



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 02:31 AM UTC

PDB ID : 7K53 / pdb_00007k53
EMDB ID : EMD-22672
Title : Pre-translocation +1-frameshifting(CCC-A) complex (Structure I-FS)
Authors : Demo, G.; Loveland, A.B.; Svidritskiy, E.; Gamper, H.B.; Hou, Y.M.; Korostelev, A.A.
Deposited on : 2020-09-16
Resolution : 3.20 Å(reported)
Based on initial models : 5UYM, 6ENJ

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:

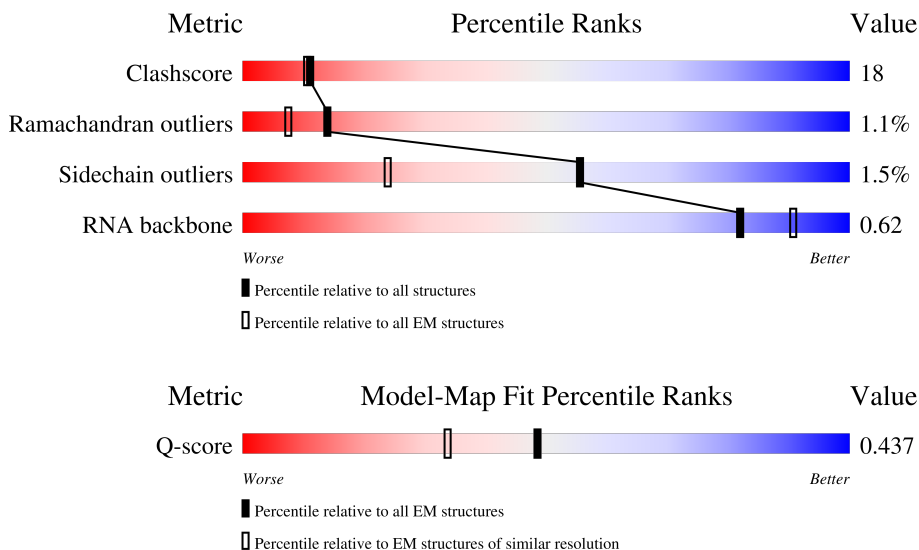
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the 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) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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






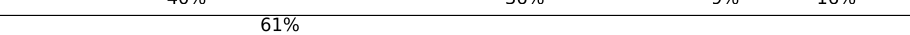
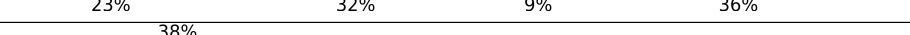
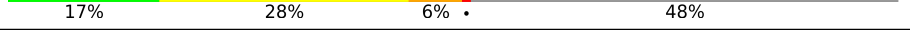






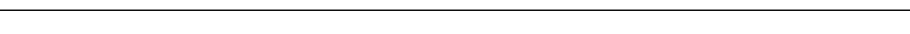
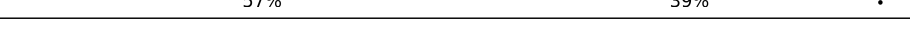
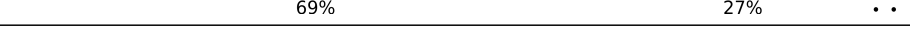










Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	b	271	55% 42% .
2	c	209	55% 43% .
3	d	201	63% 36% .




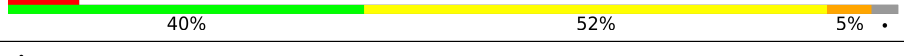
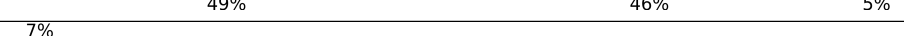
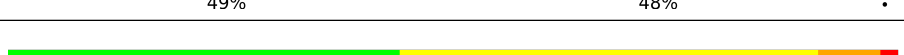
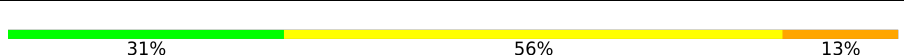
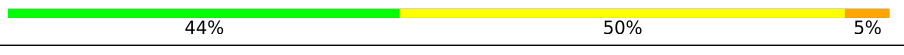
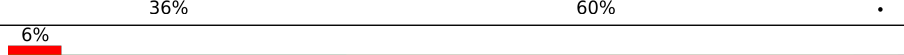
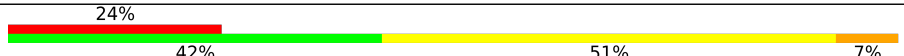
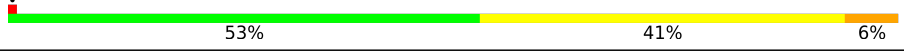
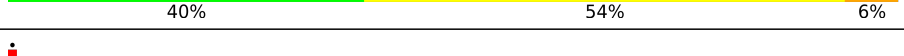
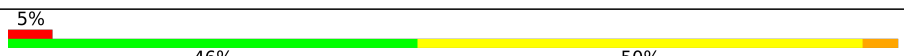

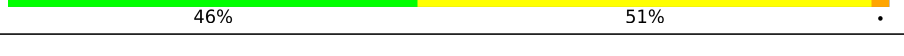
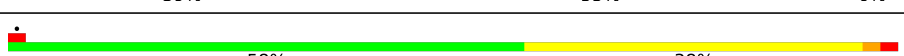







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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	A	66	
27	B	56	
28	C	50	







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Mol	Chain	Length	Quality of chain
29	D	46	
30	E	64	
31	F	38	
32	G	225	
33	H	206	
34	I	205	
35	J	157	
36	K	100	
37	L	151	
38	M	129	
39	N	127	
40	O	98	
41	P	116	
42	Q	123	
43	R	114	
44	S	100	
45	T	88	
46	U	82	
47	V	80	
48	W	65	
49	X	79	
50	Y	85	
51	Z	65	
52	a	223	
53	3	1539	

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Mol	Chain	Length	Quality of chain
54	1	2903	
55	2	120	
56	5	77	
56	6	77	
57	4	18	
58	7	77	

2 Entry composition [i](#)

There are 59 unique types of molecules in this entry. The entry contains 149698 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 50S ribosomal protein L2.

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

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	c	209	1565	979	288	294	4	0	0

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

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

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	g	125	936	590	166	179	1	0	0

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	h	84	633	397	114	118	4	0	0

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	i	74	551	358	91	99	3	0	0

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	k	122	939	587	180	166	6	0	0

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	l	143	1045	649	206	189	1	0	0

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	m	136	1074	686	205	177	6	0	0

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	n	120	961	593	196	167	5	0	0

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

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

- Molecule 20 is a protein called 50S ribosomal protein L24.

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

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

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

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	C	50	410	263	75	72	0	0

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

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

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

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

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

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

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	G	218	1705	1081	305	312	7	0	0

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	H	206	1625	1028	305	289	3	0	0

- Molecule 34 is a protein called 30S ribosomal protein S4.

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

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

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

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

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

- Molecule 45 is a protein called 30S ribosomal protein S15.

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

- Molecule 46 is a protein called 30S ribosomal protein S16.

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

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
55	2	120	2568	1145	471	833	119	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 56 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
56	5	77	1640	732	297	535	76	0	0
56	6	77	1640	732	297	535	76	0	0

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
57	4	18	388	175	78	118	17	0	0

- Molecule 58 is a RNA chain called tRNAPro.

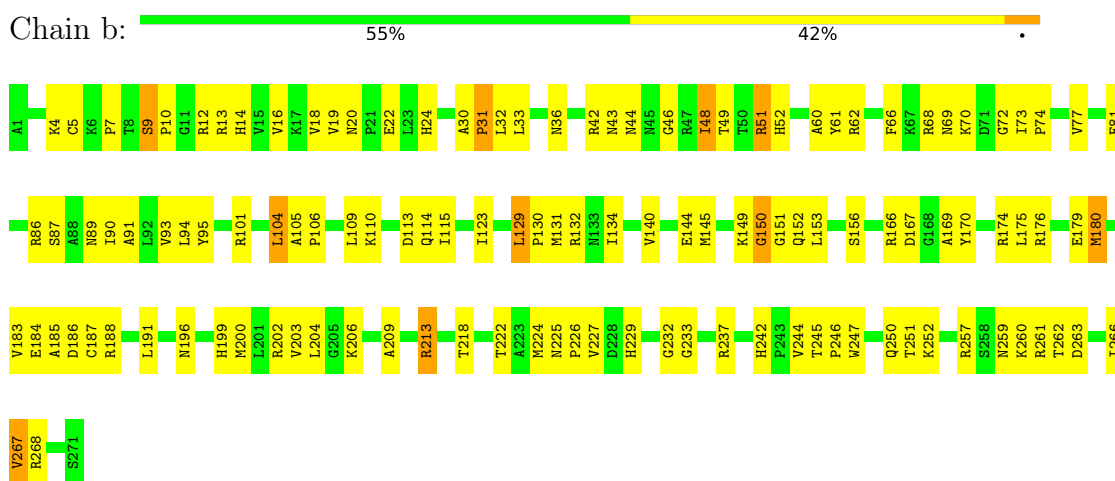
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
58	7	77	1647	733	295	542	77	0	0

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S) (labeled as "Ligand of Interest" by depositor).

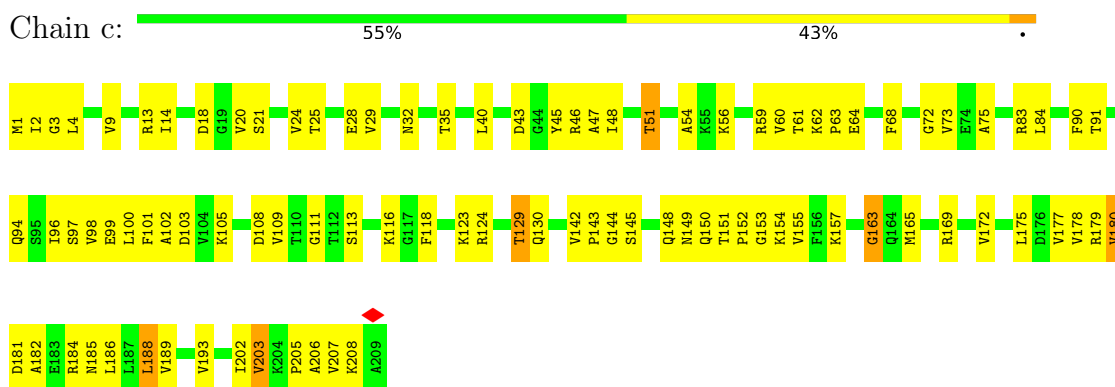
3 Residue-property plots

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.

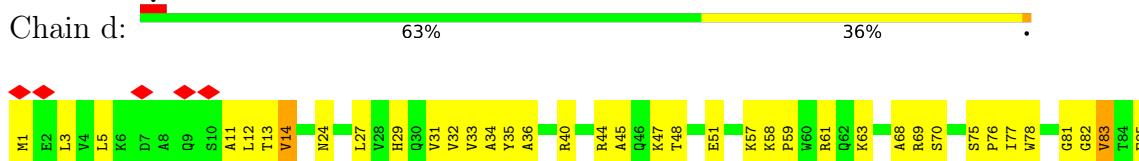
- Molecule 1: 50S ribosomal protein L2

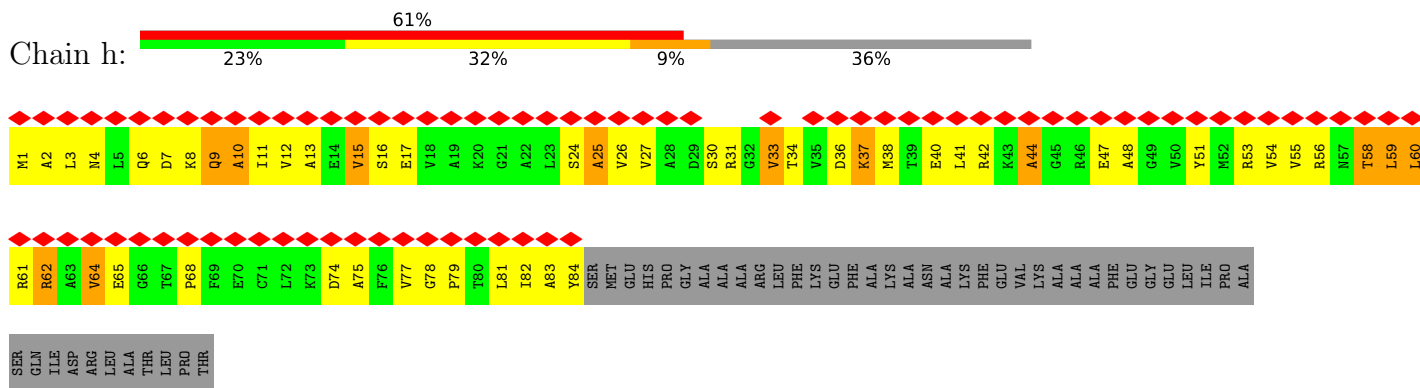


- Molecule 2: 50S ribosomal protein L3

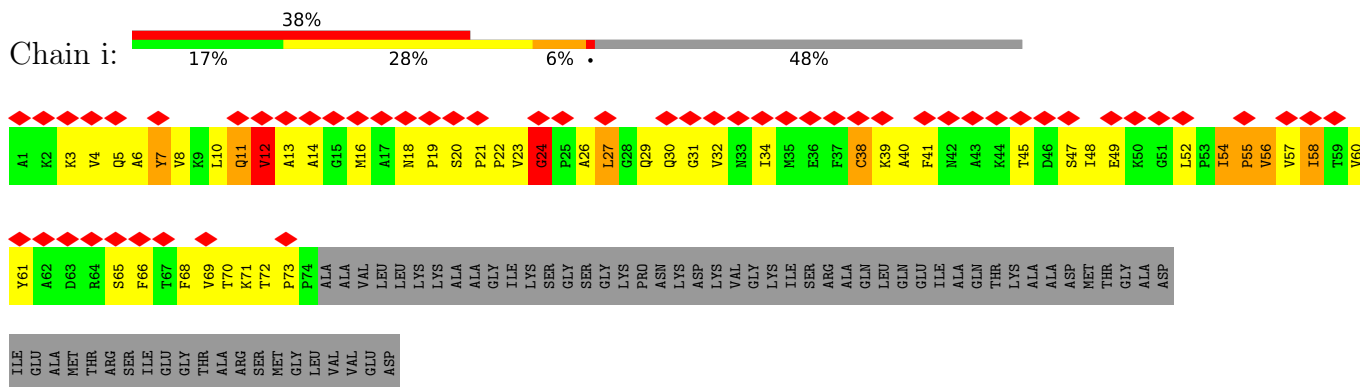


- Molecule 3: 50S ribosomal protein L4

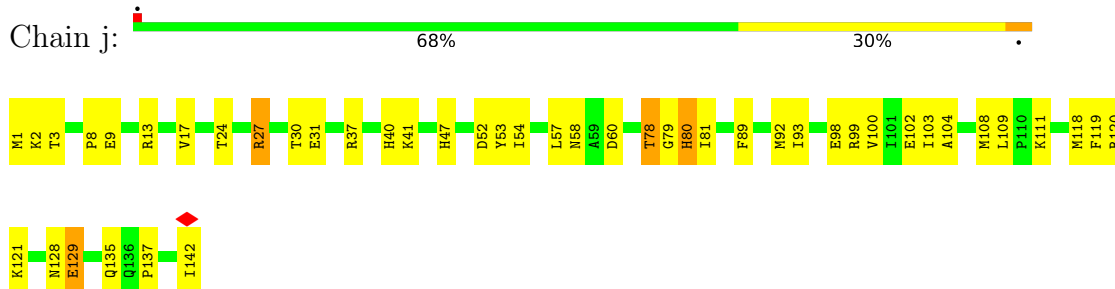




• Molecule 8: 50S ribosomal protein L11



• Molecule 9: 50S ribosomal protein L13

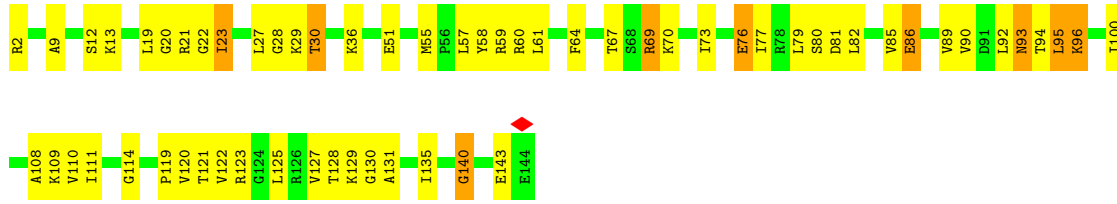


• Molecule 10: 50S ribosomal protein L14

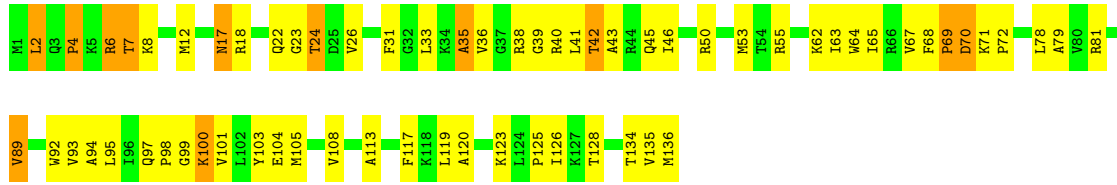


• Molecule 11: 50S ribosomal protein L15

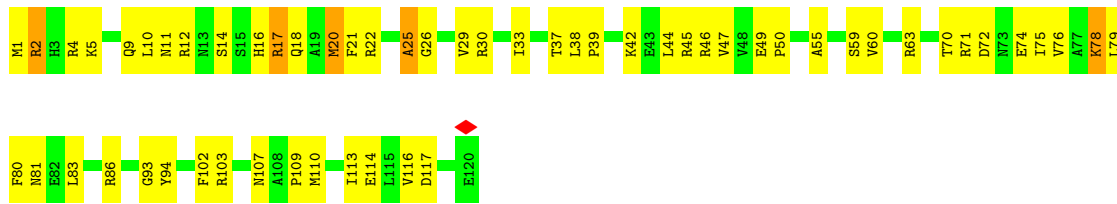




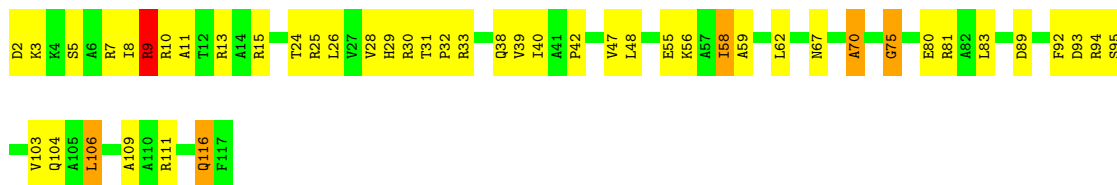
• Molecule 12: 50S ribosomal protein L16



• Molecule 13: 50S ribosomal protein L17



• Molecule 14: 50S ribosomal protein L18

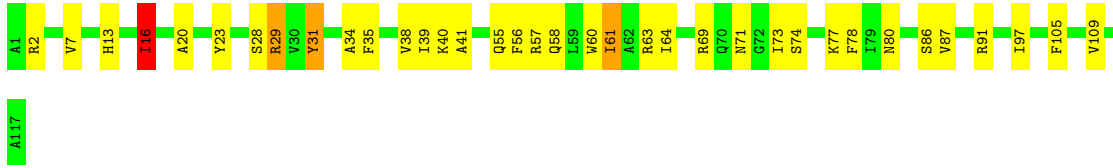


• Molecule 15: 50S ribosomal protein L19



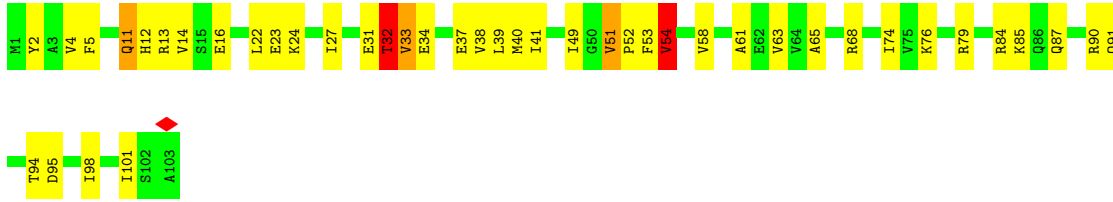
• Molecule 16: 50S ribosomal protein L20

Chain q:  69% 27%



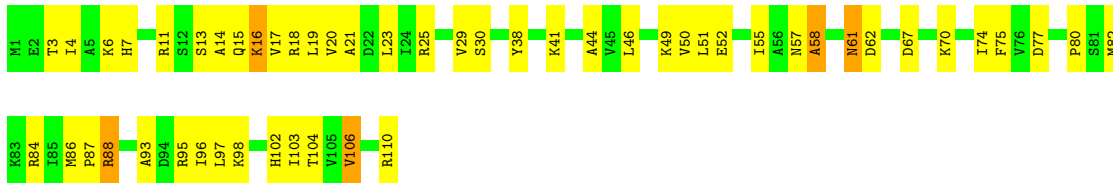
- Molecule 17: 50S ribosomal protein L21

Chain r:  58% 37%



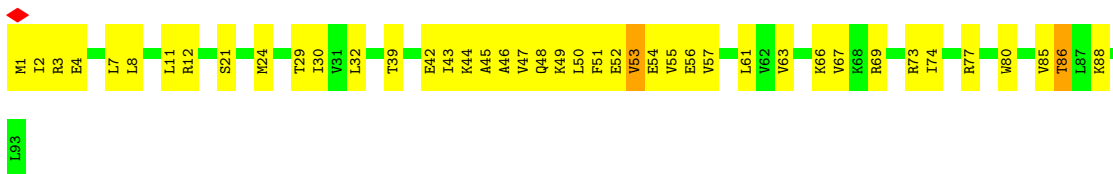
- Molecule 18: 50S ribosomal protein L22

Chain s:  53% 43% 5%



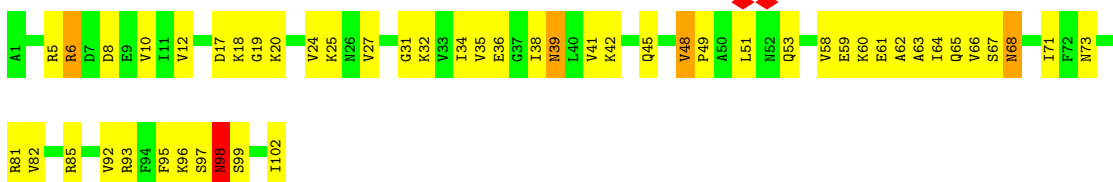
- Molecule 19: 50S ribosomal protein L23

Chain t:  55% 43%

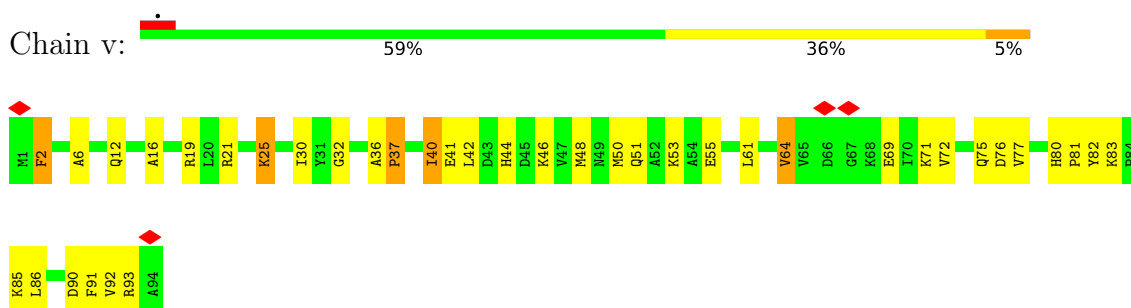


- Molecule 20: 50S ribosomal protein L24

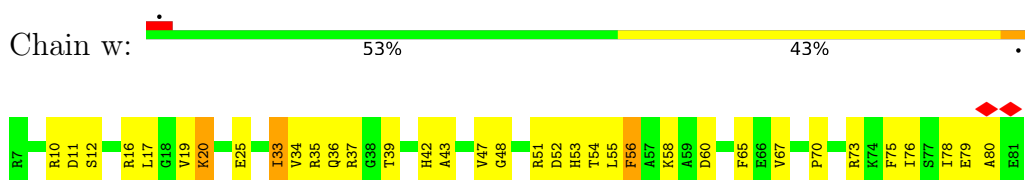
Chain u:  50% 45%



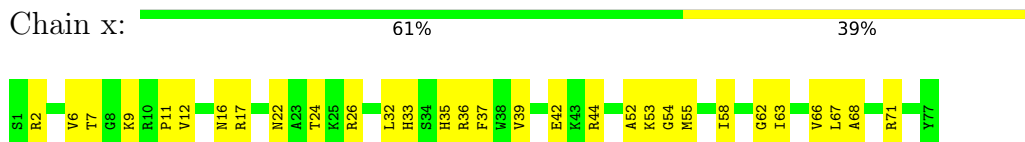
- Molecule 21: 50S ribosomal protein L25



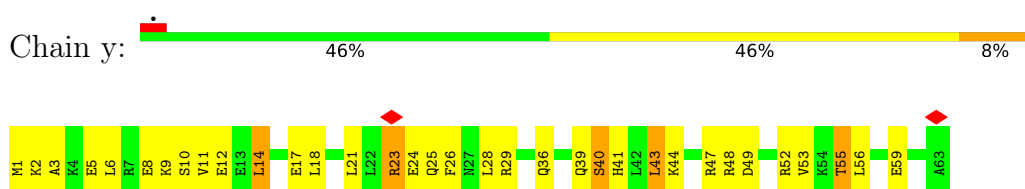
- Molecule 22: 50S ribosomal protein L27



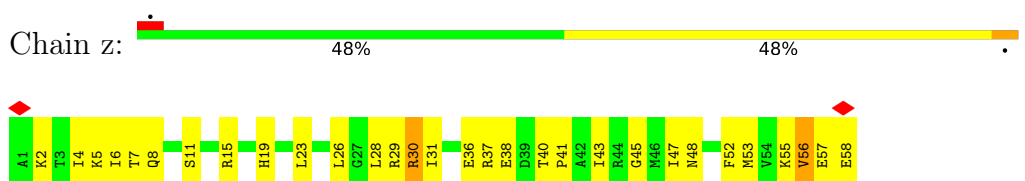
- Molecule 23: 50S ribosomal protein L28



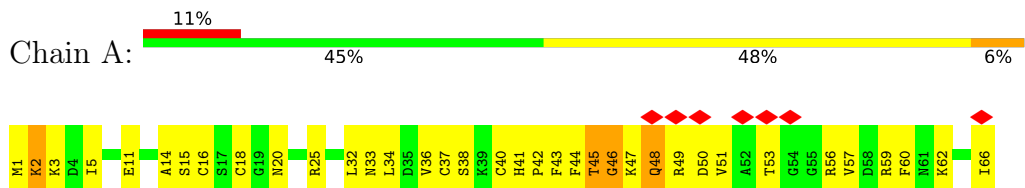
- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30



- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32



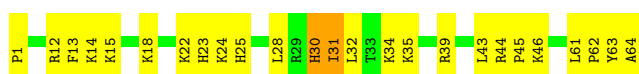
• Molecule 28: 50S ribosomal protein L33



• Molecule 29: 50S ribosomal protein L34



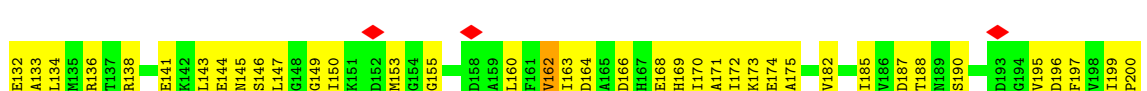
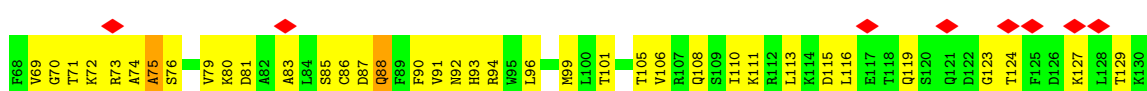
• Molecule 30: 50S ribosomal protein L35

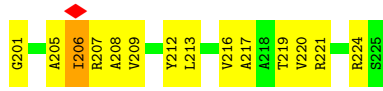


• Molecule 31: 50S ribosomal protein L36

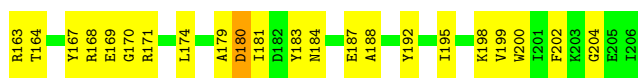
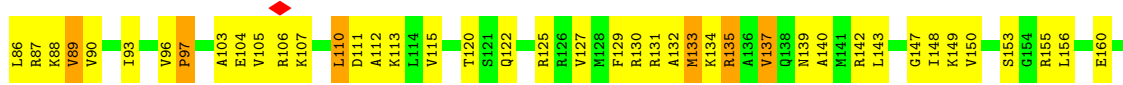
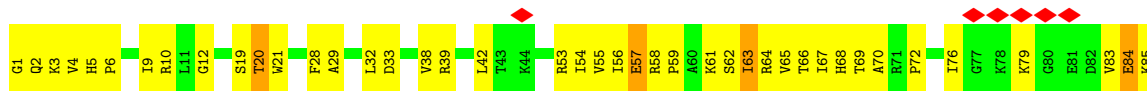


• Molecule 32: 30S ribosomal protein S2

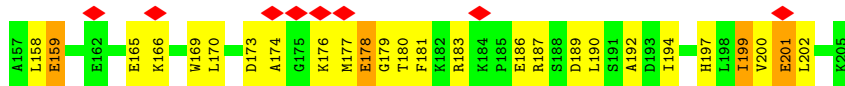
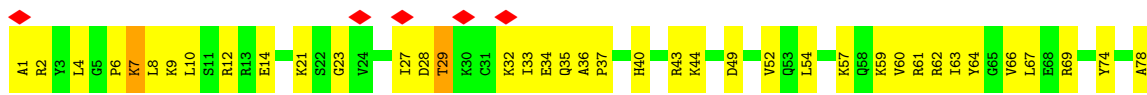




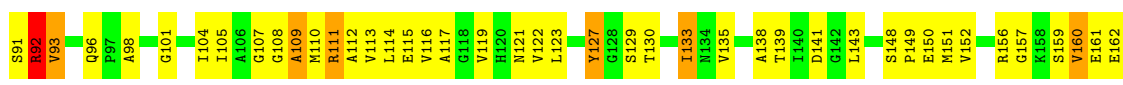
• Molecule 33: 30S ribosomal protein S3



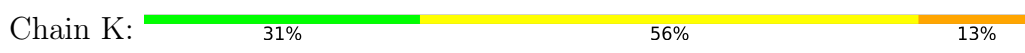
• Molecule 34: 30S ribosomal protein S4

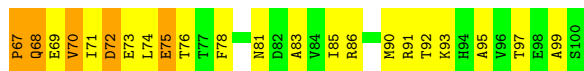


• Molecule 35: 30S ribosomal protein S5



• Molecule 36: 30S ribosomal protein S6

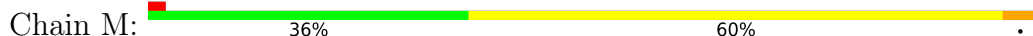




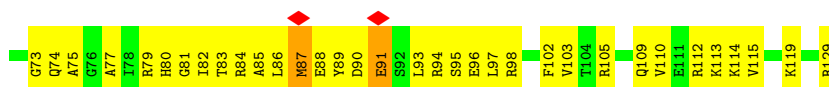
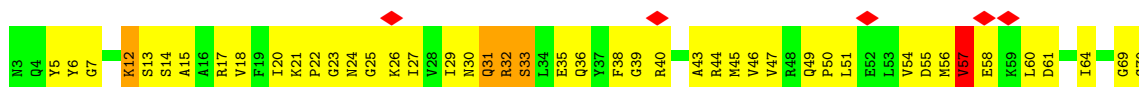
• Molecule 37: 30S ribosomal protein S7



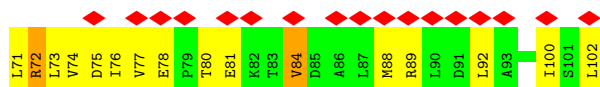
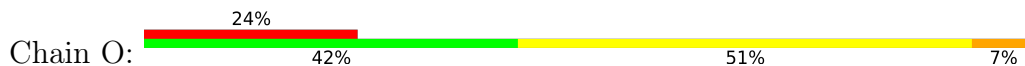
• Molecule 38: 30S ribosomal protein S8



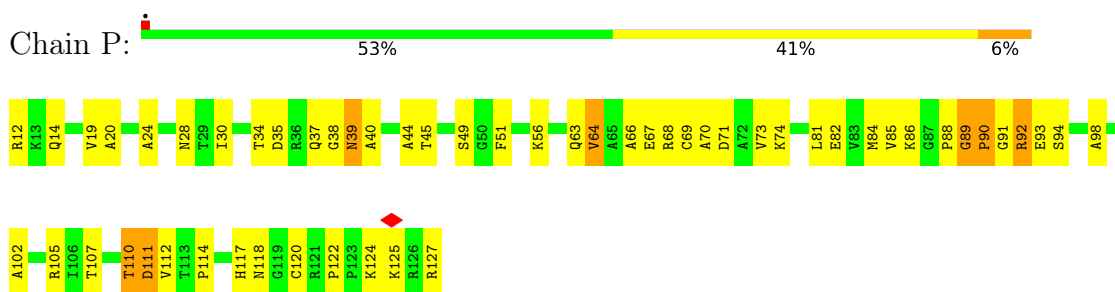
• Molecule 39: 30S ribosomal protein S9



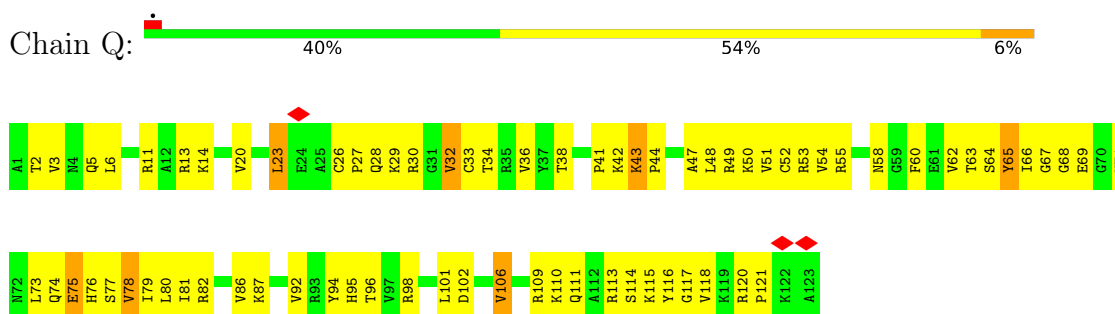
• Molecule 40: 30S ribosomal protein S10



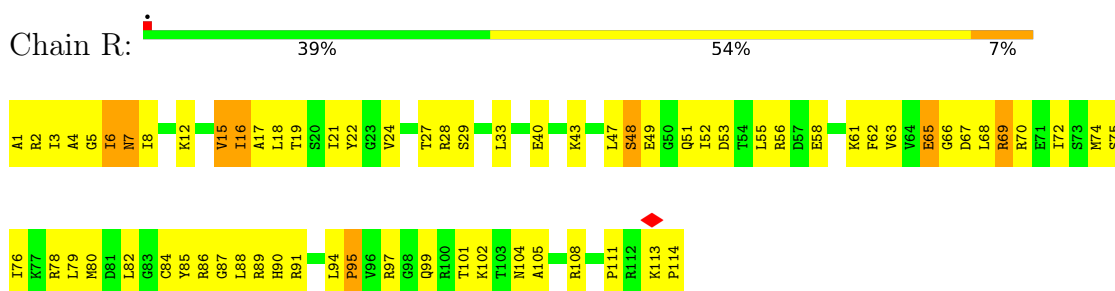
- Molecule 41: 30S ribosomal protein S11



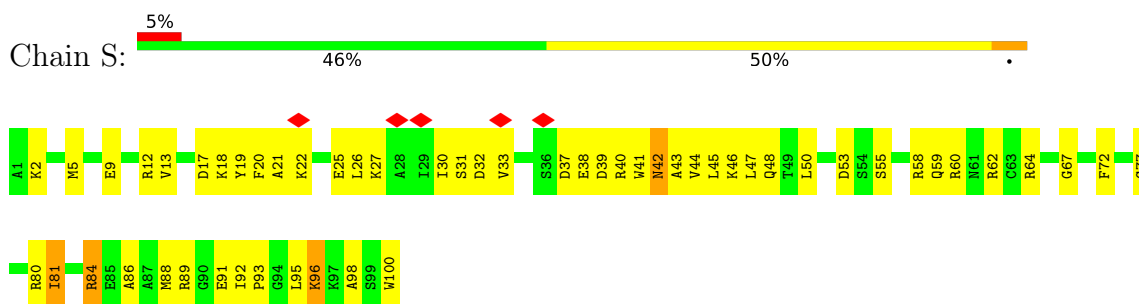
- Molecule 42: 30S ribosomal protein S12



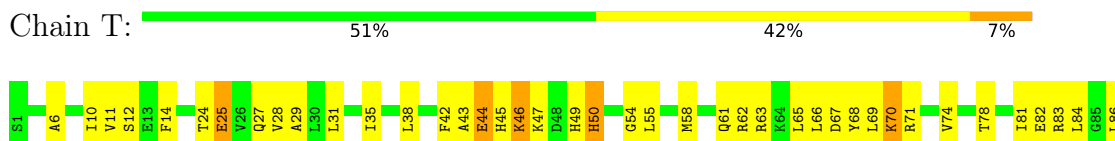
- Molecule 43: 30S ribosomal protein S13



- Molecule 44: 30S ribosomal protein S14



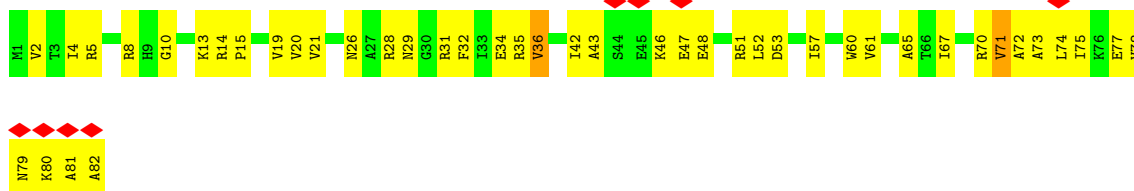
- Molecule 45: 30S ribosomal protein S15



R87
R88

• Molecule 46: 30S ribosomal protein S16

Chain U: 



• Molecule 47: 30S ribosomal protein S17

Chain V: 



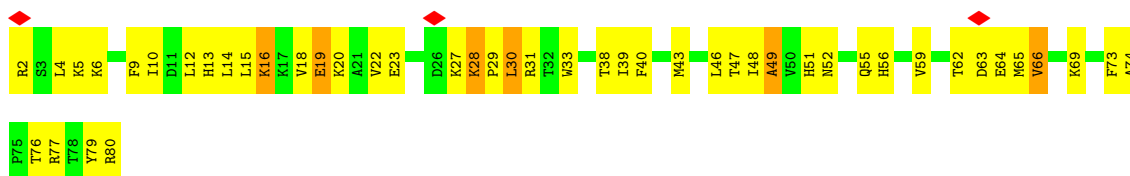
• Molecule 48: 30S ribosomal protein S18

Chain W: 



• Molecule 49: 30S ribosomal protein S19

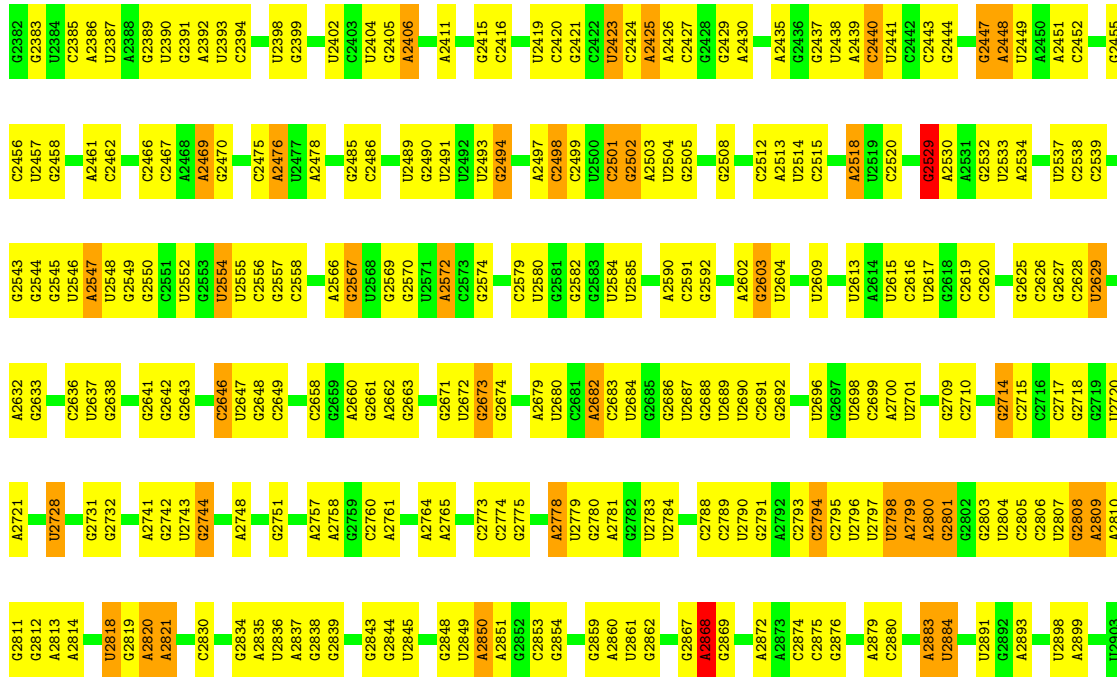
Chain X: 



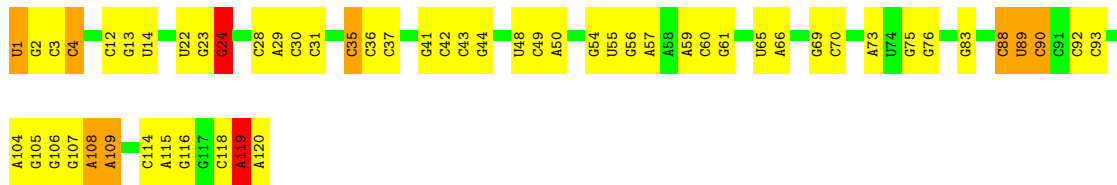
• Molecule 50: 30S ribosomal protein S20

Chain Y: 

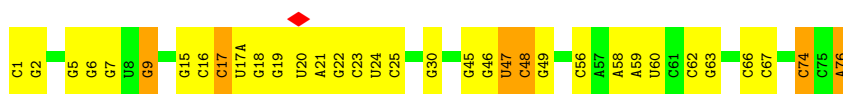




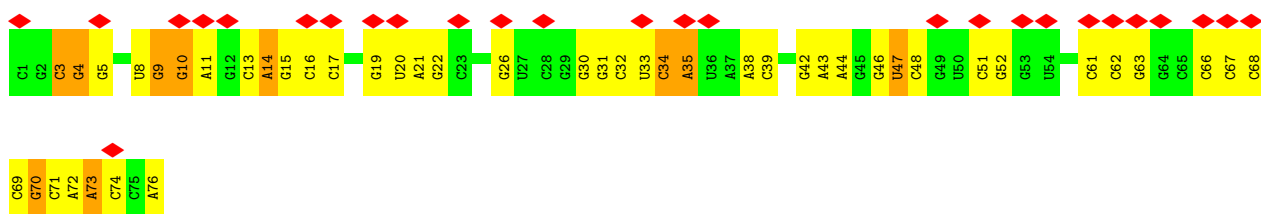
• Molecule 55: 5S ribosomal RNA



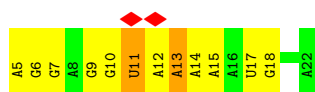
• Molecule 56: tRNAfMet



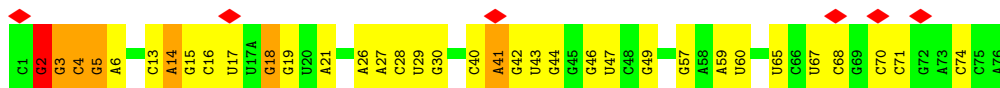
• Molecule 56: tRNAfMet



• Molecule 57: mRNA



● Molecule 58: tRNAPro



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	12108	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47.5	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	24.420	Depositor
Minimum map value	-6.345	Depositor
Average map value	0.018	Depositor
Map value standard deviation	1.346	Depositor
Recommended contour level	3.7	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality i

5.1 Standard geometry i

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

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	b	0.76	5/2122 (0.2%)	1.04	6/2852 (0.2%)
2	c	0.79	4/1586 (0.3%)	1.07	9/2134 (0.4%)
3	d	0.81	3/1571 (0.2%)	1.00	8/2113 (0.4%)
4	e	0.92	10/1435 (0.7%)	1.11	12/1926 (0.6%)
5	f	0.99	11/1343 (0.8%)	1.22	13/1816 (0.7%)
6	g	1.20	10/946 (1.1%)	1.26	12/1275 (0.9%)
7	h	1.78	17/638 (2.7%)	1.71	21/860 (2.4%)
8	i	1.50	11/564 (2.0%)	1.47	13/768 (1.7%)
9	j	0.72	2/1152 (0.2%)	1.06	4/1551 (0.3%)
10	k	0.85	3/948 (0.3%)	1.21	11/1268 (0.9%)
11	l	0.71	2/1054 (0.2%)	1.06	5/1403 (0.4%)
12	m	0.87	7/1093 (0.6%)	1.11	7/1460 (0.5%)
13	n	0.70	2/974 (0.2%)	1.00	5/1301 (0.4%)
14	o	1.07	9/902 (1.0%)	1.10	4/1209 (0.3%)
15	p	0.79	5/929 (0.5%)	1.12	9/1242 (0.7%)
16	q	0.80	2/960 (0.2%)	1.08	3/1278 (0.2%)
17	r	0.79	2/829 (0.2%)	1.09	5/1107 (0.5%)
18	s	1.07	9/864 (1.0%)	1.19	5/1156 (0.4%)
19	t	0.77	3/745 (0.4%)	1.05	3/994 (0.3%)
20	u	0.72	1/788 (0.1%)	1.03	3/1051 (0.3%)
21	v	0.67	2/766 (0.3%)	0.93	2/1025 (0.2%)
22	w	0.74	2/582 (0.3%)	1.09	2/769 (0.3%)
23	x	0.63	1/635 (0.2%)	0.98	2/848 (0.2%)
24	y	1.14	7/510 (1.4%)	1.28	5/677 (0.7%)
25	z	0.76	2/453 (0.4%)	0.95	2/605 (0.3%)
26	A	1.04	5/532 (0.9%)	1.08	8/709 (1.1%)
27	B	0.63	1/450 (0.2%)	0.98	4/599 (0.7%)
28	C	0.74	1/417 (0.2%)	0.92	3/554 (0.5%)
29	D	0.62	0/380	0.92	0/498
30	E	0.59	1/513 (0.2%)	0.84	0/676
31	F	0.73	0/303	1.05	2/397 (0.5%)
32	G	0.91	8/1736 (0.5%)	1.13	15/2338 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	H	0.94	10/1652 (0.6%)	1.04	10/2225 (0.4%)
34	I	0.89	10/1665 (0.6%)	1.08	6/2227 (0.3%)
35	J	0.99	10/1170 (0.9%)	1.24	16/1573 (1.0%)
36	K	1.54	19/836 (2.3%)	1.37	14/1128 (1.2%)
37	L	0.92	5/1196 (0.4%)	1.12	10/1602 (0.6%)
38	M	0.93	9/989 (0.9%)	1.10	13/1326 (1.0%)
39	N	0.92	7/1034 (0.7%)	1.15	7/1375 (0.5%)
40	O	0.84	4/797 (0.5%)	1.08	6/1077 (0.6%)
41	P	0.79	3/886 (0.3%)	1.04	4/1195 (0.3%)
42	Q	0.90	3/969 (0.3%)	1.23	9/1300 (0.7%)
43	R	0.97	6/893 (0.7%)	1.13	7/1193 (0.6%)
44	S	0.79	3/817 (0.4%)	1.00	1/1088 (0.1%)
45	T	0.83	4/722 (0.6%)	1.02	1/964 (0.1%)
46	U	0.74	1/659 (0.2%)	0.97	3/884 (0.3%)
47	V	0.84	5/658 (0.8%)	1.04	2/881 (0.2%)
48	W	0.74	1/545 (0.2%)	0.93	3/731 (0.4%)
49	X	1.05	4/653 (0.6%)	1.20	7/877 (0.8%)
50	Y	1.08	5/671 (0.7%)	1.17	5/888 (0.6%)
51	Z	0.95	3/551 (0.5%)	1.23	7/728 (1.0%)
52	a	1.39	15/1034 (1.5%)	1.43	27/1387 (1.9%)
53	3	0.51	0/36963	0.56	10/57662 (0.0%)
54	1	0.48	0/69796	0.57	20/108888 (0.0%)
55	2	0.48	0/2872	0.54	1/4479 (0.0%)
56	5	0.47	0/1832	0.54	0/2855
56	6	0.51	0/1832	0.60	0/2855
57	4	0.52	0/436	0.62	0/679
58	7	0.50	0/1840	0.65	2/2868 (0.1%)
All	All	0.65	275/162688 (0.2%)	0.75	394/243394 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
35	J	0	2
53	3	0	14
54	1	0	45
55	2	0	3
All	All	0	64

The worst 5 of 275 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	K	13	ASP	C-O	16.89	1.45	1.24
7	h	44	ALA	C-O	16.07	1.44	1.24
7	h	12	VAL	C-O	15.94	1.42	1.24
52	a	26	ALA	C-O	15.13	1.41	1.24
6	g	114	GLU	C-O	14.11	1.42	1.24

The worst 5 of 394 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	L	29	LEU	N-CA-C	-13.79	98.90	114.62
9	j	81	ILE	N-CA-C	12.99	125.43	110.62
36	K	13	ASP	CA-C-O	10.33	131.78	120.10
5	f	163	TYR	CA-C-N	-10.00	107.44	120.44
5	f	163	TYR	C-N-CA	-10.00	107.44	120.44

There are no chirality outliers.

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
53	3	159	G	Sidechain
53	3	324	G	Sidechain
53	3	405	U	Sidechain
35	J	86	GLY	Mainchain
35	J	92	ARG	Mainchain

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	b	2083	0	2157	109	0
2	c	1565	0	1616	87	0
3	d	1552	0	1619	60	0
4	e	1411	0	1447	102	0
5	f	1323	0	1374	87	0
6	g	936	0	961	58	0
7	h	633	0	666	57	0
8	i	551	0	577	45	0
9	j	1129	0	1162	44	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	k	939	0	1012	62	0
11	l	1045	0	1117	56	0
12	m	1074	0	1157	62	0
13	n	961	0	1000	59	0
14	o	892	0	923	38	0
15	p	917	0	965	42	0
16	q	947	0	1022	30	0
17	r	816	0	839	40	0
18	s	857	0	922	44	0
19	t	739	0	807	42	0
20	u	780	0	834	40	0
21	v	753	0	780	31	0
22	w	575	0	592	28	0
23	x	625	0	655	25	0
24	y	509	0	543	30	0
25	z	449	0	491	31	0
26	A	523	0	524	30	0
27	B	444	0	461	15	0
28	C	410	0	440	14	0
29	D	377	0	418	21	0
30	E	504	0	574	21	0
31	F	302	0	343	20	0
32	G	1705	0	1732	110	0
33	H	1625	0	1699	104	0
34	I	1643	0	1710	99	0
35	J	1157	0	1199	90	0
36	K	818	0	808	67	0
37	L	1182	0	1240	80	0
38	M	979	0	1034	77	0
39	N	1022	0	1070	70	0
40	O	787	0	828	64	0
41	P	870	0	878	53	0
42	Q	955	0	1019	81	0
43	R	884	0	944	78	0
44	S	805	0	847	74	0
45	T	714	0	737	38	0
46	U	649	0	666	52	0
47	V	649	0	691	49	0
48	W	536	0	552	26	0
49	X	638	0	665	55	0
50	Y	665	0	714	37	0
51	Z	545	0	579	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	a	1027	0	1092	100	0
53	3	33012	0	16618	688	0
54	1	62317	0	31346	1208	0
55	2	2568	0	1303	63	0
56	5	1640	0	836	22	0
56	6	1640	0	837	47	0
57	4	388	0	198	14	0
58	7	1647	0	832	27	0
59	5	10	0	10	1	0
All	All	149698	0	100682	4562	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 18.

The worst 5 of 4562 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)
54:1:45:G:H5''	54:1:46:G:H5'	1.25	1.17
55:2:119:A:C2	55:2:120:A:H1'	1.88	1.09
10:k:104:THR:HG22	10:k:106:GLU:H	1.18	1.08
52:a:6:LYS:O	52:a:8:MET:N	1.86	1.08
45:T:88:ARG:H	45:T:88:ARG:HD3	1.20	1.07

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	233 (87%)	32 (12%)	4 (2%)	8	37
2	c	207/209 (99%)	182 (88%)	24 (12%)	1 (0%)	24	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	d	199/201 (99%)	175 (88%)	23 (12%)	1 (0%)	24	59
4	e	175/177 (99%)	153 (87%)	22 (13%)	0	100	100
5	f	174/176 (99%)	156 (90%)	18 (10%)	0	100	100
6	g	121/149 (81%)	102 (84%)	17 (14%)	2 (2%)	7	35
7	h	82/131 (63%)	63 (77%)	18 (22%)	1 (1%)	10	42
8	i	72/141 (51%)	58 (81%)	12 (17%)	2 (3%)	4	25
9	j	140/142 (99%)	124 (89%)	15 (11%)	1 (1%)	18	52
10	k	120/122 (98%)	98 (82%)	20 (17%)	2 (2%)	7	35
11	l	141/143 (99%)	116 (82%)	21 (15%)	4 (3%)	4	25
12	m	134/136 (98%)	123 (92%)	9 (7%)	2 (2%)	8	37
13	n	118/120 (98%)	101 (86%)	15 (13%)	2 (2%)	7	35
14	o	114/116 (98%)	102 (90%)	12 (10%)	0	100	100
15	p	112/114 (98%)	95 (85%)	16 (14%)	1 (1%)	14	47
16	q	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
17	r	101/103 (98%)	84 (83%)	16 (16%)	1 (1%)	12	45
18	s	108/110 (98%)	97 (90%)	11 (10%)	0	100	100
19	t	91/93 (98%)	80 (88%)	11 (12%)	0	100	100
20	u	100/102 (98%)	74 (74%)	23 (23%)	3 (3%)	3	23
21	v	92/94 (98%)	77 (84%)	14 (15%)	1 (1%)	11	43
22	w	73/75 (97%)	63 (86%)	10 (14%)	0	100	100
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
25	z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
26	A	64/66 (97%)	55 (86%)	8 (12%)	1 (2%)	7	36
27	B	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
28	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
29	D	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
30	E	62/64 (97%)	53 (86%)	6 (10%)	3 (5%)	2	14
31	F	36/38 (95%)	30 (83%)	6 (17%)	0	100	100
32	G	216/225 (96%)	178 (82%)	36 (17%)	2 (1%)	14	47
33	H	204/206 (99%)	183 (90%)	21 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	I	203/205 (99%)	170 (84%)	32 (16%)	1 (0%)	24	59
35	J	155/157 (99%)	128 (83%)	24 (16%)	3 (2%)	6	33
36	K	98/100 (98%)	78 (80%)	19 (19%)	1 (1%)	12	45
37	L	149/151 (99%)	127 (85%)	21 (14%)	1 (1%)	18	52
38	M	127/129 (98%)	111 (87%)	16 (13%)	0	100	100
39	N	125/127 (98%)	98 (78%)	24 (19%)	3 (2%)	4	28
40	O	96/98 (98%)	81 (84%)	13 (14%)	2 (2%)	5	31
41	P	114/116 (98%)	87 (76%)	24 (21%)	3 (3%)	4	26
42	Q	121/123 (98%)	90 (74%)	29 (24%)	2 (2%)	7	35
43	R	112/114 (98%)	90 (80%)	19 (17%)	3 (3%)	4	25
44	S	98/100 (98%)	76 (78%)	22 (22%)	0	100	100
45	T	86/88 (98%)	71 (83%)	14 (16%)	1 (1%)	10	42
46	U	80/82 (98%)	66 (82%)	13 (16%)	1 (1%)	9	40
47	V	78/80 (98%)	61 (78%)	16 (20%)	1 (1%)	9	40
48	W	63/65 (97%)	48 (76%)	13 (21%)	2 (3%)	3	21
49	X	77/79 (98%)	68 (88%)	9 (12%)	0	100	100
50	Y	83/85 (98%)	76 (92%)	7 (8%)	0	100	100
51	Z	63/65 (97%)	39 (62%)	20 (32%)	4 (6%)	1	8
52	a	130/223 (58%)	104 (80%)	21 (16%)	5 (4%)	2	18
All	All	5836/6178 (94%)	4947 (85%)	822 (14%)	67 (1%)	14	43

5 of 67 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
6	g	9	VAL
17	r	54	VAL
30	E	30	HIS
30	E	31	ILE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	209 (97%)	7 (3%)	34	65
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	84
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	84
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	83
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	83
6	g	98/114 (86%)	97 (99%)	1 (1%)	68	80
7	h	66/100 (66%)	65 (98%)	1 (2%)	57	76
8	i	60/109 (55%)	58 (97%)	2 (3%)	33	65
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	81
10	k	103/103 (100%)	100 (97%)	3 (3%)	37	67
11	l	102/102 (100%)	99 (97%)	3 (3%)	37	67
12	m	109/109 (100%)	105 (96%)	4 (4%)	30	63
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	79
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	87 (98%)	2 (2%)	45	71
17	r	84/84 (100%)	81 (96%)	3 (4%)	31	63
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	78 (94%)	5 (6%)	17	50
21	v	78/78 (100%)	78 (100%)	0	100	100
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	66 (98%)	1 (2%)	57	76
24	y	55/55 (100%)	54 (98%)	1 (2%)	51	74
25	z	48/48 (100%)	45 (94%)	3 (6%)	16	48
26	A	59/59 (100%)	59 (100%)	0	100	100
27	B	47/47 (100%)	47 (100%)	0	100	100
28	C	45/45 (100%)	45 (100%)	0	100	100
29	D	38/38 (100%)	37 (97%)	1 (3%)	40	69
30	E	51/51 (100%)	50 (98%)	1 (2%)	48	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	F	34/34 (100%)	33 (97%)	1 (3%)	37	67
32	G	180/186 (97%)	179 (99%)	1 (1%)	78	84
33	H	170/170 (100%)	167 (98%)	3 (2%)	51	74
34	I	172/172 (100%)	169 (98%)	3 (2%)	53	75
35	J	119/119 (100%)	118 (99%)	1 (1%)	73	82
36	K	87/87 (100%)	85 (98%)	2 (2%)	44	70
37	L	124/124 (100%)	122 (98%)	2 (2%)	55	75
38	M	104/104 (100%)	104 (100%)	0	100	100
39	N	105/105 (100%)	101 (96%)	4 (4%)	29	62
40	O	86/86 (100%)	85 (99%)	1 (1%)	63	79
41	P	89/89 (100%)	87 (98%)	2 (2%)	45	71
42	Q	103/103 (100%)	103 (100%)	0	100	100
43	R	92/92 (100%)	89 (97%)	3 (3%)	33	65
44	S	83/83 (100%)	83 (100%)	0	100	100
45	T	76/76 (100%)	74 (97%)	2 (3%)	40	69
46	U	65/65 (100%)	64 (98%)	1 (2%)	57	76
47	V	74/74 (100%)	74 (100%)	0	100	100
48	W	56/56 (100%)	55 (98%)	1 (2%)	51	74
49	X	70/70 (100%)	70 (100%)	0	100	100
50	Y	65/65 (100%)	65 (100%)	0	100	100
51	Z	55/55 (100%)	54 (98%)	1 (2%)	51	74
52	a	110/174 (63%)	109 (99%)	1 (1%)	70	81
All	All	4862/5031 (97%)	4789 (98%)	73 (2%)	55	76

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	N	57	VAL
51	Z	40	PRO
39	N	110	VAL
43	R	40	GLU
12	m	17	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
20	u	68	ASN
46	U	29	ASN
29	D	29	GLN
46	U	26	ASN
50	Y	81	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	3	1538/1539 (99%)	171 (11%)	7 (0%)
54	1	2902/2903 (99%)	354 (12%)	17 (0%)
55	2	119/120 (99%)	9 (7%)	1 (0%)
56	5	76/77 (98%)	11 (14%)	0
56	6	76/77 (98%)	19 (25%)	0
57	4	17/18 (94%)	5 (29%)	0
58	7	76/77 (98%)	11 (14%)	4 (5%)
All	All	4804/4811 (99%)	580 (12%)	29 (0%)

5 of 580 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	3	4	U
53	3	6	G
53	3	7	A
53	3	9	G
53	3	22	G

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	1	858	G
58	7	40	C
54	1	1475	G
55	2	88	C
54	1	1130	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
59	FME	5	101	56	8,9,10	0.48	0	8,9,11	1.05	1 (12%)

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
59	FME	5	101	56	-	1/7/9/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	5	101	FME	O-C-CA	-2.29	118.87	124.77

There are no chirality outliers.

All (1) torsion outliers are listed below:

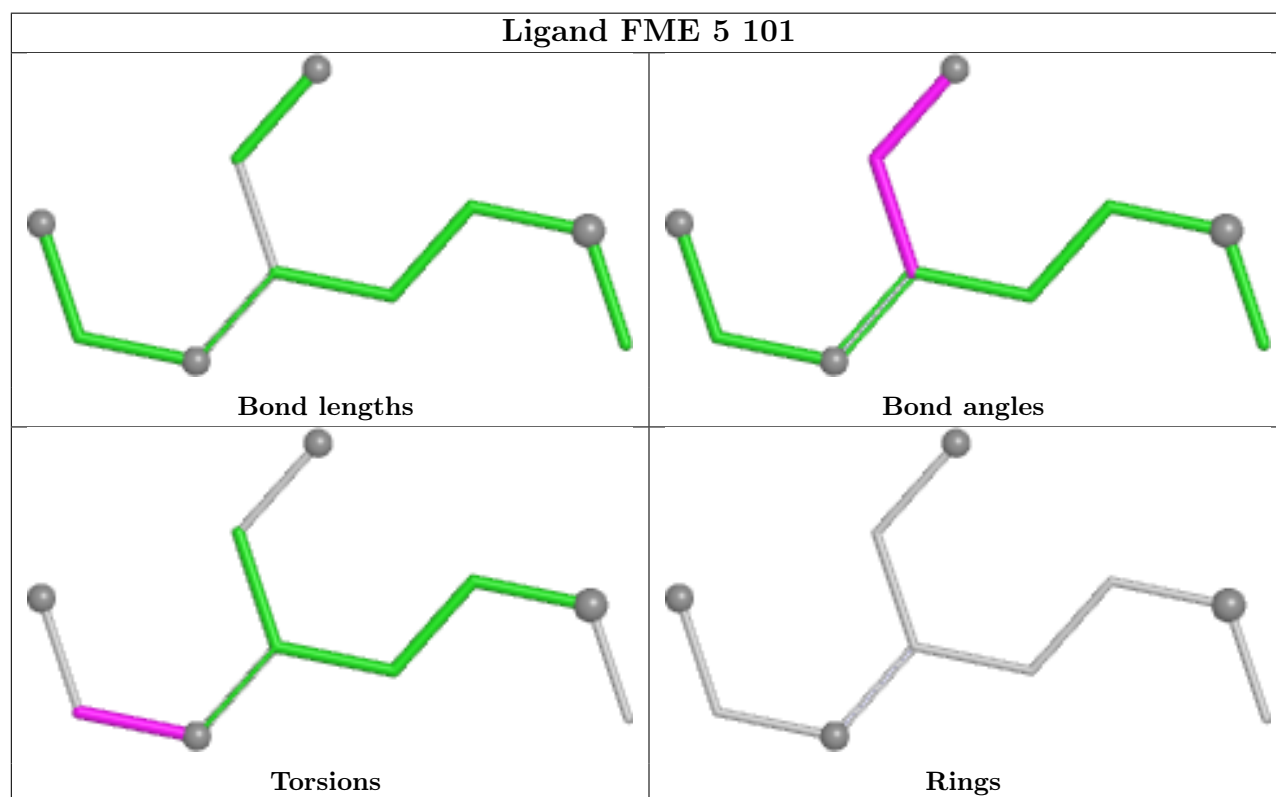
Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	5	101	FME	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.

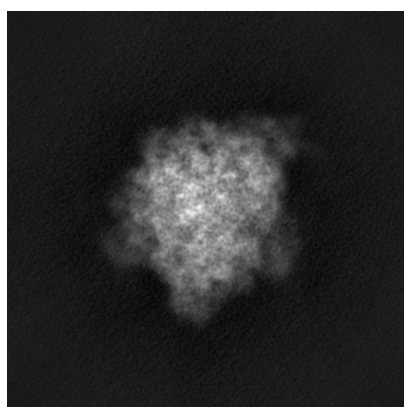
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22672. These allow visual inspection of the internal detail of the map and identification of artifacts.

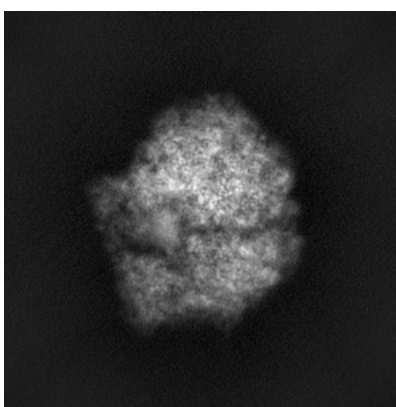
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

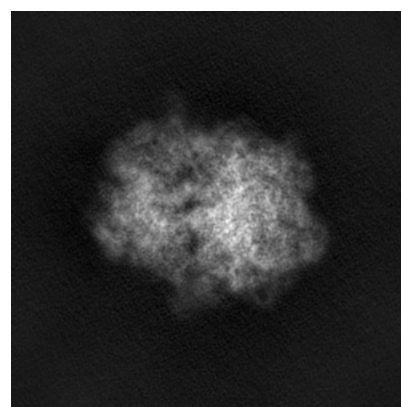
6.1.1 Primary map



X



Y

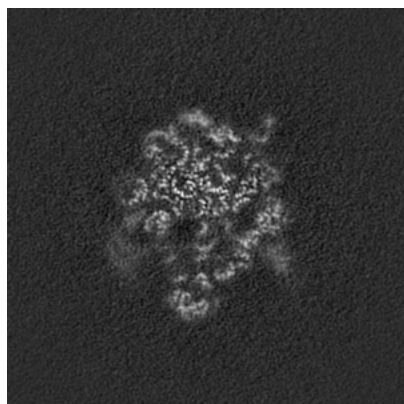


Z

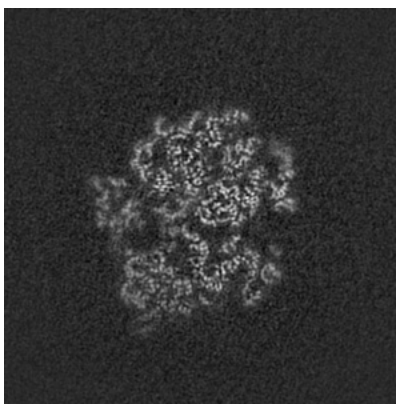
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

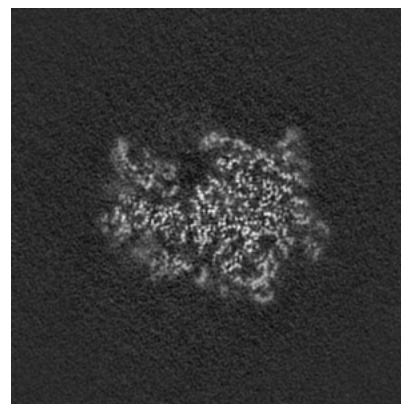
6.2.1 Primary map



X Index: 200



Y Index: 200

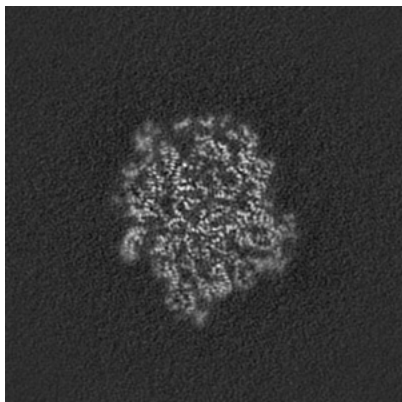


Z Index: 200

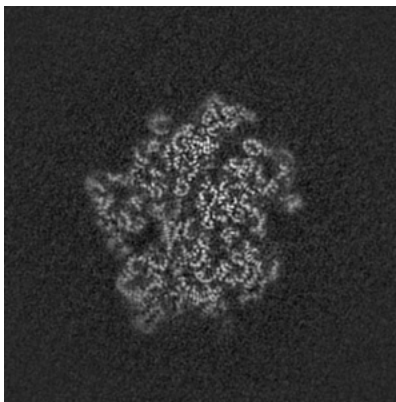
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

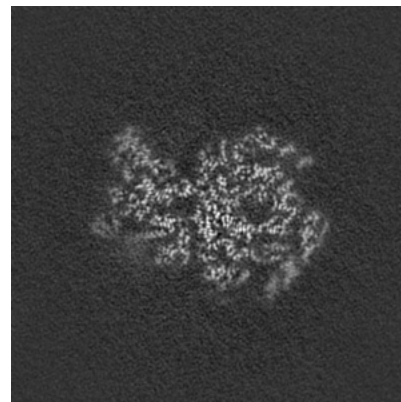
6.3.1 Primary map



X Index: 223



Y Index: 193

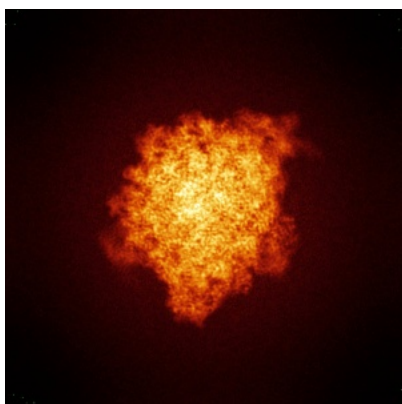


Z Index: 215

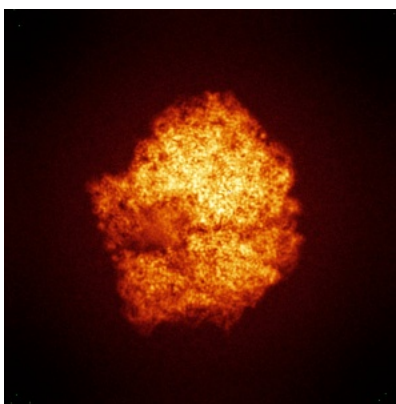
The images above show the largest variance slices of the map in three orthogonal directions.

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

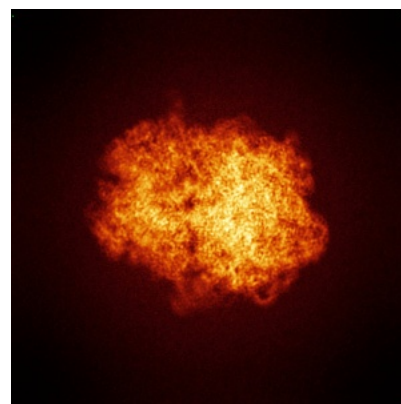
6.4.1 Primary map



X



Y

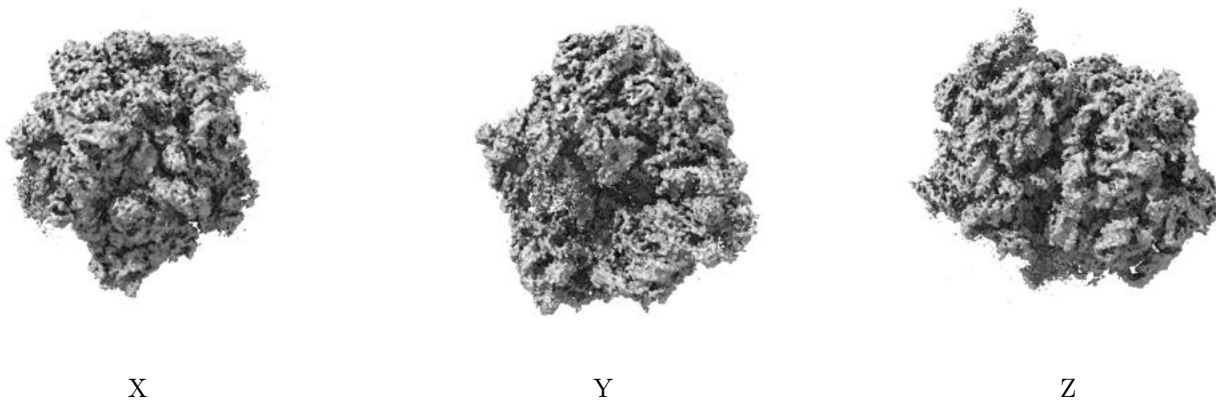


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

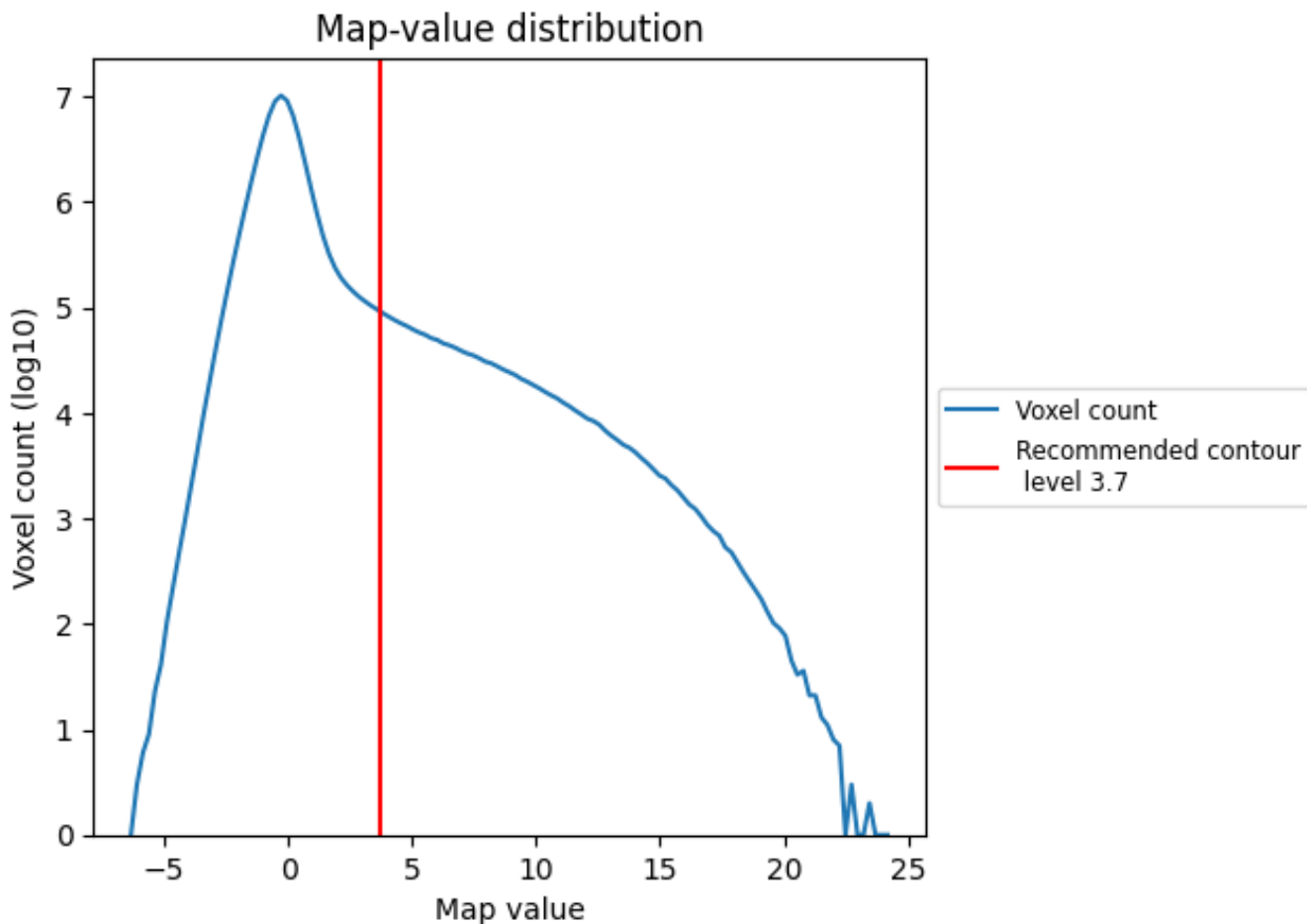
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

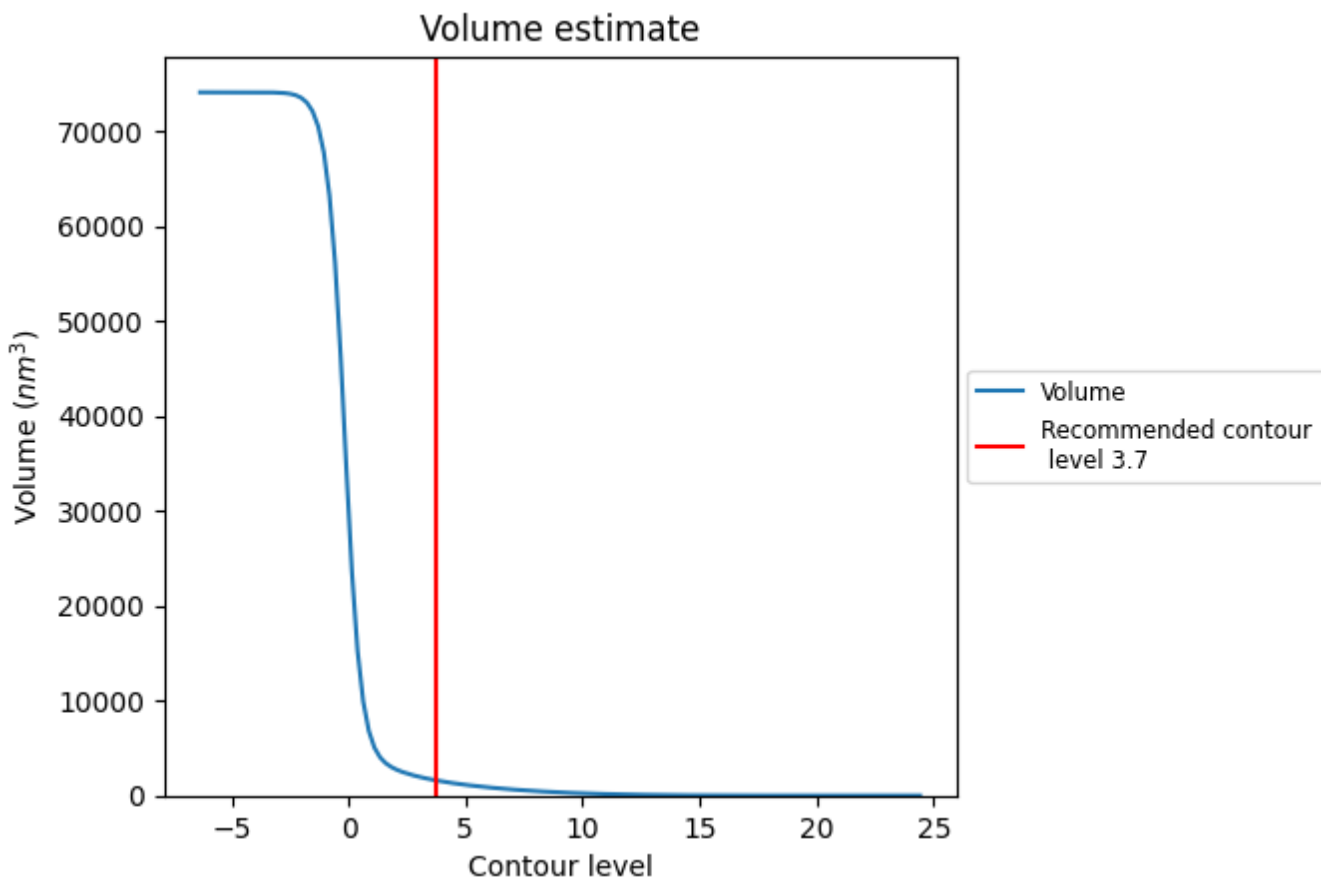
This section contains the results of statistical analysis of the map.

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.

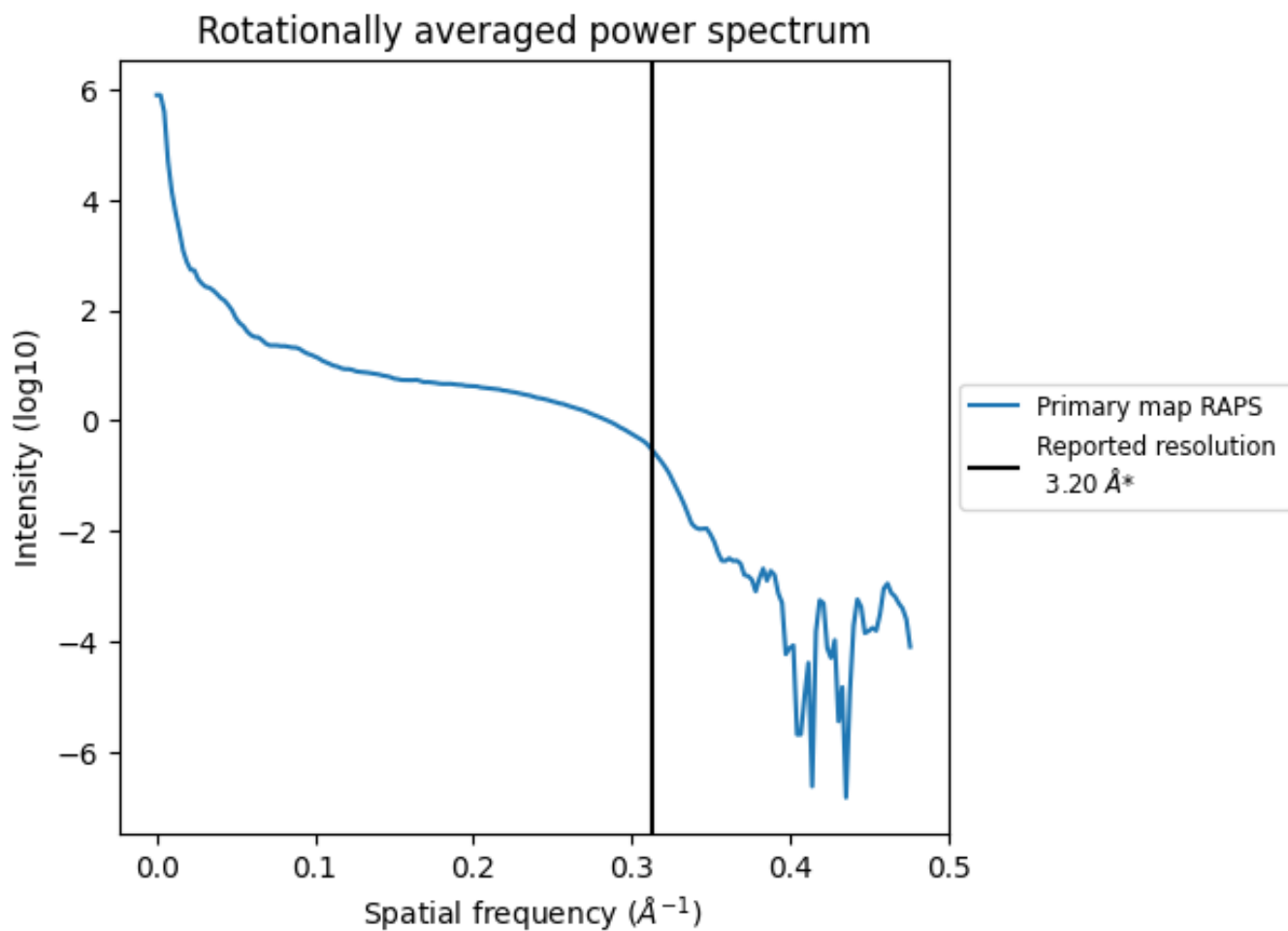
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1619 nm^3 ; this corresponds to an approximate mass of 1462 kDa.

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

7.3 Rotationally averaged power spectrum i



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

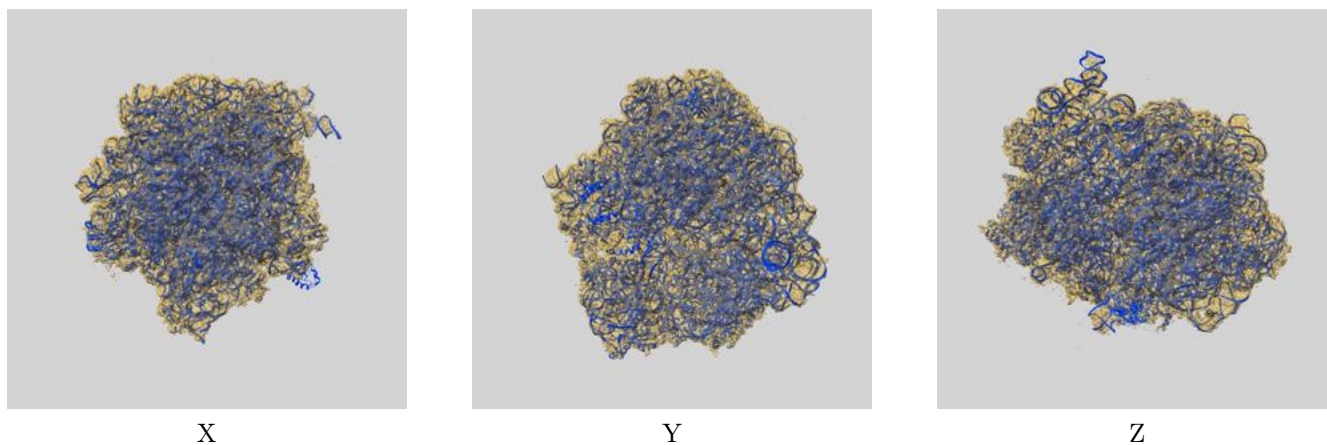
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

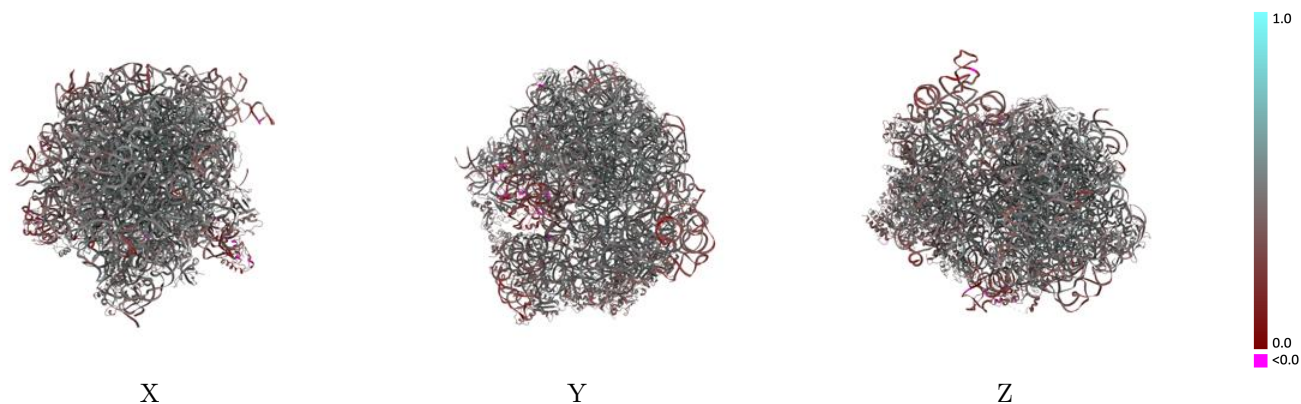
This section contains information regarding the fit between EMDB map EMD-22672 and PDB model 7K53. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



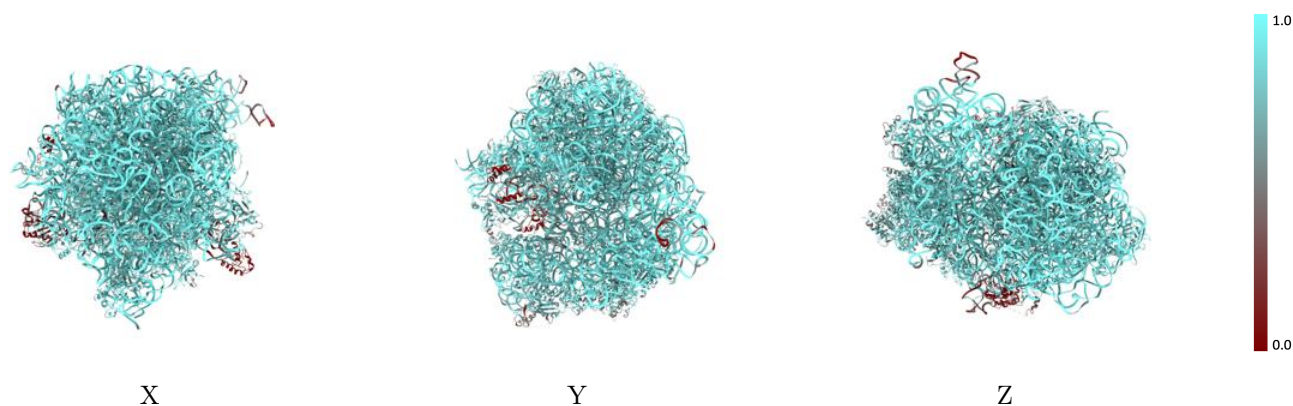
The images above show the 3D surface view of the map at the recommended contour level 3.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



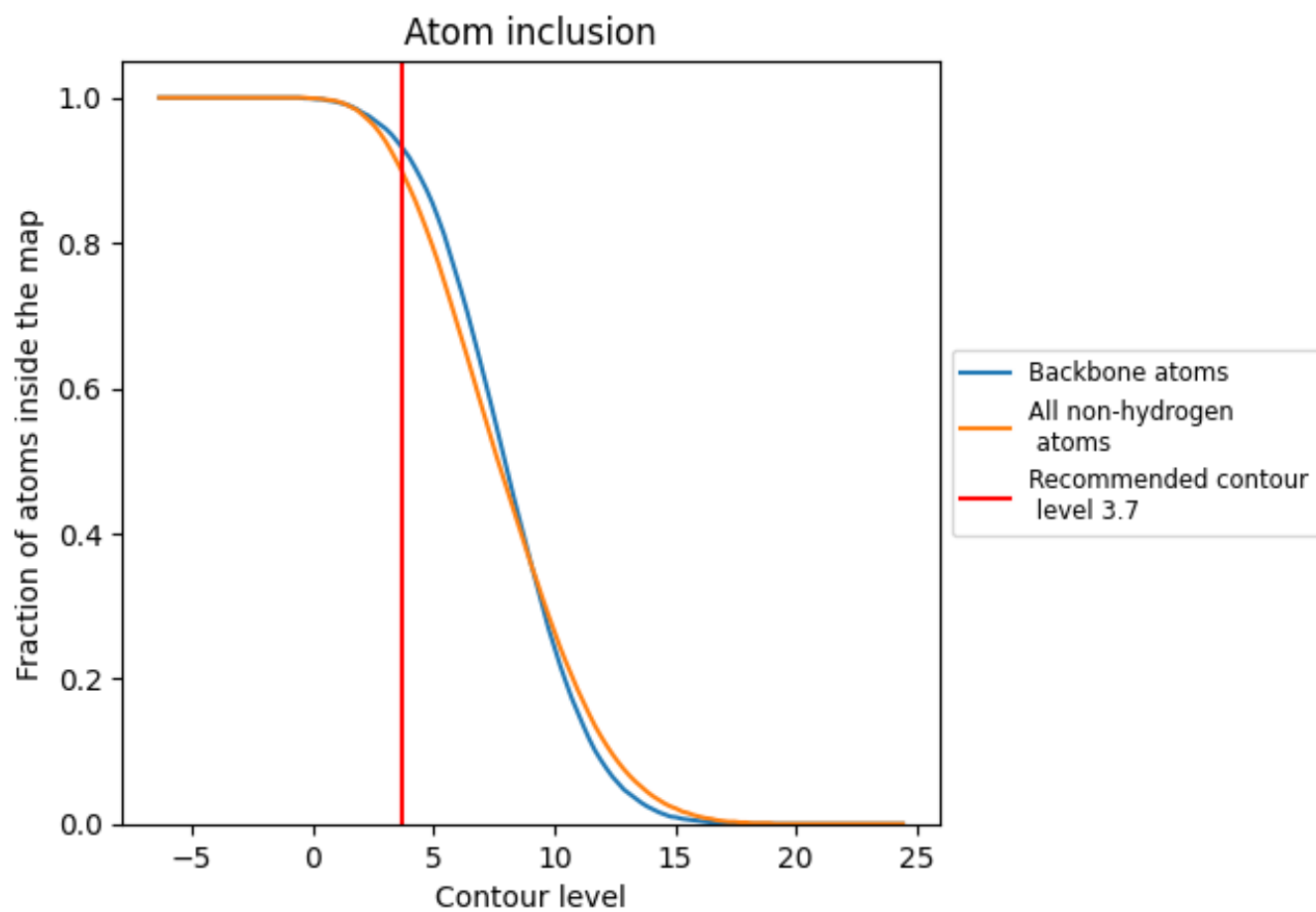
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.7).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 90% 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 (3.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8980	 0.4370
1	 0.9600	 0.4520
2	 0.9740	 0.4390
3	 0.9480	 0.4300
4	 0.7140	 0.3000
5	 0.9440	 0.4200
6	 0.5080	 0.2160
7	 0.7810	 0.3180
A	 0.7250	 0.3910
B	 0.9370	 0.4880
C	 0.7240	 0.4590
D	 0.9300	 0.5040
E	 0.9160	 0.5050
F	 0.8800	 0.4920
G	 0.6700	 0.3990
H	 0.7830	 0.4460
I	 0.7530	 0.4100
J	 0.8710	 0.4550
K	 0.8390	 0.4160
L	 0.7800	 0.4080
M	 0.8600	 0.4660
N	 0.7650	 0.4110
O	 0.6140	 0.3920
P	 0.8660	 0.4460
Q	 0.8510	 0.4510
R	 0.8120	 0.4150
S	 0.8110	 0.4260
T	 0.8930	 0.4440
U	 0.7880	 0.4340
V	 0.8860	 0.4400
W	 0.8600	 0.4410
X	 0.7940	 0.4030
Y	 0.8110	 0.4130
Z	 0.7240	 0.3640
a	 0.1600	 0.2510



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Chain	Atom inclusion	Q-score
b	 0.9200	 0.5070
c	 0.9010	 0.4820
d	 0.8150	 0.4560
e	 0.8310	 0.4230
f	 0.7900	 0.4130
g	 0.2680	 0.3300
h	 0.0530	 0.1940
i	 0.2140	 0.2370
j	 0.8980	 0.4750
k	 0.8890	 0.4850
l	 0.8870	 0.4790
m	 0.9000	 0.4870
n	 0.9100	 0.4730
o	 0.8580	 0.4360
p	 0.8910	 0.4780
q	 0.9170	 0.4910
r	 0.8580	 0.4690
s	 0.8720	 0.4750
t	 0.8660	 0.4570
u	 0.8360	 0.4280
v	 0.8280	 0.4530
w	 0.8840	 0.4760
x	 0.9030	 0.4890
y	 0.7870	 0.4060
z	 0.8760	 0.4760