



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 09:32 PM UTC

PDB ID : 6WDL / pdb_00006wdl
EMDB ID : EMD-21640
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Non-cognate Structure V-B1)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.70 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

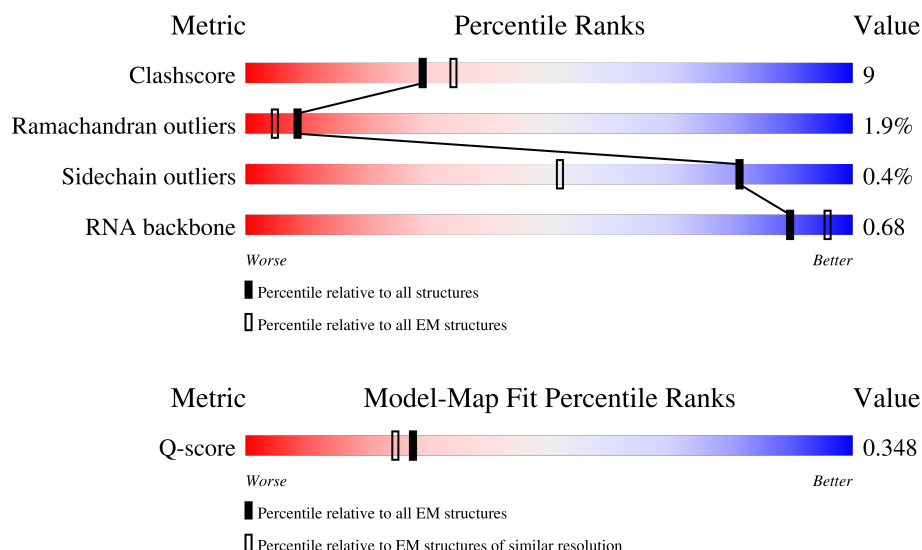
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



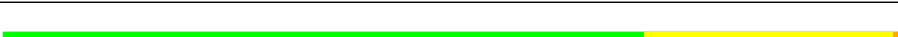
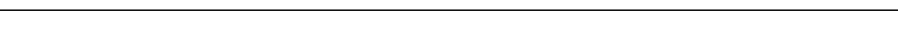
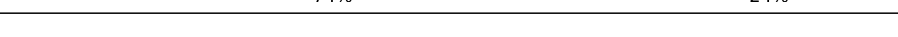
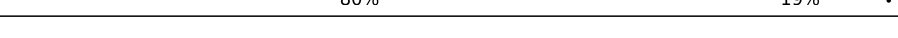
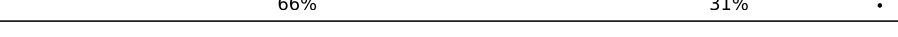
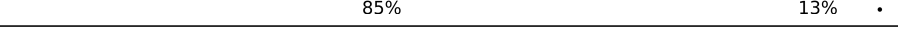
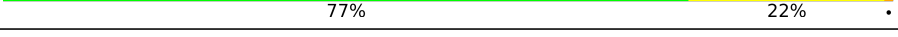
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	

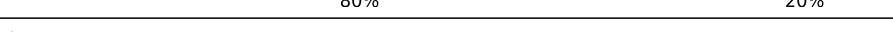
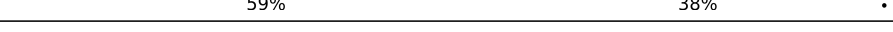
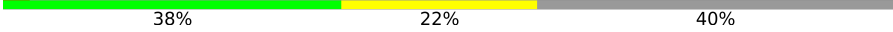
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
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	 61% 33% 6%
55	5	77	 71% 27% .
55	6	77	 66% 32% .
56	4	18	 78% 22%
57	7	76	 71% 24% 5%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 150220 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		
55	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

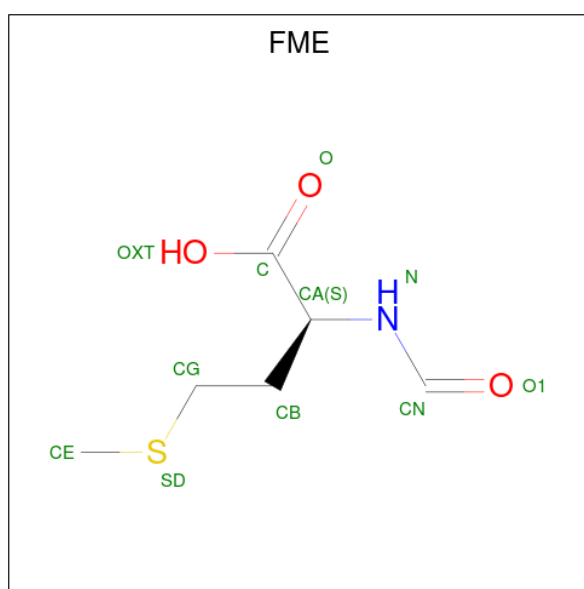
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	77	119	17		

- Molecule 57 is a RNA chain called tRNA^{Phe}.

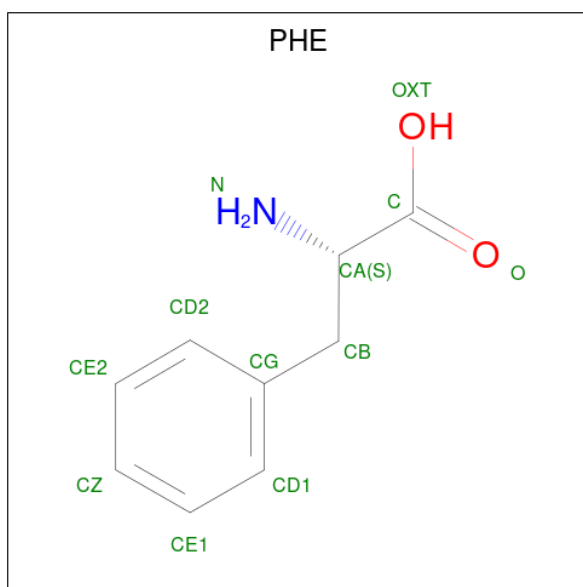
Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 58 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



Mol	Chain	Residues	Atoms					AltConf
58	1	1	Total	C	N	O	S	0
			8	5	1	1	1	

- Molecule 59 is PHENYLALANINE (CCD ID: PHE) (formula: C₉H₁₁NO₂).

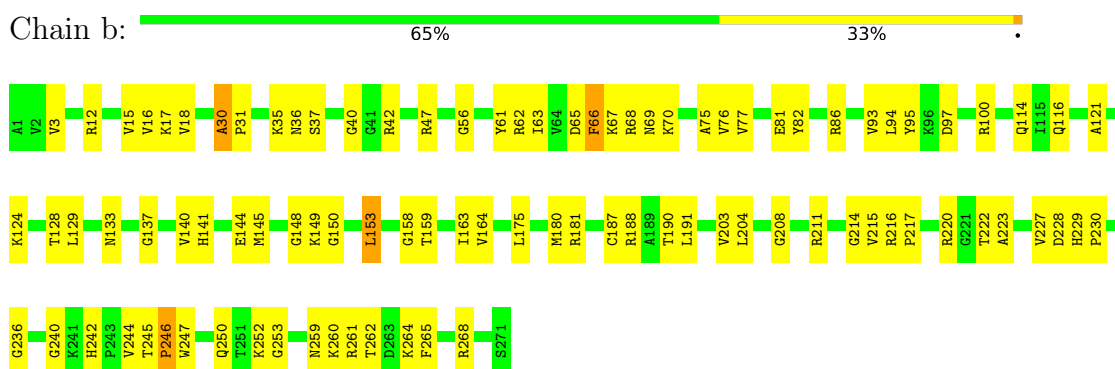


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
59	7	1	11	9	1	1	0

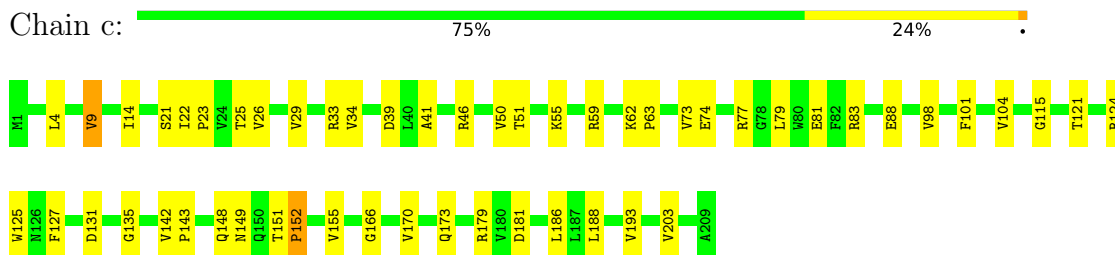
3 Residue-property plots [i](#)

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.

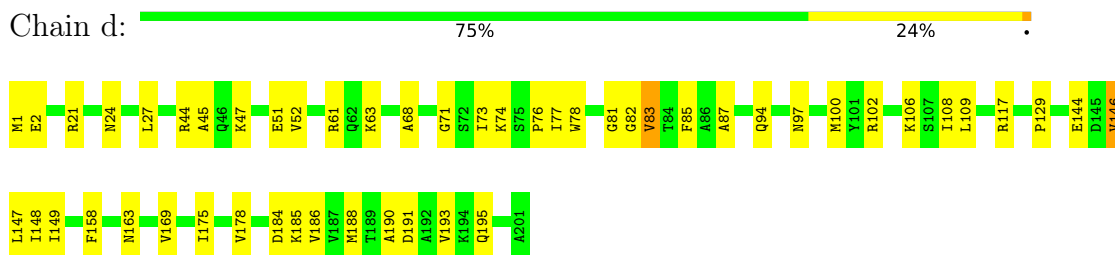
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

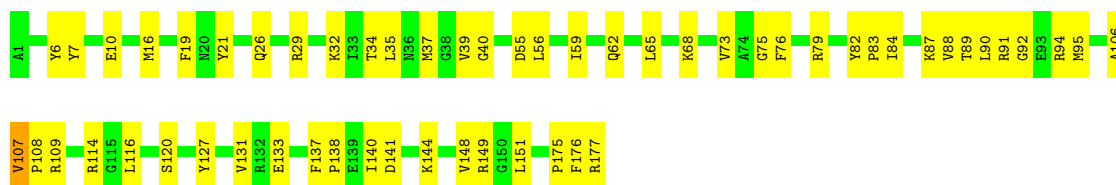


- Molecule 3: 50S ribosomal protein L4

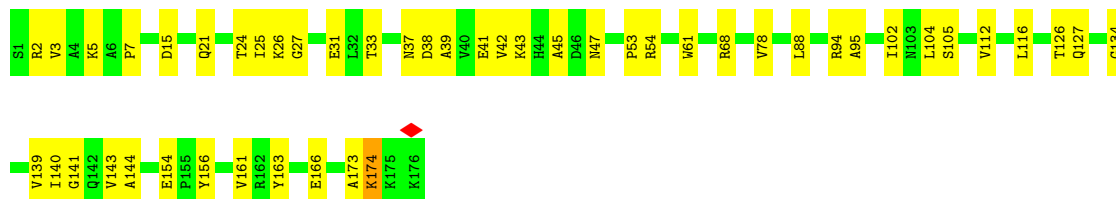


- Molecule 4: 50S ribosomal protein L5

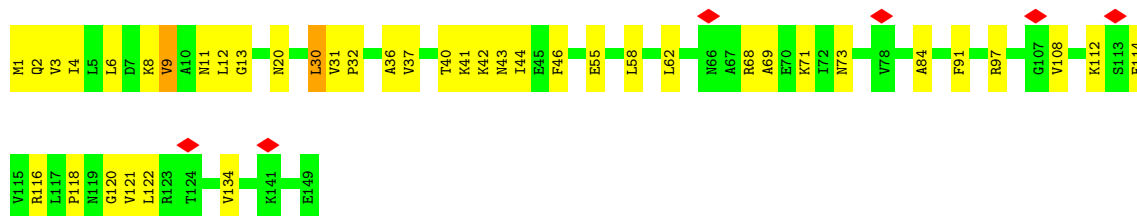




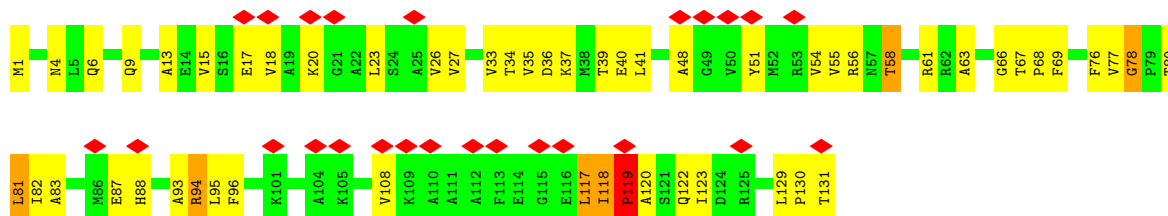
• Molecule 5: 50S ribosomal protein L6



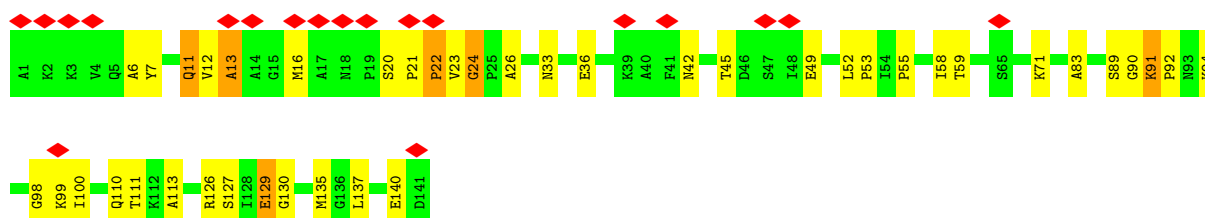
• Molecule 6: 50S ribosomal protein L9



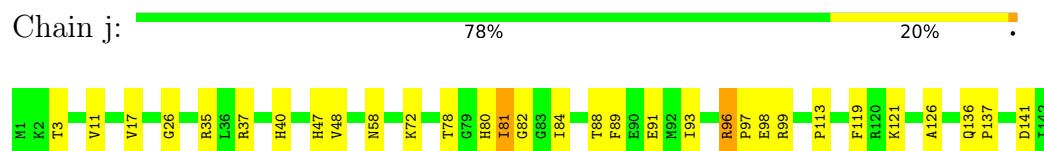
• Molecule 7: 50S ribosomal protein L10



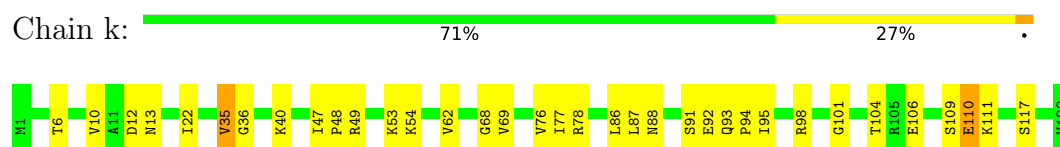
• Molecule 8: 50S ribosomal protein L11



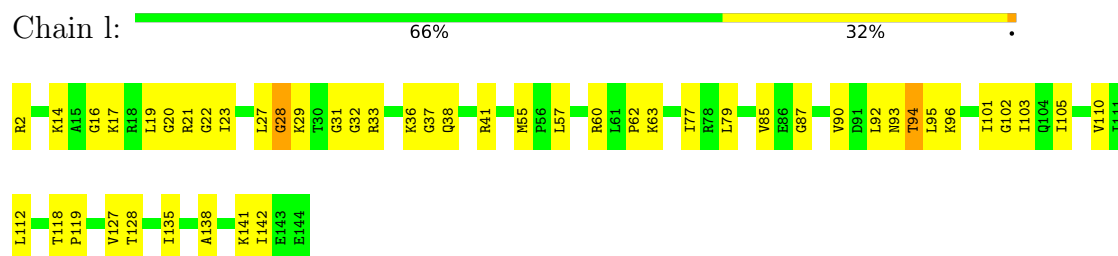
- Molecule 9: 50S ribosomal protein L13



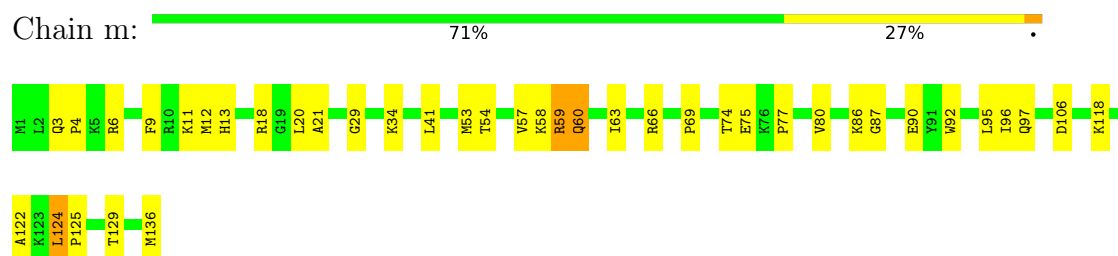
- Molecule 10: 50S ribosomal protein L14



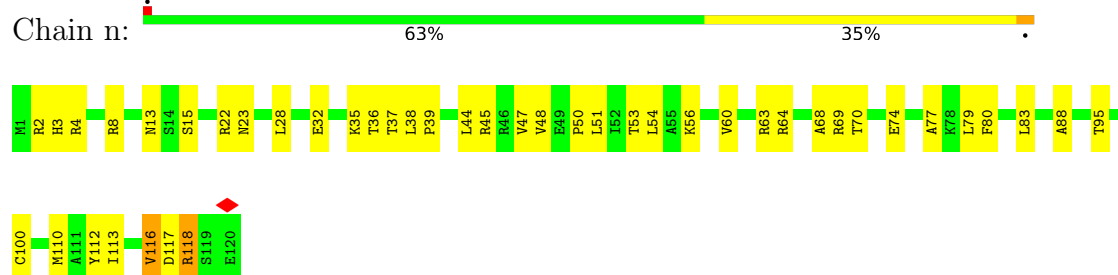
- Molecule 11: 50S ribosomal protein L15



- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17

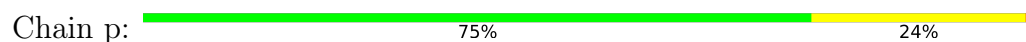


- Molecule 14: 50S ribosomal protein L18

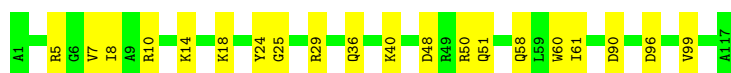
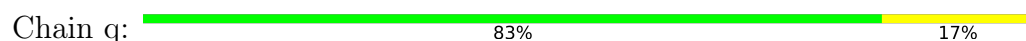




- Molecule 15: 50S ribosomal protein L19



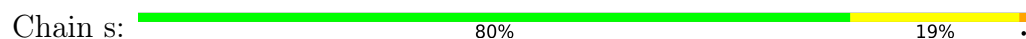
- Molecule 16: 50S ribosomal protein L20



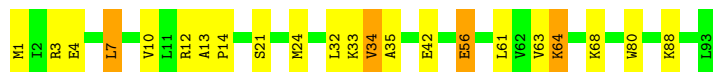
- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25





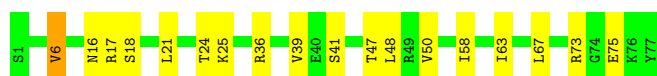
- Molecule 22: 50S ribosomal protein L27

Chain w: 85% 13%



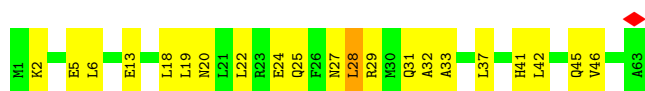
- Molecule 23: 50S ribosomal protein L28

Chain x: 77% 22%



- Molecule 24: 50S ribosomal protein L29

Chain y: 67% 32%



- Molecule 25: 50S ribosomal protein L30

Chain z: 81% 19%



- Molecule 26: 50S ribosomal protein L32

Chain B: 71% 29%



- Molecule 27: 50S ribosomal protein L33

Chain C: 78% 22%

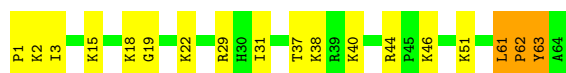


- Molecule 28: 50S ribosomal protein L34

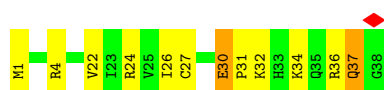
Chain D: 72% 28%



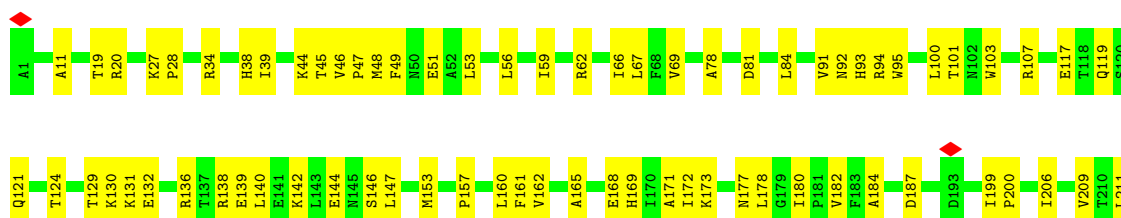
- Molecule 29: 50S ribosomal protein L35



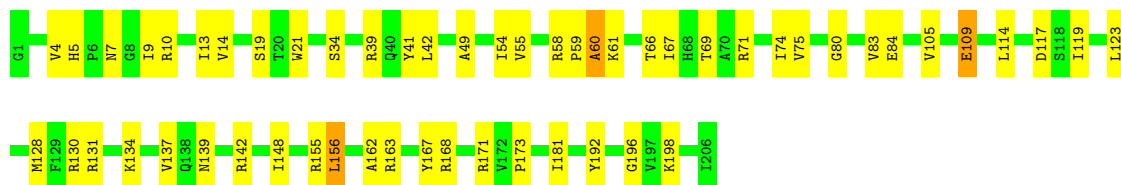
- Molecule 30: 50S ribosomal protein L36



- Molecule 31: 30S ribosomal protein S2



- Molecule 32: 30S ribosomal protein S3

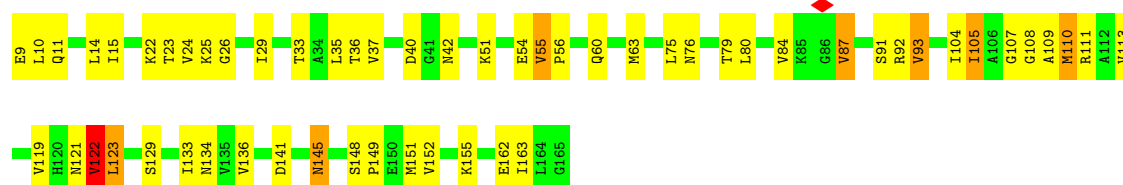


- Molecule 33: 30S ribosomal protein S4

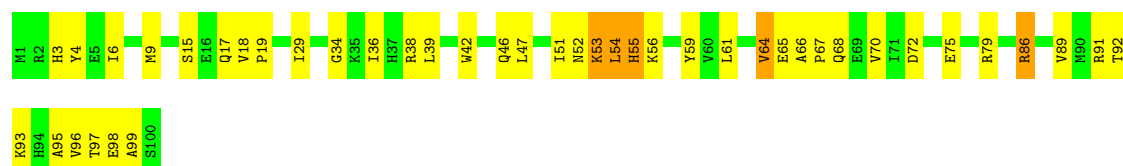




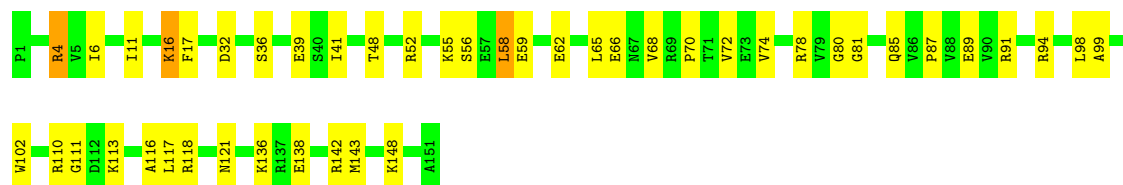
- Molecule 34: 30S ribosomal protein S5



- Molecule 35: 30S ribosomal protein S6



- Molecule 36: 30S ribosomal protein S7

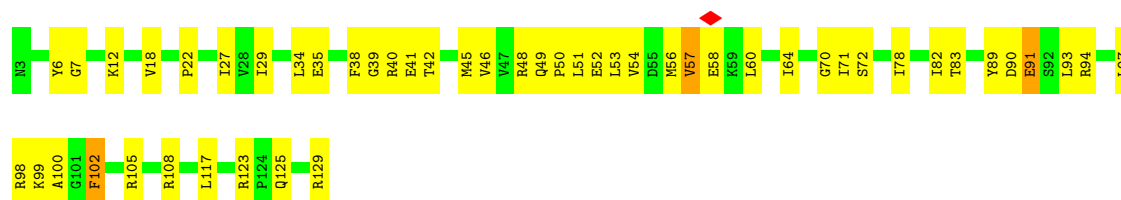


- Molecule 37: 30S ribosomal protein S8

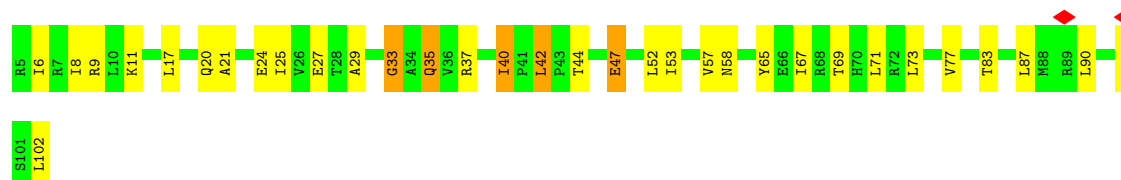


- Molecule 38: 30S ribosomal protein S9





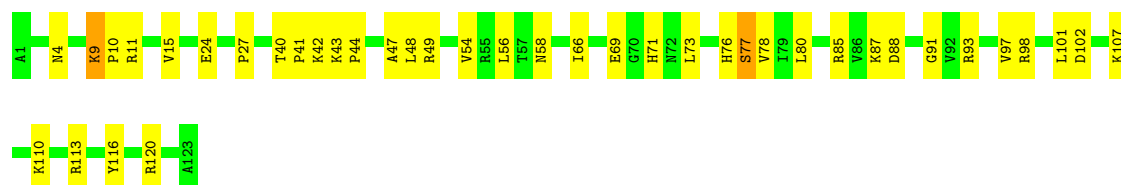
- Molecule 39: 30S ribosomal protein S10



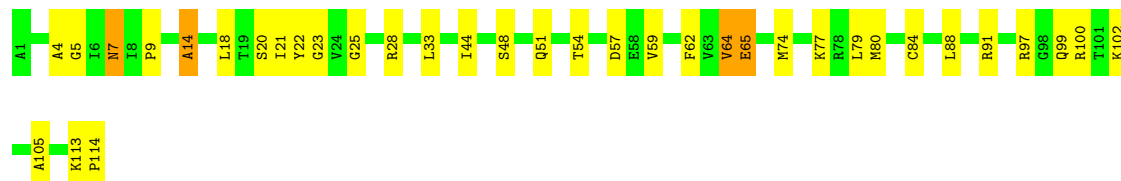
- Molecule 40: 30S ribosomal protein S11



- Molecule 41: 30S ribosomal protein S12

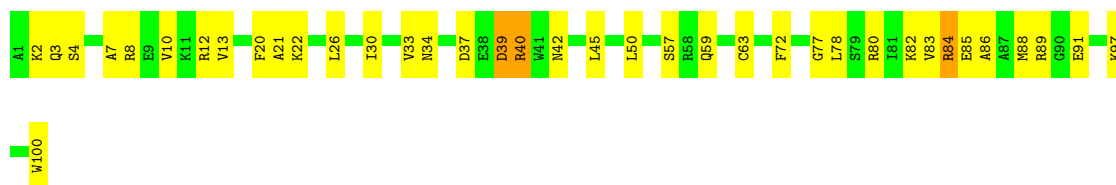


- Molecule 42: 30S ribosomal protein S13

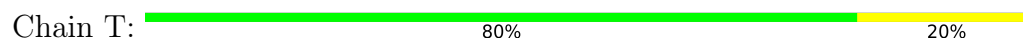


- Molecule 43: 30S ribosomal protein S14

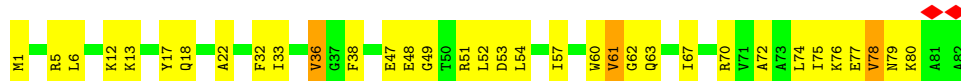




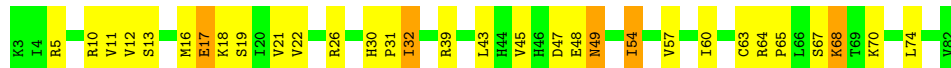
- Molecule 44: 30S ribosomal protein S15



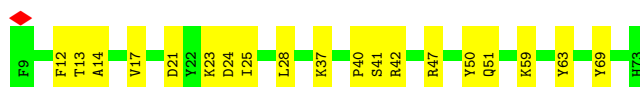
- Molecule 45: 30S ribosomal protein S16



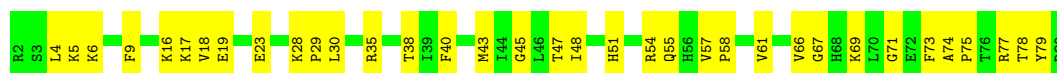
- Molecule 46: 30S ribosomal protein S17



- Molecule 47: 30S ribosomal protein S18



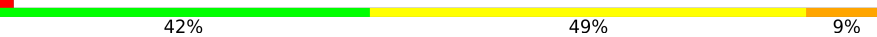
- Molecule 48: 30S ribosomal protein S19



- Molecule 49: 30S ribosomal protein S20

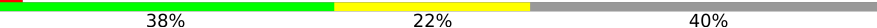


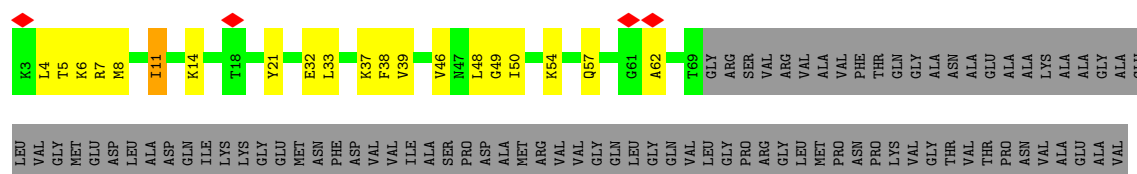
- Molecule 50: 30S ribosomal protein S21

Chain Z: 



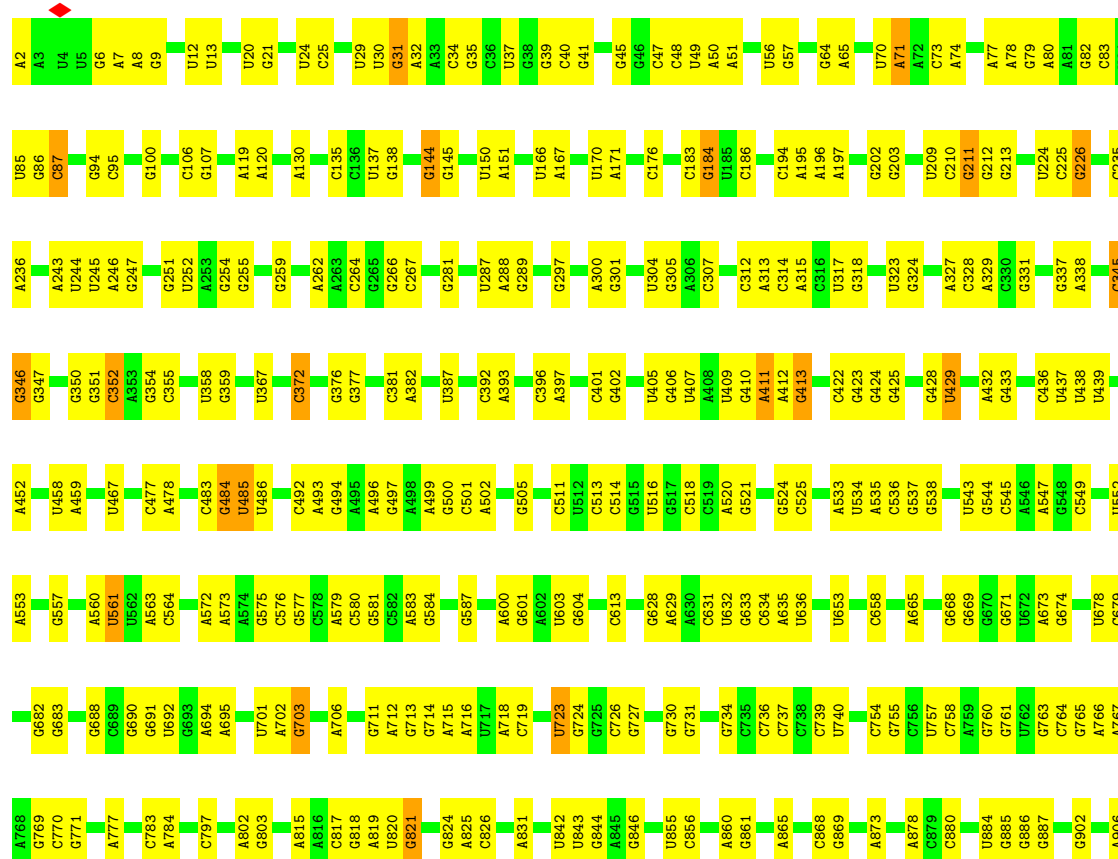
- Molecule 51: 50S ribosomal protein L1

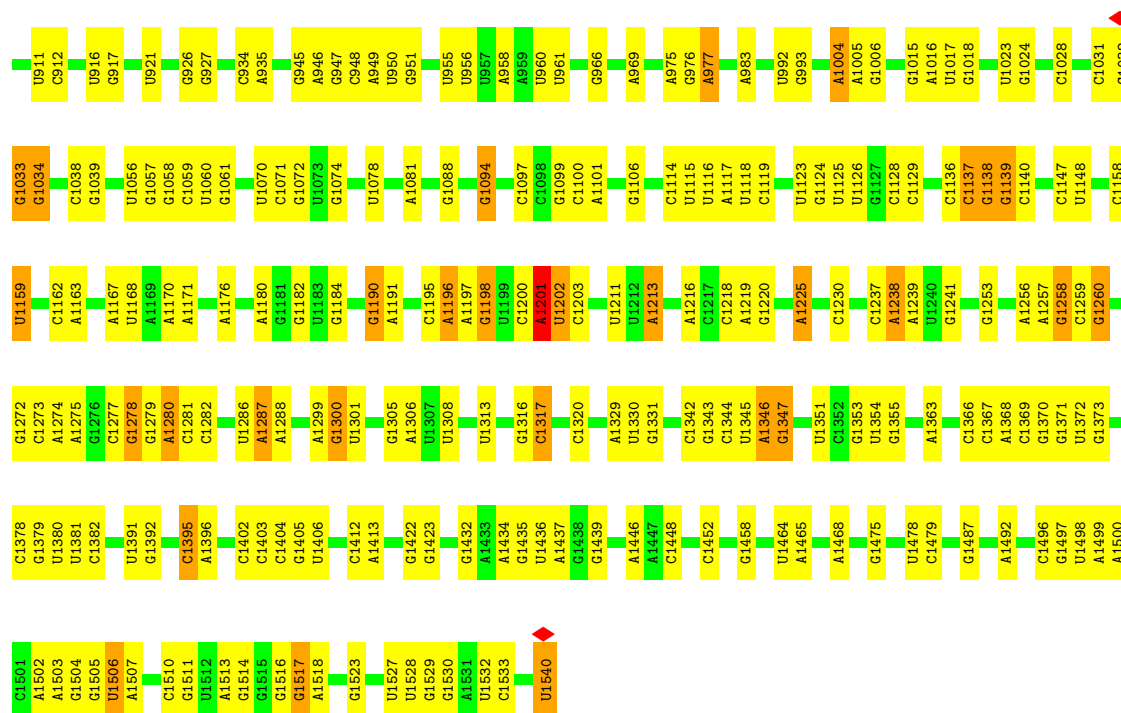
Chain a: 



- Molecule 52: 16S ribosomal RNA

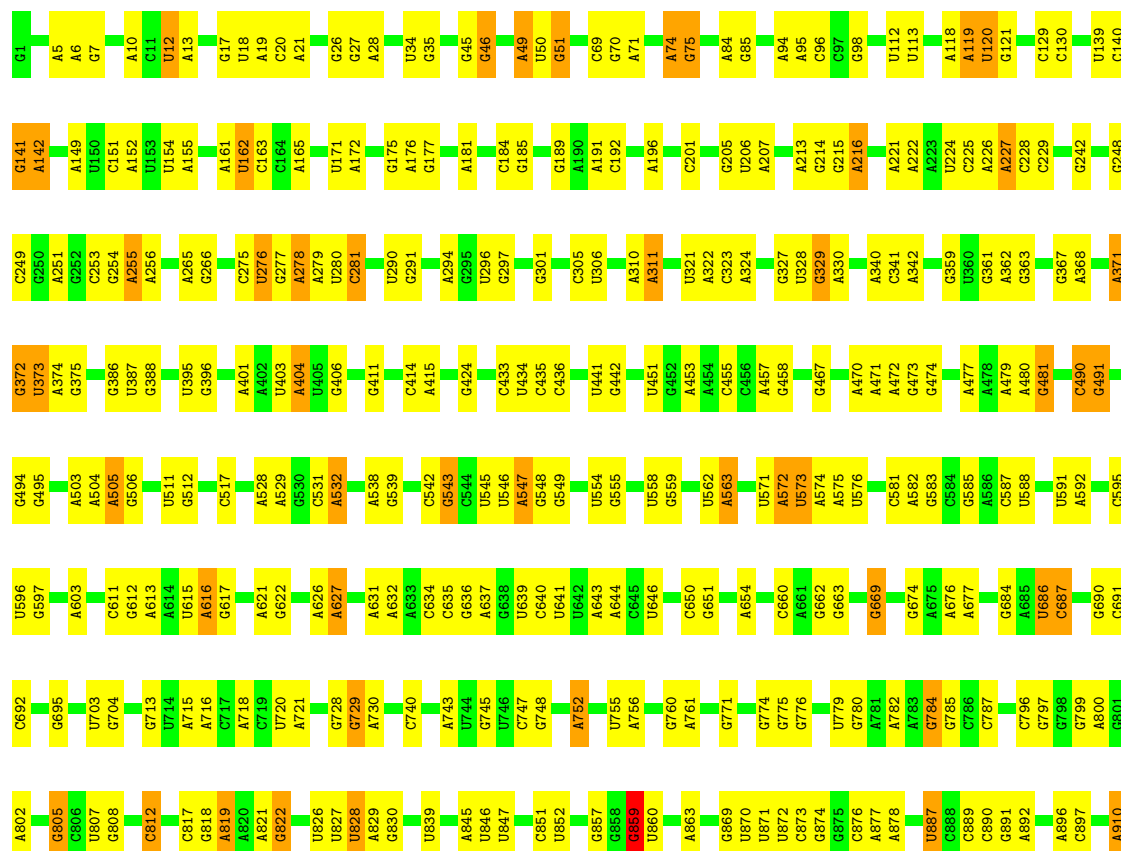
Chain 3: 



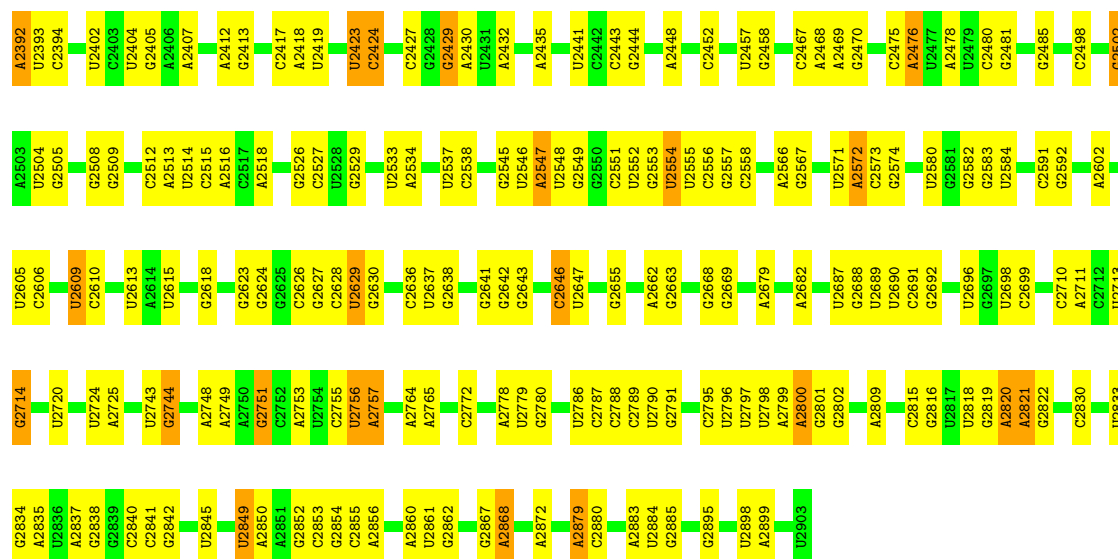


• Molecule 53: 23S ribosomal RNA

Chain 1: 62% 33% 5%

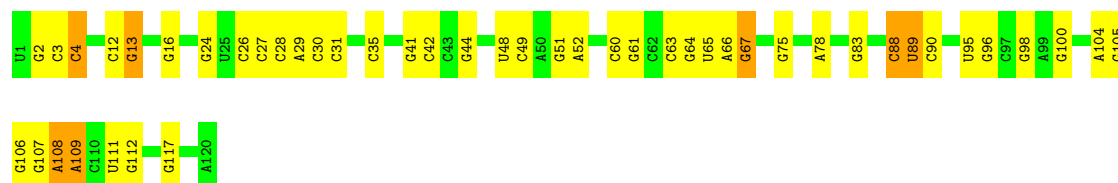


U2305	U2220	G2116	U2022	A1913	A1803	G1696	A1569	G1435	G1309	G1202	C1104	A1009	A911
G2308	G2221	A2117	C2023	C1914	G1807	G1697	G1581	G1436	G1310	G1212	G1105	A1010	A917
A2309	A2225	A2118	G2024	U1917	A1808	G1699	U1584	U1438	G1311	A1213	U1012	G1011	G924
C2313	U2229	G2121	G2029	A1918	A1809	A1919	U1584	U1439	U1316	G1216	A1014	C1013	A925
A2317	U2230	U2122	A2031	A1919	A1810	A1705	U1585	U1440	G1317	U1217	U1015	U1015	U929
G2318	U2234	G2123	G2032	G1929	G1816	C1706	C1592	G1441	A1321	G1218	G1016	G1016	U932
G2319	U2235	G2124	G2035	U1930	A1819	U1709	A1593	C1454	A1322	G1220	U1019	A1020	G935
G2325	U2236	A2125	G2036	A1931	U1820	U1710	C1600	C1461	U1326	U1231	A1021	A1021	A936
C2326	U2237	A2126	G2039	A1932	U1820	G1715	U1602	C1463	A1327	U1234	G1022	G1022	C937
A2327	U2238	G2127	G2040	G1933	G1826	U1720	A1603	G1464	U1329	G1225	U1023	U1023	G938
U2329	A2241	U2132	U2041	A1936	U1827	G1721	C1606	U1468	G1330	U1231	G1026	G1026	G939
G2330	G2242	G2133	A2042	A1938	G1828	G1721	C1607	C1462	G1331	A1127	A1027	A1027	G940
G2331	A2243	C2043	G2043	C2043	A1829	U1729	C1608	C1463	G1332	G1232	A1028	A1028	A941
C2332	U2244	U2139	C2044	U1943	C1830	C1730	U1608	U1475	G1333	G1233	A1029	A1029	G942
A2333	U2245	G2140	C2045	U1944	G1831	G1731	C1611	U1476	A1336	U1234	C1030	C1030	A943
A2336	U2246	G2141	G2048	C1947	C1837	G1732	C1614	G1482	G1341	G1236	U1033	U1033	C946
G2337	U2247	C2145	G2049	G1948	G1846	U1736	A1615	A1490	G1344	G1250	G1034	G1034	A947
U2343	U2250	U2151	G2055	U1955	A1847	G1737	A1616	G1491	U1344	G1251	U1035	U1035	C948
U2344	U2251	U2155	G2056	C1957	A1848	G1738	G1619	C1498	C1345	A1252	G1036	G1036	G949
G2345	U2252	U2156	A2060	U1963	U1856	G1740	G1645	G1501	A1365	A1253	A1039	A1039	G950
C2349	U2257	G2162	A2061	G1964	G1857	U1749	C1646	G1507	A1366	G1254	C1045	C1045	C951
G2350	U2258	A2163	A2062	C1965	G1861	A1749	U1647	C1507	A1367	G1256	C1046	C1046	U955
A2351	U2259	C2164	G2066	A1966	U1871	G1753	U1648	A1508	G1369	A1268	A1047	A1047	G956
C2352	U2260	U2172	U2067	C1967	A1872	U1758	G1651	A1509	C1370	A1269	A1048	A1048	C961
G2353	U2261	A2173	G2068	U1970	G1873	A1758	A1652	A1510	G1371	C1270	C1049	C1049	G962
A2358	U2262	U2180	A2069	G1971	G1874	U1765	G1653	A1515	A1378	A1272	C1053	C1053	U963
C2359	U2263	U2181	A2070	G1972	G1875	G1766	A1654	A1522	U1379	A1275	A1054	A1054	C968
G2360	U2264	U2182	C2072	U1978	U1880	U1765	C1658	U1523	G1380	A1276	A1057	A1057	G969
G2361	U2265	A2183	A2082	U1979	C1881	G1766	G1659	G1524	G1381	G1277	U1058	U1058	U970
A2366	U2266	U2184	G2083	G1980	G1884	U1773	A1664	A1528	G1382	C1278	G1059	G1059	G971
C2367	U2267	U2185	U2086	U1983	G1889	U1774	G1666	G1529	C1386	G1279	U1060	U1060	A972
G2368	U2268	G2190	G2087	U1991	A1890	U1775	G1666	A1535	A1387	A1286	U1061	U1061	A973
A2369	U2269	A2191	A2088	G1992	G1891	G1776	A1669	C1536	U1394	G1288	G1062	G1062	A975
G2370	U2270	C2196	G2093	U1993	C1892	U1781	G1674	U1542	A1395	U1294	U1066	U1066	A983
U2371	U2271	U2197	C2096	C1996	C1894	A1784	A1677	G1543	C1398	G1295	A1070	A1070	A988
U2372	U2272	A2198	C2096	C1997	G1899	A1784	A1677	G1543	G1416	G1296	G1071	G1071	A990
A2376	U2273	G2200	C2104	U1998	A1899	C1790	U1683	G1555	U1394	C1297	A1077	A1077	C995
C2381	U2274	U2199	U2105	C1999	A1901	A1791	G1684	G1560	A1419	G1298	U1078	U1078	A996
G2382	U2275	U2203	U2106	C2000	G1906	U1796	C1685	G1560	A1420	C1299	C1079	C1079	U1001
C2383	U2276	G2204	G2107	C2001	G1907	U1797	C1686	G1563	G1421	G1300	A1080	A1080	A1001
U2384	U2277	U2211	G2110	U2011	G1908	U1798	G1687	C1564	G1422	A1301	U1081	U1081	U1001
C2385	U2278	U2212	G2111	G2012	C1909	U1799	U1688	C1565	G1423	A1302	U1082	U1082	G1002
G2389	U2279	U2213	G2112	U2019	G1910	G1800	A1689	A1566	G1424	C1306	U1083	U1083	G1003
U2390	U2280	U2214	G2113	A2019	U1911	A1801	C1694	G1567	G1425	A1307	A1084	A1084	U1004
G2391	U2281	U2215	G2114	C2021	U1912	A1802	G1695	G1568	A1434	U1201	A1085	A1085	C1007
	U2282	U2216	G2115								A1088	A1088	A1008



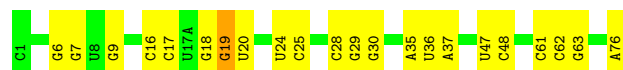
- Molecule 54: 5S ribosomal RNA

Chain 2: 61% 33% 6%



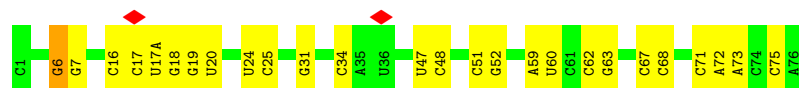
- Molecule 55: tRNA^{fMet}

Chain 5: 71% 27%



- Molecule 55: tRNA^{fMet}

Chain 6: 66% 32%

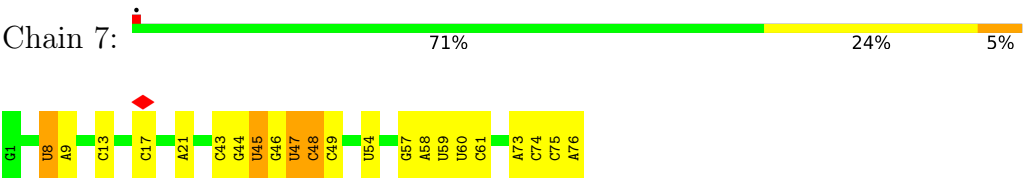


- Molecule 56: mRNA

Chain 4: 78% 22%



- Molecule 57: tRNA^{Phe}



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	7369	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	20.349	Depositor
Minimum map value	-9.493	Depositor
Average map value	0.121	Depositor
Map value standard deviation	0.931	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	0.29	0/2122	0.97	7/2852 (0.2%)
2	c	0.29	0/1586	0.82	2/2134 (0.1%)
3	d	0.28	0/1571	0.90	3/2113 (0.1%)
4	e	0.31	0/1435	0.91	4/1926 (0.2%)
5	f	0.30	0/1343	0.86	4/1816 (0.2%)
6	g	0.34	0/1122	0.99	3/1515 (0.2%)
7	h	0.34	0/1002	1.01	8/1350 (0.6%)
8	i	0.35	0/1046	0.99	8/1410 (0.6%)
9	j	0.27	0/1152	0.82	4/1551 (0.3%)
10	k	0.28	0/948	0.97	3/1268 (0.2%)
11	l	0.30	0/1054	0.91	1/1403 (0.1%)
12	m	0.29	0/1093	0.89	3/1460 (0.2%)
13	n	0.31	0/974	0.91	2/1301 (0.2%)
14	o	0.29	0/902	0.89	5/1209 (0.4%)
15	p	0.29	0/929	0.83	2/1242 (0.2%)
16	q	0.29	0/960	0.86	1/1278 (0.1%)
17	r	0.30	0/829	0.90	2/1107 (0.2%)
18	s	0.27	0/864	0.85	0/1156
19	t	0.29	0/745	0.92	2/994 (0.2%)
20	u	0.29	0/788	0.89	2/1051 (0.2%)
21	v	0.28	0/766	0.86	2/1025 (0.2%)
22	w	0.30	0/582	0.83	0/769
23	x	0.29	0/635	0.78	0/848
24	y	0.28	0/510	0.78	1/677 (0.1%)
25	z	0.29	0/453	0.73	0/605
26	B	0.27	0/450	0.76	0/599
27	C	0.32	0/417	0.82	0/554
28	D	0.31	0/380	0.88	0/498
29	E	0.30	0/513	0.95	4/676 (0.6%)
30	F	0.35	0/303	0.90	2/397 (0.5%)
31	G	0.30	0/1788	0.90	3/2408 (0.1%)
32	H	0.30	0/1652	0.87	2/2225 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.93	6/2227 (0.3%)
34	J	0.33	0/1170	1.07	11/1573 (0.7%)
35	K	0.30	0/836	0.97	3/1128 (0.3%)
36	L	0.29	0/1196	0.90	3/1602 (0.2%)
37	M	0.30	0/989	0.95	3/1326 (0.2%)
38	N	0.29	0/1034	0.90	1/1375 (0.1%)
39	O	0.33	0/797	0.95	5/1077 (0.5%)
40	P	0.31	0/886	0.95	2/1195 (0.2%)
41	Q	0.31	0/969	1.03	5/1300 (0.4%)
42	R	0.30	0/893	0.87	0/1193
43	S	0.29	0/817	0.94	4/1088 (0.4%)
44	T	0.28	0/722	0.91	2/964 (0.2%)
45	U	0.32	0/659	0.97	4/884 (0.5%)
46	V	0.28	0/658	0.99	4/881 (0.5%)
47	W	0.30	0/545	0.88	2/731 (0.3%)
48	X	0.31	0/653	0.95	3/877 (0.3%)
49	Y	0.29	0/671	0.98	5/888 (0.6%)
50	Z	0.36	0/551	1.01	3/728 (0.4%)
51	a	0.33	0/1034	0.83	1/1387 (0.1%)
52	3	0.40	0/36963	0.50	2/57662 (0.0%)
53	1	0.39	0/69796	0.51	2/108888 (0.0%)
54	2	0.40	0/2872	0.51	0/4479
55	5	0.39	0/1832	0.48	0/2855
55	6	0.40	0/1832	0.51	0/2855
56	4	0.40	0/436	0.50	0/679
57	7	0.39	0/1809	0.48	0/2819
All	All	0.37	0/163199	0.64	151/244078 (0.1%)

There are no bond length outliers.

The worst 5 of 151 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	J	163	ILE	N-CA-C	10.98	120.96	110.42
3	d	73	ILE	N-CA-C	-9.62	103.77	113.10
17	r	50	GLY	N-CA-C	-7.93	102.62	112.77
36	L	16	LYS	N-CA-C	-7.76	105.78	114.62
34	J	55	VAL	N-CA-C	7.65	121.53	112.35

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	67	0
2	c	1565	0	1616	42	0
3	d	1552	0	1619	37	0
4	e	1411	0	1447	42	0
5	f	1323	0	1374	24	0
6	g	1111	0	1148	30	0
7	h	989	0	1025	42	0
8	i	1032	0	1088	31	0
9	j	1129	0	1162	29	0
10	k	939	0	1012	30	0
11	l	1045	0	1117	39	0
12	m	1074	0	1157	39	0
13	n	961	0	1000	35	0
14	o	892	0	923	22	0
15	p	917	0	965	24	0
16	q	947	0	1022	19	0
17	r	816	0	839	27	0
18	s	857	0	922	15	0
19	t	739	0	807	17	0
20	u	780	0	834	24	0
21	v	753	0	780	21	0
22	w	575	0	592	13	0
23	x	625	0	655	9	0
24	y	509	0	543	14	0
25	z	449	0	491	9	0
26	B	444	0	461	13	0
27	C	410	0	440	9	0
28	D	377	0	418	11	0
29	E	504	0	574	17	0
30	F	302	0	343	12	0
31	G	1757	0	1787	55	0
32	H	1625	0	1699	43	0
33	I	1643	0	1710	50	0
34	J	1157	0	1199	49	0
35	K	818	0	808	38	0
36	L	1182	0	1240	35	0
37	M	979	0	1034	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	40	0
39	O	787	0	828	26	0
40	P	870	0	878	27	0
41	Q	955	0	1019	31	0
42	R	884	0	944	28	0
43	S	805	0	847	29	0
44	T	714	0	737	13	0
45	U	649	0	666	26	0
46	V	649	0	691	22	0
47	W	536	0	552	11	0
48	X	638	0	665	26	0
49	Y	665	0	714	27	0
50	Z	545	0	579	38	0
51	a	1027	0	1092	40	0
52	3	33012	0	16618	411	0
53	1	62317	0	31346	747	0
54	2	2568	0	1303	43	0
55	5	1640	0	837	10	0
55	6	1640	0	837	17	0
56	4	388	0	197	2	0
57	7	1619	0	821	9	0
58	1	8	0	8	0	0
59	7	11	0	8	0	0
All	All	150220	0	101265	2328	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 9.

The worst 5 of 2328 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)
53:1:45:G:H5''	53:1:46:G:H5'	1.23	1.11
36:L:78:ARG:HH22	52:3:1382:C:H5'	1.20	1.01
34:J:54:GLU:HG3	34:J:56:PRO:HD2	1.44	0.99
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.44	0.98
12:m:12:MET:HA	53:1:910:A:H62	1.33	0.92

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%)	236 (88%)	28 (10%)	5 (2%)	6	33
2	c	207/209 (99%)	181 (87%)	26 (13%)	0	100	100
3	d	199/201 (99%)	185 (93%)	13 (6%)	1 (0%)	24	56
4	e	175/177 (99%)	153 (87%)	21 (12%)	1 (1%)	21	52
5	f	174/176 (99%)	163 (94%)	9 (5%)	2 (1%)	11	42
6	g	147/149 (99%)	128 (87%)	17 (12%)	2 (1%)	9	37
7	h	129/131 (98%)	98 (76%)	25 (19%)	6 (5%)	2	18
8	i	139/141 (99%)	120 (86%)	15 (11%)	4 (3%)	3	26
9	j	140/142 (99%)	129 (92%)	10 (7%)	1 (1%)	18	50
10	k	120/122 (98%)	102 (85%)	15 (12%)	3 (2%)	4	29
11	l	141/143 (99%)	114 (81%)	22 (16%)	5 (4%)	3	24
12	m	134/136 (98%)	120 (90%)	11 (8%)	3 (2%)	5	31
13	n	118/120 (98%)	99 (84%)	16 (14%)	3 (2%)	4	29
14	o	114/116 (98%)	103 (90%)	11 (10%)	0	100	100
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%)	88 (87%)	12 (12%)	1 (1%)	12	43
18	s	108/110 (98%)	98 (91%)	8 (7%)	2 (2%)	6	33
19	t	91/93 (98%)	84 (92%)	7 (8%)	0	100	100
20	u	100/102 (98%)	83 (83%)	13 (13%)	4 (4%)	2	21
21	v	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
22	w	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
23	x	75/77 (97%)	68 (91%)	3 (4%)	4 (5%)	1	16
24	y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
25	z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	51 (94%)	2 (4%)	1 (2%)	6	33
27	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
28	D	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
29	E	62/64 (97%)	52 (84%)	8 (13%)	2 (3%)	3	25
30	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	27
31	G	223/225 (99%)	202 (91%)	21 (9%)	0	100	100
32	H	204/206 (99%)	183 (90%)	18 (9%)	3 (2%)	8	36
33	I	203/205 (99%)	177 (87%)	23 (11%)	3 (2%)	8	36
34	J	155/157 (99%)	131 (84%)	20 (13%)	4 (3%)	4	28
35	K	98/100 (98%)	83 (85%)	9 (9%)	6 (6%)	1	14
36	L	149/151 (99%)	131 (88%)	17 (11%)	1 (1%)	18	50
37	M	127/129 (98%)	113 (89%)	13 (10%)	1 (1%)	16	48
38	N	125/127 (98%)	100 (80%)	19 (15%)	6 (5%)	2	17
39	O	96/98 (98%)	79 (82%)	12 (12%)	5 (5%)	1	17
40	P	114/116 (98%)	93 (82%)	19 (17%)	2 (2%)	6	34
41	Q	121/123 (98%)	91 (75%)	24 (20%)	6 (5%)	1	17
42	R	112/114 (98%)	99 (88%)	8 (7%)	5 (4%)	2	18
43	S	98/100 (98%)	87 (89%)	9 (9%)	2 (2%)	6	32
44	T	86/88 (98%)	76 (88%)	9 (10%)	1 (1%)	10	40
45	U	80/82 (98%)	66 (82%)	12 (15%)	2 (2%)	4	29
46	V	78/80 (98%)	61 (78%)	15 (19%)	2 (3%)	4	28
47	W	63/65 (97%)	58 (92%)	3 (5%)	2 (3%)	3	25
48	X	77/79 (98%)	67 (87%)	9 (12%)	1 (1%)	9	38
49	Y	83/85 (98%)	80 (96%)	2 (2%)	1 (1%)	10	40
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	7
51	a	130/223 (58%)	124 (95%)	6 (5%)	0	100	100
All	All	5919/6112 (97%)	5178 (88%)	631 (11%)	110 (2%)	8	33

5 of 110 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
6	g	9	VAL

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Mol	Chain	Res	Type
7	h	78	GLY
7	h	81	LEU
7	h	108	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100
7	h	100/100 (100%)	99 (99%)	1 (1%)	68	74
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	75
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	74
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	74
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	84 (98%)	2 (2%)	44	62
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	74
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	73
19	t	80/80 (100%)	78 (98%)	2 (2%)	42	61
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	78 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	67
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	80
32	H	170/170 (100%)	170 (100%)	0	100	100
33	I	172/172 (100%)	172 (100%)	0	100	100
34	J	119/119 (100%)	119 (100%)	0	100	100
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	73
36	L	124/124 (100%)	123 (99%)	1 (1%)	73	76
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	74
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	85 (99%)	1 (1%)	63	72
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	90 (98%)	2 (2%)	45	63
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%)	64 (98%)	1 (2%)	57	68
46	V	74/74 (100%)	74 (100%)	0	100	100
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%)	55 (100%)	0	100	100
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4908/4972 (99%)	4888 (100%)	20 (0%)	81	81

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	L	65	LEU
42	R	18	LEU
45	U	36	VAL
42	R	64	VAL
14	o	65	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 119 such sidechains are listed below:

Mol	Chain	Res	Type
21	v	78	GLN
46	V	30	HIS
31	G	50	ASN
45	U	29	ASN
51	a	188	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	136 (8%)	2 (0%)
53	1	2902/2903 (99%)	333 (11%)	11 (0%)
54	2	119/120 (99%)	12 (10%)	1 (0%)
55	5	76/77 (98%)	8 (10%)	0
55	6	76/77 (98%)	6 (7%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	13 (17%)	0
All	All	4803/4810 (99%)	510 (10%)	14 (0%)

5 of 510 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	7	A
52	3	9	G
52	3	31	G
52	3	32	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	1475	G
53	1	2286	G
54	2	88	C
53	1	2391	G
53	1	2756	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	FME	1	3001	59	6,7,10	0.60	0	2,7,11	0.20	0
59	PHE	7	101	57,58	10,11,12	0.68	0	8,13,15	0.35	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	FME	1	3001	59	-	0/5/6/11	-
59	PHE	7	101	57,58	-	3/5/6/8	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	7	101	PHE	O-C-CA-CB
59	7	101	PHE	CA-CB-CG-CD1
59	7	101	PHE	CA-CB-CG-CD2

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.

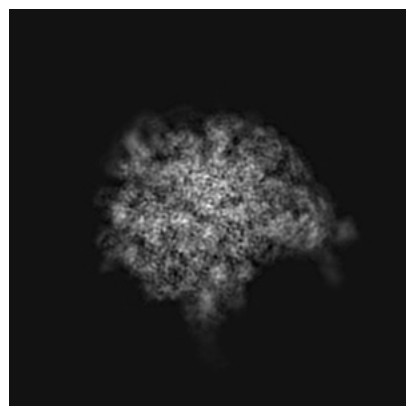
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21640. These allow visual inspection of the internal detail of the map and identification of artifacts.

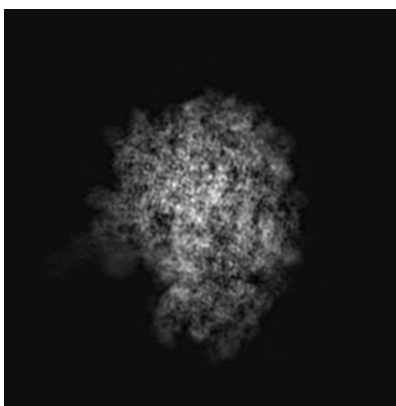
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

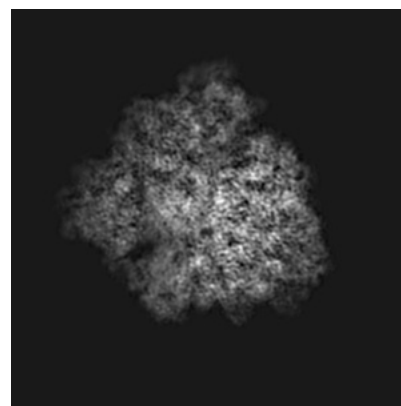
6.1.1 Primary map



X

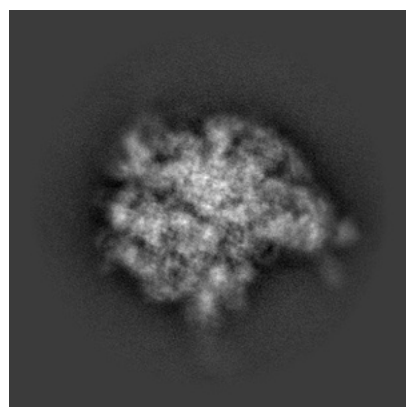


Y

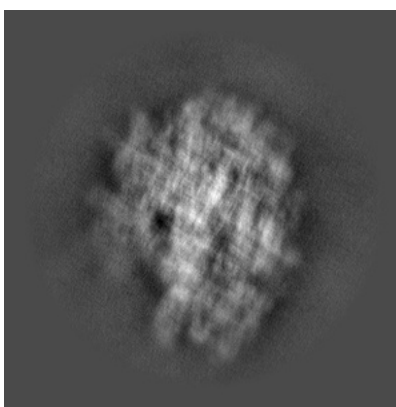


Z

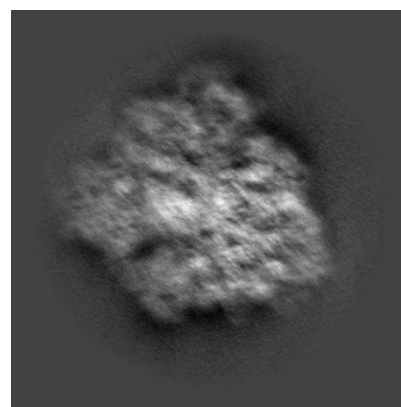
6.1.2 Raw map



X



Y

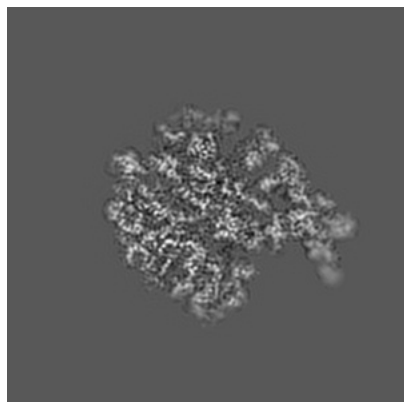


Z

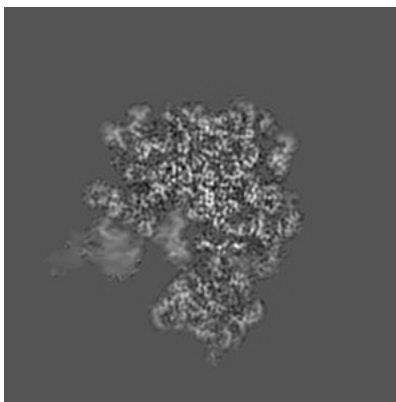
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

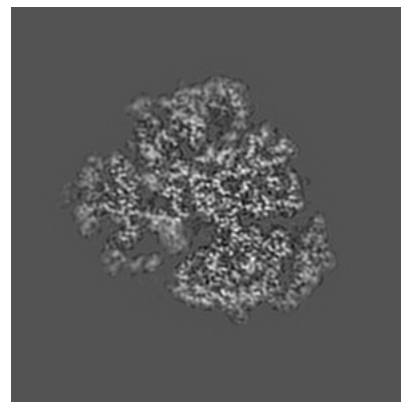
6.2.1 Primary map



X Index: 144

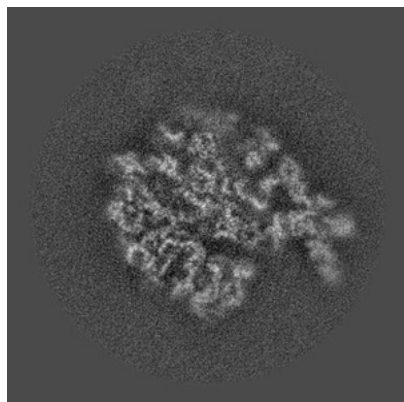


Y Index: 144

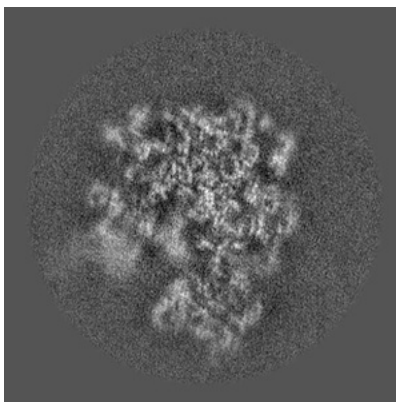


Z Index: 144

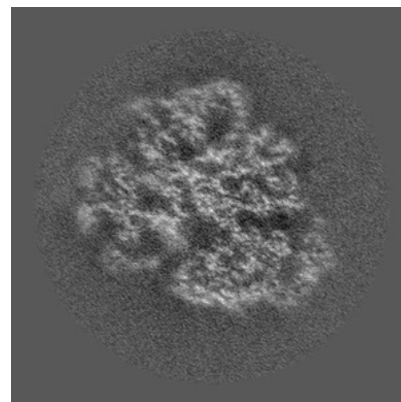
6.2.2 Raw map



X Index: 144



Y Index: 144

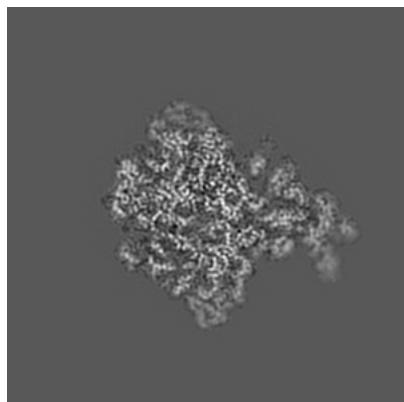


Z Index: 144

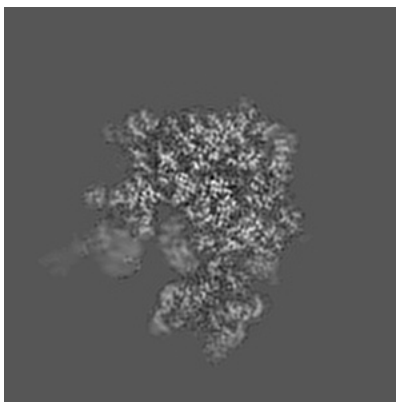
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

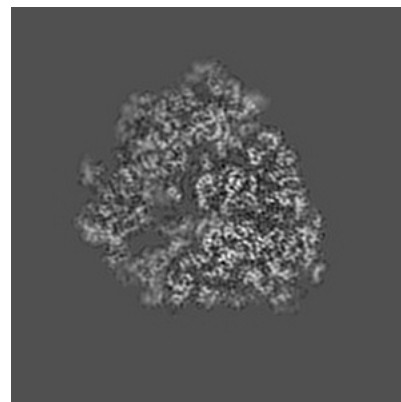
6.3.1 Primary map



X Index: 150

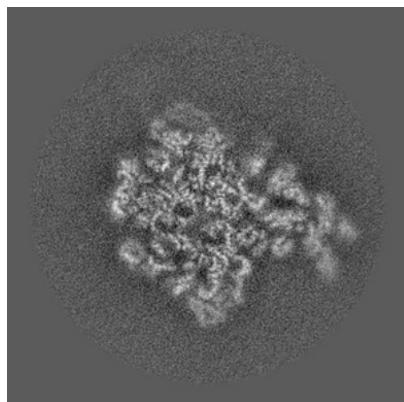


Y Index: 148

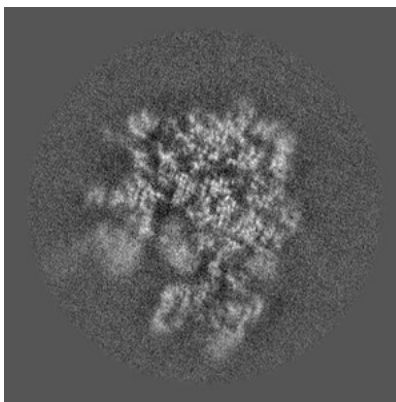


Z Index: 135

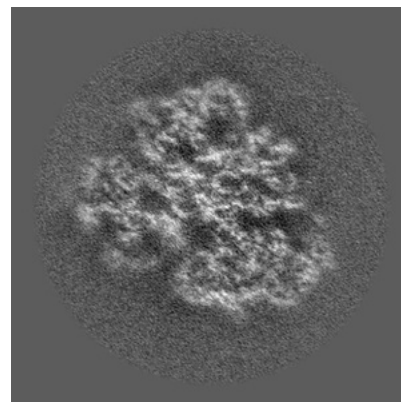
6.3.2 Raw map



X Index: 150



Y Index: 148

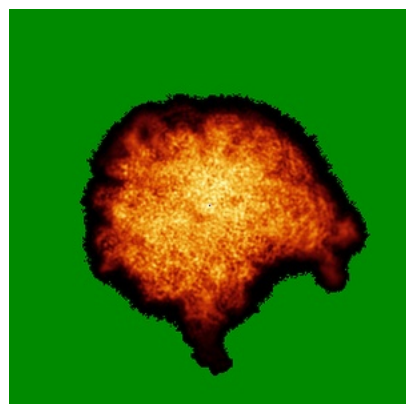


Z Index: 145

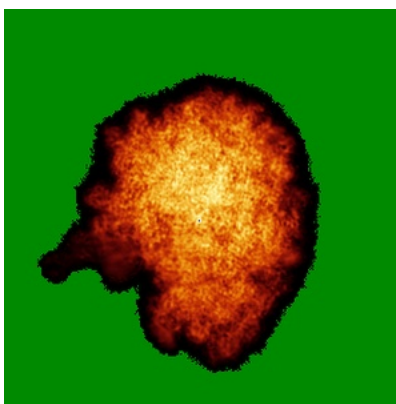
The images above show the largest variance slices of the map in three orthogonal directions.

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

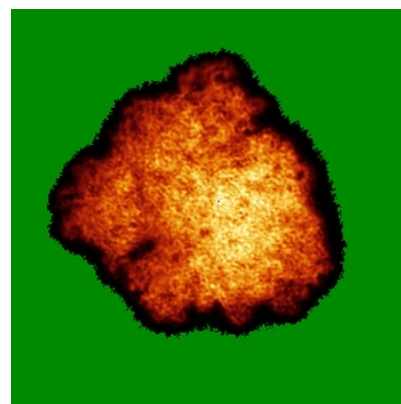
6.4.1 Primary map



X

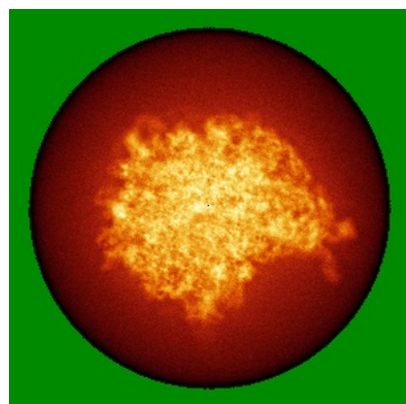


Y

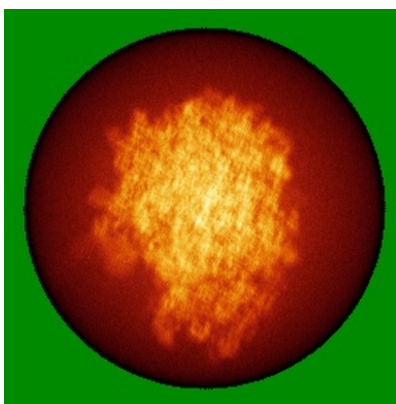


Z

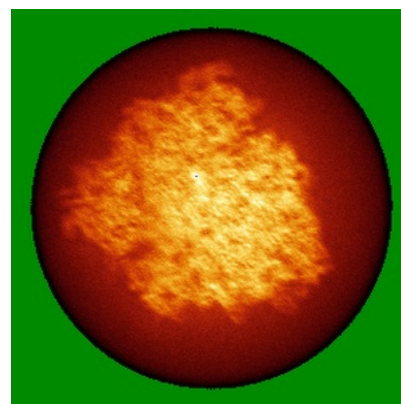
6.4.2 Raw map



X



Y

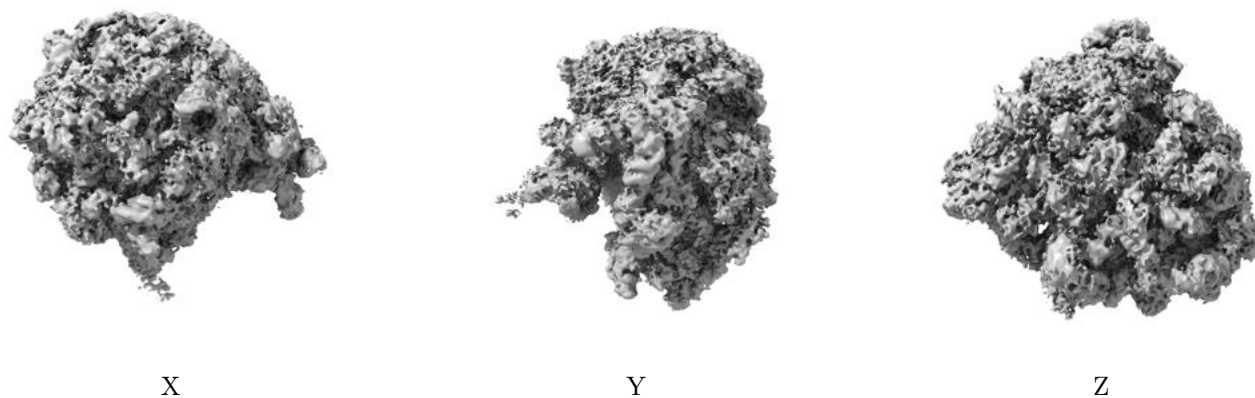


Z

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.

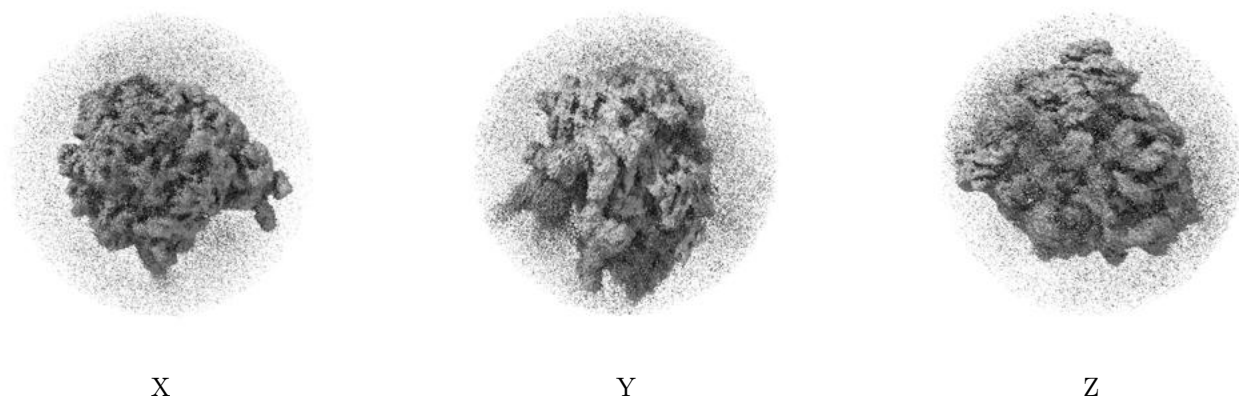
6.5 Orthogonal surface views [i](#)

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.

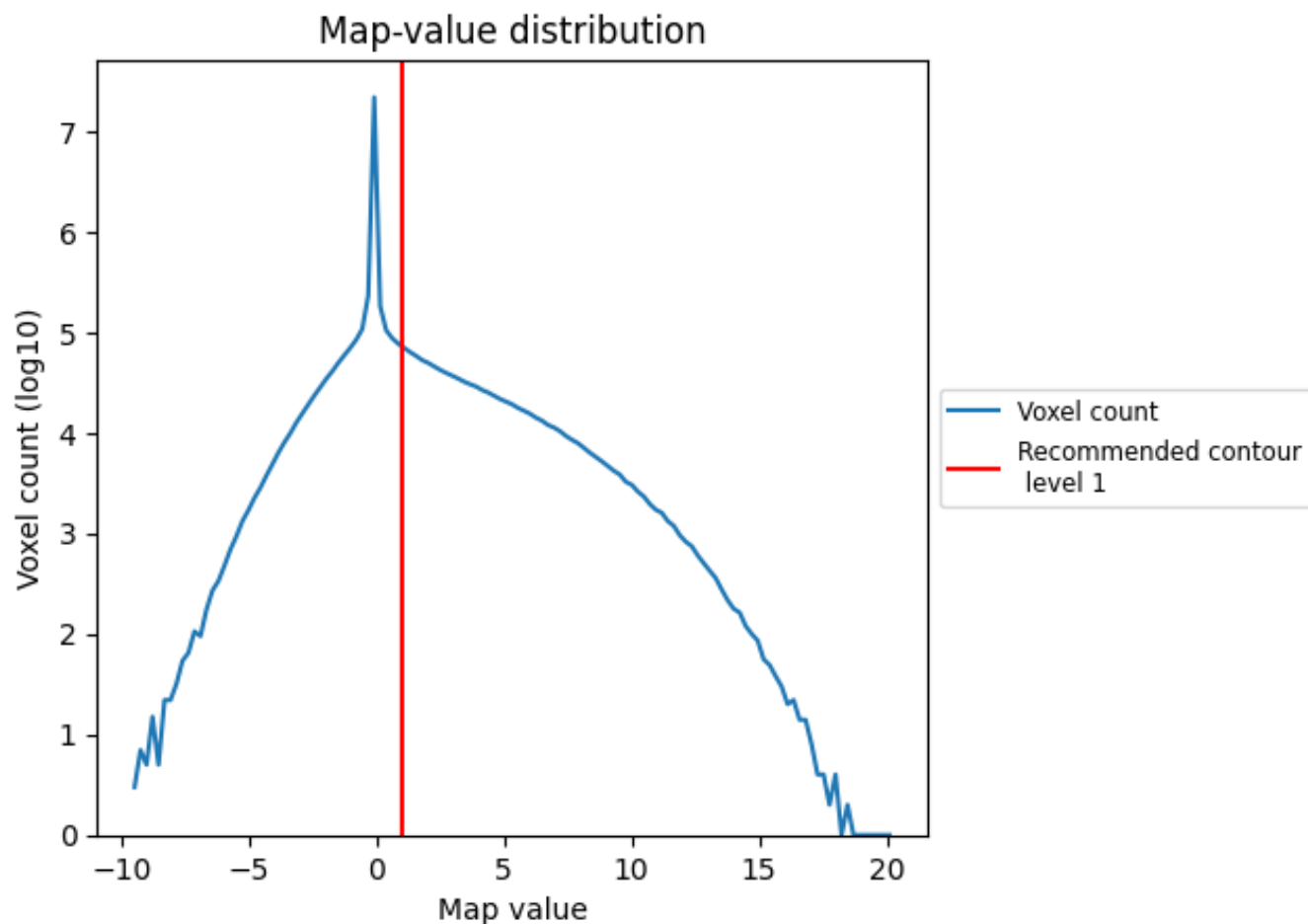
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

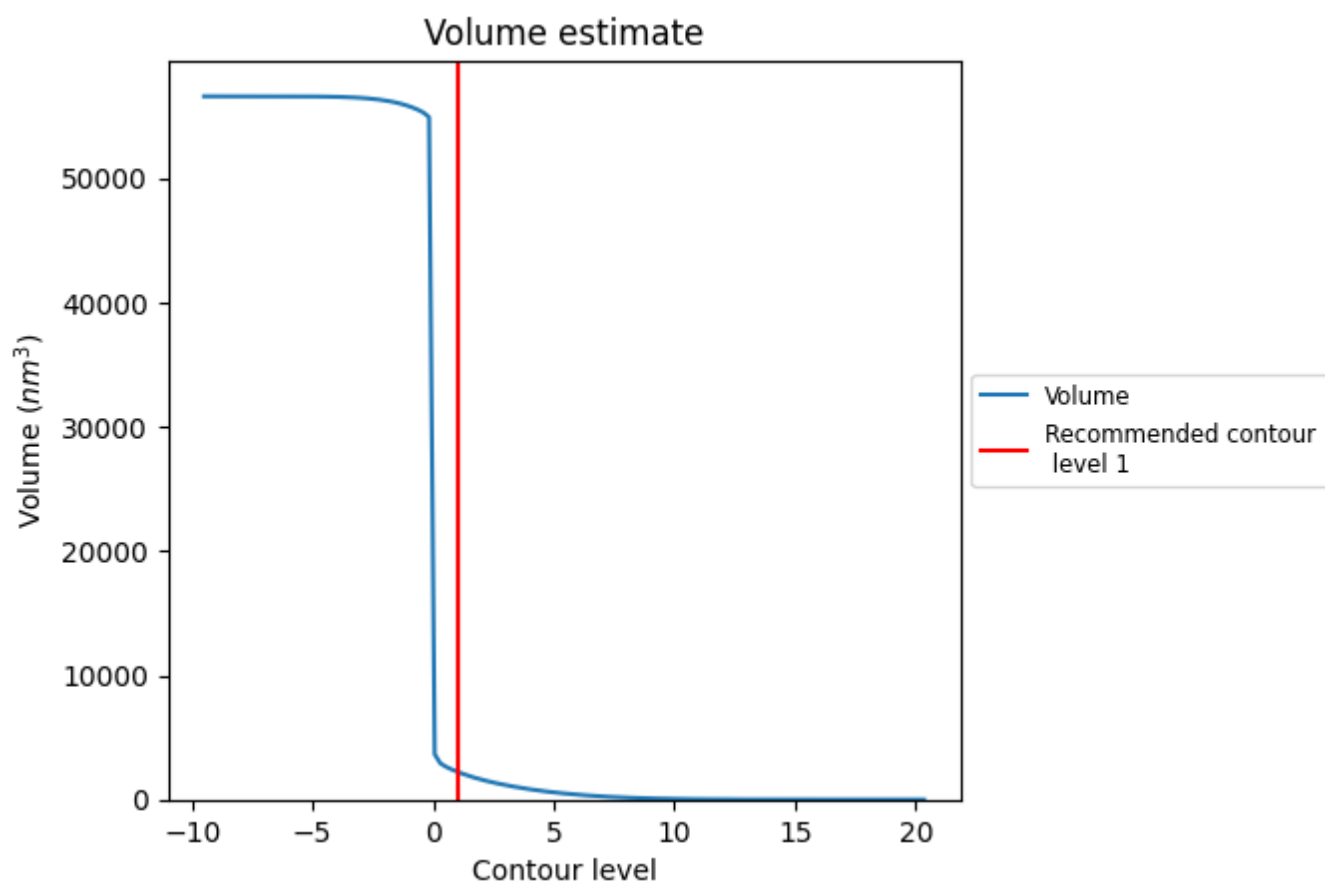
This section contains the results of statistical analysis of the map.

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.

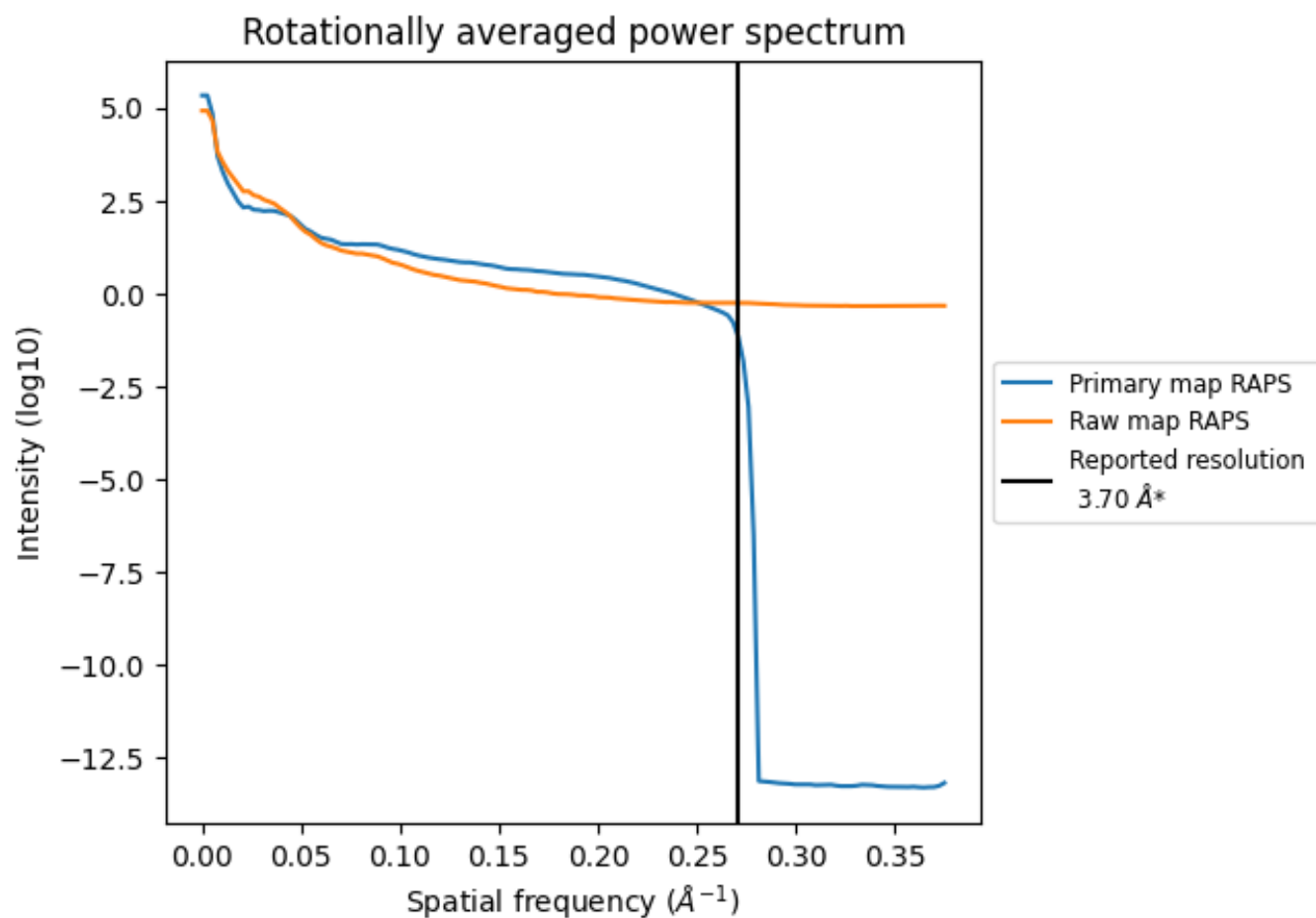
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2237 nm³; this corresponds to an approximate mass of 2021 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 ⓘ

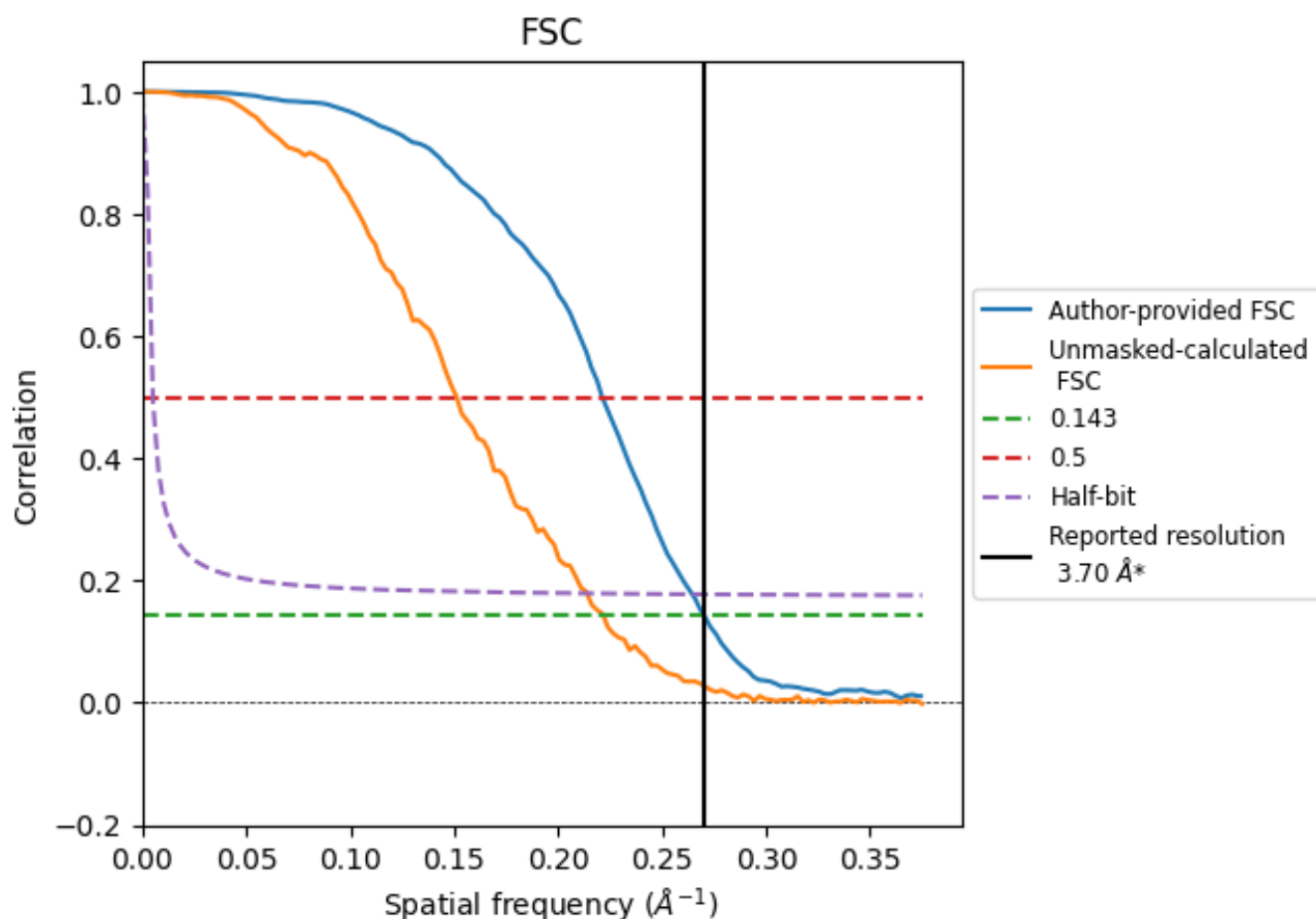


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

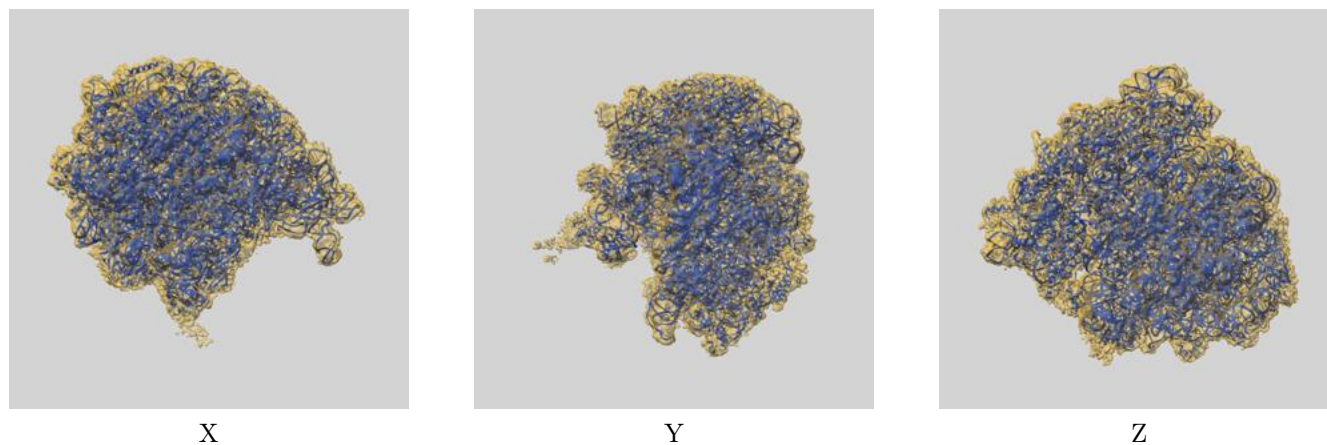
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.70	4.52	3.78
Unmasked-calculated*	4.51	6.61	4.67

*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 4.51 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21640 and PDB model 6WDL. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



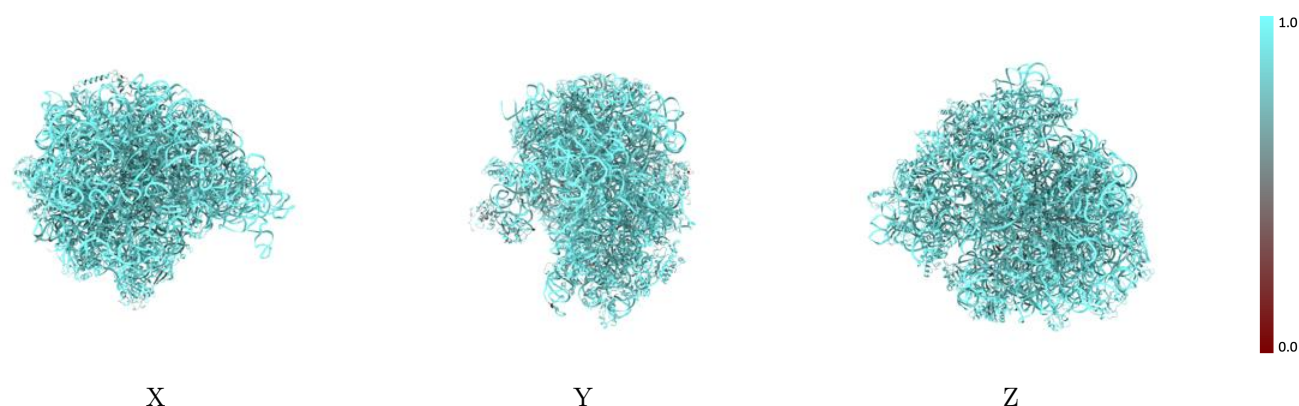
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



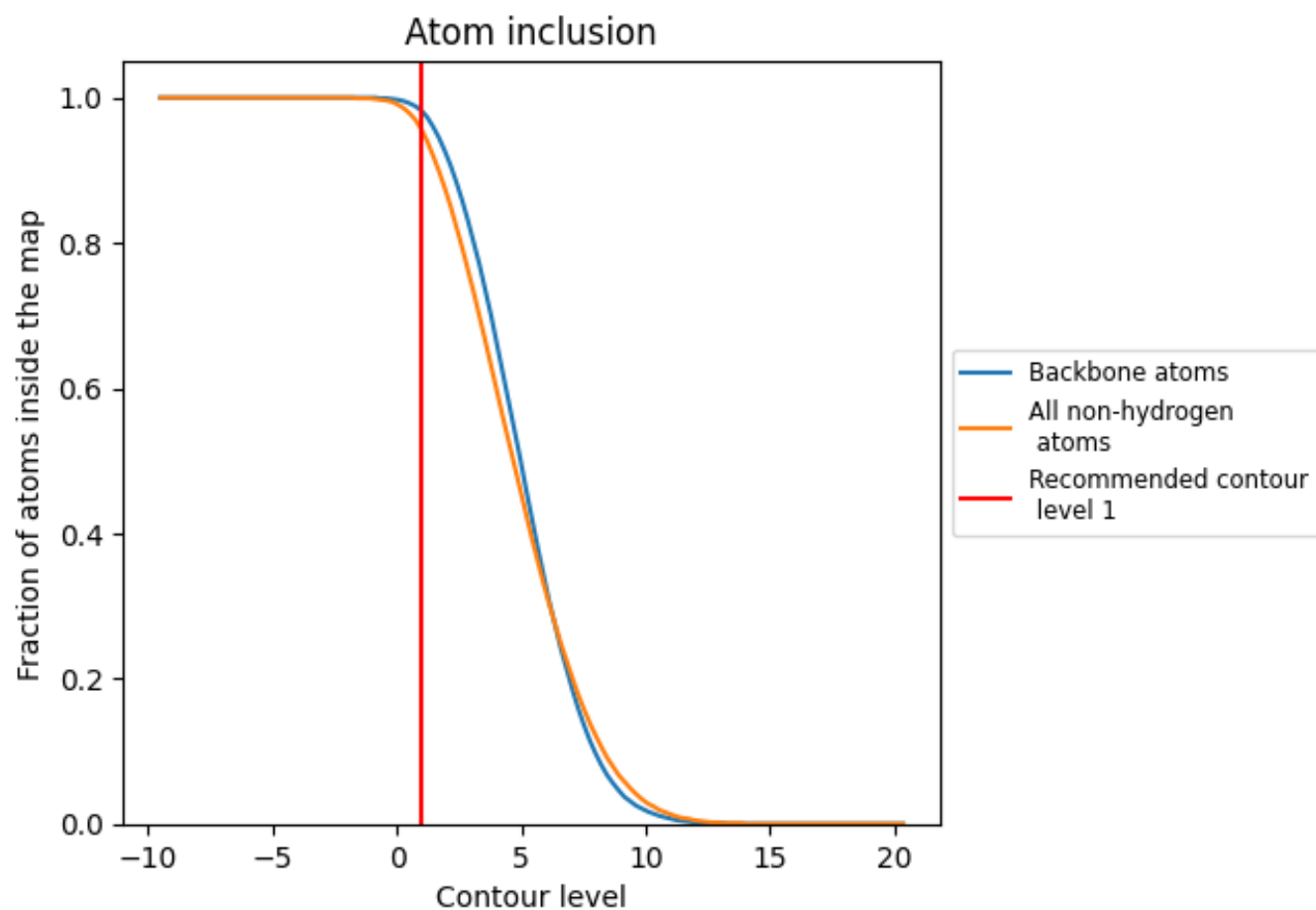
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (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	 0.9560	 0.3480
1	 0.9780	 0.3620
2	 0.9820	 0.3340
3	 0.9750	 0.3330
4	 0.8690	 0.2310
5	 0.9580	 0.2750
6	 0.8350	 0.1260
7	 0.9100	 0.1960
B	 0.9420	 0.4080
C	 0.8900	 0.3680
D	 0.9410	 0.4340
E	 0.9470	 0.4510
F	 0.8120	 0.3780
G	 0.8930	 0.3180
H	 0.9180	 0.3740
I	 0.8210	 0.2640
J	 0.9110	 0.3880
K	 0.9560	 0.3490
L	 0.9350	 0.3190
M	 0.9260	 0.3960
N	 0.9170	 0.3230
O	 0.8700	 0.3240
P	 0.9480	 0.3810
Q	 0.9490	 0.3770
R	 0.9430	 0.3180
S	 0.8990	 0.3650
T	 0.9550	 0.3800
U	 0.8980	 0.3290
V	 0.9450	 0.3730
W	 0.9160	 0.3810
X	 0.9600	 0.3270
Y	 0.9290	 0.3330
Z	 0.8880	 0.3090
a	 0.8740	 0.1620
b	 0.9490	 0.4350



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Chain	Atom inclusion	Q-score
c	 0.9400	 0.4200
d	 0.9380	 0.3820
e	 0.9480	 0.3130
f	 0.9530	 0.3320
g	 0.8330	 0.2700
h	 0.7230	 0.1520
i	 0.7960	 0.1050
j	 0.9470	 0.4270
k	 0.9380	 0.4240
l	 0.9360	 0.4090
m	 0.9220	 0.4160
n	 0.9420	 0.4170
o	 0.9470	 0.3670
p	 0.9440	 0.4010
q	 0.9350	 0.4130
r	 0.9590	 0.4110
s	 0.9160	 0.4210
t	 0.9220	 0.4100
u	 0.9310	 0.3750
v	 0.9570	 0.3990
w	 0.9280	 0.4320
x	 0.9480	 0.4080
y	 0.9210	 0.3300
z	 0.9430	 0.4150