



wwPDB EM Validation Summary Report ⓘ

Jul 6, 2026 – 04:46 PM JST

PDB ID : 9VTG / pdb_00009vtg
EMDB ID : EMD-65327
Title : cryoEM structure of tobacco mosaic virus tRNA-like structure complexed with tobacco 60S
Authors : Lu, G.; Lin, J.
Deposited on : 2025-07-10
Resolution : 3.80 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.dev133
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

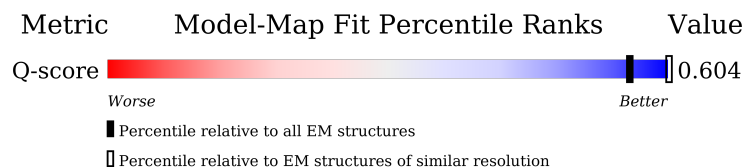
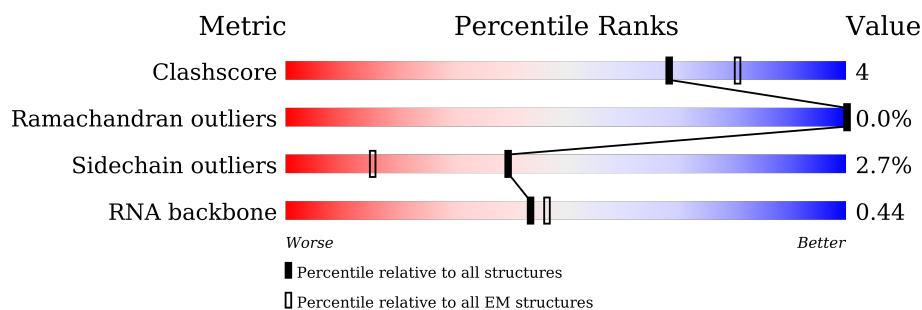
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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)	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	10198 (3.30 - 4.30)

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	LA	217	
2	LB	260	
3	LC	389	

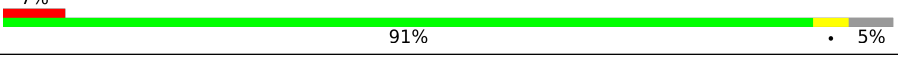
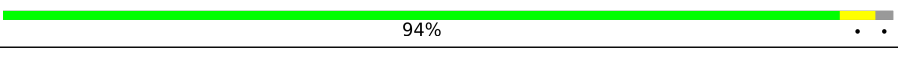
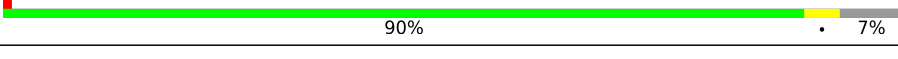
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Mol	Chain	Length	Quality of chain
4	LD	405	
5	LE	181	
6	LF	194	
7	LG	206	
8	LH	140	
9	LI	148	
10	LJ	219	
11	LK	293	
12	LL	175	
13	LM	154	
14	LN	146	
15	LO	123	
16	LP	242	
17	LQ	230	
18	LR	237	
19	LS	200	
20	LT	130	
21	LU	204	
22	LV	187	
23	LW	211	
24	LX	178	
25	LY	164	
26	LZ	108	
27	La	164	
28	Lb	135	

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Mol	Chain	Length	Quality of chain
29	Lc	143	
30	Ld	50	
31	Le	113	
32	Lf	120	
33	Lg	133	
34	Lh	112	
35	Li	120	
36	Lj	110	
37	Lk	95	
38	Ll	69	
39	Lm	51	
40	Ln	128	
41	Lp	105	
42	Lq	77	
43	10	204	
44	12	119	
45	13	163	
46	14	3390	

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 129544 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 protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	215	Total	C	N	O	S	0	0
			1710	1092	300	307	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LA	2	SER	-	insertion	UNP A0A1S3Y379
LA	216	ILE	VAL	conflict	UNP A0A1S3Y379

- Molecule 2 is a protein called 60S ribosomal protein L8-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	245	Total	C	N	O	S	0	0
			1880	1174	381	315	10		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LC	386	Total	C	N	O	S	0	0
			3107	1983	577	532	15		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LC	200	SER	GLY	conflict	UNP A0A1S3ZLI9
LC	308	GLU	ASP	conflict	UNP A0A1S3ZLI9
LC	381	GLU	GLN	conflict	UNP A0A1S3ZLI9

- Molecule 4 is a protein called 60S ribosomal protein L4-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LD	398	Total	C	N	O	S	0	0
			3099	1958	583	548	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LD	27	VAL	LEU	conflict	UNP A0A1S4BWA4

- Molecule 5 is a protein called 60S ribosomal protein L11-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LE	169	Total	C	N	O	S	0	0
			1356	859	251	239	7		

- Molecule 6 is a protein called 60S ribosomal protein L9-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LF	191	Total	C	N	O	S	0	0
			1520	966	274	275	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LF	125	LYS	ARG	conflict	UNP A0A1S4CJ62
LF	191	VAL	ALA	conflict	UNP A0A1S4CJ62

- Molecule 7 is a protein called 60S ribosomal protein L13a-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LG	205	Total	C	N	O	S	0	0
			1644	1046	320	270	8		

- Molecule 8 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LH	131	Total	C	N	O	S	0	0
			985	623	183	170	9		

- Molecule 9 is a protein called 60s ribosomal protein l27a-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	147	Total	C	N	O	S	0	0
			1155	735	226	191	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	94	SER	ASN	conflict	UNP A0A1J6IJF4

- Molecule 10 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	209	Total	C	N	O	S	0	0
			1671	1058	329	273	11		

- Molecule 11 is a protein called 60S ribosomal protein L5-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LK	288	Total	C	N	O	S	0	0
			2342	1482	428	427	5		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LK	85	ARG	GLN	conflict	UNP A0A1S3XE16
LK	126	THR	SER	conflict	UNP A0A1S3XE16
LK	150	VAL	ILE	conflict	UNP A0A1S3XE16
LK	218	PHE	TYR	conflict	UNP A0A1S3XE16

- Molecule 12 is a protein called 60S ribosomal protein L17-1 isoform X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	154	Total	C	N	O	S	0	0
			1236	769	245	217	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LL	46	LYS	ARG	conflict	UNP A0A1S4DQP0
LL	168	SER	PRO	conflict	UNP A0A1S4DQP0

- Molecule 13 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LM	117	Total	C	N	O	S	0	0
			950	609	170	169	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LM	31	PHE	LEU	conflict	UNP Q07761

- Molecule 14 is a protein called 60S ribosomal protein L26-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LN	126	Total	C	N	O	S	0	0
			1023	635	209	176	3		

- Molecule 15 is a protein called 60S ribosomal protein L35-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LO	122	Total	C	N	O	S	0	0
			997	640	191	165	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LO	100	ALA	VAL	conflict	UNP A0A1S3WY31

- Molecule 16 is a protein called 60S ribosomal protein L7-4-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LP	238	Total	C	N	O	S	0	0
			1958	1255	361	338	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LP	7	PRO	LEU	conflict	UNP A0A1U7X2X8
LP	64	ARG	GLN	conflict	UNP A0A1U7X2X8
LP	157	ASP	GLU	conflict	UNP A0A1U7X2X8

- Molecule 17 is a protein called 60S ribosomal protein L6-like isoform X1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LQ	207	Total	C	N	O	S	0	0
			1600	1040	285	272	3		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LQ	60	ILE	PHE	conflict	UNP A0A1U7WD54

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Chain	Residue	Modelled	Actual	Comment	Reference
LQ	97	LYS	ARG	conflict	UNP A0A1U7WD54
LQ	144	VAL	ILE	conflict	UNP A0A1U7WD54
LQ	148	SER	ASN	conflict	UNP A0A1U7WD54
LQ	152	PHE	ILE	conflict	UNP A0A1U7WD54
LQ	187	GLU	GLY	conflict	UNP A0A1U7WD54

- Molecule 18 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LR	233	Total	C	N	O	S	0	0
			1874	1206	343	318	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LR	108	ILE	VAL	conflict	UNP A0A1U7XNI3
LR	110	LYS	ARG	conflict	UNP A0A1U7XNI3

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LS	200	Total	C	N	O	S	0	0
			1608	1010	324	270	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LS	139	VAL	ALA	conflict	UNP A0A1S4CSN1
LS	163	GLU	ASP	conflict	UNP A0A1S4CSN1

- Molecule 20 is a protein called 60S ribosomal protein L14-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LT	129	Total	C	N	O	S	0	0
			1046	673	195	175	3		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LT	82	THR	ASN	conflict	UNP A0A1U7UYX7
LT	86	ASN	SER	conflict	UNP A0A1U7UYX7

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Chain	Residue	Modelled	Actual	Comment	Reference
LT	101	ALA	SER	conflict	UNP A0A1U7UYX7

- Molecule 21 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	203	Total	C	N	O	S	0	0
			1701	1072	350	276	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LV	186	Total	C	N	O	S	0	0
			1462	931	283	245	3		

- Molecule 23 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LW	182	Total	C	N	O	S	0	0
			1519	940	323	247	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	190	VAL	ALA	conflict	UNP A0A1S4A7M5
LW	195	SER	PRO	conflict	UNP A0A1S4A7M5
LW	197	THR	ALA	conflict	UNP A0A1S4A7M5
LW	198	PRO	SER	conflict	UNP A0A1S4A7M5

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LX	177	Total	C	N	O	S	0	0
			1505	969	277	251	8		

- Molecule 25 is a protein called 60S ribosomal protein L21-1-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LY	163	Total	C	N	O	S	0	0
			1306	823	255	224	4		

- Molecule 26 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LZ	98	Total	C	N	O	S	0	0
			799	510	140	147	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LZ	61	ALA	THR	conflict	UNP A0A1S4BSU3
LZ	63	ALA	THR	conflict	UNP A0A1S4BSU3

- Molecule 27 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	La	62	Total	C	N	O	S	0	0
			526	341	101	81	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lb	134	Total	C	N	O	S	0	0
			1091	704	203	182	2		

- Molecule 29 is a protein called 60S ribosomal protein L28-1-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lc	142	Total	C	N	O	S	0	0
			1107	700	206	199	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lc	53	TYR	ASN	conflict	UNP A0A1U7WYY1
Lc	98	ALA	THR	conflict	UNP A0A1U7WYY1

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ld	49	Total	C	N	O	S	0	0
			407	249	87	70	1		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Le	97	Total	C	N	O	S	0	0
			745	475	130	135	5		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lf	108	Total	C	N	O	S	0	0
			875	549	168	156	2		

- Molecule 33 is a protein called 60S ribosomal protein L32-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lg	126	Total	C	N	O	S	0	0
			1034	653	206	170	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lg	9	THR	LYS	conflict	UNP A0A1U7YAK1

- Molecule 34 is a protein called 60S ribosomal protein L35a-3-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lh	103	Total	C	N	O	S	0	0
			836	534	155	142	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lh	57	VAL	ILE	conflict	UNP A0A1S4AHL7
Lh	91	LYS	ASN	conflict	UNP A0A1S4AHL7

- Molecule 35 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	114	Total	C	N	O	S	0	0
			926	579	193	153	1		

- Molecule 36 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	98	Total	C	N	O	S	0	0
			784	491	162	129	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lj	45	SER	GLY	conflict	UNP A0A1U7VXX3

- Molecule 37 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lk	86	Total	C	N	O	S	0	0
			701	429	155	112	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ll	68	Total	C	N	O	S	0	0
			558	358	99	98	3		

- Molecule 39 is a protein called 60S ribosomal protein L39-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lm	50	Total	C	N	O	S	0	0
			448	286	96	64	2		

- Molecule 40 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ln	51	Total	C	N	O	S	0	0
			420	261	88	65	6		

- Molecule 41 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lp	98	Total	C	N	O	S	0	0
			785	493	157	131	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lp	17	GLY	CYS	conflict	UNP A0A1U7YPT7

- Molecule 42 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lq	76	Total	C	N	O	S	0	0
			593	377	109	102	5		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lq	8	THR	ALA	conflict	UNP A0A1U7XSD1
Lq	35	ASN	SER	conflict	UNP A0A1U7XSD1
Lq	59	TYR	ASP	conflict	UNP A0A1U7XSD1
Lq	62	ASN	LYS	conflict	UNP A0A1U7XSD1
Lq	65	VAL	ALA	conflict	UNP A0A1U7XSD1
Lq	76	ASP	ALA	conflict	UNP A0A1U7XSD1

- Molecule 43 is a RNA chain called RNA (204-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
43	10	158	Total	C	N	O	P	0	0
			3359	1500	590	1111	158		

- Molecule 44 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	12	119	Total	C	N	O	P	0	0
			2538	1133	457	829	119		

- Molecule 45 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	13	163	Total	C	N	O	P	0	0
			3478	1553	628	1134	163		

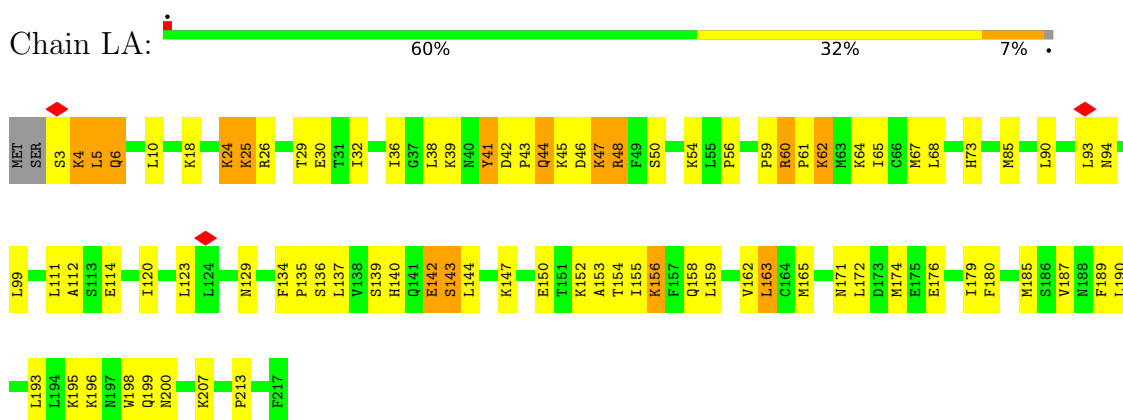
- Molecule 46 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	14	3142	Total	C	N	O	P	0	0
			67280	30009	12243	21886	3142		

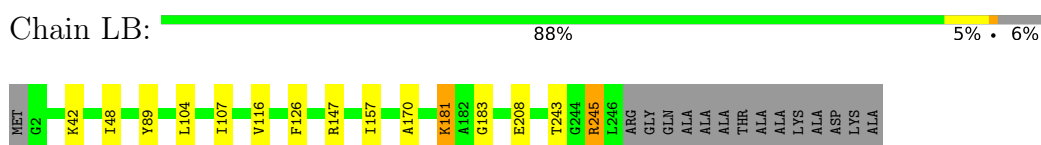
3 Residue-property plots

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.

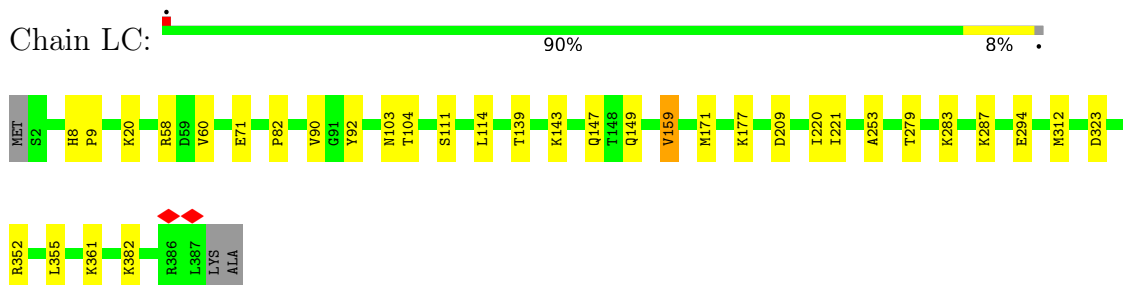
- Molecule 1: Ribosomal protein



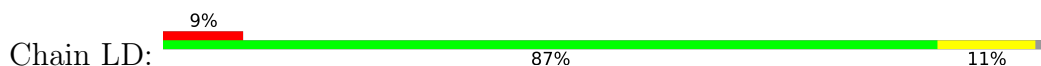
- Molecule 2: 60S ribosomal protein L8-like

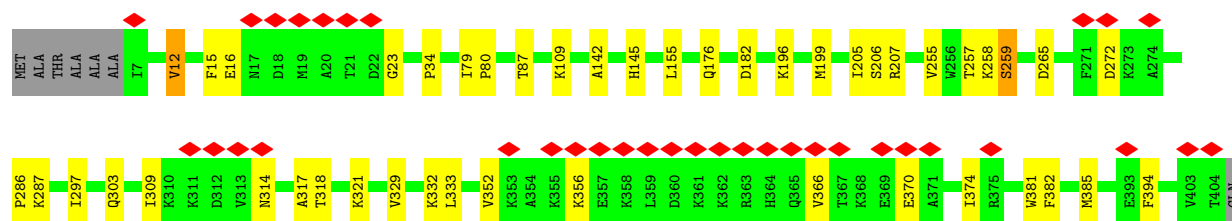


- Molecule 3: 60S ribosomal protein L3

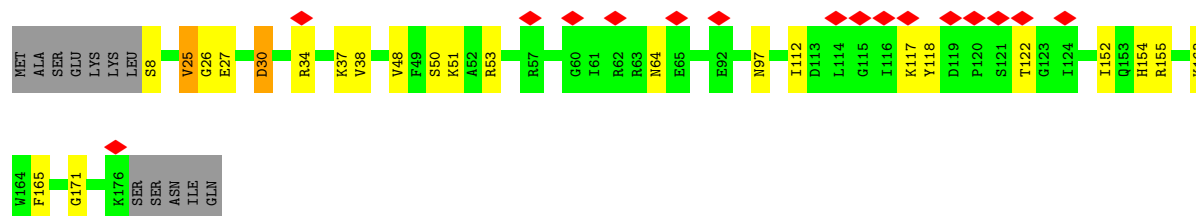
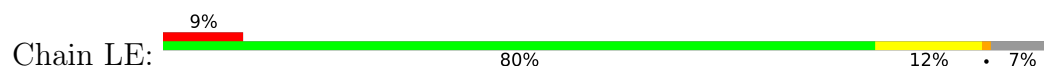


- Molecule 4: 60S ribosomal protein L4-like

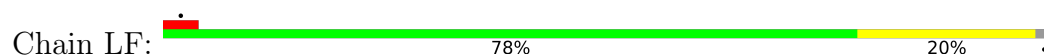




• Molecule 5: 60S ribosomal protein L11-1



• Molecule 6: 60S ribosomal protein L9-1



• Molecule 7: 60S ribosomal protein L13a-4



• Molecule 8: 60S ribosomal protein L23

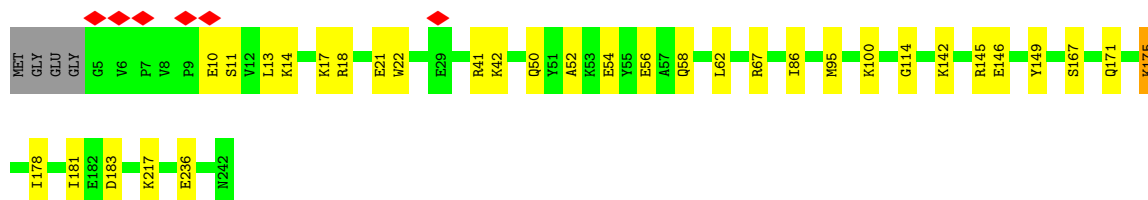
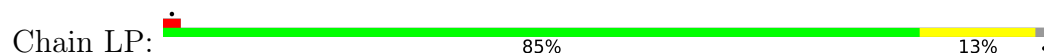


• Molecule 9: 60s ribosomal protein l27a-3

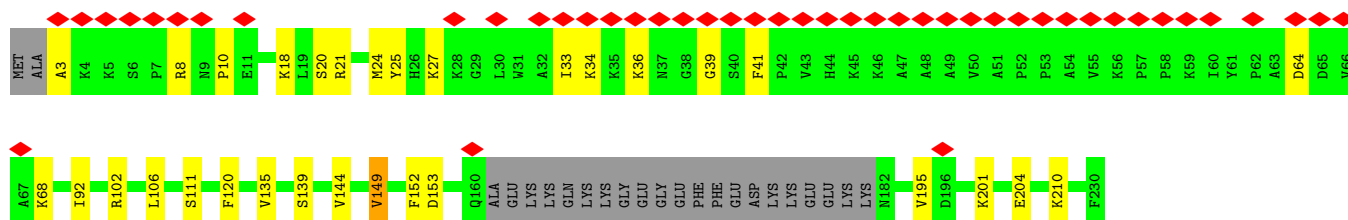
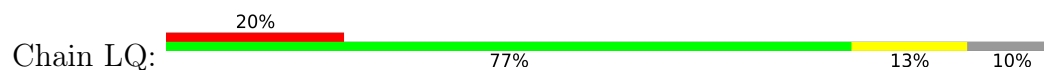




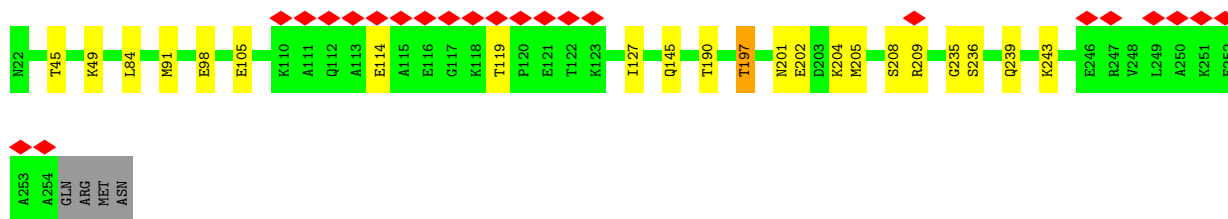
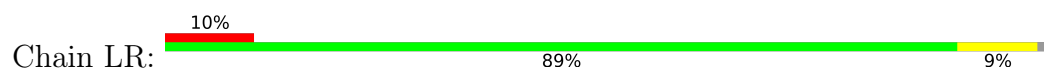
- Molecule 16: 60S ribosomal protein L7-4-like



- Molecule 17: 60S ribosomal protein L6-like isoform X1



- Molecule 18: 60S ribosomal protein L7a



- Molecule 19: 60S ribosomal protein L13

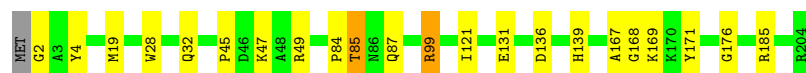
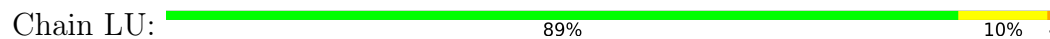


- Molecule 20: 60S ribosomal protein L14-1





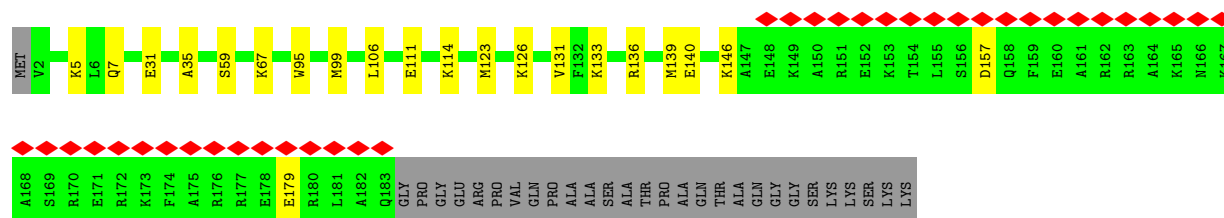
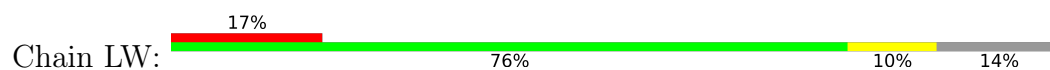
- Molecule 21: Ribosomal protein L15



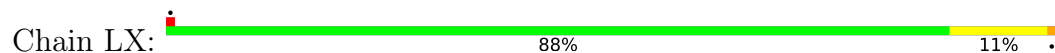
- Molecule 22: 60S ribosomal protein L18-2



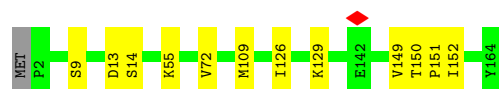
- Molecule 23: Ribosomal protein L19



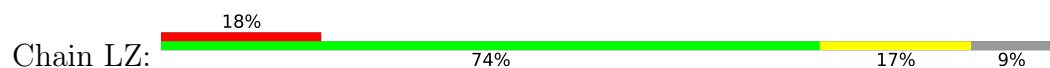
- Molecule 24: 60S ribosomal protein L18a

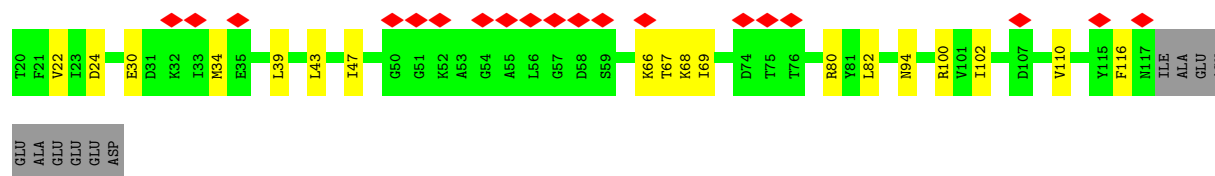


- Molecule 25: 60S ribosomal protein L21-1-like

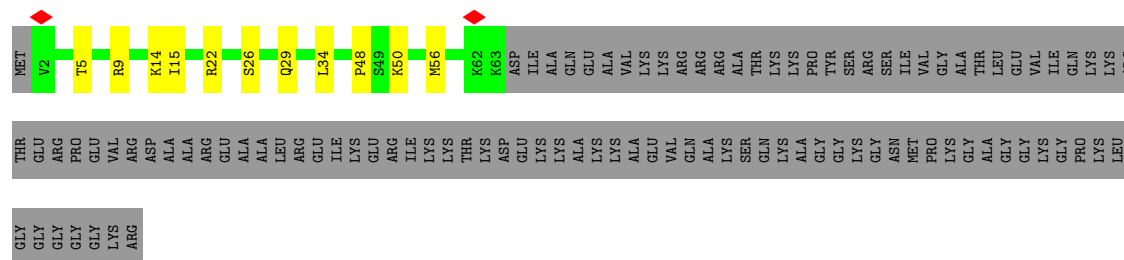


- Molecule 26: Large ribosomal subunit protein eL22

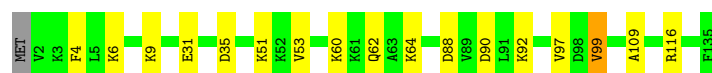
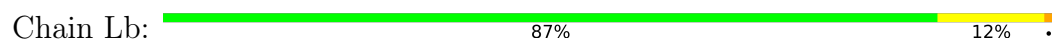




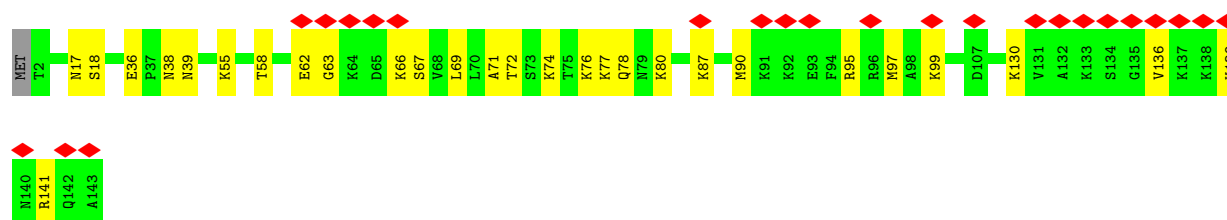
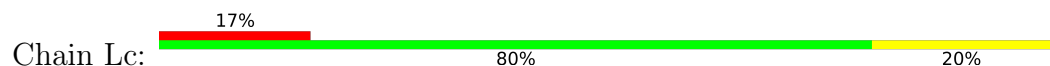
- Molecule 27: 60S ribosomal protein L24



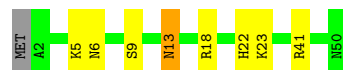
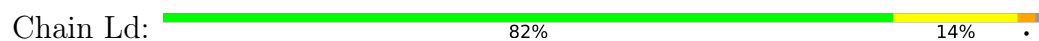
- Molecule 28: 60S ribosomal protein L27



- Molecule 29: 60S ribosomal protein L28-1-like

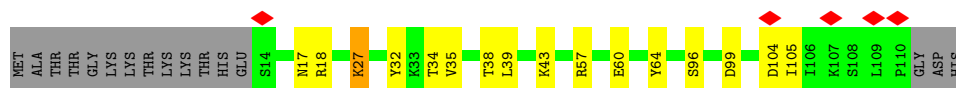


- Molecule 30: 60S ribosomal protein L29

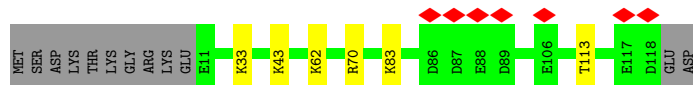
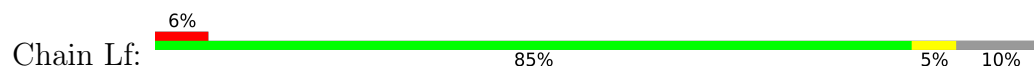


- Molecule 31: 60S ribosomal protein L30

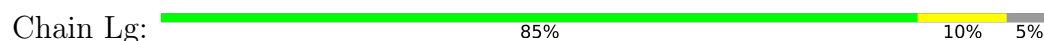




- Molecule 32: 60S ribosomal protein L31



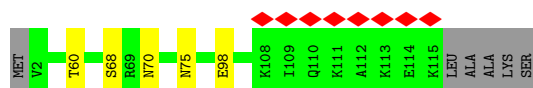
- Molecule 33: 60S ribosomal protein L32-1



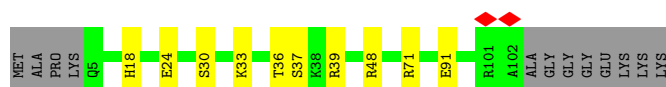
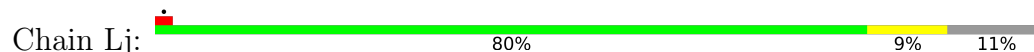
- Molecule 34: 60S ribosomal protein L35a-3-like



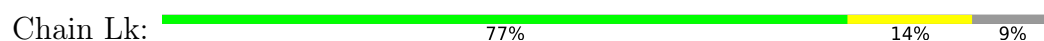
- Molecule 35: Large ribosomal subunit protein eL34



- Molecule 36: 60S ribosomal protein L36

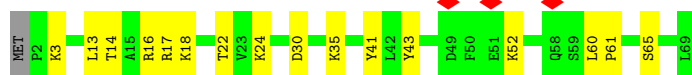


- Molecule 37: Ribosomal protein L37

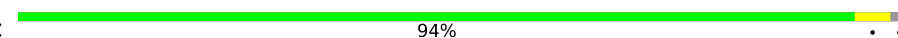


- Molecule 38: 60S ribosomal protein L38

Chain Ll:  75% 23%



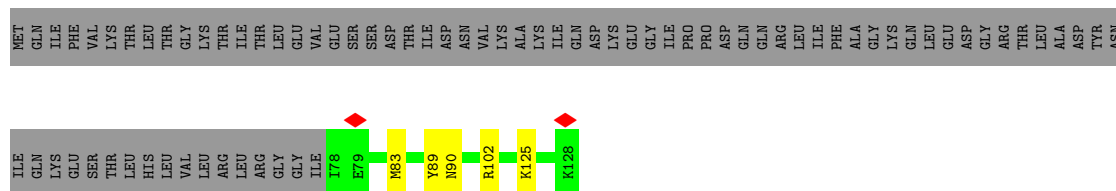
- Molecule 39: 60S ribosomal protein L39-3

Chain Lm:  94%

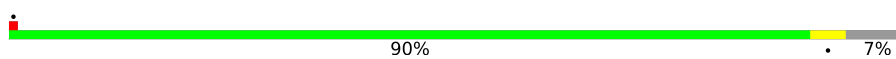


- Molecule 40: Ubiquitin-60S ribosomal protein L40

Chain Ln:  36% 60%



- Molecule 41: 60S ribosomal protein L44

Chain Lp:  90% 7%



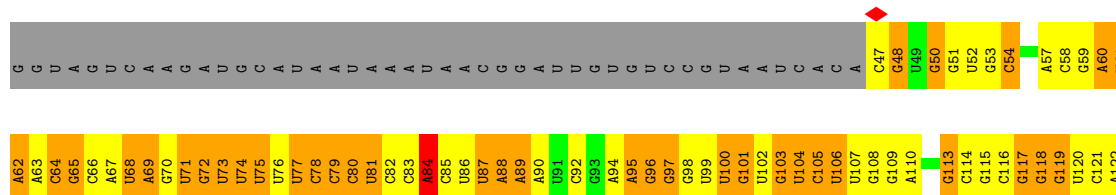
- Molecule 42: 60S ribosomal protein L37a

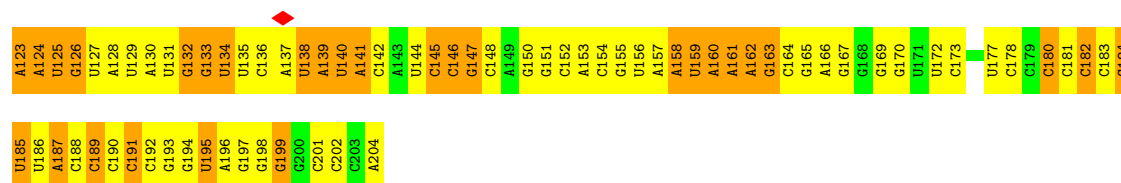
Chain Lq:  88% 10%



- Molecule 43: RNA (204-MER)

Chain 10:  8% 37% 32% 23%





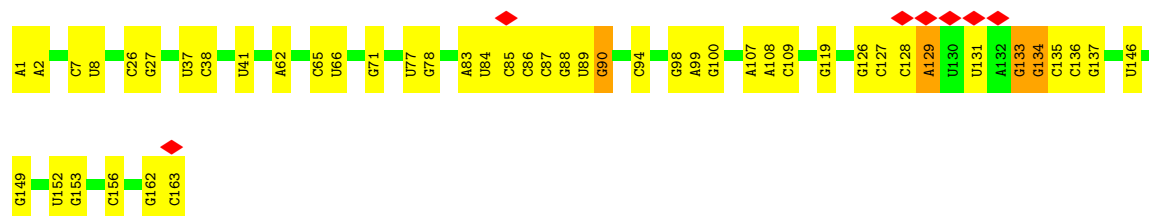
• Molecule 44: 5S rRNA

Chain 12: 85% 12% .



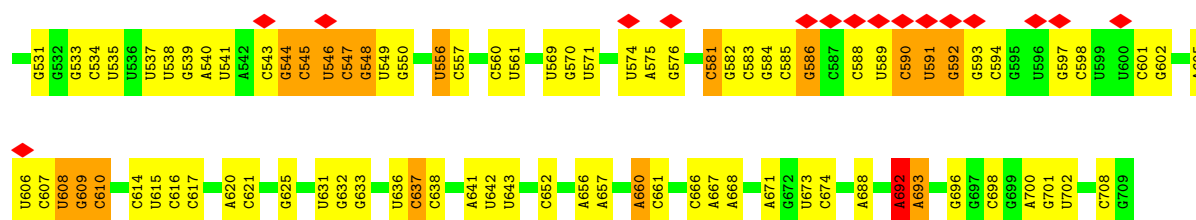
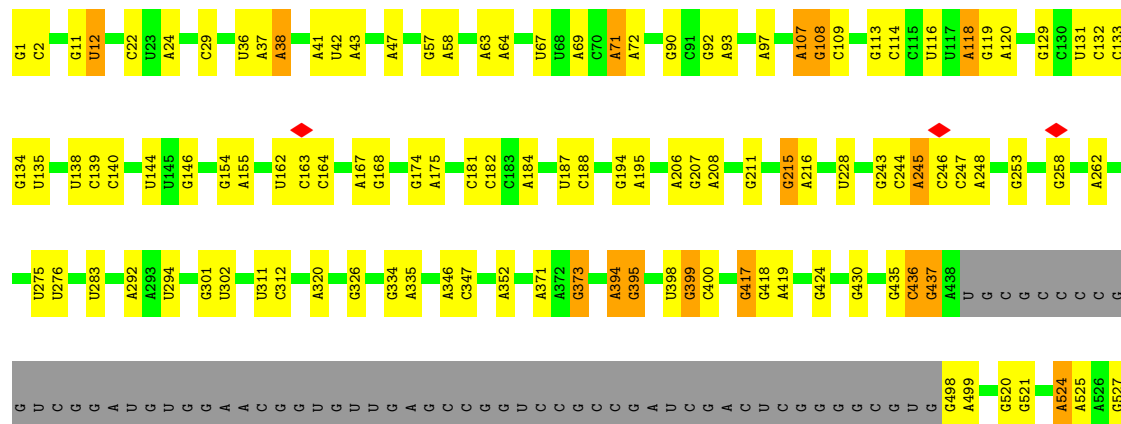
• Molecule 45: 5.8S rRNA

Chain 13: 71% 27% .



• Molecule 46: 25S rRNA

Chain 14: 67% 22% 7% .







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53930	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	1.904	Depositor
Minimum map value	-0.681	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.056	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	460.32, 460.32, 460.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.959, 0.959, 0.959	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	LA	0.75	0/1735	1.11	2/2318 (0.1%)
2	LB	0.36	0/1924	0.53	0/2585
3	LC	0.42	0/3175	0.61	0/4253
4	LD	0.37	0/3161	0.60	0/4263
5	LE	0.30	0/1378	0.52	0/1845
6	LF	0.38	0/1539	0.55	0/2058
7	LG	0.28	0/1673	0.42	0/2241
8	LH	0.27	0/1001	0.47	0/1345
9	LI	0.43	0/1183	0.65	2/1581 (0.1%)
10	LJ	0.25	0/1707	0.39	0/2283
11	LK	0.35	0/2387	0.53	0/3201
12	LL	0.36	0/1261	0.59	0/1693
13	LM	0.27	0/965	0.45	0/1295
14	LN	0.35	0/1037	0.54	0/1385
15	LO	0.24	0/1007	0.37	0/1340
16	LP	0.32	0/1993	0.50	0/2672
17	LQ	0.19	0/1634	0.37	0/2196
18	LR	0.23	0/1907	0.36	0/2555
19	LS	0.31	0/1638	0.47	0/2198
20	LT	0.25	0/1059	0.40	0/1415
21	LU	0.32	0/1740	0.49	0/2333
22	LV	0.29	0/1487	0.45	0/1989
23	LW	0.32	0/1538	0.49	0/2031
24	LX	0.33	0/1544	0.44	0/2071
25	LY	0.29	0/1331	0.44	0/1784
26	LZ	0.21	0/810	0.45	0/1085
27	La	0.23	0/539	0.39	0/716
28	Lb	0.30	0/1110	0.43	0/1482
29	Lc	0.29	0/1122	0.49	0/1503
30	Ld	0.57	0/417	0.82	0/555
31	Le	0.27	0/757	0.42	0/1018
32	Lf	0.27	0/885	0.37	0/1184
33	Lg	0.37	0/1051	0.56	0/1407
34	Lh	0.28	0/856	0.43	0/1149

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Li	0.27	0/939	0.42	0/1251
36	Lj	0.24	0/793	0.44	0/1050
37	Lk	0.36	0/714	0.60	0/949
38	Ll	0.34	0/566	0.49	0/752
39	Lm	0.29	0/460	0.41	0/611
40	Ln	0.17	0/426	0.36	0/561
41	Lp	0.30	0/799	0.43	0/1055
42	Lq	0.40	0/603	0.55	0/802
43	10	0.67	0/3752	1.05	1/5844 (0.0%)
44	12	0.31	0/2837	0.35	0/4420
45	13	0.35	0/3889	0.41	0/6060
46	14	0.42	0/75291	0.53	3/117423 (0.0%)
All	All	0.40	0/139620	0.54	8/205807 (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	LA	0	3
2	LB	0	1
3	LC	0	2
4	LD	0	1
14	LN	0	1
16	LP	0	1
24	LX	0	1
30	Ld	0	1
All	All	0	11

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	LI	15	VAL	N-CA-CB	-6.85	102.91	110.51
9	LI	15	VAL	N-CA-C	6.83	117.53	110.36
46	14	692	A	C3'-C2'-C1'	-6.68	94.82	101.50
46	14	883	C	C2'-C3'-O3'	-6.52	103.93	113.70
46	14	926	G	C2'-C3'-O3'	-5.61	105.29	113.70

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	LA	26	ARG	Sidechain
1	LA	48	ARG	Sidechain
1	LA	60	ARG	Sidechain
2	LB	245	ARG	Sidechain
3	LC	58	ARG	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	LA	1710	0	1812	55	0
2	LB	1880	0	1915	9	0
3	LC	3107	0	3232	18	0
4	LD	3099	0	3229	30	0
5	LE	1356	0	1394	17	0
6	LF	1520	0	1614	24	0
7	LG	1644	0	1773	8	0
8	LH	985	0	1046	6	0
9	LI	1155	0	1197	8	0
10	LJ	1671	0	1731	15	0
11	LK	2342	0	2379	20	0
12	LL	1236	0	1262	5	0
13	LM	950	0	1029	12	0
14	LN	1023	0	1105	7	0
15	LO	997	0	1136	8	0
16	LP	1958	0	2057	20	0
17	LQ	1600	0	1731	24	0
18	LR	1874	0	2030	10	0
19	LS	1608	0	1697	14	0
20	LT	1046	0	1144	12	0
21	LU	1701	0	1771	14	0
22	LV	1462	0	1581	5	0
23	LW	1519	0	1630	10	0
24	LX	1505	0	1557	11	0
25	LY	1306	0	1367	8	0
26	LZ	799	0	836	11	0
27	La	526	0	554	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	Lb	1091	0	1171	8	0
29	Lc	1107	0	1182	19	0
30	Ld	407	0	393	4	0
31	Le	745	0	783	10	0
32	Lf	875	0	934	4	0
33	Lg	1034	0	1110	8	0
34	Lh	836	0	865	4	0
35	Li	926	0	1013	3	0
36	Lj	784	0	871	6	0
37	Lk	701	0	729	10	0
38	Ll	558	0	604	9	0
39	Lm	448	0	480	1	0
40	Ln	420	0	461	5	0
41	Lp	785	0	844	2	0
42	Lq	593	0	618	6	0
43	10	3359	0	1699	98	0
44	12	2538	0	1286	6	0
45	13	3478	0	1761	17	0
46	14	67280	0	33921	282	0
All	All	129544	0	94534	802	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 4.

The worst 5 of 802 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:LA:4:LYS:NZ	1:LA:198:TRP:HB3	1.76	1.00
1:LA:39:LYS:HE3	1:LA:199:GLN:O	1.70	0.92
25:LY:129:LYS:HB3	46:14:1109:A:H5'	1.51	0.91
26:LZ:39:LEU:HD23	26:LZ:69:ILE:HD12	1.54	0.86
1:LA:171:ASN:OD1	1:LA:174:MET:HG3	1.74	0.86

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	
1	LA	213/217 (98%)	190 (89%)	21 (10%)	2 (1%)	14	45
2	LB	243/260 (94%)	231 (95%)	12 (5%)	0	100	100
3	LC	384/389 (99%)	374 (97%)	10 (3%)	0	100	100
4	LD	396/405 (98%)	384 (97%)	12 (3%)	0	100	100
5	LE	167/181 (92%)	163 (98%)	4 (2%)	0	100	100
6	LF	189/194 (97%)	184 (97%)	5 (3%)	0	100	100
7	LG	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
8	LH	129/140 (92%)	127 (98%)	2 (2%)	0	100	100
9	LI	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
10	LJ	205/219 (94%)	201 (98%)	4 (2%)	0	100	100
11	LK	286/293 (98%)	277 (97%)	9 (3%)	0	100	100
12	LL	152/175 (87%)	150 (99%)	2 (1%)	0	100	100
13	LM	115/154 (75%)	114 (99%)	1 (1%)	0	100	100
14	LN	124/146 (85%)	120 (97%)	4 (3%)	0	100	100
15	LO	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
16	LP	236/242 (98%)	229 (97%)	7 (3%)	0	100	100
17	LQ	203/230 (88%)	199 (98%)	4 (2%)	0	100	100
18	LR	231/237 (98%)	228 (99%)	3 (1%)	0	100	100
19	LS	198/200 (99%)	192 (97%)	6 (3%)	0	100	100
20	LT	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
21	LU	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
22	LV	184/187 (98%)	180 (98%)	4 (2%)	0	100	100
23	LW	180/211 (85%)	179 (99%)	1 (1%)	0	100	100
24	LX	175/178 (98%)	174 (99%)	1 (1%)	0	100	100
25	LY	161/164 (98%)	157 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	LZ	96/108 (89%)	94 (98%)	2 (2%)	0	100	100
27	La	60/164 (37%)	59 (98%)	1 (2%)	0	100	100
28	Lb	132/135 (98%)	130 (98%)	2 (2%)	0	100	100
29	Lc	140/143 (98%)	139 (99%)	1 (1%)	0	100	100
30	Ld	47/50 (94%)	46 (98%)	1 (2%)	0	100	100
31	Le	95/113 (84%)	93 (98%)	2 (2%)	0	100	100
32	Lf	106/120 (88%)	105 (99%)	1 (1%)	0	100	100
33	Lg	124/133 (93%)	123 (99%)	1 (1%)	0	100	100
34	Lh	101/112 (90%)	100 (99%)	1 (1%)	0	100	100
35	Li	112/120 (93%)	111 (99%)	1 (1%)	0	100	100
36	Lj	96/110 (87%)	94 (98%)	2 (2%)	0	100	100
37	Lk	84/95 (88%)	83 (99%)	1 (1%)	0	100	100
38	Ll	66/69 (96%)	66 (100%)	0	0	100	100
39	Lm	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
40	Ln	49/128 (38%)	49 (100%)	0	0	100	100
41	Lp	96/105 (91%)	93 (97%)	3 (3%)	0	100	100
42	Lq	74/77 (96%)	70 (95%)	4 (5%)	0	100	100
All	All	6493/7066 (92%)	6328 (98%)	163 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	LA	59	PRO
1	LA	143	SER

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	
1	LA	192/196 (98%)	168 (88%)	24 (12%)	4	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	LB	190/197 (96%)	186 (98%)	4 (2%)	47	64
3	LC	331/333 (99%)	324 (98%)	7 (2%)	47	64
4	LD	327/331 (99%)	319 (98%)	8 (2%)	43	62
5	LE	144/157 (92%)	141 (98%)	3 (2%)	47	64
6	LF	167/170 (98%)	161 (96%)	6 (4%)	31	54
7	LG	174/175 (99%)	170 (98%)	4 (2%)	44	63
8	LH	103/109 (94%)	100 (97%)	3 (3%)	37	58
9	LI	119/120 (99%)	117 (98%)	2 (2%)	53	67
10	LJ	173/180 (96%)	167 (96%)	6 (4%)	32	54
11	LK	244/246 (99%)	235 (96%)	9 (4%)	30	54
12	LL	133/151 (88%)	132 (99%)	1 (1%)	73	76
13	LM	106/134 (79%)	105 (99%)	1 (1%)	70	74
14	LN	115/132 (87%)	113 (98%)	2 (2%)	53	67
15	LO	108/109 (99%)	106 (98%)	2 (2%)	50	66
16	LP	207/209 (99%)	203 (98%)	4 (2%)	50	66
17	LQ	174/194 (90%)	170 (98%)	4 (2%)	44	63
18	LR	201/205 (98%)	192 (96%)	9 (4%)	24	48
19	LS	166/166 (100%)	165 (99%)	1 (1%)	78	79
20	LT	112/113 (99%)	109 (97%)	3 (3%)	39	59
21	LU	176/177 (99%)	173 (98%)	3 (2%)	53	67
22	LV	154/155 (99%)	151 (98%)	3 (2%)	50	66
23	LW	158/180 (88%)	151 (96%)	7 (4%)	25	49
24	LX	163/164 (99%)	159 (98%)	4 (2%)	42	61
25	LY	140/141 (99%)	138 (99%)	2 (1%)	59	70
26	LZ	89/97 (92%)	87 (98%)	2 (2%)	45	63
27	La	57/133 (43%)	56 (98%)	1 (2%)	51	67
28	Lb	115/117 (98%)	110 (96%)	5 (4%)	26	50
29	Lc	121/123 (98%)	119 (98%)	2 (2%)	53	67
30	Ld	42/43 (98%)	38 (90%)	4 (10%)	8	30
31	Le	85/98 (87%)	83 (98%)	2 (2%)	43	62
32	Lf	95/106 (90%)	93 (98%)	2 (2%)	47	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Lg	114/121 (94%)	113 (99%)	1 (1%)	70	74
34	Lh	92/99 (93%)	92 (100%)	0	100	100
35	Li	100/104 (96%)	99 (99%)	1 (1%)	68	74
36	Lj	84/91 (92%)	82 (98%)	2 (2%)	43	62
37	Lk	72/77 (94%)	71 (99%)	1 (1%)	59	70
38	Ll	64/65 (98%)	61 (95%)	3 (5%)	23	48
39	Lm	47/48 (98%)	46 (98%)	1 (2%)	47	64
40	Ln	46/114 (40%)	46 (100%)	0	100	100
41	Lp	85/91 (93%)	84 (99%)	1 (1%)	63	72
42	Lq	61/62 (98%)	58 (95%)	3 (5%)	22	47
All	All	5646/6033 (94%)	5493 (97%)	153 (3%)	40	59

5 of 153 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	LW	179	GLU
36	Lj	91	GLU
24	LX	168	THR
29	Lc	18	SER
42	Lq	6	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

Mol	Chain	Res	Type
18	LR	239	GLN
24	LX	175	ASN
19	LS	149	GLN
22	LV	150	HIS
25	LY	114	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
43	10	157/204 (76%)	111 (70%)	19 (12%)
44	12	118/119 (99%)	12 (10%)	0
45	13	162/163 (99%)	33 (20%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	14	3138/3390 (92%)	569 (18%)	21 (0%)
All	All	3575/3876 (92%)	725 (20%)	40 (1%)

5 of 725 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	10	48	G
43	10	50	G
43	10	54	C
43	10	58	C
43	10	59	G

5 of 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	14	1847	A
46	14	2553	U
46	14	1848	A
46	14	2376	A
46	14	2731	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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 ⓘ

There are no chain breaks in this entry.

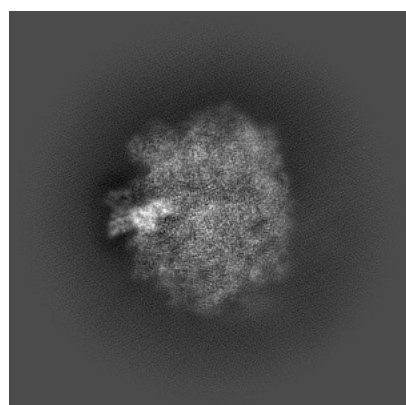
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65327. These allow visual inspection of the internal detail of the map and identification of artifacts.

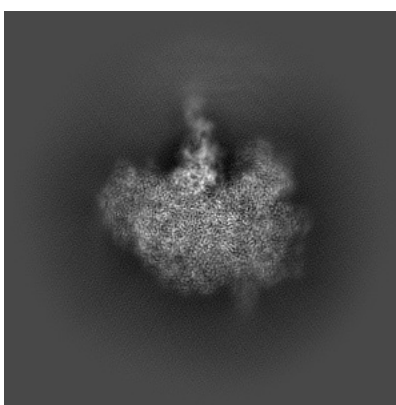
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

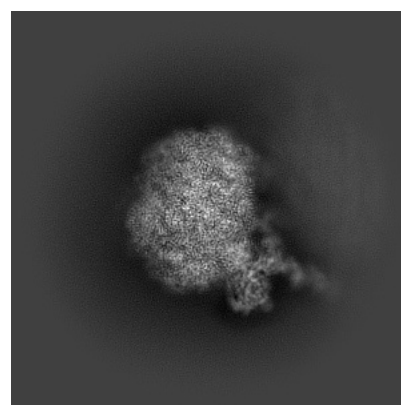
6.1.1 Primary map



X



Y

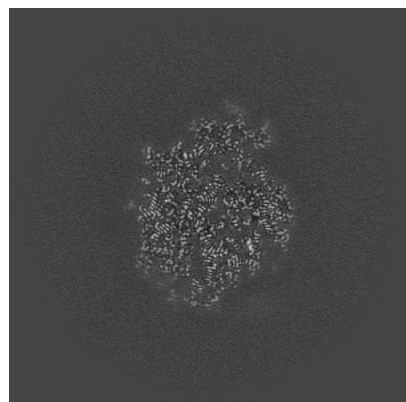


Z

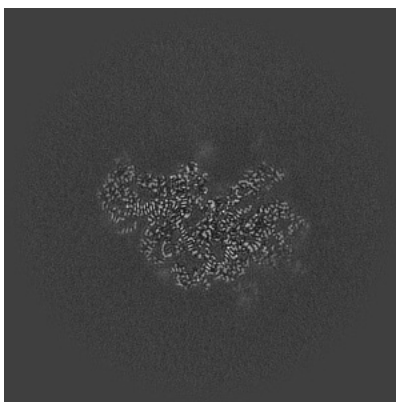
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

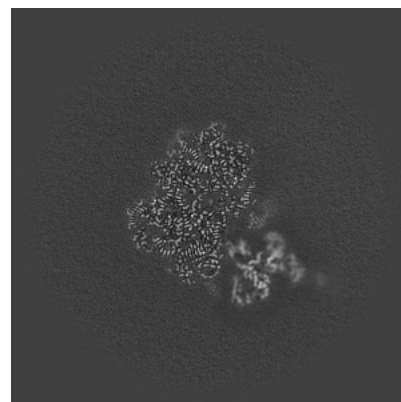
6.2.1 Primary map



X Index: 240



Y Index: 240

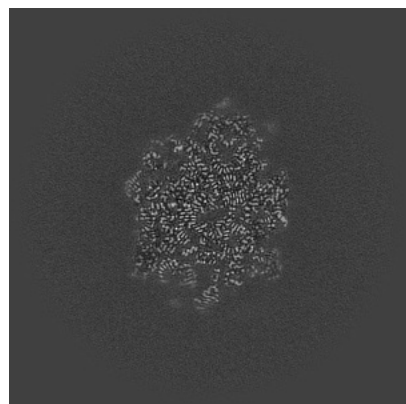


Z Index: 240

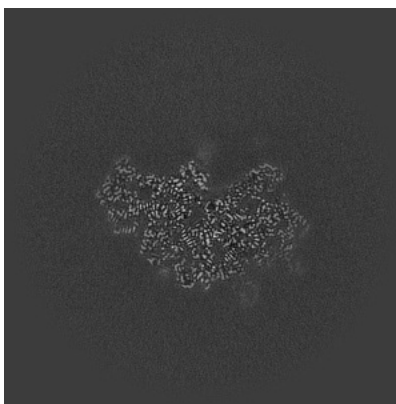
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

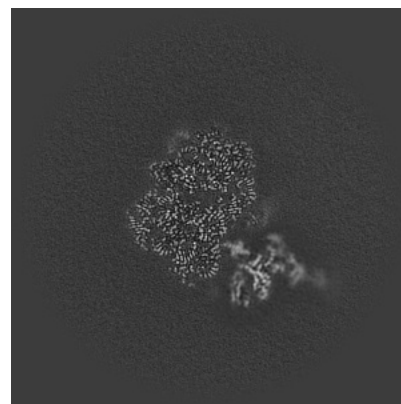
6.3.1 Primary map



X Index: 227



Y Index: 242

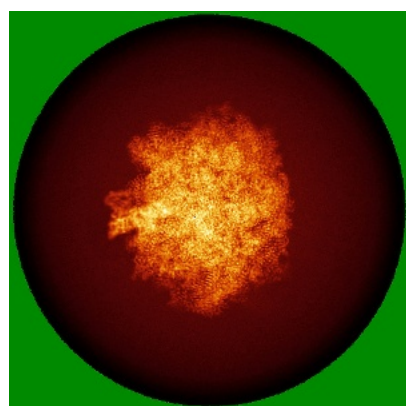


Z Index: 237

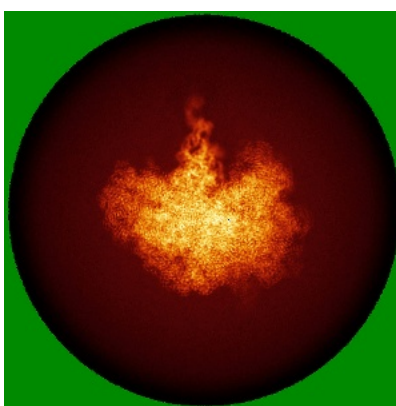
The images above show the largest variance slices of the map in three orthogonal directions.

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

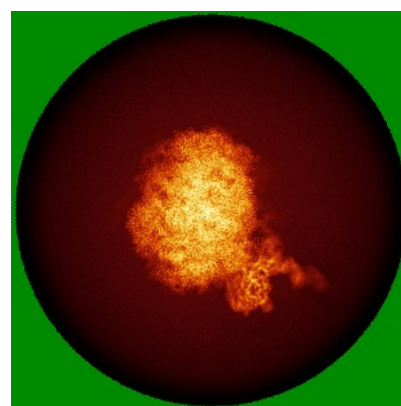
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.18. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

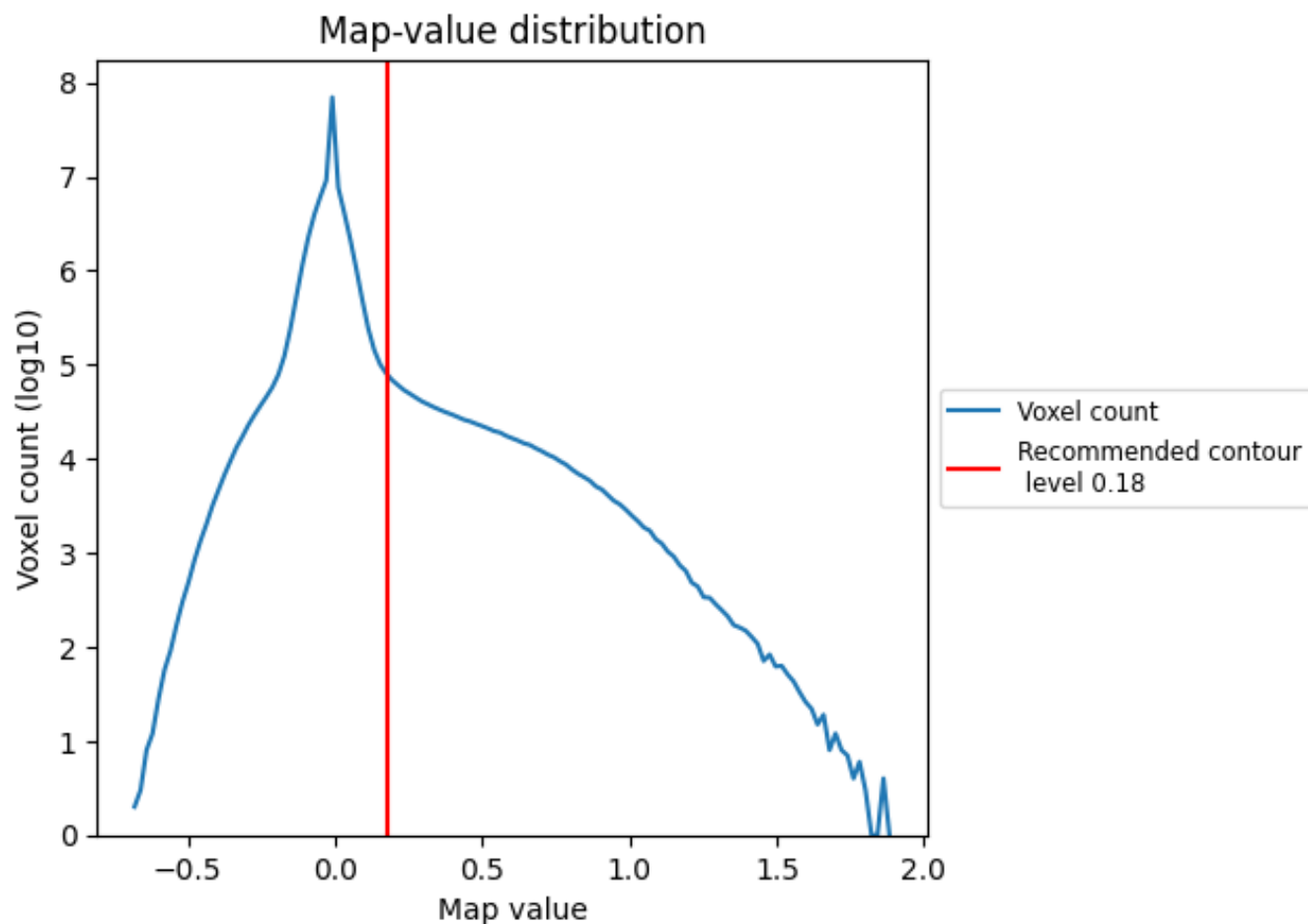
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

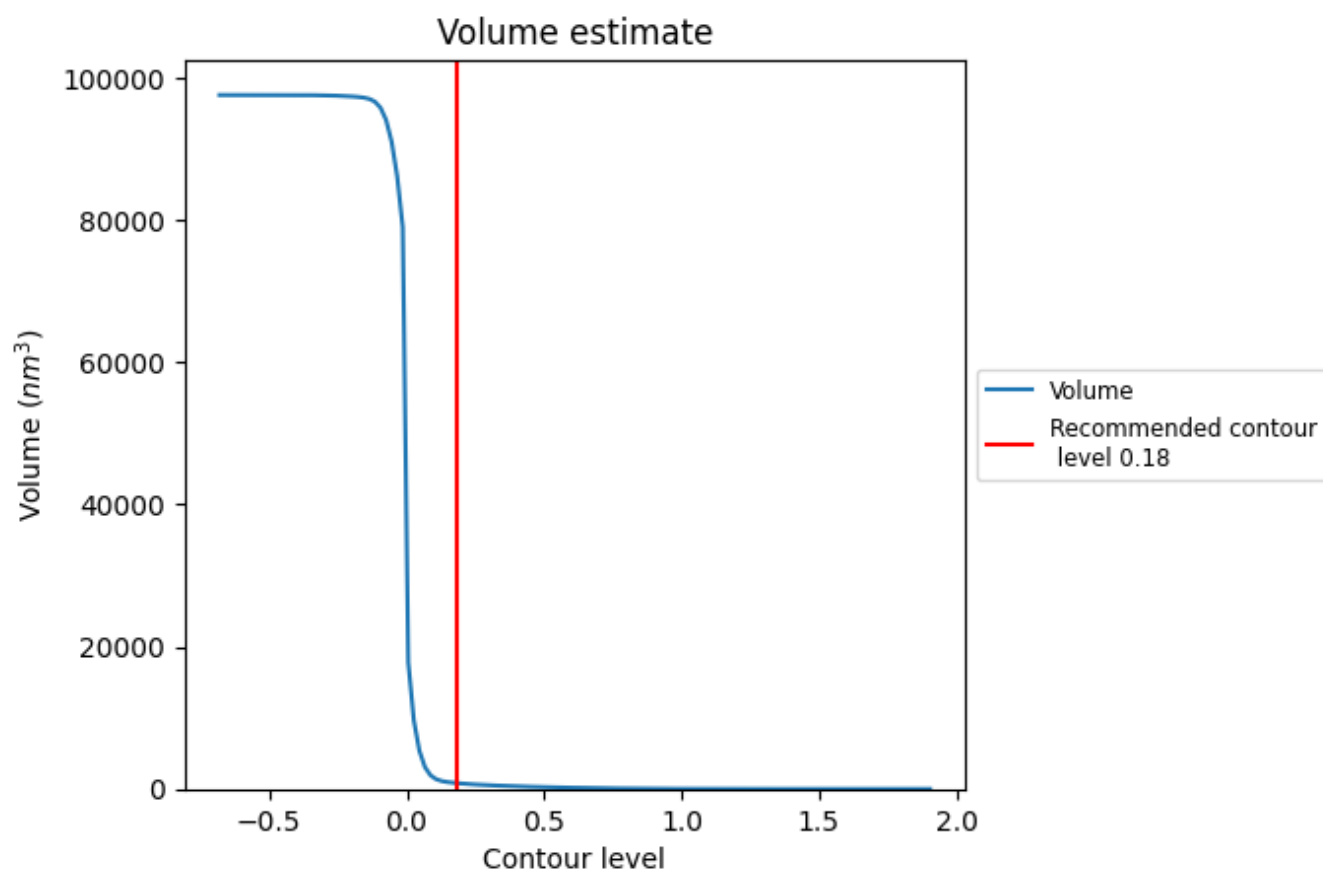
This section contains the results of statistical analysis of the map.

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.

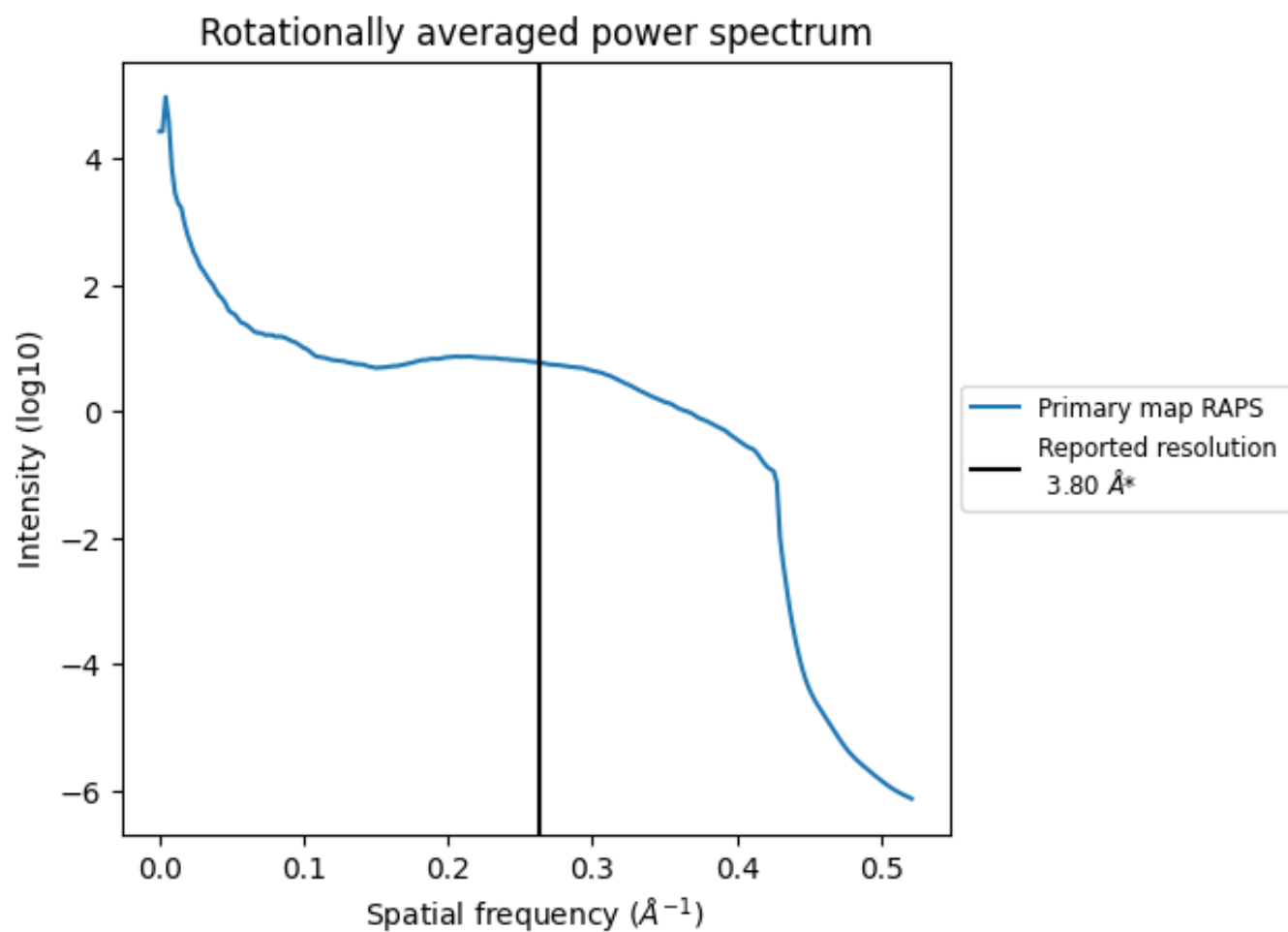
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 827 nm^3 ; this corresponds to an approximate mass of 747 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 0.263 Å⁻¹

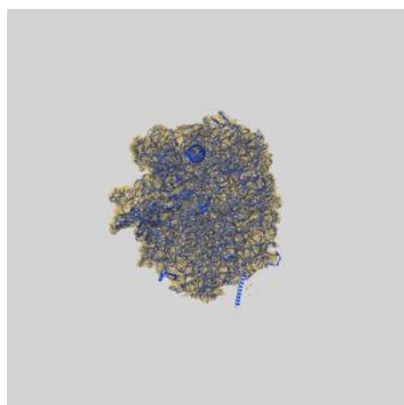
8 Fourier-Shell correlation ⓘ

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

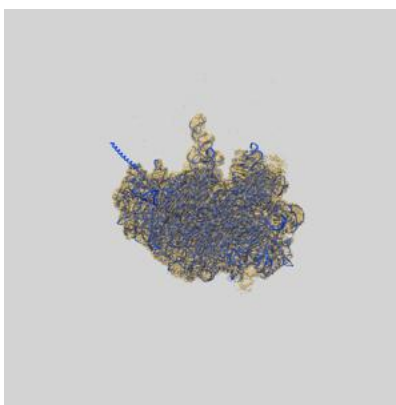
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65327 and PDB model 9VTG. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

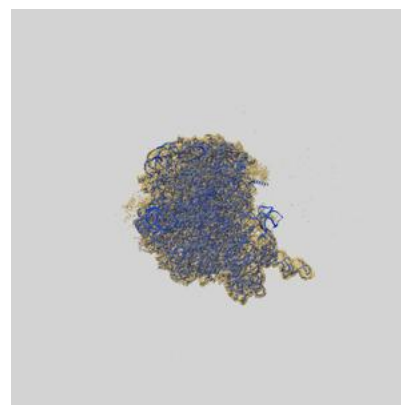
9.1 Map-model overlay [i](#)



X



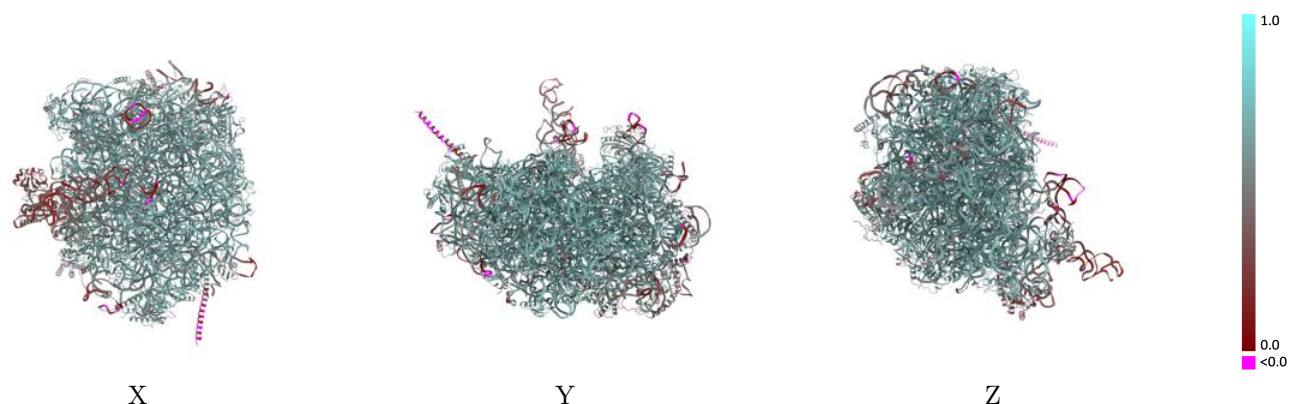
Y



Z

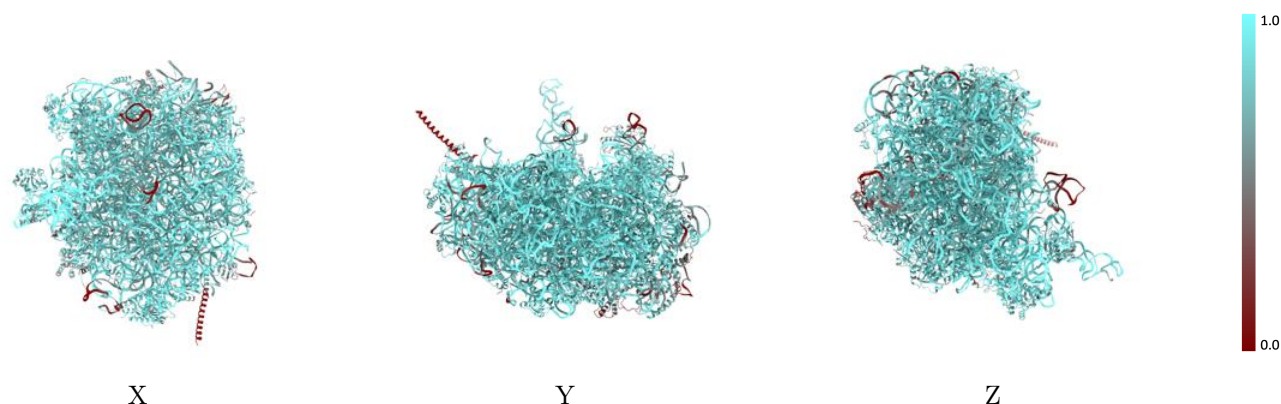
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



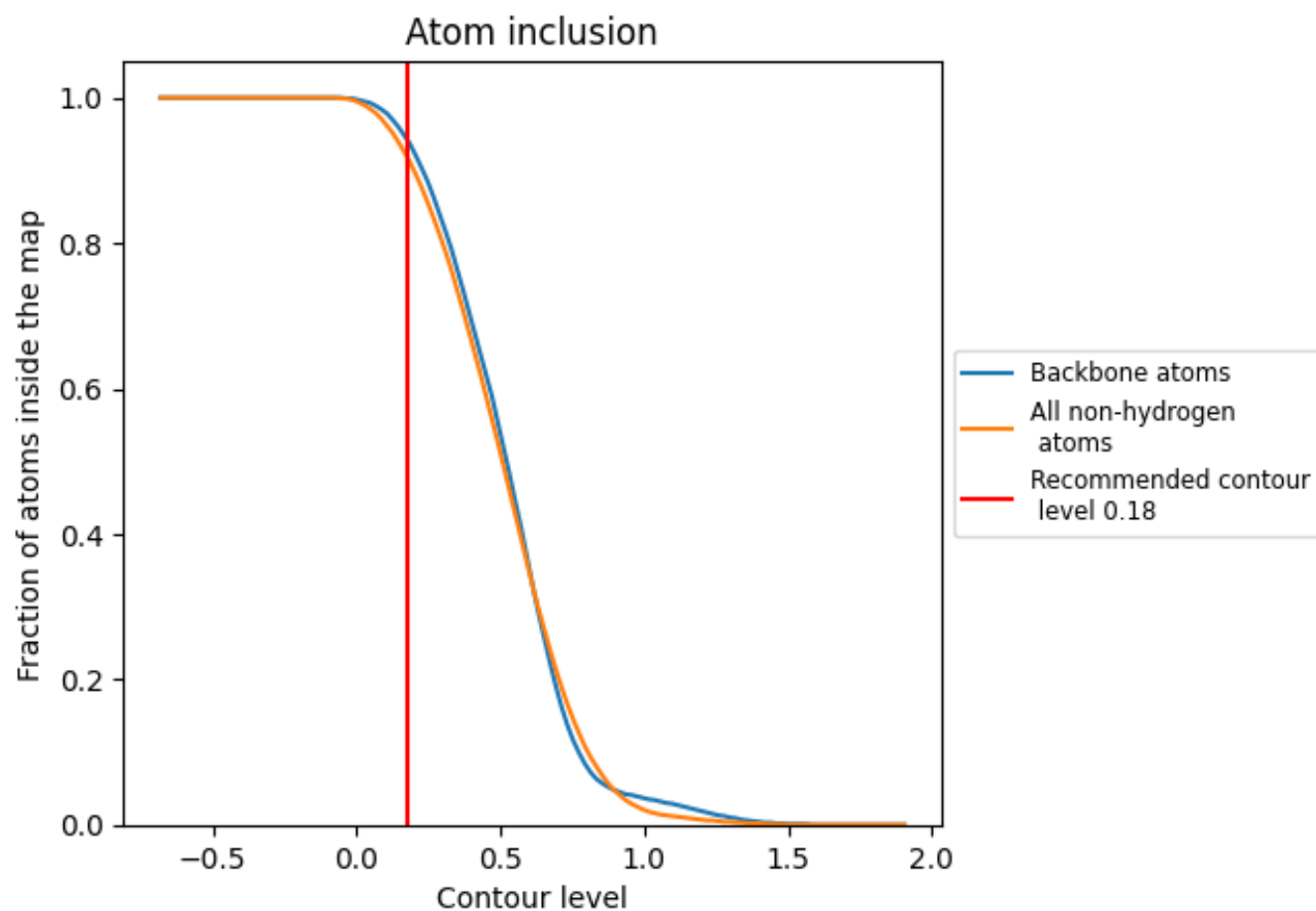
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9160	 0.6040
10	 0.9450	 0.3020
12	 0.9960	 0.6450
13	 0.9230	 0.6120
14	 0.9400	 0.6180
LA	 0.8010	 0.3190
LB	 0.9780	 0.6670
LC	 0.9500	 0.6620
LD	 0.8410	 0.5880
LE	 0.7370	 0.5300
LF	 0.8230	 0.5740
LG	 0.9330	 0.6370
LH	 0.9500	 0.6510
LI	 0.9600	 0.6560
LJ	 0.9160	 0.6310
LK	 0.8660	 0.5970
LL	 0.9500	 0.6550
LM	 0.8970	 0.6220
LN	 0.9420	 0.6370
LO	 0.8780	 0.6030
LP	 0.8810	 0.6180
LQ	 0.6650	 0.5060
LR	 0.7910	 0.5510
LS	 0.9160	 0.6280
LT	 0.8700	 0.5940
LU	 0.9860	 0.6740
LV	 0.9670	 0.6600
LW	 0.7390	 0.5160
LX	 0.9370	 0.6410
LY	 0.9230	 0.6360
LZ	 0.6290	 0.4970
La	 0.8190	 0.6190
Lb	 0.8960	 0.6080
Lc	 0.6620	 0.5600
Ld	 0.9120	 0.6300



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Chain	Atom inclusion	Q-score
Le	 0.8690	 0.5900
Lf	 0.8780	 0.6040
Lg	 0.9620	 0.6580
Lh	 0.9620	 0.6680
Li	 0.8830	 0.6110
Lj	 0.8770	 0.6020
Lk	 0.9770	 0.6690
Ll	 0.8010	 0.5610
Lm	 0.9530	 0.6600
Ln	 0.8080	 0.6160
Lp	 0.9440	 0.6590
Lq	 0.9240	 0.6470