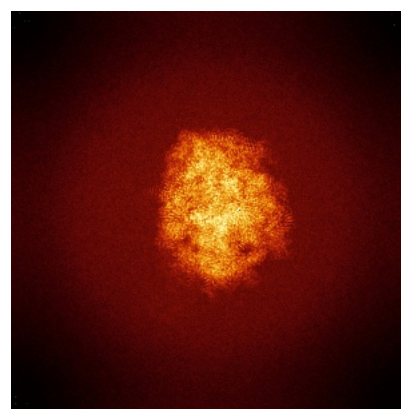
6.4.1 Primary map



X



Y

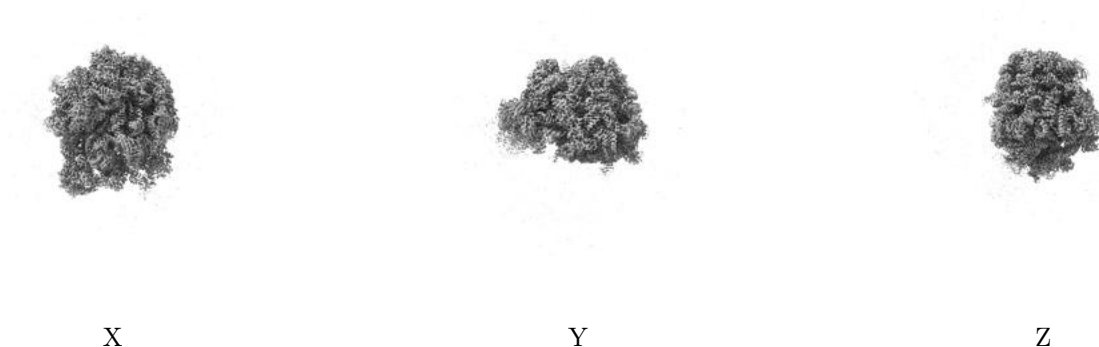


Z

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

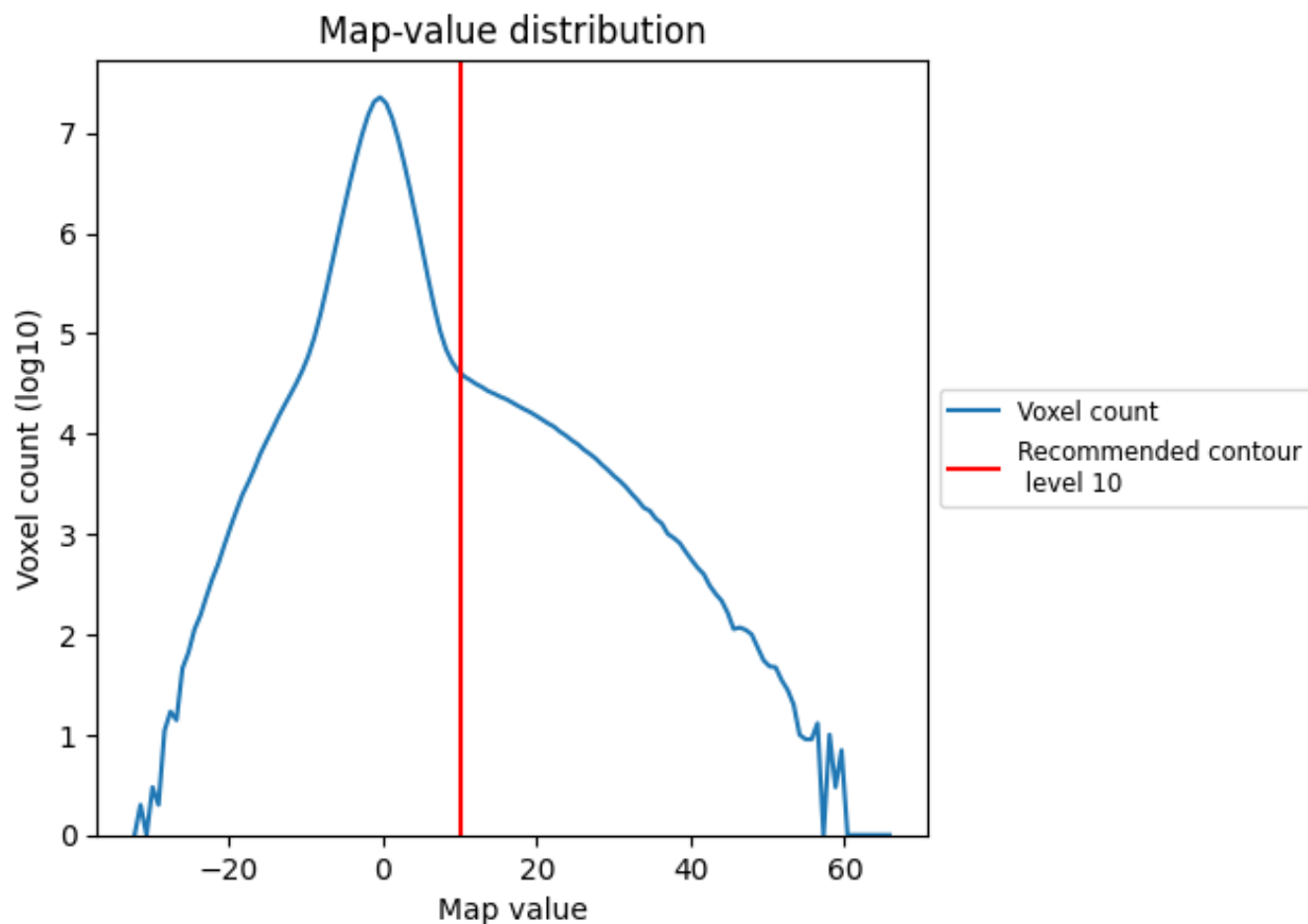
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

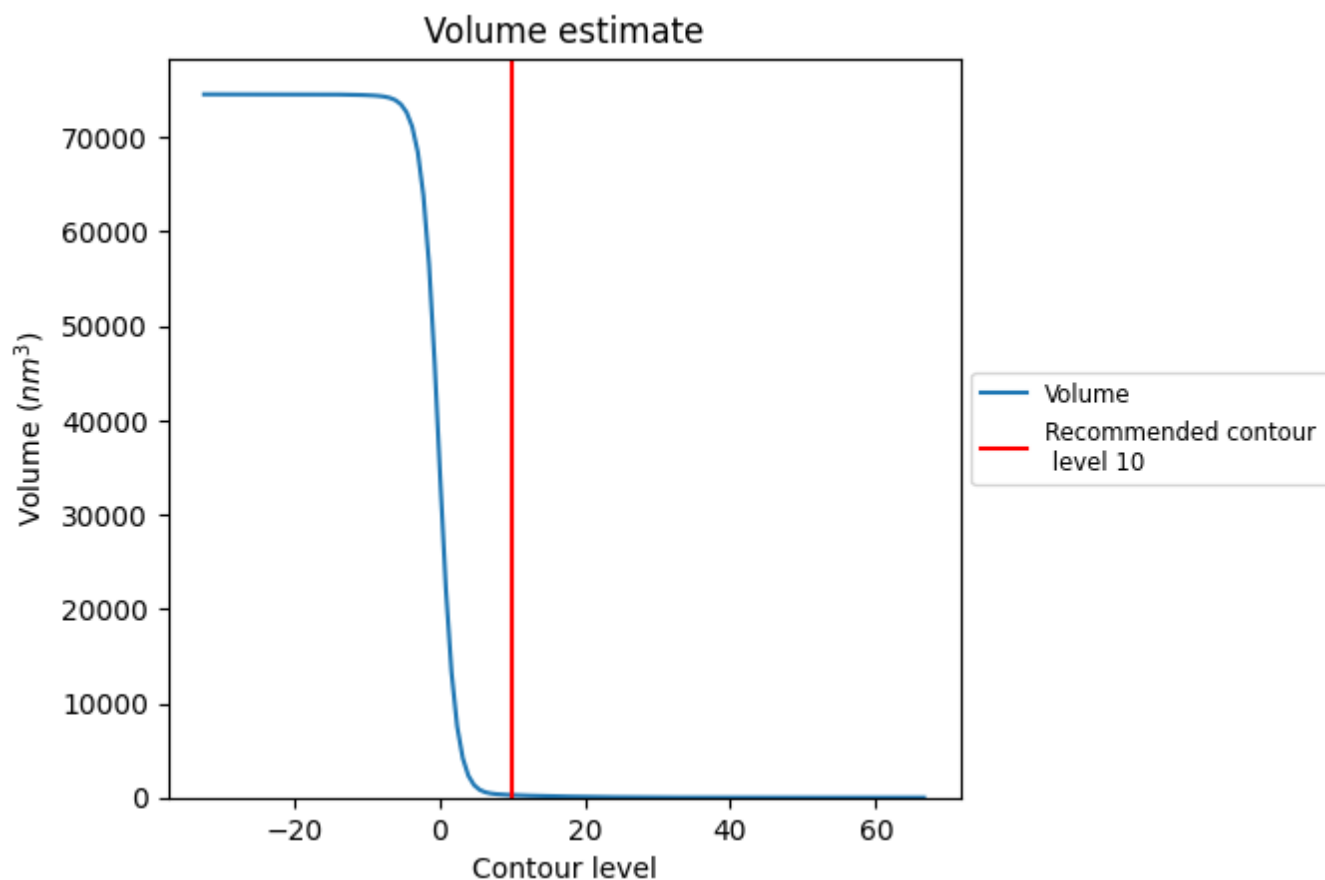
This section contains the results of statistical analysis of the map.

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.

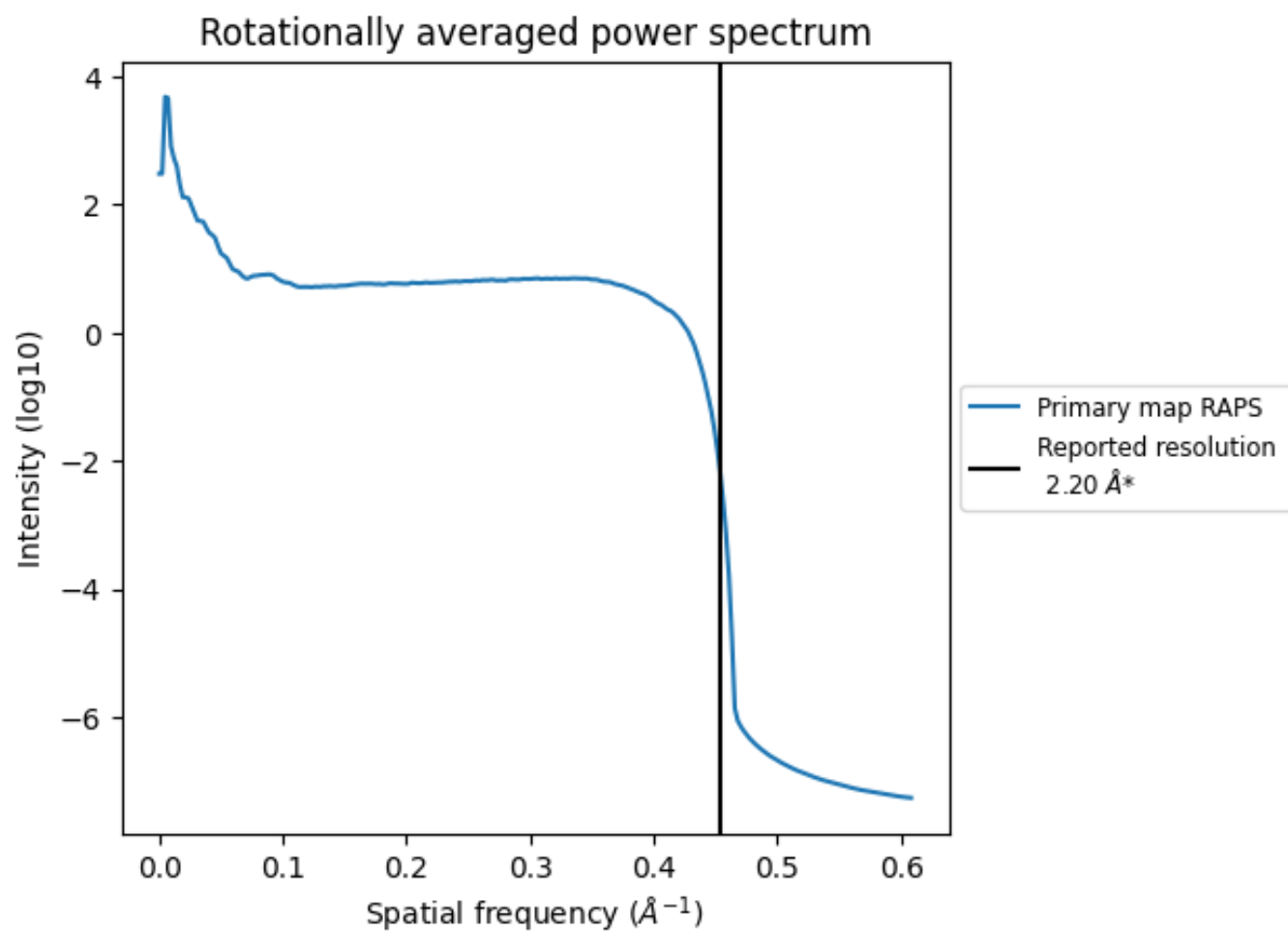
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 266 nm³; this corresponds to an approximate mass of 240 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 0.455 Å⁻¹

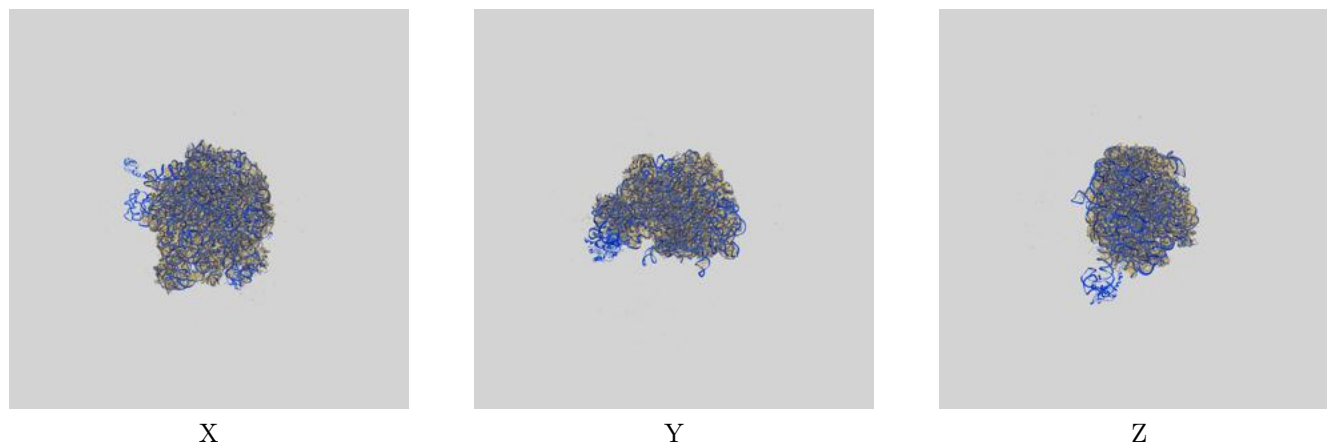
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

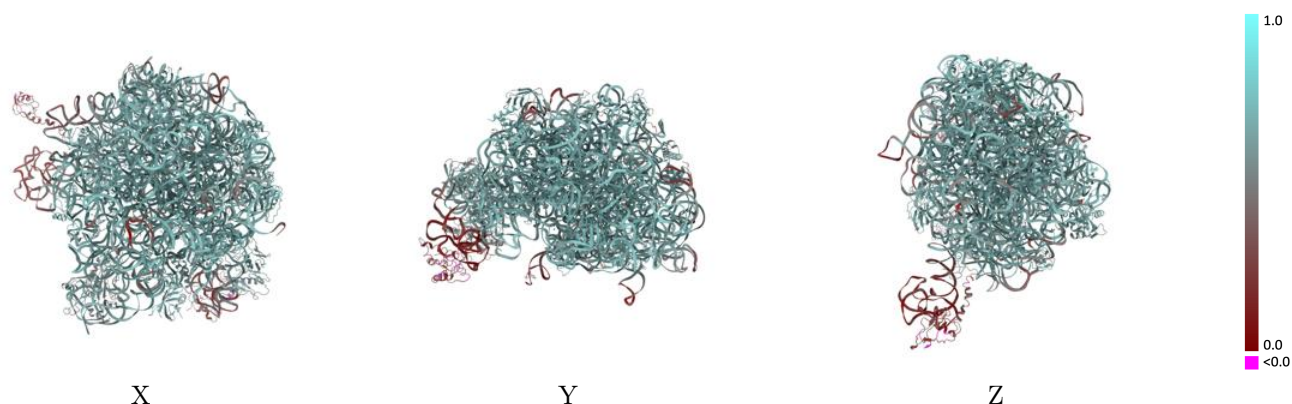
This section contains information regarding the fit between EMDB map EMD-20353 and PDB model 6PJ6. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



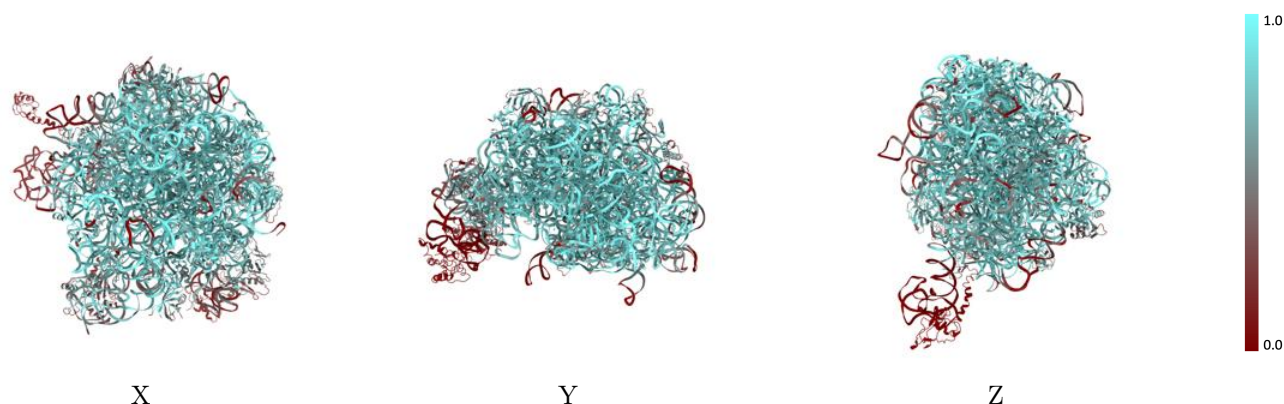
The images above show the 3D surface view of the map at the recommended contour level 10.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



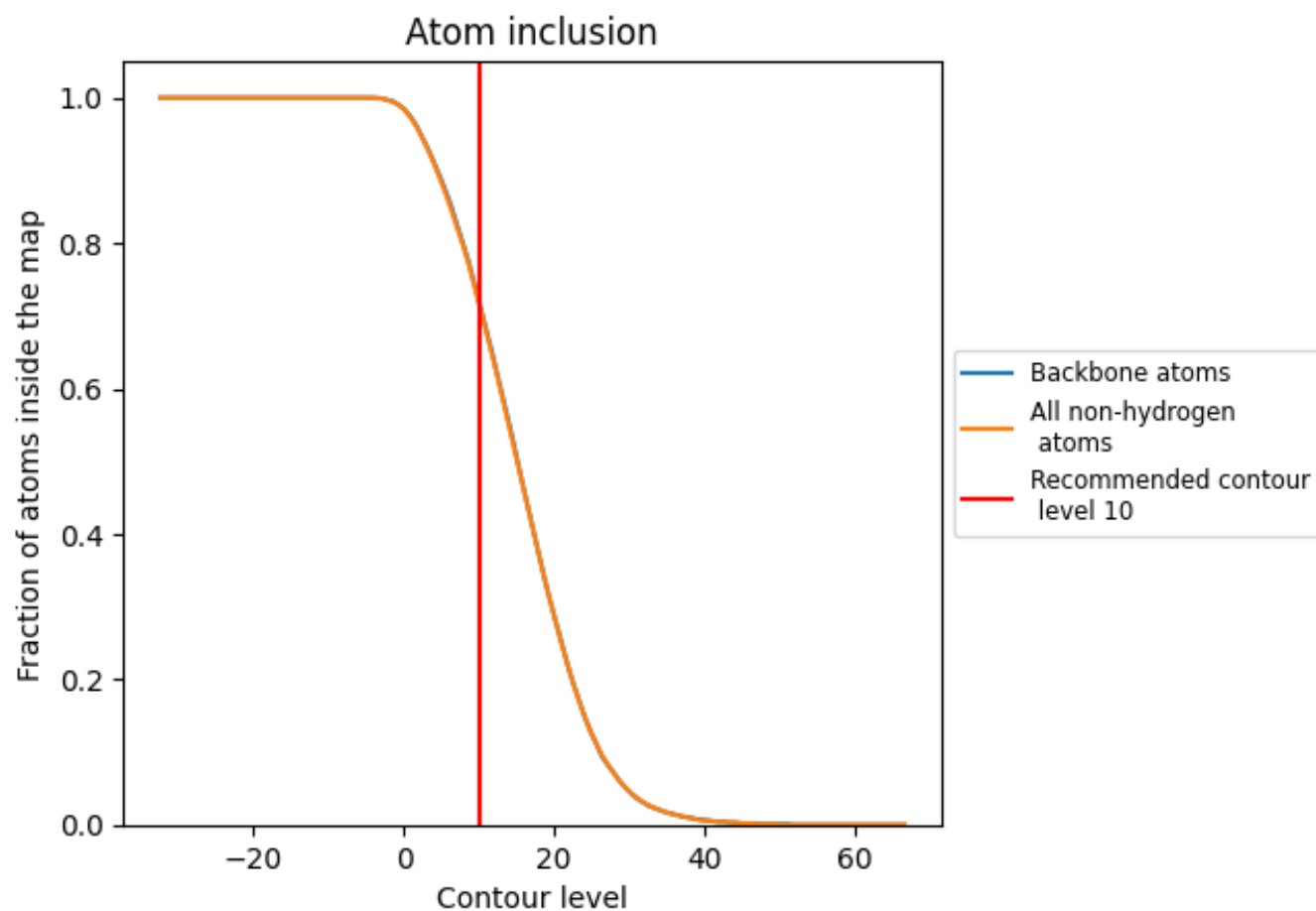
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (10).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 72% 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 (10) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7190	 0.6160
I	 0.7610	 0.6180
J	 0.6860	 0.6150
K	 0.7910	 0.6730
L	 0.7800	 0.6700
M	 0.6780	 0.6470
N	 0.1220	 0.4500
O	 0.4460	 0.5820
P	 0.1270	 0.3310
Q	 0.0000	 0.2260
R	 0.7690	 0.6740
S	 0.6980	 0.6520
T	 0.7520	 0.6650
U	 0.7400	 0.6650
V	 0.8400	 0.6810
W	 0.5700	 0.6060
X	 0.6670	 0.6330
Y	 0.8390	 0.6930
Z	 0.7290	 0.6440
a	 0.7490	 0.6570
b	 0.6390	 0.6360
c	 0.5990	 0.6150
d	 0.6350	 0.6360
e	 0.7910	 0.6630
f	 0.7140	 0.6620
g	 0.5400	 0.6070
h	 0.7480	 0.6580
i	 0.7520	 0.6600
j	 0.5960	 0.6200
k	 0.8370	 0.6900
l	 0.8370	 0.6870
m	 0.7070	 0.6500

