



wwPDB EM Validation Summary Report ⓘ

Sep 14, 2026 – 10:14 PM JST

PDB ID : 44BB / pdb_000044bb
EMDB ID : EMD-65330
Title : cryoEM structure of tobacco mosaic virus tRNA-like structure complexed with tobacco 60S and cycloheximide (CHX)
Authors : Lu, G.; Lin, J.
Deposited on : 2026-07-23
Resolution : 2.50 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD 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

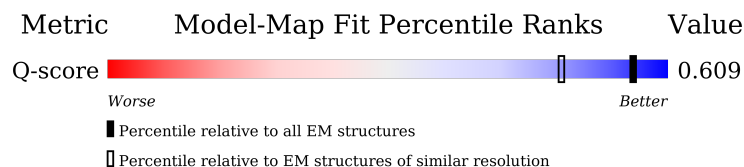
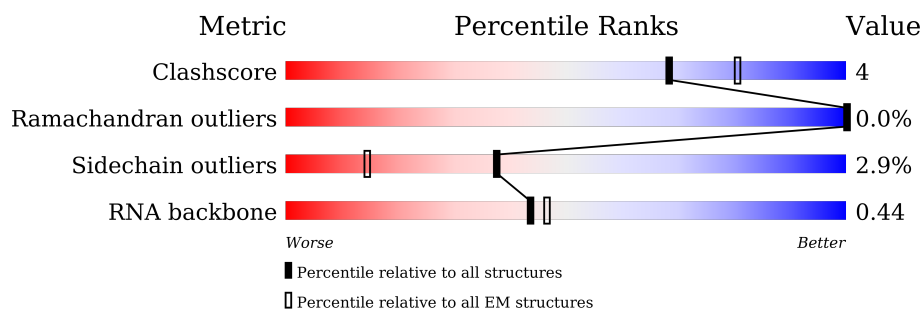
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.50 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.



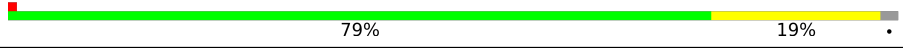
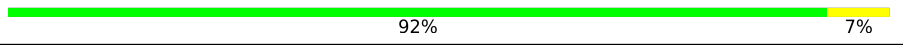
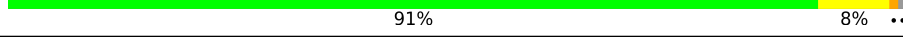
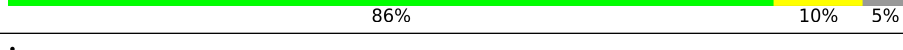
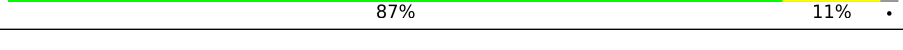
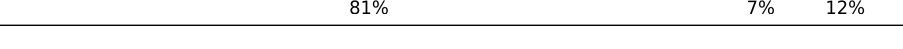
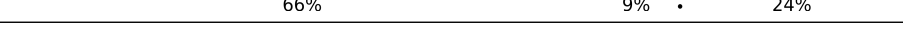
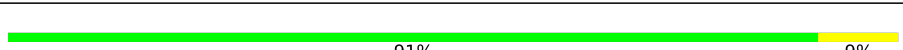
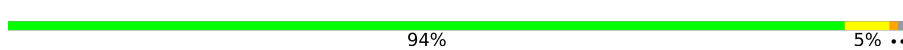
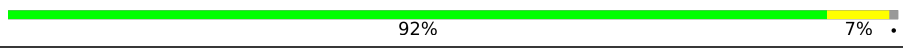
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7115 (2.00 - 3.00)

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	69% 56% 35% 9% .
2	LB	260	88% 5% . 6%
3	LC	389	91% 8% .

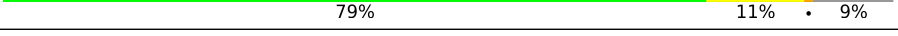
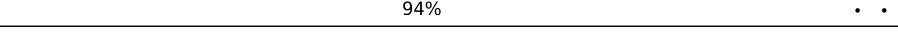
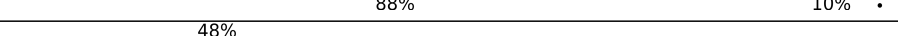
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Mol	Chain	Length	Quality of chain
4	LD	405	
5	LE	181	
6	LF	194	
7	LG	206	
8	LH	140	
9	LI	148	
10	LJ	219	
11	LK	293	
12	LL	175	
13	LM	154	
14	LN	146	
15	LO	123	
16	LP	242	
17	LQ	230	
18	LR	237	
19	LS	200	
20	LT	130	
21	LU	204	
22	LV	187	
23	LW	211	
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 47 unique types of molecules in this entry. The entry contains 129518 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
			1706	1089	299	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 TLSh.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	10	156	Total	C	N	O	P	0	0
			3317	1481	582	1098	156		

- 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		

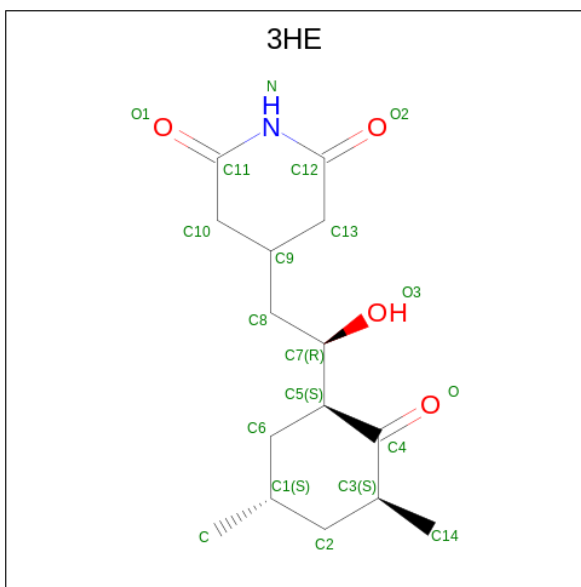
- Molecule 45 is a RNA chain called 5.8S rRNA.

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		

- Molecule 47 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: C₁₅H₂₃NO₄).

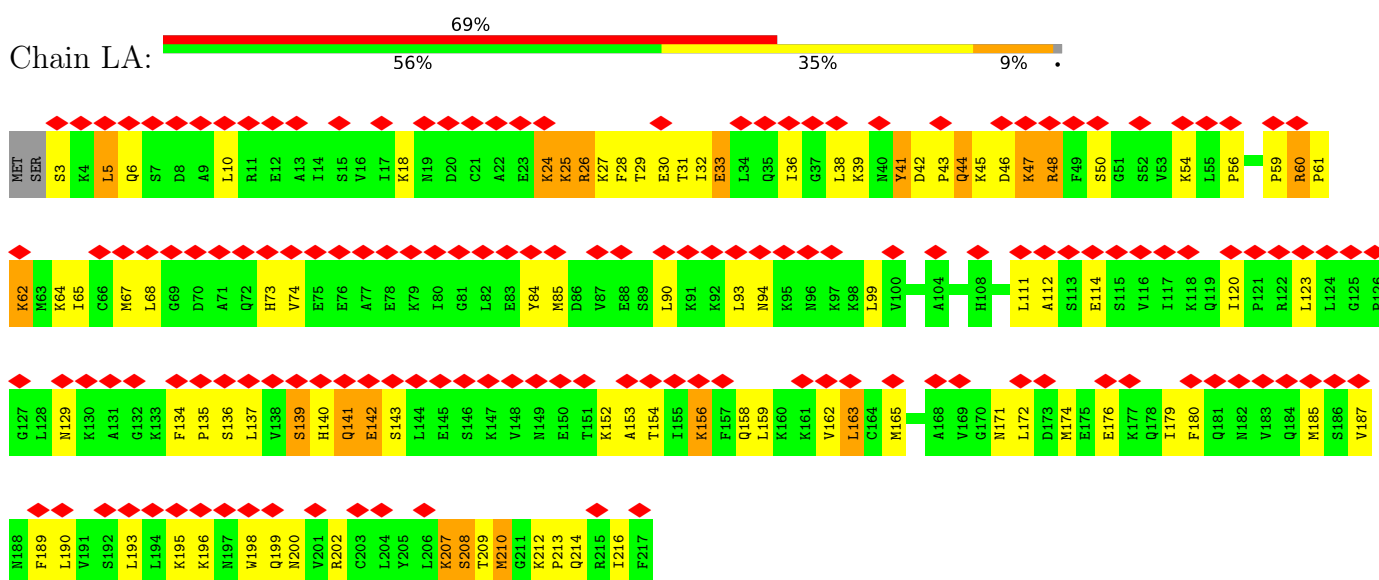


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
47	14	1	20	15	1	4	0

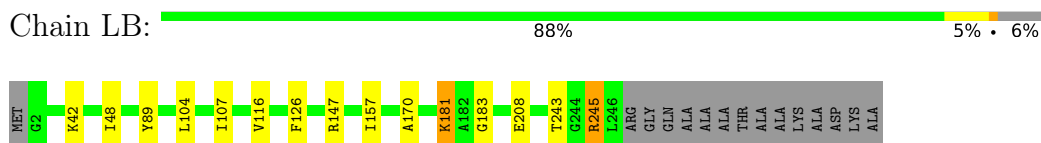
3 Residue-property plots

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

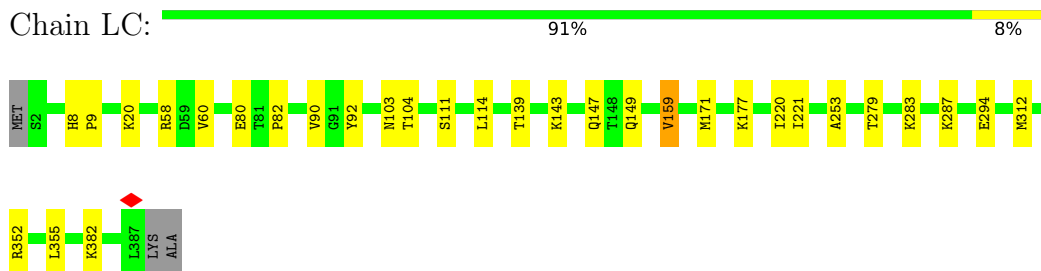
• Molecule 1: Ribosomal protein



• Molecule 2: 60S ribosomal protein L8-like

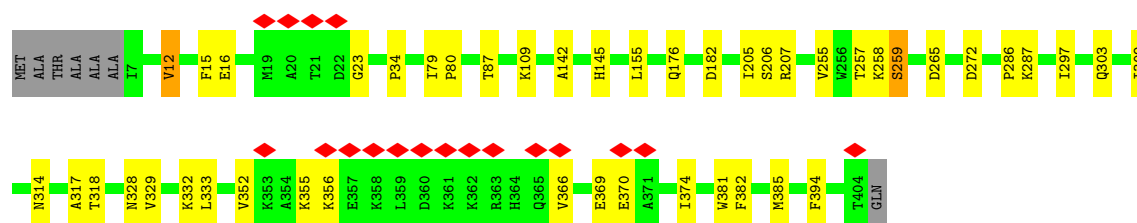


• Molecule 3: 60S ribosomal protein L3



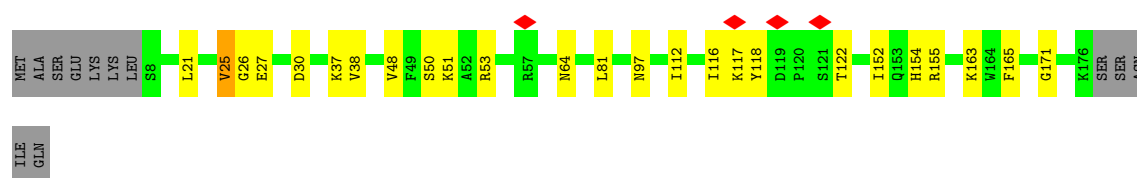
• Molecule 4: 60S ribosomal protein L4-like

Chain LD:  87% 11%



- Molecule 5: 60S ribosomal protein L11-1

Chain LE:  80% 13% 7%



- Molecule 6: 60S ribosomal protein L9-1

Chain LF:  79% 19%



- Molecule 7: 60S ribosomal protein L13a-4

Chain LG:  92% 7%



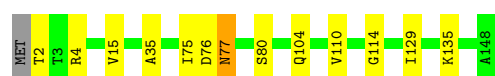
- Molecule 8: 60S ribosomal protein L23

Chain LH:  89% 5% 6%



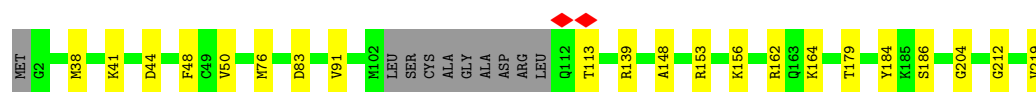
- Molecule 9: 60s ribosomal protein l27a-3

Chain LI:  91% 8%



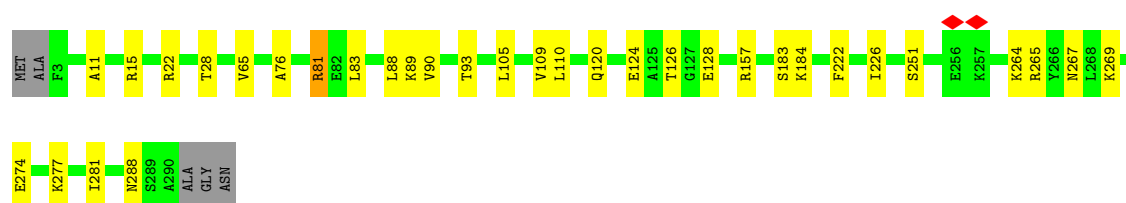
- Molecule 10: 60S ribosomal protein L10

Chain LJ:  86% 10% 5%



- Molecule 11: 60S ribosomal protein L5-like

Chain LK:  87% 11% .



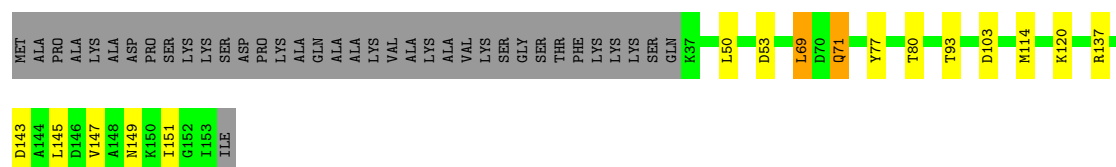
- Molecule 12: 60S ribosomal protein L17-1 isoform X2

Chain LL:  81% 7% 12%



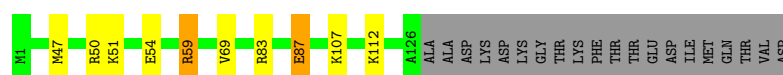
- Molecule 13: Large ribosomal subunit protein uL23

Chain LM:  66% 9% 24%

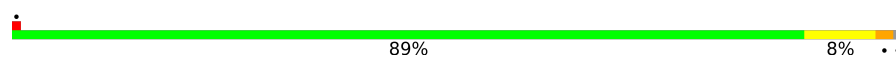


- Molecule 14: 60S ribosomal protein L26-1

Chain LN:  79% 5% 14%



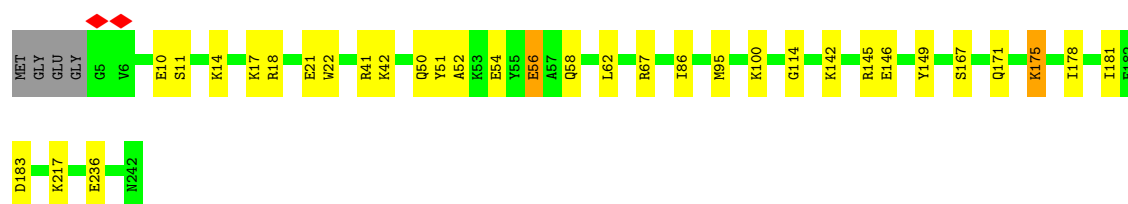
- Molecule 15: 60S ribosomal protein L35-like

Chain LO:  89% 8% .



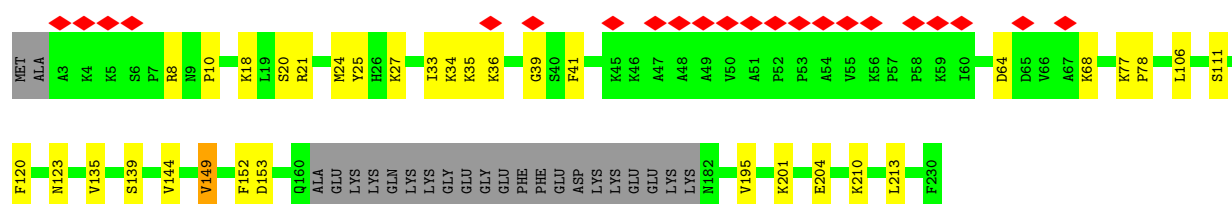
- Molecule 16: 60S ribosomal protein L7-4-like

Chain LP:  85% 13% ..



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

Chain LQ:  10% 76% 14% 10%



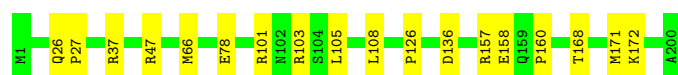
- Molecule 18: 60S ribosomal protein L7a

Chain LR:  5% 89% 9%



- Molecule 19: 60S ribosomal protein L13

Chain LS:  91% 9%



- Molecule 20: 60S ribosomal protein L14-1

Chain LT:  86% 12% ..



- Molecule 21: Ribosomal protein L15

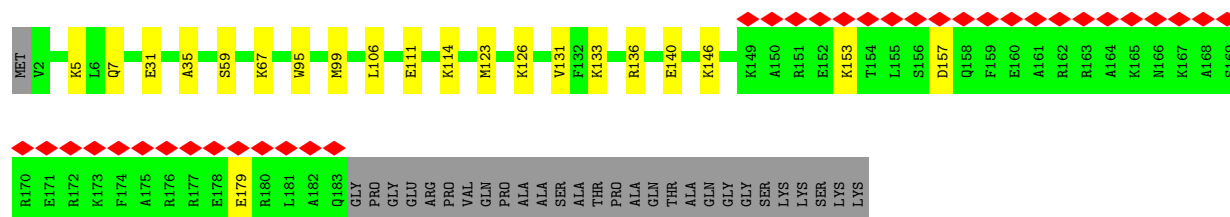
Chain LU:  89% 9%



- Molecule 22: 60S ribosomal protein L18-2

Amino Acid	Percentage (%)
MET	~1
G2	~2
S21	~3
D22	~4
D23	~5
K27	~6
L36	~7
T40	~15
V79	~8
K98	~9
D123	~10
Q124	~11
T162	~12
A187	~13

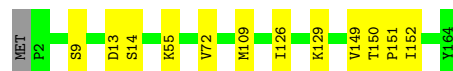
Chain LW:



Chain LX: 88% 11%



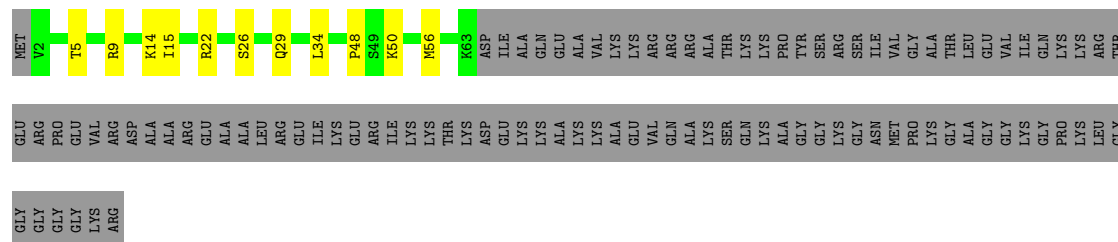
Chain LY: 92% 7%



Chain LZ: 73% 18% 9%

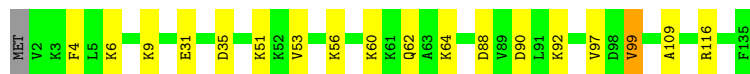


Chain La: 31% 7% 62%



- Molecule 28: 60S ribosomal protein L27

Chain Lb:  86% 13% ..



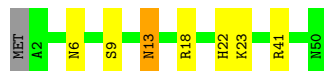
- Molecule 29: 60S ribosomal protein L28-1-like

Chain Lc:  7% 81% 18% .



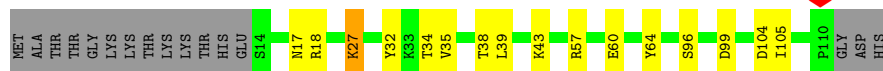
- Molecule 30: 60S ribosomal protein L29

Chain Ld:  84% 12% ..



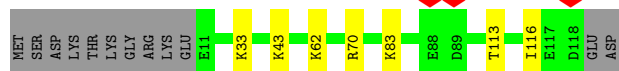
- Molecule 31: 60S ribosomal protein L30

Chain Le:  72% 13% 14%



- Molecule 32: 60S ribosomal protein L31

Chain Lf:  84% 6% 10%



- Molecule 33: 60S ribosomal protein L32-1

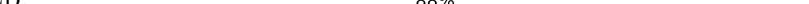
Chain Lg:  85% 10% 5%



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

Chain Lh:  87% 5% 8%



- Chain Lp:  88% 5% • 7%



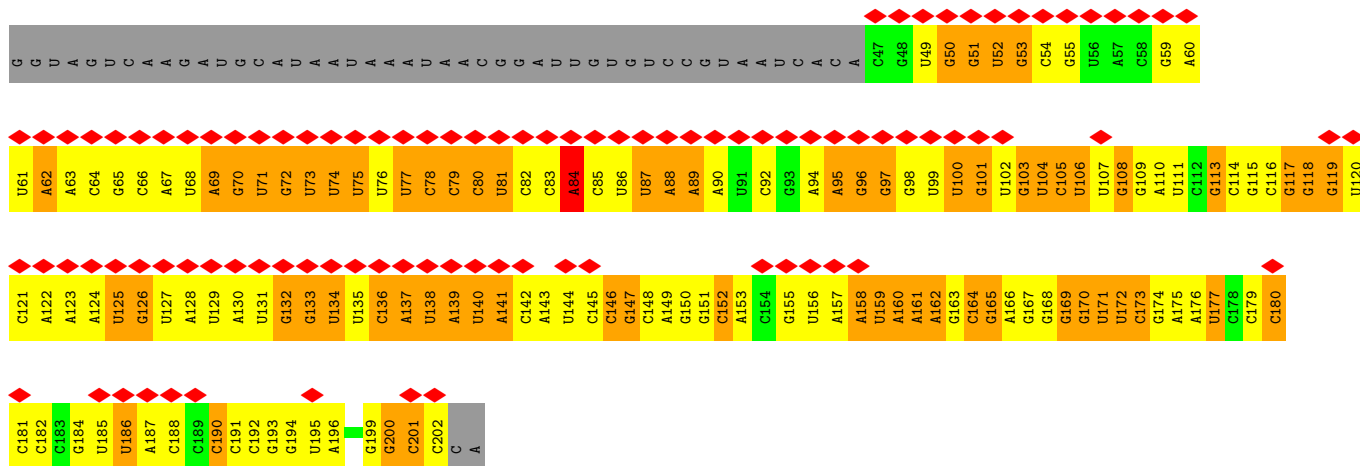
- Molecule 42: 60S ribosomal protein L37a

Chain Lq: 88% 10%



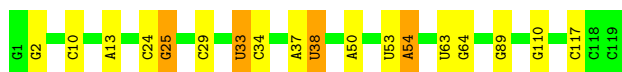
- Molecule 43: TLSh

Chain 10: 7% 48% 37% 32% 24%



- Molecule 44: 5S rRNA

Chain 12: 85% 12%



- Molecule 45: 5.8S rRNA

Chain 13: 71% 25%



- Molecule 46: 25S rRNA

Chain 14: 67% 23% 7%

G1	C2	G134	U135	U275	U276	G	G	A526	G527	U606	C607	C708	A858	G992	A1109	A1232	C1480	U1633	C1828
G11	U12	U138	C139	U136	U137	U	U	G531	G532	U608	G609	G709	C859	C993	A1114	A1233	A1486	C1643	A1847
C22	U23	C140	U144	A292	A293	A	A	G533	G534	C610	C614	A711	C867	G1006	G1115	G1234	A1491	U1646	C1849
U24	A24	U145	U146	A294	U294	U	U	U535	U536	C615	U616	C725	C870	C1013	U1119	A1237	G1491	G1649	C1852
C29				U301	U302	G	G	U537	U538	C617	U617	U726	C871	A1014	C1120	C1239	A1492	U1652	C1853
U36	A37	G154	A155	G301	U302	A	A	U539	U540	A620	U621	U727	C874	G1022	G1128	A	A1493	U1653	C1855
A39		G155		U311	U312	C	C	U541	U542	C621	U622	U728	U879	G1027	U1131	G	A1494	U1654	U1861
U42	U43	U162	C163	U312	C312	G	G	C543	G544	C625	U625	C742	U889	A1028	C1130	U	C1508	C1661	C1872
U43	A43	C164	A167	A320	U320	U	U	U545	U546	U631	U632	C743	U894	C1029	U1132	G	A1509	G1679	A1873
A47		A168	G174	G326	U326	U	U	C547	U548	U633	U634	C744	U898	C1030	U1133	G	C1543	A1680	G1884
G57	A58	A175	A176	G334	U334	G	G	C549	U550	U635	U636	C745	U906	G1032	A1140	U	A1544	U1686	G1885
U67		C181	C182	A335	U335	A	A	C551	U551	C637	U637	C746	U917	G1033	G1145	A	A1545	U1696	A1907
U68	A69	C183	C188	A346	U346	C	C	C552	U552	C638	U638	C747	G917	C1034	A1146	G	U1546	U1697	G1912
A71	A72	G194	A195	A347	U347	C	C	C553	U553	U642	U643	C748	G918	C1035	U1155	U	A1547	U1698	A1914
G90	G91	A206	G207	A352	U352	G	G	C554	U554	U643	U644	C749	G920	C1040	A1164	A	G1548	U1699	G1921
G92	A93	A208	G211	A371	U371	U	U	C555	U555	U644	U645	C750	G927	C1041	A1165	U	G1549	U1700	U1922
A97		G215	A216	A372	U372	C	C	C556	U556	U645	U646	C751	G931	C1042	C1166	G	U1550	G1733	G1933
A107	G108	U228	G243	A394	U394	C	C	C557	U557	U646	U647	C752	G932	C1043	G1169	A	A1558	G1748	C1949
C109		G244	A245	G395	U395	G	G	C558	U558	C661	U661	C753	G933	C1044	A1170	U	C1559	G1749	G1958
G113	C114	G245	A246	G399	U399	U	U	C559	U559	C662	U662	C754	G934	C1045	A1171	C	G1560	A1755	G1959
C115	U116	C247	A248	C400	U400	C	C	C560	U560	C663	U663	C755	G935	C1046	C1186	G	A1561	G1756	G
U117	G119	G253	G258	C436	U436	A	A	C561	U561	C664	U664	C756	G936	C1047	A1189	U	G1562	G1767	C
G129	C130		A262	G437	U437	C	C	C562	U562	C665	U665	C757	G937	C1048	U1192	A	A1563	U1768	A
U131	C132			U	U	C	C	C563	U563	C666	U666	C758	G938	C1049	C1193	G	G1564	C1769	G
C133				G	G	C	C	C564	U564	C667	U667	C759	G939	C1050	A1200	U	G1565	G1770	C
				A498	A499			C565	U565	C668	U668	C760	G940	C1051	A1201	A	A1566	C1771	G
				G518	G519			C566	U566	C669	U669	C761	G941	C1052	A1205	G	G1567	G1772	G
				G520	G521			C567	U567	C670	U670	C762	G942	C1053	G1206	U	A1568	G1773	C
				A524	A525			C568	U568	C671	U671	C763	G943	C1054	A1207	U	A1569	G1774	G
								C569	U569	C672	U672	C764	G944	C1055	A1208	A	G1570	G1775	U
								C570	U570	C673	U673	C765	G945	C1056	A1209	G	A1571	U1577	
								C571	U571	C674	U674	C766	G946	C1057	A1210	U	G1572	U1578	
								C572	U572	C675	U675	C767	G947	C1058	A1211	A	U1579	U1579	
								C573	U573	C676	U676	C768	G948	C1059	A1212	G	U1580	U1580	
								C574	U574	C677	U677	C769	G949	C1060	A1213	U	A1581	U1581	
								C575	U575	C678	U678	C770	G950	C1061	A1214	A	A1582	U1582	
								C576	U576	C679	U679	C771	G951	C1062	A1215	G	A1583	U1583	
								C577	U577	C680	U680	C772	G952	C1063	A1216	U	A1584	U1584	
								C578	U578	C681	U681	C773	G953	C1064	A1217	A	A1585	U1585	
								C579	U579	C682	U682	C774	G954	C1065	A1218	G	A1586	U1586	
								C580	U580	C683	U683	C775	G955	C1066	A1219	U	A1587	U1587	
								C581	U581	C684	U684	C776	G956	C1067	A1220	A	A1588	U1588	
								C582	U582	C685	U685	C777	G957	C1068	A1221	G	A1589	U1589	
								C583	U583	C686	U686	C778	G958	C1069	A1222	U	A1590	U1590	
								C584	U584	C687	U687	C779	G959	C1070	A1223	A	A1591	U1591	
								C585	U585	C688	U688	C780	G960	C1071	A1224	G	A1592	U1592	
								C586	U586	C689	U689	C781	G961	C1072			A1593	U1593	
								C587	U587	C690	U690	C782	G962	C1073			A1594	U1594	
								C588	U588	C691	U691	C783	G963	C1074			A1595	U1595	
								C589	U589	C692	U692	C784	G964	C1075			A1596	U1596	
								C590	U590	C693	U693	C785	G965	C1076			A1597	U1597	
								C591	U591	C694	U694	C786	G966	C1077			A1598	U1598	
								C592	U592	C695	U695	C787	G967	C1078			A1599	U1599	
								C593	U593	C696	U696	C788	G968	C1079			A1600	U1600	
								C594	U594	C697	U697	C789	G969	C1080			A1601	U1601	
								C595	U595	C698	U698	C790	G970	C1081			A1602	U1602	
								C596	U596	C699	U699	C791	G971	C1082			A1603	U1603	
								C597	U597	C700	U700	C792	G972	C1083			A1604	U1604	
								C598	U598	C701	U701	C793	G973	C1084			A1605	U1605	
								C599	U599	C702	U702	C794	G974	C1085			A1606	U1606	
								C600	U600	C703	U703	C795	G975	C1086			A1607	U1607	
								C601	U601	C704	U704	C796	G976	C1087			A1608	U1608	
								C602	U602	C705	U705	C797	G977	C1088			A1609	U1609	
								C603	U603	C706	U706	C798	G978	C1089			A1610	U1610	
								C604	U604	C707	U707	C799	G979	C1090			A1611	U1611	
								C605	U605	C708	U708	C800	G980	C1091			A1612	U1612	
								C606	U606	C709	U709	C801	G981	C1092			A1613	U1613	
								C607	U607	C710	U710	C802	G982	C1093			A1614	U1614	
								C608	U608	C711	U711	C803	G983	C1094			A1615	U1615	
								C609	U609	C712	U712	C804	G984	C1095			A1616	U1616	
								C610	U610	C713	U713	C805	G985	C1096			A1617	U1617	
								C611	U611	C714	U714	C806	G986	C1097			A1618	U1618	
								C612	U612	C715	U715	C807	G987	C1098			A1619	U1619	
								C613	U613	C716	U716	C808	G988	C1099			A1620	U1620	
								C614	U614	C717	U717	C809	G989	C1100			A1621	U1621	
								C615	U615	C718	U718	C810	G990	C1101			A1622	U1622	
								C616	U616	C719	U719	C811	G991	C1102			A1623	U1623	
								C617	U617	C720	U720	C812	G992	C1103			A1624	U1624	
								C618	U618	C721	U721	C813	G993	C1104			A1625	U1625	
								C619	U619	C722	U722	C814	G994	C1105			A1626	U1626	
								C620	U620	C723	U723	C815	G995	C1106			A1627	U1627	
								C621	U621	C724	U724	C816	G996	C1107			A1628	U1628	
								C622	U622	C725	U725	C817	G997	C1108			A1629	U1629	
								C623	U623	C726	U726	C818	G998	C1109			A1630	U1630	
								C624	U624	C727	U727	C819	G999	C1110			A1631	U1631	
								C625	U625	C728	U728	C820	G1000	C1111			A1632	U1632	
								C626	U626	C729	U729	C821	G1001	C1112			A1633	U1633	
								C											

A3285	C3190	G3030	A2903	G2622	U2514	A2443	C2118	G
C3296	U3191	A3031	G2904	A2629	U2515	U2444	C2122	U
A3299	U3192	G3032	C2912	U2636	U2519	A2445	C2123	C
A3307	U3193	C3049	A2913	U2637	A2520	A2446	U2285	G
A3308	G3194	A3050	A2914	A2638	A2528	C2447	G2126	C
C3311	G3195	U3059	G2917	A2639	A2529	U2448	A2135	U
U3321	C3060	C3061	U2926	A2640	A2537	G2450	G2309	G
A3334	A3072	A3073	U2927	A2645	G2536	A2451	U2144	U
G3337	G3080	G3073	C2928	U2655	G2537	G2452	A2152	G
U3343	C3208	G3080	A2933	U2658	G2538	G2453	A2153	G
U3344	U3210	U2938	U2938	A2659	G2539	G2454	U2162	U
G3345	U3211	A2939	A2939	A2677	G2540	G2455	A2163	G
G3346	U3212	C2945	C2945	G2680	G2541	G2456	G2164	C
U3347	G3213	G2948	G2948	A2683	G2542	U2457	G2165	U
G3348	G3214	A2949	A2949	U2684	A2543	A2458	C2199	C
G3361	G3215	C3119	C3119	A2684	U2544	G2460	C2200	C
C3370	A3226	C3120	C2951	U2706	U2545	U2461	A2201	G
U3374	G3235	A3132	G2954	A2707	U2546	U2462	U2337	C
U3377	A3236	U3133	G2954	U2711	U2547	U2463	U2338	C
C3380	G3240	G3153	C2963	C2712	C2547	A2464	G2209	A
U3381	C3253	C3154	C2964	G2717	C2548	G2470	G2209	G
C3382	C3254	G3156	U2965	U2722	C2549	A2471	A2211	C
U3390	G3257	G3160	U2966	U2725	U2550	G2472	G2212	U
	A3258	C3161	U2967	U2726	U2551	C2473	G2213	C
	G3260	A2999	G3000	U2727	U2552	G2474	A2216	U
	A3264	U3164	U3001	U2731	U2553	G2475	A2217	C
	A3265	C3165	G3002	U2732	U2554	A2476	G2226	C
	U3266	C3166	U3003	U2733	U2555	A2477	A2227	C
	U3267	C3167	C3006	U2734	U2556	A2478	U2228	G
	U3268	U3169	A3007	U2735	U2557	G2479	A2231	C
	C3269	C3172	U3014	U2736	U2558	G2482	A2236	G
	A3270	C3173	U3015	U2737	U2559	A2483	A2236	C
	U3271	G3174	U3016	U2738	U2560	U2489	A2245	G
	G3274	A3179	C3017	U2739	U2561	A2490	G2252	C
	A3275	G3180	A3018	U2740	U2562	A2491	G2253	G
	G3278	A3181	A3019	U2741	U2563	U2492	A2258	C
	G3279	G3185	U3025	U2742	U2564	A2496	A2259	U
	G3281	A3026	U3026	U2743	U2565	U2497	C2260	C
				U2744	U2566	U2498	U2261	C
				U2745	U2567	A2499	A2262	G
				U2746	U2568	C2500	U2263	C
				U2747	U2569	U2501	U2264	U
				U2748	U2570	U2502	A2273	G
				U2749	U2571	U2503	A2274	C
				U2750	U2572	U2504	U2116	C
				U2751	U2573	A2505	A2117	C
				U2752	U2574	A2506	G2275	C
				U2753	U2575	U2507	G2276	G
				U2754	U2576	U2508	U2277	G
				U2755	U2577	U2509		
				U2756	U2578	U2510		
				U2757	U2579	U2511		
				U2758	U2580	U2512		
				U2759	U2581	U2513		
				U2760	U2582			
				U2761	U2583			
				U2762	U2584			
				U2763	U2585			
				U2764	U2586			
				U2765	U2587			
				U2766	U2588			
				U2767	U2589			
				U2768	U2590			
				U2769	U2591			
				U2770	U2592			
				U2771	U2593			
				U2772	U2594			
				U2773	U2595			
				U2774	U2596			
				U2775	U2597			
				U2776	U2598			
				U2777	U2599			
				U2778	U2600			
				U2779	U2601			
				U2780	U2602			
				U2781	U2603			
				U2782	U2604			
				U2783	U2605			
				U2784	U2606			
				U2785	U2607			
				U2786	U2608			
				U2787	U2609			
				U2788	U2610			
				U2789	U2611			
				U2790	U2612			
				U2791	U2613			
				U2792	U2614			
				U2793	U2615			
				U2794	U2616			
				U2795	U2617			
				U2796	U2618			
				U2797	U2619			
				U2798	U2620			
				U2799	U2621			
				U2800	U2622			
				U2801	U2623			
				U2802	U2624			
				U2803	U2625			
				U2804	U2626			
				U2805	U2627			
				U2806	U2628			
				U2807	U2629			
				U2808	U2630			
				U2809	U2631			
				U2810	U2632			
				U2811	U2633			
				U2812	U2634			
				U2813	U2635			
				U2814	U2636			
				U2815	U2637			
				U2816	U2638			
				U2817	U2639			
				U2818	U2640			
				U2819	U2641			
				U2820	U2642			
				U2821	U2643			
				U2822	U2644			
				U2823	U2645			
				U2824	U2646			
				U2825	U2647			
				U2826	U2648			
				U2827	U2649			
				U2828	U2650			
				U2829	U2651			
				U2830	U2652			
				U2831	U2653			
				U2832	U2654			
				U2833	U2655			
				U2834	U2656			
				U2835	U2657			
				U2836	U2658			
				U2837	U2659			
				U2838	U2660			
				U2839	U2661			
				U2840	U2662			
				U2841	U2663			
				U2842	U2664			
				U2843	U2665			
				U2844	U2666			
				U2845	U2667			
				U2846	U2668			
				U2847	U2669			
				U2848	U2670			
				U2849	U2671			
				U2850	U2672			
				U2851	U2673			
				U2852	U2674			
				U2853	U2675			
				U2854	U2676			
				U2855	U2677			
				U2856	U2678			
				U2857	U2679			
				U2858	U2680			
				U2859	U2681			
				U2860	U2682			
				U2861	U2683			
				U2862	U2684			
				U2863	U2685			
				U2864	U2686			
				U2865	U2687			
				U2866	U2688			
				U2867	U2689			
				U2868	U2690			
				U2869	U2691			
				U2870	U2692			
				U2871	U2693			
				U2872	U2694			
				U2873	U2695			
				U2874	U2696			
				U2875	U2697			
				U2876	U2698			
				U2877	U2699			
				U2878	U2700			
				U2879	U2701			
				U2880	U2702			
				U2881	U2703			
				U2882	U2704			
				U2883	U2705			
				U2884	U2706			
				U2885	U2707			
				U2886	U2708			
				U2887	U2709			
				U2888	U2710			
				U2889	U2711			
				U2890	U2712			
				U2891	U2713			
				U2892	U2714			
				U2893	U2715			
				U2894	U2716			
				U2895	U2717			
				U2896	U2718			
				U2897	U2719			
				U2898	U2720			
				U2899	U2721			
				U2900	U2722			
				U2901	U2723			
				U2902	U2724			
				U2903	U2725			
				U2904	U2726			
				U2905	U2727			
				U2906	U2728			
				U2907	U2729			
				U2908	U2730			
				U2909	U2731			
				U2910	U2732			
				U2911	U2733			
				U2912	U2734			
				U2913	U2735			
				U2914	U2736			
				U2915	U2737			
				U2916	U			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14049	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	5000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.817	Depositor
Minimum map value	-0.607	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	460.32, 460.32, 460.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.959, 0.959, 0.959	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 3HE

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	0.77	0/1731	1.13	2/2314 (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	0.31	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	3/1581 (0.2%)
10	LJ	0.25	0/1707	0.39	0/2283
11	LK	0.35	0/2387	0.53	0/3201
12	LL	0.38	0/1261	0.63	0/1693
13	LM	0.27	0/965	0.45	0/1295
14	LN	0.35	0/1037	0.55	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	0.24	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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
33	Lg	0.38	0/1051	0.56	0/1407
34	Lh	0.28	0/856	0.43	0/1149
35	Li	0.27	0/939	0.42	0/1251
36	Lj	0.24	0/793	0.45	0/1050
37	Lk	0.37	0/714	0.60	0/949
38	Ll	0.34	0/566	0.49	0/752
39	Lm	0.29	0/460	0.42	0/611
40	Ln	0.17	0/426	0.36	0/561
41	Lp	0.41	0/799	0.54	0/1055
42	Lq	0.40	0/603	0.55	0/802
43	10	0.70	0/3705	1.03	2/5771 (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	4/117423 (0.0%)
All	All	0.40	0/139569	0.54	11/205730 (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
12	LL	0	1
14	LN	0	1
16	LP	0	1
24	LX	0	1
30	Ld	0	1
All	All	0	12

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
9	LI	15	VAL	N-CA-CB	-6.83	102.93	110.51
9	LI	15	VAL	N-CA-C	6.81	117.51	110.36
46	14	883	C	C2'-C3'-O3'	-6.54	103.89	113.70
43	10	134	U	O3'-P-O5'	-5.96	95.06	104.00
46	14	692	A	C3'-C2'-C1'	-5.86	95.64	101.50

There are no chirality outliers.

5 of 12 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

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	1706	0	1801	62	0
2	LB	1880	0	1915	9	0
3	LC	3107	0	3232	17	0
4	LD	3099	0	3229	31	0
5	LE	1356	0	1394	18	0
6	LF	1520	0	1614	22	0
7	LG	1644	0	1773	9	0
8	LH	985	0	1046	4	0
9	LI	1155	0	1197	8	0
10	LJ	1671	0	1731	12	0
11	LK	2342	0	2379	18	0
12	LL	1236	0	1262	5	0
13	LM	950	0	1029	13	0
14	LN	1023	0	1105	8	0
15	LO	997	0	1136	8	0
16	LP	1958	0	2057	21	0
17	LQ	1600	0	1731	25	0
18	LR	1874	0	2030	11	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	7	0
23	LW	1519	0	1630	10	0
24	LX	1505	0	1557	12	0
25	LY	1306	0	1367	8	0
26	LZ	799	0	836	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	La	526	0	554	10	0
28	Lb	1091	0	1171	9	0
29	Lc	1107	0	1182	17	0
30	Ld	407	0	393	3	0
31	Le	745	0	783	10	0
32	Lf	875	0	934	5	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	9	0
37	Lk	701	0	729	8	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	4	0
42	Lq	593	0	618	6	0
43	10	3317	0	1677	94	0
44	12	2538	0	1286	6	0
45	13	3478	0	1761	15	0
46	14	67280	0	33921	300	0
47	14	20	0	23	1	0
All	All	129518	0	94524	814	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 814 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)
25:LY:129:LYS:HB3	46:14:1109:A:H5'	1.51	0.91
1:LA:39:LYS:HE3	1:LA:199:GLN:O	1.70	0.90
1:LA:171:ASN:OD1	1:LA:174:MET:HG3	1.74	0.88
26:LZ:39:LEU:HD23	26:LZ:69:ILE:HD12	1.54	0.87
1:LA:36:ILE:HG21	1:LA:190:LEU:HD21	1.58	0.83

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%)	189 (89%)	23 (11%)	1 (0%)	24	43
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%)	6327 (97%)	165 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	LA	59	PRO

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	191/196 (97%)	160 (84%)	31 (16%)	2	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	LB	190/197 (96%)	186 (98%)	4 (2%)	47	74
3	LC	331/333 (99%)	324 (98%)	7 (2%)	47	74
4	LD	327/331 (99%)	319 (98%)	8 (2%)	43	70
5	LE	144/157 (92%)	141 (98%)	3 (2%)	47	74
6	LF	167/170 (98%)	161 (96%)	6 (4%)	31	58
7	LG	174/175 (99%)	170 (98%)	4 (2%)	44	72
8	LH	103/109 (94%)	100 (97%)	3 (3%)	37	65
9	LI	119/120 (99%)	117 (98%)	2 (2%)	53	78
10	LJ	173/180 (96%)	167 (96%)	6 (4%)	32	58
11	LK	244/246 (99%)	235 (96%)	9 (4%)	30	57
12	LL	133/151 (88%)	130 (98%)	3 (2%)	44	72
13	LM	106/134 (79%)	104 (98%)	2 (2%)	50	76
14	LN	115/132 (87%)	113 (98%)	2 (2%)	53	78
15	LO	108/109 (99%)	106 (98%)	2 (2%)	50	76
16	LP	207/209 (99%)	202 (98%)	5 (2%)	43	70
17	LQ	174/194 (90%)	170 (98%)	4 (2%)	44	72
18	LR	201/205 (98%)	193 (96%)	8 (4%)	28	54
19	LS	166/166 (100%)	165 (99%)	1 (1%)	78	91
20	LT	112/113 (99%)	109 (97%)	3 (3%)	39	67
21	LU	176/177 (99%)	173 (98%)	3 (2%)	53	78
22	LV	154/155 (99%)	151 (98%)	3 (2%)	50	76
23	LW	158/180 (88%)	151 (96%)	7 (4%)	25	50
24	LX	163/164 (99%)	159 (98%)	4 (2%)	42	69
25	LY	140/141 (99%)	138 (99%)	2 (1%)	59	81
26	LZ	89/97 (92%)	87 (98%)	2 (2%)	45	73
27	La	57/133 (43%)	56 (98%)	1 (2%)	51	77
28	Lb	115/117 (98%)	110 (96%)	5 (4%)	26	51
29	Lc	121/123 (98%)	119 (98%)	2 (2%)	53	78
30	Ld	42/43 (98%)	38 (90%)	4 (10%)	8	17
31	Le	85/98 (87%)	83 (98%)	2 (2%)	43	70
32	Lf	95/106 (90%)	93 (98%)	2 (2%)	47	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Lg	114/121 (94%)	113 (99%)	1 (1%)	70	87
34	Lh	92/99 (93%)	92 (100%)	0	100	100
35	Li	100/104 (96%)	99 (99%)	1 (1%)	68	86
36	Lj	84/91 (92%)	82 (98%)	2 (2%)	43	70
37	Lk	72/77 (94%)	71 (99%)	1 (1%)	59	81
38	Ll	64/65 (98%)	62 (97%)	2 (3%)	35	62
39	Lm	47/48 (98%)	46 (98%)	1 (2%)	47	74
40	Ln	46/114 (40%)	46 (100%)	0	100	100
41	Lp	85/91 (93%)	82 (96%)	3 (4%)	32	58
42	Lq	61/62 (98%)	58 (95%)	3 (5%)	22	45
All	All	5645/6033 (94%)	5481 (97%)	164 (3%)	38	65

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	LU	169	LYS
30	Ld	13	ASN
23	LW	31	GLU
25	LY	14	SER
33	Lg	111	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
21	LU	86	ASN
27	La	29	GLN
21	LU	144	ASN
24	LX	64	ASN
30	Ld	13	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
43	10	155/204 (75%)	113 (72%)	15 (9%)
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%)	572 (18%)	21 (0%)
All	All	3573/3876 (92%)	730 (20%)	36 (1%)

5 of 730 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	10	49	U
43	10	50	G
43	10	51	G
43	10	52	U
43	10	53	G

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	14	2455	G
46	14	3168	C
46	14	2544	C
46	14	2556	U
43	10	177	U

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](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
47	3HE	14	3401	-	21,21,21	0.44	0	19,30,30	0.59	0

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
47	3HE	14	3401	-	-	2/8/36/36	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

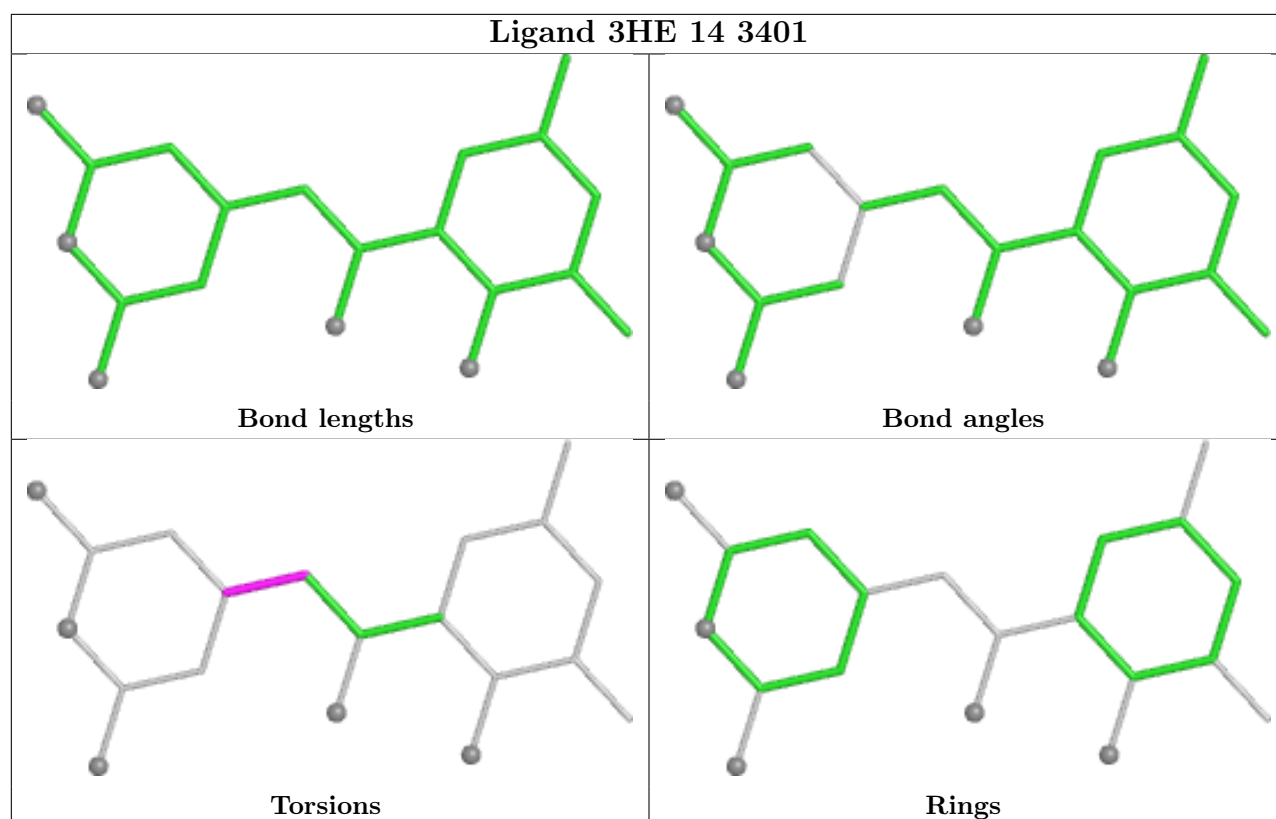
Mol	Chain	Res	Type	Atoms
47	14	3401	3HE	C7-C8-C9-C10
47	14	3401	3HE	C7-C8-C9-C13

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
47	14	3401	3HE	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

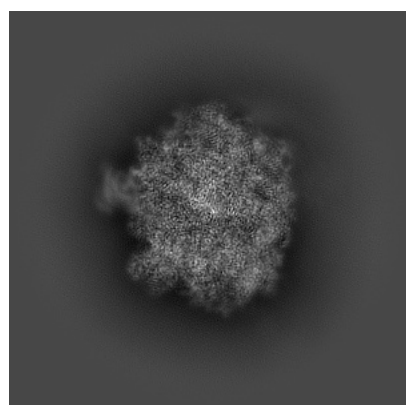
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65330. These allow visual inspection of the internal detail of the map and identification of artifacts.

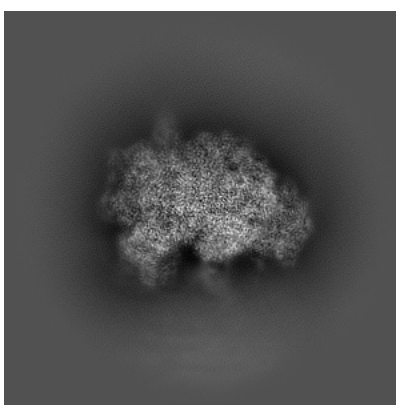
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

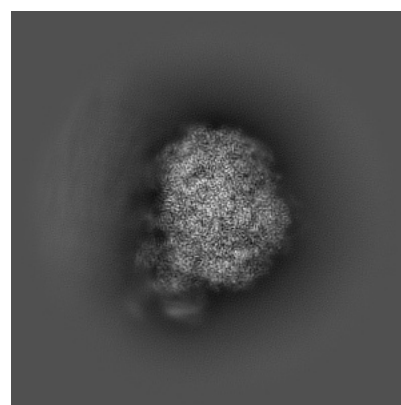
6.1.1 Primary map



X



Y

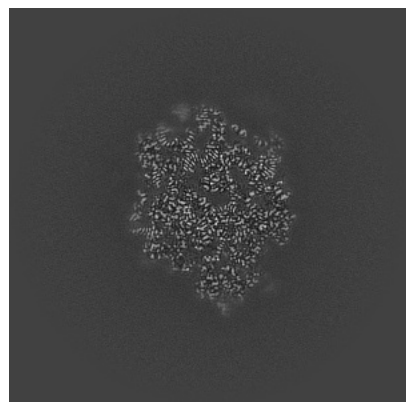


Z

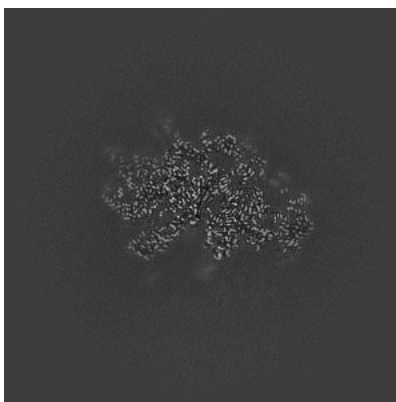
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

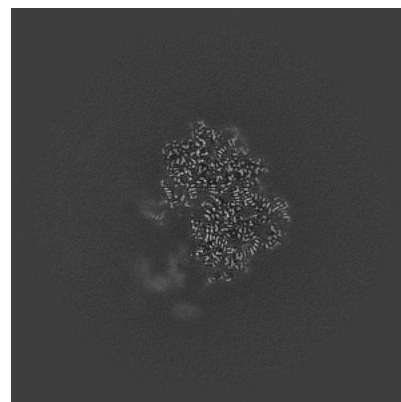
6.2.1 Primary map



X Index: 240



Y Index: 240

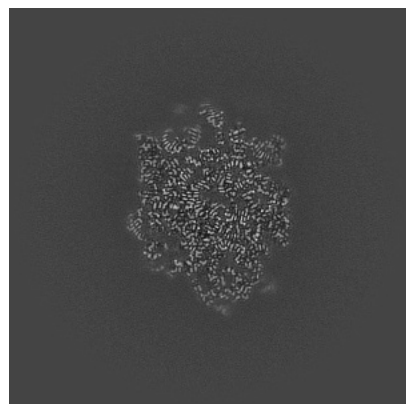


Z Index: 240

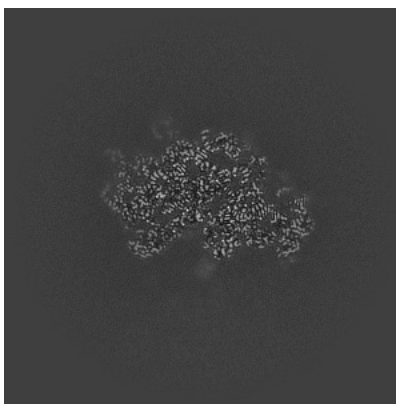
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

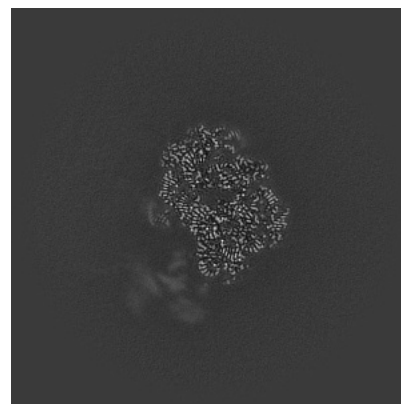
6.3.1 Primary map



X Index: 246



Y Index: 242

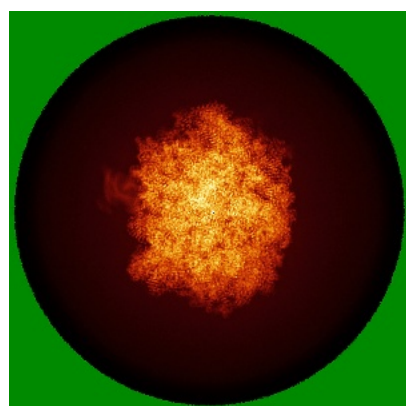


Z Index: 247

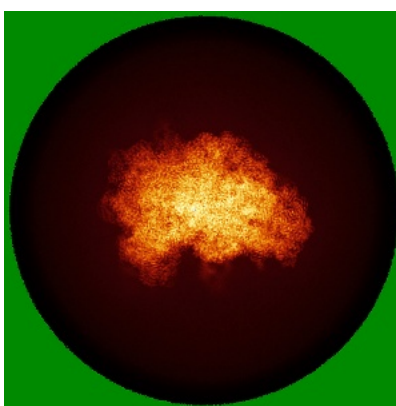
The images above show the largest variance slices of the map in three orthogonal directions.

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

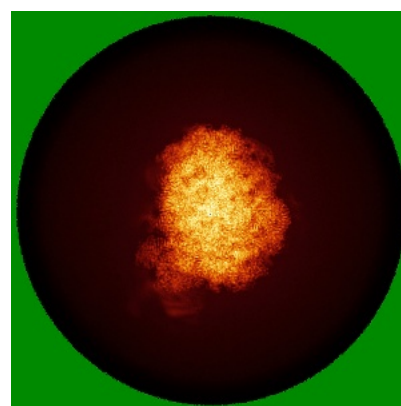
6.4.1 Primary map



X



Y

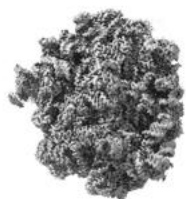


Z

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

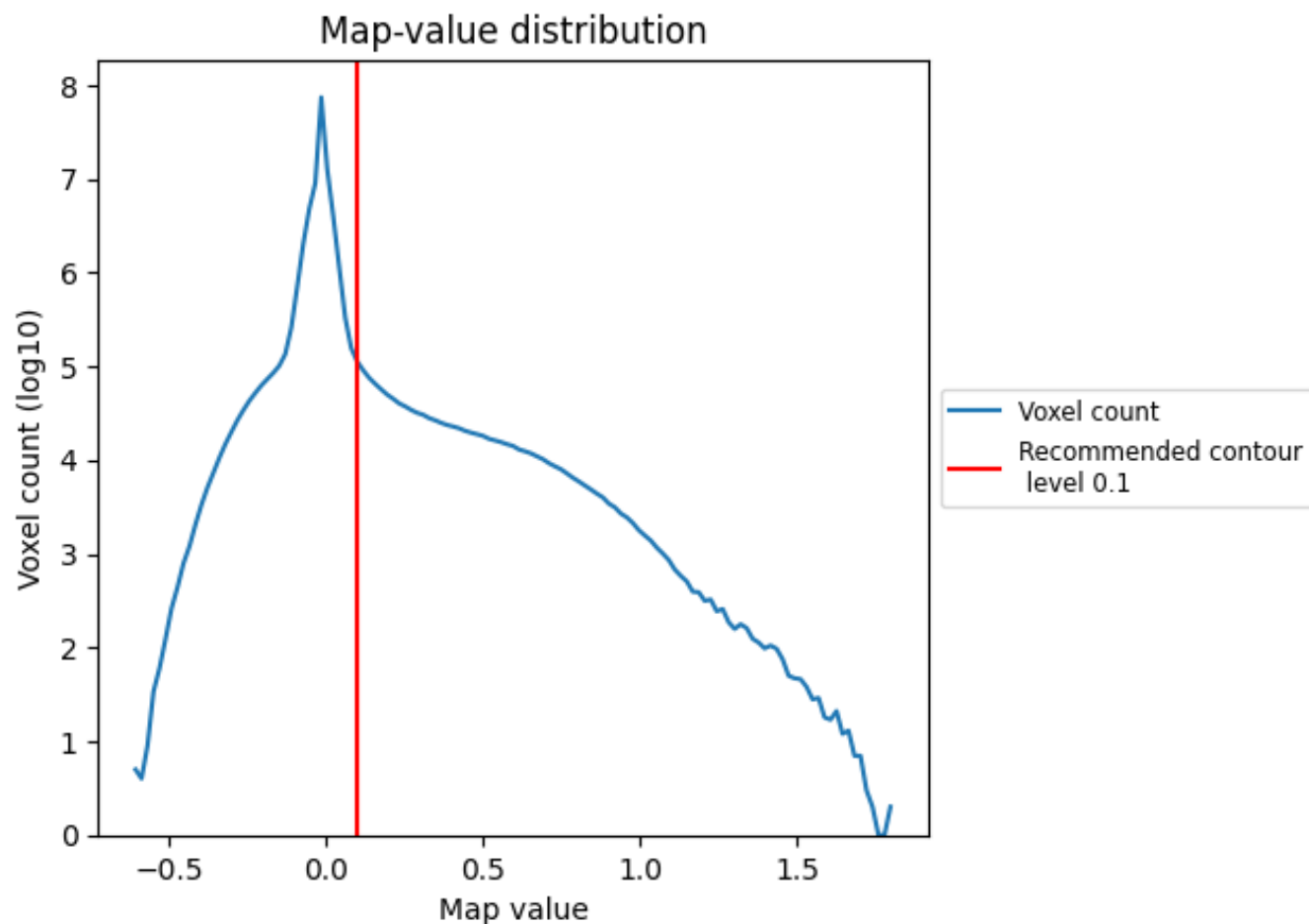
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

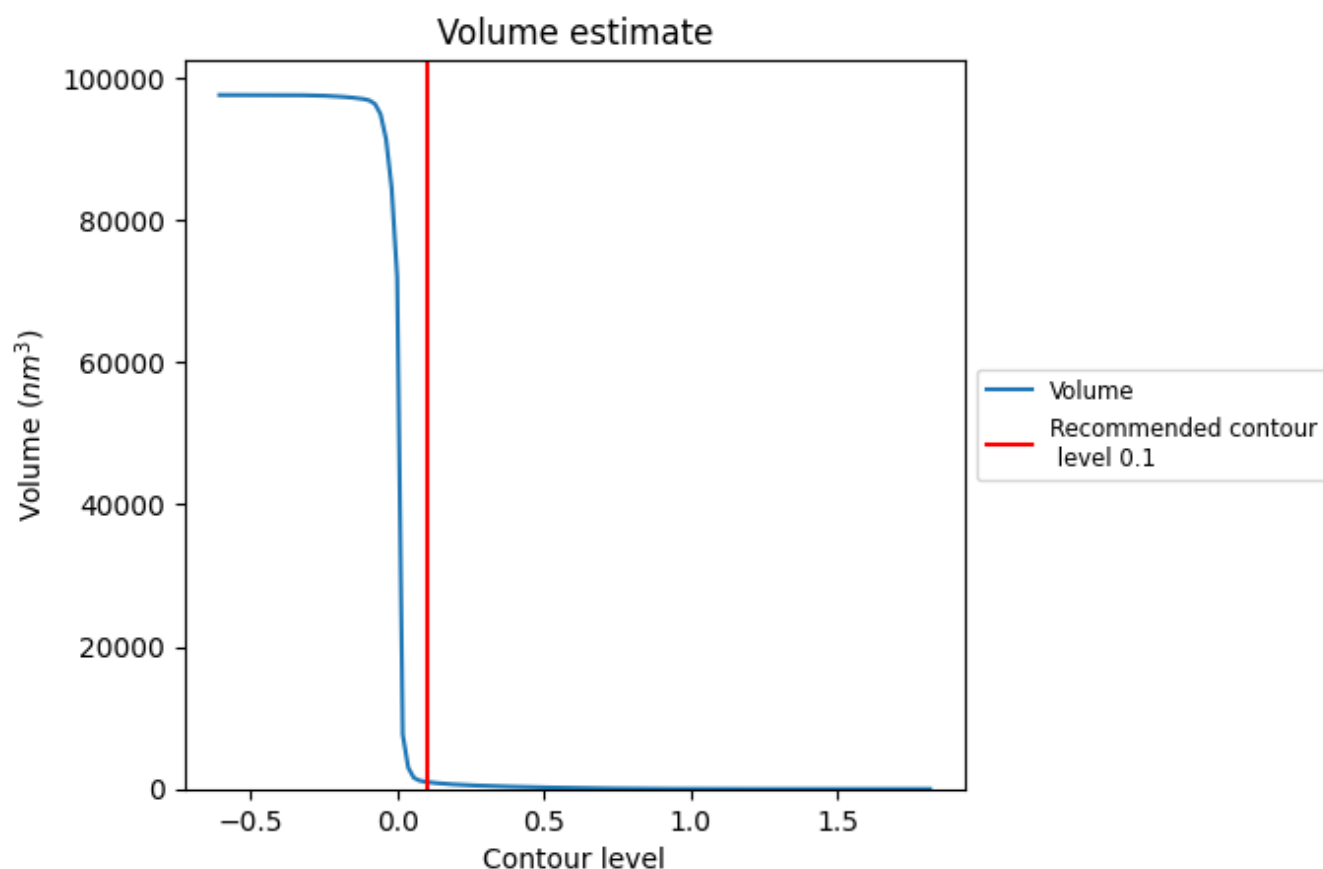
This section contains the results of statistical analysis of the map.

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.

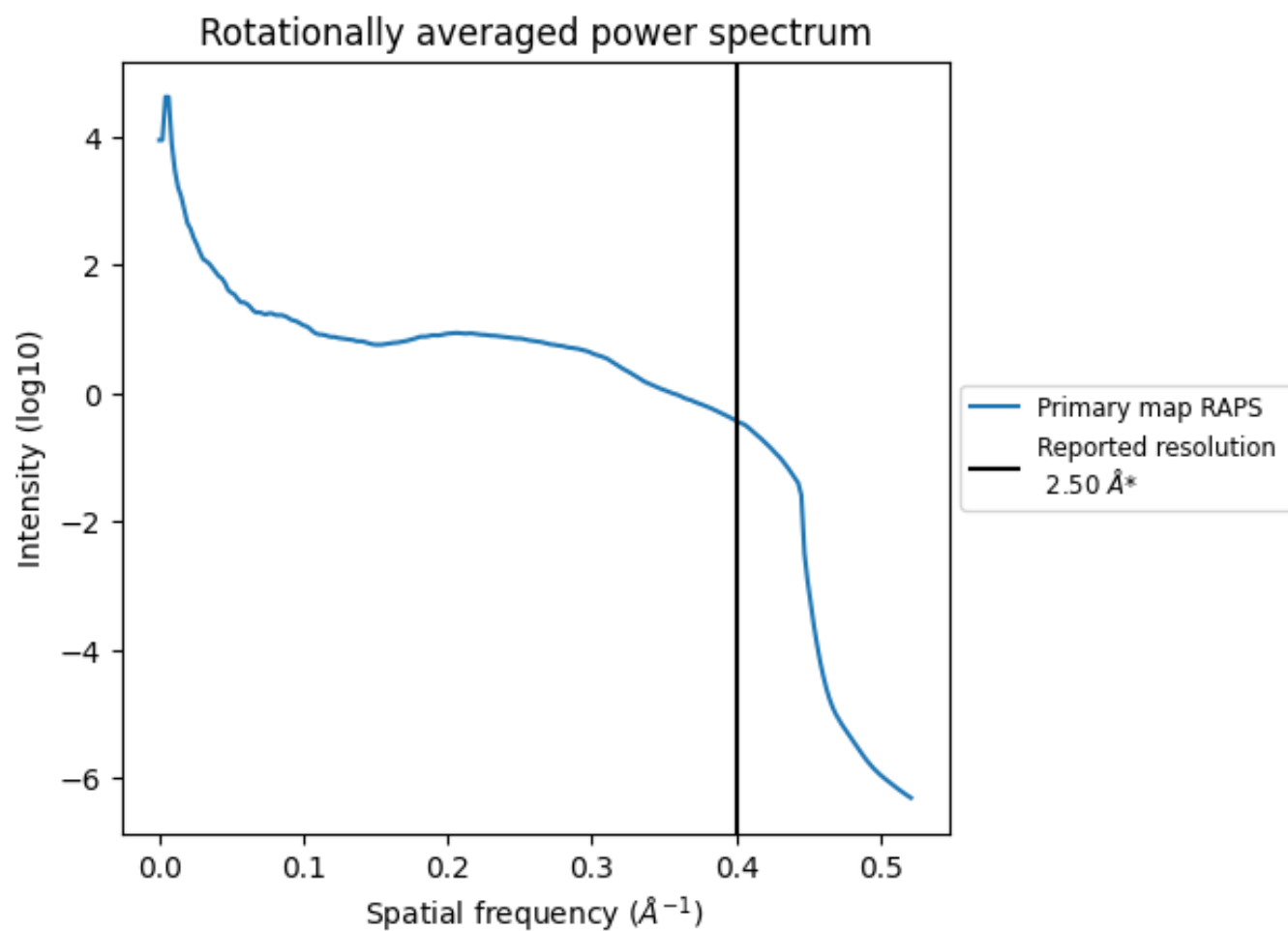
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 986 nm^3 ; this corresponds to an approximate mass of 891 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 0.400 Å⁻¹

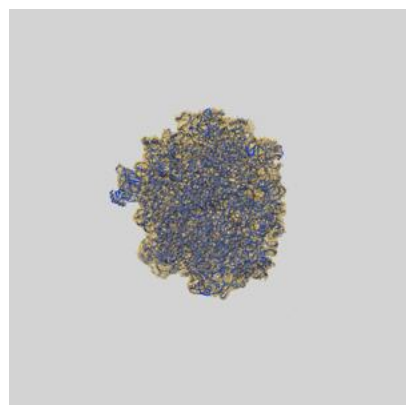
8 Fourier-Shell correlation

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

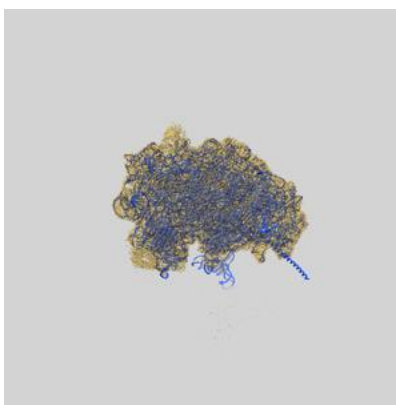
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65330 and PDB model 44BB. Per-residue inclusion information can be found in section [3](#) on page [16](#).

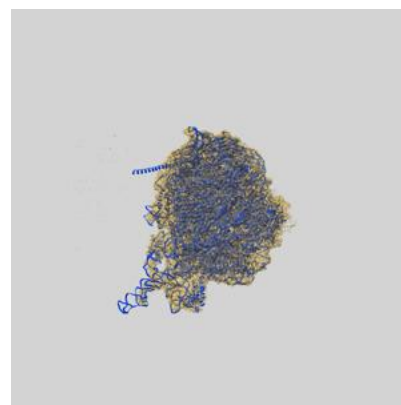
9.1 Map-model overlay [i](#)



X



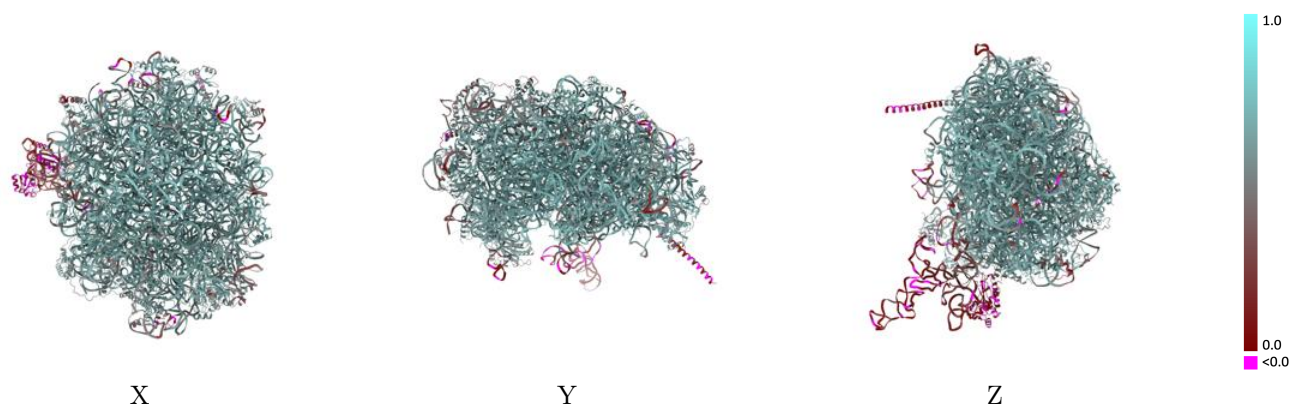
Y



Z

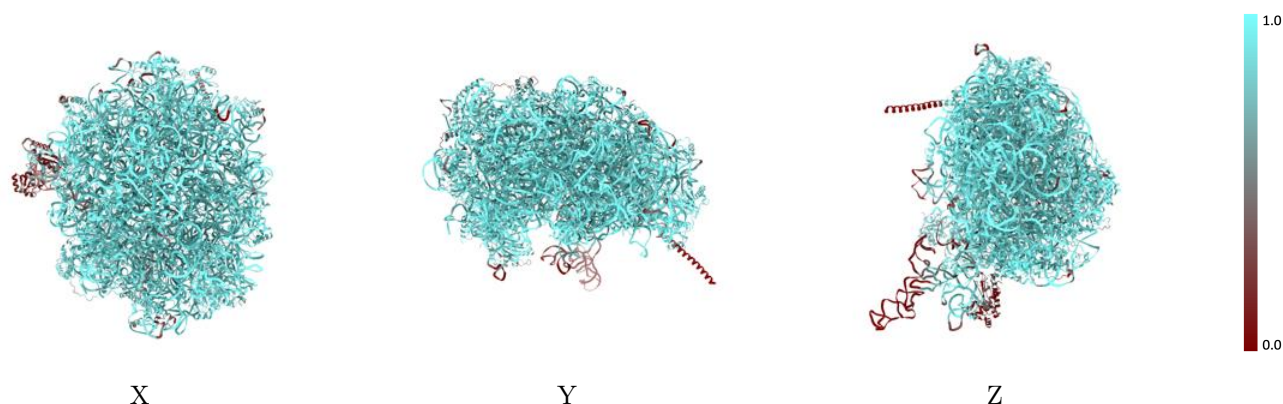
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



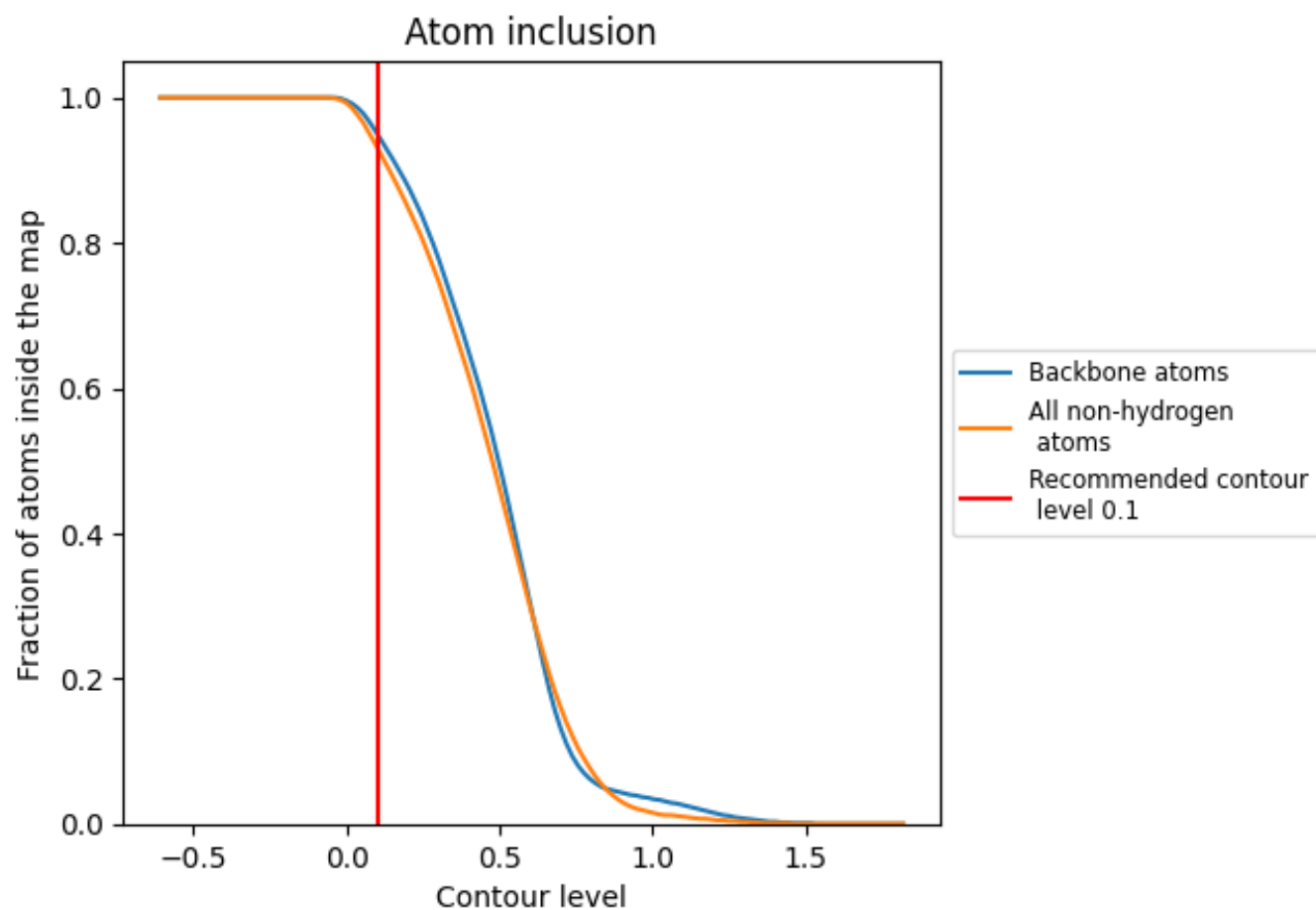
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion ⓘ



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9320	 0.6090
10	 0.3370	 0.1250
12	 0.9990	 0.6510
13	 0.9610	 0.6270
14	 0.9700	 0.6280
LA	 0.2910	 0.0720
LB	 0.9930	 0.6860
LC	 0.9750	 0.6780
LD	 0.9070	 0.5960
LE	 0.8670	 0.5500
LF	 0.9190	 0.5920
LG	 0.9680	 0.6560
LH	 0.9790	 0.6680
LI	 0.9760	 0.6630
LJ	 0.9620	 0.6440
LK	 0.9280	 0.6100
LL	 0.9700	 0.6660
LM	 0.9500	 0.6470
LN	 0.9680	 0.6480
LO	 0.9360	 0.6210
LP	 0.9290	 0.6260
LQ	 0.8060	 0.5270
LR	 0.8900	 0.5820
LS	 0.9600	 0.6430
LT	 0.9440	 0.6190
LU	 0.9960	 0.6870
LV	 0.9860	 0.6670
LW	 0.7810	 0.5430
LX	 0.9700	 0.6510
LY	 0.9630	 0.6510
LZ	 0.8360	 0.5400
La	 0.9350	 0.6500
Lb	 0.9640	 0.6430
Lc	 0.8360	 0.5920
Ld	 0.9320	 0.6260



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Chain	Atom inclusion	Q-score
Le	 0.9320	 0.6210
Lf	 0.9170	 0.6270
Lg	 0.9780	 0.6610
Lh	 0.9830	 0.6710
Li	 0.9340	 0.6350
Lj	 0.9510	 0.6220
Lk	 0.9960	 0.6850
Ll	 0.8850	 0.5840
Lm	 0.9860	 0.6760
Ln	 0.9290	 0.6370
Lp	 0.9730	 0.6680
Lq	 0.9590	 0.6630