



wwPDB EM Validation Summary Report ⓘ

Dec 4, 2024 – 04:01 am GMT

PDB ID : 9GUT
EMDB ID : EMD-51619
Title : 30S mRNA delivery complex (bS1 resolved)
Authors : Rahil, H.; Weixlbaumer, A.; Webster, M.W.
Deposited on : 2024-09-20
Resolution : 2.80 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:

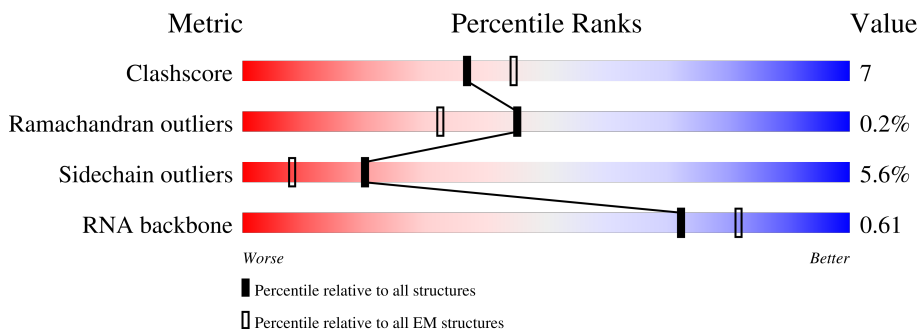
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

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 2.80 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.




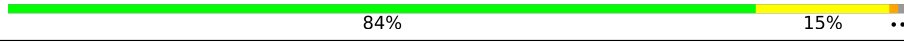
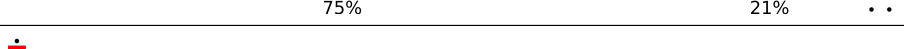
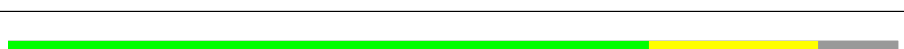



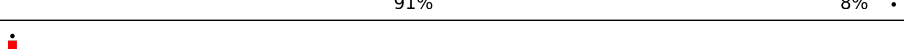



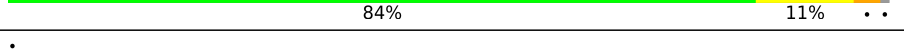





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	3082	33% 15% 50%
2	B	557	52% 62% 29% 7%
3	C	241	66% 24% 6%
4	D	233	75% 16% 9%
5	E	206	77% 18%
6	F	156	72% 26%
7	G	131	50% 26% 21%

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Mol	Chain	Length	Quality of chain
8	H	156	 80% 17% ..
9	I	130	 84% 15% ..
10	J	130	 75% 21% ..
11	K	103	 71% 25% ...
12	L	129	 72% 19% 9%
13	M	124	 65% 31% ..
14	N	118	 72% 23% ..
15	O	101	 83% 16% .
16	P	89	 91% 8% .
17	Q	82	 79% 20% .
18	R	84	 71% 23% . 5%
19	S	75	 76% 13% 11%
20	T	92	 72% 17% . 10%
21	U	87	 84% 11% ..
22	V	71	 77% 20% ..
23	W	77	 35% 83% 52% 13%
24	X	53	 11% 13% 6% 68%

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 58183 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1539	33023	14736	6046	10702	1539	0	0

- Molecule 2 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	516	3988	2503	691	787	7	0	0

- Molecule 3 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	226	1765	1116	317	324	8	0	0

- Molecule 4 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	211	1653	1046	310	293	4	0	0

- Molecule 5 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 6 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	156	1152	717	217	212	6	0	0

- Molecule 7 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	104	848	536	153	152	7	0	0

- Molecule 8 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	153	1203	750	231	218	4	0	0

- Molecule 9 is a protein called 30S ribosomal protein S8.

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

- Molecule 10 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	128	1031	639	207	182	3	0	0

- Molecule 11 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	101	808	504	155	148	1	0	0

- Molecule 12 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	117	877	540	174	160	3	0	0

- Molecule 13 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	122	951	588	195	163	5	0	0

- Molecule 14 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 15 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 16 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 17 is a protein called 30S ribosomal protein S16.

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

- Molecule 18 is a protein called 30S ribosomal protein S17.

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

- Molecule 19 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	67	Total	C	N	O	S	0	0
			554	350	104	99	1		

- Molecule 20 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 21 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 22 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 23 is a RNA chain called tRNA(fmet) P-site.

Mol	Chain	Residues	Atoms					AltConf	Trace	
23	W	77	Total	C	N	O	P	S	0	0
			1645	734	297	536	77	1		

- Molecule 24 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	17	Total	C	N	O	P	0	0
			296	128	49	102	17		

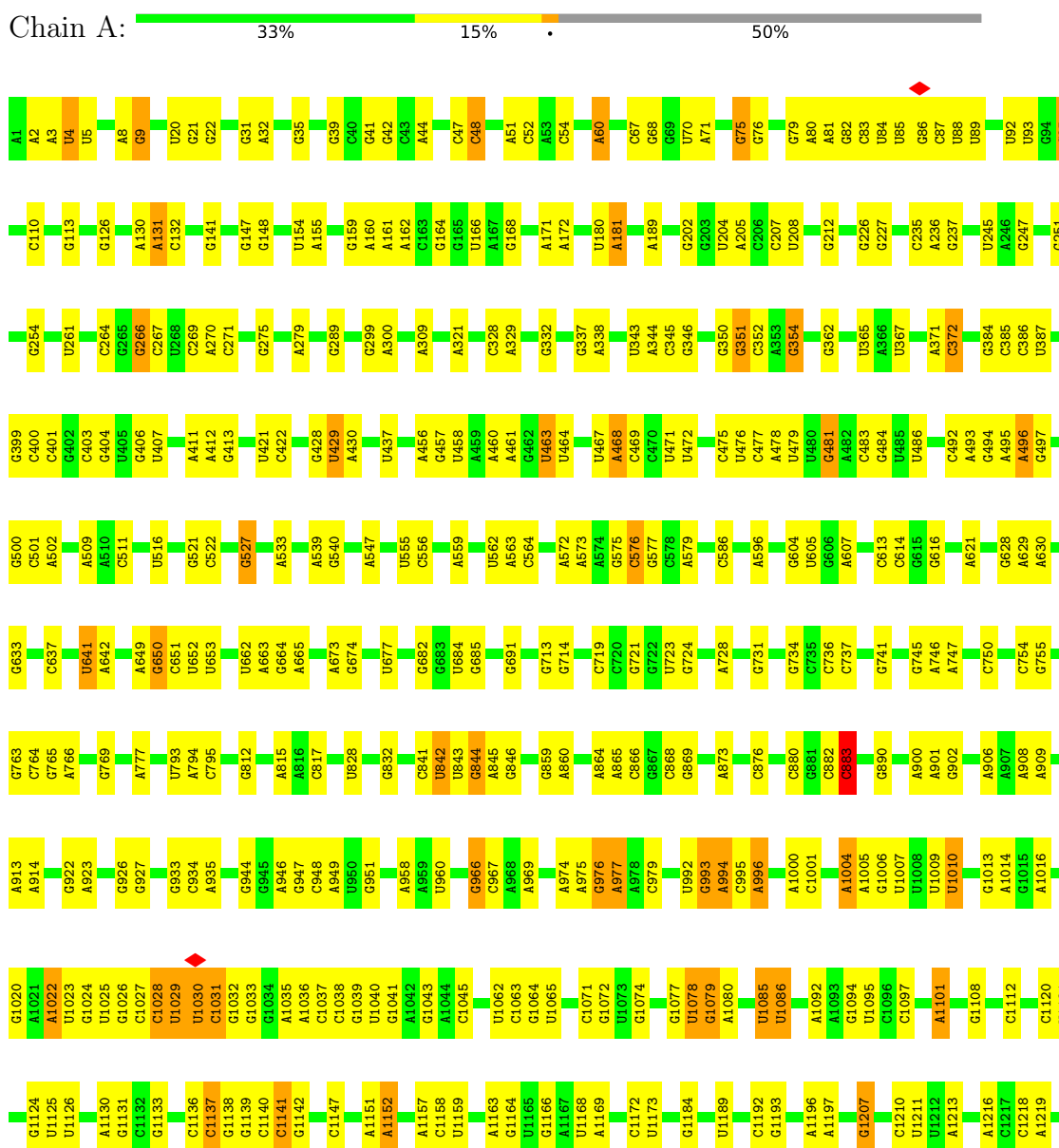
- Molecule 25 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
25	A	135	Total	Mg	0
			135	135	
25	M	1	Total	Mg	0
			1	1	
25	O	1	Total	Mg	0
			1	1	

3 Residue-property plots [i](#)

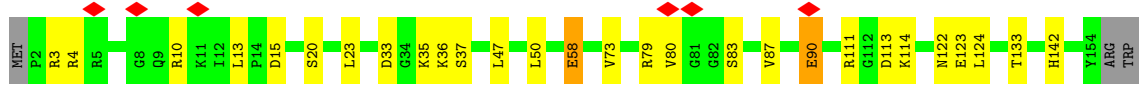
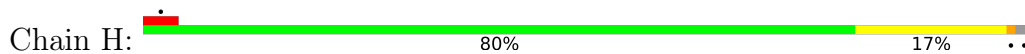
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 16S ribosomal RNA

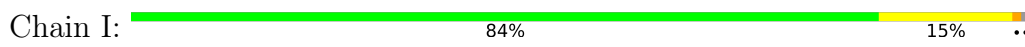




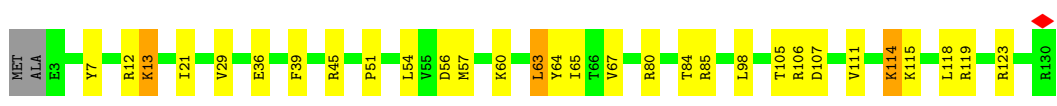
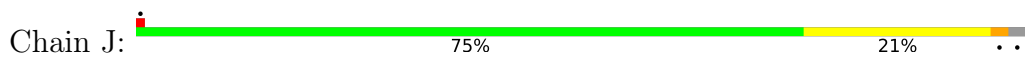
• Molecule 8: 30S ribosomal protein S7



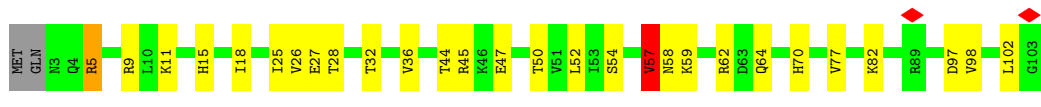
• Molecule 9: 30S ribosomal protein S8



• Molecule 10: 30S ribosomal protein S9



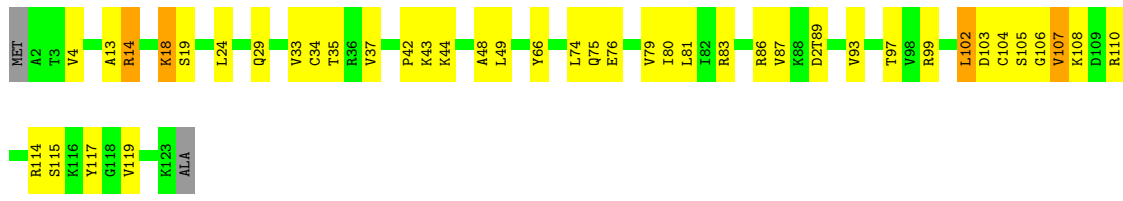
• Molecule 11: 30S ribosomal protein S10



• Molecule 12: 30S ribosomal protein S11

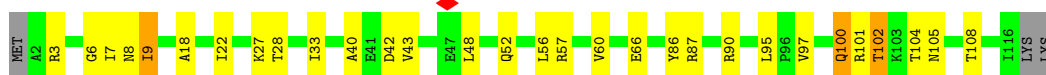


• Molecule 13: 30S ribosomal protein S12




- Molecule 14: 30S ribosomal protein S13

Chain N:  72% 23%



- Molecule 15: 30S ribosomal protein S14

Chain O:  83% 16%




- Molecule 16: Small ribosomal subunit protein uS15

Chain P:  91% 8%



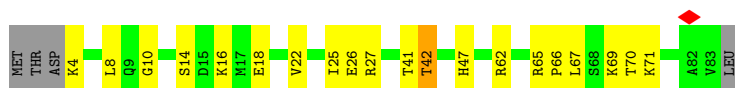
- Molecule 17: 30S ribosomal protein S16

Chain Q:  79% 20%



- Molecule 18: 30S ribosomal protein S17

Chain R:  71% 23% 5%



- Molecule 19: 30S ribosomal protein S18

Chain S:  76% 13% 11%

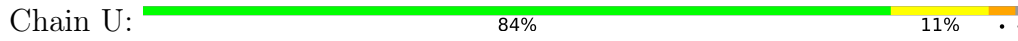


- Molecule 20: 30S ribosomal protein S19

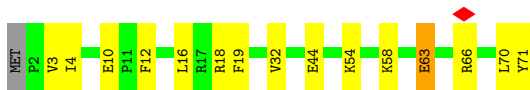
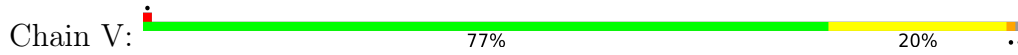
Chain T:  72% 17% 10%



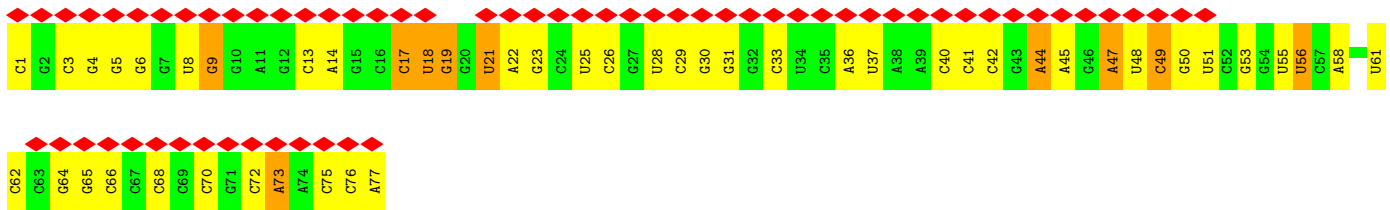
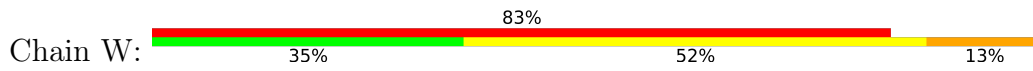
• Molecule 21: 30S ribosomal protein S20



• Molecule 22: 30S ribosomal protein S21



• Molecule 23: tRNA(fmet) P-site



• Molecule 24: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51717	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.95	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	3.562	Depositor
Minimum map value	-0.504	Depositor
Average map value	0.032	Depositor
Map value standard deviation	0.073	Depositor
Recommended contour level	0.328	Depositor
Map size (Å)	503.99997, 503.99997, 503.99997	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: H2U, 4OC, PSU, G7M, 4SU, D2T, MG, 2MG, OMC, 5MU, UR3, MA6, 5MC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.41	9/36692 (0.0%)	0.88	13/57230 (0.0%)
2	B	0.29	0/4039	0.49	0/5455
3	C	0.41	0/1796	0.48	0/2420
4	D	0.53	0/1680	0.48	0/2263
5	E	0.53	0/1665	0.50	0/2227
6	F	0.49	0/1165	0.54	0/1568
7	G	0.52	0/867	0.50	0/1171
8	H	0.39	0/1219	0.48	0/1635
9	I	0.53	0/989	0.52	0/1326
10	J	0.57	0/1043	0.54	0/1387
11	K	0.46	0/818	0.52	0/1105
12	L	0.42	0/893	0.49	0/1205
13	M	0.57	0/954	0.55	0/1279
14	N	0.47	0/900	0.51	0/1204
15	O	0.54	0/817	0.47	0/1088
16	P	0.45	0/722	0.48	0/964
17	Q	0.64	0/659	0.52	0/884
18	R	0.51	0/657	0.53	0/881
19	S	0.60	0/563	0.50	0/754
20	T	0.51	0/680	0.49	0/915
21	U	0.46	0/676	0.41	0/895
22	V	0.42	0/598	0.44	0/792
23	W	0.38	1/1725 (0.1%)	0.78	0/2687
24	X	0.35	0/327	0.81	0/503
All	All	1.12	10/62144 (0.0%)	0.77	13/91838 (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
1	A	0	2

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	W	1	C	OP3-P	-10.49	1.48	1.61
1	A	1287	A	N9-C4	-6.41	1.34	1.37
1	A	60	A	N9-C4	-5.85	1.34	1.37
1	A	387	U	C2-N3	-5.43	1.33	1.37
1	A	1157	A	N9-C4	-5.25	1.34	1.37

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	60	A	C8-N9-C4	-11.98	101.01	105.80
1	A	883	C	C6-N1-C2	-8.65	116.84	120.30
1	A	60	A	N3-C4-N9	-7.12	121.70	127.40
1	A	60	A	N9-C4-C5	6.72	108.49	105.80
1	A	1279	G	N7-C8-N9	6.09	116.15	113.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	60	A	Sidechain
1	A	883	C	Sidechain

5.2 Too-close contacts [\(i\)](#)

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	A	33023	0	16642	272	0
2	B	3988	0	4015	120	0
3	C	1765	0	1792	41	0
4	D	1653	0	1727	18	0
5	E	1643	0	1707	33	0
6	F	1152	0	1196	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	848	0	846	25	0
8	H	1203	0	1254	18	0
9	I	979	0	1031	10	0
10	J	1031	0	1076	14	0
11	K	808	0	845	20	0
12	L	877	0	887	17	0
13	M	951	0	1010	21	0
14	N	891	0	952	19	0
15	O	805	0	844	12	0
16	P	714	0	734	6	0
17	Q	649	0	666	10	0
18	R	648	0	691	15	0
19	S	554	0	573	9	0
20	T	663	0	688	16	0
21	U	670	0	719	8	0
22	V	590	0	629	12	0
23	W	1645	0	842	32	0
24	X	296	0	137	10	0
25	A	135	0	0	0	0
25	M	1	0	0	0	0
25	O	1	0	0	0	0
All	All	58183	0	41503	695	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 7.

The worst 5 of 695 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)
23:W:51:U:H3	23:W:65:G:H1	1.19	0.89
1:A:1277:C:HO2'	1:A:1279:G:H8	1.21	0.85
2:B:361:HIS:ND1	2:B:365:ASP:OD2	2.10	0.82
1:A:407:U:O2'	5:E:113:GLU:OE1	1.96	0.82
1:A:1097:C:OP1	3:C:143:LYS:NZ	2.12	0.82

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	512/557 (92%)	495 (97%)	15 (3%)	2 (0%)	30	61
3	C	224/241 (93%)	217 (97%)	5 (2%)	2 (1%)	14	42
4	D	209/233 (90%)	204 (98%)	5 (2%)	0	100	100
5	E	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
6	F	154/156 (99%)	147 (96%)	7 (4%)	0	100	100
7	G	102/131 (78%)	100 (98%)	2 (2%)	0	100	100
8	H	151/156 (97%)	147 (97%)	4 (3%)	0	100	100
9	I	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
10	J	126/130 (97%)	120 (95%)	5 (4%)	1 (1%)	16	44
11	K	99/103 (96%)	93 (94%)	5 (5%)	1 (1%)	13	39
12	L	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
13	M	119/124 (96%)	113 (95%)	6 (5%)	0	100	100
14	N	113/118 (96%)	112 (99%)	1 (1%)	0	100	100
15	O	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
16	P	86/89 (97%)	86 (100%)	0	0	100	100
17	Q	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
18	R	78/84 (93%)	75 (96%)	3 (4%)	0	100	100
19	S	65/75 (87%)	62 (95%)	3 (5%)	0	100	100
20	T	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
21	U	84/87 (97%)	84 (100%)	0	0	100	100
22	V	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
All	All	2894/3095 (94%)	2808 (97%)	80 (3%)	6 (0%)	45	73

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	175	GLU
2	B	172	ALA
10	J	13	LYS
11	K	57	VAL
3	C	127	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	431/461 (94%)	421 (98%)	10 (2%)	45 78
3	C	187/199 (94%)	172 (92%)	15 (8%)	10 30
4	D	172/190 (90%)	164 (95%)	8 (5%)	22 54
5	E	172/173 (99%)	159 (92%)	13 (8%)	11 32
6	F	119/119 (100%)	113 (95%)	6 (5%)	20 51
7	G	91/112 (81%)	80 (88%)	11 (12%)	4 13
8	H	126/129 (98%)	121 (96%)	5 (4%)	27 60
9	I	104/105 (99%)	100 (96%)	4 (4%)	28 62
10	J	106/107 (99%)	97 (92%)	9 (8%)	8 27
11	K	88/90 (98%)	82 (93%)	6 (7%)	13 38
12	L	90/99 (91%)	87 (97%)	3 (3%)	33 67
13	M	102/103 (99%)	89 (87%)	13 (13%)	3 12
14	N	93/96 (97%)	84 (90%)	9 (10%)	6 21
15	O	83/84 (99%)	80 (96%)	3 (4%)	30 64
16	P	76/77 (99%)	76 (100%)	0	100 100
17	Q	65/65 (100%)	60 (92%)	5 (8%)	10 31
18	R	74/78 (95%)	70 (95%)	4 (5%)	18 48
19	S	58/65 (89%)	57 (98%)	1 (2%)	56 84
20	T	72/79 (91%)	70 (97%)	2 (3%)	38 72
21	U	65/66 (98%)	60 (92%)	5 (8%)	10 31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	V	60/61 (98%)	56 (93%)	4 (7%)	13	38
All	All	2434/2558 (95%)	2298 (94%)	136 (6%)	20	47

5 of 136 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	Q	5	ARG
17	Q	69	ASP
21	U	66	LEU
6	F	117	VAL
6	F	105	ILE

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

Mol	Chain	Res	Type
14	N	52	GLN
16	P	46	HIS
15	O	49	GLN
16	P	80	GLN
6	F	73	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1534/3082 (49%)	199 (12%)	4 (0%)
23	W	76/77 (98%)	18 (23%)	2 (2%)
24	X	11/53 (20%)	2 (18%)	1 (9%)
All	All	1621/3212 (50%)	219 (13%)	7 (0%)

5 of 219 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	4	U
1	A	5	U
1	A	9	G
1	A	32	A

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1078	U
23	W	21	H2U
24	X	11	U
23	W	48	U
1	A	641	U

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

17 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	4OC	A	1402	1	20,23,24	3.34	9 (45%)	26,32,35	0.87	1 (3%)
23	H2U	W	21	23	18,21,22	3.11	5 (27%)	21,30,33	2.03	5 (23%)
23	PSU	W	56	23	18,21,22	1.11	1 (5%)	22,30,33	1.79	5 (22%)
1	2MG	A	966	25,1	18,26,27	2.26	7 (38%)	16,38,41	1.48	4 (25%)
1	2MG	A	1207	1	18,26,27	2.14	6 (33%)	16,38,41	1.65	4 (25%)
23	5MU	W	55	23	19,22,23	1.41	6 (31%)	28,32,35	2.06	6 (21%)
1	2MG	A	1516	1	18,26,27	2.20	7 (38%)	16,38,41	1.66	4 (25%)
1	G7M	A	527	1	20,26,27	2.27	8 (40%)	17,39,42	1.20	2 (11%)
1	MA6	A	1518	1	18,26,27	1.33	3 (16%)	19,38,41	4.25	2 (10%)
1	5MC	A	967	1	18,22,23	3.91	7 (38%)	26,32,35	1.03	2 (7%)
23	OMC	W	33	23	19,22,23	3.10	8 (42%)	26,31,34	0.87	0
1	MA6	A	1519	1	18,26,27	1.37	3 (16%)	19,38,41	4.45	3 (15%)
1	UR3	A	1498	1	19,22,23	2.48	6 (31%)	26,32,35	1.28	1 (3%)
23	4SU	W	8	23	18,21,22	4.13	8 (44%)	26,30,33	2.30	5 (19%)
1	PSU	A	516	1	18,21,22	1.09	3 (16%)	22,30,33	1.95	4 (18%)
1	5MC	A	1407	1	18,22,23	3.92	7 (38%)	26,32,35	1.05	1 (3%)
13	D2T	M	89	13	7,9,10	0.99	0	6,11,13	2.15	2 (33%)

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	4OC	A	1402	1	-	0/9/29/30	0/2/2/2
23	H2U	W	21	23	-	4/7/38/39	0/2/2/2
23	PSU	W	56	23	-	0/7/25/26	0/2/2/2
1	2MG	A	966	25,1	-	2/5/27/28	0/3/3/3
1	2MG	A	1207	1	-	2/5/27/28	0/3/3/3
23	5MU	W	55	23	-	0/7/25/26	0/2/2/2
1	2MG	A	1516	1	-	2/5/27/28	0/3/3/3
1	G7M	A	527	1	-	3/3/25/26	0/3/3/3
1	MA6	A	1518	1	-	3/7/29/30	0/3/3/3
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
23	OMC	W	33	23	-	1/9/27/28	0/2/2/2
1	MA6	A	1519	1	-	5/7/29/30	0/3/3/3
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
23	4SU	W	8	23	-	0/7/25/26	0/2/2/2
1	PSU	A	516	1	-	0/7/25/26	0/2/2/2
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
13	D2T	M	89	13	-	2/7/12/14	-

The worst 5 of 94 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1407	5MC	C6-C5	9.91	1.50	1.34
1	A	967	5MC	C6-C5	9.80	1.50	1.34
23	W	21	H2U	C2-N1	9.54	1.49	1.35
23	W	8	4SU	C4-N3	9.29	1.47	1.37
23	W	8	4SU	C2-N1	7.71	1.50	1.38

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1519	MA6	N1-C6-N6	-18.21	97.89	117.06
1	A	1518	MA6	N1-C6-N6	-17.45	98.70	117.06
23	W	8	4SU	C4-N3-C2	-8.26	119.32	127.34
23	W	21	H2U	C4-N3-C2	-7.00	119.98	125.79
1	A	1519	MA6	N3-C2-N1	-5.53	120.03	128.68

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	M	89	D2T	SB-CB-CG-OD2
23	W	21	H2U	O4'-C1'-N1-C6
1	A	1207	2MG	O4'-C4'-C5'-O5'
1	A	1207	2MG	C3'-C4'-C5'-O5'
1	A	1516	2MG	O4'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	W	56	PSU	1	0
1	A	1516	2MG	1	0
1	A	1518	MA6	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 137 ligands modelled in this entry, 137 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

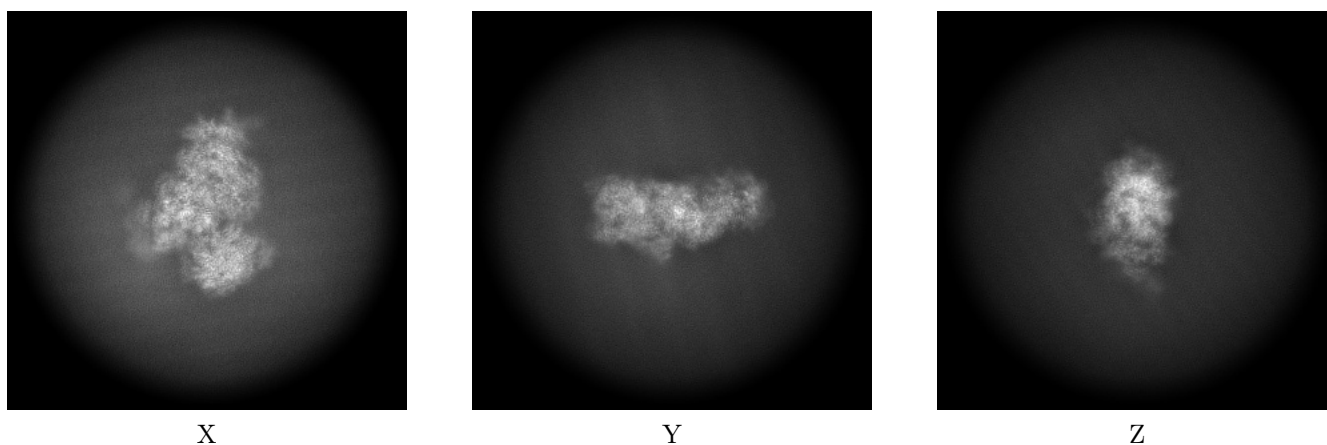
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51619. 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](#)

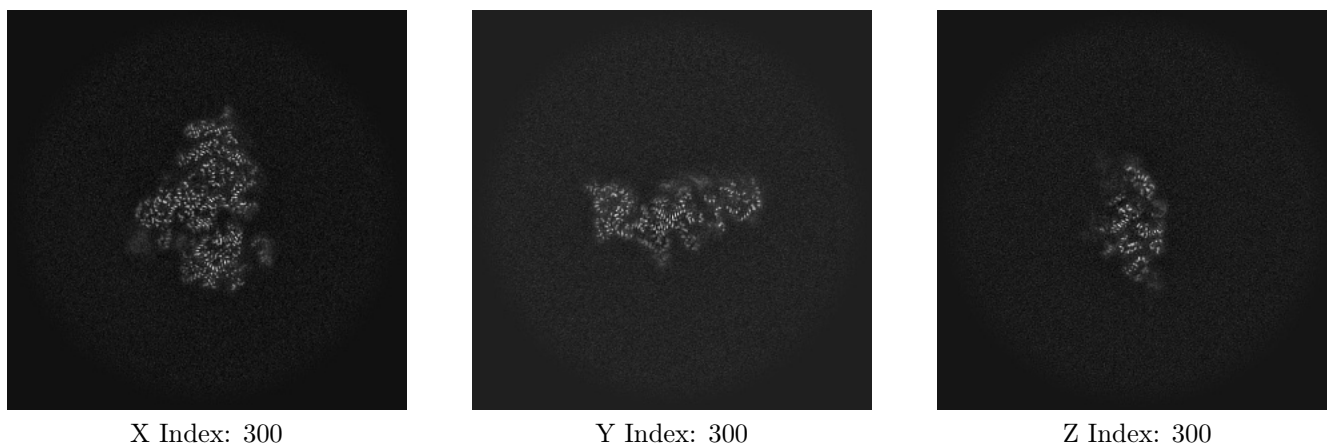
6.1.1 Primary map



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

6.2 Central slices [i](#)

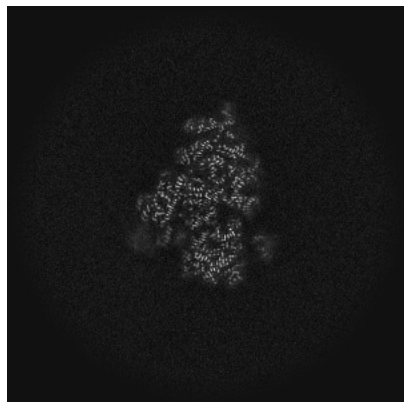
6.2.1 Primary map



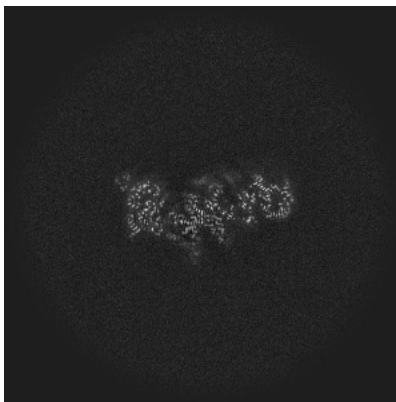
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

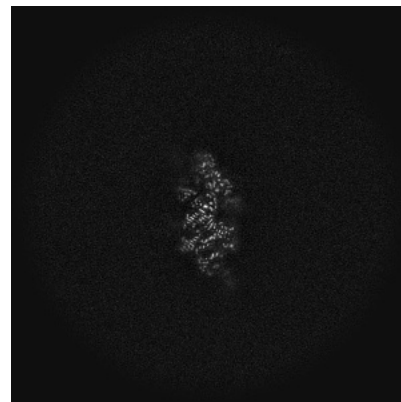
6.3.1 Primary map



X Index: 297



Y Index: 303

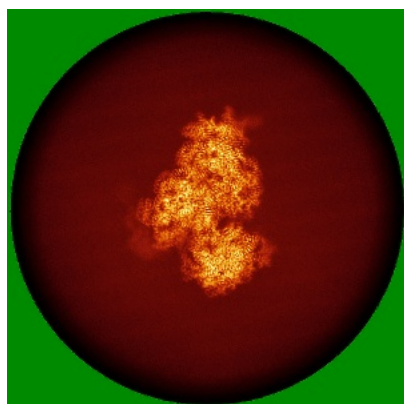


Z Index: 305

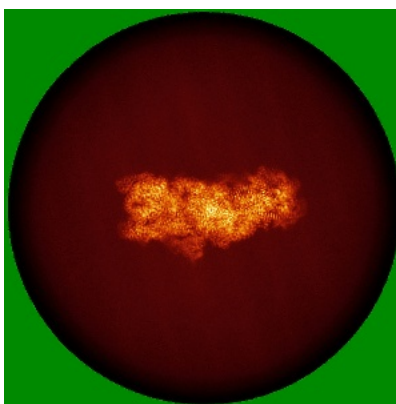
The images above show the largest variance slices of the map in three orthogonal directions.

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

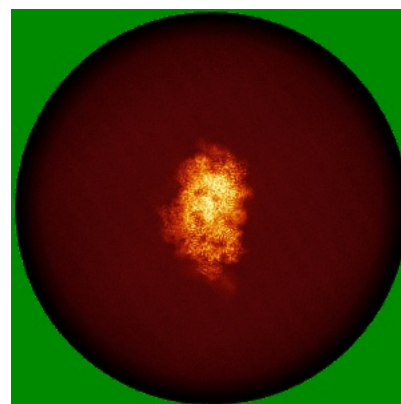
6.4.1 Primary map



X



Y

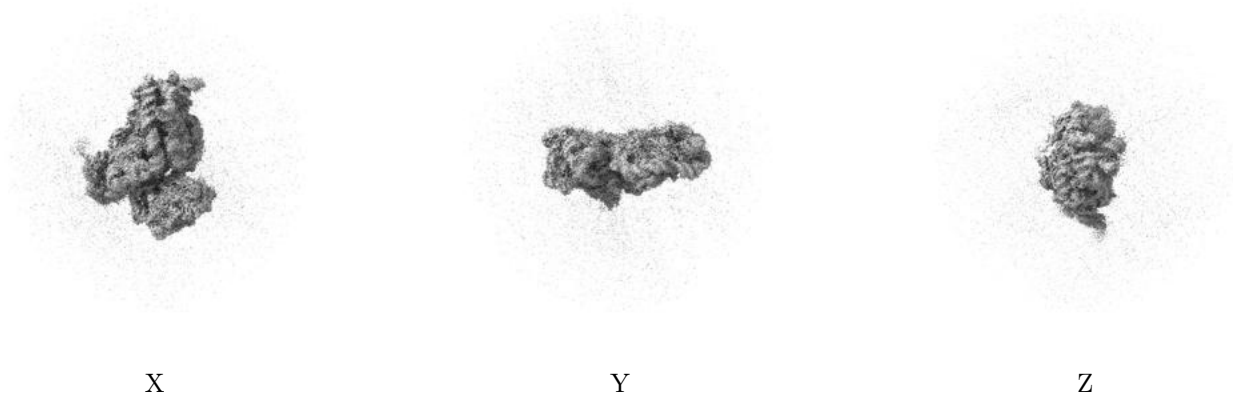


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.328. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

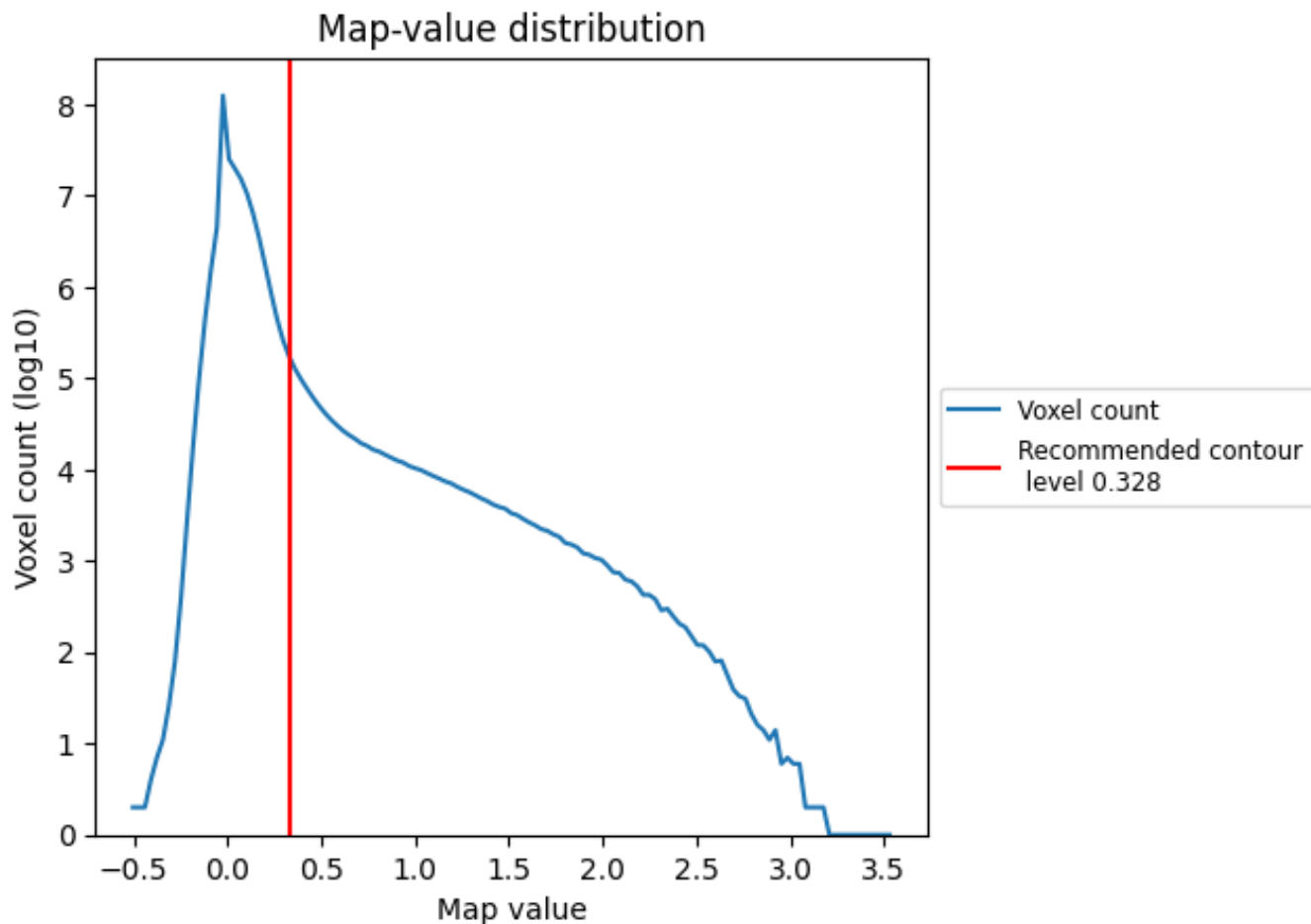
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

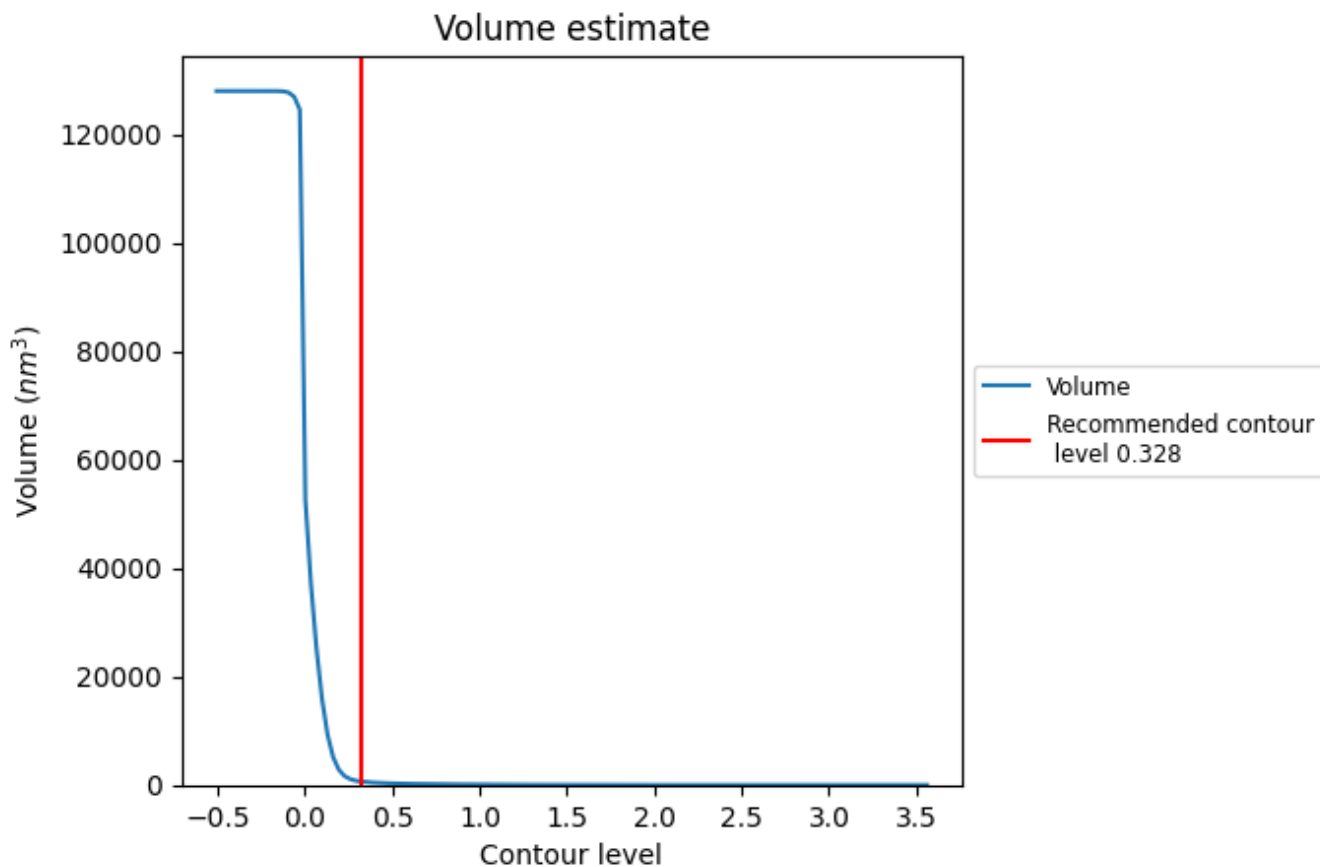
This section contains the results of statistical analysis of the map.

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.

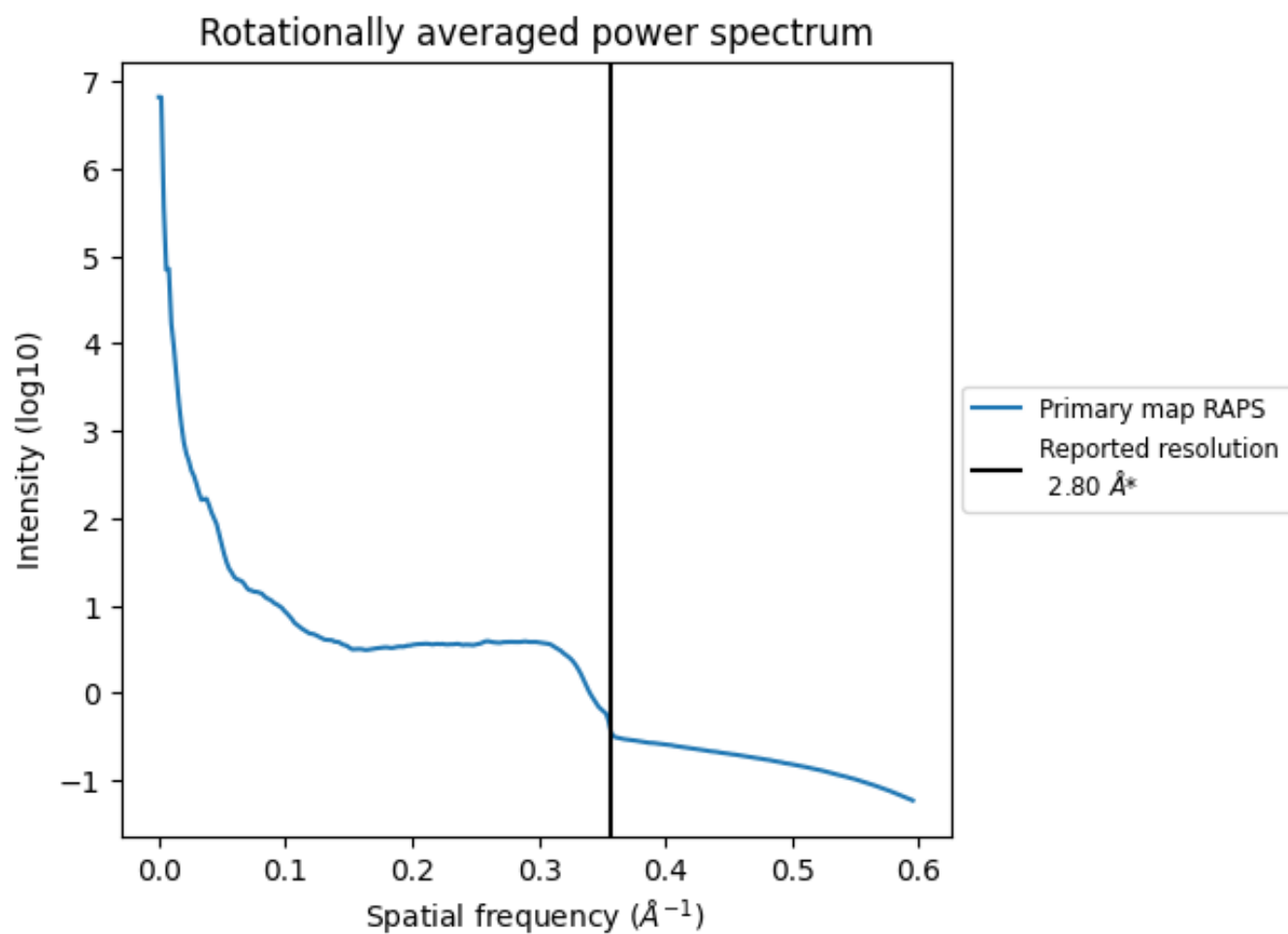
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 622 nm^3 ; this corresponds to an approximate mass of 562 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

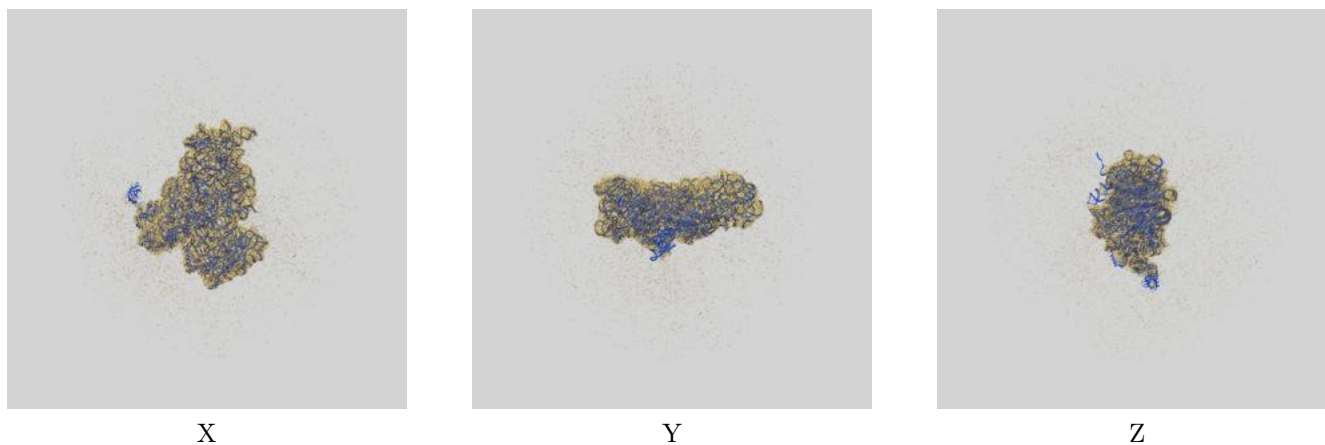
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

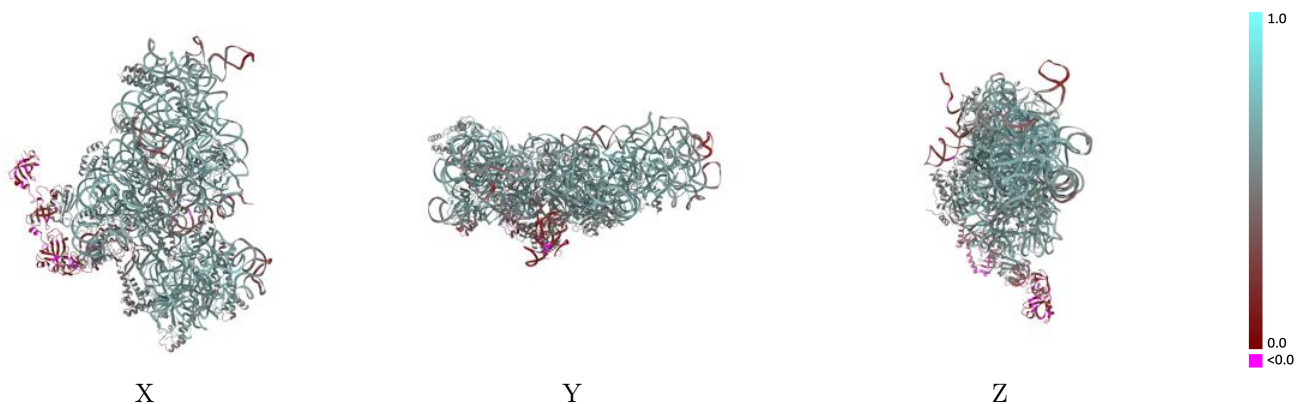
This section contains information regarding the fit between EMDB map EMD-51619 and PDB model 9GUT. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



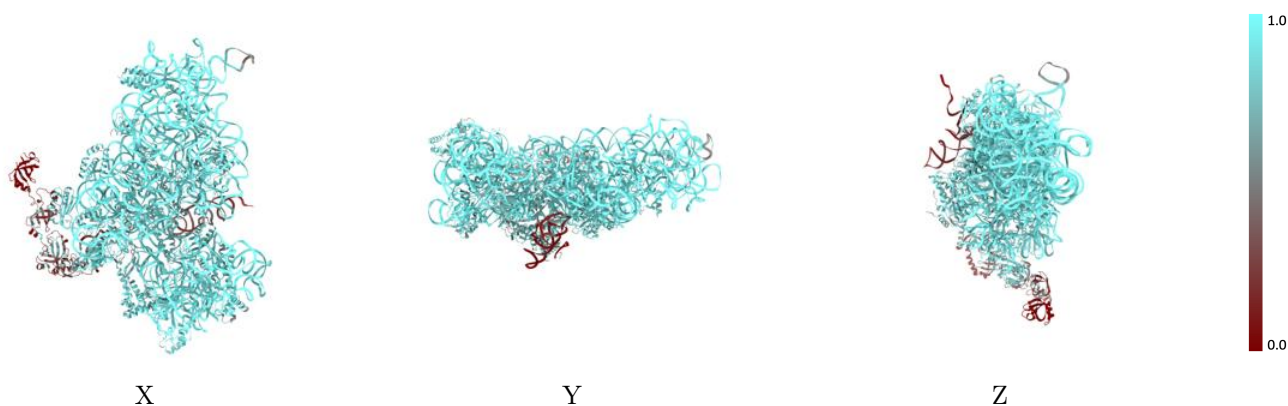
The images above show the 3D surface view of the map at the recommended contour level 0.328 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



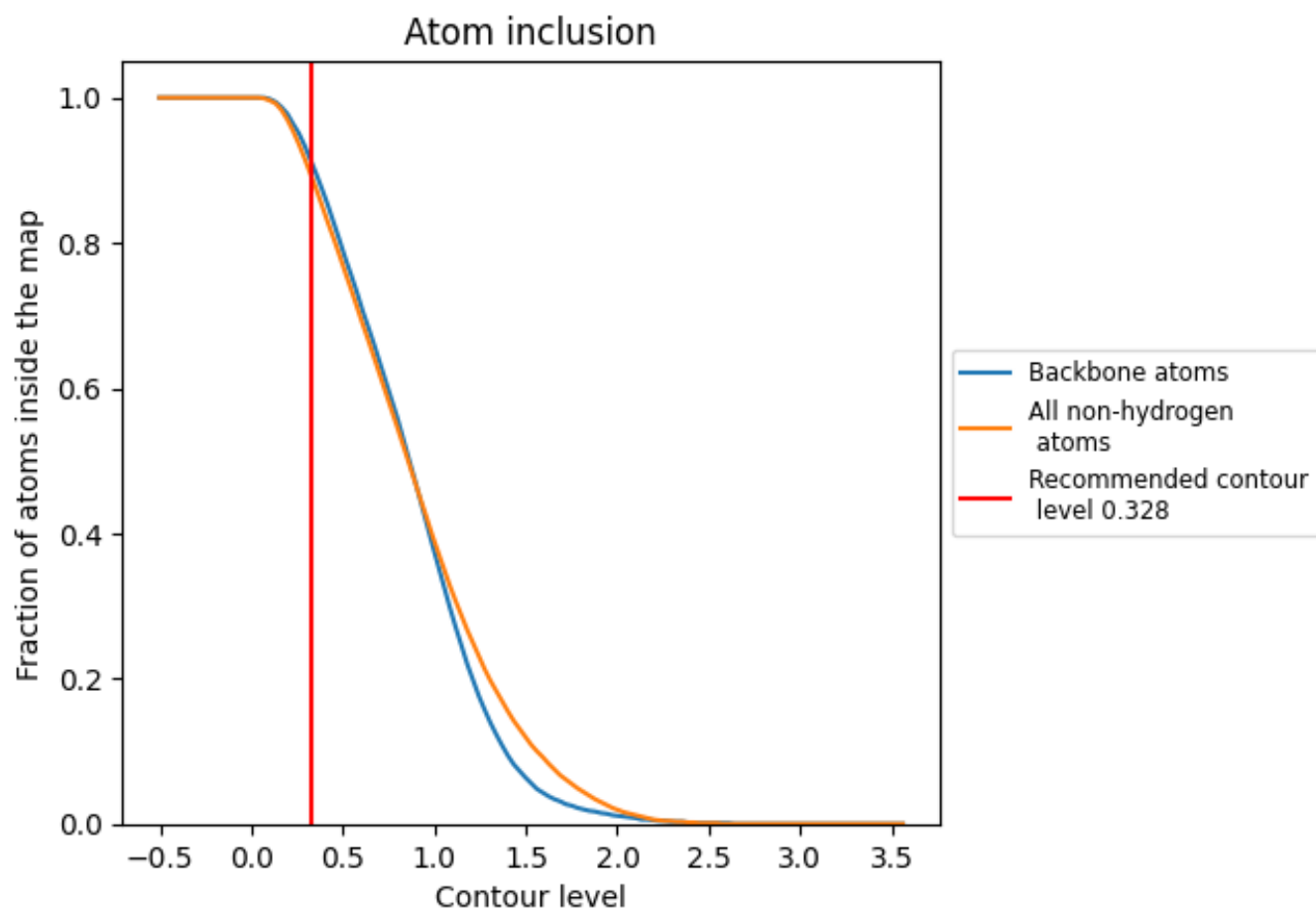
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.328).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.328) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.5360
A	 0.9830	 0.5930
B	 0.3770	 0.1900
C	 0.8700	 0.5020
D	 0.9020	 0.5580
E	 0.9140	 0.5570
F	 0.9260	 0.5630
G	 0.8810	 0.5230
H	 0.8290	 0.4680
I	 0.9120	 0.5670
J	 0.9160	 0.5690
K	 0.8610	 0.5060
L	 0.9170	 0.5300
M	 0.9350	 0.5730
N	 0.9060	 0.5280
O	 0.9410	 0.5790
P	 0.9220	 0.5630
Q	 0.9390	 0.5880
R	 0.8970	 0.5420
S	 0.8970	 0.5630
T	 0.9300	 0.5780
U	 0.9450	 0.5690
V	 0.8020	 0.4640
W	 0.1890	 0.2160
X	 0.5780	 0.2110

