



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 12:52 AM EST

PDB ID : 6U48
EMDB ID : EMD-20638
Title : E. coli 50S with phazolicin (PHZ) bound in exit tunnel
Authors : Watson, Z.L.; Cate, J.H.D.; Polikanov, Y.S.; Severinov, K.
Deposited on : 2019-08-23
Resolution : 2.87 Å (reported)
Based on initial model : 4YBB

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

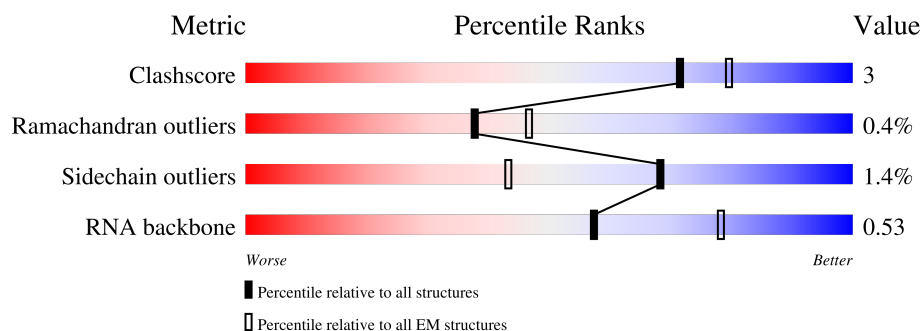
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.87 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	CA	2904	<div> <div>31%</div> <div>68%</div> <div>27%</div> <div>5%</div> </div>
2	CB	118	<div> <div>77%</div> <div>66%</div> <div>31%</div> <div>.</div> </div>
3	CC	271	<div> <div>35%</div> <div>79%</div> <div>20%</div> <div>.</div> </div>
4	CD	209	<div> <div>35%</div> <div>92%</div> <div>8%</div> </div>
5	CE	201	<div> <div>59%</div> <div>89%</div> <div>10%</div> <div>.</div> </div>
6	CF	177	<div> <div>100%</div> <div>77%</div> <div>20%</div> <div>..</div> </div>
7	CG	176	<div> <div>100%</div> <div>89%</div> <div>10%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
8	CH	149	
9	CJ	134	
10	CK	142	
11	CL	122	
12	CM	144	
13	CN	136	
14	CO	120	
15	CP	116	
16	CQ	114	
17	CR	117	
18	CS	103	
19	CT	110	
20	CU	93	
21	CV	102	
22	CW	94	
23	CX	75	
24	CY	77	
25	CZ	62	
26	C0	58	
27	C1	56	
28	C2	50	
29	C3	46	
30	C4	64	
31	C5	38	
32	A	22	

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 90950 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CA	2898	Total	C	N	O	P	0	0
			62229	27768	11448	20115	2898		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CB	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 3 is a protein called 50S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CC	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 4 is a protein called 50S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CD	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 5 is a protein called 50S ribosomal protein uL4.

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

- Molecule 6 is a protein called 50S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CF	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 7 is a protein called 50S ribosomal protein uL6.

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

- Molecule 8 is a protein called 50S ribosomal protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CH	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 9 is a protein called 50S ribosomal protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CJ	134	Total	C	N	O	S	0	0
			979	619	169	185	6		

- Molecule 10 is a protein called 50S ribosomal protein uL13.

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

- Molecule 11 is a protein called 50S ribosomal protein uL14.

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

- Molecule 12 is a protein called 50S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CM	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 13 is a protein called 50S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CN	136	Total	C	N	O	S	0	0
			1075	686	205	178	6		

- Molecule 14 is a protein called 50S ribosomal protein bL17.

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

- Molecule 15 is a protein called 50S ribosomal protein uL18.

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

- Molecule 16 is a protein called 50S ribosomal protein bL19.

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

- Molecule 17 is a protein called 50S ribosomal protein bL20.

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

- Molecule 18 is a protein called 50S ribosomal protein bL21.

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

- Molecule 19 is a protein called 50S ribosomal protein uL22.

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

- Molecule 20 is a protein called 50S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CU	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 21 is a protein called 50S ribosomal protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	CV	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 22 is a protein called 50S ribosomal protein bL25.

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

- Molecule 23 is a protein called 50S ribosomal protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	CX	75	Total	C	N	O	S	0
			569	353	113	102	1	0

- Molecule 24 is a protein called 50S ribosomal protein bL28.

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

- Molecule 25 is a protein called 50S ribosomal protein uL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	CZ	62	Total	C	N	O	S	0
			501	308	98	94	1	0

- Molecule 26 is a protein called 50S ribosomal protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	C0	58	Total	C	N	O	S	0
			449	281	87	79	2	0

- Molecule 27 is a protein called 50S ribosomal protein bL32.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	C1	56	Total	C	N	O	S	0
			444	269	94	80	1	0

- Molecule 28 is a protein called 50S ribosomal protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	C2	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 29 is a protein called 50S ribosomal protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	C3	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	C4	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	C5	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

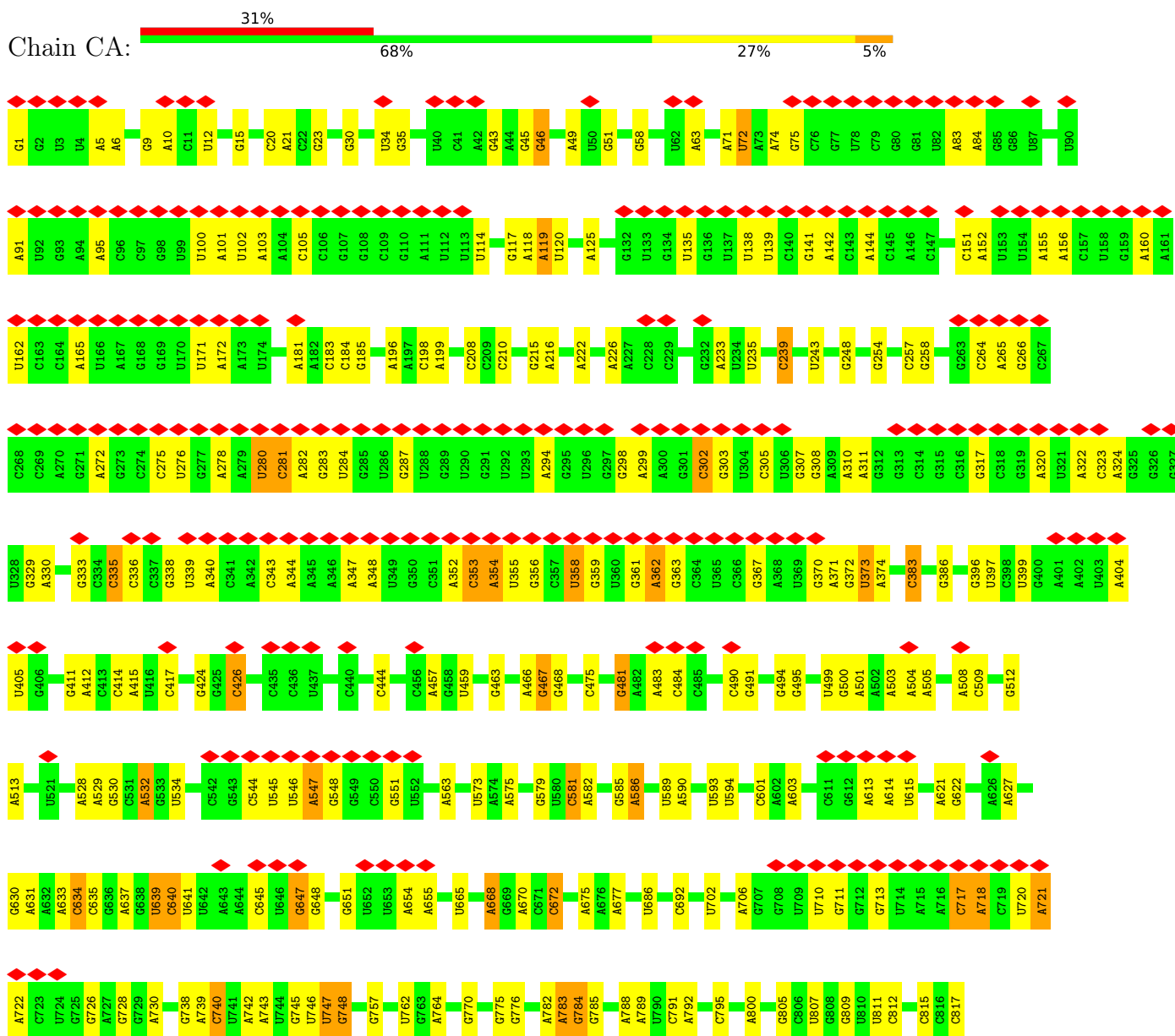
- Molecule 32 is a protein called phazolicin.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	A	22	Total	C	N	O	S	0	0
			132	74	29	26	3		

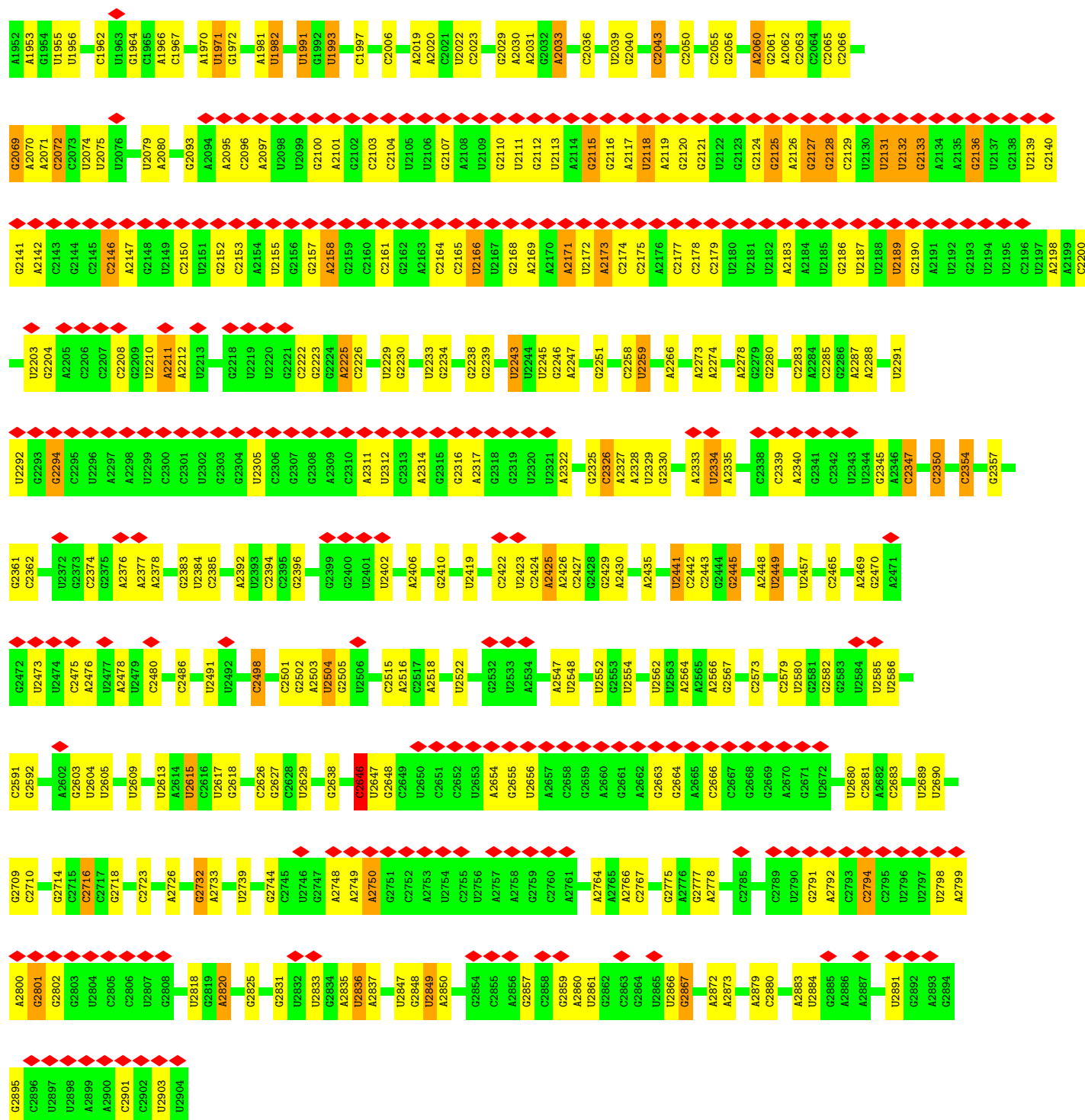
3 Residue-property plots

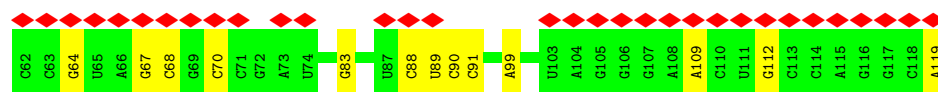
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

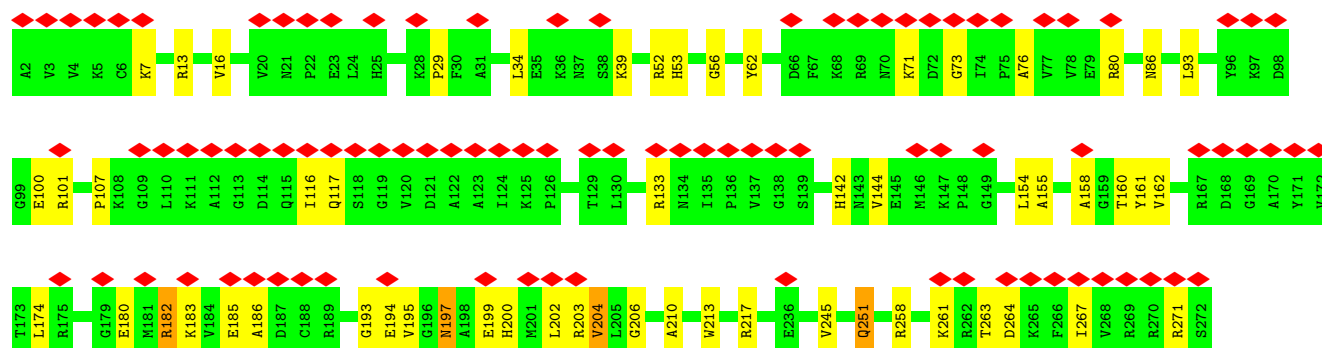
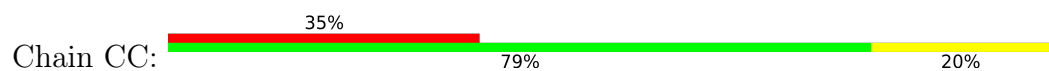




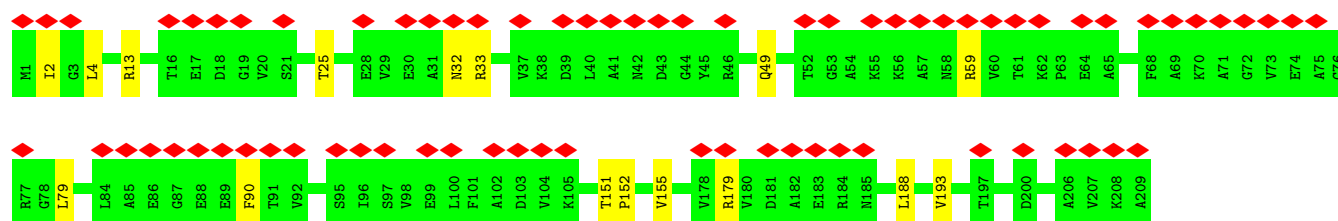




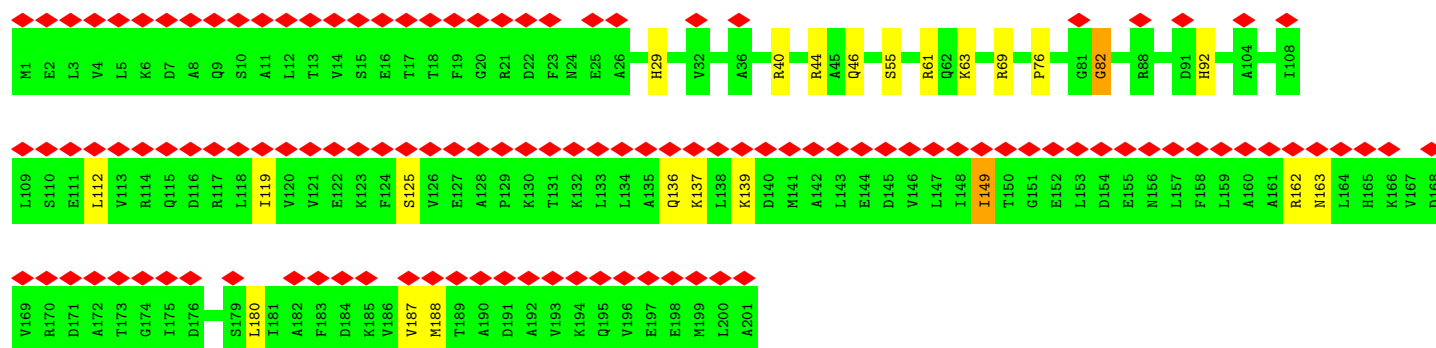
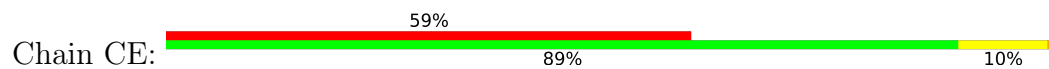
• Molecule 3: 50S ribosomal protein uL2



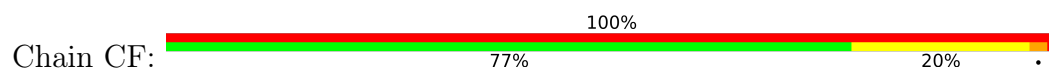
• Molecule 4: 50S ribosomal protein uL3

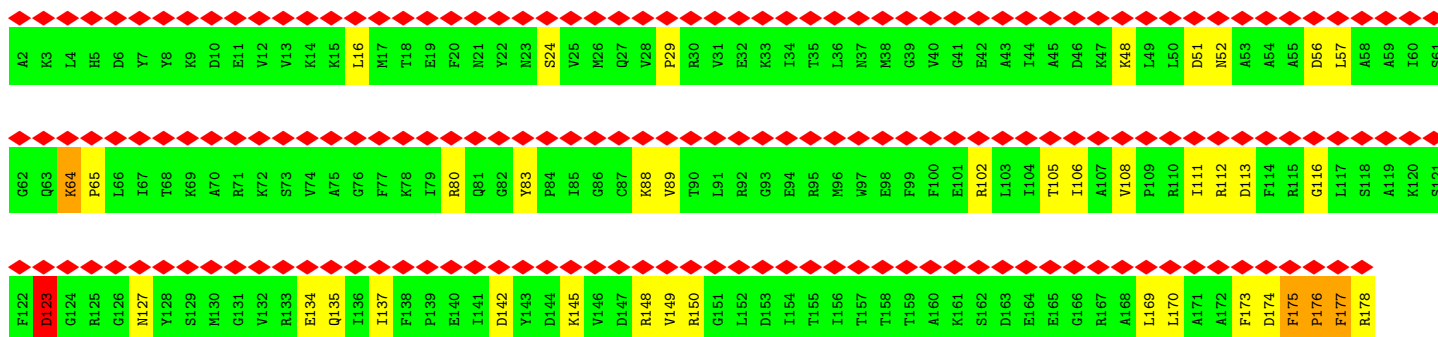


• Molecule 5: 50S ribosomal protein uL4

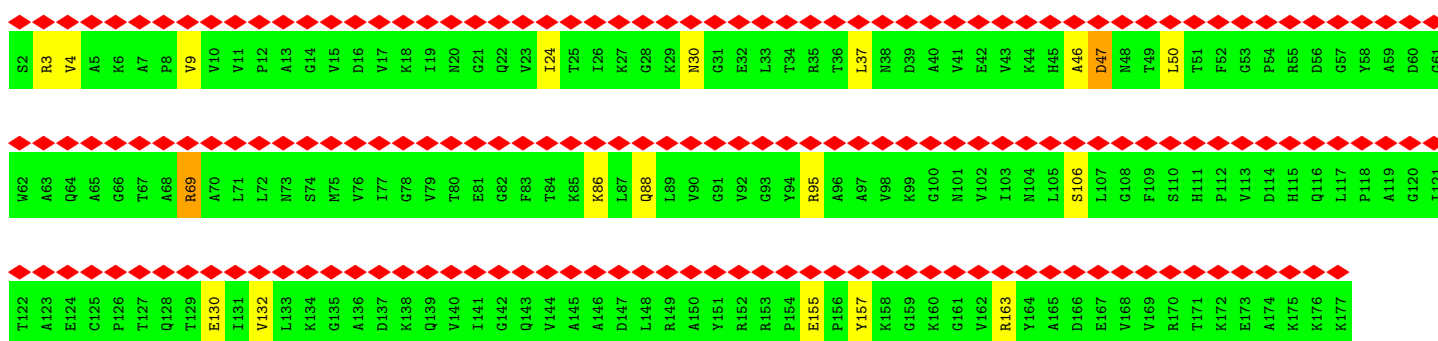
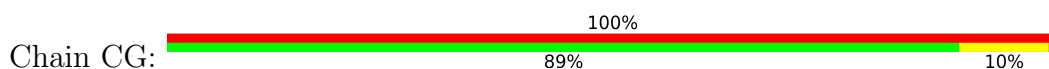


• Molecule 6: 50S ribosomal protein uL5





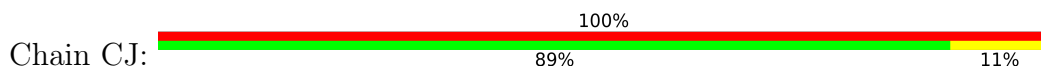
• Molecule 7: 50S ribosomal protein uL6

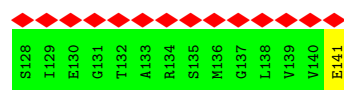


• Molecule 8: 50S ribosomal protein bL9

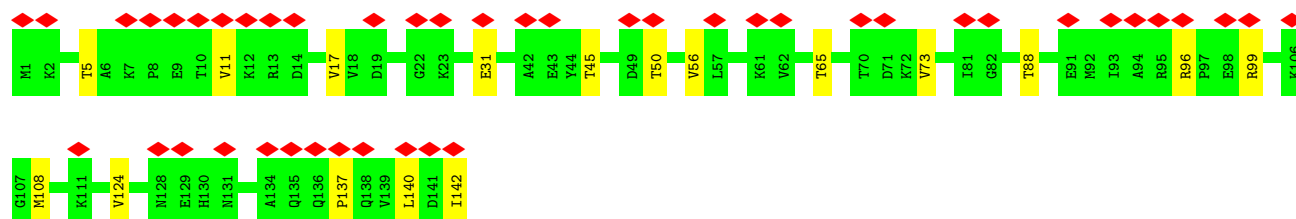
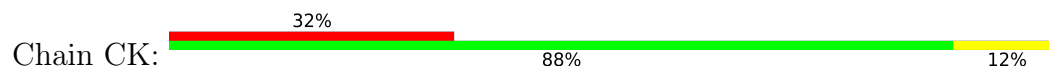


• Molecule 9: 50S ribosomal protein uL11

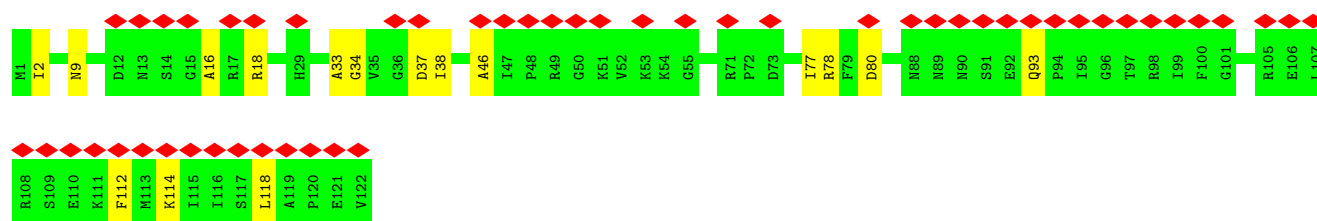
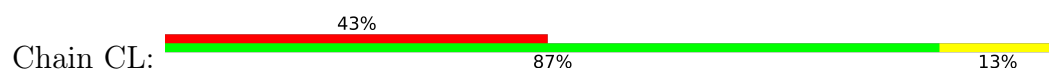




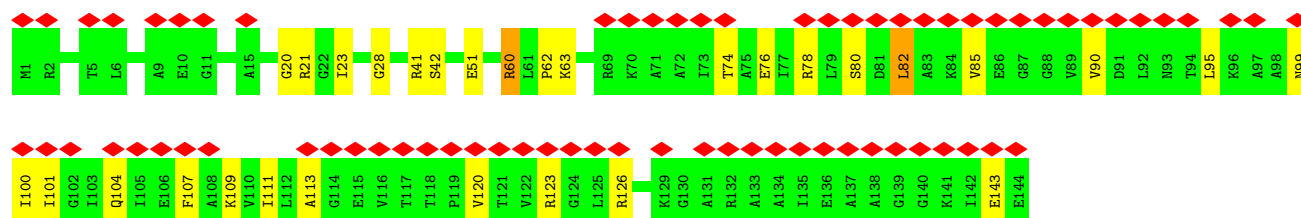
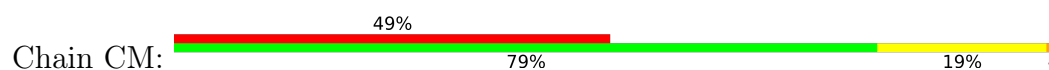
- Molecule 10: 50S ribosomal protein uL13



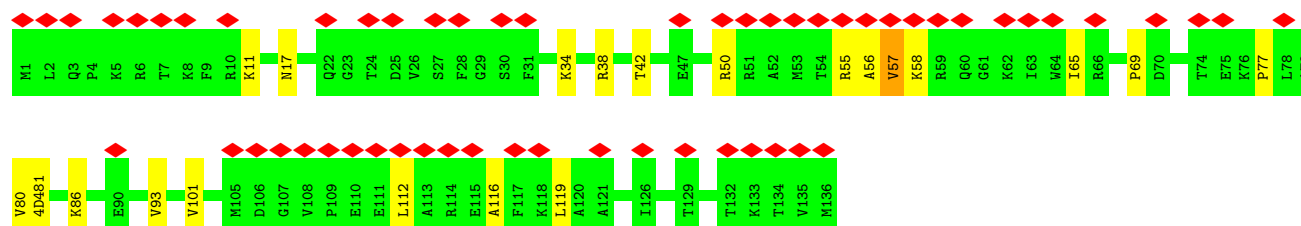
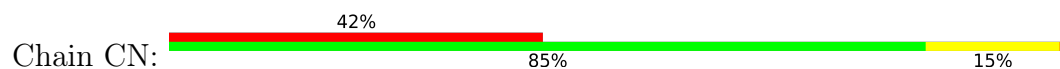
- Molecule 11: 50S ribosomal protein uL14



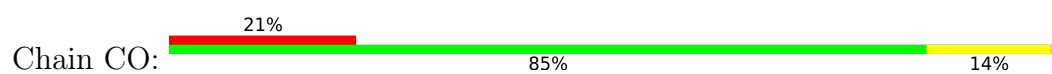
- Molecule 12: 50S ribosomal protein uL15



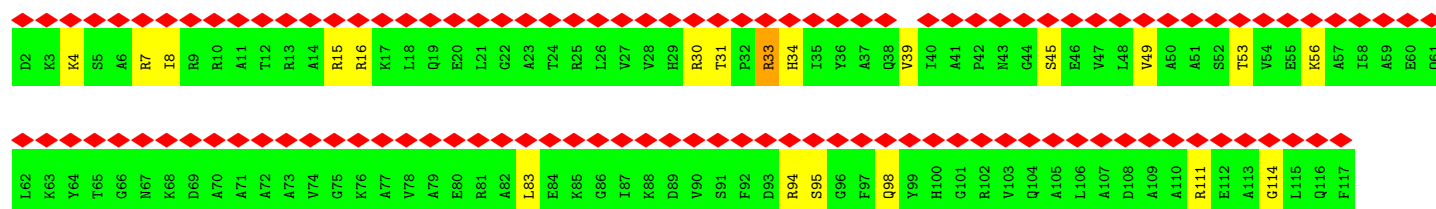
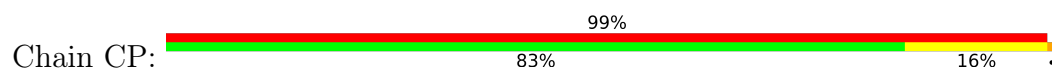
- Molecule 13: 50S ribosomal protein uL16



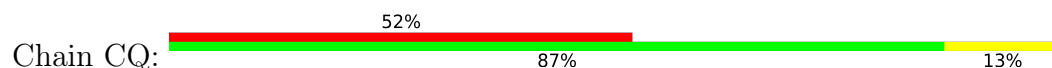
- Molecule 14: 50S ribosomal protein bL17



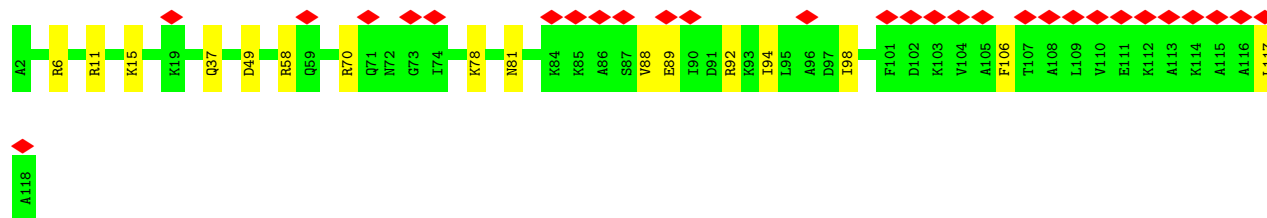
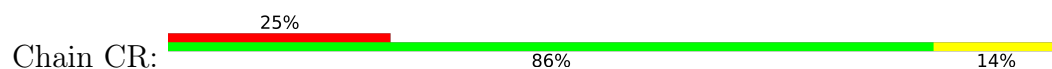
• Molecule 15: 50S ribosomal protein uL18



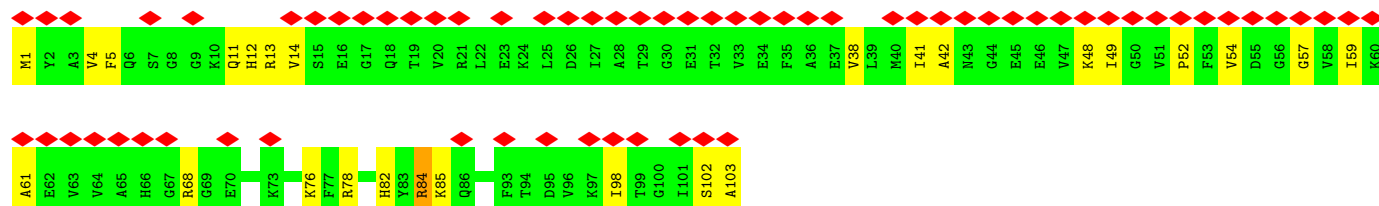
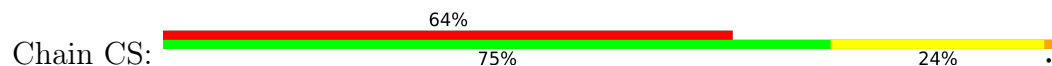
• Molecule 16: 50S ribosomal protein bL19



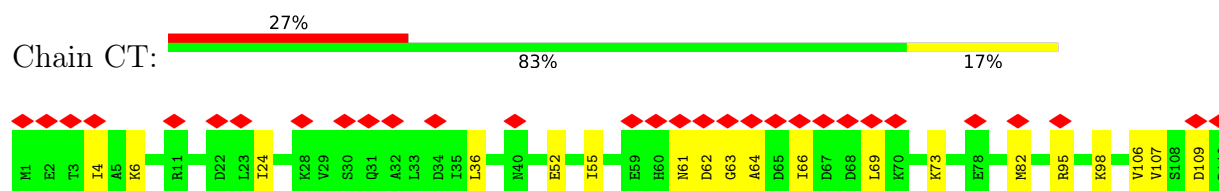
• Molecule 17: 50S ribosomal protein bL20



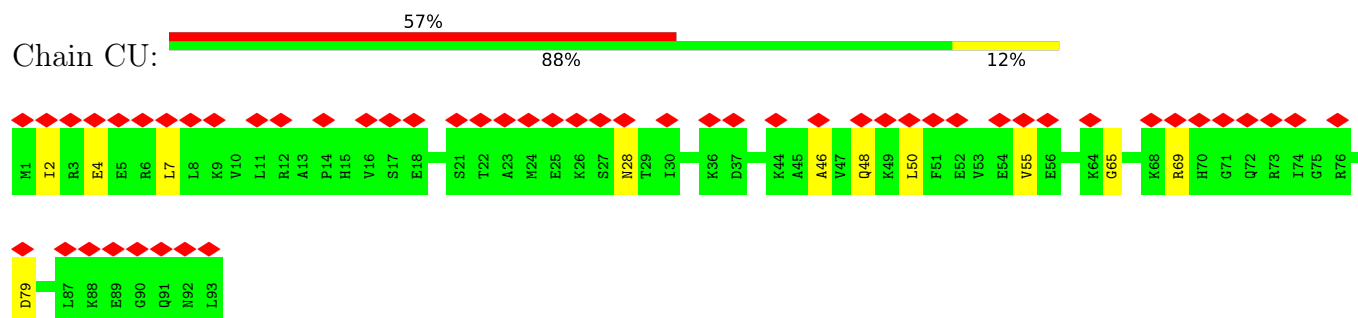
• Molecule 18: 50S ribosomal protein bL21



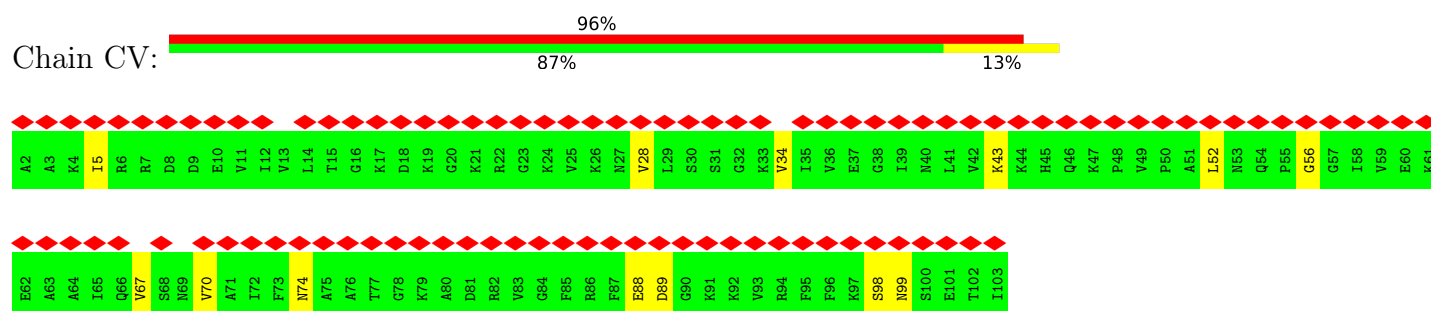
- Molecule 19: 50S ribosomal protein uL22



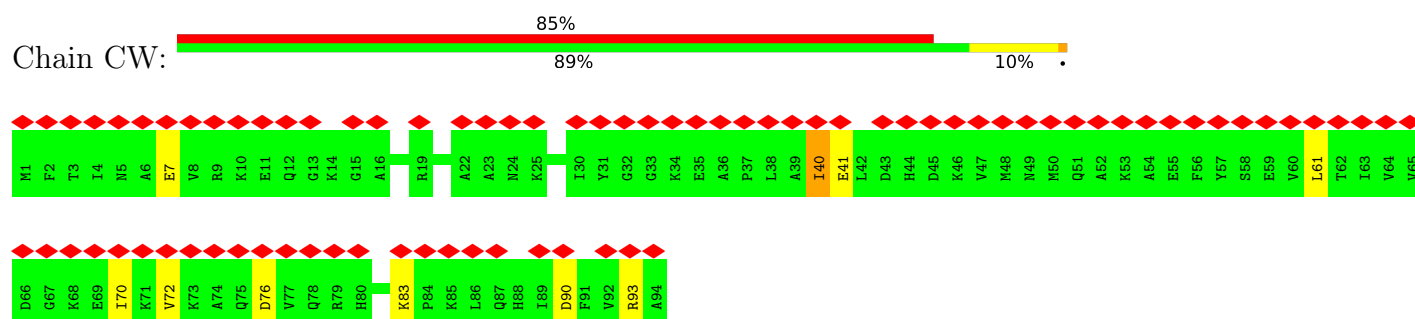
- Molecule 20: 50S ribosomal protein uL23



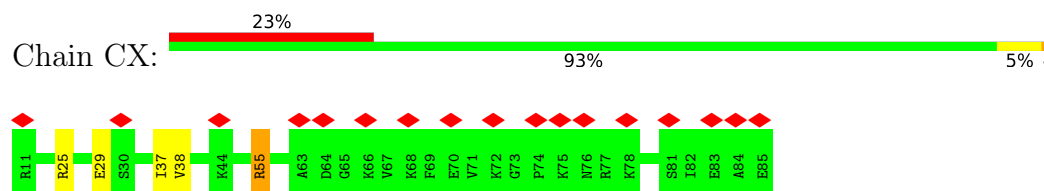
- Molecule 21: 50S ribosomal protein uL24



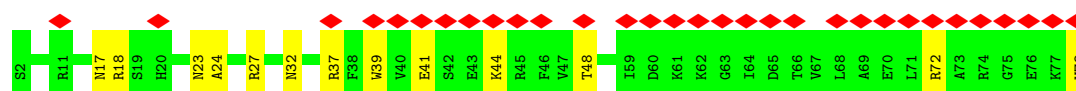
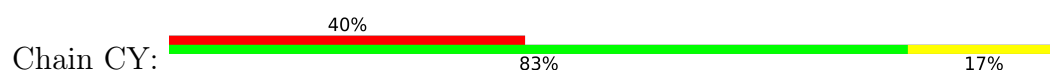
- Molecule 22: 50S ribosomal protein bL25



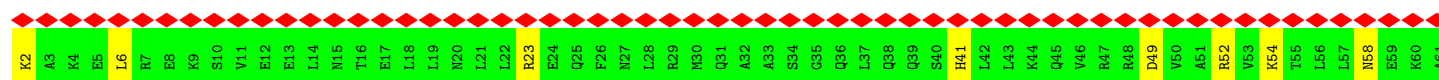
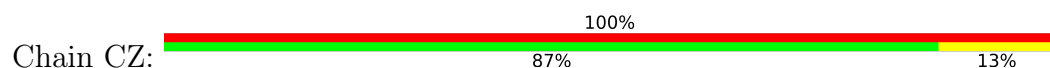
- Molecule 23: 50S ribosomal protein bL27



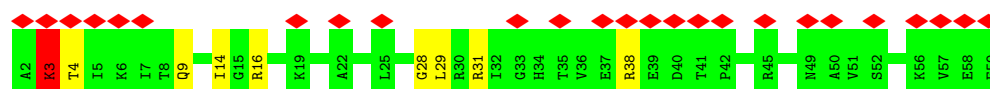
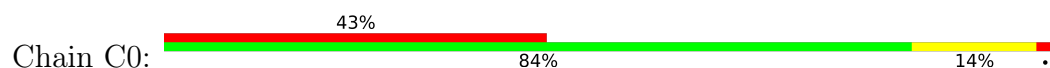
- Molecule 24: 50S ribosomal protein bL28



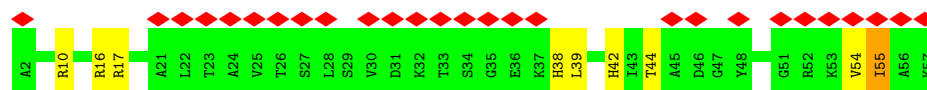
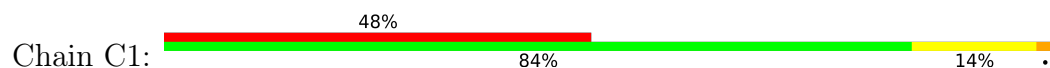
- Molecule 25: 50S ribosomal protein uL29



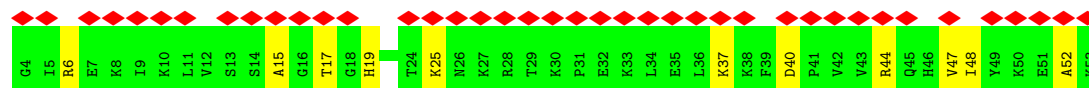
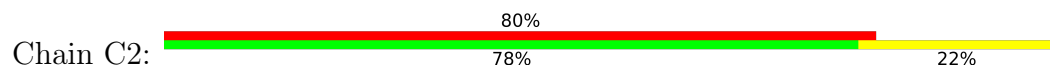
- Molecule 26: 50S ribosomal protein uL30



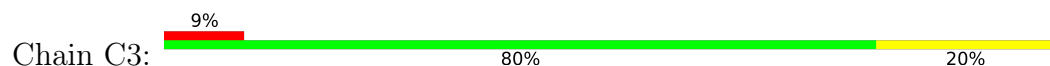
- Molecule 27: 50S ribosomal protein bL32



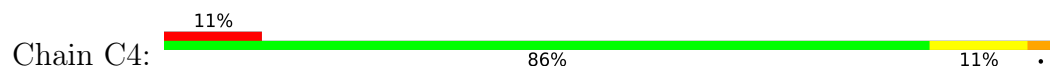
- Molecule 28: 50S ribosomal protein bL33

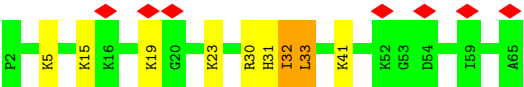


- Molecule 29: 50S ribosomal protein bL34

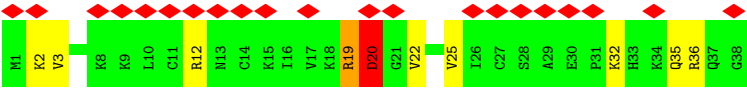
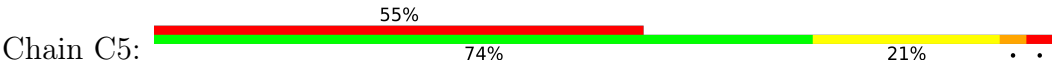


- Molecule 30: 50S ribosomal protein bL35

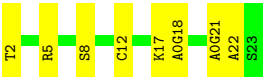




• Molecule 31: 50S ribosomal protein bL36



• Molecule 32: phazolicin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	65393	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 ($e^-/\text{\AA}^2$)	30.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.214	Depositor
Minimum map value	-0.141	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.027	Depositor
Map size (\AA)	356.352, 356.352, 356.352	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1136, 1.1136, 1.1136	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: A0G, PSU, MEQ, OMC, BB9, G7M, OMG, 4D4, 2MG, 6MZ, 5MU, 2MA, 5MC, H2U, OMU, 3TD, 1MG

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	CA	0.56	0/69143	1.09	259/107862 (0.2%)
2	CB	0.40	0/2828	1.10	15/4410 (0.3%)
3	CC	0.33	0/2122	0.61	0/2852
4	CD	0.36	0/1576	0.61	0/2119
5	CE	0.32	0/1571	0.57	0/2113
6	CF	0.31	0/1435	0.63	1/1926 (0.1%)
7	CG	0.28	0/1343	0.59	0/1816
8	CH	0.29	0/1121	0.60	0/1515
9	CJ	0.30	0/993	0.60	0/1341
10	CK	0.33	0/1152	0.55	0/1551
11	CL	0.35	0/947	0.62	0/1268
12	CM	0.33	0/1062	0.70	2/1413 (0.1%)
13	CN	0.33	0/1081	0.59	0/1443
14	CO	0.33	0/973	0.60	0/1301
15	CP	0.29	0/902	0.56	0/1209
16	CQ	0.31	0/929	0.57	1/1242 (0.1%)
17	CR	0.36	0/960	0.53	0/1278
18	CS	0.34	0/829	0.60	0/1107
19	CT	0.32	0/864	0.60	0/1156
20	CU	0.30	0/745	0.60	0/994
21	CV	0.33	0/788	0.68	2/1051 (0.2%)
22	CW	0.29	0/766	0.56	0/1025
23	CX	0.35	0/576	0.52	0/762
24	CY	0.31	0/635	0.54	0/848
25	CZ	0.27	0/502	0.58	0/667
26	C0	0.29	0/453	0.61	0/605
27	C1	0.35	0/450	0.71	0/599
28	C2	0.33	0/416	0.64	0/554
29	C3	0.35	0/380	0.64	0/498
30	C4	0.34	0/513	0.72	1/676 (0.1%)
31	C5	0.35	0/303	0.76	2/397 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	A	0.35	0/82	0.49	0/97
All	All	0.50	0/98440	1.00	283/147695 (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
4	CD	0	1
5	CE	0	1
6	CF	0	1
7	CG	0	2
8	CH	0	1
11	CL	0	1
13	CN	0	1
15	CP	0	1
19	CT	0	1
21	CV	0	1
26	C0	0	1
27	C1	0	1
30	C4	0	1
31	C5	0	3
All	All	0	17

There are no bond length outliers.

The worst 5 of 283 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1313	U	C2-N1-C1'	10.11	129.83	117.70
1	CA	1313	U	N3-C2-O2	-9.92	115.25	122.20
1	CA	1313	U	N1-C2-O2	9.66	129.56	122.80
1	CA	426	C	N1-C2-O2	9.14	124.39	118.90
2	CB	31	C	N1-C2-O2	8.90	124.24	118.90

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	CD	151	THR	Peptide
5	CE	82	GLY	Peptide

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Mol	Chain	Res	Type	Group
6	CF	174	ASP	Peptide
7	CG	46	ALA	Peptide
7	CG	47	ASP	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	CA	62229	0	31320	258	0
2	CB	2529	0	1281	14	0
3	CC	2083	0	2154	34	0
4	CD	1566	0	1618	8	0
5	CE	1552	0	1619	16	0
6	CF	1411	0	1444	22	0
7	CG	1323	0	1371	8	0
8	CH	1110	0	1148	11	0
9	CJ	979	0	1028	8	0
10	CK	1129	0	1162	10	0
11	CL	938	0	1012	8	0
12	CM	1053	0	1129	19	0
13	CN	1075	0	1155	10	0
14	CO	960	0	1000	11	0
15	CP	892	0	923	16	0
16	CQ	917	0	962	10	0
17	CR	947	0	1019	14	0
18	CS	816	0	839	17	0
19	CT	857	0	922	12	0
20	CU	739	0	807	5	0
21	CV	780	0	831	5	0
22	CW	753	0	780	7	0
23	CX	569	0	581	3	0
24	CY	625	0	652	8	0
25	CZ	501	0	531	5	0
26	C0	449	0	488	7	0
27	C1	444	0	458	6	0
28	C2	409	0	440	6	0
29	C3	377	0	418	8	0
30	C4	504	0	572	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	C5	302	0	343	4	0
32	A	132	0	95	3	0
All	All	90950	0	60102	491	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 3.

The worst 5 of 491 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)
1:CA:1093:G:H21	1:CA:1098:A:H62	1.01	0.99
1:CA:1093:G:N2	1:CA:1098:A:H62	1.64	0.95
1:CA:284:U:H3	1:CA:356:G:H1	1.25	0.81
1:CA:1607:C:N4	1:CA:1622:G:OP2	2.15	0.79
1:CA:1715:G:N2	1:CA:1744:A:OP2	2.15	0.79

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	CC	269/271 (99%)	254 (94%)	15 (6%)	0	100	100
4	CD	206/209 (99%)	197 (96%)	8 (4%)	1 (0%)	29	59
5	CE	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
6	CF	175/177 (99%)	155 (89%)	17 (10%)	3 (2%)	9	28
7	CG	174/176 (99%)	155 (89%)	18 (10%)	1 (1%)	25	55
8	CH	147/149 (99%)	134 (91%)	13 (9%)	0	100	100
9	CJ	132/134 (98%)	124 (94%)	8 (6%)	0	100	100
10	CK	140/142 (99%)	137 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	CL	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
12	CM	142/144 (99%)	130 (92%)	12 (8%)	0	100	100
13	CN	133/136 (98%)	127 (96%)	4 (3%)	2 (2%)	10	32
14	CO	118/120 (98%)	111 (94%)	7 (6%)	0	100	100
15	CP	114/116 (98%)	103 (90%)	11 (10%)	0	100	100
16	CQ	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
17	CR	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
18	CS	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
19	CT	108/110 (98%)	101 (94%)	6 (6%)	1 (1%)	17	45
20	CU	91/93 (98%)	85 (93%)	6 (7%)	0	100	100
21	CV	100/102 (98%)	80 (80%)	18 (18%)	2 (2%)	7	25
22	CW	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
23	CX	73/75 (97%)	70 (96%)	3 (4%)	0	100	100
24	CY	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
25	CZ	60/62 (97%)	56 (93%)	4 (7%)	0	100	100
26	C0	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
27	C1	54/56 (96%)	47 (87%)	6 (11%)	1 (2%)	8	26
28	C2	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
29	C3	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
30	C4	62/64 (97%)	56 (90%)	4 (6%)	2 (3%)	4	14
31	C5	36/38 (95%)	34 (94%)	1 (3%)	1 (3%)	5	17
32	A	5/22 (23%)	5 (100%)	0	0	100	100
All	All	3301/3378 (98%)	3081 (93%)	206 (6%)	14 (0%)	38	64

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	CG	47	ASP
13	CN	58	LYS
21	CV	89	ASP
30	C4	32	ILE
30	C4	33	LEU

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	CC	216/216 (100%)	211 (98%)	5 (2%)	50	79
4	CD	163/163 (100%)	162 (99%)	1 (1%)	86	95
5	CE	165/165 (100%)	163 (99%)	2 (1%)	71	89
6	CF	148/148 (100%)	145 (98%)	3 (2%)	55	81
7	CG	137/137 (100%)	134 (98%)	3 (2%)	52	80
8	CH	114/114 (100%)	113 (99%)	1 (1%)	78	92
9	CJ	104/104 (100%)	104 (100%)	0	100	100
10	CK	116/116 (100%)	116 (100%)	0	100	100
11	CL	103/103 (100%)	102 (99%)	1 (1%)	76	91
12	CM	103/103 (100%)	102 (99%)	1 (1%)	76	91
13	CN	108/108 (100%)	108 (100%)	0	100	100
14	CO	100/100 (100%)	99 (99%)	1 (1%)	76	91
15	CP	86/86 (100%)	84 (98%)	2 (2%)	50	79
16	CQ	99/99 (100%)	98 (99%)	1 (1%)	76	91
17	CR	89/89 (100%)	88 (99%)	1 (1%)	73	90
18	CS	84/84 (100%)	82 (98%)	2 (2%)	49	78
19	CT	93/93 (100%)	92 (99%)	1 (1%)	73	90
20	CU	80/80 (100%)	78 (98%)	2 (2%)	47	77
21	CV	83/83 (100%)	82 (99%)	1 (1%)	71	89
22	CW	78/78 (100%)	77 (99%)	1 (1%)	69	88
23	CX	56/57 (98%)	55 (98%)	1 (2%)	59	83
24	CY	67/67 (100%)	65 (97%)	2 (3%)	41	73
25	CZ	54/54 (100%)	53 (98%)	1 (2%)	57	82
26	C0	48/48 (100%)	47 (98%)	1 (2%)	53	80
27	C1	47/47 (100%)	46 (98%)	1 (2%)	53	80
28	C2	45/45 (100%)	45 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	C3	38/38 (100%)	38 (100%)	0	100	100
30	C4	51/51 (100%)	51 (100%)	0	100	100
31	C5	34/34 (100%)	33 (97%)	1 (3%)	42	74
32	A	9/9 (100%)	8 (89%)	1 (11%)	6	17
All	All	2718/2719 (100%)	2681 (99%)	37 (1%)	68	87

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	CW	40	ILE
31	C5	12	ARG
23	CX	55	ARG
25	CZ	58	ASN
7	CG	30	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
17	CR	37	GLN
19	CT	61	ASN
18	CS	82	HIS
20	CU	28	ASN
6	CF	52	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CA	2892/2904 (99%)	517 (17%)	12 (0%)
2	CB	117/118 (99%)	18 (15%)	0
All	All	3009/3022 (99%)	535 (17%)	12 (0%)

5 of 535 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	CA	10	A
1	CA	15	G
1	CA	23	G
1	CA	34	U
1	CA	35	G

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	CA	2146	C
1	CA	2225	A
1	CA	2680	U
1	CA	2326	C
1	CA	647	G

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

32 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	OMG	CA	2251	1	18,26,27	0.94	1 (5%)	19,38,41	1.09	2 (10%)
1	PSU	CA	1911	1	18,21,22	1.37	2 (11%)	22,30,33	1.84	3 (13%)
1	OMU	CA	2552	1	19,22,23	1.24	3 (15%)	26,31,34	1.65	5 (19%)
1	PSU	CA	746	1	18,21,22	1.36	4 (22%)	22,30,33	1.83	4 (18%)
1	2MA	CA	2503	1	17,25,26	0.89	0	17,37,40	1.19	1 (5%)
1	PSU	CA	2580	1	18,21,22	1.58	5 (27%)	22,30,33	1.85	4 (18%)
32	BB9	A	3	32	3,5,6	0.55	0	1,5,7	1.83	0
13	4D4	CN	81	13	9,11,12	1.96	2 (22%)	8,13,15	0.85	0
1	1MG	CA	745	1	18,26,27	0.69	0	19,39,42	1.04	2 (10%)
32	BB9	A	6	32	3,5,6	0.56	0	1,5,7	0.95	0
1	6MZ	CA	2030	1	18,25,26	0.79	1 (5%)	16,36,39	2.61	5 (31%)
1	5MU	CA	747	1	19,22,23	1.40	4 (21%)	28,32,35	2.06	7 (25%)
32	A0G	A	15	32	4,5,6	0.55	0	1,5,7	1.47	0
1	2MG	CA	2445	1	18,26,27	1.07	1 (5%)	16,38,41	1.01	1 (6%)
1	H2U	CA	2449	1	18,21,22	1.14	3 (16%)	21,30,33	1.62	1 (4%)
1	PSU	CA	955	1	18,21,22	1.40	3 (16%)	22,30,33	1.96	4 (18%)
1	OMC	CA	2498	1	19,22,23	0.91	0	26,31,34	1.19	1 (3%)
1	PSU	CA	2457	1	18,21,22	1.43	4 (22%)	22,30,33	1.96	3 (13%)
1	3TD	CA	1915	1	18,22,23	1.61	4 (22%)	22,32,35	1.97	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	A0G	A	21	32	4,5,6	0.59	0	1,5,7	3.39	1 (100%)
32	A0G	A	18	32	4,5,6	0.58	0	1,5,7	2.13	1 (100%)
4	MEQ	CD	150	4	8,9,10	0.70	0	5,10,12	0.79	0
1	PSU	CA	2504	1	18,21,22	1.50	4 (22%)	22,30,33	1.83	4 (18%)
1	5MC	CA	1962	1	18,22,23	0.89	2 (11%)	26,32,35	1.07	2 (7%)
32	BB9	A	12	32	3,5,6	0.37	0	1,5,7	2.25	1 (100%)
1	2MG	CA	1835	1	18,26,27	0.93	1 (5%)	16,38,41	1.10	2 (12%)
1	5MU	CA	1939	1	19,22,23	1.42	4 (21%)	28,32,35	2.33	6 (21%)
1	G7M	CA	2069	1	20,26,27	1.26	2 (10%)	17,39,42	0.77	0
32	A0G	A	9	32	4,5,6	0.59	0	1,5,7	0.95	0
1	PSU	CA	2605	1	18,21,22	1.34	3 (16%)	22,30,33	1.91	3 (13%)
1	PSU	CA	1917	1	18,21,22	1.40	3 (16%)	22,30,33	1.92	4 (18%)
1	6MZ	CA	1618	1	18,25,26	0.81	1 (5%)	16,36,39	2.05	4 (25%)

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	OMG	CA	2251	1	-	0/5/27/28	0/3/3/3
1	PSU	CA	1911	1	-	0/7/25/26	0/2/2/2
1	OMU	CA	2552	1	-	0/9/27/28	0/2/2/2
1	PSU	CA	746	1	-	2/7/25/26	0/2/2/2
1	2MA	CA	2503	1	-	2/3/25/26	0/3/3/3
1	PSU	CA	2580	1	-	0/7/25/26	0/2/2/2
32	BB9	A	3	32	-	0/0/4/6	-
13	4D4	CN	81	13	-	1/11/12/14	-
1	1MG	CA	745	1	-	0/3/25/26	0/3/3/3
32	BB9	A	6	32	-	0/0/4/6	-
1	6MZ	CA	2030	1	-	2/5/27/28	0/3/3/3
1	5MU	CA	747	1	-	1/7/25/26	0/2/2/2
32	A0G	A	15	32	-	0/0/4/6	-
1	2MG	CA	2445	1	-	2/5/27/28	0/3/3/3
1	H2U	CA	2449	1	-	2/7/38/39	0/2/2/2
1	PSU	CA	955	1	-	0/7/25/26	0/2/2/2
1	OMC	CA	2498	1	-	0/9/27/28	0/2/2/2
1	PSU	CA	2457	1	-	0/7/25/26	0/2/2/2
1	3TD	CA	1915	1	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	A0G	A	21	32	-	0/0/4/6	-
32	A0G	A	18	32	-	0/0/4/6	-
4	MEQ	CD	150	4	-	6/8/9/11	-
1	PSU	CA	2504	1	-	2/7/25/26	0/2/2/2
1	5MC	CA	1962	1	-	0/7/25/26	0/2/2/2
32	BB9	A	12	32	-	0/0/4/6	-
1	2MG	CA	1835	1	-	0/5/27/28	0/3/3/3
1	5MU	CA	1939	1	-	0/7/25/26	0/2/2/2
1	G7M	CA	2069	1	-	1/3/25/26	0/3/3/3
32	A0G	A	9	32	-	0/0/4/6	-
1	PSU	CA	2605	1	-	0/7/25/26	0/2/2/2
1	PSU	CA	1917	1	-	1/7/25/26	0/2/2/2
1	6MZ	CA	1618	1	-	0/5/27/28	0/3/3/3

The worst 5 of 57 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	CN	81	4D4	CZ-NE	4.13	1.41	1.33
1	CA	2069	G7M	C5-C4	3.55	1.46	1.39
1	CA	1917	PSU	C6-C5	3.41	1.39	1.35
1	CA	2580	PSU	C4-N3	-3.36	1.32	1.38
1	CA	1911	PSU	C6-C5	3.33	1.39	1.35

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	2030	6MZ	C2-N1-C6	7.52	123.04	116.59
1	CA	1915	3TD	N1-C2-N3	7.31	121.91	116.14
1	CA	2449	H2U	C4-N3-C2	-6.39	120.49	125.79
1	CA	2457	PSU	N1-C2-N3	6.16	122.10	115.13
1	CA	2580	PSU	N1-C2-N3	6.08	122.01	115.13

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	CD	150	MEQ	O-C-CA-CB
4	CD	150	MEQ	CG-CD-NE2-CE
1	CA	746	PSU	C2'-C1'-C5-C6
1	CA	2030	6MZ	O4'-C4'-C5'-O5'
1	CA	2445	2MG	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	CA	1915	3TD	2	0
1	CA	1939	5MU	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

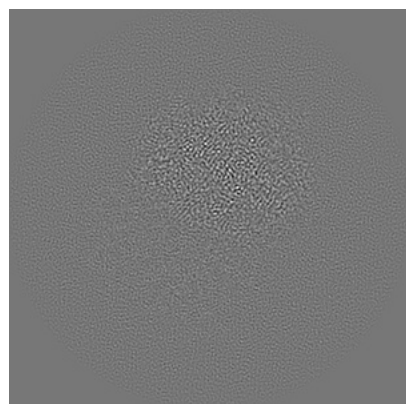
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20638. These allow visual inspection of the internal detail of the map and identification of artifacts.

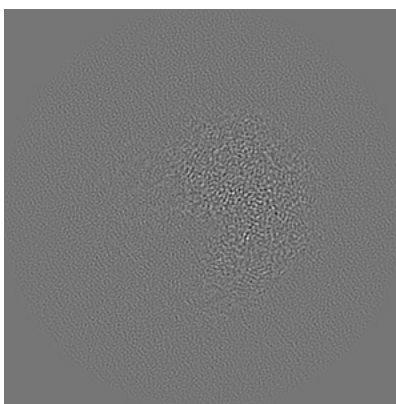
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

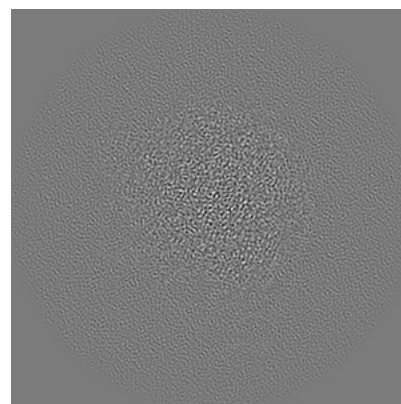
6.1.1 Primary map



X

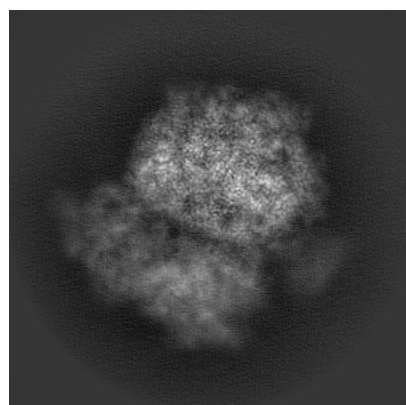


Y

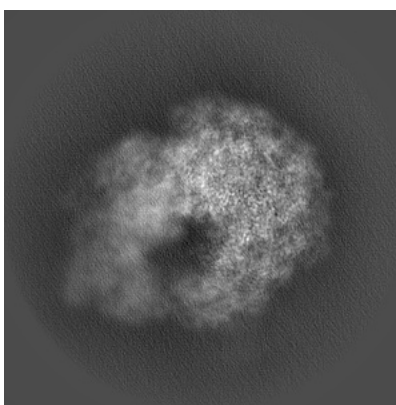


Z

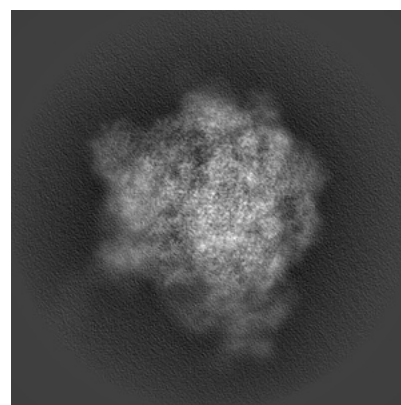
6.1.2 Raw map



X



Y

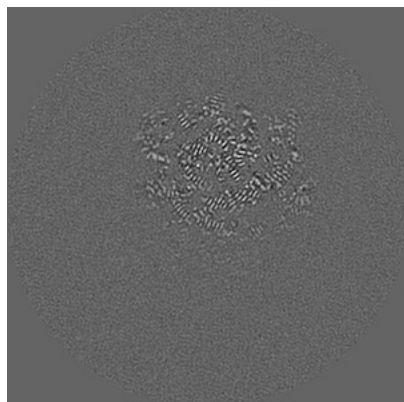


Z

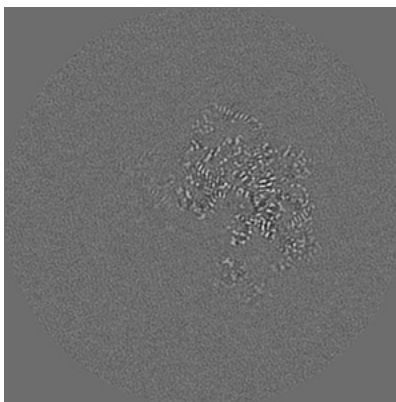
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

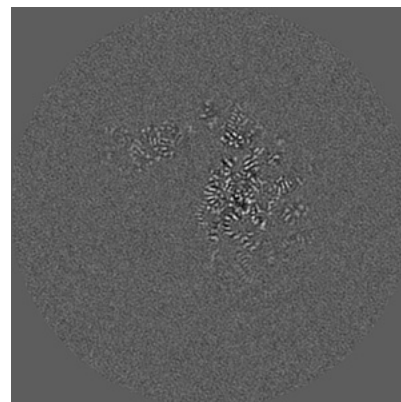
6.2.1 Primary map



X Index: 160

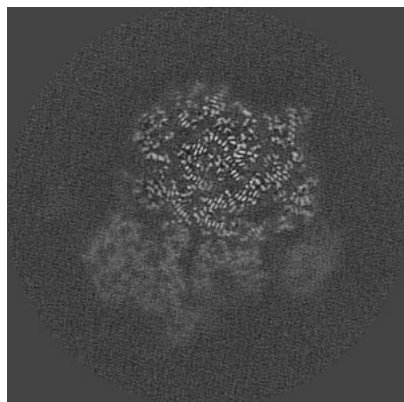


Y Index: 160

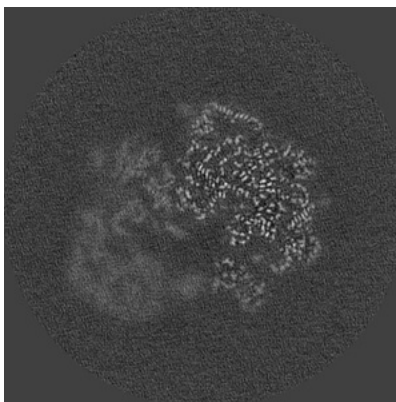


Z Index: 160

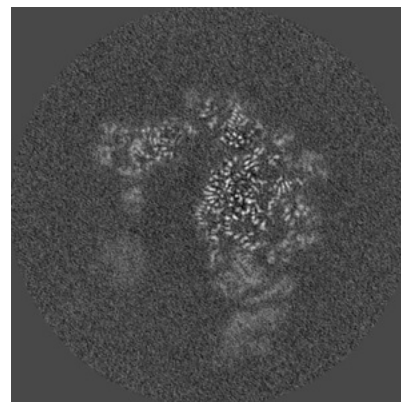
6.2.2 Raw map



X Index: 160



Y Index: 160

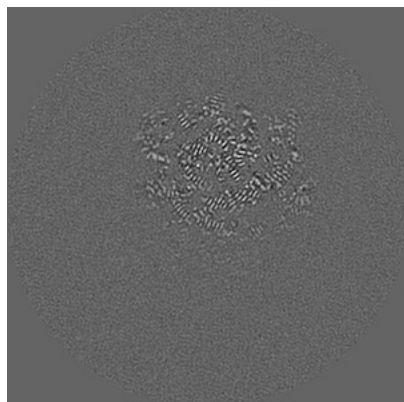


Z Index: 160

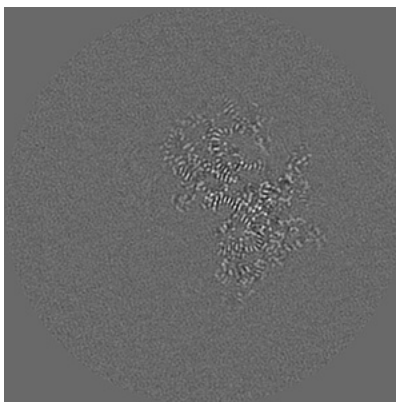
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

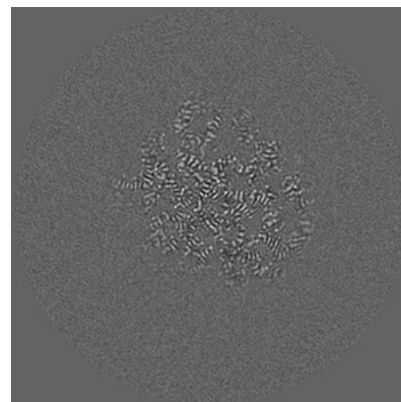
6.3.1 Primary map



X Index: 160

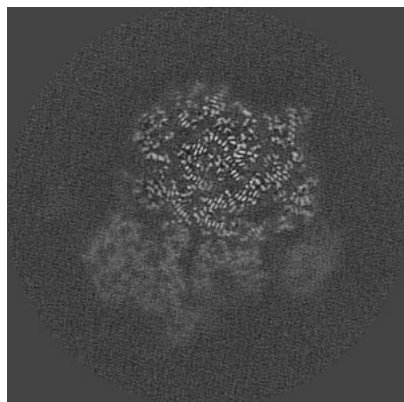


Y Index: 182

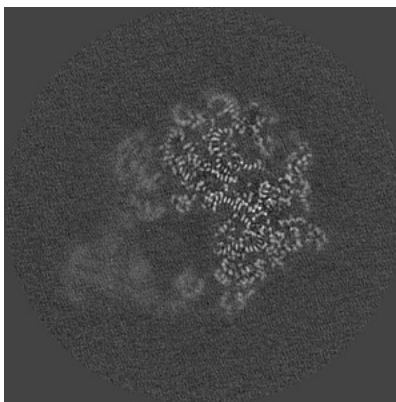


Z Index: 191

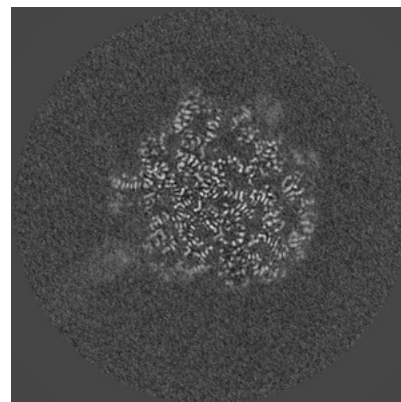
6.3.2 Raw map



X Index: 160



Y Index: 182

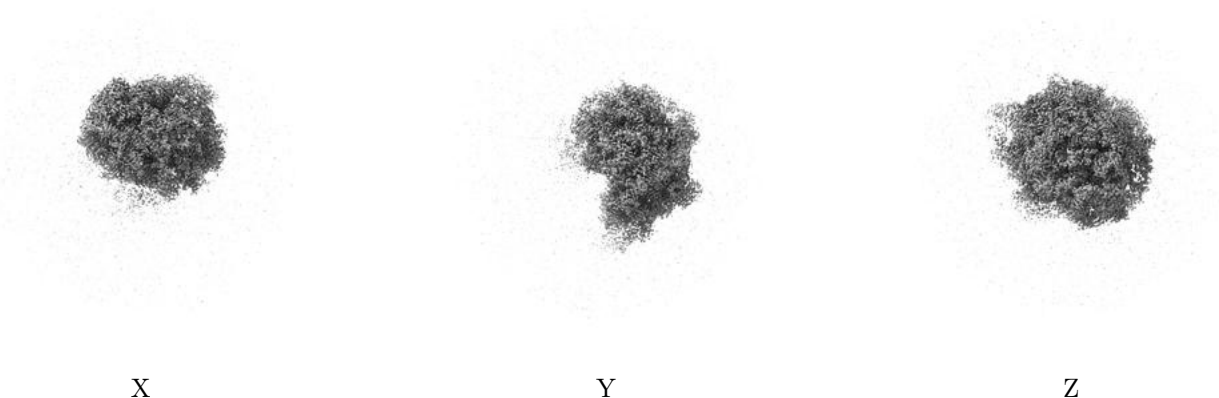


Z Index: 191

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

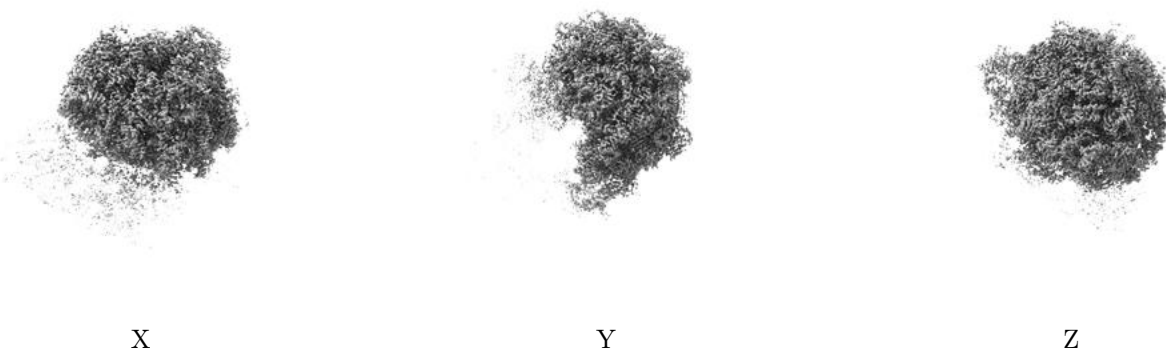
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.027. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

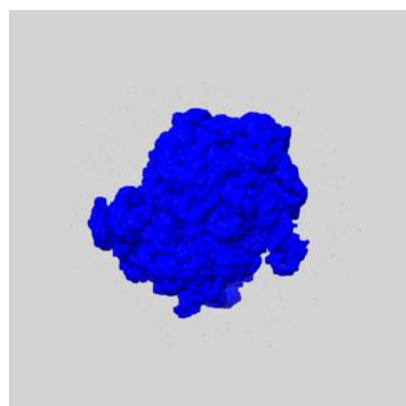
6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

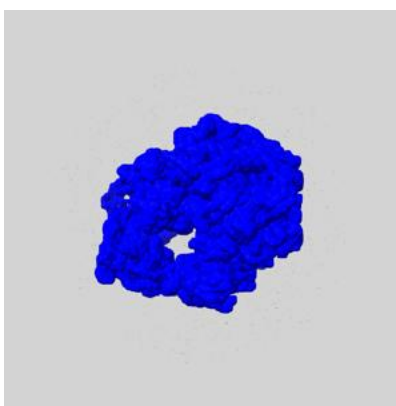
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

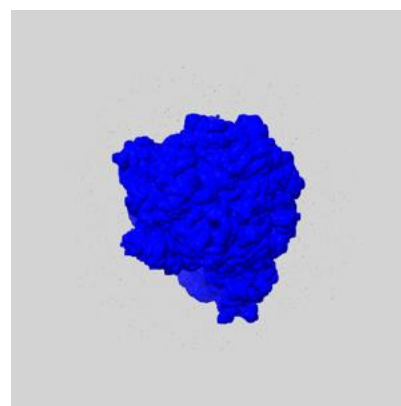
6.5.1 emd_20638_msk_1.map [i](#)



X



Y

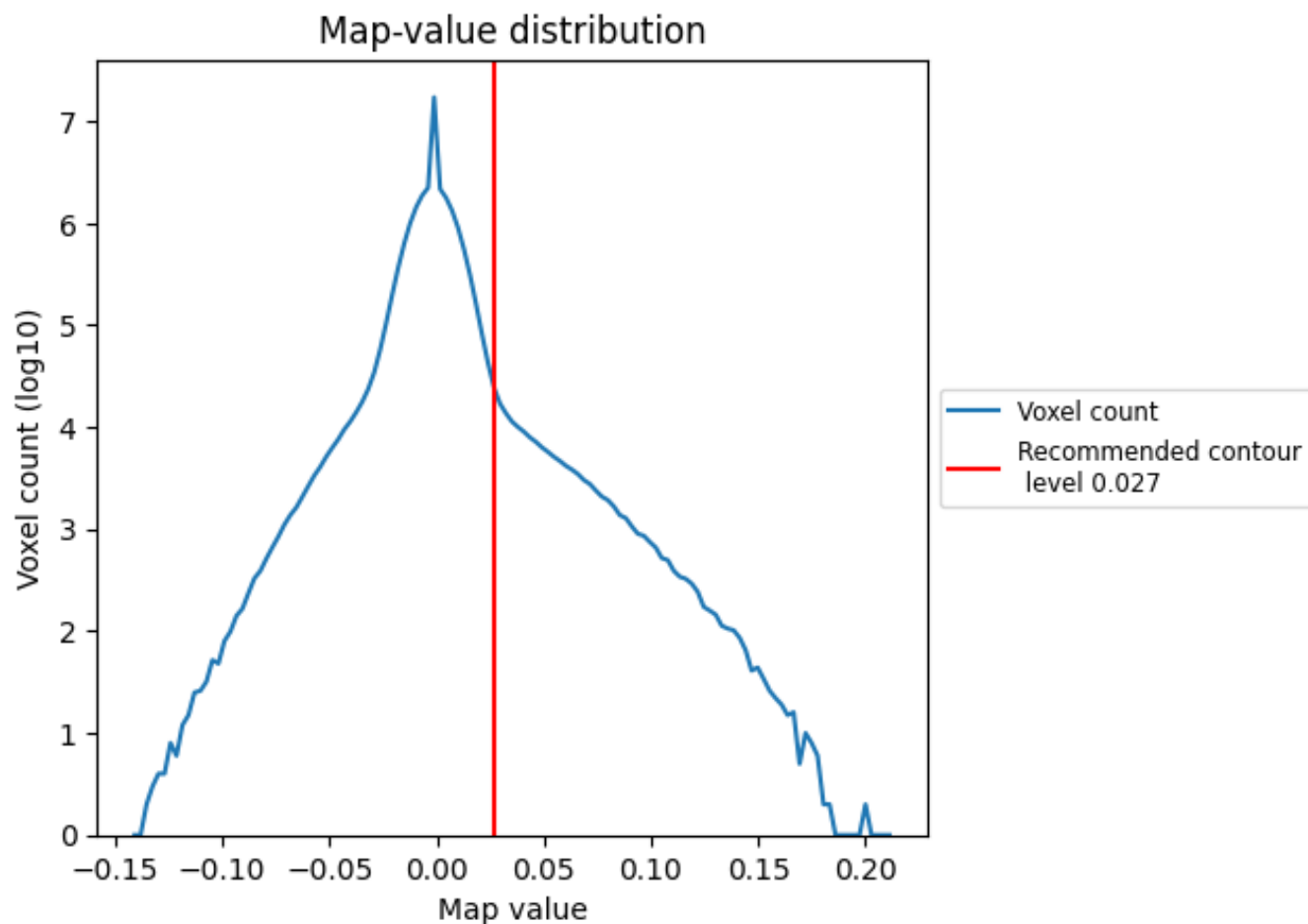


Z

7 Map analysis [i](#)

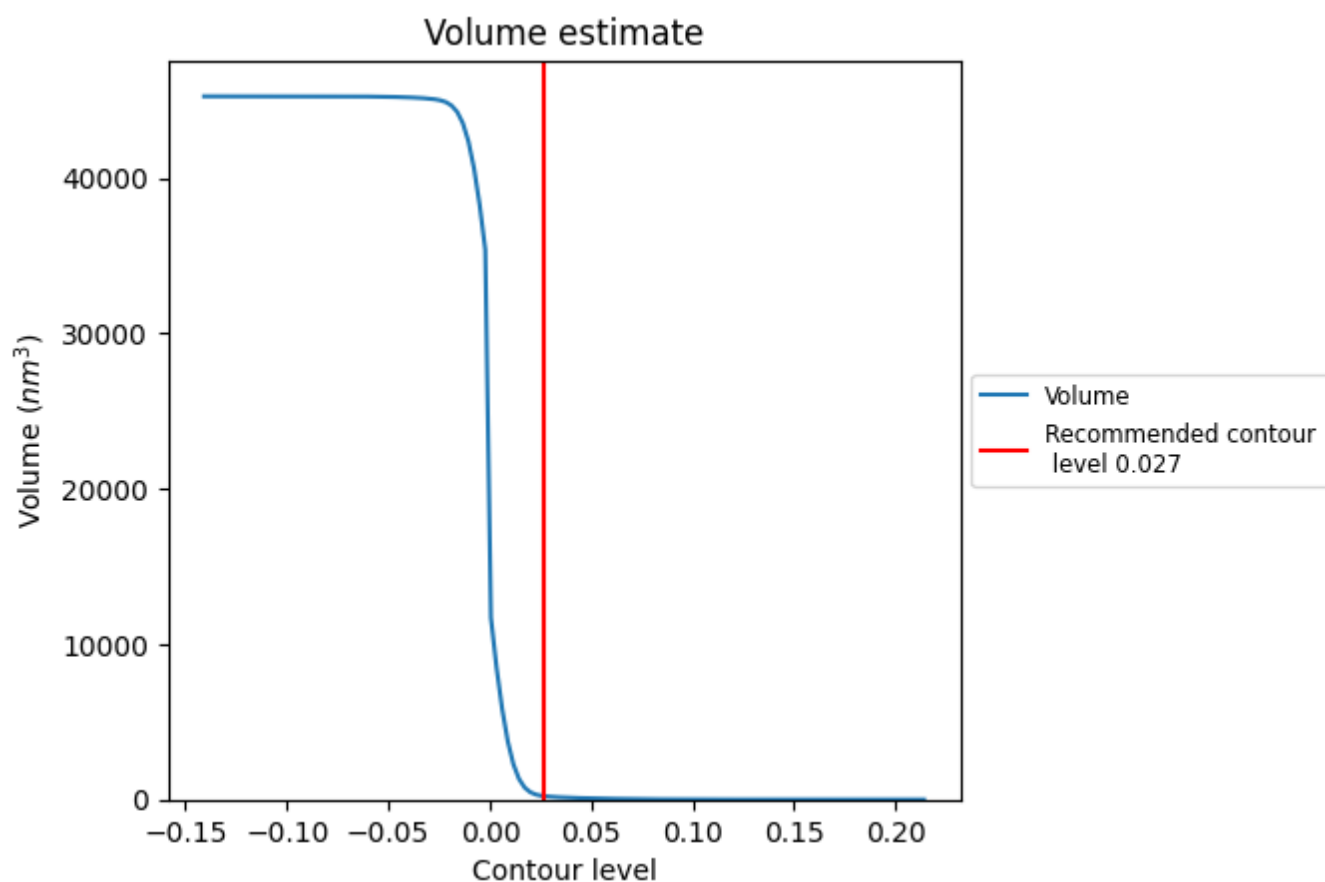
This section contains the results of statistical analysis of the map.

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.

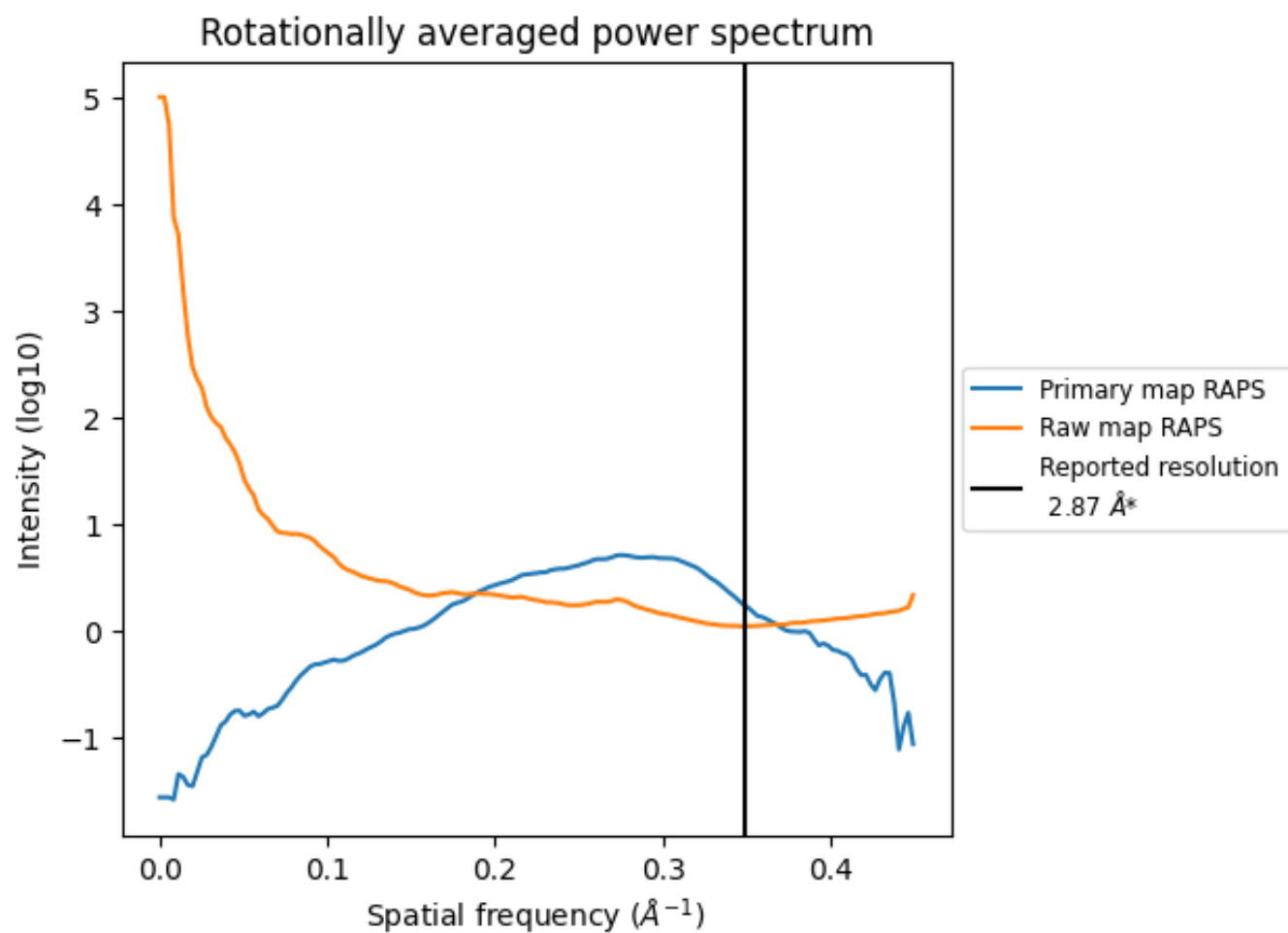
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 219 nm^3 ; this corresponds to an approximate mass of 198 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 ⓘ

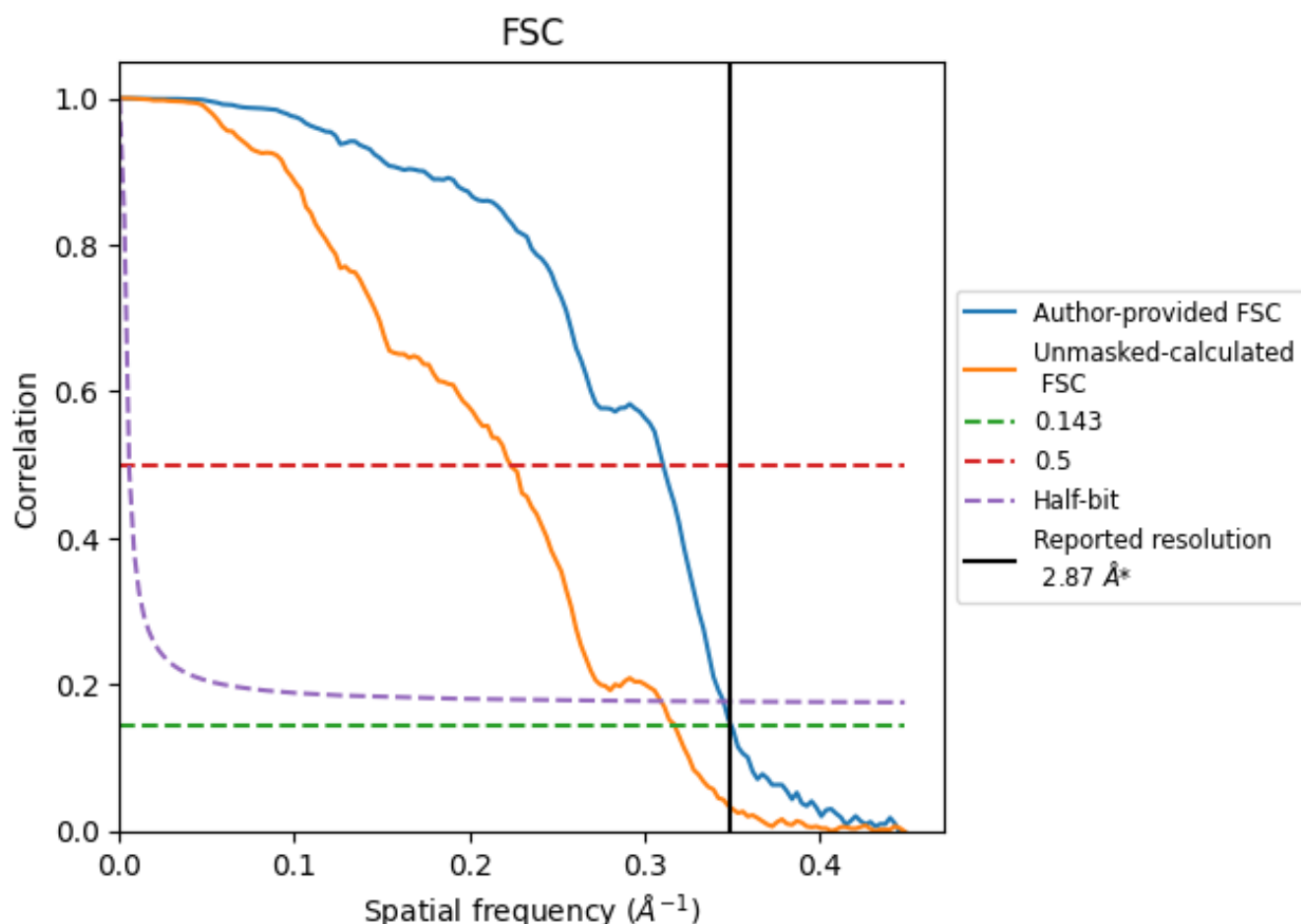


*Reported resolution corresponds to spatial frequency of 0.348 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.348 Å⁻¹

8.2 Resolution estimates [i](#)

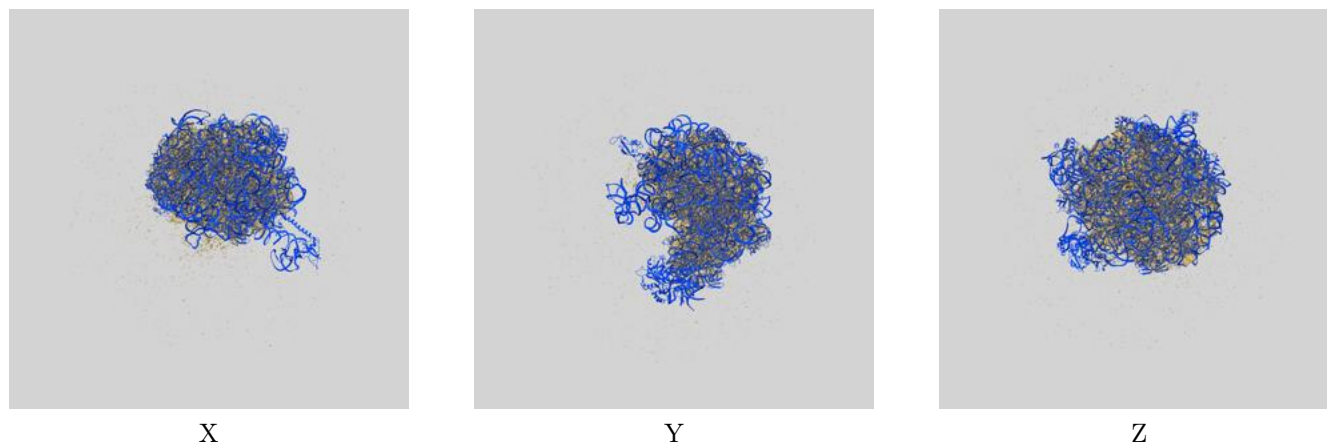
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.87	-	-
Author-provided FSC curve	2.86	3.22	2.90
Unmasked-calculated*	3.15	4.47	3.23

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

9 Map-model fit [i](#)

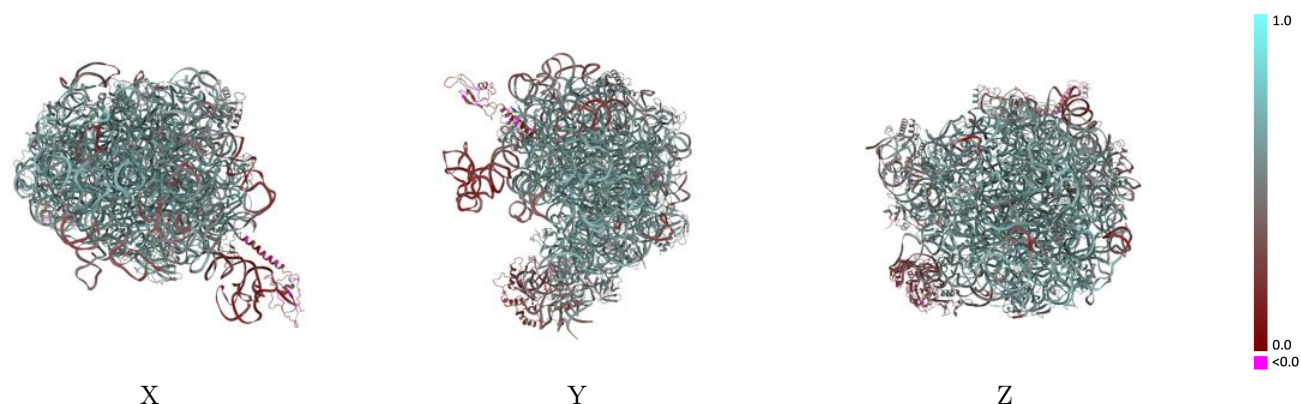
This section contains information regarding the fit between EMDB map EMD-20638 and PDB model 6U48. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



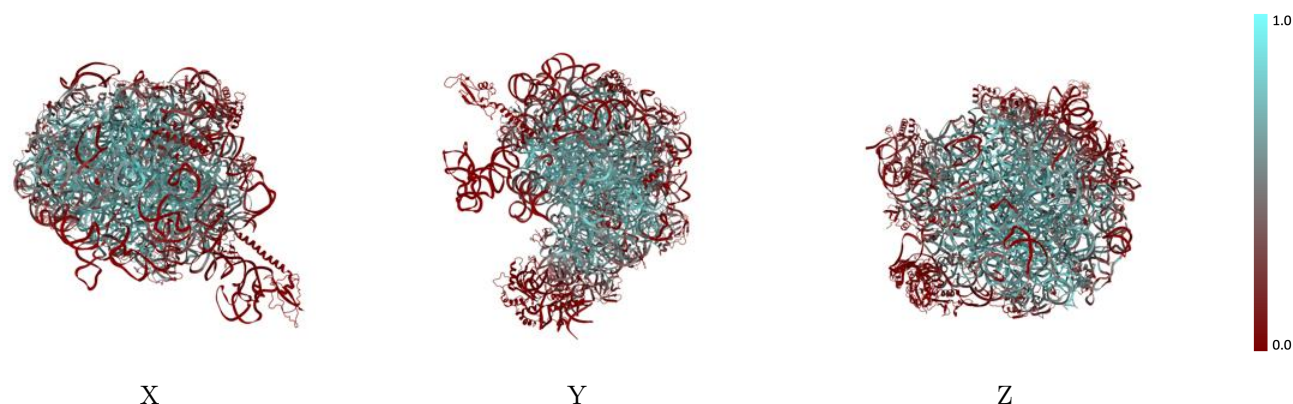
The images above show the 3D surface view of the map at the recommended contour level 0.027 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



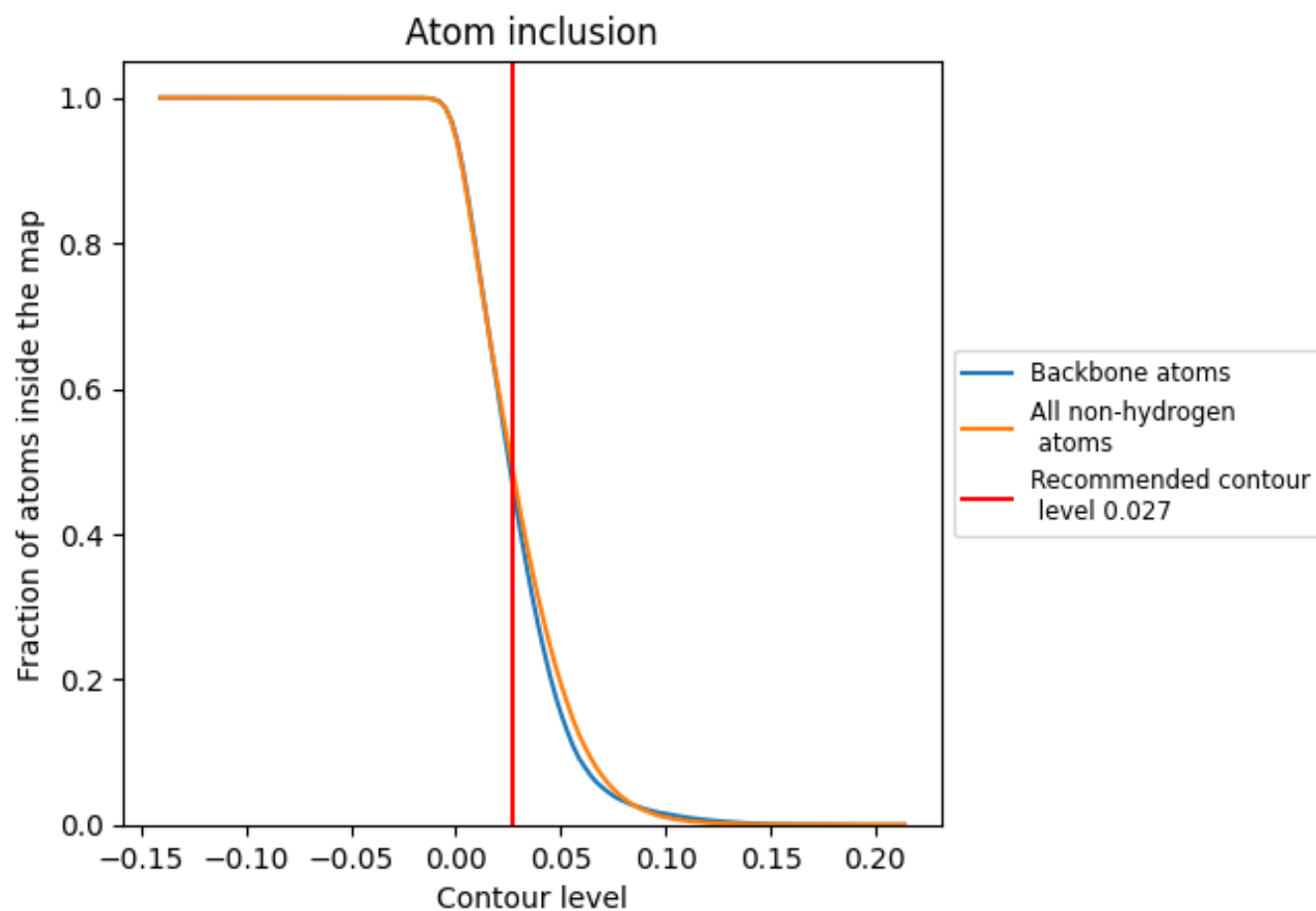
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.027).

9.4 Atom inclusion [i](#)



At the recommended contour level, 47% of all backbone atoms, 49% 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 (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4899	0.5490
A	0.8359	0.6630
C0	0.4439	0.5520
C1	0.4860	0.5580
C2	0.2469	0.5150
C3	0.7014	0.6180
C4	0.6904	0.6200
C5	0.3767	0.5490
CA	0.5559	0.5680
CB	0.2115	0.5010
CC	0.5350	0.5950
CD	0.5296	0.5850
CE	0.3487	0.5270
CF	0.0007	0.2810
CG	0.0254	0.3930
CH	0.0192	0.2610
CJ	0.0000	0.1940
CK	0.5300	0.5870
CL	0.4469	0.5610
CM	0.4521	0.5610
CN	0.4573	0.5690
CO	0.6074	0.6050
CP	0.0765	0.4580
CQ	0.3908	0.5560
CR	0.6289	0.6030
CS	0.3676	0.5450
CT	0.5215	0.5770
CU	0.3651	0.5250
CV	0.0964	0.4640
CW	0.1829	0.4930
CX	0.5766	0.5950
CY	0.4426	0.5650
CZ	0.0982	0.4650

