



wwPDB EM Validation Summary Report ⓘ

Sep 15, 2026 – 12:53 PM EDT

PDB ID : 6V3A / pdb_00006v3a
EMDB ID : EMD-21031
Title : Cryo-EM structure of the Acinetobacter baumannii Ribosome: 70S with E-site tRNA
Authors : Morgan, C.E.; Yu, E.W.
Deposited on : 2019-11-25
Resolution : 2.82 Å(reported)
Based on initial model : 5AFI

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:

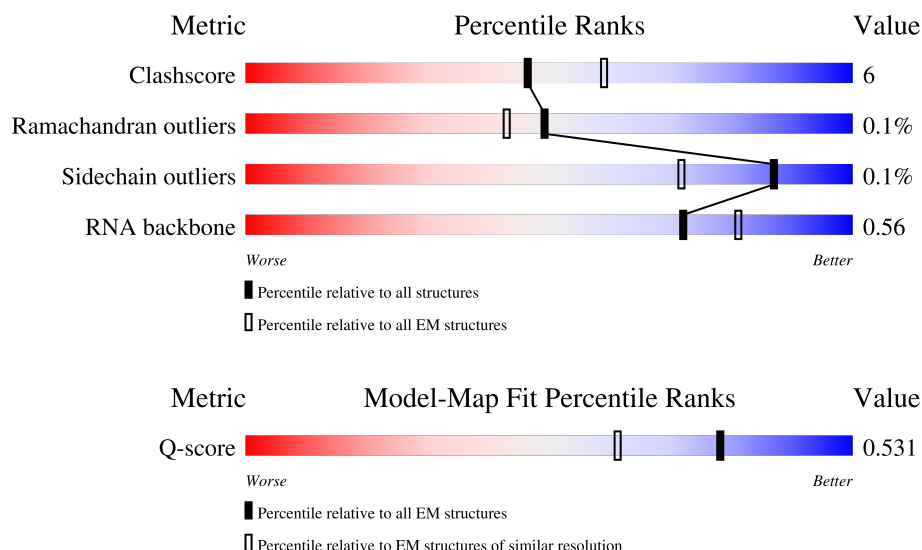
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 2.82 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	11795 (2.32 - 3.32)

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	0	51	16% 90% 10%
2	1	44	84% 16%
3	2	64	81% 12% 5%

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Mol	Chain	Length	Quality of chain
4	3	38	
5	AN1	2918	
6	B	115	
7	C	274	
8	D	212	
9	E	200	
10	F	178	
11	G	177	
12	H	148	
13	I	142	
14	J	122	
15	K	146	
16	L	137	
17	M	125	
18	N	116	
19	O	122	
20	P	119	
21	Q	103	
22	R	109	
23	S	106	
24	T	105	
25	U	98	
26	V	85	
27	W	78	
28	X	65	

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Mol	Chain	Length	Quality of chain
29	Y	58	
30	Z	61	
31	sN1	1544	
32	b	250	
33	c	250	
34	d	208	
35	e	165	
36	f	127	
37	g	156	
38	h	131	
39	i	128	
40	j	103	
41	k	128	
42	l	124	
43	m	118	
44	n	101	
45	o	89	
46	p	101	
47	q	85	
48	r	75	
49	s	91	
50	t	88	
51	u	71	
52	v	77	
53	w	3	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 142113 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 L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	51	Total	C	N	O	S	0	0
			427	274	77	73	3		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	44	Total	C	N	O	S	0	0
			363	222	85	54	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			509	319	110	76	4		

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			295	179	64	48	4		

- Molecule 5 is a RNA chain called 23s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AN1	2892	Total	C	N	O	P	0	0
			62023	27689	11345	20098	2891		

- Molecule 6 is a RNA chain called 5s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	115	Total	C	N	O	P	0	0
			2450	1095	440	800	115		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	270	Total	C	N	O	S	0	0
			2096	1291	434	363	8		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	211	Total	C	N	O	S	0	0
			1572	972	297	300	3		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	186	Total	C	N	O	S	0	0
			1419	893	265	257	4		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	175	Total	C	N	O	S	0	0
			1381	877	247	249	8		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	174	Total	C	N	O	S	0	0
			1318	832	236	249	1		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	60	Total	C	N	O	S	0	0
			458	287	84	86	1		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	142	Total	C	N	O	S	0	0
			1125	718	200	203	4		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	122	Total	C	N	O	S	0	0
			946	592	180	169	5		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	146	Total	C	N	O	S	0	0
			1089	673	215	200	1		

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	137	Total	C	N	O	S	0	0
			1087	687	210	185	5		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	119	Total	C	N	O	S	0	0
			942	590	186	163	3		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	114	Total	C	N	O	S	0	0
			857	528	173	155	1		

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	O	117	Total	C	N	O	0	0
			919	578	177	164		

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	117	Total	C	N	O	S	0	0
			934	589	197	146	2		

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	103	Total	C	N	O	S	0	0
			807	506	155	143	3		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	109	Total	C	N	O	S	0	0
			826	514	158	150	4		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	90	Total	C	N	O		0	0
			702	447	127	128			

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	100	Total	C	N	O		0	0
			749	465	139	145			

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	97	Total	C	N	O	S	0	0
			760	477	143	139	1		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	80	Total	C	N	O	S	0	0
			598	370	115	111	2		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	77	Total	C	N	O	S	0	0
			632	395	130	105	2		

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	62	Total	C	N	O	S	0	0
			498	308	96	93	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	58	Total	C	N	O	S	0	0
			463	286	88	85	4		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	55	Total	C	N	O	S	0	0
			456	271	102	82	1		

- Molecule 31 is a RNA chain called 16s Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	sN1	1528	Total	C	N	O	P	0	0
			32782	14631	5994	10630	1527		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	225	Total	C	N	O	S	0	0
			1769	1110	328	325	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	215	Total	C	N	O	S	0	0
			1690	1065	318	299	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	207	Total	C	N	O	S	0	0
			1631	1017	313	299	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	155	Total	C	N	O	S	0	0
			1129	700	217	207	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	94	Total	C	N	O	S	0	0
			793	499	147	143	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	141	Total	C	N	O	S	0	0
			1111	696	210	199	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	130	Total	C	N	O	S	0	0
			985	615	177	187	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	127	Total	C	N	O	S	0	0
			995	621	198	175	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	100	Total	C	N	O	S	0	0
			801	500	150	148	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	117	Total	C	N	O	S	0	0
			862	535	167	159	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	122	Total	C	N	O	S	0	0
			945	580	193	167	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	115	Total	C	N	O	S	0	0
			903	558	184	158	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	100	Total	C	N	O	S	0	0
			792	493	158	137	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	88	Total	C	N	O	S	0	0
			705	434	144	126	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	83	Total	C	N	O	S	0	0
			649	406	129	113	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	80	Total	C	N	O	S	0	0
			630	396	118	115	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
48	r	53	Total	C	N	O	0	0
			438	282	75	81		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	82	Total	C	N	O	S	0	0
			646	412	125	107	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	85	Total	C	N	O	S	0	0
			658	406	138	112	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
51	u	21	Total	C	N	O	0	0
			182	115	37	30		

- Molecule 52 is a RNA chain called tRNA-met.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	v	77	Total	C	N	O	P	S	0	0
			1636	733	291	535	76	1		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	3	Total	C	N	O	P	0	0
			65	29	12	21	3		

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
54	3	1	Total	Zn	0
			1	1	

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	AN1	49	Total	Mg	0
			49	49	
55	sN1	44	Total	Mg	0
			44	44	

- Molecule 56 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
56	AN1	1	Total	Na	0
			1	1	

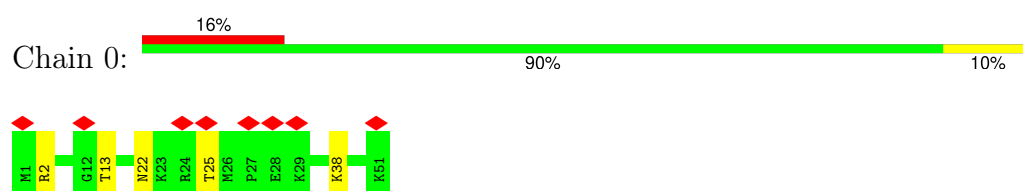
- Molecule 57 is water.

Mol	Chain	Residues	Atoms		AltConf
57	AN1	319	Total	O	0
			319	319	
57	B	4	Total	O	0
			4	4	
57	C	5	Total	O	0
			5	5	
57	D	3	Total	O	0
			3	3	
57	E	3	Total	O	0
			3	3	
57	K	3	Total	O	0
			3	3	
57	O	1	Total	O	0
			1	1	
57	P	3	Total	O	0
			3	3	
57	Q	1	Total	O	0
			1	1	
57	U	1	Total	O	0
			1	1	
57	sN1	163	Total	O	0
			163	163	
57	i	5	Total	O	0
			5	5	
57	j	2	Total	O	0
			2	2	
57	m	1	Total	O	0
			1	1	
57	o	1	Total	O	0
			1	1	
57	p	1	Total	O	0
			1	1	
57	q	2	Total	O	0
			2	2	
57	t	2	Total	O	0
			2	2	

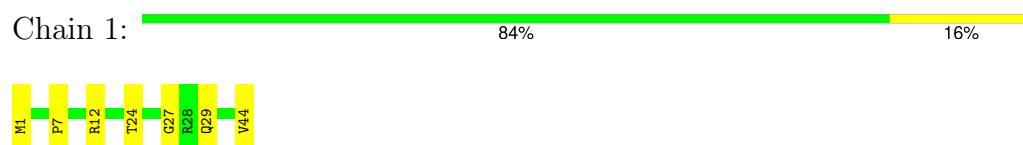
3 Residue-property plots [i](#)

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

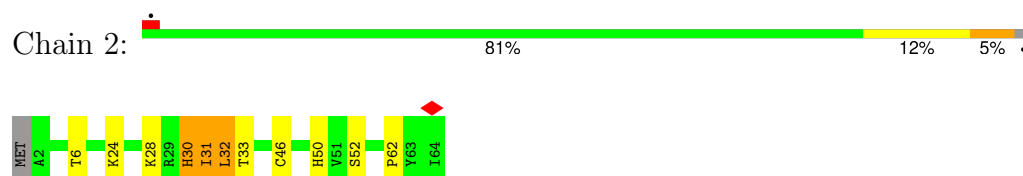
- Molecule 1: 50S ribosomal protein L33



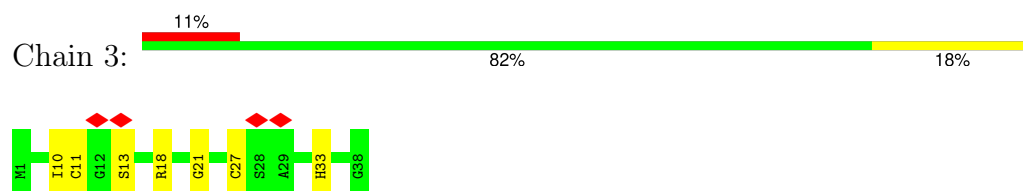
- Molecule 2: 50S ribosomal protein L34



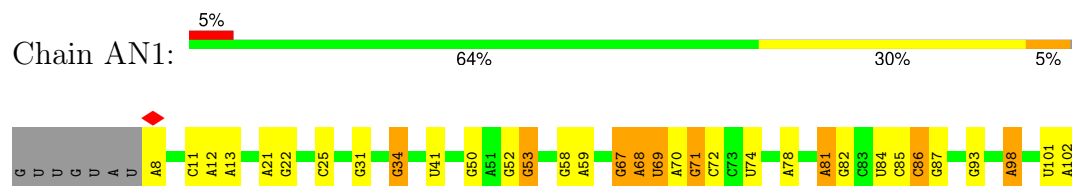
- Molecule 3: 50S ribosomal protein L35

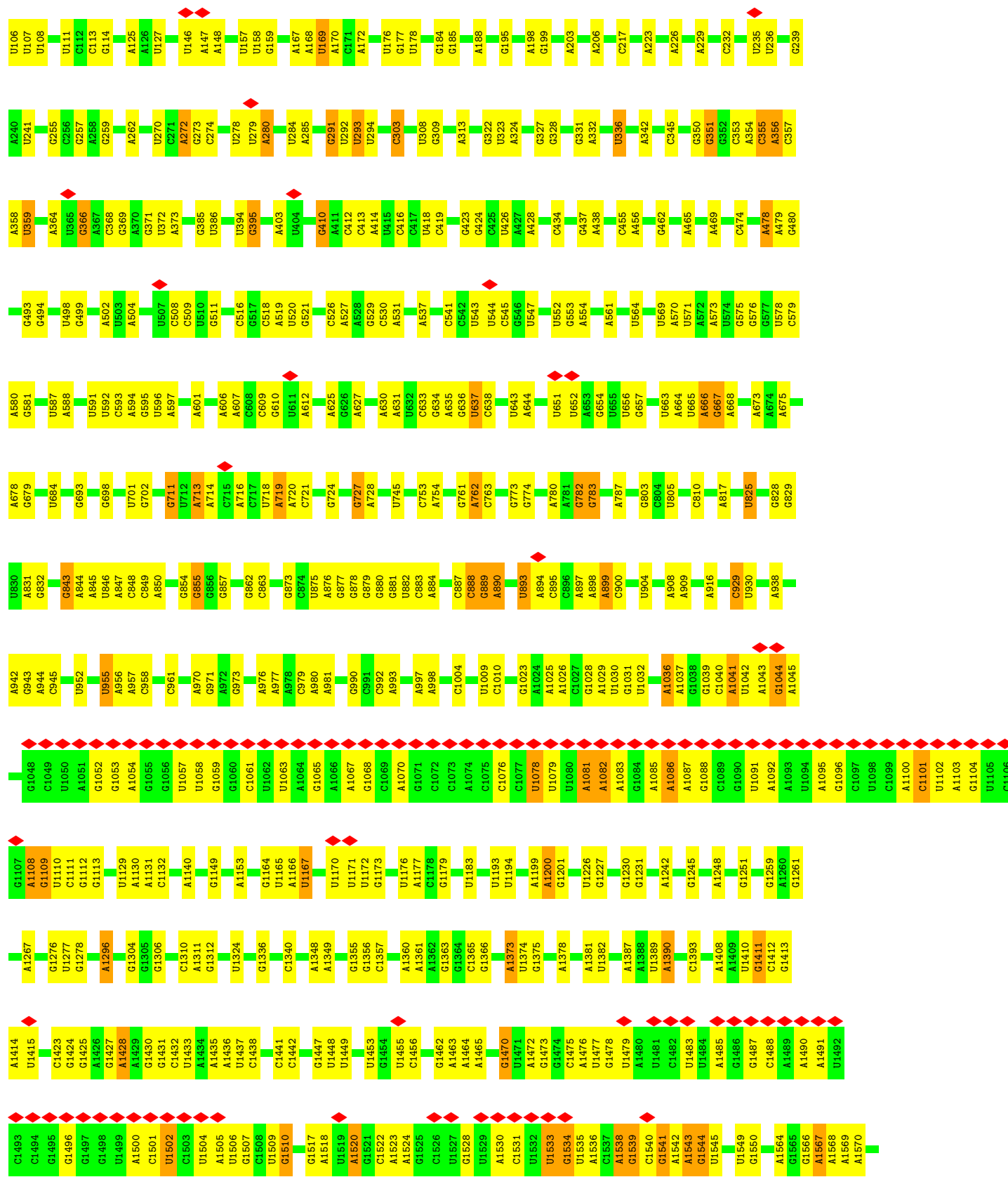


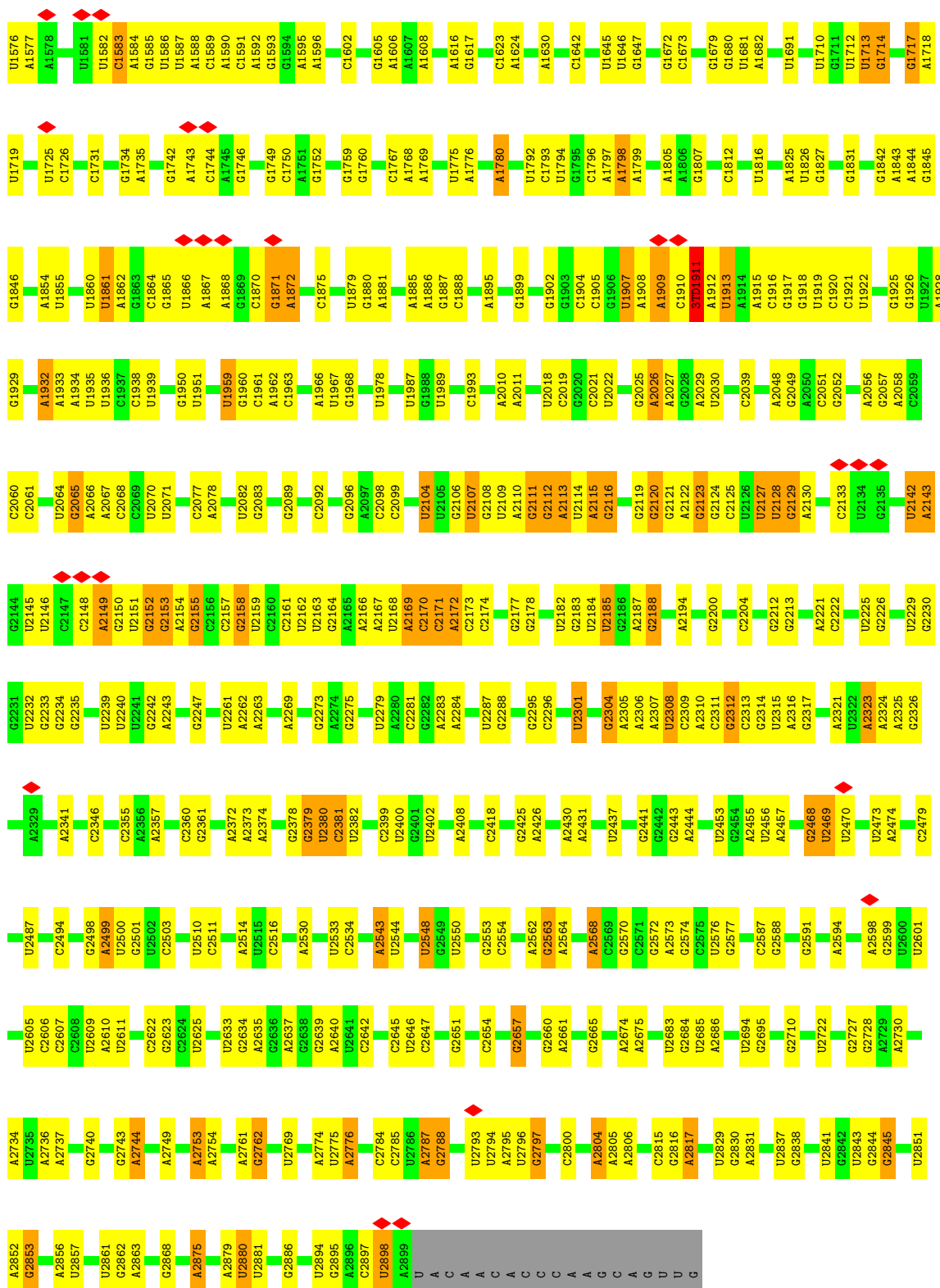
- Molecule 4: 50S ribosomal protein L36

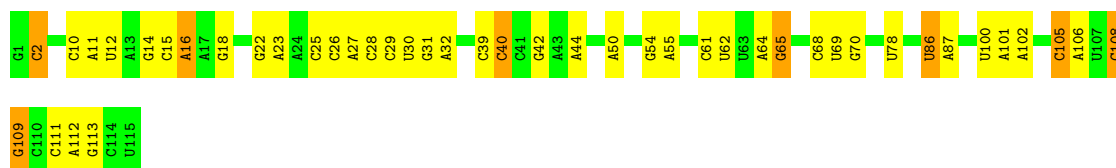


- Molecule 5: 23s ribosomal RNA

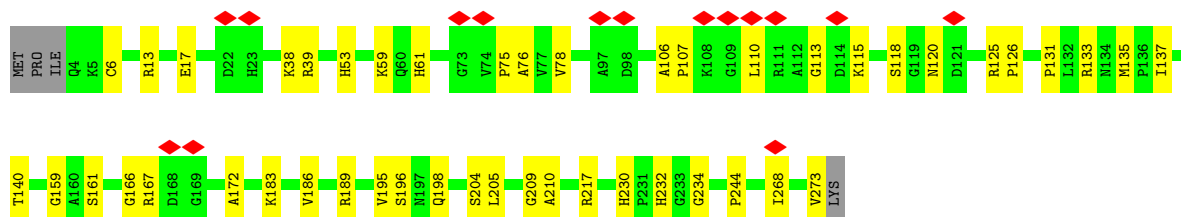
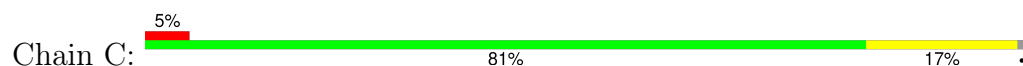




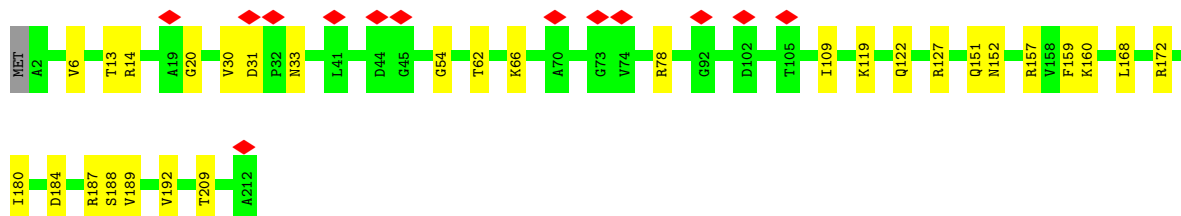
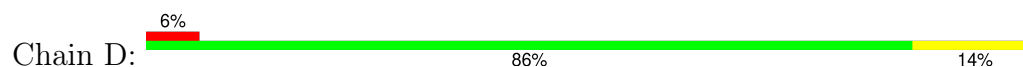




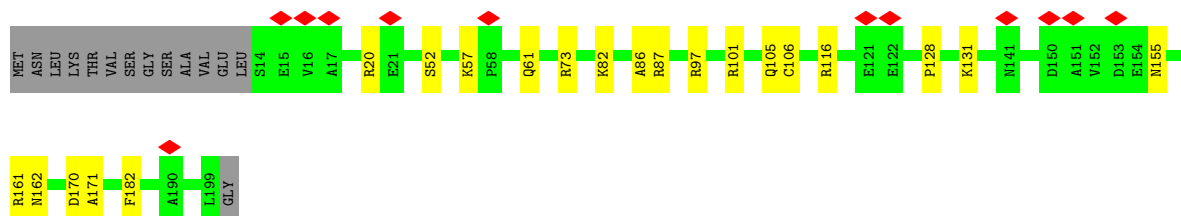
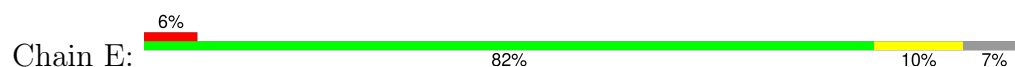
• Molecule 7: 50S ribosomal protein L2



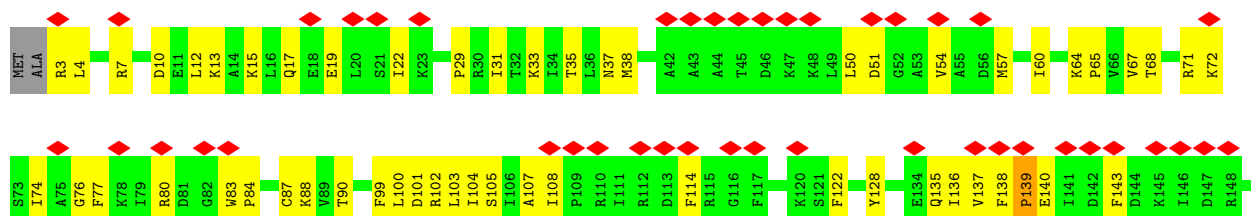
• Molecule 8: 50S ribosomal protein L3

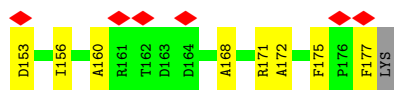


• Molecule 9: 50S ribosomal protein L4

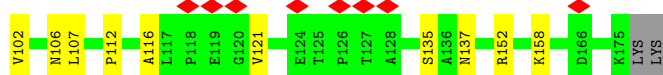
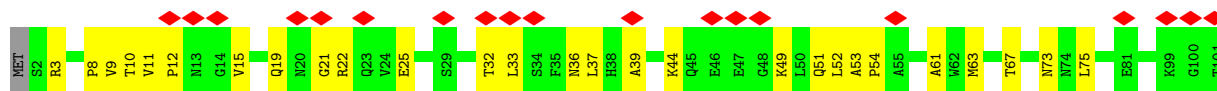
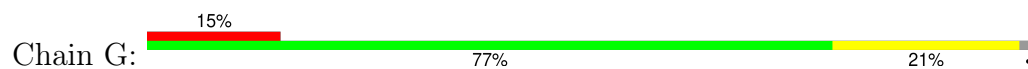


• Molecule 10: 50S ribosomal protein L5

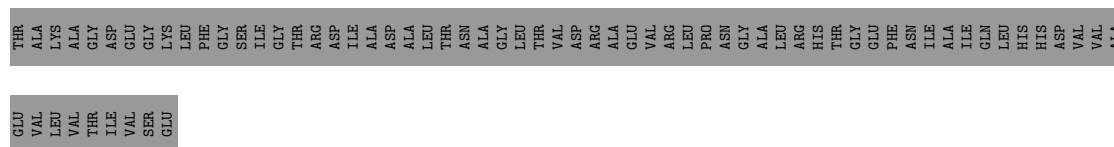
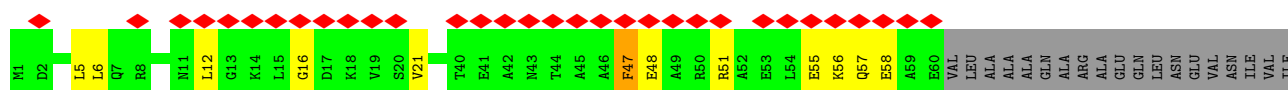




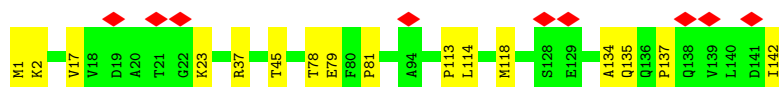
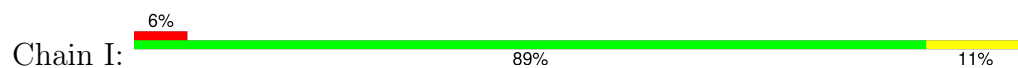
- Molecule 11: 50S ribosomal protein L6



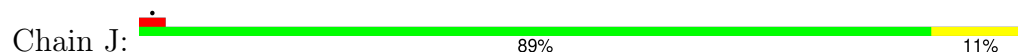
- Molecule 12: 50S ribosomal protein L9



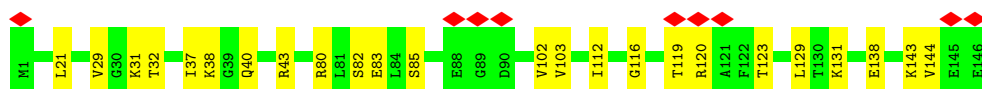
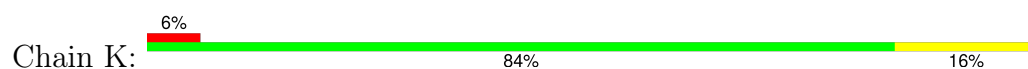
- Molecule 13: 50S ribosomal protein L13



- Molecule 14: 50S ribosomal protein L14

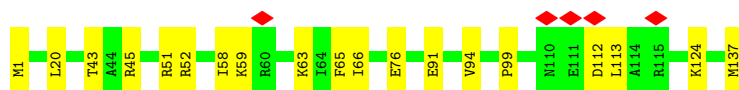


- Molecule 15: 50S ribosomal protein L15



- Molecule 16: 50S ribosomal protein L16

Chain L:  86% 14%



- Molecule 17: 50S ribosomal protein L17

Chain M:  84% 11% 5%



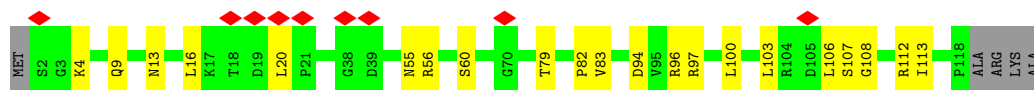
- Molecule 18: 50S ribosomal protein L18

Chain N:  84% 14% 10%

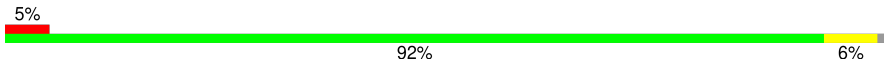


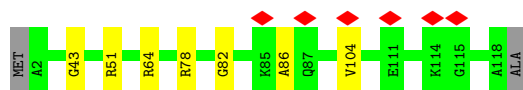
- Molecule 19: 50S ribosomal protein L19

Chain O:  79% 17% 7%



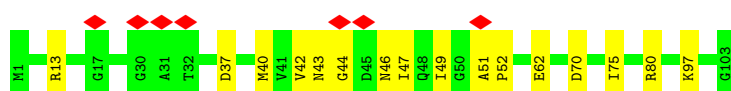
- Molecule 20: 50S ribosomal protein L20

Chain P:  92% 6% 5%

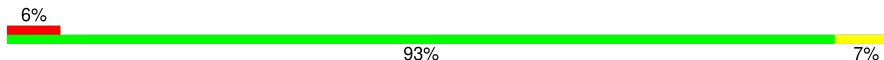


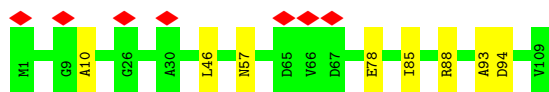
- Molecule 21: 50S ribosomal protein L21

Chain Q:  84% 16% 7%

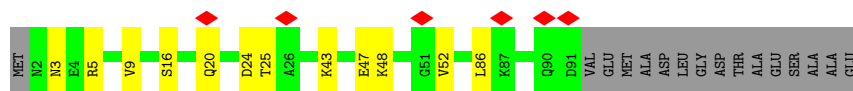
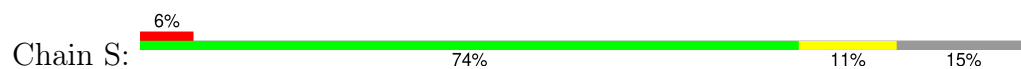


- Molecule 22: 50S ribosomal protein L22

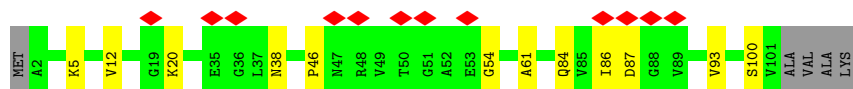
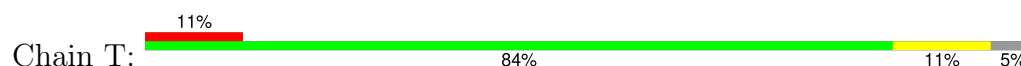
Chain R:  93% 7% 6%



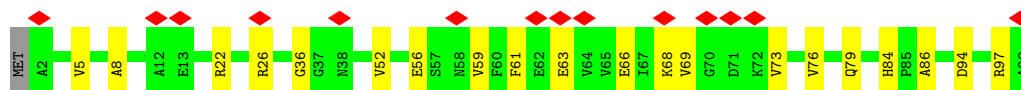
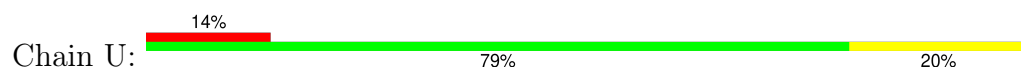
- Molecule 23: 50S ribosomal protein L23



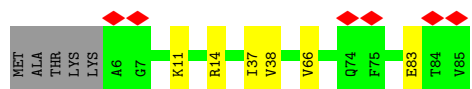
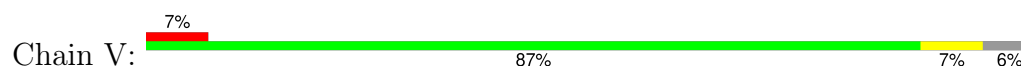
- Molecule 24: 50S ribosomal protein L24



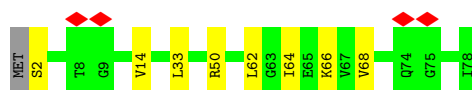
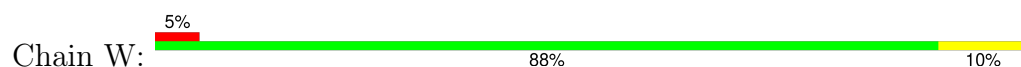
- Molecule 25: 50S ribosomal protein L25



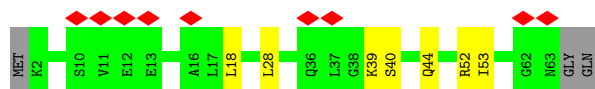
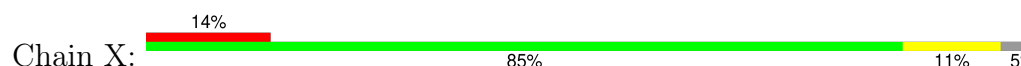
- Molecule 26: 50S ribosomal protein L27



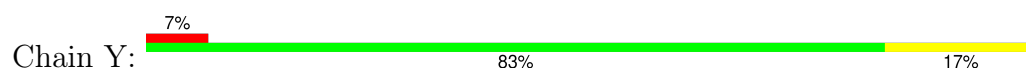
- Molecule 27: 50S ribosomal protein L28



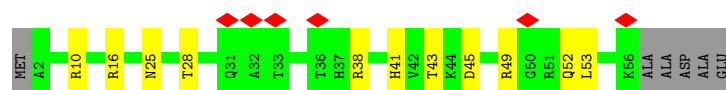
- Molecule 28: 50S ribosomal protein L29



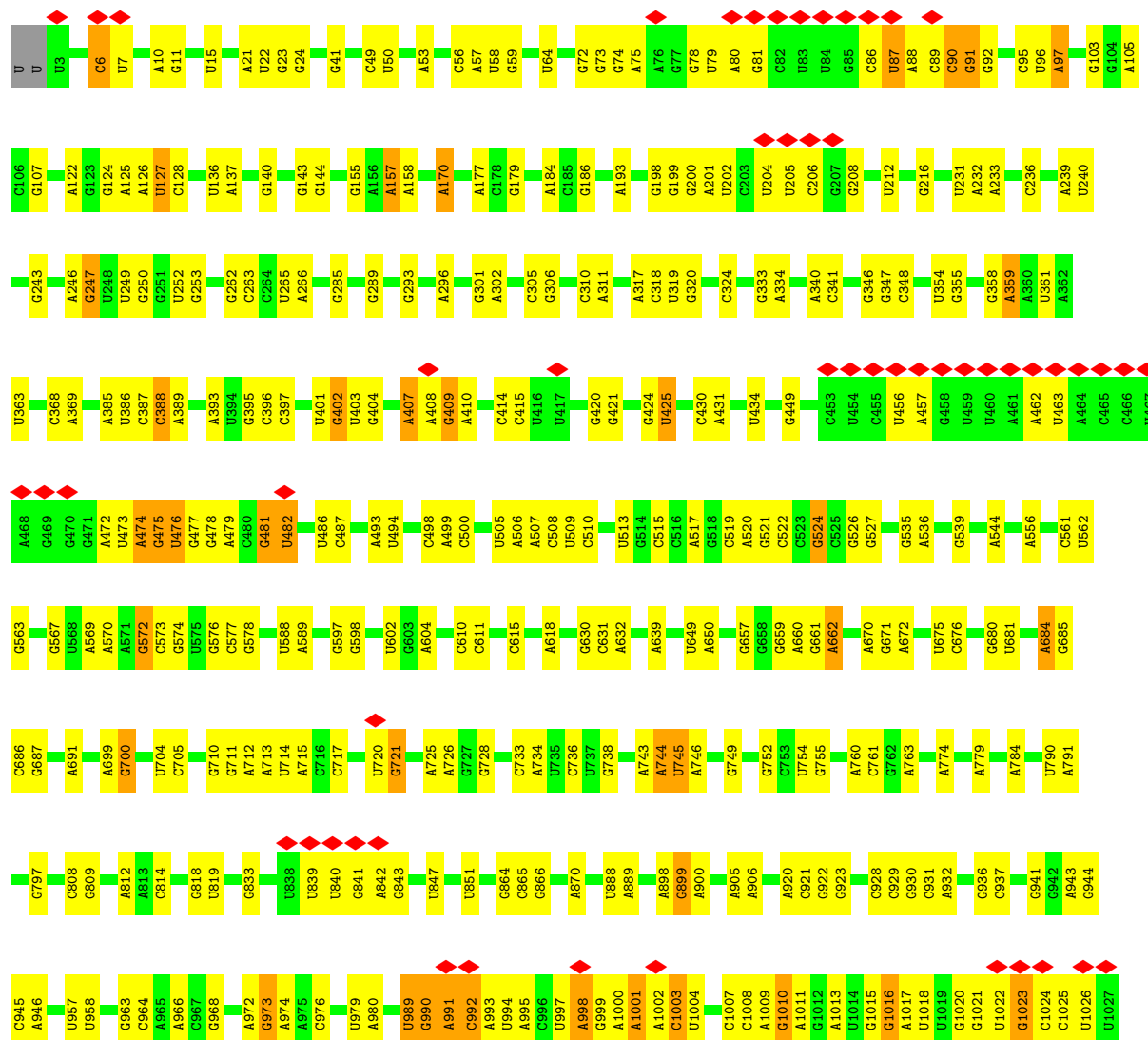
- Molecule 29: 50S ribosomal protein L30

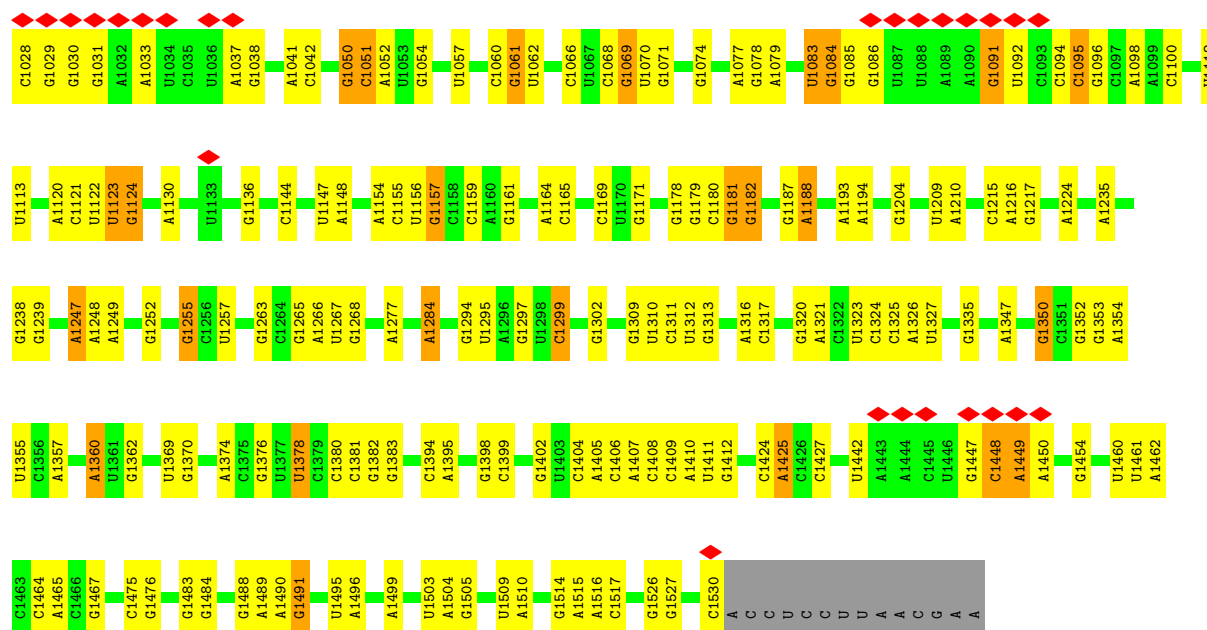


- Molecule 30: 50S ribosomal protein L32

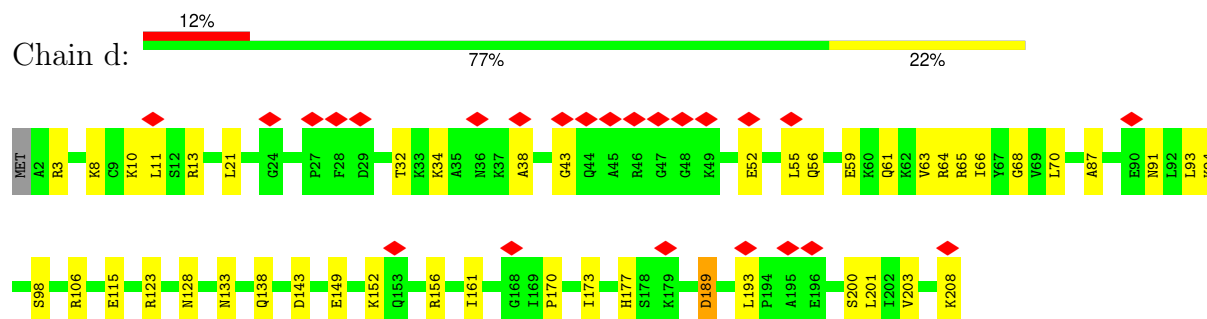


- Molecule 31: 16s Ribosomal RNA

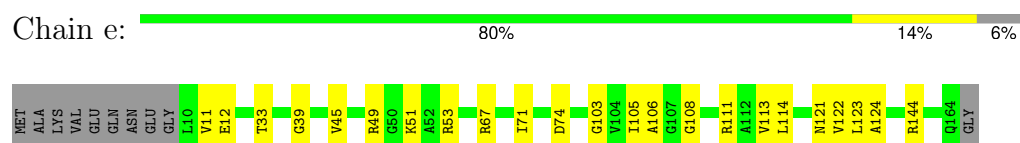




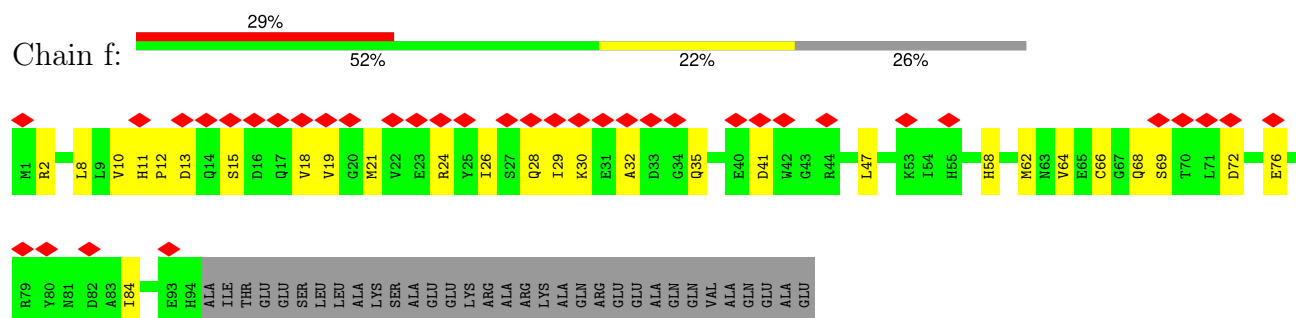
- Molecule 34: 30S ribosomal protein S4



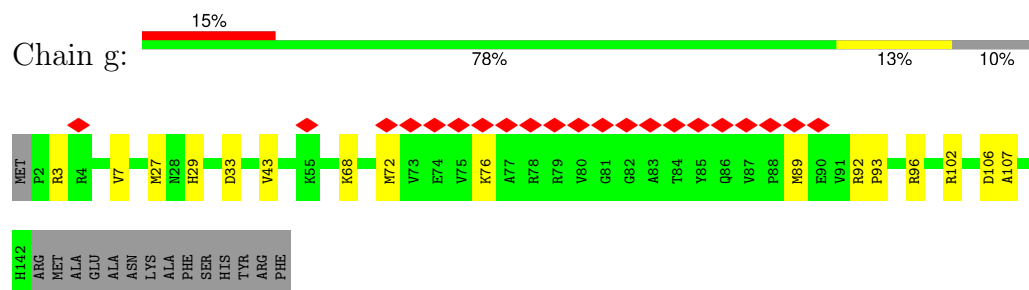
- Molecule 35: 30S ribosomal protein S5



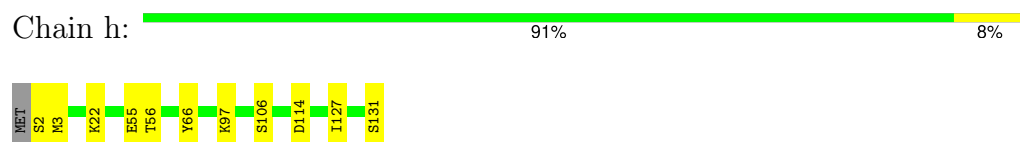
- Molecule 36: 30S ribosomal protein S6



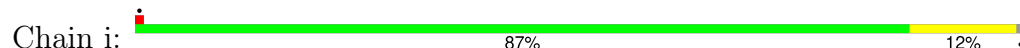
- Molecule 37: 30S ribosomal protein S7



- Molecule 38: 30S ribosomal protein S8

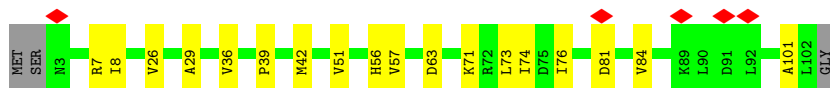
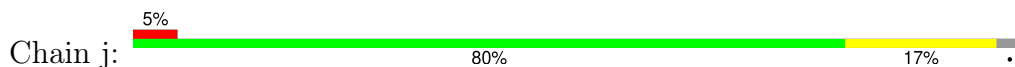


- Molecule 39: 30S ribosomal protein S9

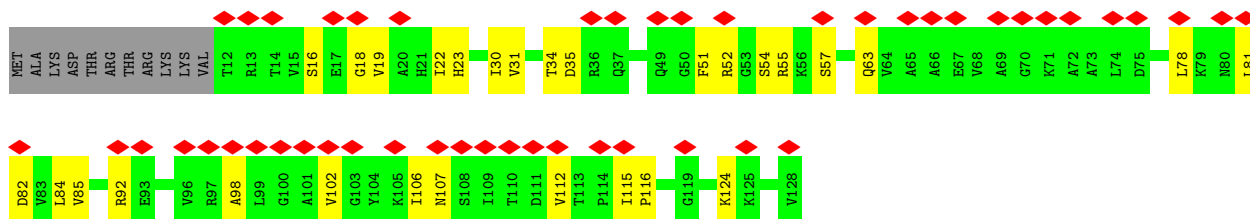




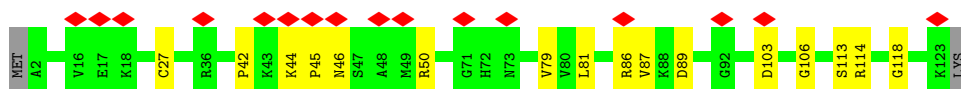
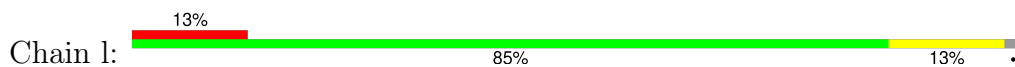
- Molecule 40: 30S ribosomal protein S10



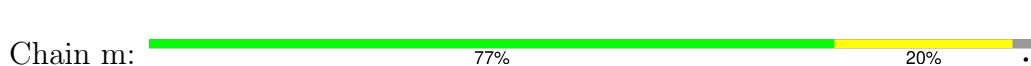
- Molecule 41: 30S ribosomal protein S11



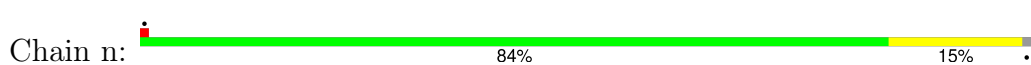
- Molecule 42: 30S ribosomal protein S12



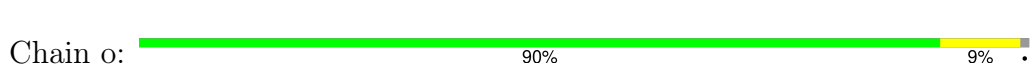
- Molecule 43: 30S ribosomal protein S13

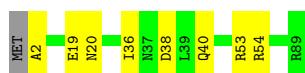


- Molecule 44: 30S ribosomal protein S14

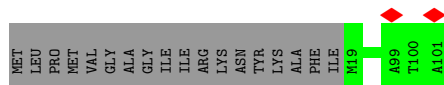
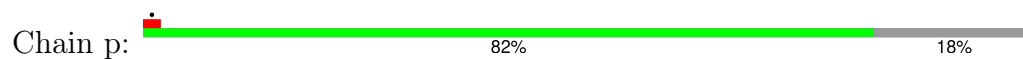


- Molecule 45: 30S ribosomal protein S15

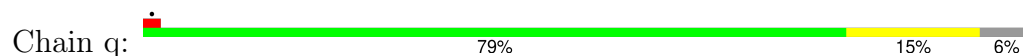




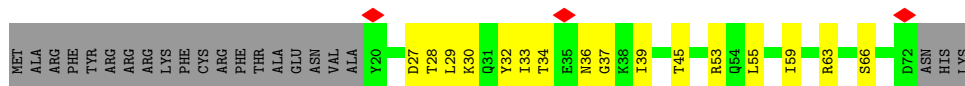
- Molecule 46: 30S ribosomal protein S16



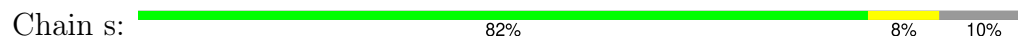
- Molecule 47: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S18



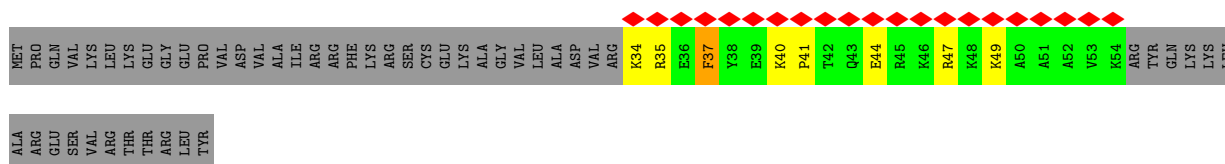
- Molecule 49: 30S ribosomal protein S19



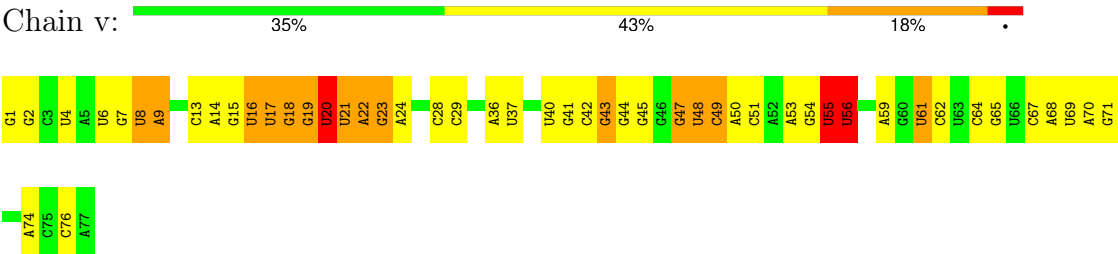
- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21



● Molecule 52: tRNA-met



● Molecule 53: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	90845	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	7.935	Depositor
Minimum map value	-2.795	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.117	Depositor
Recommended contour level	0.45	Depositor
Map size ($\text{\AA}$)	544.768, 544.768, 544.768	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.064, 1.064, 1.064	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: ZN, MG, 3TD, 6MZ, 4SU, 2MA, OMU, 2MG, PSU, OMG, MA6, 7MG, 4OC, 5MU, UR3, NA, H2U, 5MC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.11	0/434	0.32	0/573
2	1	0.15	0/367	0.37	0/481
3	2	0.17	0/515	0.55	0/678
4	3	0.16	0/296	0.47	0/389
5	AN1	0.10	0/69101	0.24	0/107780
6	B	0.09	0/2739	0.22	0/4266
7	C	0.14	0/2136	0.37	0/2869
8	D	0.13	0/1590	0.34	0/2142
9	E	0.12	0/1440	0.32	0/1944
10	F	0.18	0/1401	0.46	0/1877
11	G	0.14	0/1337	0.39	0/1807
12	H	0.18	0/461	0.52	0/616
13	I	0.13	0/1151	0.34	0/1551
14	J	0.12	0/956	0.35	0/1286
15	K	0.13	0/1097	0.38	0/1461
16	L	0.13	0/1104	0.34	0/1475
17	M	0.14	0/956	0.38	0/1282
18	N	0.14	0/865	0.37	0/1156
19	O	0.13	0/931	0.34	0/1249
20	P	0.14	0/947	0.33	0/1262
21	Q	0.14	0/818	0.39	0/1094
22	R	0.12	0/831	0.32	0/1113
23	S	0.12	0/708	0.32	0/947
24	T	0.15	0/753	0.43	0/1010
25	U	0.13	0/770	0.37	0/1036
26	V	0.12	0/606	0.33	0/810
27	W	0.12	0/642	0.34	0/856
28	X	0.12	0/499	0.33	0/662
29	Y	0.13	0/468	0.34	0/624
30	Z	0.12	0/462	0.35	0/615
31	sN1	0.09	0/36476	0.21	0/56895

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	b	0.18	0/1799	0.51	0/2429
33	c	0.12	0/1714	0.35	0/2304
34	d	0.12	0/1653	0.36	0/2213
35	e	0.13	0/1141	0.33	0/1537
36	f	0.15	0/808	0.45	0/1089
37	g	0.14	0/1127	0.36	0/1511
38	h	0.11	0/993	0.29	0/1331
39	i	0.13	0/1006	0.35	0/1346
40	j	0.15	0/811	0.39	0/1096
41	k	0.14	0/878	0.37	0/1189
42	l	0.16	0/958	0.44	0/1284
43	m	0.14	0/913	0.40	0/1226
44	n	0.13	0/803	0.35	0/1071
45	o	0.11	0/715	0.28	0/958
46	p	0.10	0/660	0.29	0/886
47	q	0.13	0/637	0.32	0/858
48	r	0.11	0/445	0.32	0/601
49	s	0.12	0/664	0.33	0/897
50	t	0.14	0/664	0.29	0/885
51	u	0.28	0/184	0.63	0/240
52	v	0.15	1/1739 (0.1%)	0.23	0/2709
53	w	0.11	0/72	0.30	0/110
All	All	0.11	1/153241 (0.0%)	0.27	0/229576

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
3	2	0	1
12	H	0	1
51	u	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	v	8	4SU	O3'-P	5.25	1.61	1.56

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	2	30	HIS	Peptide
12	H	47	PHE	Peptide
51	u	37	PHE	Peptide

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	0	427	0	462	3	0
2	1	363	0	401	5	0
3	2	509	0	566	9	0
4	3	295	0	327	5	0
5	AN1	62023	0	31193	502	0
6	B	2450	0	1241	34	0
7	C	2096	0	2157	33	0
8	D	1572	0	1610	22	0
9	E	1419	0	1464	17	0
10	F	1381	0	1433	54	0
11	G	1318	0	1373	26	0
12	H	458	0	480	10	0
13	I	1125	0	1148	13	0
14	J	946	0	1007	8	0
15	K	1089	0	1159	15	0
16	L	1087	0	1162	11	0
17	M	942	0	987	9	0
18	N	857	0	899	12	0
19	O	919	0	973	15	0
20	P	934	0	997	6	0
21	Q	807	0	842	12	0
22	R	826	0	894	6	0
23	S	702	0	756	6	0
24	T	749	0	797	8	0
25	U	760	0	783	13	0
26	V	598	0	600	3	0
27	W	632	0	667	5	0
28	X	498	0	537	4	0
29	Y	463	0	488	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Z	456	0	448	10	0
31	sN1	32782	0	16506	304	0
32	b	1769	0	1787	43	0
33	c	1690	0	1774	29	0
34	d	1631	0	1691	32	0
35	e	1129	0	1174	16	0
36	f	793	0	788	18	0
37	g	1111	0	1163	13	0
38	h	985	0	1047	6	0
39	i	995	0	1053	10	0
40	j	801	0	832	11	0
41	k	862	0	877	16	0
42	l	945	0	996	14	0
43	m	903	0	962	15	0
44	n	792	0	833	11	0
45	o	705	0	712	6	0
46	p	649	0	660	0	0
47	q	630	0	678	9	0
48	r	438	0	456	10	0
49	s	646	0	663	4	0
50	t	658	0	710	2	0
51	u	182	0	198	7	0
52	v	1636	0	832	36	0
53	w	65	0	33	0	0
54	3	1	0	0	0	0
55	AN1	49	0	0	0	0
55	sN1	44	0	0	0	0
56	AN1	1	0	0	0	0
57	AN1	319	0	0	2	0
57	B	4	0	0	0	0
57	C	5	0	0	0	0
57	D	3	0	0	0	0
57	E	3	0	0	0	0
57	K	3	0	0	0	0
57	O	1	0	0	0	0
57	P	3	0	0	0	0
57	Q	1	0	0	0	0
57	U	1	0	0	0	0
57	i	5	0	0	0	0
57	j	2	0	0	0	0
57	m	1	0	0	0	0
57	o	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	p	1	0	0	0	0
57	q	2	0	0	0	0
57	sN1	163	0	0	2	0
57	t	2	0	0	0	0
All	All	142113	0	94276	1362	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 6.

The worst 5 of 1362 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)
5:AN1:1462:G:H1	5:AN1:1520:A:N6	1.45	1.15
5:AN1:1463:A:N7	5:AN1:1544:G:O6	1.99	0.96
6:B:70:G:H21	6:B:101:A:H62	1.00	0.93
31:sN1:1157:G:N7	31:sN1:1179:G:N2	2.17	0.92
43:m:23:PHE:HB3	43:m:66:GLU:HG2	1.53	0.90

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	0	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
2	1	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
3	2	61/64 (95%)	58 (95%)	1 (2%)	2 (3%)	3	10
4	3	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
7	C	268/274 (98%)	260 (97%)	8 (3%)	0	100	100
8	D	209/212 (99%)	204 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	E	184/200 (92%)	184 (100%)	0	0	100	100
10	F	173/178 (97%)	151 (87%)	21 (12%)	1 (1%)	21	48
11	G	172/177 (97%)	167 (97%)	5 (3%)	0	100	100
12	H	58/148 (39%)	56 (97%)	1 (2%)	1 (2%)	7	23
13	I	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
14	J	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
15	K	144/146 (99%)	140 (97%)	4 (3%)	0	100	100
16	L	135/137 (98%)	133 (98%)	2 (2%)	0	100	100
17	M	117/125 (94%)	117 (100%)	0	0	100	100
18	N	112/116 (97%)	111 (99%)	1 (1%)	0	100	100
19	O	115/122 (94%)	112 (97%)	3 (3%)	0	100	100
20	P	115/119 (97%)	115 (100%)	0	0	100	100
21	Q	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
22	R	107/109 (98%)	107 (100%)	0	0	100	100
23	S	88/106 (83%)	85 (97%)	3 (3%)	0	100	100
24	T	98/105 (93%)	94 (96%)	4 (4%)	0	100	100
25	U	95/98 (97%)	93 (98%)	2 (2%)	0	100	100
26	V	78/85 (92%)	78 (100%)	0	0	100	100
27	W	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
28	X	60/65 (92%)	60 (100%)	0	0	100	100
29	Y	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
30	Z	53/61 (87%)	52 (98%)	1 (2%)	0	100	100
32	b	223/250 (89%)	207 (93%)	16 (7%)	0	100	100
33	c	213/250 (85%)	207 (97%)	6 (3%)	0	100	100
34	d	205/208 (99%)	200 (98%)	5 (2%)	0	100	100
35	e	153/165 (93%)	152 (99%)	1 (1%)	0	100	100
36	f	92/127 (72%)	89 (97%)	3 (3%)	0	100	100
37	g	139/156 (89%)	138 (99%)	1 (1%)	0	100	100
38	h	128/131 (98%)	124 (97%)	4 (3%)	0	100	100
39	i	125/128 (98%)	123 (98%)	2 (2%)	0	100	100
40	j	98/103 (95%)	94 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	k	115/128 (90%)	113 (98%)	2 (2%)	0	100	100
42	l	120/124 (97%)	114 (95%)	6 (5%)	0	100	100
43	m	113/118 (96%)	106 (94%)	7 (6%)	0	100	100
44	n	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
45	o	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
46	p	81/101 (80%)	80 (99%)	1 (1%)	0	100	100
47	q	78/85 (92%)	78 (100%)	0	0	100	100
48	r	51/75 (68%)	51 (100%)	0	0	100	100
49	s	80/91 (88%)	80 (100%)	0	0	100	100
50	t	83/88 (94%)	83 (100%)	0	0	100	100
51	u	19/71 (27%)	16 (84%)	3 (16%)	0	100	100
All	All	5361/5872 (91%)	5209 (97%)	148 (3%)	4 (0%)	49	75

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	31	ILE
3	2	32	LEU
10	F	139	PRO
12	H	48	GLU

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	0	47/47 (100%)	47 (100%)	0	100	100
2	1	36/36 (100%)	36 (100%)	0	100	100
3	2	52/53 (98%)	52 (100%)	0	100	100
4	3	33/33 (100%)	33 (100%)	0	100	100
7	C	216/220 (98%)	216 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	D	166/167 (99%)	166 (100%)	0	100	100
9	E	144/155 (93%)	144 (100%)	0	100	100
10	F	145/147 (99%)	145 (100%)	0	100	100
11	G	139/142 (98%)	139 (100%)	0	100	100
12	H	45/112 (40%)	45 (100%)	0	100	100
13	I	118/118 (100%)	118 (100%)	0	100	100
14	J	103/103 (100%)	103 (100%)	0	100	100
15	K	108/108 (100%)	108 (100%)	0	100	100
16	L	113/113 (100%)	113 (100%)	0	100	100
17	M	96/101 (95%)	96 (100%)	0	100	100
18	N	83/85 (98%)	83 (100%)	0	100	100
19	O	99/102 (97%)	99 (100%)	0	100	100
20	P	85/86 (99%)	85 (100%)	0	100	100
21	Q	84/84 (100%)	84 (100%)	0	100	100
22	R	88/88 (100%)	88 (100%)	0	100	100
23	S	76/87 (87%)	76 (100%)	0	100	100
24	T	82/85 (96%)	82 (100%)	0	100	100
25	U	79/80 (99%)	79 (100%)	0	100	100
26	V	60/64 (94%)	60 (100%)	0	100	100
27	W	69/70 (99%)	69 (100%)	0	100	100
28	X	54/56 (96%)	54 (100%)	0	100	100
29	Y	54/54 (100%)	54 (100%)	0	100	100
30	Z	47/50 (94%)	47 (100%)	0	100	100
32	b	185/200 (92%)	184 (100%)	1 (0%)	81	93
33	c	175/198 (88%)	175 (100%)	0	100	100
34	d	170/171 (99%)	169 (99%)	1 (1%)	78	92
35	e	113/120 (94%)	113 (100%)	0	100	100
36	f	86/111 (78%)	86 (100%)	0	100	100
37	g	116/128 (91%)	116 (100%)	0	100	100
38	h	108/109 (99%)	108 (100%)	0	100	100
39	i	99/100 (99%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	j	89/91 (98%)	89 (100%)	0	100	100
41	k	88/98 (90%)	88 (100%)	0	100	100
42	l	104/106 (98%)	104 (100%)	0	100	100
43	m	95/98 (97%)	95 (100%)	0	100	100
44	n	81/82 (99%)	80 (99%)	1 (1%)	63	86
45	o	71/72 (99%)	71 (100%)	0	100	100
46	p	63/77 (82%)	63 (100%)	0	100	100
47	q	72/76 (95%)	72 (100%)	0	100	100
48	r	47/66 (71%)	47 (100%)	0	100	100
49	s	70/78 (90%)	70 (100%)	0	100	100
50	t	65/67 (97%)	65 (100%)	0	100	100
51	u	18/62 (29%)	18 (100%)	0	100	100
All	All	4436/4756 (93%)	4433 (100%)	3 (0%)	87	96

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	b	144	GLU
34	d	189	ASP
44	n	27	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 89 such sidechains are listed below:

Mol	Chain	Res	Type
35	e	121	ASN
40	j	56	HIS
36	f	17	GLN
37	g	142	HIS
41	k	117	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	sN1	1527/1544 (98%)	204 (13%)	0
5	AN1	2891/2918 (99%)	496 (17%)	10 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	v	76/77 (98%)	28 (36%)	0
53	w	2/3 (66%)	1 (50%)	0
6	B	114/115 (99%)	21 (18%)	1 (0%)
All	All	4610/4657 (98%)	750 (16%)	11 (0%)

5 of 750 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	AN1	21	A
5	AN1	22	G
5	AN1	34	G
5	AN1	41	U
5	AN1	50	G

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	AN1	1538	A
5	AN1	2170	C
6	B	108	C
5	AN1	2379	G
5	AN1	782	G

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

28 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
31	PSU	sN1	513	31	18,21,22	1.18	1 (5%)	21,30,33	1.65	4 (19%)
31	MA6	sN1	1516	31	23,26,27	1.37	4 (17%)	33,38,41	3.41	12 (36%)
52	5MU	v	55	52	19,22,23	5.05	7 (36%)	27,32,35	3.67	9 (33%)
31	2MG	sN1	1204	31	23,26,27	2.91	8 (34%)	33,38,41	2.19	11 (33%)
5	OMG	AN1	2247	5	23,26,27	2.39	8 (34%)	32,38,41	1.91	8 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
31	UR3	sN1	1495	31	19,22,23	2.95	6 (31%)	26,32,35	1.60	3 (11%)
31	2MG	sN1	963	31	23,26,27	2.90	8 (34%)	33,38,41	2.22	11 (33%)
5	PSU	AN1	2601	5	18,21,22	1.08	1 (5%)	21,30,33	1.91	4 (19%)
31	7MG	sN1	524	31	23,26,27	3.64	11 (47%)	27,39,42	2.19	9 (33%)
5	OMU	AN1	2548	5	19,22,23	3.10	8 (42%)	25,31,34	1.80	4 (16%)
5	PSU	AN1	952	5	18,21,22	1.10	1 (5%)	21,30,33	1.92	4 (19%)
31	4OC	sN1	1399	31	20,23,24	3.23	8 (40%)	25,32,35	0.94	1 (4%)
52	PSU	v	56	52	18,21,22	1.11	1 (5%)	21,30,33	1.73	5 (23%)
5	2MG	AN1	2441	5	23,26,27	2.88	8 (34%)	33,38,41	2.19	11 (33%)
5	PSU	AN1	2500	5	18,21,22	1.12	1 (5%)	21,30,33	1.91	4 (19%)
5	3TD	AN1	1911	5	19,22,23	4.30	7 (36%)	23,32,35	1.83	3 (13%)
52	4SU	v	8	52	18,21,22	4.47	8 (44%)	25,30,33	2.27	5 (20%)
31	MA6	sN1	1515	31	23,26,27	1.37	4 (17%)	33,38,41	3.29	12 (36%)
5	6MZ	AN1	2026	5	22,25,26	2.49	4 (18%)	29,36,39	3.40	11 (37%)
5	PSU	AN1	2576	5	18,21,22	1.10	1 (5%)	21,30,33	1.94	6 (28%)
5	PSU	AN1	2453	5	18,21,22	1.11	1 (5%)	21,30,33	1.95	6 (28%)
5	PSU	AN1	1913	5	18,21,22	1.14	1 (5%)	21,30,33	1.80	5 (23%)
5	2MA	AN1	2499	5,55	22,25,26	3.98	9 (40%)	32,37,40	2.77	11 (34%)
5	7MG	AN1	2065	5	23,26,27	3.56	10 (43%)	27,39,42	2.17	9 (33%)
52	H2U	v	20	52	18,21,22	3.18	4 (22%)	19,30,33	1.37	4 (21%)
5	PSU	AN1	1907	5	18,21,22	1.13	1 (5%)	21,30,33	1.91	5 (23%)
31	5MC	sN1	964	31	19,22,23	3.93	8 (42%)	26,32,35	0.99	2 (7%)
5	5MU	AN1	1935	5	19,22,23	4.99	7 (36%)	27,32,35	3.61	9 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	PSU	sN1	513	31	-	0/7/25/26	0/2/2/2
31	MA6	sN1	1516	31	-	4/11/29/30	0/3/3/3
52	5MU	v	55	52	-	6/7/25/26	0/2/2/2
31	2MG	sN1	1204	31	-	0/9/27/28	0/3/3/3
5	OMG	AN1	2247	5	-	0/9/27/28	0/3/3/3
31	UR3	sN1	1495	31	-	1/7/25/26	0/2/2/2
31	2MG	sN1	963	31	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PSU	AN1	2601	5	-	0/7/25/26	0/2/2/2
31	7MG	sN1	524	31	-	3/7/37/38	0/3/3/3
5	OMU	AN1	2548	5	-	2/9/27/28	0/2/2/2
5	PSU	AN1	952	5	-	0/7/25/26	0/2/2/2
31	4OC	sN1	1399	31	-	2/9/29/30	0/2/2/2
52	PSU	v	56	52	-	0/7/25/26	0/2/2/2
5	2MG	AN1	2441	5	-	1/9/27/28	0/3/3/3
5	PSU	AN1	2500	5	-	0/7/25/26	0/2/2/2
5	3TD	AN1	1911	5	-	5/7/25/26	0/2/2/2
52	4SU	v	8	52	-	4/7/25/26	0/2/2/2
31	MA6	sN1	1515	31	-	3/11/29/30	0/3/3/3
5	6MZ	AN1	2026	5	-	2/9/27/28	0/3/3/3
5	PSU	AN1	2576	5	-	0/7/25/26	0/2/2/2
5	PSU	AN1	2453	5	-	0/7/25/26	0/2/2/2
5	PSU	AN1	1913	5	-	3/7/25/26	0/2/2/2
5	2MA	AN1	2499	5,55	-	2/7/25/26	0/3/3/3
5	7MG	AN1	2065	5	-	3/7/37/38	0/3/3/3
52	H2U	v	20	52	-	2/7/38/39	0/2/2/2
5	PSU	AN1	1907	5	-	1/7/25/26	0/2/2/2
31	5MC	sN1	964	31	-	0/7/25/26	0/2/2/2
5	5MU	AN1	1935	5	-	0/7/25/26	0/2/2/2

The worst 5 of 146 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AN1	1911	3TD	C6-C5	12.79	1.49	1.35
5	AN1	2499	2MA	C4-N3	12.22	1.50	1.34
52	v	55	5MU	C2-N1	11.72	1.56	1.38
5	AN1	1935	5MU	C2-N1	11.61	1.56	1.38
52	v	55	5MU	C6-N1	11.17	1.57	1.38

The worst 5 of 188 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	sN1	1516	MA6	N1-C6-N6	-12.78	101.28	116.86
52	v	55	5MU	C5-C4-N3	12.26	125.98	115.32
31	sN1	1515	MA6	N1-C6-N6	-12.04	102.19	116.86
5	AN1	1935	5MU	C5-C4-N3	11.91	125.67	115.32
5	AN1	2026	6MZ	C4-N9-C1'	-9.90	103.48	126.63

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
31	sN1	1515	MA6	C5-C6-N6-C9
31	sN1	1516	MA6	C5-C6-N6-C10
31	sN1	1516	MA6	N1-C6-N6-C10
5	AN1	1911	3TD	O4'-C4'-C5'-O5'
5	AN1	1913	PSU	O4'-C1'-C5-C4

There are no ring outliers.

6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
52	v	55	5MU	2	0
52	v	56	PSU	2	0
5	AN1	1911	3TD	2	0
52	v	8	4SU	2	0
5	AN1	1913	PSU	1	0
52	v	20	H2U	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 95 ligands modelled in this entry, 95 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

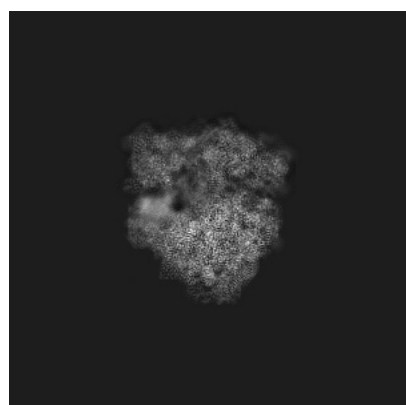
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21031. These allow visual inspection of the internal detail of the map and identification of artifacts.

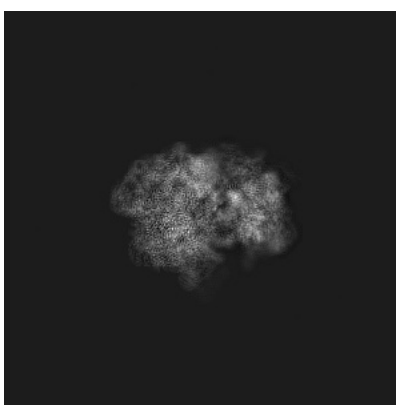
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

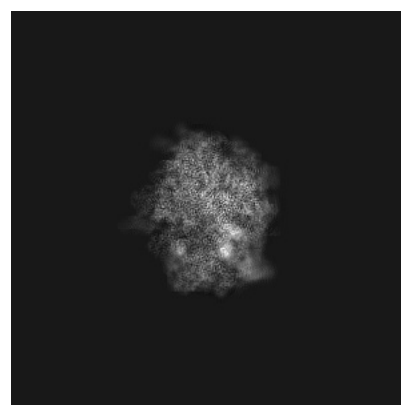
6.1.1 Primary map



X



Y



Z

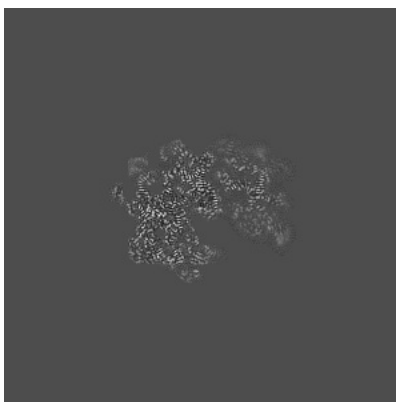
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

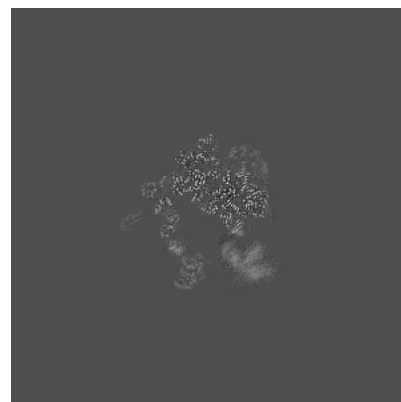
6.2.1 Primary map



X Index: 256



Y Index: 256



Z Index: 256

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: 256



Y Index: 270

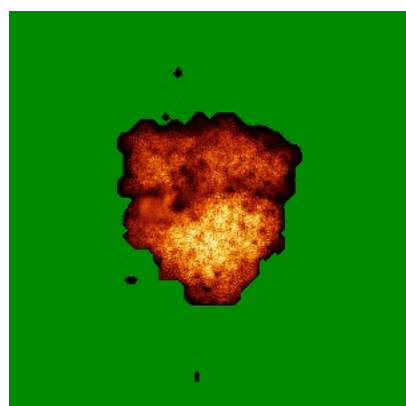


Z Index: 219

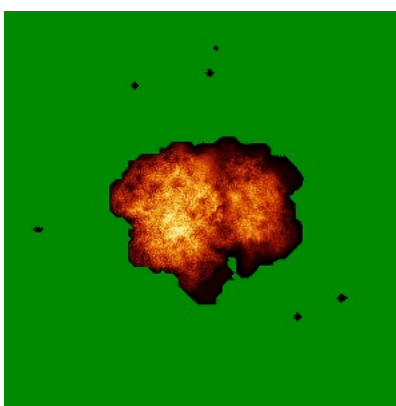
The images above show the largest variance slices of the map in three orthogonal directions.

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

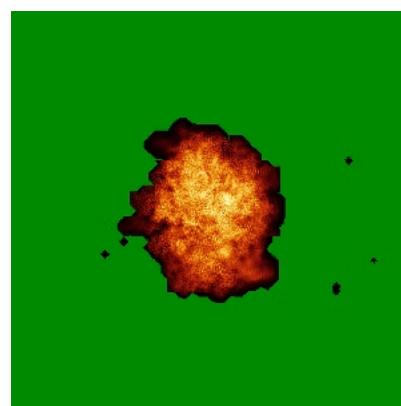
6.4.1 Primary map



X



Y



Z

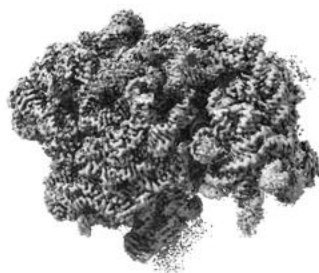
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

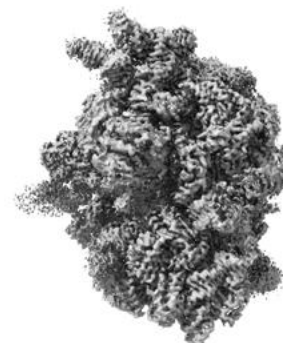
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

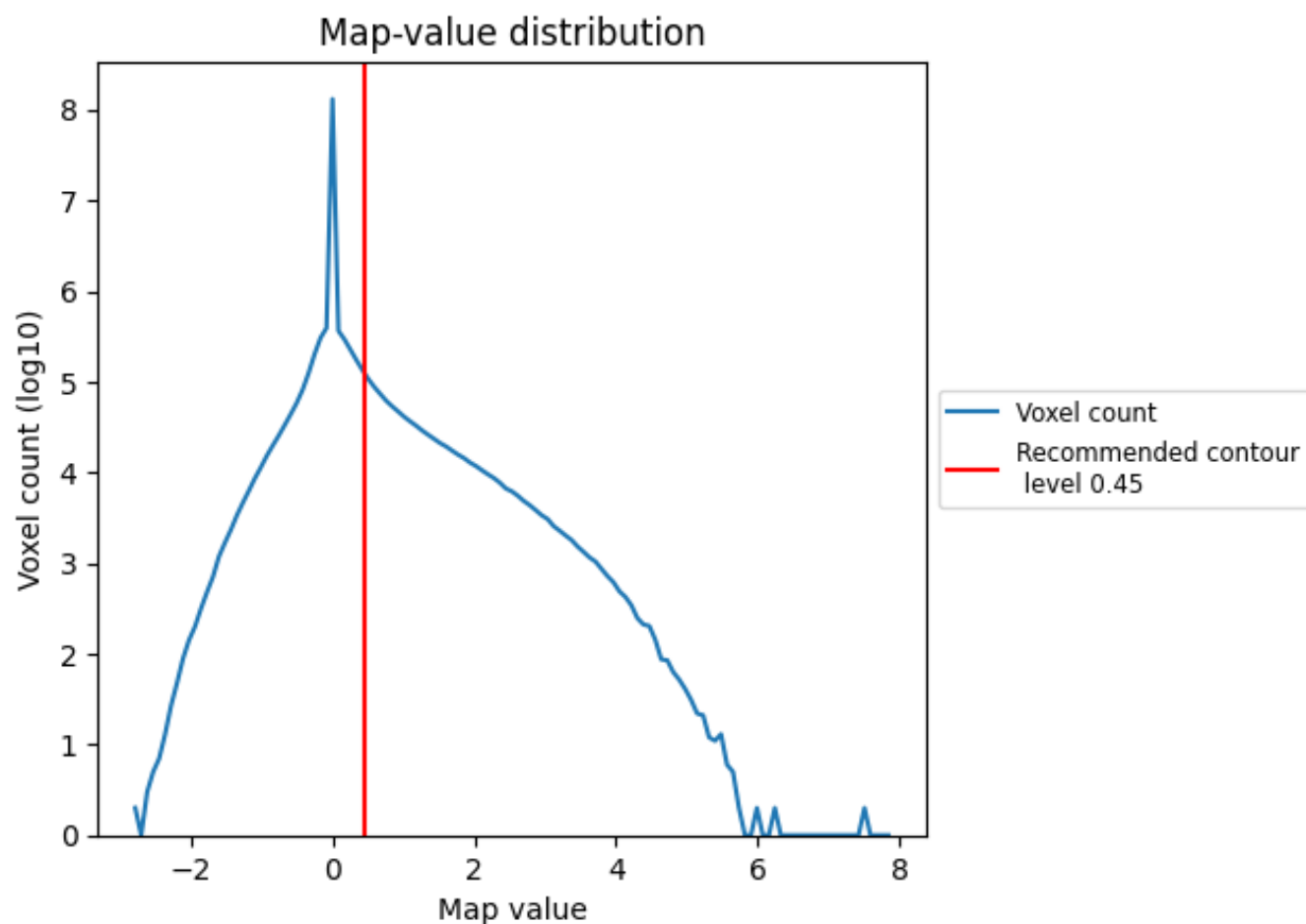
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

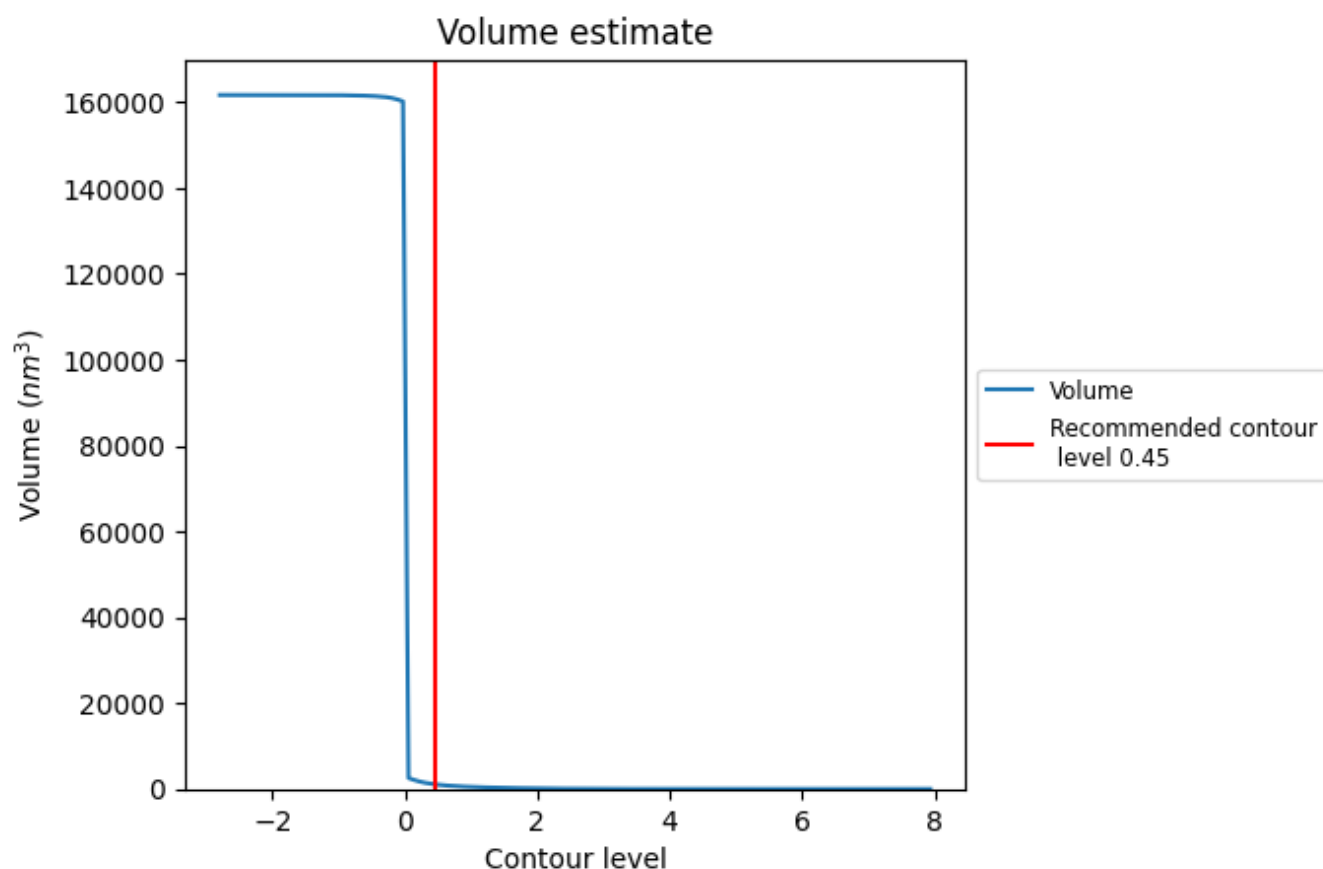
This section contains the results of statistical analysis of the map.

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.

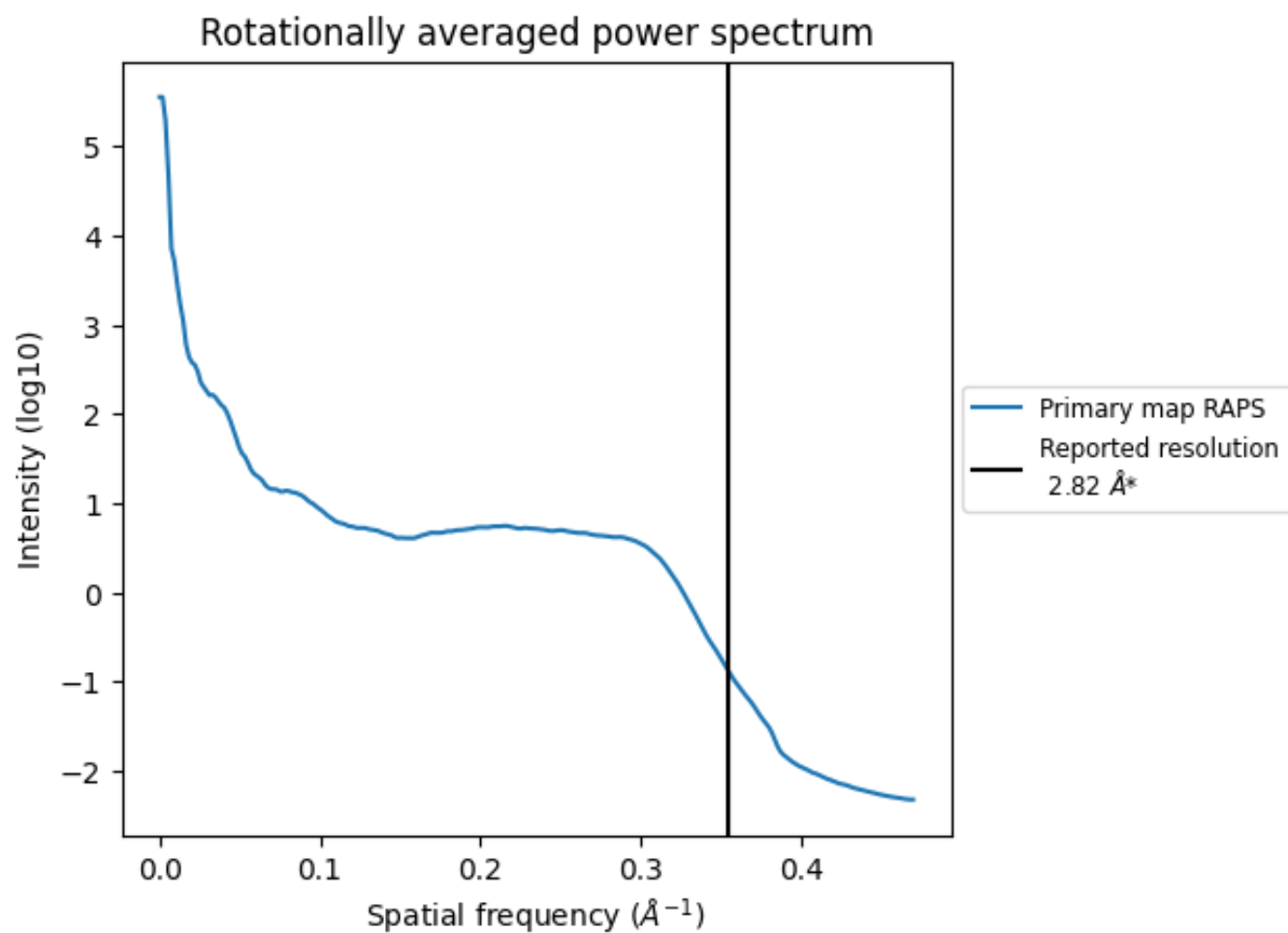
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1088 nm^3 ; this corresponds to an approximate mass of 983 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 0.355 Å⁻¹

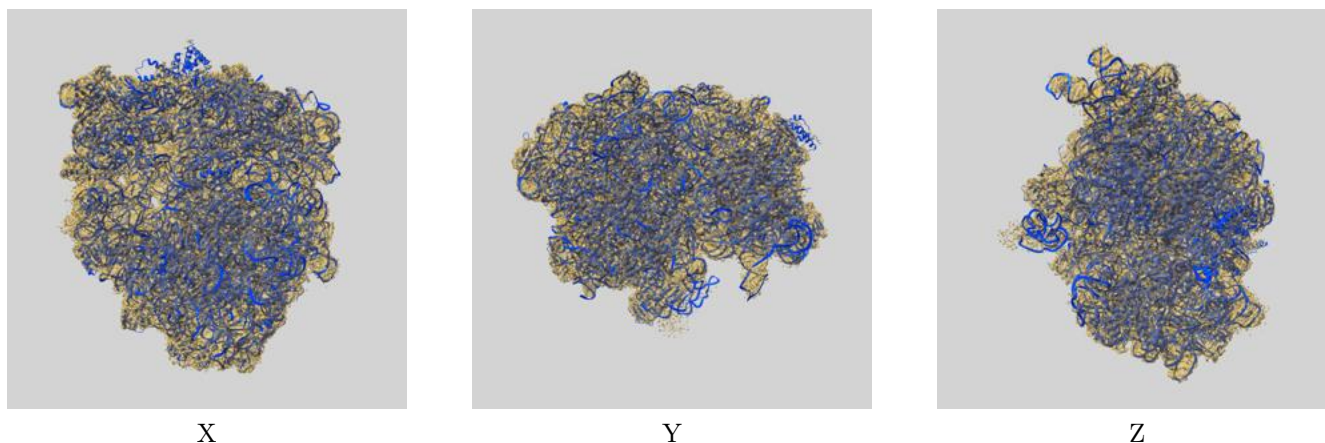
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

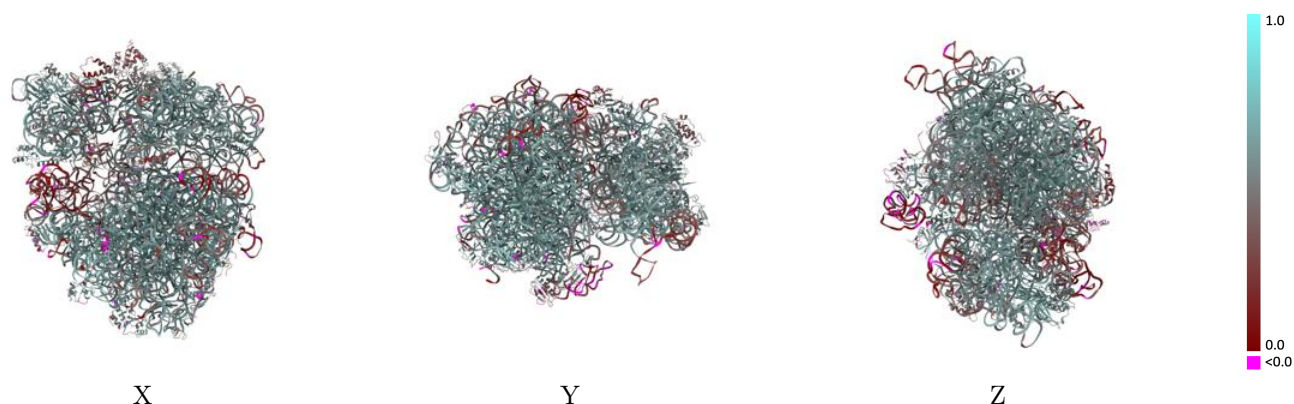
This section contains information regarding the fit between EMDB map EMD-21031 and PDB model 6V3A. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



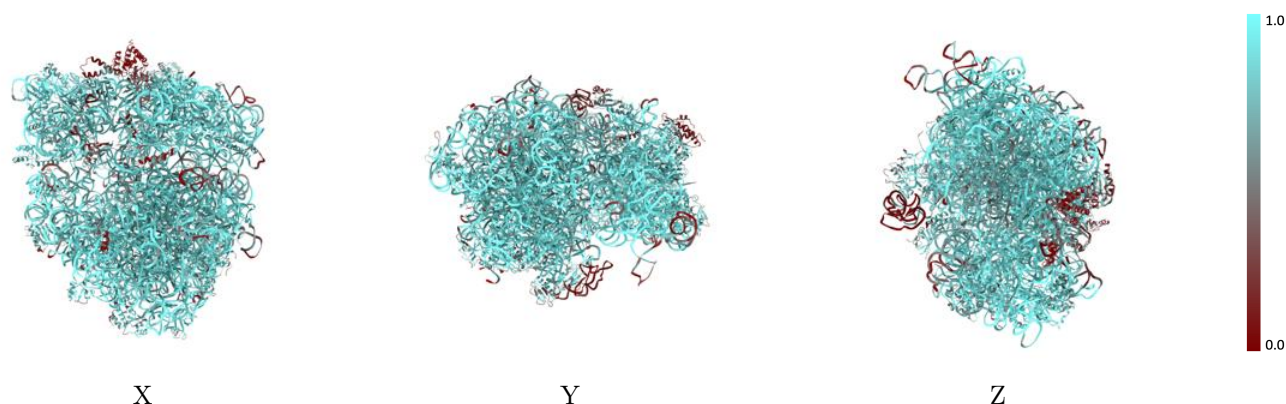
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



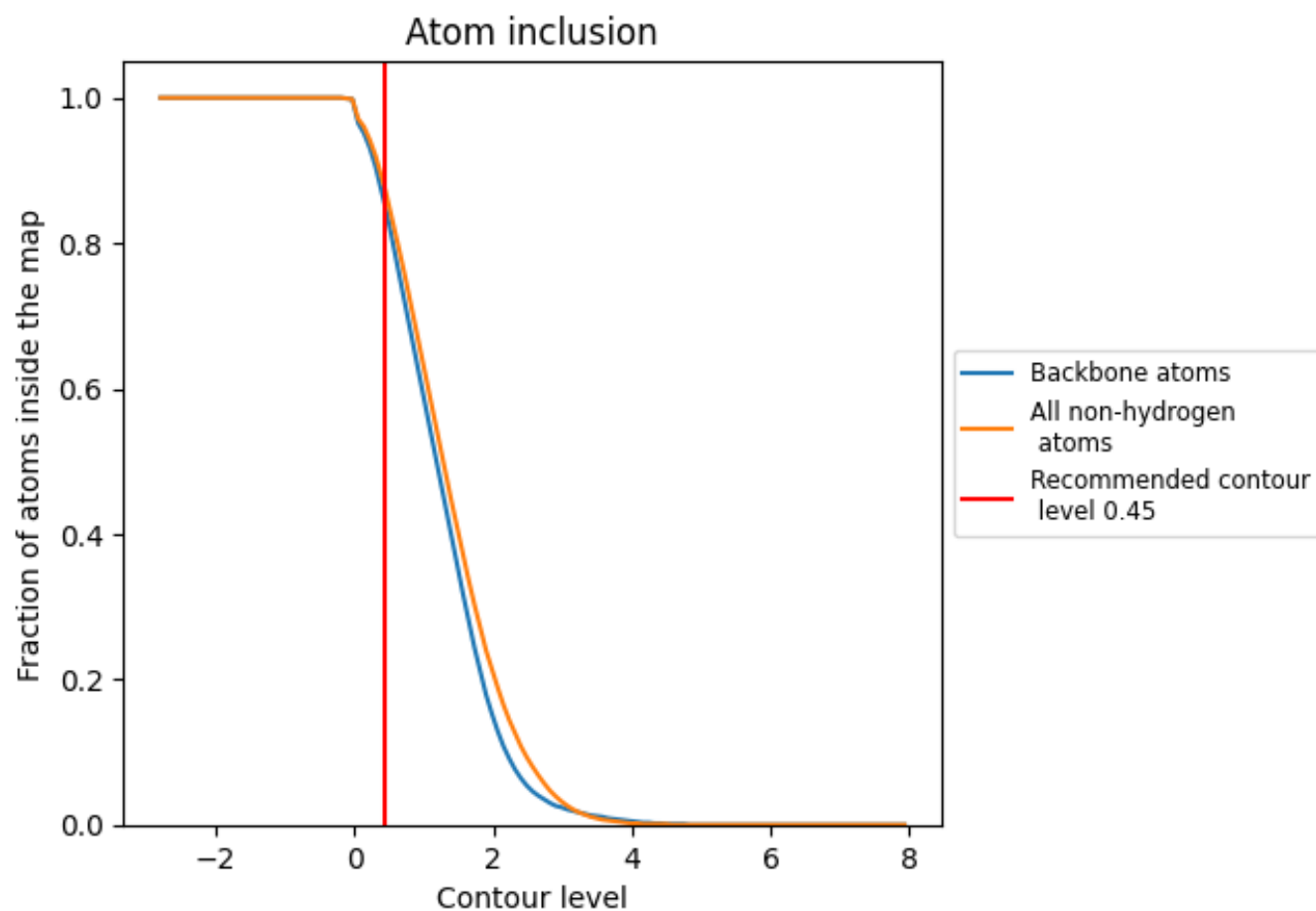
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 87% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8720	 0.5310
0	 0.8200	 0.5320
1	 0.9590	 0.6400
2	 0.9550	 0.6160
3	 0.8850	 0.5580
AN1	 0.9080	 0.5450
B	 0.9050	 0.4910
C	 0.8990	 0.5900
D	 0.8730	 0.5680
E	 0.8690	 0.5660
F	 0.5720	 0.3150
G	 0.6860	 0.4070
H	 0.3760	 0.2790
I	 0.8650	 0.5610
J	 0.9000	 0.5900
K	 0.8800	 0.5680
L	 0.8900	 0.5740
M	 0.9690	 0.6260
N	 0.8360	 0.5020
O	 0.8430	 0.5540
P	 0.9230	 0.5980
Q	 0.8780	 0.5650
R	 0.8490	 0.5590
S	 0.8570	 0.5430
T	 0.7830	 0.4870
U	 0.7900	 0.5080
V	 0.8820	 0.5960
W	 0.8860	 0.5860
X	 0.7380	 0.4540
Y	 0.8260	 0.5280
Z	 0.8320	 0.5500
b	 0.2030	 0.3490
c	 0.8660	 0.5540
d	 0.6950	 0.4610
e	 0.8840	 0.5550



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Chain	Atom inclusion	Q-score
f	 0.4880	 0.3840
g	 0.6410	 0.4680
h	 0.9140	 0.5900
i	 0.9180	 0.5950
j	 0.8240	 0.5440
k	 0.5050	 0.3910
l	 0.6920	 0.5210
m	 0.8880	 0.5580
n	 0.8950	 0.5770
o	 0.8800	 0.5490
p	 0.9250	 0.5870
q	 0.8560	 0.5650
r	 0.7050	 0.4950
s	 0.9440	 0.5980
sN1	 0.9040	 0.5300
t	 0.8990	 0.5640
u	 0.0910	 0.2790
v	 0.9440	 0.3080
w	 0.9540	 0.2530