



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 08:19 AM UTC

PDB ID : 6WDG / pdb_00006wdg
EMDB ID : EMD-21635
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure VI-B)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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) : 2.49

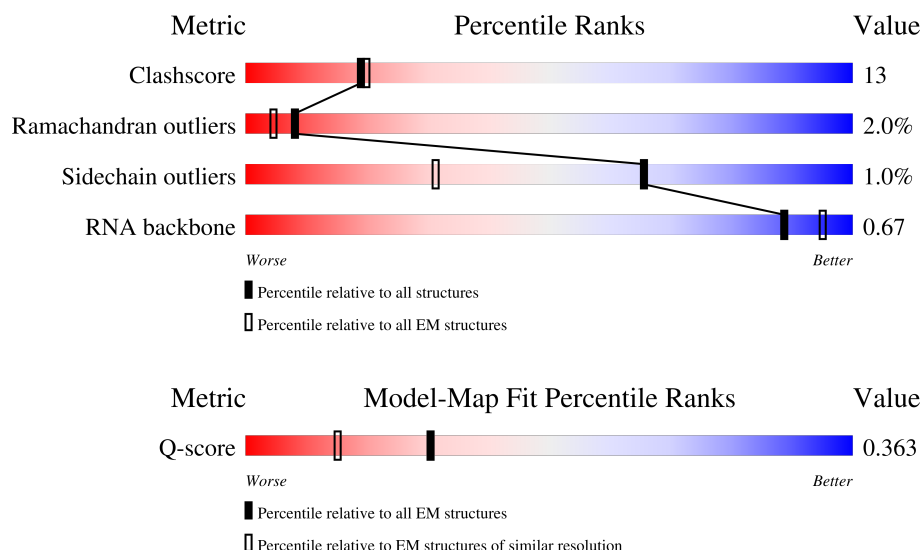
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.



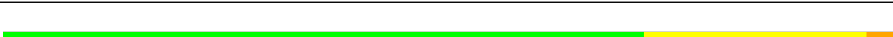
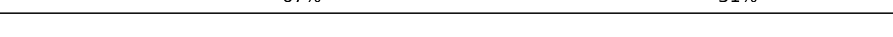
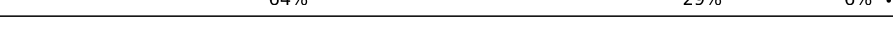
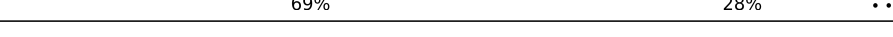
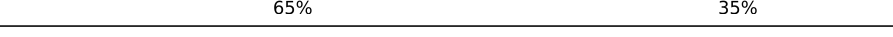
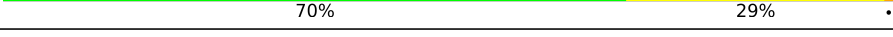
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	
2	c	209	
3	d	201	

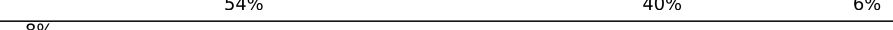
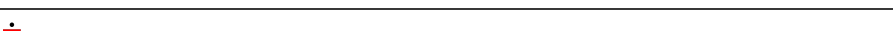
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

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Mol	Chain	Length	Quality of chain
29	E	64	
30	F	38	
31	G	225	
32	H	206	
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	223	
52	3	1539	
53	1	2903	

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Mol	Chain	Length	Quality of chain
54	2	120	58%37%5%
55	5	77	40%38%21%
56	4	18	6%72%22%6%
57	7	76	54%36%11%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 148582 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
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

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

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

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

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

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

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

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

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

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

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

- 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
			917	574	179	163	1	0

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

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

- 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
			816	516	153	145	2	0

- 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
			857	532	166	156	3	0

- 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
			739	466	139	132	2	0

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

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

- 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 L32.

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

- Molecule 27 is a protein called 50S ribosomal protein L33.

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

- Molecule 28 is a protein called 50S ribosomal protein L34.

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

- Molecule 29 is a protein called 50S ribosomal protein L35.

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

- Molecule 30 is a protein called 50S ribosomal protein L36.

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

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 32 is a protein called 30S ribosomal protein S3.

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

- Molecule 33 is a protein called 30S ribosomal protein S4.

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

- Molecule 34 is a protein called 30S ribosomal protein S5.

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

- Molecule 35 is a protein called 30S ribosomal protein S6.

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

- Molecule 36 is a protein called 30S ribosomal protein S7.

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

- Molecule 37 is a protein called 30S ribosomal protein S8.

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

- Molecule 38 is a protein called 30S ribosomal protein S9.

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

- Molecule 39 is a protein called 30S ribosomal protein S10.

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

- Molecule 40 is a protein called 30S ribosomal protein S11.

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

- Molecule 41 is a protein called 30S ribosomal protein S12.

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

- Molecule 42 is a protein called 30S ribosomal protein S13.

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

- Molecule 43 is a protein called 30S ribosomal protein S14.

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

- Molecule 44 is a protein called 30S ribosomal protein S15.

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

- Molecule 45 is a protein called 30S ribosomal protein S16.

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

- Molecule 46 is a protein called 30S ribosomal protein S17.

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

- Molecule 47 is a protein called 30S ribosomal protein S18.

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

- Molecule 48 is a protein called 30S ribosomal protein S19.

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

- Molecule 49 is a protein called 30S ribosomal protein S20.

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

- Molecule 50 is a protein called 30S ribosomal protein S21.

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

- Molecule 51 is a protein called 50S ribosomal protein L1.

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

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	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 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 55 is a RNA chain called tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

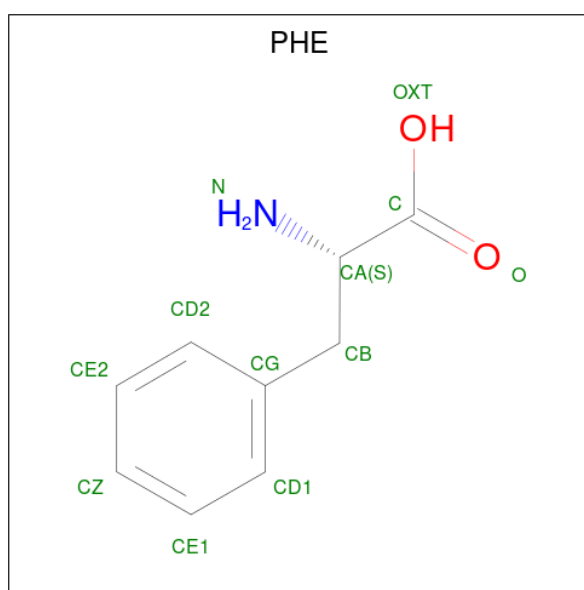
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 57 is a RNA chain called tRNA^PPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 58 is PHENYLALANINE (CCD ID: PHE) (formula: C₉H₁₁NO₂).



Mol	Chain	Residues	Atoms				AltConf
58	7	1	Total	C	N	O	0
			11	9	1	1	

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).

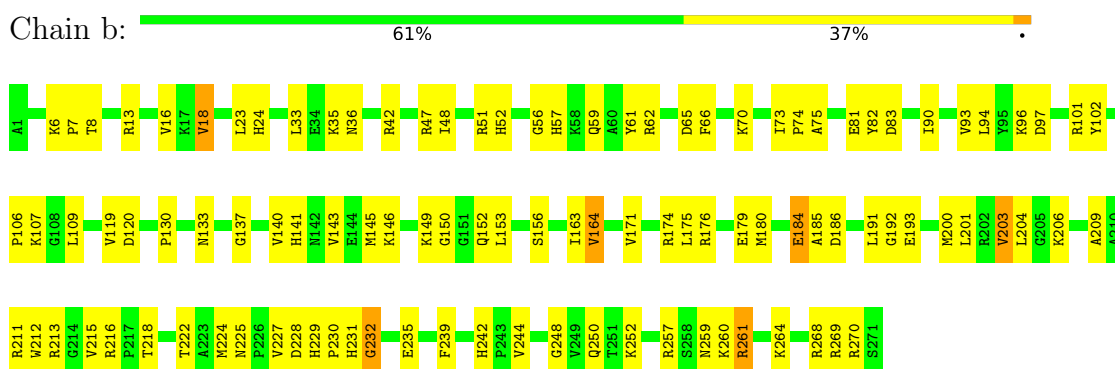


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
59	7	1	10	6	1	2	1	0

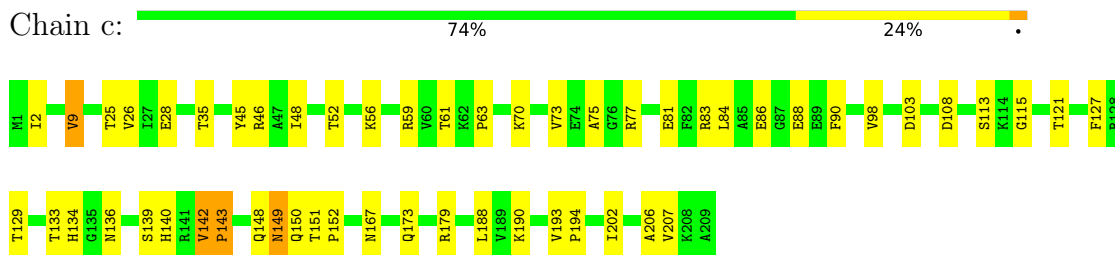
3 Residue-property plots [i](#)

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.

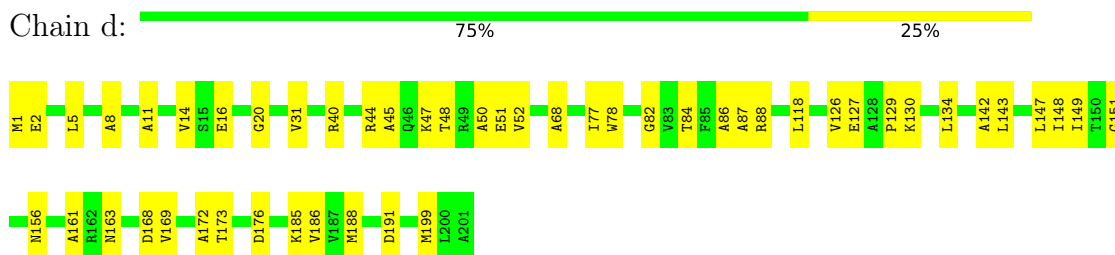
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

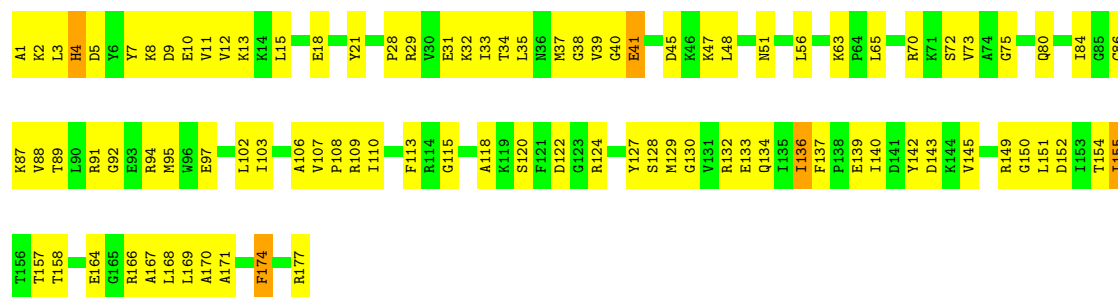


- Molecule 3: 50S ribosomal protein L4

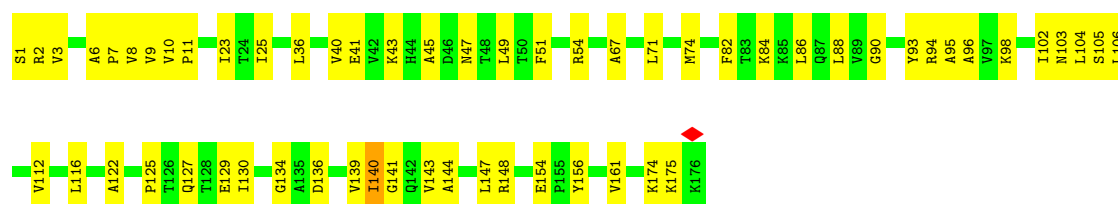


- Molecule 4: 50S ribosomal protein L5

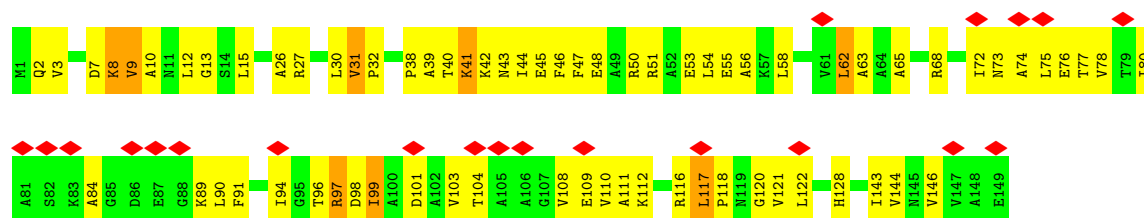




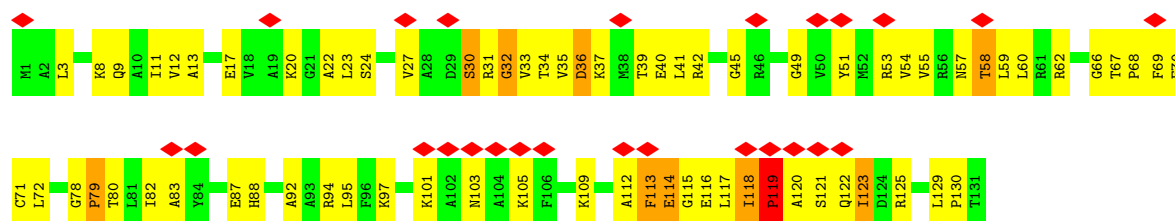
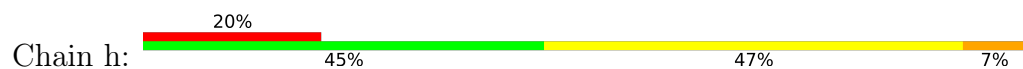
• Molecule 5: 50S ribosomal protein L6



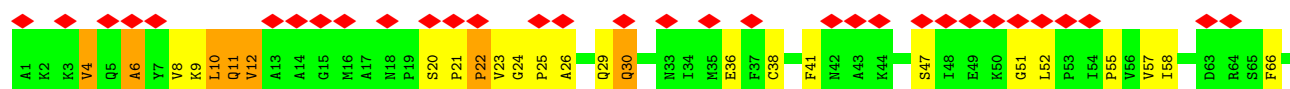
• Molecule 6: 50S ribosomal protein L9

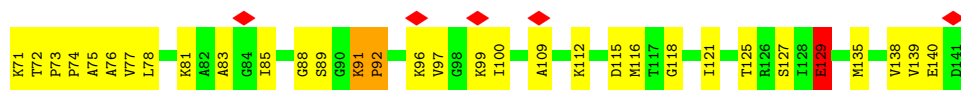


• Molecule 7: 50S ribosomal protein L10

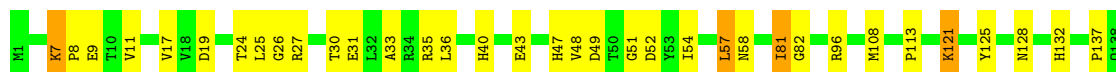


• Molecule 8: 50S ribosomal protein L11

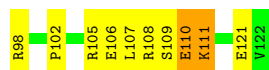




- Molecule 9: 50S ribosomal protein L13



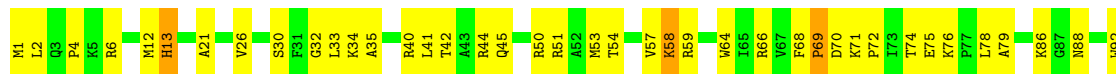
- Molecule 10: 50S ribosomal protein L14



- Molecule 11: 50S ribosomal protein L15

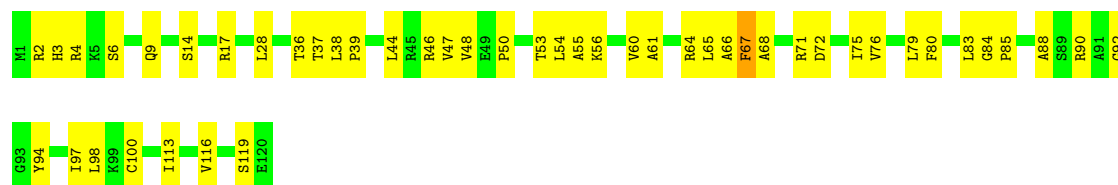


- Molecule 12: 50S ribosomal protein L16

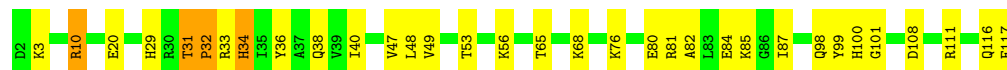


- Molecule 13: 50S ribosomal protein L17

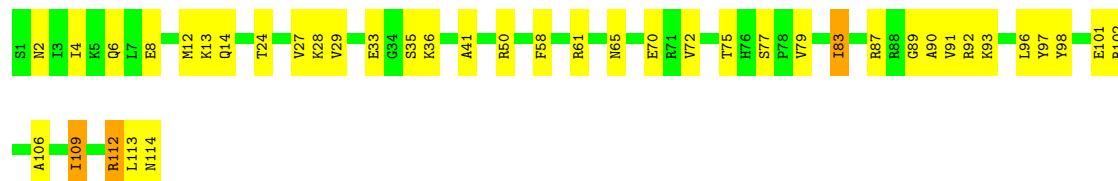




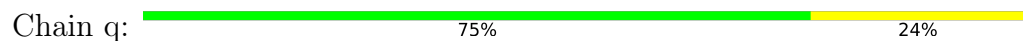
- Molecule 14: 50S ribosomal protein L18



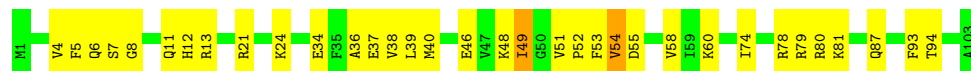
- Molecule 15: 50S ribosomal protein L19



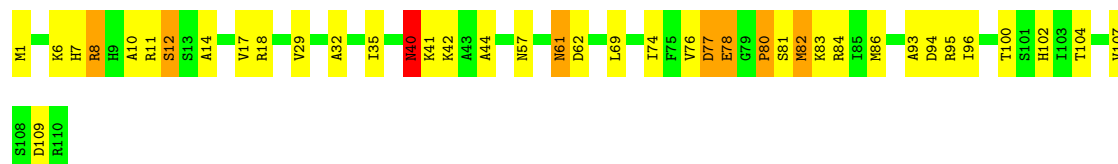
- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23

Chain t:  74% 25%



- Molecule 20: 50S ribosomal protein L24

Chain u:  69% 28%



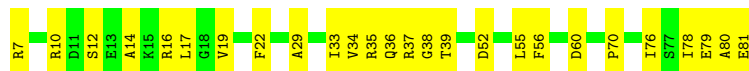
- Molecule 21: 50S ribosomal protein L25

Chain v:  65% 33%



- Molecule 22: 50S ribosomal protein L27

Chain w:  65% 35%



- Molecule 23: 50S ribosomal protein L28

Chain x:  70% 29%



- Molecule 24: 50S ribosomal protein L29

Chain y:  57% 43%



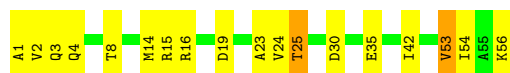
- Molecule 25: 50S ribosomal protein L30

Chain z:  76% 24%



- Molecule 26: 50S ribosomal protein L32

Chain B:  68% 29% .



- Molecule 27: 50S ribosomal protein L33

Chain C:  76% 24%



- Molecule 28: 50S ribosomal protein L34

Chain D:  61% 39%



- Molecule 29: 50S ribosomal protein L35

Chain E:  77% 20% .



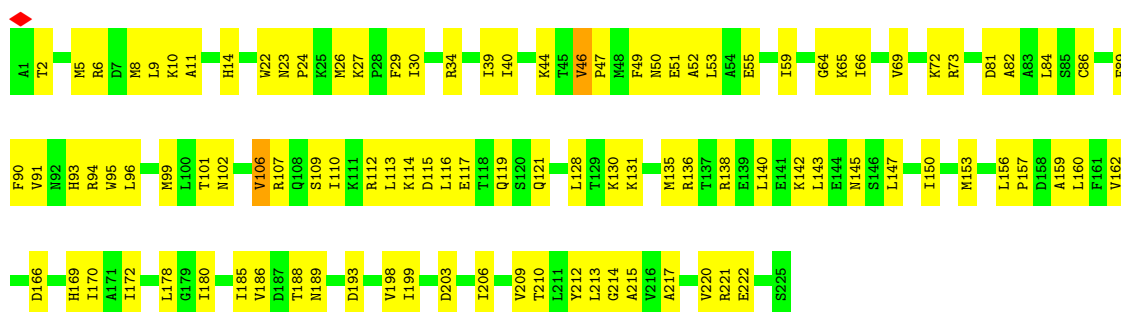
- Molecule 30: 50S ribosomal protein L36

Chain F:  66% 34%

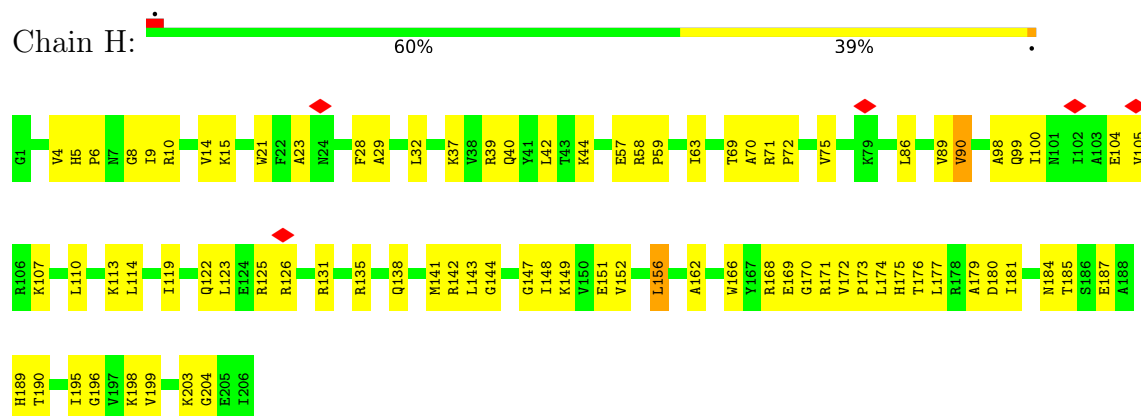


- Molecule 31: 30S ribosomal protein S2

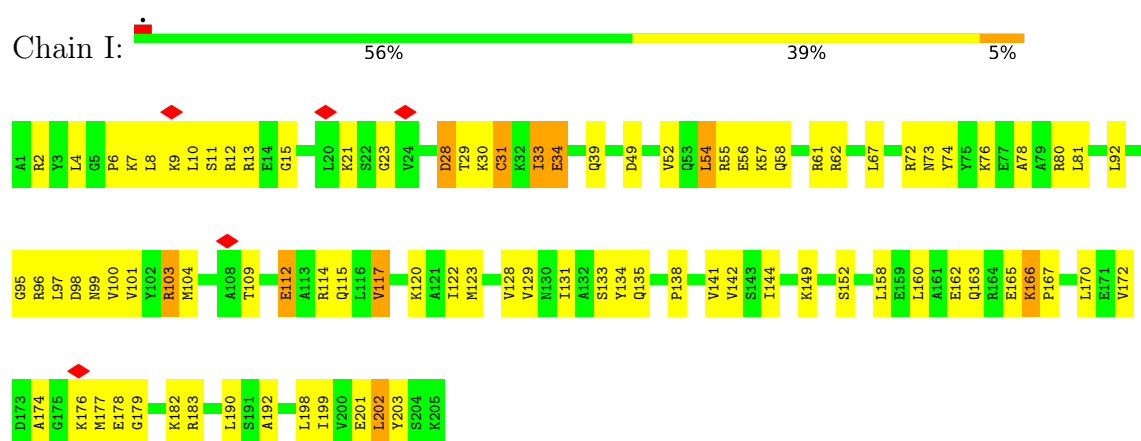
Chain G:  54% 45% .



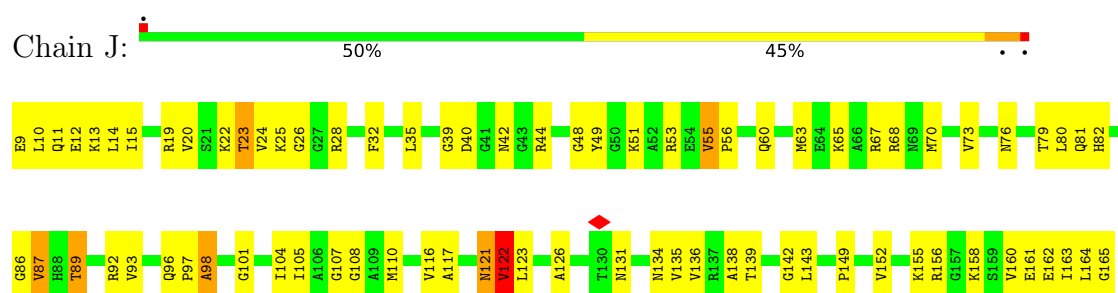
- Molecule 32: 30S ribosomal protein S3



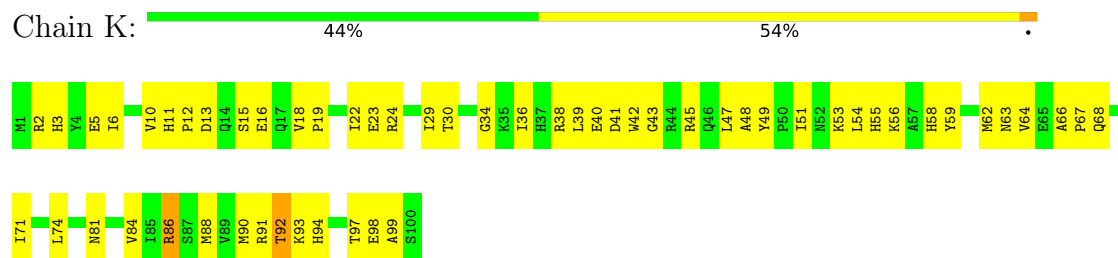
- Molecule 33: 30S ribosomal protein S4



- Molecule 34: 30S ribosomal protein S5

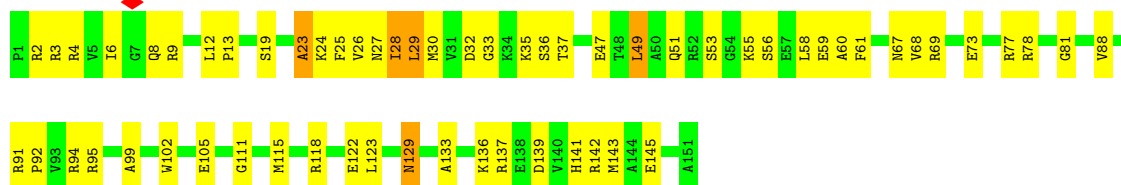


- Molecule 35: 30S ribosomal protein S6



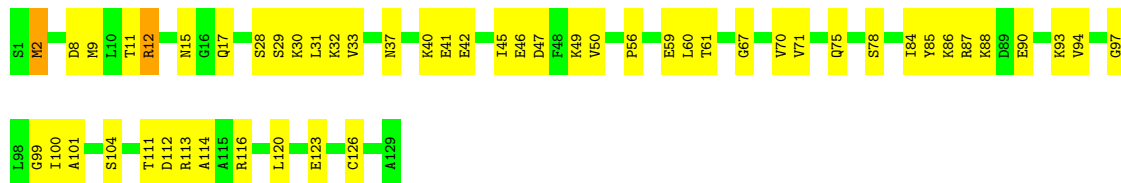
- Molecule 36: 30S ribosomal protein S7

Chain L:  60% 37%



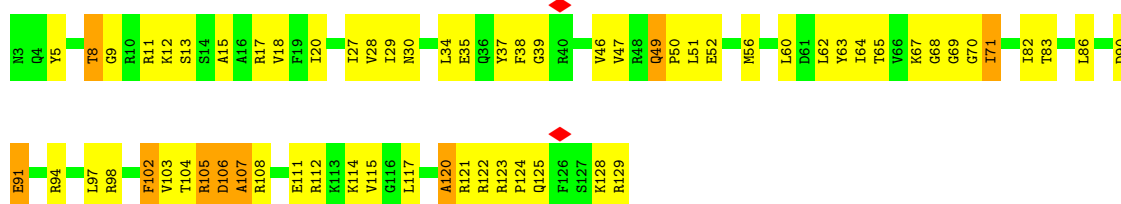
- Molecule 37: 30S ribosomal protein S8

Chain M:  60% 39%



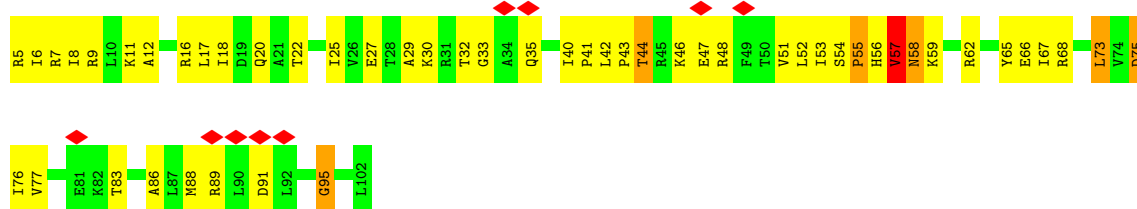
- Molecule 38: 30S ribosomal protein S9

Chain N:  50% 43% 7%



- Molecule 39: 30S ribosomal protein S10

Chain O:  9% 48% 45% 6%



- Molecule 40: 30S ribosomal protein S11

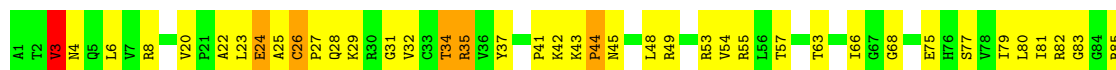
Chain P:  56% 39% 5%





- Molecule 41: 30S ribosomal protein S12

Chain Q: 53% 41% 6%



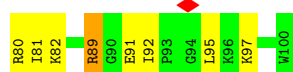
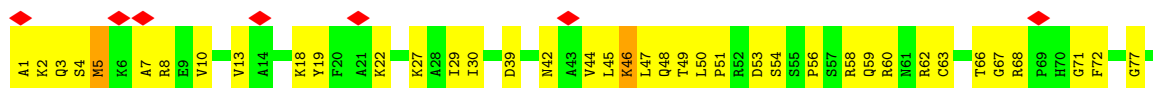
- Molecule 42: 30S ribosomal protein S13

Chain R: 54% 40% 6%



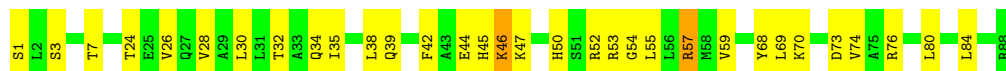
- Molecule 43: 30S ribosomal protein S14

Chain S: 8% 53% 44%



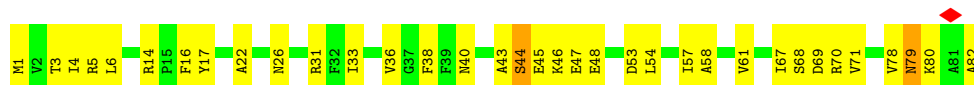
- Molecule 44: 30S ribosomal protein S15

Chain T: 64% 34% 2%



- Molecule 45: 30S ribosomal protein S16

Chain U: 57% 40% 3%



- Molecule 46: 30S ribosomal protein S17

Chain V:  58% 40%

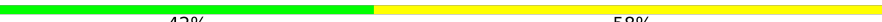


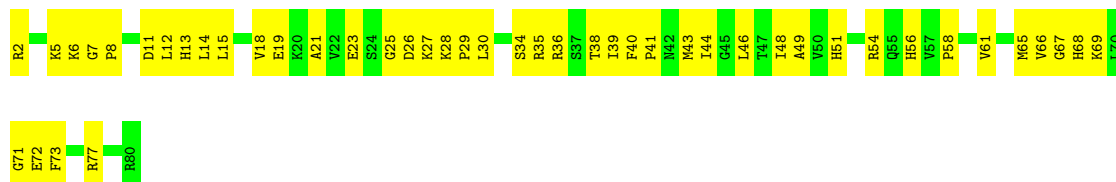
- Molecule 47: 30S ribosomal protein S18

Chain W:  74% 26%



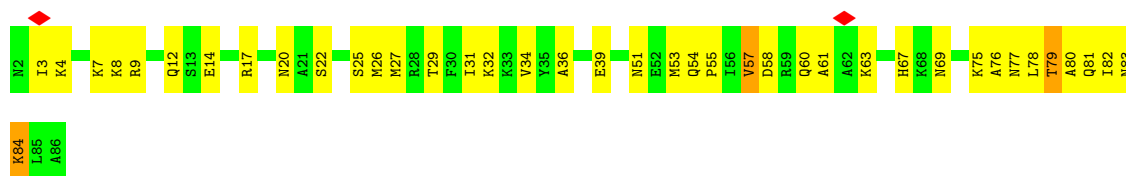
- Molecule 48: 30S ribosomal protein S19

Chain X:  42% 58%



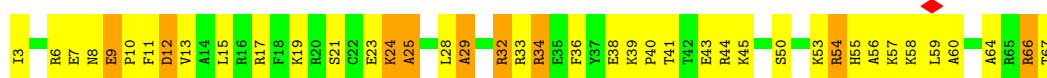
- Molecule 49: 30S ribosomal protein S20

Chain Y:  53% 44%

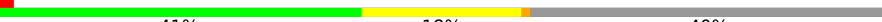


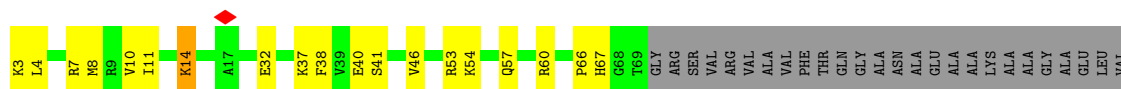
- Molecule 50: 30S ribosomal protein S21

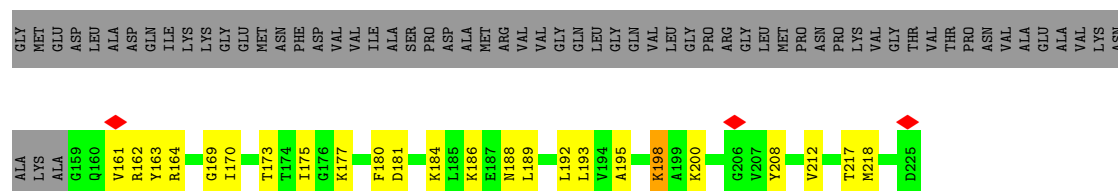
Chain Z:  37% 49% 14%



- Molecule 51: 50S ribosomal protein L1

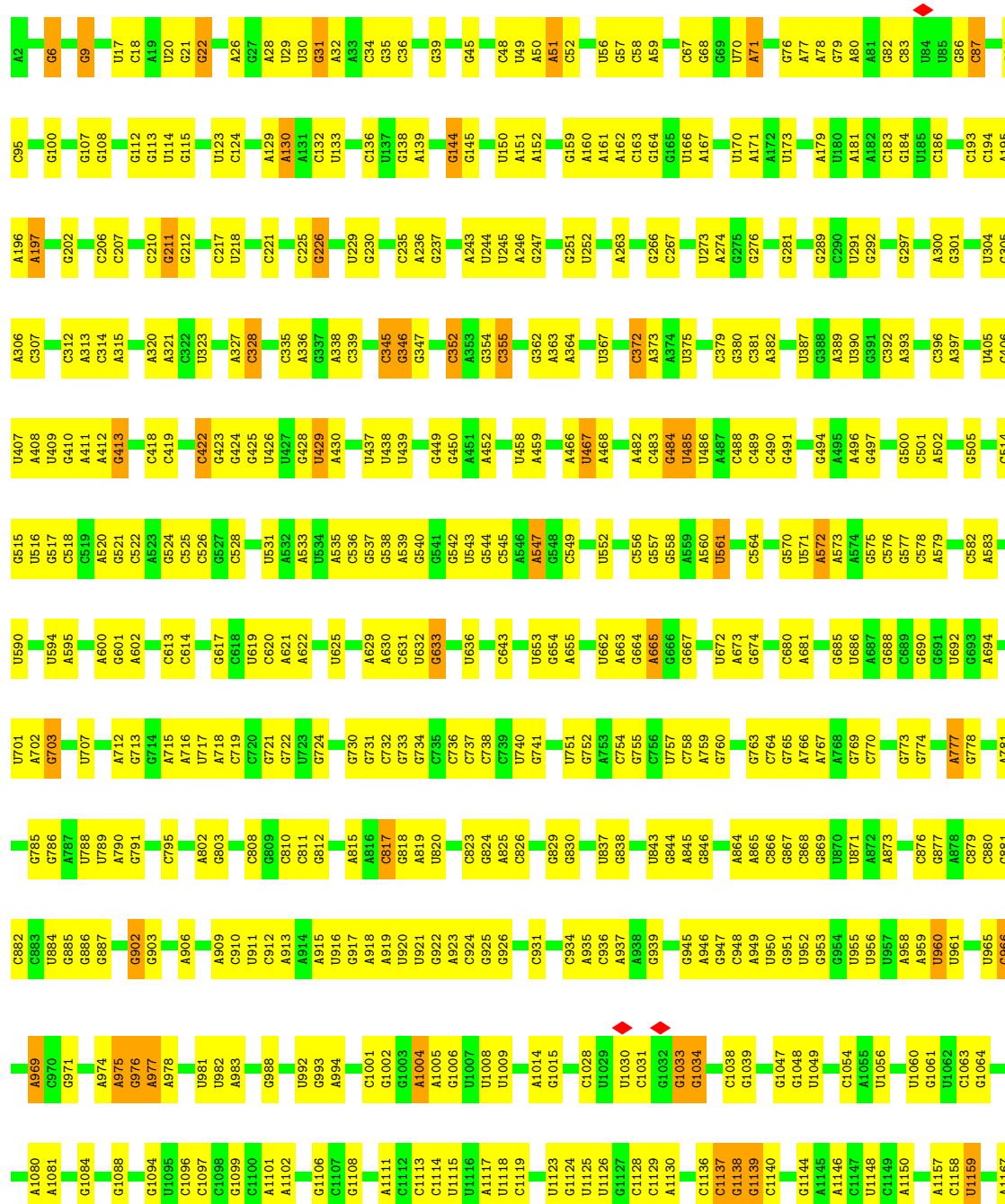
Chain a:  41% 18% 40%

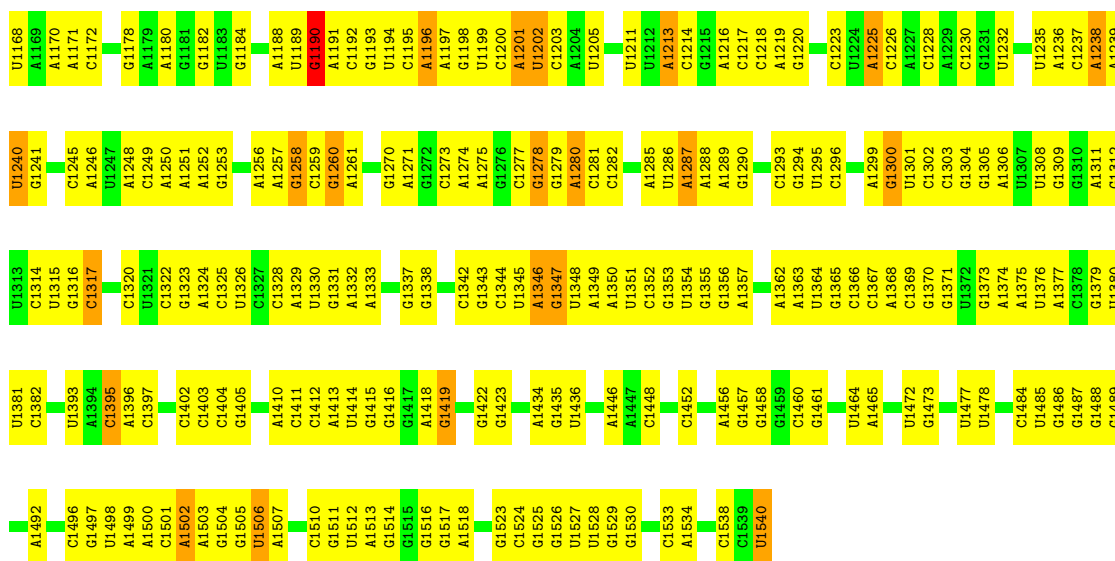




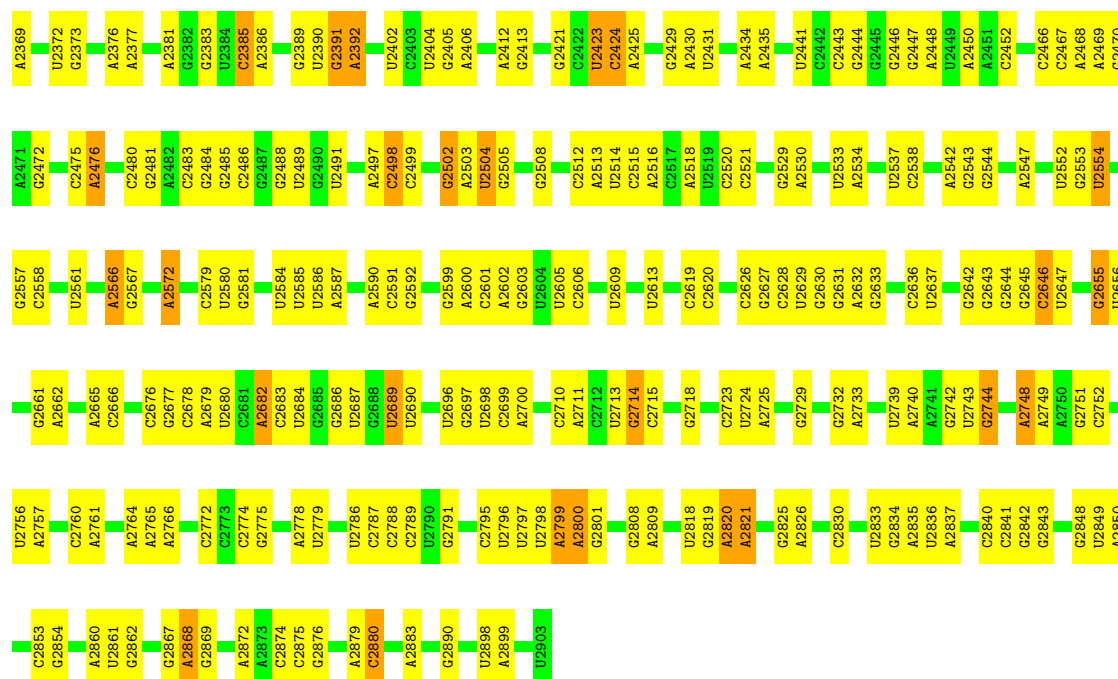
• Molecule 52: 16S ribosomal RNA

Chain 3: 53% 43%



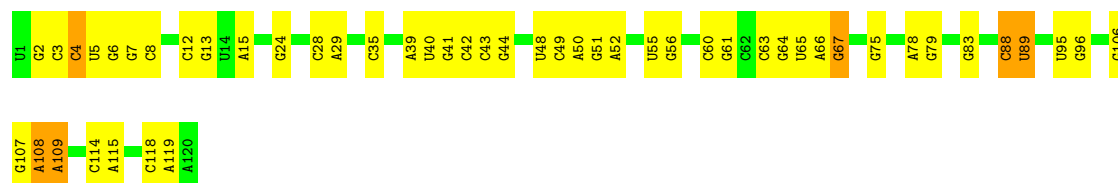


A2297	U2213	A2126	G2040	U1943	A1829	A1745	C1639	G1529	U1394	G1288	G1179	U1083	A996
A2298	G2217	G2127	U2041	U1944	G1842	U1747	A1640	C1533	U1415	C1295	U1180	A1084	G997
G2303	G2218	G2128	A2042	C1947	C1843	G1748	G1642	C1534	U1416	G1296	U1181	A1085	A1001
G2304	G2219	U2132	C2044	G1948	G1846	A1749	C1644	A1535	A1534	G1300	U1183	A1088	G1002
U2305	U2220	G2133	C2045	G1949	A1847	G1752	G1645	G1537	G1417	A1301	U1184	G1092	C1005
C2306	G2221	A2134	G2049	A1952	A1847	G1753	C1646	U1538	A1420	C1306	G1186	G1093	
G2307			G2049				U1647	G1539	G1421	A1307	G1187	U1097	U1012
G2308	G2224	U2139	G2053	U1955	A1854	U1758	U1648	G1540	G1424	A1308	U1188	A1014	C1013
A2309	A2225	G2140	A2054	U1956	U1855	G1764	U1648	C1541	U1424	U1316	U1189		U1019
C2310			C2055	C1957	G1857		G1651	U1542	G1425	U1317	A1205	C1102	U1019
U2312	U2234	G2144	C2056	U1963	G1862	U1769	U1657	G1543	G1432	G1317	G1206	A1103	A1020
C2313	G2235	A2147	A2060	G1964	G1863	G1770	C1658	A1549	A1433	U1318	C1211	A1104	A1021
A2314	U2236	U2148	G2061	C1965	A1871	A1773	G1663	C1550	A1434	C1319	U1105	G1022	G1022
	G2237	G2149	A2062	U1966	A1872	G1774	G1664	G1555	G1435	C1320	G1212	U1106	U1023
G2318	G2238	C2150	C2063	C1967	G1873	U1775	A1665	G1560	G1441	U1321	A1213	G1107	
G2319	G2239				G1874	G1776	G1666		U1442	U1326	G1215	G1110	G1026
U2320		U2155	C2066	A1970	G1875	U1779	G1667	G1560	U1443	A1327	G1216	A1111	A1027
A2321	U2243	G2156	G2067	U1971	G1876	U1780	C1670	U1563	U1444	U1328	G1112	U1033	
A2322	U2244	G2157	C2068	G1972	A1877	U1781	U1671	C1564	G1445	U1329	C1229	U1034	
G2323	U2245	G2162	U2069	G1973	G1878	U1781	U1671	C1565	C1446	C1330	G1122	U1035	
U2324	G2246	A2163	A2070	G1974	G1878			C1566	C1447	G1331	C1230	G1036	
G2325	A2247	C2164	A2071	U1979				C1567	G1448	G1332	G1124		
C2326	C2248		C2072	G1980	G1884	A1784	G1674	G1568					
A2327	U2249					A1785	C1675	C1569					
A2328	G2250	A2170	C2073	U1991	G1888	A1786	C1676	A1568	C1451	G1341	A1127	A1040	
U2329	U2244	A2171	U2074	G1992	G1888	A1787	A1677	A1570	G1475	U1344	A1128	C1045	
G2330	U2257	U2172	C2078	U1993	A1900	A1787	G1678	C1584	U1476	C1345	U1130	A1046	
G2331	C2258	A2173	U2079	C1994	A1901	A1791	U1680	U1584	G1482		U1131	G1047	
		C2174		U1995			U1680	G1587			U1248		
	U2262	A2175	U2086	C1997	G1906	A1794	U1680	G1587			U1249		
	C2263	C2177	G2087	C2001	G1907	U1795	G1682	G1581	G1475	C1349	U1250	A1054	
	U2264		A2088	G2002	G1909	U1796	G1683	G1584	U1476	C1350	C1251	A1056	
	A2266				G1910	U1797	G1684			C1351	G1252	C1135	
	A2267		G2093		U1911	U1798				U1352	A1253		
	A2268			G2010	A1912	G1799	A1690	G1587		A1353	A1254	G1138	
		A2181	C2096		A1913	C1800	C1691				U1255	G1139	
	G2271	A2182			A1914	A1801	U1692	A1590	A1490	C1357	U1256	C1140	
	U2272	A2183		A2014	C1914	A1802	U1693	A1591	G1491	G1358	G1257	U1141	
	A2273	U2185	U2105			A1803	G1694			A1359	U1258	U1061	
		G2186	G2107	U2017	U1917	A1807	G1695	G1601	A1494	G1360	G1259	A1143	
	G2277		A2108	A2018	A1918	G1807	G1696	U1602		G1361			
	A2278	U2189	U2109	A2019	A1919	A1808	G1696	A1603			A1264	C1146	
		A2191	A2020	A2020	C1920	A1809	G1715			A1365	A1268	A1147	
	A2281		G2021	C2021	C1924	A1810	U1720	C1606	G1501	A1366	A1268		
	C2282	U2197	U2022	U2022	U1925	G1811	G1721	A1608	C1507	A1367	C1270	C1153	
	A2284	C2023	G2024	G2024	U1926	G1816	U1729	A1609	A1508	G1368	G1271	G1154	
	C2285	U1926						A1610	A1509		A1272	G1157	
		G1930	G2029	G2029	G1930	G1817	C1730	C1611	G1510	A1373			
	U2203	U1931	A2030	A2030	U1931	A1818	U1736	C1612	A1515	A1378	A1275	A1169	
	G2204	A2031	A2031	A2031	A1932	A1819	G1737	G1613		U1379	A1275	C1170	
		G1933	G2032	G2032	G1933	U1820	G1738	A1614			G1278	C1170	
		A1936	A2033	A2033	A1936	G1824	G1738	C1615	G1524	A1383	G1279	U1174	
	C2208	U1937	U2034	U2034	A1937	U1825	A1739	A1616	A1525		G1279	A1175	
	U2212	A1938	G2036	G2036	A1938	G1826	G1740		C1526	C1386	U1285	U1078	
	G2124					U1827		A1637	G1527	A1387	A1286	G1079	
	A2211					G1828	A1744		A1528		U1287	G1177	A1080
	A2212											C1178	U1082



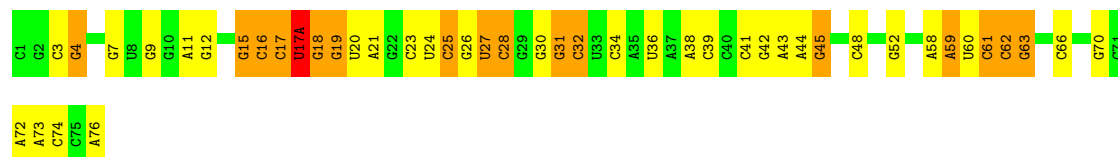
• Molecule 54: 5S ribosomal RNA

Chain 2: 58% 37% 5%



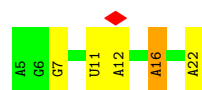
• Molecule 55: tRNA^{fMet}

Chain 5: 40% 38% 21%



• Molecule 56: mRNA

Chain 4: 6% 72% 22% 6%



• Molecule 57: tRNA^{Phe}

Chain 7: 54% 36% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	19875	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 ($e^-/\text{\AA}^2$)	35	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	23.377	Depositor
Minimum map value	-14.097	Depositor
Average map value	0.117	Depositor
Map value standard deviation	0.965	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.30	0/2122	0.96	4/2852 (0.1%)
2	c	0.29	0/1586	0.95	1/2134 (0.0%)
3	d	0.29	0/1571	0.91	5/2113 (0.2%)
4	e	0.31	0/1435	0.94	6/1926 (0.3%)
5	f	0.31	0/1343	0.94	3/1816 (0.2%)
6	g	0.33	0/1122	1.05	11/1515 (0.7%)
7	h	0.36	0/1002	0.99	6/1350 (0.4%)
8	i	0.35	0/1046	1.05	8/1410 (0.6%)
9	j	0.30	0/1152	1.00	7/1551 (0.5%)
10	k	0.29	0/948	0.99	5/1268 (0.4%)
11	l	0.29	0/1054	1.00	5/1403 (0.4%)
12	m	0.30	0/1093	0.93	3/1460 (0.2%)
13	n	0.31	0/974	0.96	4/1301 (0.3%)
14	o	0.29	0/902	0.95	3/1209 (0.2%)
15	p	0.29	0/929	0.87	3/1242 (0.2%)
16	q	0.28	0/960	0.94	4/1278 (0.3%)
17	r	0.27	0/829	0.84	1/1107 (0.1%)
18	s	0.29	0/864	0.94	4/1156 (0.3%)
19	t	0.27	0/745	0.83	1/994 (0.1%)
20	u	0.30	0/788	0.92	3/1051 (0.3%)
21	v	0.29	0/766	0.89	4/1025 (0.4%)
22	w	0.28	0/582	0.91	1/769 (0.1%)
23	x	0.29	0/635	0.89	0/848
24	y	0.29	0/510	0.85	0/677
25	z	0.30	0/453	0.86	1/605 (0.2%)
26	B	0.29	0/450	0.87	1/599 (0.2%)
27	C	0.32	0/417	0.93	4/554 (0.7%)
28	D	0.31	0/380	0.98	0/498
29	E	0.30	0/513	1.02	2/676 (0.3%)
30	F	0.31	0/303	0.87	0/397
31	G	0.30	0/1788	0.98	12/2408 (0.5%)
32	H	0.33	0/1652	0.91	5/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.31	0/1665	0.99	10/2227 (0.4%)
34	J	0.33	0/1170	1.00	5/1573 (0.3%)
35	K	0.30	0/836	0.90	1/1128 (0.1%)
36	L	0.31	0/1196	1.01	7/1602 (0.4%)
37	M	0.30	0/989	0.95	4/1326 (0.3%)
38	N	0.33	0/1034	0.97	5/1375 (0.4%)
39	O	0.33	0/797	1.06	9/1077 (0.8%)
40	P	0.33	0/886	0.99	4/1195 (0.3%)
41	Q	0.33	0/969	1.02	7/1300 (0.5%)
42	R	0.33	0/893	1.05	5/1193 (0.4%)
43	S	0.33	0/817	0.94	5/1088 (0.5%)
44	T	0.29	0/722	0.95	3/964 (0.3%)
45	U	0.33	0/659	0.96	3/884 (0.3%)
46	V	0.32	0/658	0.94	1/881 (0.1%)
47	W	0.32	0/545	0.86	0/731
48	X	0.34	0/653	0.86	0/877
49	Y	0.29	0/671	0.99	5/888 (0.6%)
50	Z	0.32	0/551	0.97	5/728 (0.7%)
51	a	0.31	0/1034	0.87	3/1387 (0.2%)
52	3	0.43	0/36963	0.47	1/57662 (0.0%)
53	1	0.40	0/69796	0.47	2/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.42	0/1832	0.52	1/2855 (0.0%)
56	4	0.49	0/436	0.51	0/679
57	7	0.65	0/1809	0.56	0/2819
All	All	0.39	0/161367	0.64	203/241223 (0.1%)

There are no bond length outliers.

The worst 5 of 203 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	g	10	ALA	N-CA-C	9.68	121.43	111.07
29	E	61	LEU	CA-C-N	9.41	128.76	118.97
29	E	61	LEU	C-N-CA	9.41	128.76	118.97
42	R	3	ILE	N-CA-C	9.41	121.28	108.11
9	j	121	LYS	N-CA-C	-9.12	101.93	113.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2083	0	2157	95	0
2	c	1565	0	1616	40	0
3	d	1552	0	1619	35	0
4	e	1411	0	1447	87	0
5	f	1323	0	1374	43	0
6	g	1111	0	1148	48	0
7	h	989	0	1025	77	0
8	i	1032	0	1088	56	0
9	j	1129	0	1162	29	0
10	k	939	0	1012	45	0
11	l	1045	0	1117	39	0
12	m	1074	0	1157	43	0
13	n	961	0	1000	35	0
14	o	892	0	923	29	0
15	p	917	0	965	34	0
16	q	947	0	1022	26	0
17	r	816	0	839	37	0
18	s	857	0	922	30	0
19	t	739	0	807	22	0
20	u	780	0	834	24	0
21	v	753	0	780	22	0
22	w	575	0	592	25	0
23	x	625	0	655	16	0
24	y	509	0	543	23	0
25	z	449	0	491	16	0
26	B	444	0	461	15	0
27	C	410	0	440	10	0
28	D	377	0	418	21	0
29	E	504	0	574	15	0
30	F	302	0	343	9	0
31	G	1757	0	1787	68	0
32	H	1625	0	1699	73	0
33	I	1643	0	1710	90	0
34	J	1157	0	1199	62	0
35	K	818	0	808	50	0
36	L	1182	0	1240	55	0
37	M	979	0	1034	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	58	0
39	O	787	0	828	43	0
40	P	870	0	878	41	0
41	Q	955	0	1019	61	0
42	R	884	0	944	47	0
43	S	805	0	847	51	0
44	T	714	0	737	27	0
45	U	649	0	666	35	0
46	V	649	0	691	26	0
47	W	536	0	552	16	0
48	X	638	0	665	41	0
49	Y	665	0	714	29	0
50	Z	545	0	579	46	0
51	a	1027	0	1092	44	0
52	3	33012	0	16618	663	0
53	1	62317	0	31346	912	0
54	2	2568	0	1303	57	0
55	5	1640	0	837	53	0
56	4	388	0	196	4	0
57	7	1619	0	821	24	0
58	7	11	0	8	0	0
59	7	10	0	10	0	0
All	All	148582	0	100429	3185	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 13.

The worst 5 of 3185 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)
7:h:23:LEU:HD22	7:h:118:ILE:HB	1.33	1.10
53:1:45:G:H5''	53:1:46:G:H5'	1.24	1.08
6:g:97:ARG:HH22	53:1:2220:U:H4'	1.18	1.06
6:g:84:ALA:HB2	6:g:90:LEU:HD23	1.41	1.02
53:1:2277:G:H2'	53:1:2278:A:H5''	1.40	1.02

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	233 (87%)	33 (12%)	3 (1%)	11	39
2	c	207/209 (99%)	173 (84%)	29 (14%)	5 (2%)	4	24
3	d	199/201 (99%)	180 (90%)	19 (10%)	0	100	100
4	e	175/177 (99%)	158 (90%)	17 (10%)	0	100	100
5	f	174/176 (99%)	156 (90%)	17 (10%)	1 (1%)	21	52
6	g	147/149 (99%)	125 (85%)	18 (12%)	4 (3%)	4	22
7	h	129/131 (98%)	100 (78%)	22 (17%)	7 (5%)	1	10
8	i	139/141 (99%)	114 (82%)	21 (15%)	4 (3%)	3	21
9	j	140/142 (99%)	125 (89%)	14 (10%)	1 (1%)	18	49
10	k	120/122 (98%)	93 (78%)	22 (18%)	5 (4%)	2	14
11	l	141/143 (99%)	112 (79%)	23 (16%)	6 (4%)	2	14
12	m	134/136 (98%)	117 (87%)	14 (10%)	3 (2%)	5	26
13	n	118/120 (98%)	98 (83%)	19 (16%)	1 (1%)	16	45
14	o	114/116 (98%)	101 (89%)	10 (9%)	3 (3%)	4	23
15	p	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
16	q	115/117 (98%)	106 (92%)	9 (8%)	0	100	100
17	r	101/103 (98%)	86 (85%)	14 (14%)	1 (1%)	12	40
18	s	108/110 (98%)	93 (86%)	13 (12%)	2 (2%)	6	28
19	t	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
20	u	100/102 (98%)	82 (82%)	15 (15%)	3 (3%)	3	20
21	v	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	w	73/75 (97%)	65 (89%)	7 (10%)	1 (1%)	9	33
23	x	75/77 (97%)	69 (92%)	4 (5%)	2 (3%)	4	22
24	y	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	48 (89%)	5 (9%)	1 (2%)	6	28
27	C	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
28	D	44/46 (96%)	36 (82%)	8 (18%)	0	100	100
29	E	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	31
30	F	36/38 (95%)	30 (83%)	6 (17%)	0	100	100
31	G	223/225 (99%)	202 (91%)	19 (8%)	2 (1%)	14	43
32	H	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
33	I	203/205 (99%)	181 (89%)	18 (9%)	4 (2%)	6	27
34	J	155/157 (99%)	123 (79%)	25 (16%)	7 (4%)	2	13
35	K	98/100 (98%)	73 (74%)	22 (22%)	3 (3%)	3	20
36	L	149/151 (99%)	131 (88%)	17 (11%)	1 (1%)	18	49
37	M	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	7	31
38	N	125/127 (98%)	101 (81%)	16 (13%)	8 (6%)	1	8
39	O	96/98 (98%)	78 (81%)	13 (14%)	5 (5%)	1	11
40	P	114/116 (98%)	88 (77%)	20 (18%)	6 (5%)	1	10
41	Q	121/123 (98%)	94 (78%)	19 (16%)	8 (7%)	1	7
42	R	112/114 (98%)	99 (88%)	8 (7%)	5 (4%)	2	13
43	S	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
44	T	86/88 (98%)	74 (86%)	11 (13%)	1 (1%)	10	37
45	U	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	23
46	V	78/80 (98%)	60 (77%)	13 (17%)	5 (6%)	1	8
47	W	63/65 (97%)	54 (86%)	9 (14%)	0	100	100
48	X	77/79 (98%)	65 (84%)	11 (14%)	1 (1%)	9	35
49	Y	83/85 (98%)	76 (92%)	6 (7%)	1 (1%)	10	37
50	Z	63/65 (97%)	39 (62%)	18 (29%)	6 (10%)	0	3
51	a	130/223 (58%)	119 (92%)	11 (8%)	0	100	100
All	All	5919/6112 (97%)	5078 (86%)	720 (12%)	121 (2%)	8	27

5 of 121 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
5	f	45	ALA

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Mol	Chain	Res	Type
6	g	41	LYS
7	h	118	ILE
8	i	92	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	212 (98%)	4 (2%)	50	68
2	c	164/164 (100%)	161 (98%)	3 (2%)	51	70
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	81
4	e	148/148 (100%)	145 (98%)	3 (2%)	48	68
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	80
6	g	114/114 (100%)	112 (98%)	2 (2%)	51	70
7	h	100/100 (100%)	98 (98%)	2 (2%)	48	68
8	i	109/109 (100%)	107 (98%)	2 (2%)	51	70
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	78
10	k	103/103 (100%)	103 (100%)	0	100	100
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	78
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	84 (98%)	2 (2%)	44	66
15	p	99/99 (100%)	96 (97%)	3 (3%)	36	61
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	76
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	89 (96%)	4 (4%)	26	54
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	74
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	185 (100%)	1 (0%)	81	83
32	H	170/170 (100%)	170 (100%)	0	100	100
33	I	172/172 (100%)	168 (98%)	4 (2%)	44	66
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	79
35	K	87/87 (100%)	87 (100%)	0	100	100
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	104 (100%)	0	100	100
38	N	105/105 (100%)	103 (98%)	2 (2%)	50	68
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	66
40	P	89/89 (100%)	87 (98%)	2 (2%)	45	66
41	Q	103/103 (100%)	101 (98%)	2 (2%)	50	68
42	R	92/92 (100%)	91 (99%)	1 (1%)	65	76
43	S	83/83 (100%)	83 (100%)	0	100	100
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	73
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	54 (98%)	1 (2%)	51	70
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4908/4972 (99%)	4859 (99%)	49 (1%)	65	76

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	s	77	ASP
33	I	54	LEU
18	s	109	ASP
31	G	46	VAL
34	J	55	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 124 such sidechains are listed below:

Mol	Chain	Res	Type
20	u	65	GLN
43	S	34	ASN
29	E	27	ASN
42	R	99	GLN
49	Y	83	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	143 (9%)	2 (0%)
53	1	2902/2903 (99%)	326 (11%)	11 (0%)
54	2	119/120 (99%)	11 (9%)	1 (0%)
55	5	76/77 (98%)	24 (31%)	1 (1%)
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	14 (18%)	0
All	All	4727/4733 (99%)	520 (11%)	15 (0%)

5 of 520 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	1130	U

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Mol	Chain	Res	Type
54	2	88	C
53	1	1475	G
55	5	17(A)	U
53	1	2326	C

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](#)

2 ligands 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	$\# Z > 2$
58	PHE	7	101	59,57	10,11,12	0.43	0	8,13,15	0.60	0
59	FME	7	102	58	8,9,10	1.41	1 (12%)	8,9,11	1.36	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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	PHE	7	101	59,57	-	2/5/6/8	0/1/1/1
59	FME	7	102	58	-	3/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	7	102	FME	CN-N	3.73	1.45	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	7	102	FME	O1-CN-N	-2.05	120.01	125.32

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	7	101	PHE	N-CA-CB-CG
58	7	101	PHE	C-CA-CB-CG
59	7	102	FME	O1-CN-N-CA
59	7	102	FME	CB-CG-SD-CE
59	7	102	FME	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

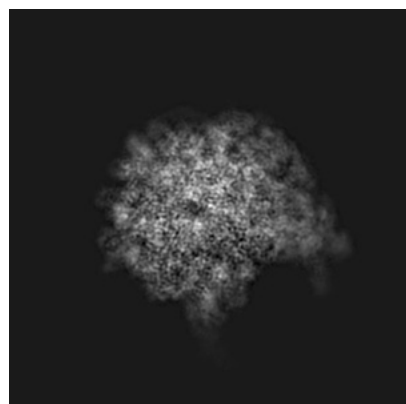
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21635. These allow visual inspection of the internal detail of the map and identification of artifacts.

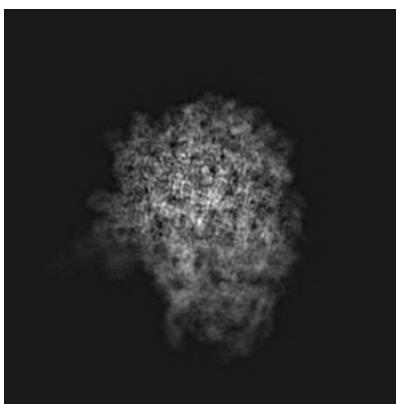
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

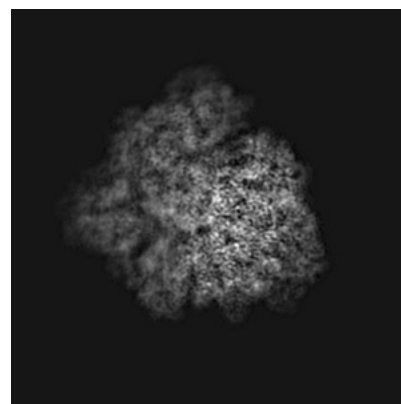
6.1.1 Primary map



X

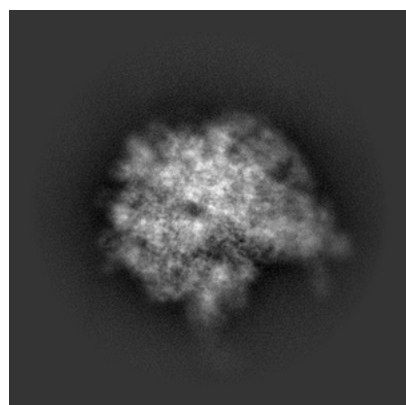


Y

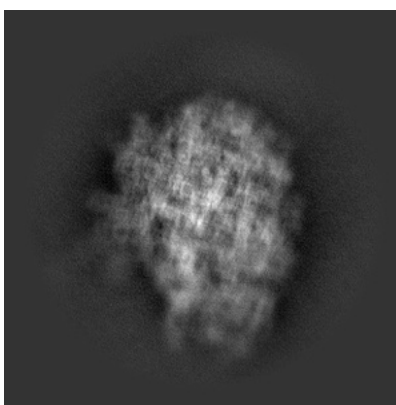


Z

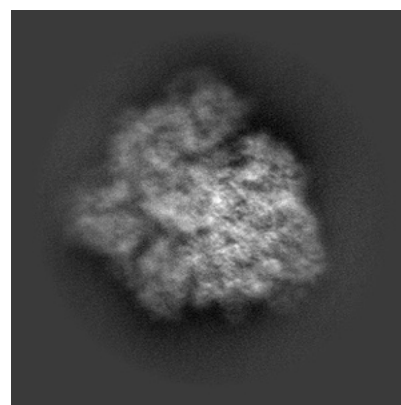
6.1.2 Raw map



X



Y

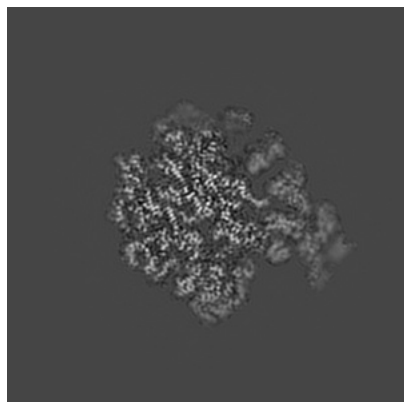


Z

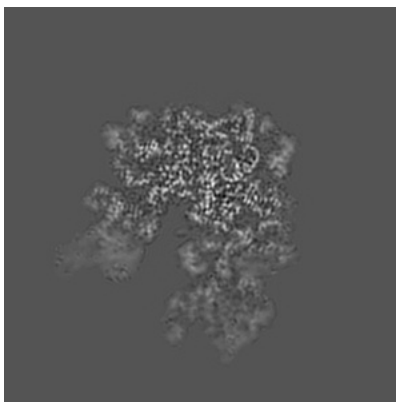
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

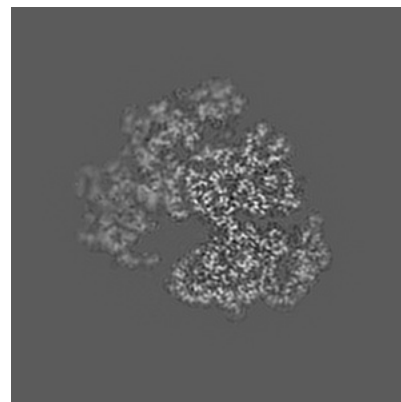
6.2.1 Primary map



X Index: 144

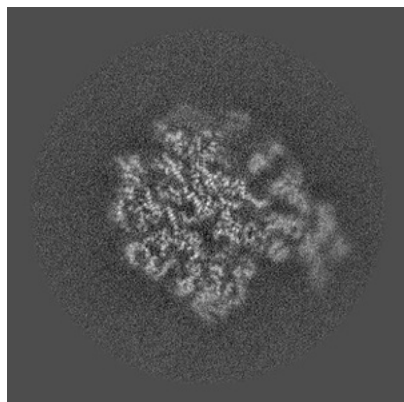


Y Index: 144

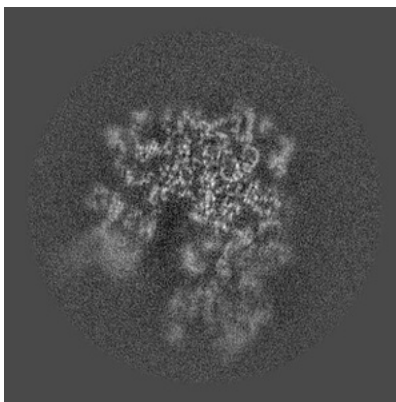


Z Index: 144

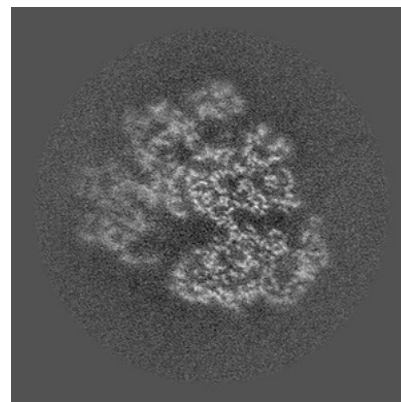
6.2.2 Raw map



X Index: 144



Y Index: 144

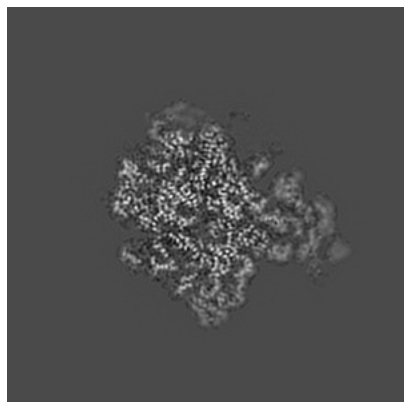


Z Index: 144

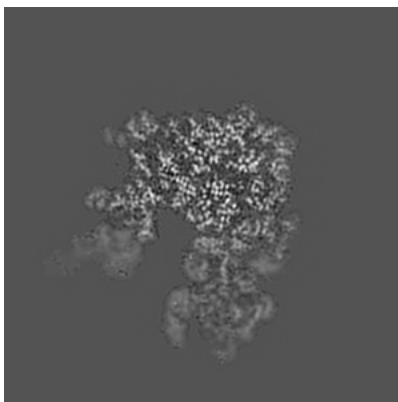
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

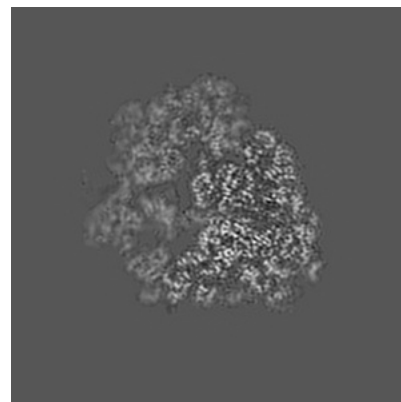
6.3.1 Primary map



X Index: 148

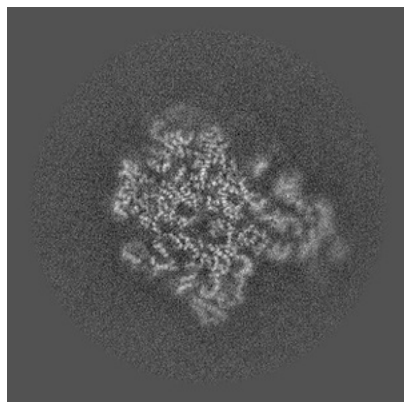


Y Index: 149

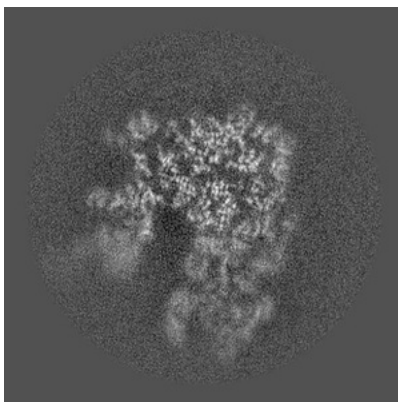


Z Index: 135

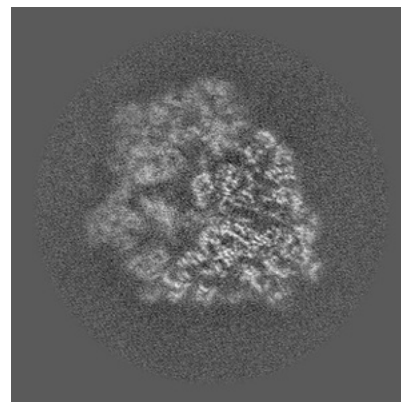
6.3.2 Raw map



X Index: 148



Y Index: 149

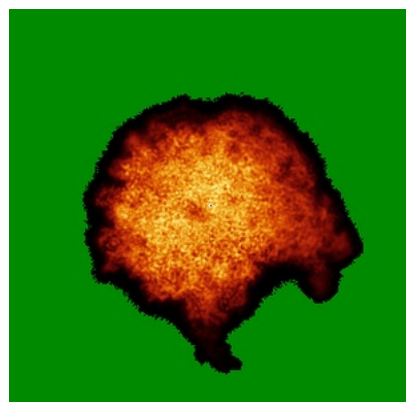


Z Index: 135

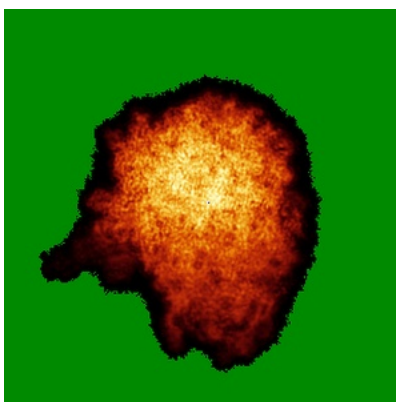
The images above show the largest variance slices of the map in three orthogonal directions.

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

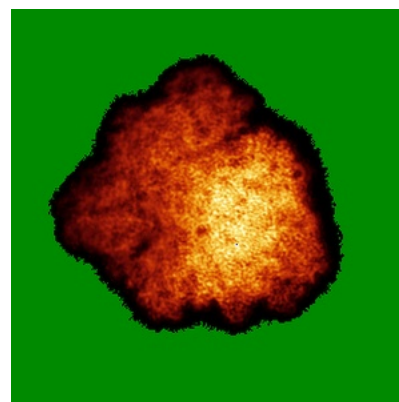
6.4.1 Primary map



X

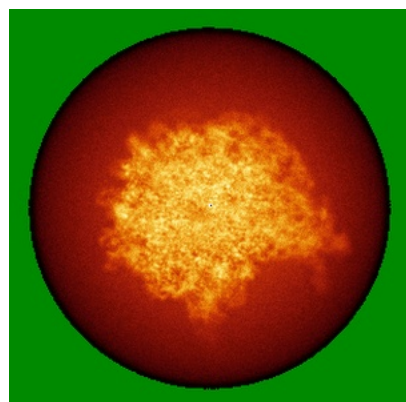


Y

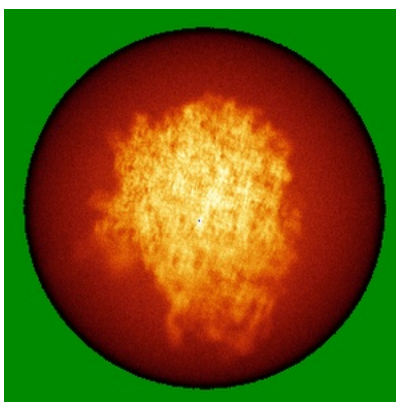


Z

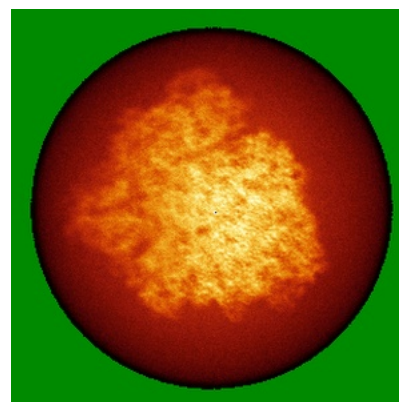
6.4.2 Raw map



X



Y

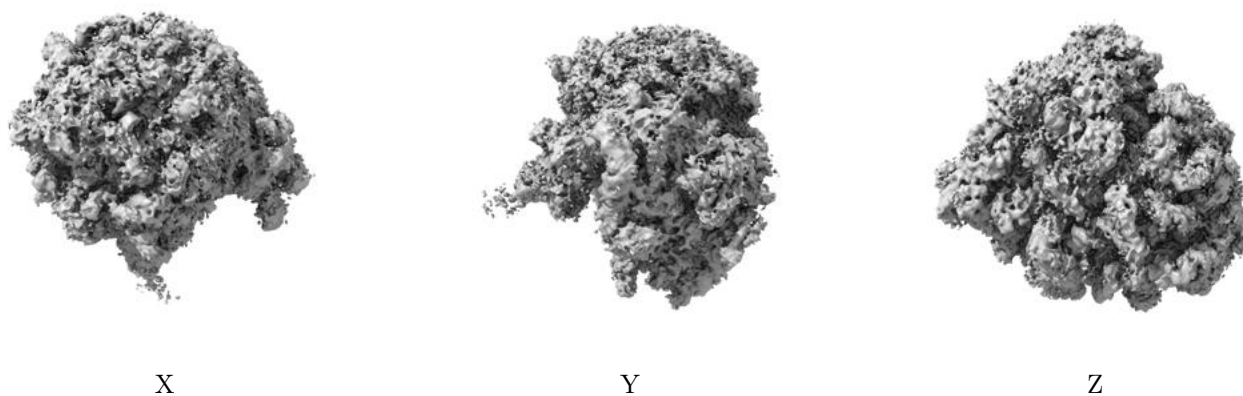


Z

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.

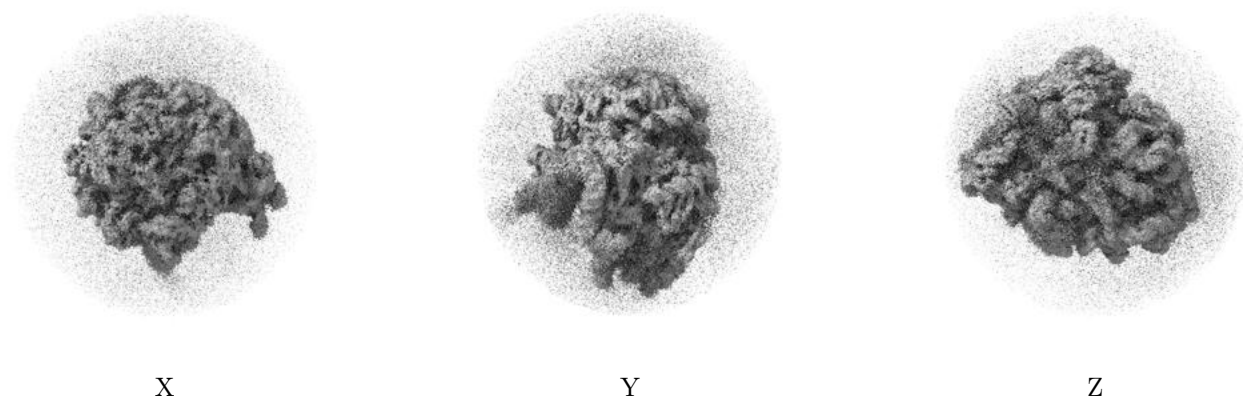
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

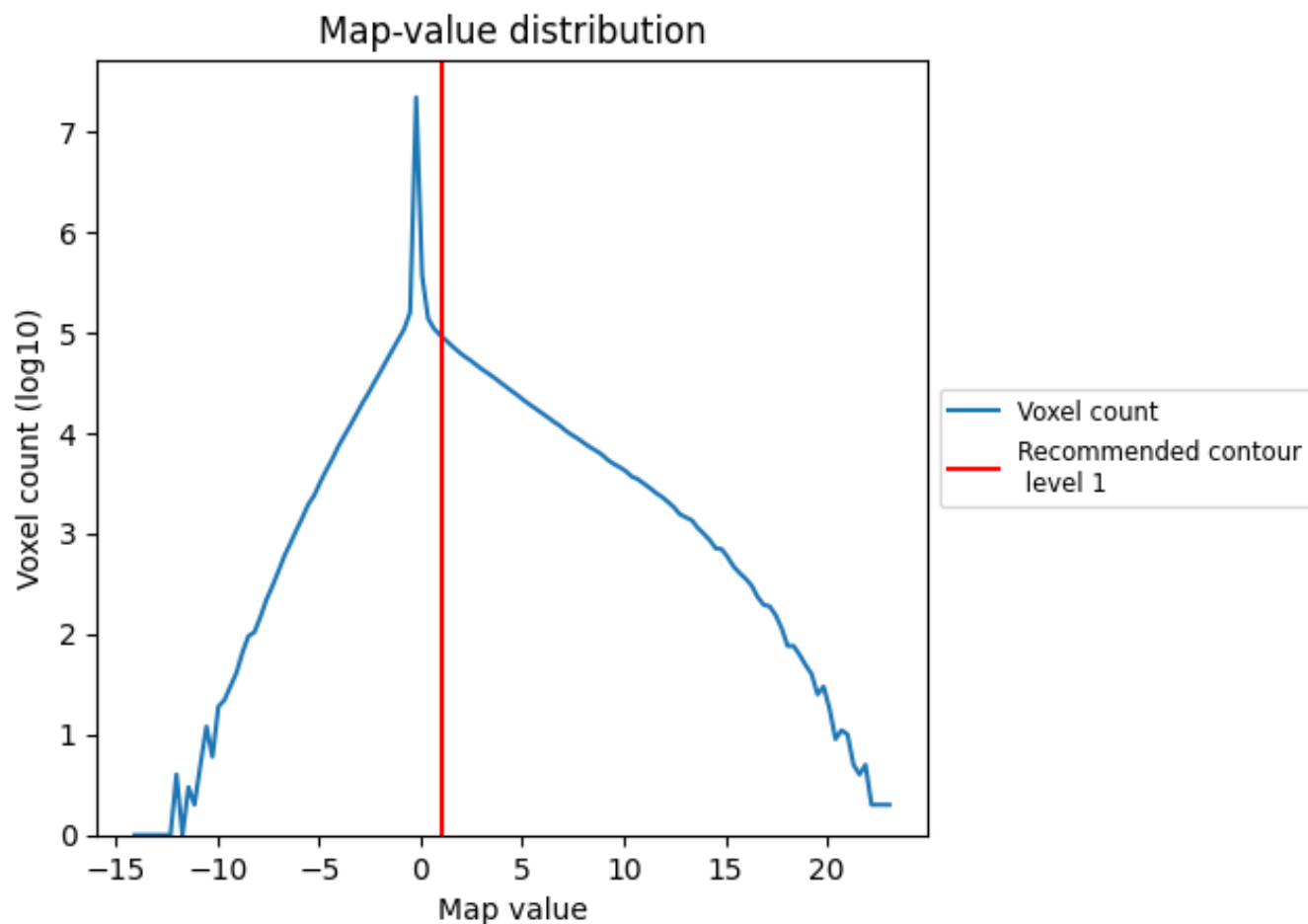
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

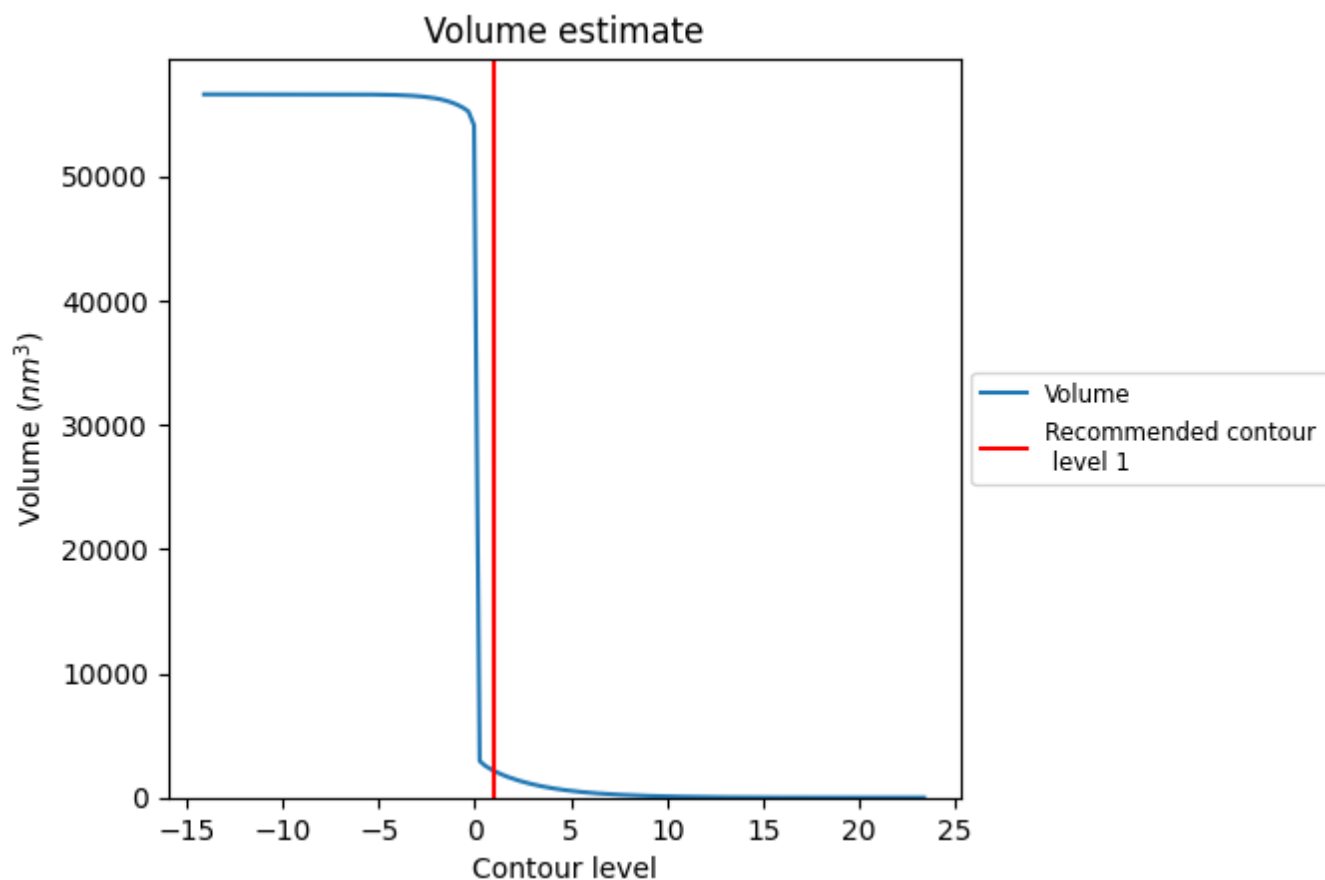
This section contains the results of statistical analysis of the map.

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.

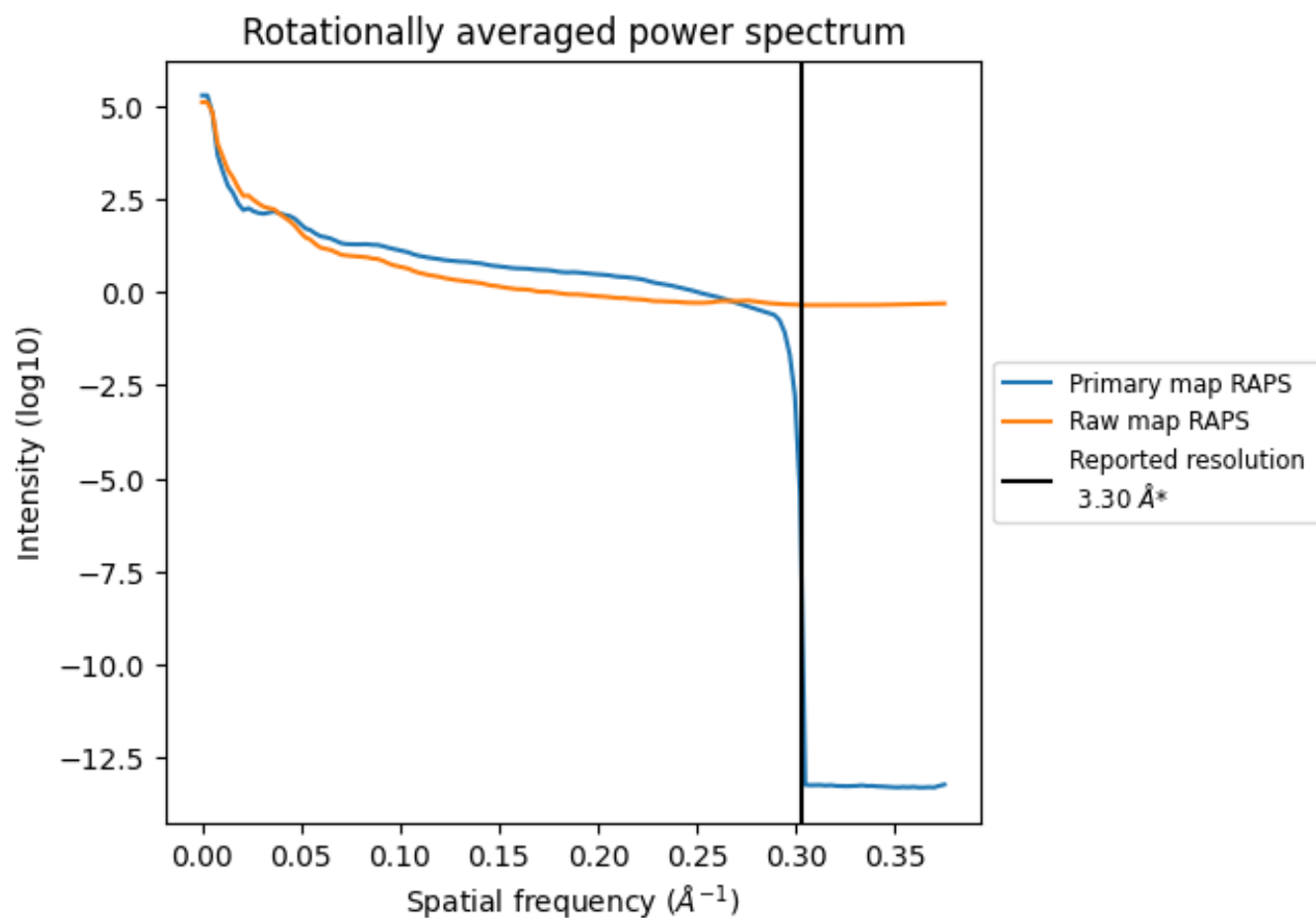
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2148 nm³; this corresponds to an approximate mass of 1940 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 ⓘ

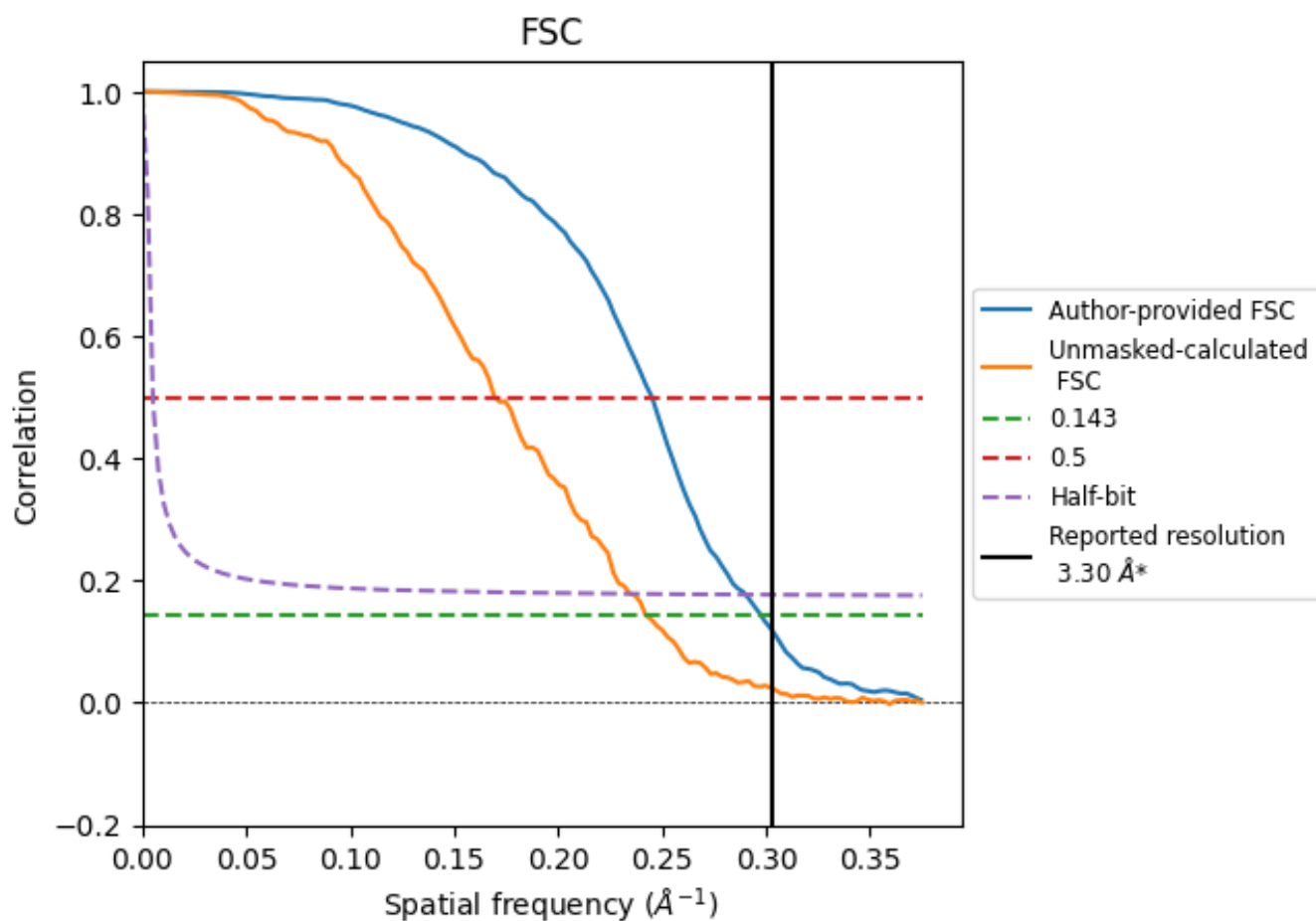


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.303 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.36	4.08	3.45
Unmasked-calculated*	4.13	5.89	4.26

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.13 differs from the reported value 3.3 by more than 10 %

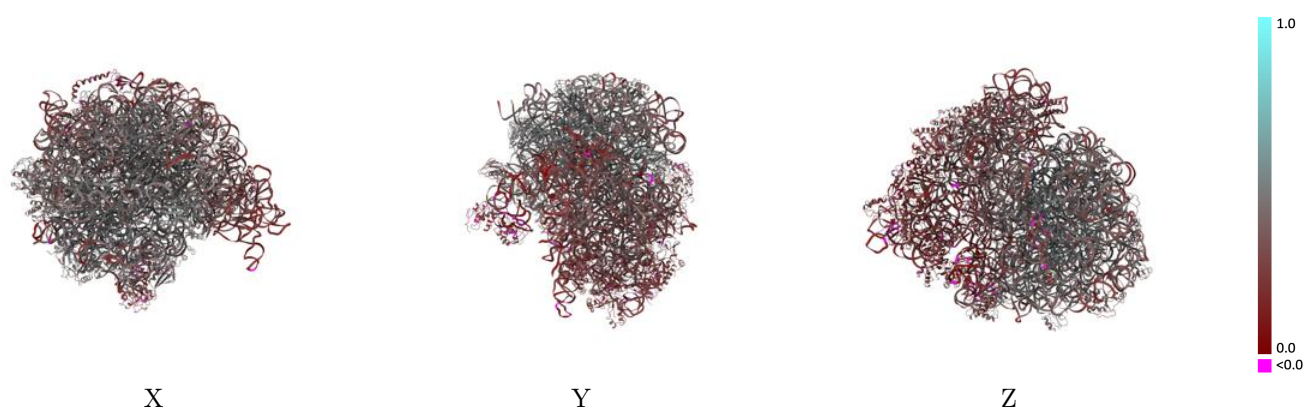
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21635 and PDB model 6WDG. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

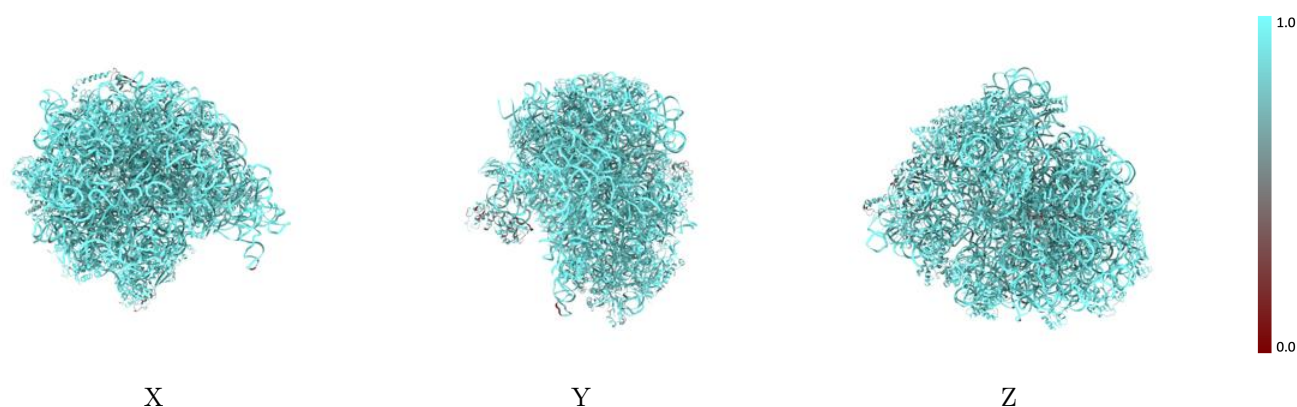
This section was not generated.

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



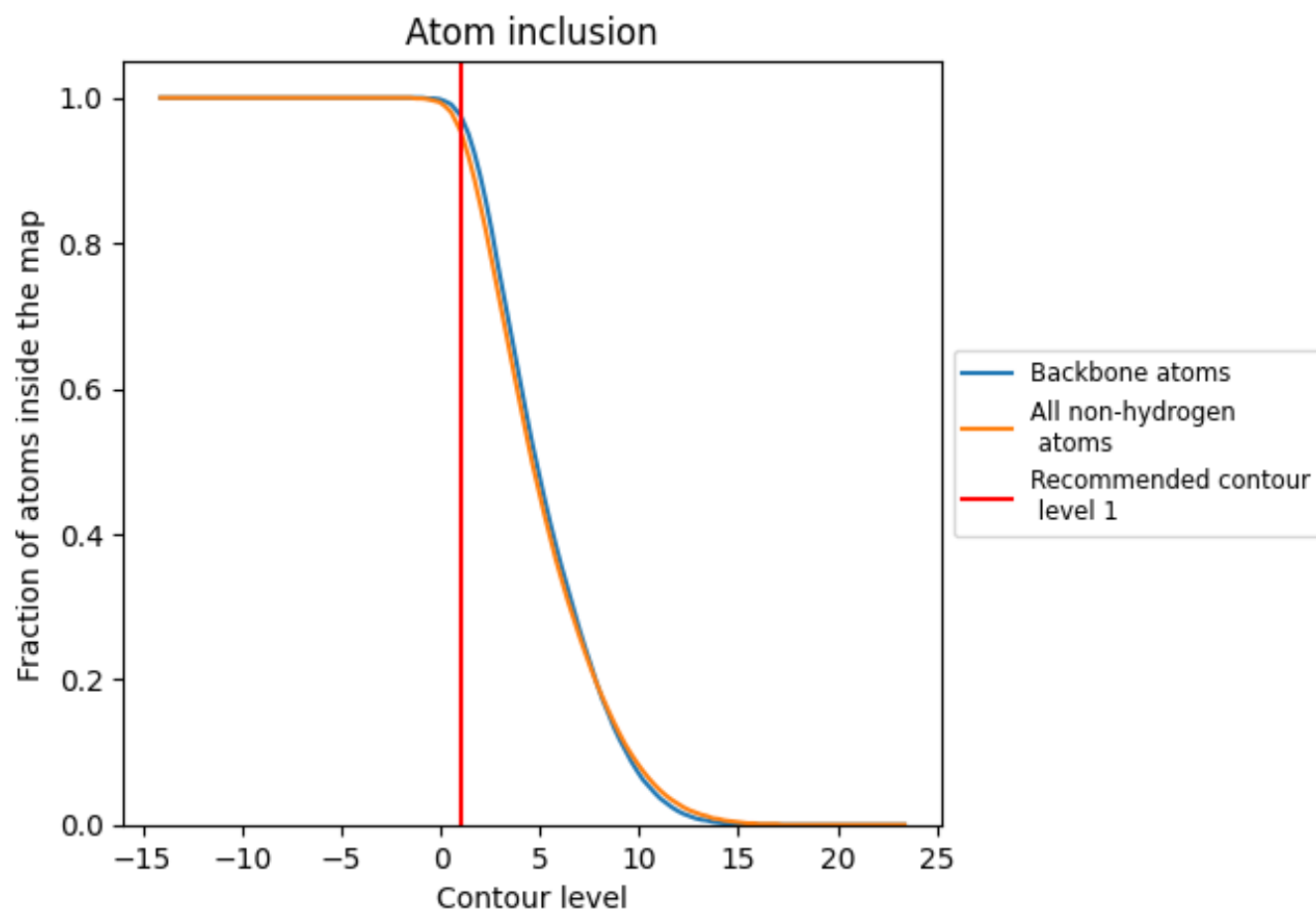
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9550	 0.3630
1	 0.9790	 0.4080
2	 0.9860	 0.3620
3	 0.9660	 0.2890
4	 0.8630	 0.2300
5	 0.9710	 0.2360
7	 0.9570	 0.2520
B	 0.9700	 0.4740
C	 0.8480	 0.4140
D	 0.9630	 0.4860
E	 0.9800	 0.5080
F	 0.8770	 0.4470
G	 0.8740	 0.2800
H	 0.8200	 0.2450
I	 0.8700	 0.2590
J	 0.9210	 0.3350
K	 0.9670	 0.3500
L	 0.9150	 0.2370
M	 0.9130	 0.3490
N	 0.8580	 0.2050
O	 0.7570	 0.2490
P	 0.9460	 0.3660
Q	 0.9360	 0.3900
R	 0.9050	 0.2570
S	 0.7950	 0.2330
T	 0.9640	 0.3670
U	 0.9040	 0.3360
V	 0.9430	 0.3520
W	 0.9380	 0.3400
X	 0.9310	 0.2300
Y	 0.9010	 0.2800
Z	 0.8900	 0.2880
a	 0.9100	 0.1860
b	 0.9690	 0.4860
c	 0.9670	 0.4890



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Chain	Atom inclusion	Q-score
d	 0.9590	 0.4480
e	 0.9350	 0.3080
f	 0.9600	 0.3870
g	 0.7890	 0.2690
h	 0.7090	 0.1550
i	 0.6440	 0.1660
j	 0.9580	 0.4740
k	 0.9510	 0.4810
l	 0.9590	 0.4660
m	 0.9670	 0.4710
n	 0.9710	 0.4790
o	 0.9590	 0.4020
p	 0.9630	 0.4690
q	 0.9530	 0.4780
r	 0.9600	 0.4500
s	 0.9340	 0.4740
t	 0.9540	 0.4480
u	 0.9540	 0.4200
v	 0.9680	 0.4400
w	 0.9540	 0.4890
x	 0.9700	 0.4840
y	 0.9480	 0.3830
z	 0.9680	 0.4610