



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:07 AM UTC

PDB ID : 6WDE / pdb_00006wde
EMDB ID : EMD-21633
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure V-B)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.00 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

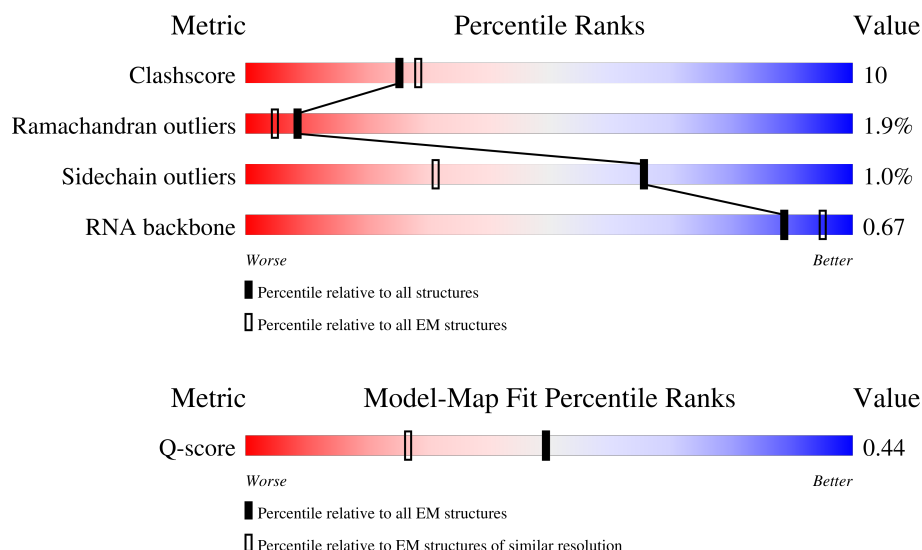
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	

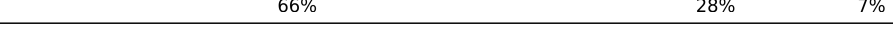
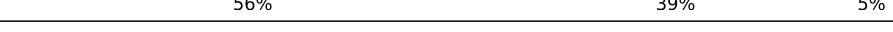
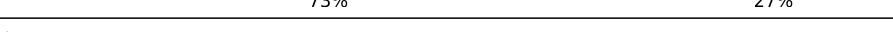
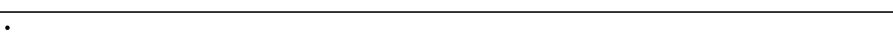
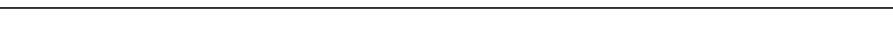
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
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	55% 38% 8%
55	5	77	66% 31%
55	6	77	64% 35%
56	4	18	72% 22% 6%
57	7	77	62% 29% 8%

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		

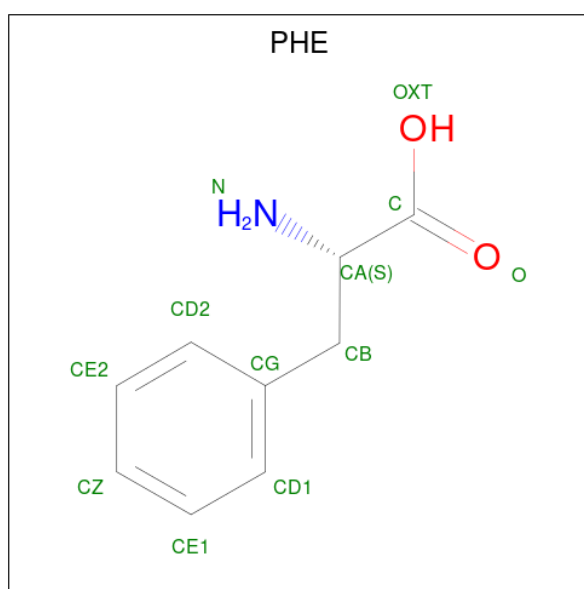
- Molecule 56 is a RNA chain called mRNA.

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

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

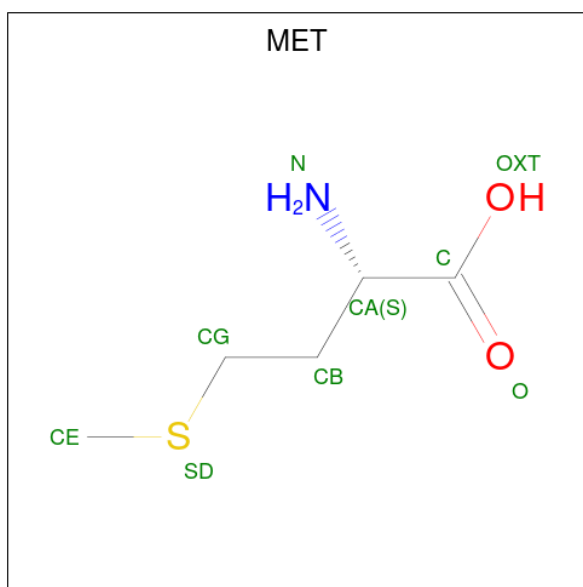
Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 58 is 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 METHIONINE (CCD ID: MET) (formula: C₅H₁₁NO₂S).

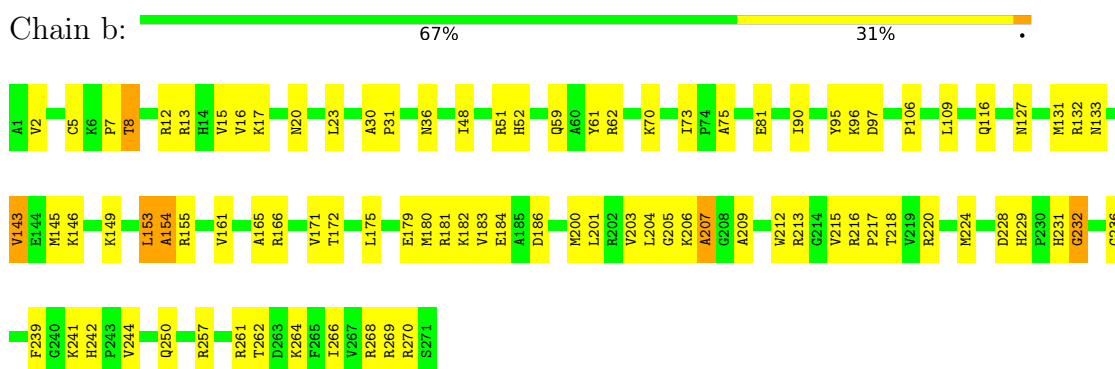


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
59	7	1	8	5	1	1	1	0

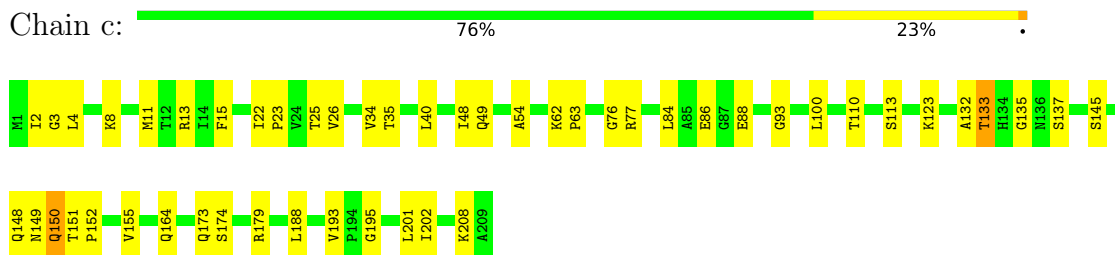
3 Residue-property plots

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

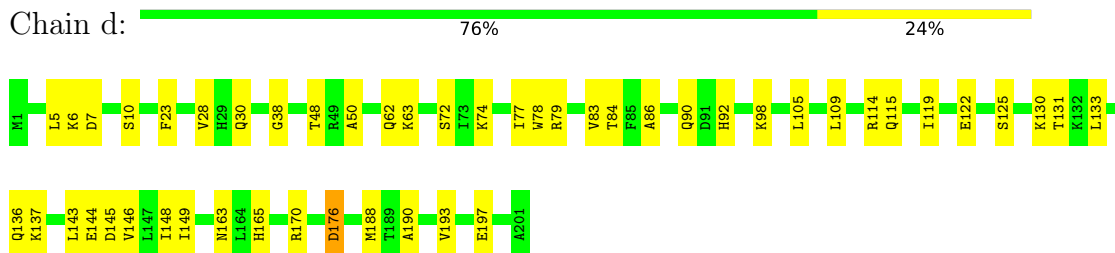
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

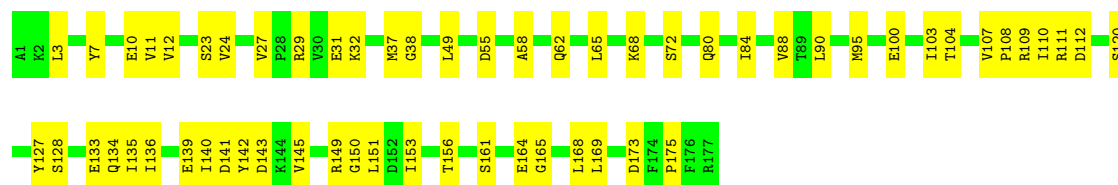


• Molecule 3: 50S ribosomal protein L4

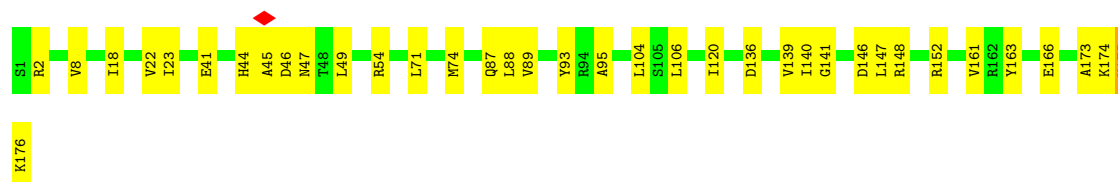
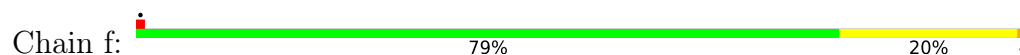


• Molecule 4: 50S ribosomal protein L5

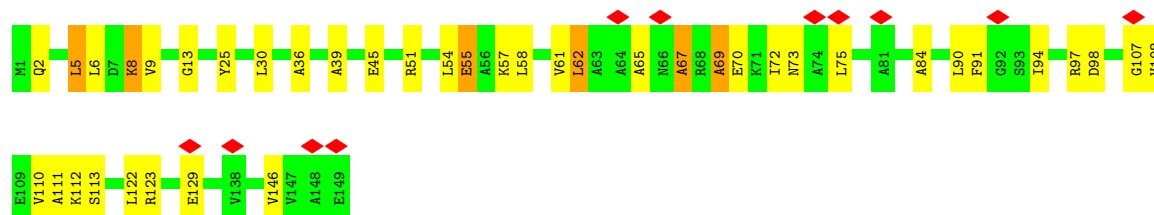
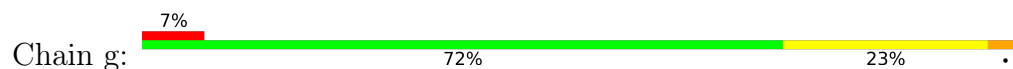




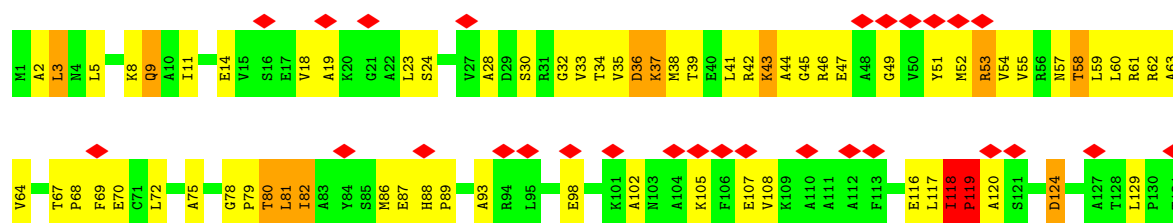
• Molecule 5: 50S ribosomal protein L6



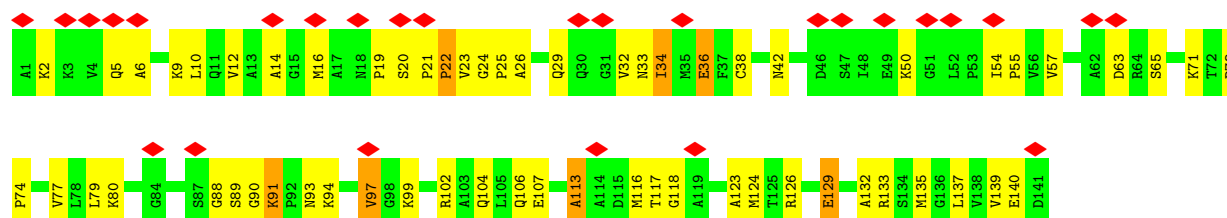
• Molecule 6: 50S ribosomal protein L9



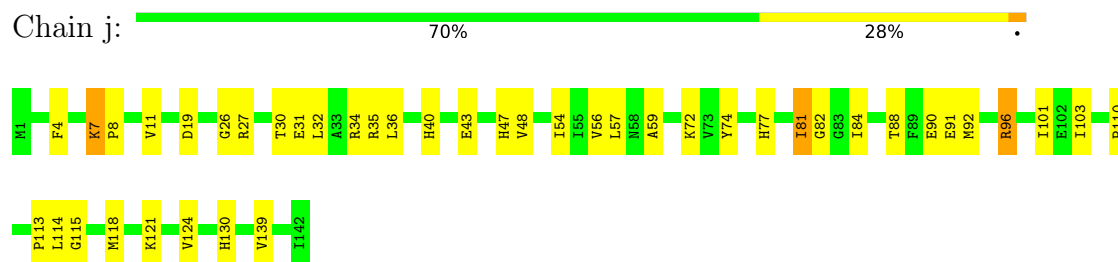
• Molecule 7: 50S ribosomal protein L10



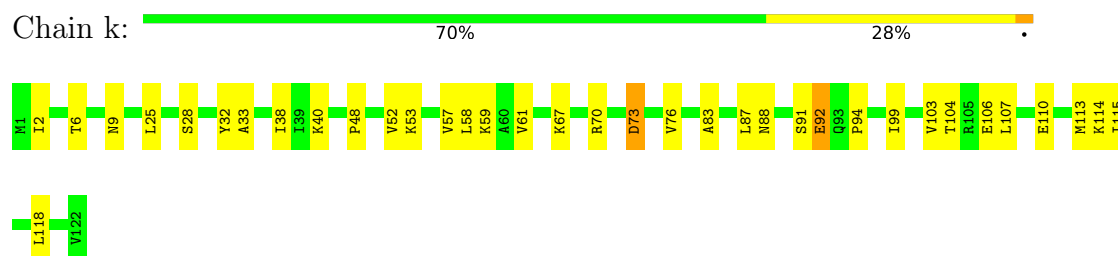
• Molecule 8: 50S ribosomal protein L11



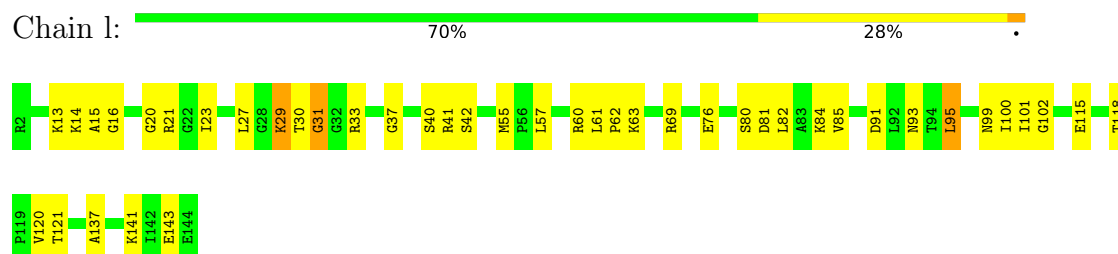
- Molecule 9: 50S ribosomal protein L13



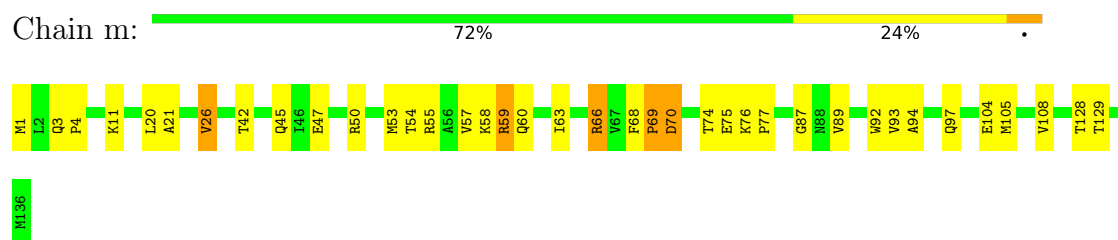
- Molecule 10: 50S ribosomal protein L14



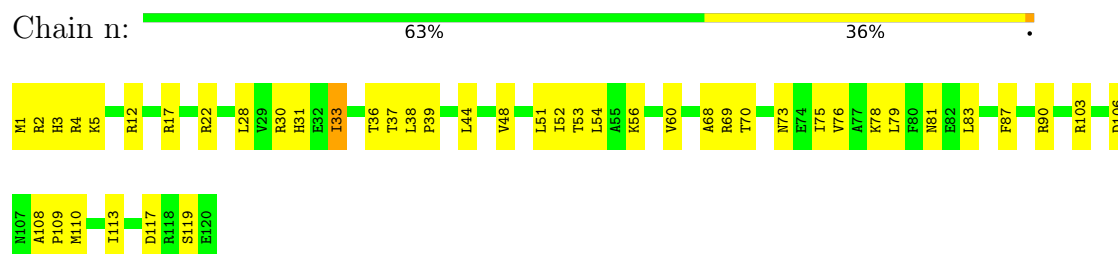
- Molecule 11: 50S ribosomal protein L15



- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17



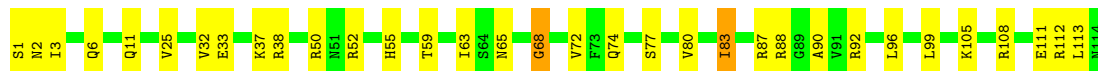
- Molecule 14: 50S ribosomal protein L18

Chain o:  78% 21%



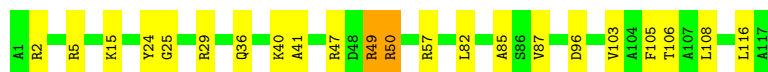
- Molecule 15: 50S ribosomal protein L19

Chain p:  71% 27%



- Molecule 16: 50S ribosomal protein L20

Chain q:  81% 17%



- Molecule 17: 50S ribosomal protein L21

Chain r:  72% 27%



- Molecule 18: 50S ribosomal protein L22

Chain s:  76% 23%



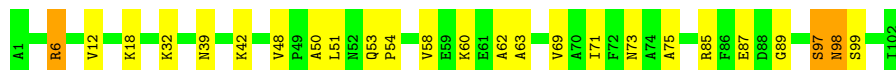
- Molecule 19: 50S ribosomal protein L23

Chain t:  74% 25%

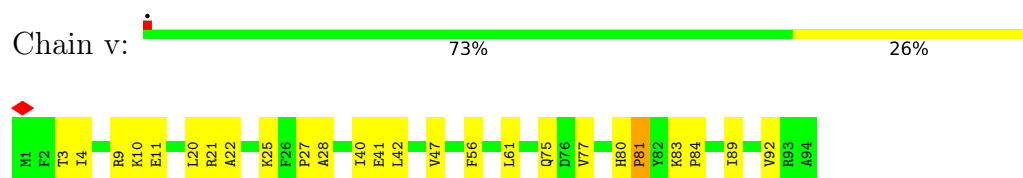


- Molecule 20: 50S ribosomal protein L24

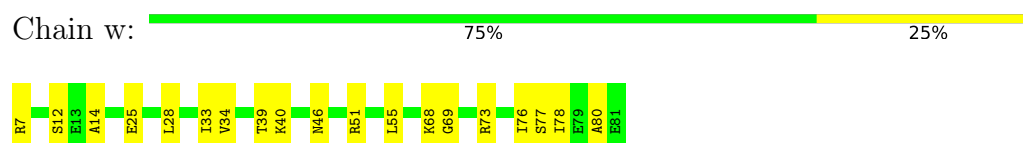
Chain u:  75% 22%



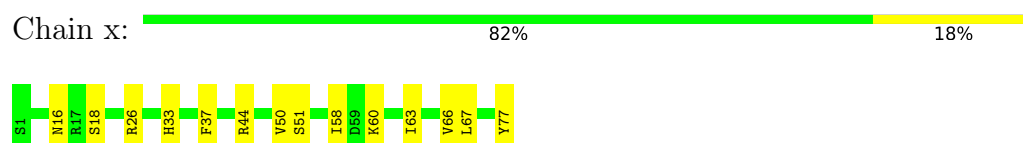
- Molecule 21: 50S ribosomal protein L25



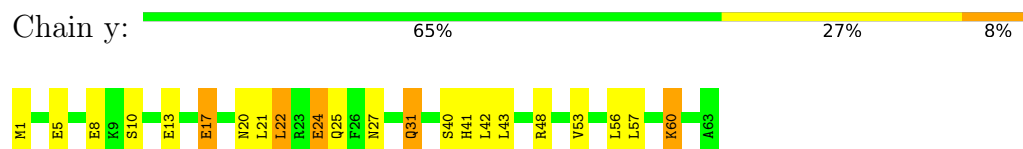
- Molecule 22: 50S ribosomal protein L27



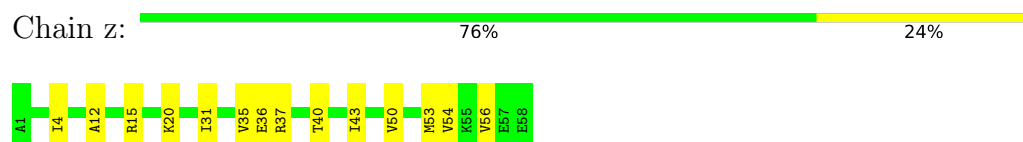
- Molecule 23: 50S ribosomal protein L28



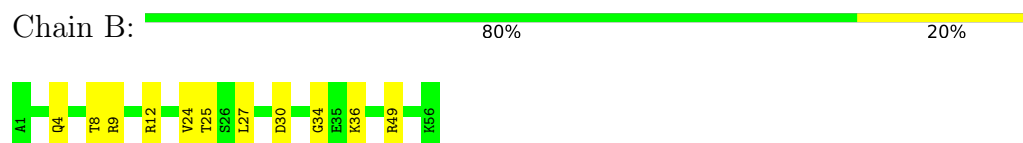
- Molecule 24: 50S ribosomal protein L29



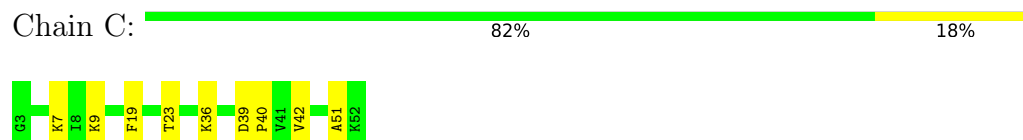
- Molecule 25: 50S ribosomal protein L30



- Molecule 26: 50S ribosomal protein L32

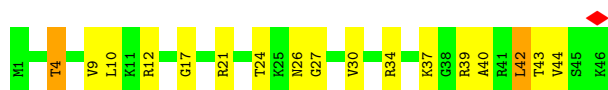


- Molecule 27: 50S ribosomal protein L33



- Molecule 28: 50S ribosomal protein L34

Chain D:  63% 33%



- Molecule 29: 50S ribosomal protein L35

Chain E:  75% 23%



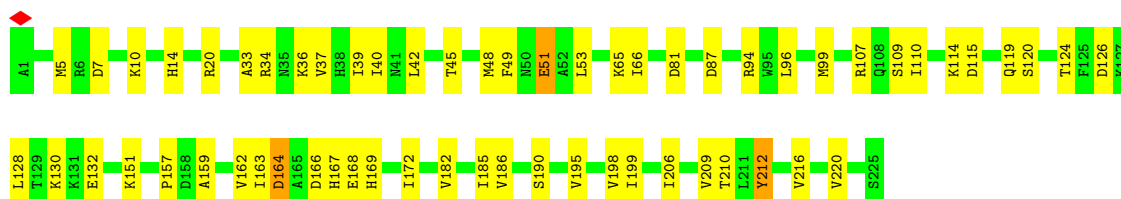
- Molecule 30: 50S ribosomal protein L36

Chain F:  53% 45%



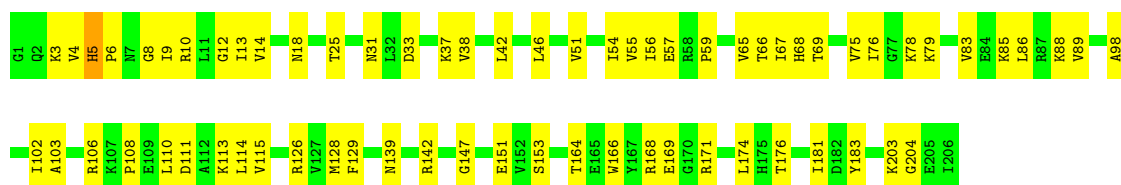
- Molecule 31: 30S ribosomal protein S2

Chain G:  73% 25%



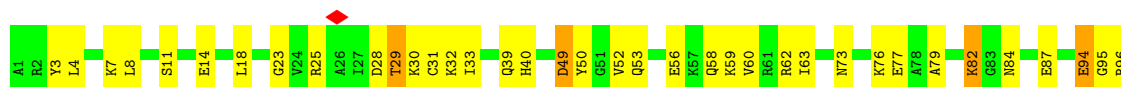
- Molecule 32: 30S ribosomal protein S3

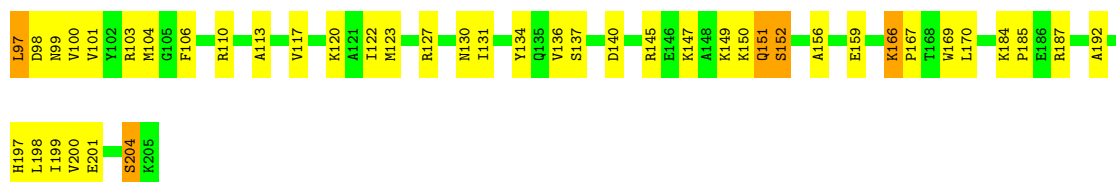
Chain H:  67% 32%



- Molecule 33: 30S ribosomal protein S4

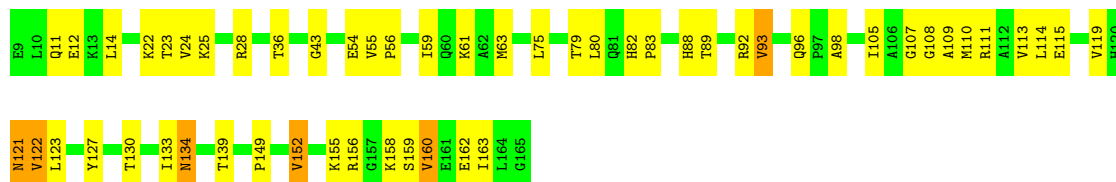
Chain I:  61% 35%





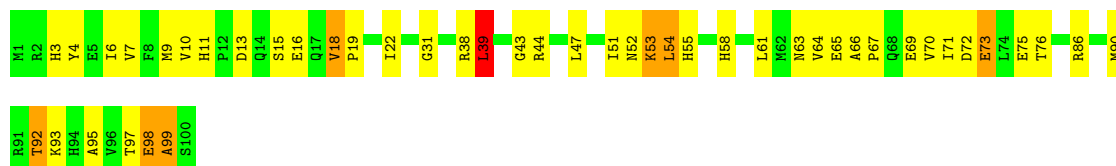
• Molecule 34: 30S ribosomal protein S5

Chain J: 66% 31% .



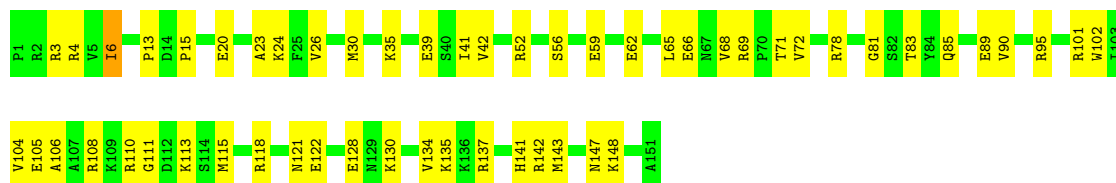
• Molecule 35: 30S ribosomal protein S6

Chain K: 54% 38% 7% .



• Molecule 36: 30S ribosomal protein S7

Chain L: 64% 35% .



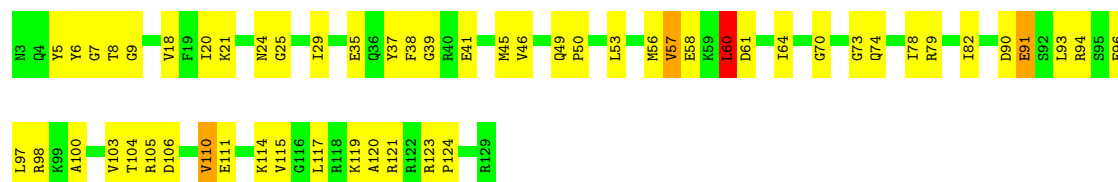
• Molecule 37: 30S ribosomal protein S8

Chain M: 74% 26%

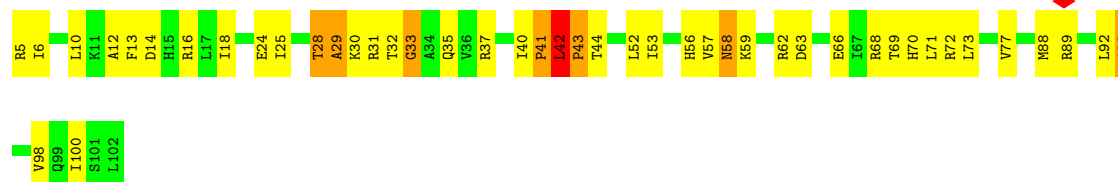


• Molecule 38: 30S ribosomal protein S9

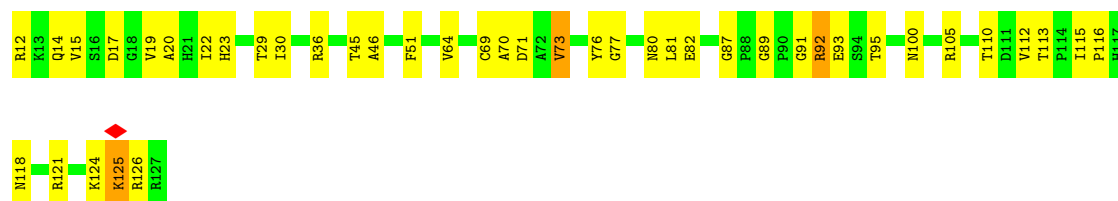
Chain N: 57% 40% ..



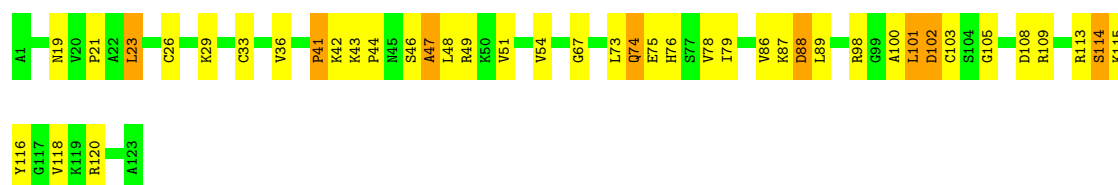
- Molecule 39: 30S ribosomal protein S10



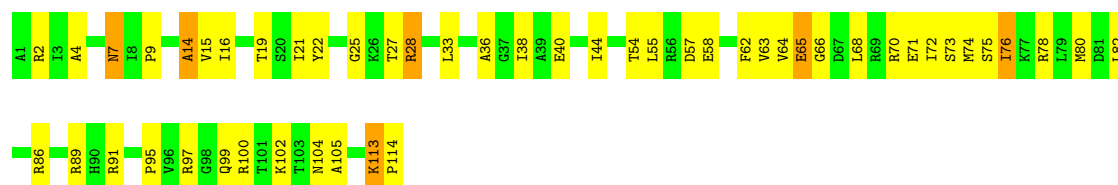
- Molecule 40: 30S ribosomal protein S11



- Molecule 41: 30S ribosomal protein S12

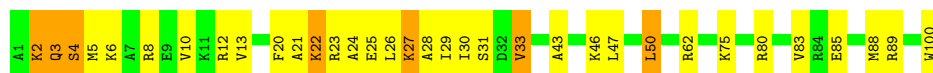


- Molecule 42: 30S ribosomal protein S13



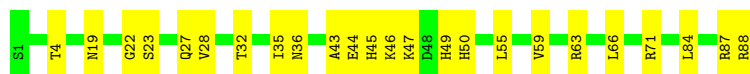
- Molecule 43: 30S ribosomal protein S14

Chain S:  66% 27% 7%



- Molecule 44: 30S ribosomal protein S15

Chain T:  73% 27%



- Molecule 45: 30S ribosomal protein S16

Chain U:  56% 38% 6%



- Molecule 46: 30S ribosomal protein S17

Chain V:  60% 38%



- Molecule 47: 30S ribosomal protein S18

Chain W:  72% 28%



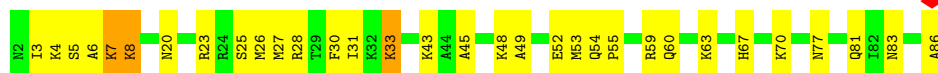
- Molecule 48: 30S ribosomal protein S19

Chain X:  61% 37%

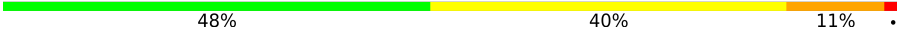


- Molecule 49: 30S ribosomal protein S20

Chain Y:  62% 34%

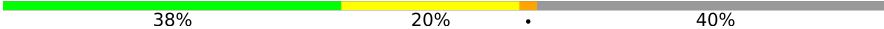


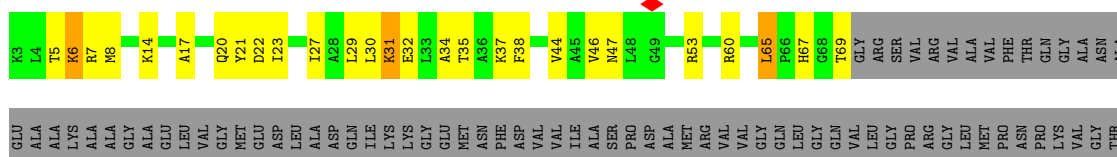
- Molecule 50: 30S ribosomal protein S21

Chain Z:  48% 40% 11%



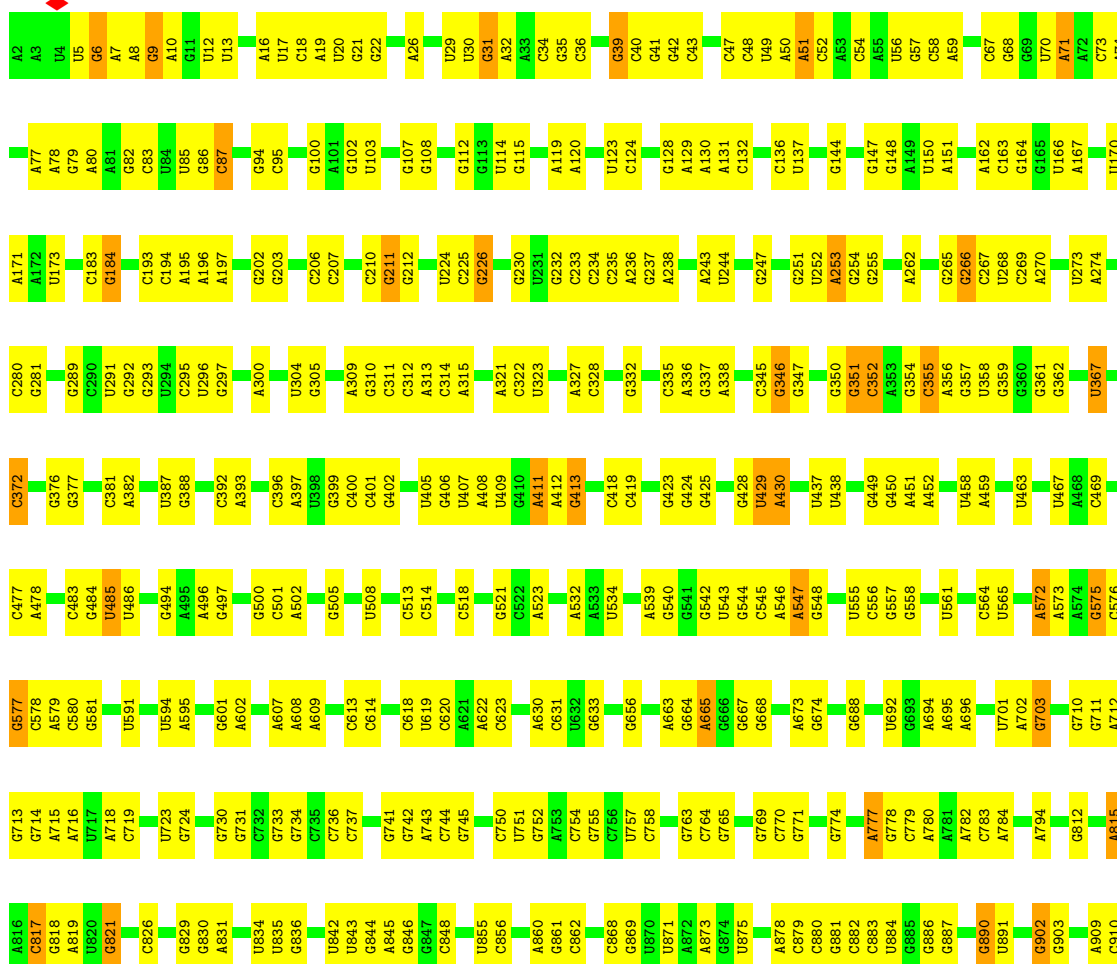
• Molecule 51: 50S ribosomal protein L1

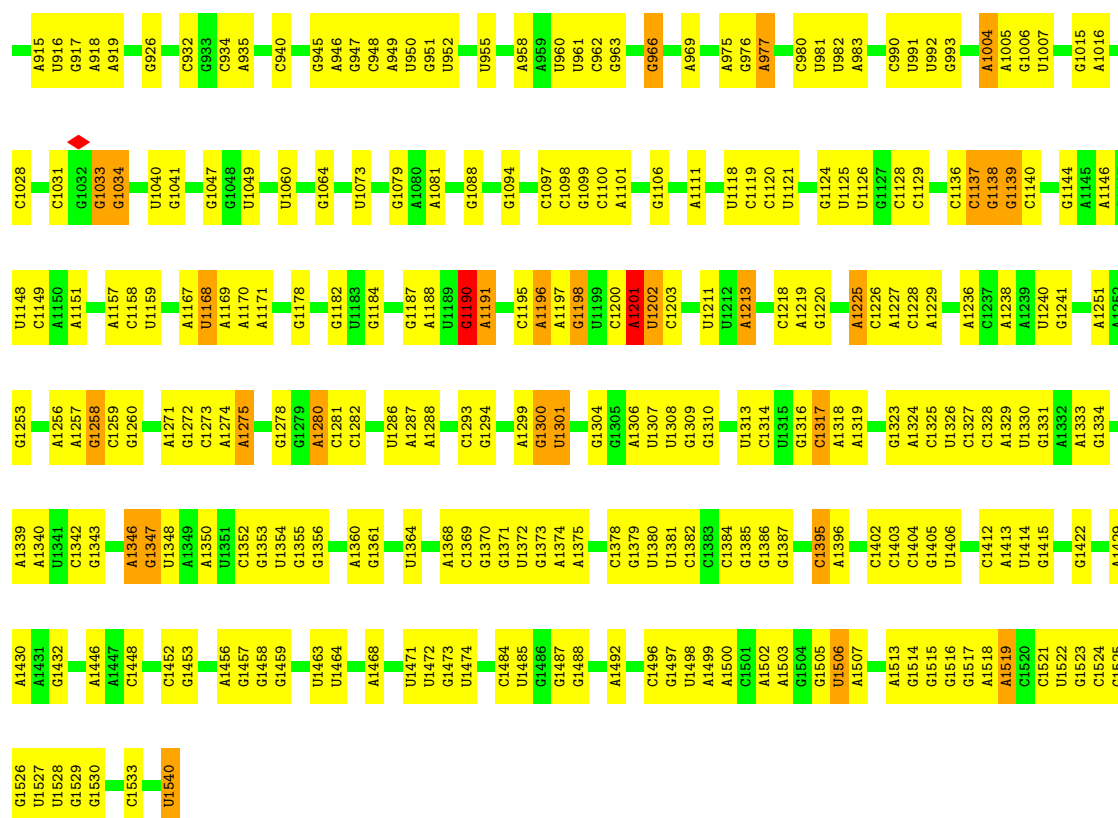
Chain a:  38% 20% 40%



• Molecule 52: 16S ribosomal RNA

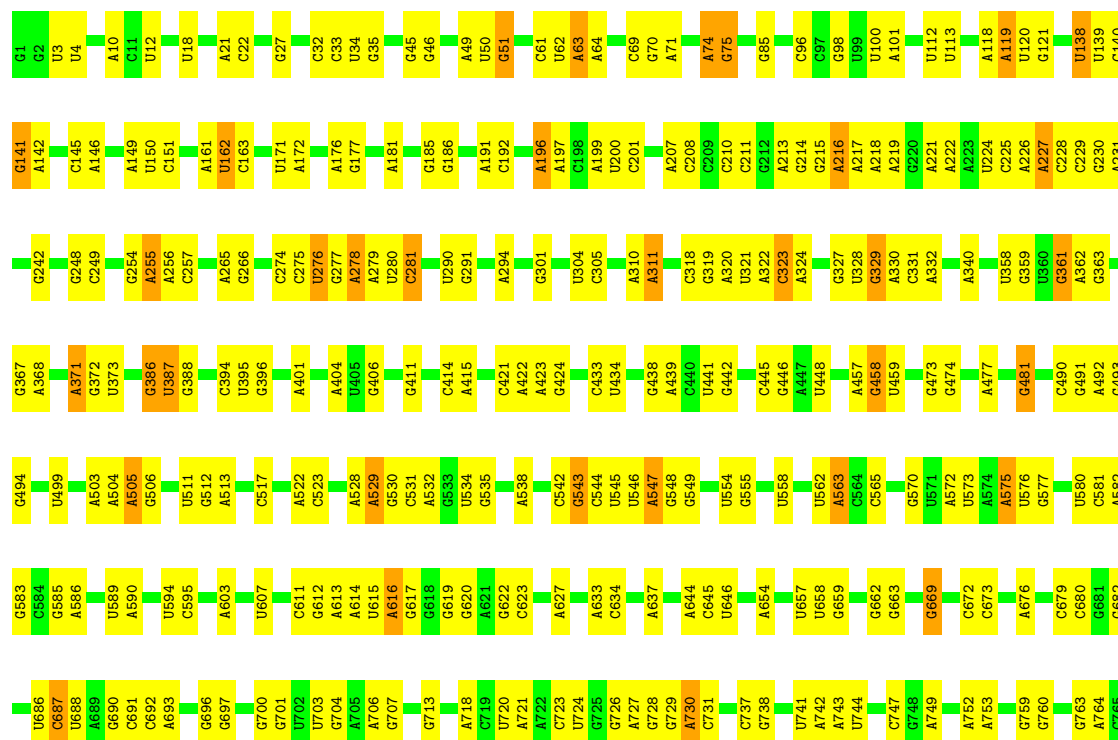
Chain 3:  58% 38%



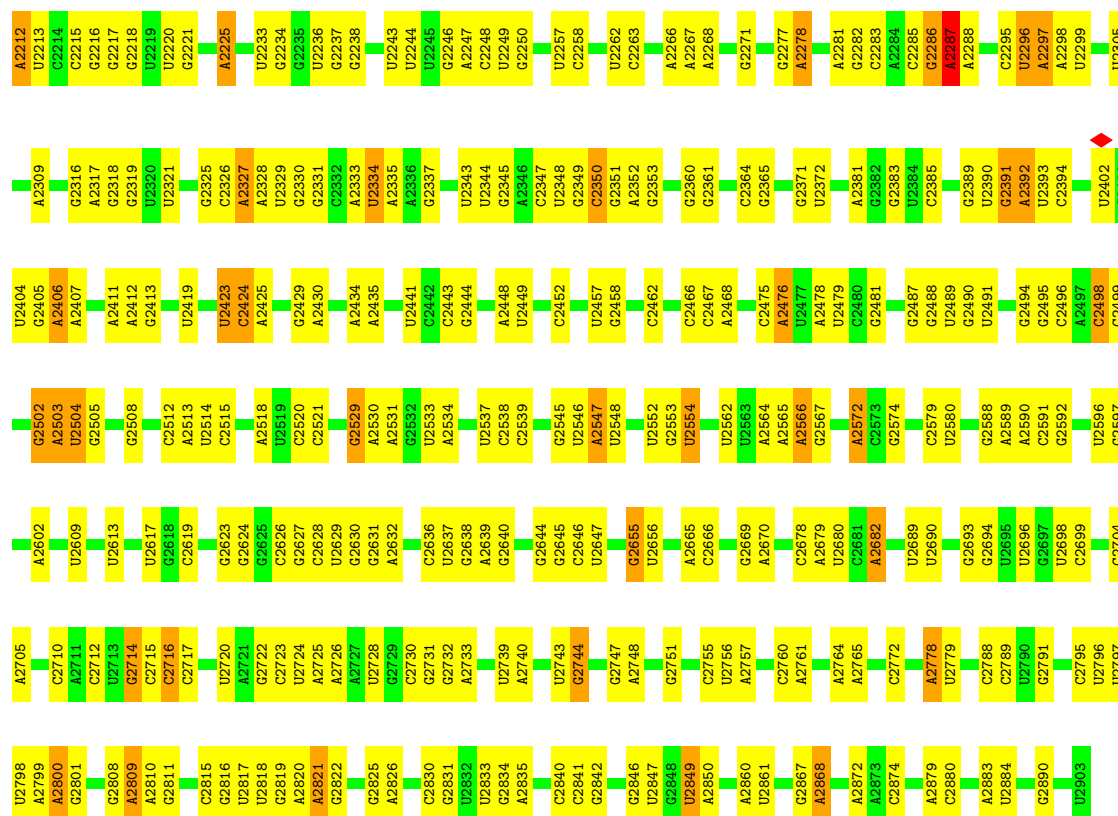


• Molecule 53: 23S ribosomal RNA

Chain 1: 59% 36% 5%

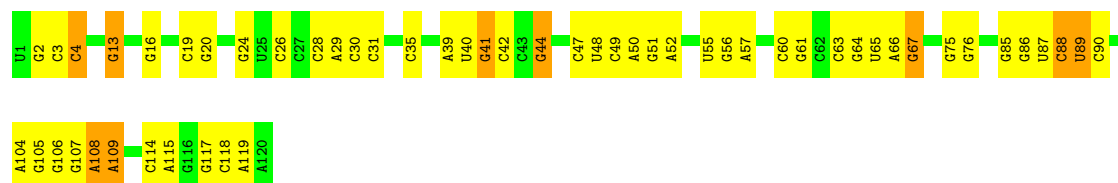


U2118	U2119	C2036	U1943	A1848	C1764	A1634	A1509	A1383	G1281	G1177	A1070	C968	G858	U766
A2120	G2120	A2042	U1944	U1856	C1765	A1635	G1510	C1386	A1287	C1178	A1071	G974	G859	U767
G2121	G2121	C2043	U1857	G1857	G1766	U1636	G1514	A1387	G1288	G1179	G1071	A975	U860	G770
G2123	G2123	G1948	G1949	G1860	A1773	A1637	A1515	U1394	C1289	U1181	C1075	A983	A861	G771
G2124	G2124	G1955	G1955	G1861	C1774	G1642	G1524	A1395	C1296	U1182	C1076	A984	A862	G772
G2125	A2126	G2048	U1956	G1862	U1775	G1643	A1525	U1396	C1297	U1183	C1077	A985	A863	U773
G2127	G2127	C2050	C1957	G1863	U1776	C1644	G1526	U1397	G1296	G1186	C1078	C986	G864	G776
G2128	C1958	A2052	C1958	A1871	U1779	G1645	A1528	G1416	G1300	U1188	A1080	C987	G869	U779
G2129	G1959	A1872	G1959	A1872	U1780	G1646	G1529	C1417	A1301	U1189	U1081	A988	U870	G780
U2132	U1963	C1874	U1963	C1874	A1784	U1648	G1535	G1418	A1302	A1189	U1082	A990	A781	A782
G2133	G1964	G1875	C1965	G1875	A1785	G1651	A1536	A1419	G1309	G1190	A1084	C991	A783	A784
G2134	C1965	G1876	A1786	A1664	U1786	A1665	G1537	A1420	A1322	G1191	A1085	C992	A875	G785
U2139	A1966	G1884	G1966	A1665	A1790	G1666	A1548	G1424	A1321	U1188	U1083	A996	A877	A794
G2140	C1967	A1885	A1967	G1666	A1791	G1666	A1549	G1425	A1322	A1205	A1095	A997	U887	C795
G2141	A1885	A1890	A1890	G1674	A1794	G1674	A1550	G1432	A1322	G1212	A1103	C1005	C888	C796
G2145	A1891	A1891	A1891	A1676	C1795	C1675	A1555	A1433	U1326	A1213	A1104	C1006	C889	G797
U2151	C1892	C1892	C1892	A1676	U1796	A1676	G1555	G1434	A1327	A1214	U1105	C1007	C890	G801
U2155	C1893	C1893	C1893	A1676	G1797	A1676	G1555	G1435	A1328	G1215	U1106	C1008	G891	A802
G2156	C1894	C1894	C1894	A1676	U1797	A1676	G1555	G1436	A1328	G1215	U1107	C1009	A892	U803
G2157	A1900	A1900	A1900	A1680	U1798	U1680	G1560	C1437	C1330	G1223	U1019	A998	A896	A804
U2162	U1901	A1901	A1901	G1681	G1799	G1681	C1564	U1438	G1332	G1227	A1020	A999	C897	A805
A2163	G1904	A1904	A1904	A1690	A1800	A1690	C1565	G1441	A1331	G1227	A1021	A999	C897	C806
C2164	C1905	C1905	C1905	C1691	A1801	C1691	A1566	G1442	G1337	G1228	A1022	A999	U906	U807
U2172	G1906	G1906	G1906	G1695	G1807	G1695	G1567	U1441	G1337	G1229	U1023	A999	G907	G808
A2173	A1907	A1907	A1907	G1696	A1808	G1696	G1568	C1447	U1344	G1236	G1026	A910	A910	C812
C2175	C1908	C1908	C1908	G1697	A1809	G1697	A1570	G1448	C1345	A1237	A1027	G914	C915	C817
C2177	A1910	A1910	A1910	A1700	A1810	A1700	A1571	G1451	C1348	G1238	A1028	G915	C915	G818
U2180	U1911	U1911	U1911	A1701	G1816	A1701	G1581	A1453	C1349	G1239	A1029	A915	A819	A819
U2181	A1912	A1912	A1912	G1702	U1817	G1702	U1584	C1454	C1350	U1240	G1030	A920	A820	A820
A2183	A1913	A1913	A1913	A1709	U1818	A1709	U1585	C1461	C1351	G1245	A1032	A921	A821	A821
A2184	C1914	C1914	C1914	G1710	A1821	G1710	A1586	C1461	U1352	G1245	A1033	A925	G822	G822
U2185	U1917	U1917	U1917	G1715	C1822	G1715	G1587	U1474	C1357	G1248	C1045	U932	U932	U827
G2186	A1918	A1918	A1918	U1715	G1823	U1715	A1590	G1475	G1358	U1249	A1046	U928	U828	U828
U2189	A1919	A1919	A1919	U1729	G1824	U1729	A1591	U1476	A1359	G1250	G1047	G840	A829	A829
C2196	G1921	G1921	G1921	C1730	U1825	C1730	A1594	G1482	G1360	C1251	A1048	A941	G830	G830
U2197	U1922	U1922	U1922	U1736	G1826	U1736	C1595	G1482	G1361	G1252	C1049	G942	G831	G831
U2198	A1924	A1924	A1924	G1737	A1827	G1737	A1596	C1482	A1365	G1256	A1053	A943	U832	U832
A2198	C1925	C1925	C1925	G1738	G1828	G1738	C1597	A1490	A1366	G1256	A1054	C946	G834	G834
U2203	U1926	U1926	U1926	U1740	A1829	U1740	G1601	G1491	A1367	A1268	C1152	A947	C838	C838
G2204	G1929	G1929	G1929	G1753	C1832	G1753	U1602	G1492	G1368	A1269	C1153	G949	U839	U839
A2205	U1930	U1930	U1930	A1754	G1833	A1754	A1603	C1493	G1369	G1270	C1154	C957	A845	A845
C2206	A1931	A1931	A1931	G1755	C1834	G1755	A1604	A1494	A1371	G1271	A1156	U1060	U846	U846
C2207	C1934	C1934	C1934	G1756	A1839	G1756	A1611	C1498	U1372	A1272	A1156	U1061	U847	U847
U2211	G1935	G1935	G1935	A1757	U1845	A1757	A1612	A1502	A1373	A1275	C1170	U1062	C961	C961
G2212	A1936	A1936	A1936	U1758	G1846	U1758	A1615	U1506	A1378	C1278	A1175	U1065	G962	G962
G2213	A1937	A1937	A1937	A1759	A1847	A1759	A1616	C1507	A1379	G1279	U1176	U1066	U963	U963
A2211	A1938	A1938	A1938	C1760	A1847	C1760	A1616	A1508	G1280	U1275	U1176	U1066	U967	U967



• Molecule 54: 5S ribosomal RNA

Chain 2: 55% 38% 8%



• Molecule 55: tRNA^{fMet}

Chain 5: 66% 31% 3%



• Molecule 55: tRNA^{fMet}

Chain 6: 64% 35% 1%



• Molecule 56: mRNA

Diagram of a 1D lattice with 8 sites. Sites 1, 3, 5, and 7 are green and labeled A5, A12, U17, and C21 respectively. Sites 2, 4, 6, and 8 are yellow and labeled A13, G18, and A22 respectively. Site 4 is also labeled G18. Horizontal lines connect sites 1-2, 2-3, 3-4, 4-5, 5-6, 6-7, and 7-8. Vertical lines connect sites 1-2, 3-4, 5-6, and 7-8.

Chain 7: 62% 29% 8%

G1	G6	A7	A9	A14	C17	A21	G27	G28	A35	A36	C43	G44	U45	G46	U47	C48	C49	G53	U54	U55	C56	G57	A58	C61	C68	G69	C74	C75	A77	A
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	51727	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	30.349	Depositor
Minimum map value	-17.455	Depositor
Average map value	0.118	Depositor
Map value standard deviation	1.163	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 [i](#)

5.1 Standard geometry [i](#)

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	0.93	8/2852 (0.3%)
2	c	0.30	0/1586	0.87	4/2134 (0.2%)
3	d	0.28	0/1571	0.87	4/2113 (0.2%)
4	e	0.31	0/1435	0.89	3/1926 (0.2%)
5	f	0.31	0/1343	0.84	2/1816 (0.1%)
6	g	0.32	0/1122	1.04	8/1515 (0.5%)
7	h	0.36	0/1002	1.14	12/1350 (0.9%)
8	i	0.35	0/1046	1.01	10/1410 (0.7%)
9	j	0.30	0/1152	0.89	6/1551 (0.4%)
10	k	0.28	0/948	0.89	3/1268 (0.2%)
11	l	0.31	0/1054	0.94	5/1403 (0.4%)
12	m	0.29	0/1093	0.85	2/1460 (0.1%)
13	n	0.30	0/974	0.87	4/1301 (0.3%)
14	o	0.29	0/902	0.88	2/1209 (0.2%)
15	p	0.29	0/929	0.88	1/1242 (0.1%)
16	q	0.30	0/960	0.90	4/1278 (0.3%)
17	r	0.29	0/829	0.84	0/1107
18	s	0.28	0/864	0.88	1/1156 (0.1%)
19	t	0.29	0/745	0.79	1/994 (0.1%)
20	u	0.29	0/788	0.88	2/1051 (0.2%)
21	v	0.30	0/766	0.89	2/1025 (0.2%)
22	w	0.28	0/582	0.78	0/769
23	x	0.28	0/635	0.84	0/848
24	y	0.27	0/510	1.00	5/677 (0.7%)
25	z	0.30	0/453	0.77	0/605
26	B	0.28	0/450	0.70	0/599
27	C	0.34	0/417	1.01	4/554 (0.7%)
28	D	0.30	0/380	0.91	2/498 (0.4%)
29	E	0.29	0/513	0.89	1/676 (0.1%)
30	F	0.31	0/303	0.88	0/397
31	G	0.30	0/1788	0.92	7/2408 (0.3%)
32	H	0.32	0/1652	0.92	8/2225 (0.4%)
33	I	0.31	0/1665	0.97	10/2227 (0.4%)
34	J	0.32	0/1170	0.91	5/1573 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	K	0.33	0/836	1.03	6/1128 (0.5%)
36	L	0.30	0/1196	0.92	2/1602 (0.1%)
37	M	0.30	0/989	0.96	4/1326 (0.3%)
38	N	0.32	0/1034	0.93	3/1375 (0.2%)
39	O	0.32	0/797	1.04	8/1077 (0.7%)
40	P	0.32	0/886	1.02	8/1195 (0.7%)
41	Q	0.30	0/969	1.00	6/1300 (0.5%)
42	R	0.31	0/893	0.98	3/1193 (0.3%)
43	S	0.31	0/817	1.04	7/1088 (0.6%)
44	T	0.29	0/722	0.88	3/964 (0.3%)
45	U	0.35	0/659	1.01	3/884 (0.3%)
46	V	0.30	0/658	0.86	1/881 (0.1%)
47	W	0.31	0/545	0.80	1/731 (0.1%)
48	X	0.31	0/653	0.90	1/877 (0.1%)
49	Y	0.29	0/671	1.09	8/888 (0.9%)
50	Z	0.34	0/551	1.18	6/728 (0.8%)
51	a	0.34	0/1034	1.01	10/1387 (0.7%)
52	3	0.41	0/36963	0.48	3/57662 (0.0%)
53	1	0.40	0/69796	0.48	3/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.41	0/1832	0.44	0/2855
55	6	0.43	0/1832	0.48	0/2855
56	4	0.42	0/436	0.49	0/679
57	7	0.41	0/1809	0.45	0/2819
All	All	0.38	0/163199	0.63	212/244078 (0.1%)

There are no bond length outliers.

The worst 5 of 212 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	Z	45	LYS	N-CA-C	-9.98	100.86	113.23
50	Z	58	LYS	N-CA-C	-9.54	100.96	111.36
45	U	78	VAL	N-CA-C	-9.44	100.14	113.07
43	S	4	SER	N-CA-C	-9.39	100.93	111.82
40	P	73	VAL	N-CA-C	-8.04	105.03	112.43

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	64	0
2	c	1565	0	1616	34	0
3	d	1552	0	1619	35	0
4	e	1411	0	1447	40	0
5	f	1323	0	1374	22	0
6	g	1111	0	1148	35	0
7	h	989	0	1025	68	0
8	i	1032	0	1088	59	0
9	j	1129	0	1162	30	0
10	k	939	0	1012	25	0
11	l	1045	0	1117	27	0
12	m	1074	0	1157	31	0
13	n	961	0	1000	32	0
14	o	892	0	923	18	0
15	p	917	0	965	30	0
16	q	947	0	1022	27	0
17	r	816	0	839	33	0
18	s	857	0	922	20	0
19	t	739	0	807	16	0
20	u	780	0	834	15	0
21	v	753	0	780	15	0
22	w	575	0	592	16	0
23	x	625	0	655	9	0
24	y	509	0	543	14	0
25	z	449	0	491	8	0
26	B	444	0	461	10	0
27	C	410	0	440	5	0
28	D	377	0	418	14	0
29	E	504	0	574	12	0
30	F	302	0	343	15	0
31	G	1757	0	1787	41	0
32	H	1625	0	1699	44	0
33	I	1643	0	1710	69	0
34	J	1157	0	1199	45	0
35	K	818	0	808	48	0
36	L	1182	0	1240	42	0
37	M	979	0	1034	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	43	0
39	O	787	0	828	45	0
40	P	870	0	878	30	0
41	Q	955	0	1019	33	0
42	R	884	0	944	36	0
43	S	805	0	847	27	0
44	T	714	0	737	20	0
45	U	649	0	666	31	0
46	V	649	0	691	21	0
47	W	536	0	552	12	0
48	X	638	0	665	25	0
49	Y	665	0	714	24	0
50	Z	545	0	579	32	0
51	a	1027	0	1092	48	0
52	3	33012	0	16618	488	0
53	1	62317	0	31346	850	0
54	2	2568	0	1303	54	0
55	5	1640	0	837	14	0
55	6	1640	0	837	18	0
56	4	388	0	196	4	0
57	7	1619	0	821	22	0
58	7	11	0	8	0	0
59	7	8	0	8	0	0
All	All	150220	0	101264	2604	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 10.

The worst 5 of 2604 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)
12:m:55:ARG:HH22	57:7:53:G:H4'	1.09	1.09
44:T:88:ARG:HD2	44:T:88:ARG:H	1.17	1.06
53:1:1906:G:H2'	53:1:1907:G:H5''	1.34	1.04
53:1:45:G:H5''	53:1:46:G:H5'	1.33	1.04
53:1:962:G:H21	53:1:2250:G:H1	1.14	0.95

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%)	237 (88%)	29 (11%)	3 (1%)	11	43
2	c	207/209 (99%)	183 (88%)	23 (11%)	1 (0%)	24	60
3	d	199/201 (99%)	179 (90%)	19 (10%)	1 (0%)	24	60
4	e	175/177 (99%)	161 (92%)	13 (7%)	1 (1%)	21	56
5	f	174/176 (99%)	157 (90%)	15 (9%)	2 (1%)	11	43
6	g	147/149 (99%)	127 (86%)	20 (14%)	0	100	100
7	h	129/131 (98%)	92 (71%)	27 (21%)	10 (8%)	1	4
8	i	139/141 (99%)	121 (87%)	15 (11%)	3 (2%)	5	26
9	j	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	9	36
10	k	120/122 (98%)	104 (87%)	15 (12%)	1 (1%)	16	50
11	l	141/143 (99%)	114 (81%)	23 (16%)	4 (3%)	4	21
12	m	134/136 (98%)	117 (87%)	13 (10%)	4 (3%)	3	19
13	n	118/120 (98%)	101 (86%)	15 (13%)	2 (2%)	7	32
14	o	114/116 (98%)	102 (90%)	11 (10%)	1 (1%)	14	48
15	p	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
16	q	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
17	r	101/103 (98%)	88 (87%)	11 (11%)	2 (2%)	6	28
18	s	108/110 (98%)	93 (86%)	12 (11%)	3 (3%)	4	21
19	t	91/93 (98%)	83 (91%)	8 (9%)	0	100	100
20	u	100/102 (98%)	88 (88%)	7 (7%)	5 (5%)	1	10
21	v	92/94 (98%)	84 (91%)	7 (8%)	1 (1%)	11	43
22	w	73/75 (97%)	66 (90%)	6 (8%)	1 (1%)	9	36
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	56 (92%)	2 (3%)	3 (5%)	1	10
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%)	51 (94%)	3 (6%)	0	100	100
27	C	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
28	D	44/46 (96%)	39 (89%)	4 (9%)	1 (2%)	5	25
29	E	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	34
30	F	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	4	21
31	G	223/225 (99%)	205 (92%)	15 (7%)	3 (1%)	9	38
32	H	204/206 (99%)	186 (91%)	18 (9%)	0	100	100
33	I	203/205 (99%)	178 (88%)	22 (11%)	3 (2%)	8	35
34	J	155/157 (99%)	128 (83%)	23 (15%)	4 (3%)	4	23
35	K	98/100 (98%)	81 (83%)	12 (12%)	5 (5%)	1	10
36	L	149/151 (99%)	131 (88%)	17 (11%)	1 (1%)	18	53
37	M	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
38	N	125/127 (98%)	103 (82%)	18 (14%)	4 (3%)	3	18
39	O	96/98 (98%)	79 (82%)	11 (12%)	6 (6%)	1	6
40	P	114/116 (98%)	97 (85%)	14 (12%)	3 (3%)	4	23
41	Q	121/123 (98%)	96 (79%)	17 (14%)	8 (7%)	1	5
42	R	112/114 (98%)	96 (86%)	10 (9%)	6 (5%)	1	9
43	S	98/100 (98%)	81 (83%)	15 (15%)	2 (2%)	6	28
44	T	86/88 (98%)	80 (93%)	5 (6%)	1 (1%)	10	40
45	U	80/82 (98%)	71 (89%)	7 (9%)	2 (2%)	4	23
46	V	78/80 (98%)	62 (80%)	13 (17%)	3 (4%)	2	15
47	W	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
48	X	77/79 (98%)	69 (90%)	5 (6%)	3 (4%)	2	14
49	Y	83/85 (98%)	76 (92%)	7 (8%)	0	100	100
50	Z	63/65 (97%)	42 (67%)	16 (25%)	5 (8%)	1	3
51	a	130/223 (58%)	122 (94%)	8 (6%)	0	100	100
All	All	5919/6112 (97%)	5196 (88%)	611 (10%)	112 (2%)	8	30

5 of 112 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
3	d	83	VAL

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Mol	Chain	Res	Type
5	f	45	ALA
7	h	80	THR
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%)	214 (99%)	2 (1%)	70	85
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	88
3	d	165/165 (100%)	163 (99%)	2 (1%)	63	82
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	86
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	86
6	g	114/114 (100%)	112 (98%)	2 (2%)	51	77
7	h	100/100 (100%)	94 (94%)	6 (6%)	17	50
8	i	109/109 (100%)	107 (98%)	2 (2%)	51	77
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	85
10	k	103/103 (100%)	101 (98%)	2 (2%)	50	76
11	l	102/102 (100%)	100 (98%)	2 (2%)	48	76
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	85
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	86 (100%)	0	100	100
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	84
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	82
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	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%)	57 (100%)	0	100	100
23	x	67/67 (100%)	66 (98%)	1 (2%)	57	80
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%)	37 (97%)	1 (3%)	40	72
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	89
32	H	170/170 (100%)	168 (99%)	2 (1%)	63	82
33	I	172/172 (100%)	170 (99%)	2 (1%)	63	82
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	86
35	K	87/87 (100%)	84 (97%)	3 (3%)	32	66
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	84
38	N	105/105 (100%)	104 (99%)	1 (1%)	68	84
39	O	86/86 (100%)	86 (100%)	0	100	100
40	P	89/89 (100%)	88 (99%)	1 (1%)	65	83
41	Q	103/103 (100%)	102 (99%)	1 (1%)	68	84
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	81 (98%)	2 (2%)	43	73
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	63 (97%)	2 (3%)	35	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%)	52 (94%)	3 (6%)	19	53
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4908/4972 (99%)	4861 (99%)	47 (1%)	65	84

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	H	31	ASN
35	K	98	GLU
32	H	128	MET
34	J	130	THR
38	N	60	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 117 such sidechains are listed below:

Mol	Chain	Res	Type
22	w	8	ASN
49	Y	51	ASN
31	G	167	HIS
49	Y	47	GLN
44	T	27	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	142 (9%)	3 (0%)
53	1	2902/2903 (99%)	331 (11%)	12 (0%)
54	2	119/120 (99%)	11 (9%)	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	75/77 (97%)	10 (13%)	0
All	All	4803/4811 (99%)	510 (10%)	16 (0%)

5 of 510 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 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	2391	G
53	1	2326	C
53	1	1130	U
53	1	2296	U
53	1	1020	A

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	57	10,11,12	0.65	0	8,13,15	0.30	0
59	MET	7	102	-	6,7,8	1.02	0	2,7,9	0.12	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	PHE	7	101	57	-	0/5/6/8	0/1/1/1
59	MET	7	102	-	-	0/5/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

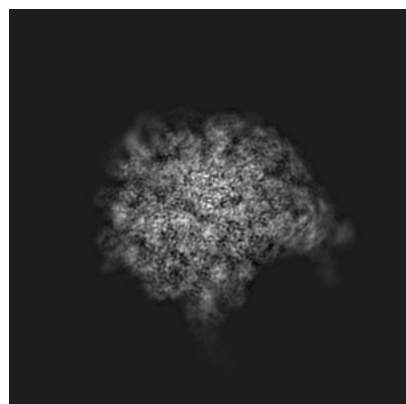
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21633. These allow visual inspection of the internal detail of the map and identification of artifacts.

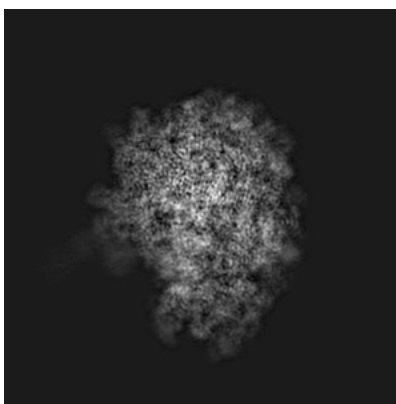
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

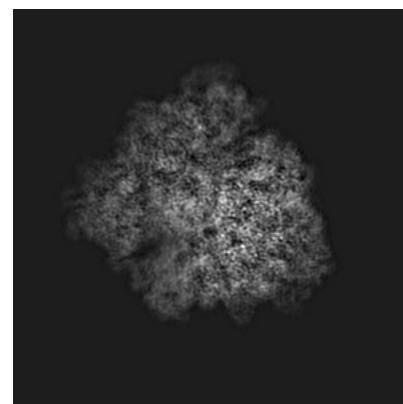
6.1.1 Primary map



X

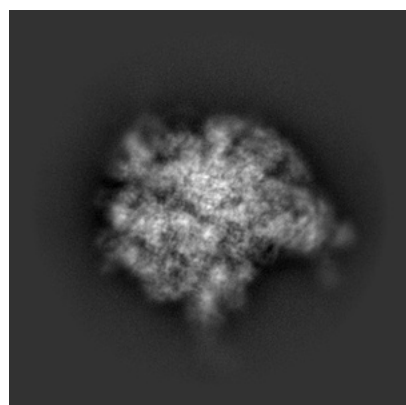


Y

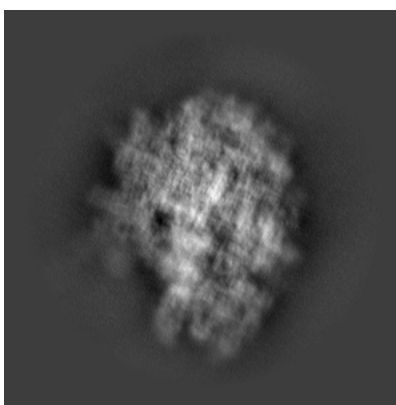


Z

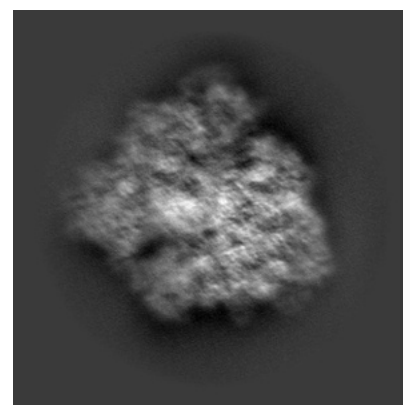
6.1.2 Raw map



X



Y

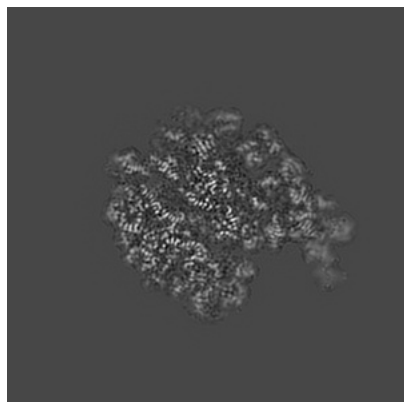


Z

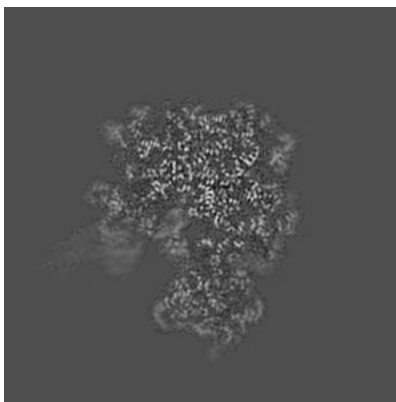
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

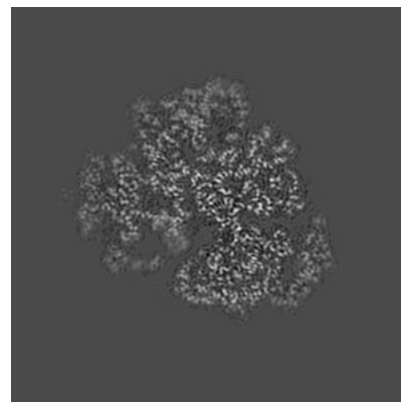
6.2.1 Primary map



X Index: 144

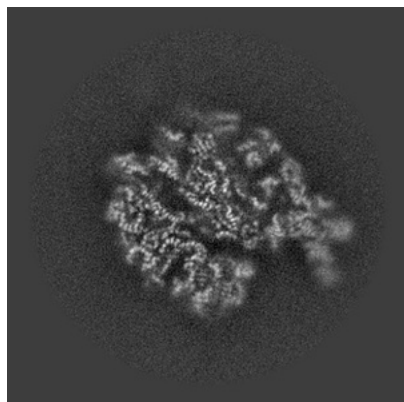


Y Index: 144

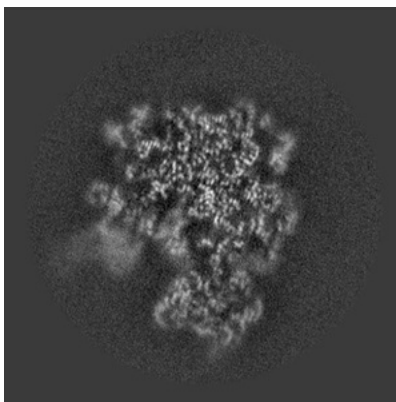


Z Index: 144

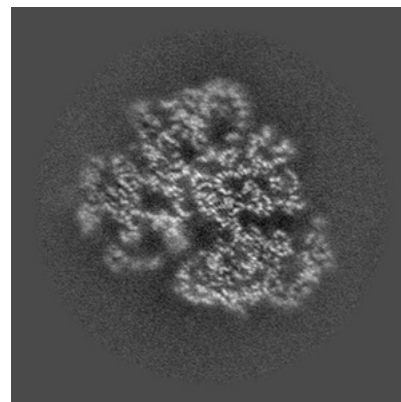
6.2.2 Raw map



X Index: 144



Y Index: 144

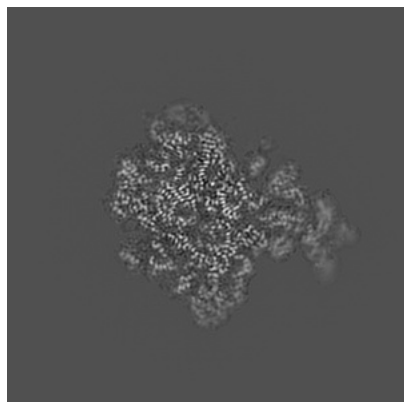


Z Index: 144

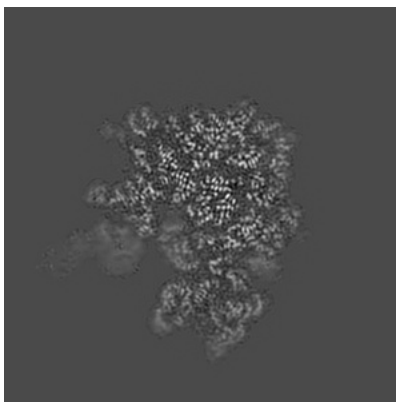
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

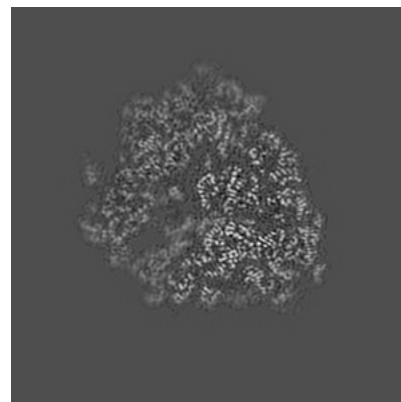
6.3.1 Primary map



X Index: 151

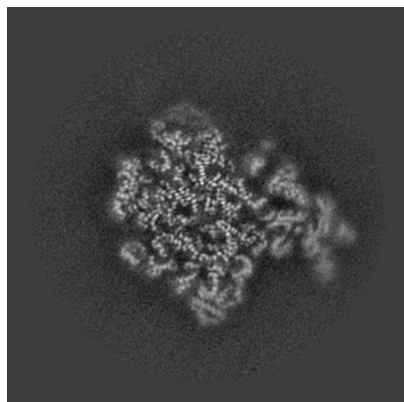


Y Index: 148

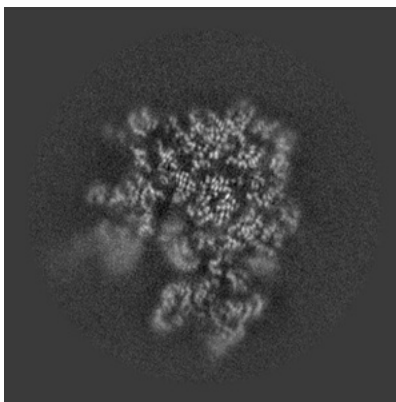


Z Index: 135

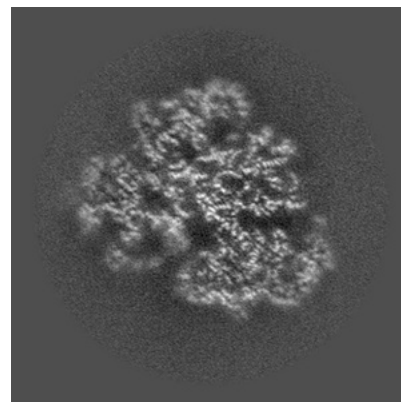
6.3.2 Raw map



X Index: 150



Y Index: 148

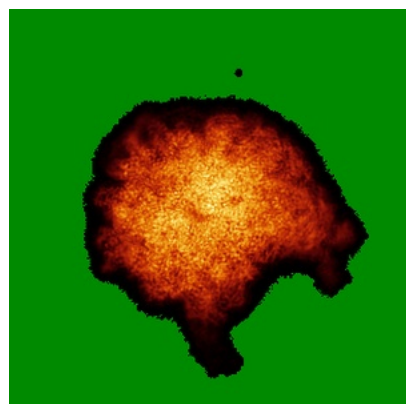


Z Index: 145

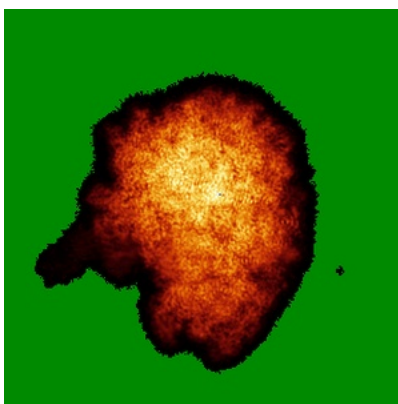
The images above show the largest variance slices of the map in three orthogonal directions.

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

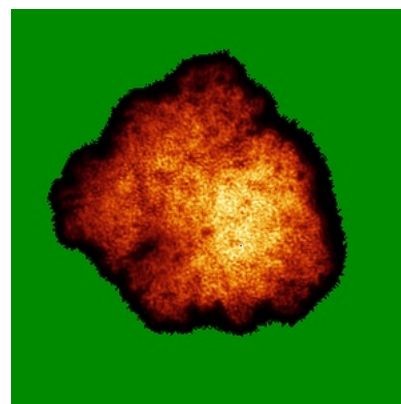
6.4.1 Primary map



X

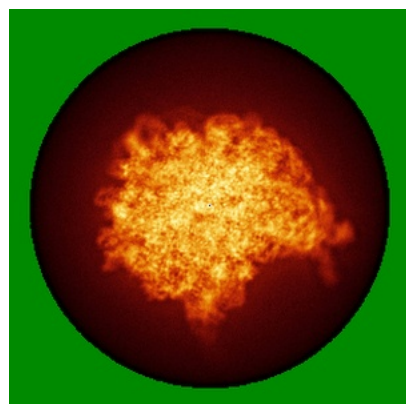


Y

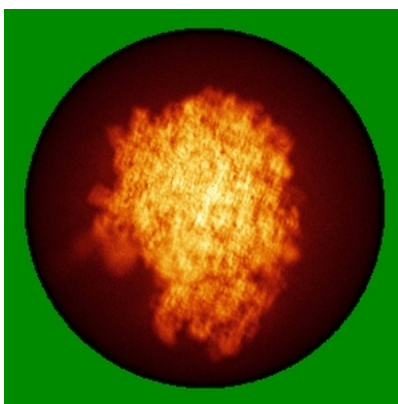


Z

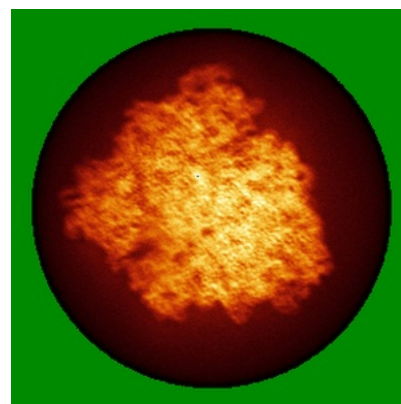
6.4.2 Raw map



X



Y

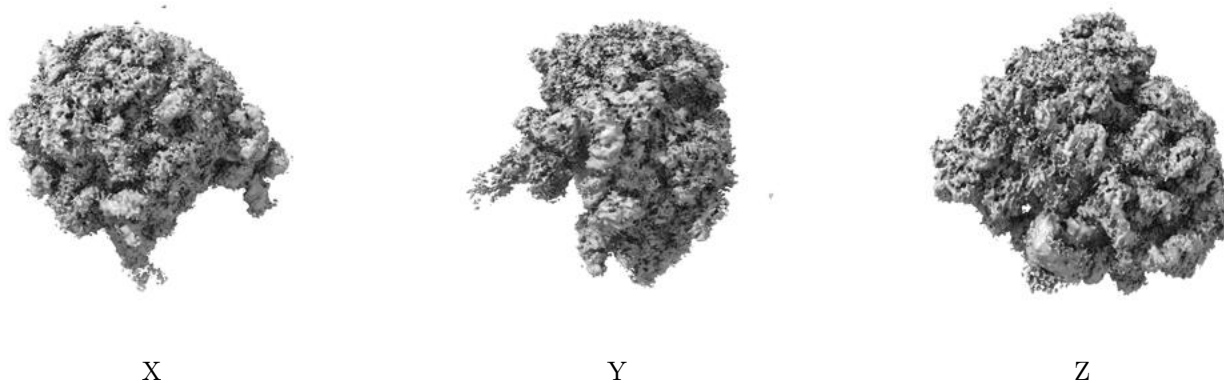


Z

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.

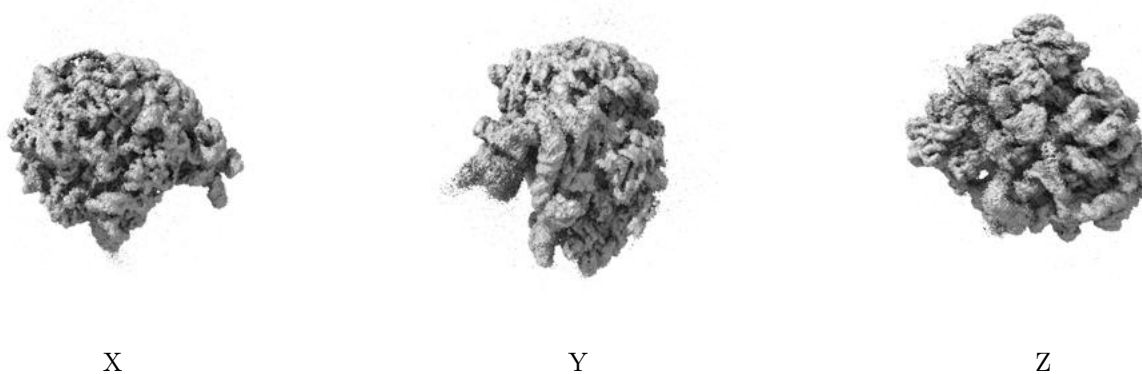
6.5 Orthogonal surface views [i](#)

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.

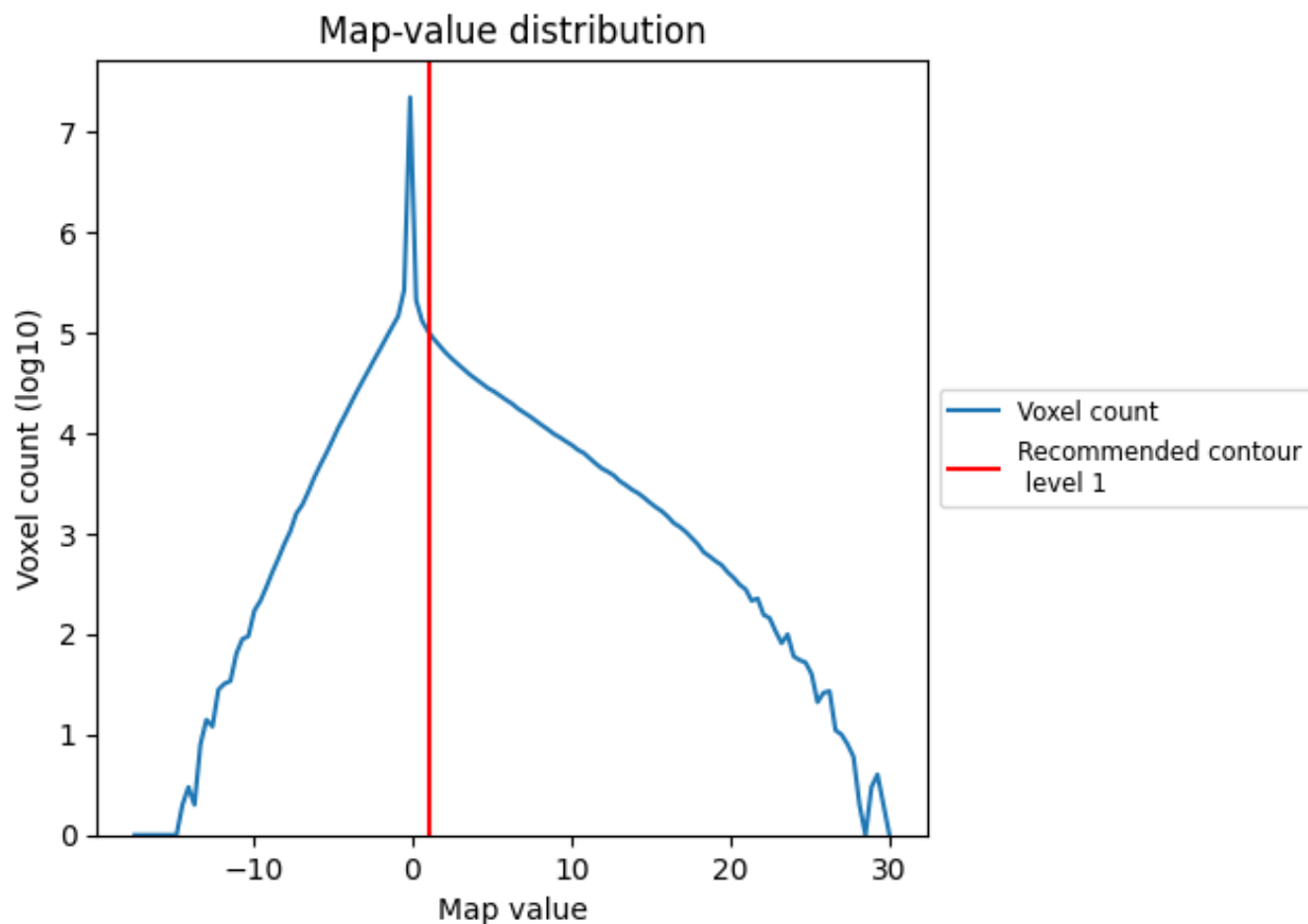
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

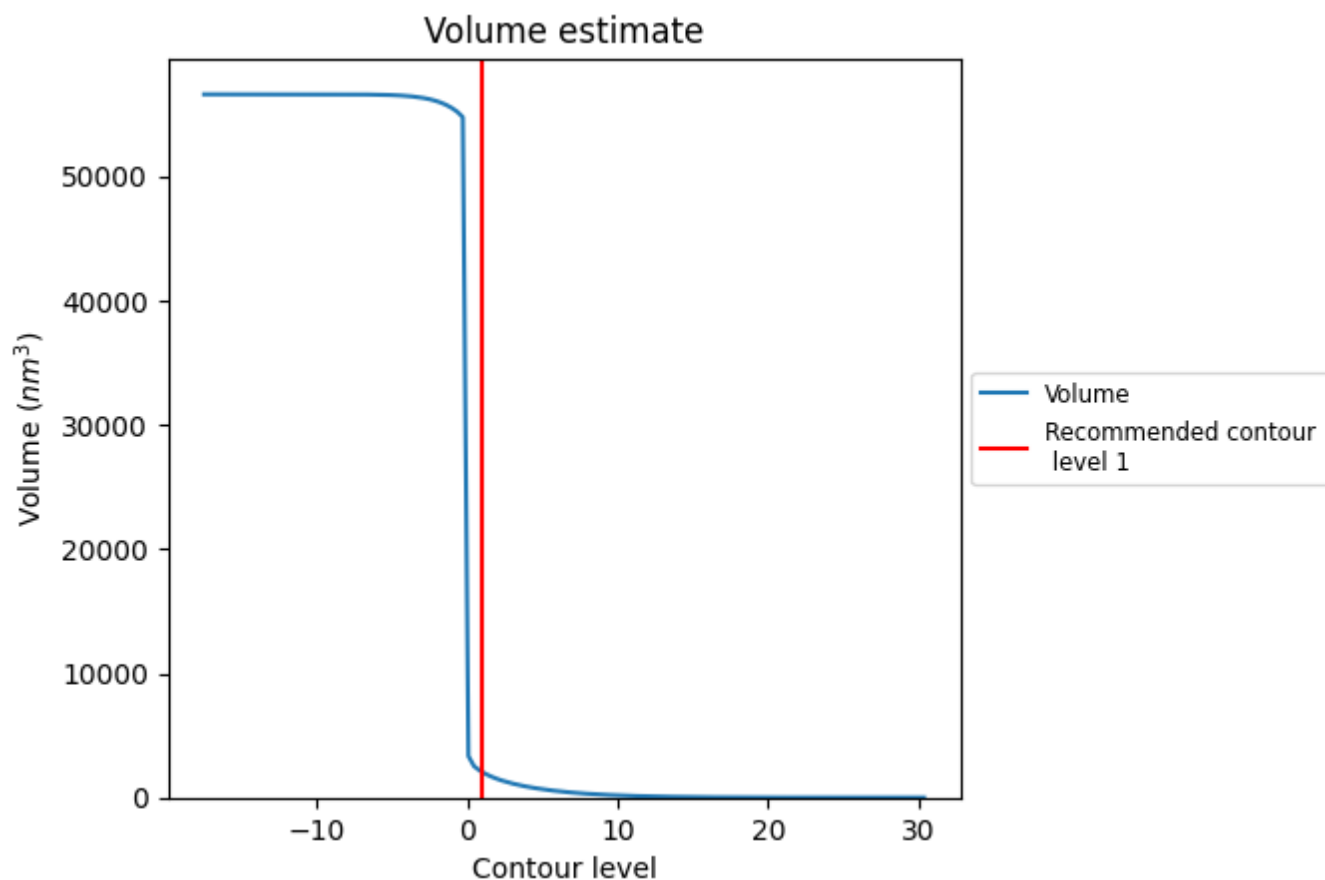
This section contains the results of statistical analysis of the map.

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.

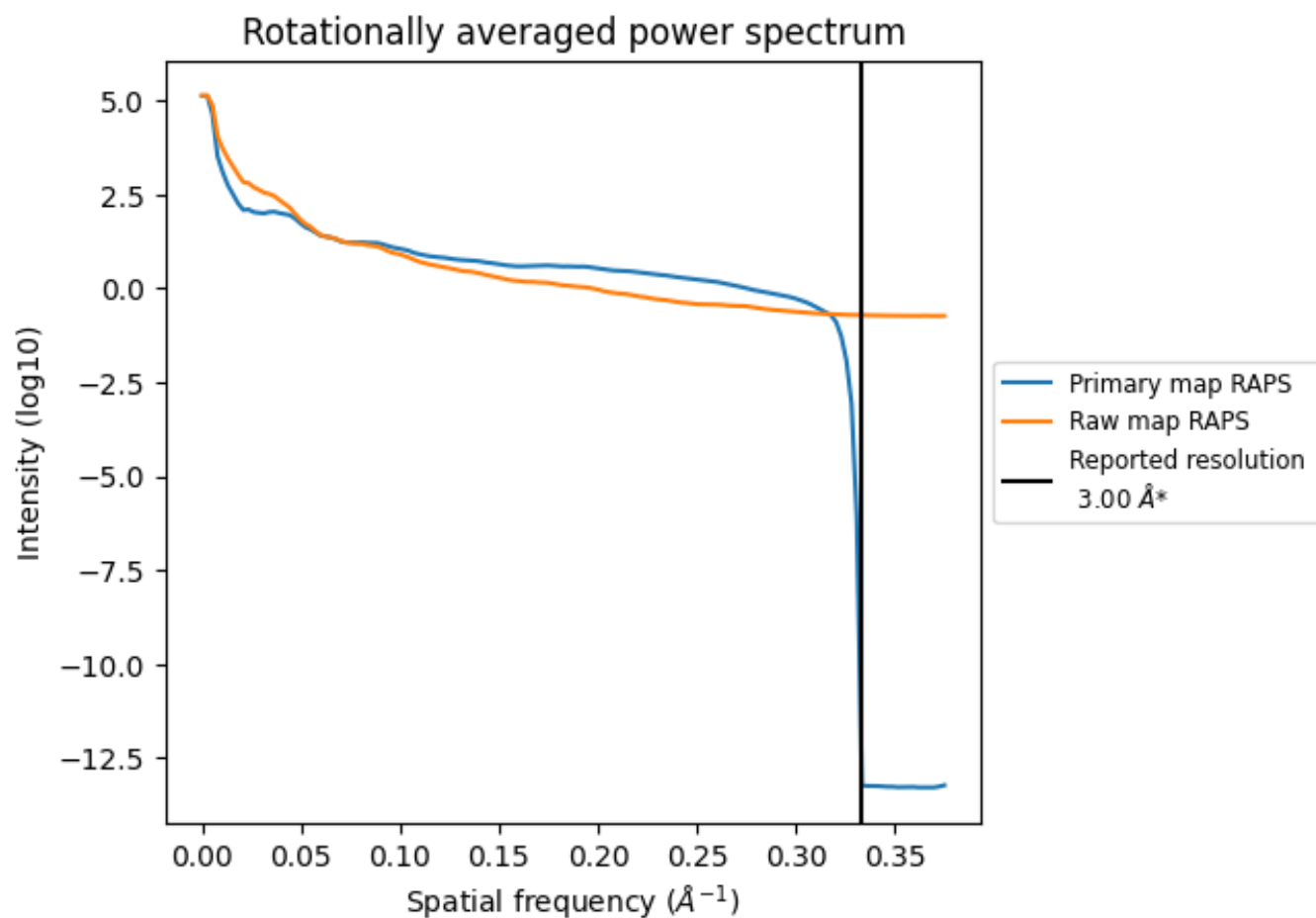
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2068 nm³; this corresponds to an approximate mass of 1868 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 ⓘ

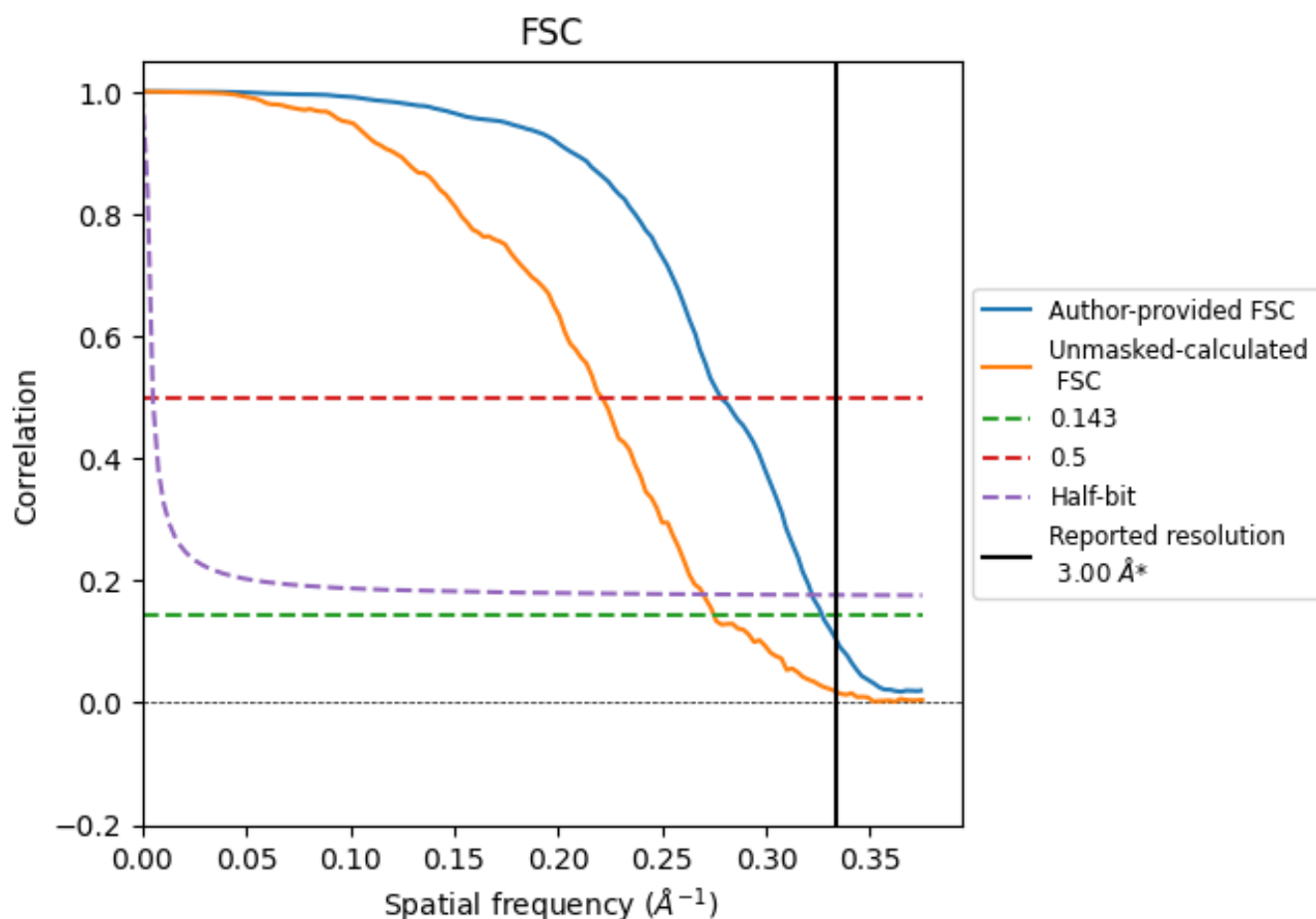


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 $0.333 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

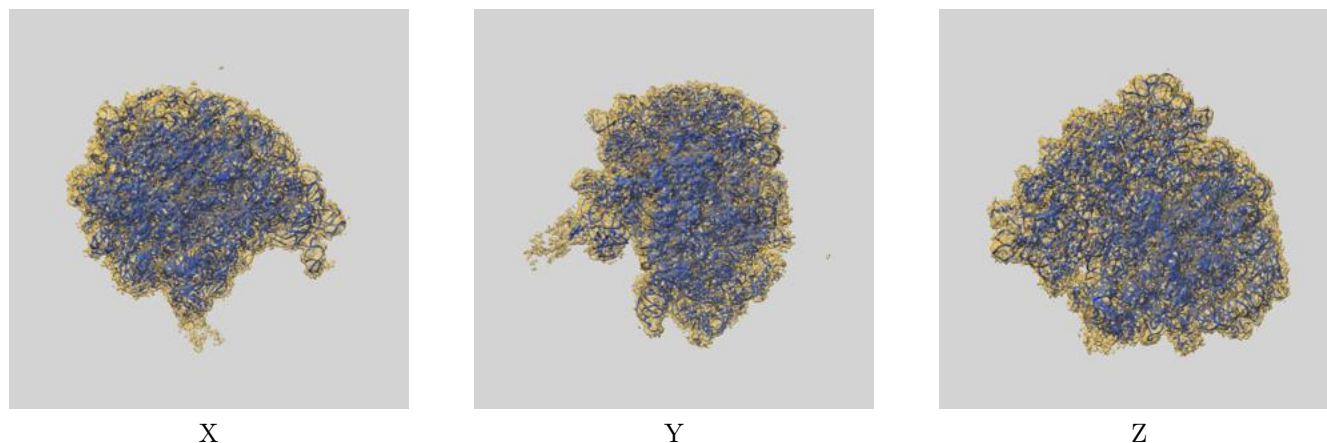
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.06	3.59	3.10
Unmasked-calculated*	3.64	4.53	3.71

*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 3.64 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

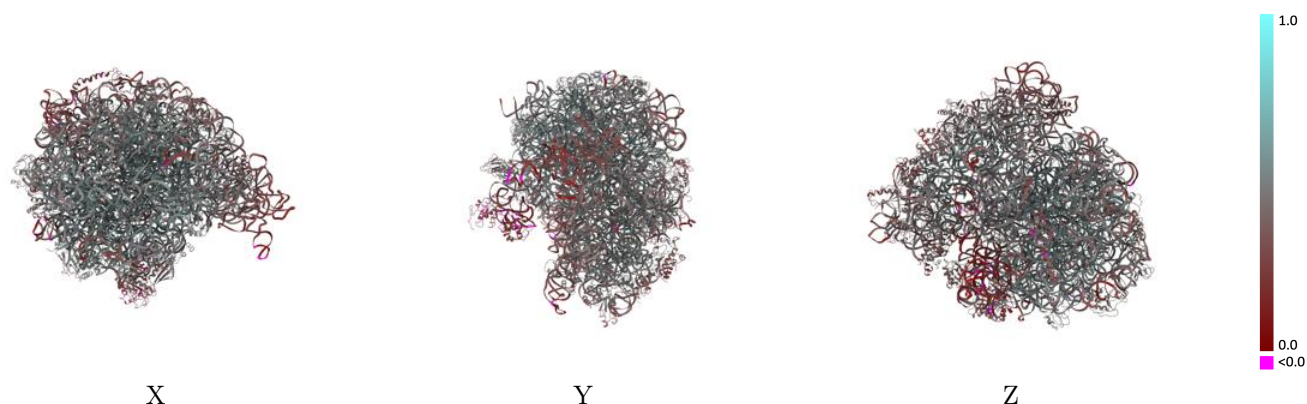
This section contains information regarding the fit between EMDB map EMD-21633 and PDB model 6WDE. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



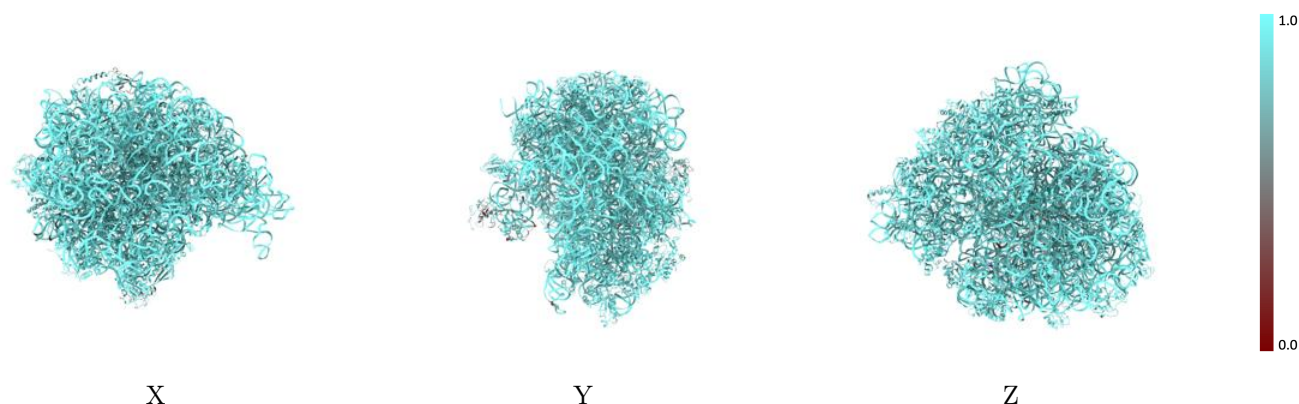
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



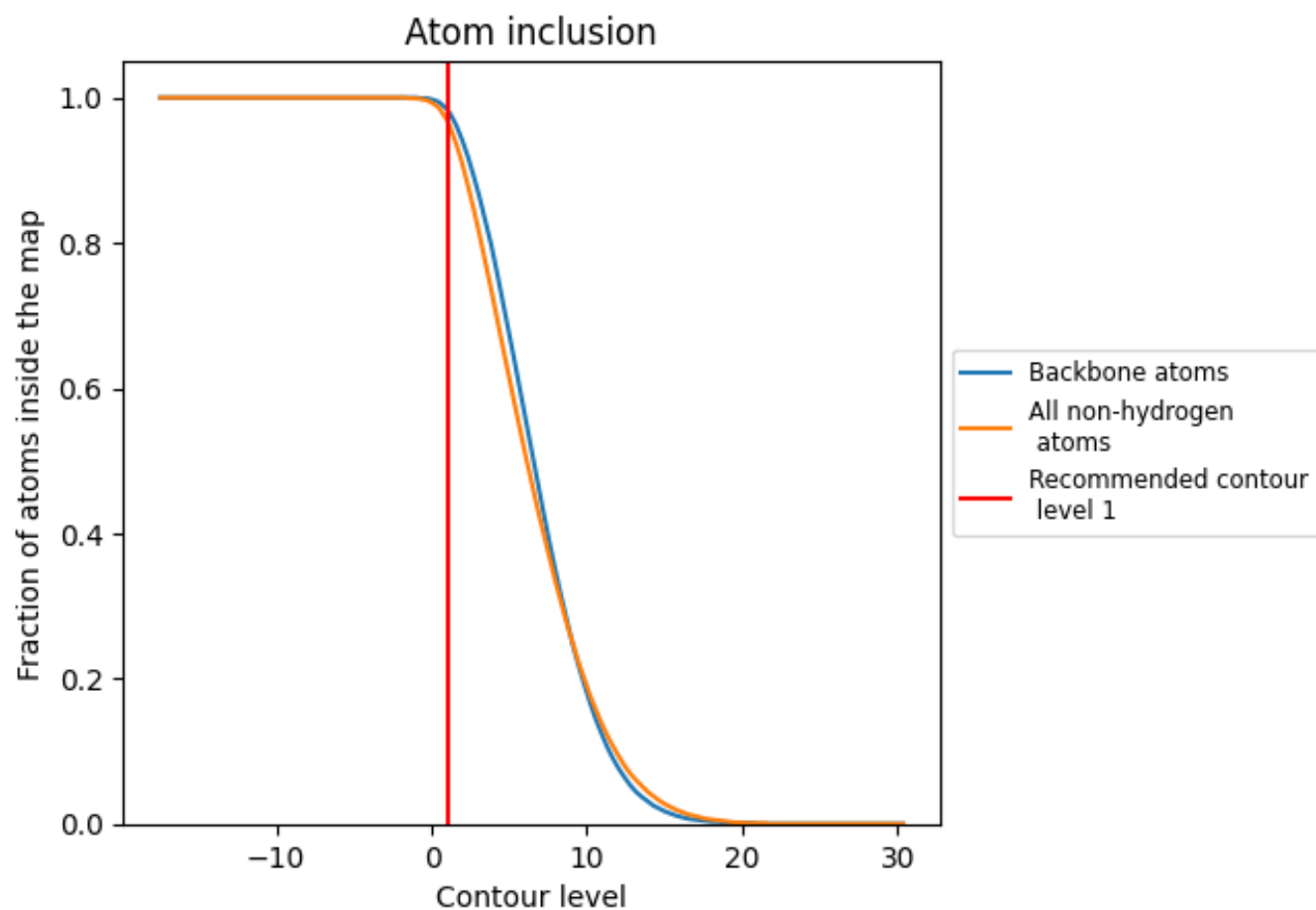
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 97% 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	 0.9690	 0.4400
1	 0.9860	 0.4670
2	 0.9910	 0.4080
3	 0.9840	 0.4260
4	 0.9170	 0.3620
5	 0.9840	 0.3820
6	 0.8460	 0.1450
7	 0.9600	 0.3240
B	 0.9630	 0.5190
C	 0.9180	 0.4600
D	 0.9550	 0.5250
E	 0.9840	 0.5430
F	 0.9310	 0.4870
G	 0.9180	 0.3970
H	 0.9360	 0.4510
I	 0.9200	 0.4000
J	 0.9550	 0.4710
K	 0.9490	 0.4120
L	 0.9560	 0.3940
M	 0.9530	 0.4710
N	 0.9360	 0.4010
O	 0.8680	 0.3730
P	 0.9670	 0.4570
Q	 0.9560	 0.4760
R	 0.9610	 0.3800
S	 0.9340	 0.4270
T	 0.9550	 0.4380
U	 0.9310	 0.4140
V	 0.9590	 0.4500
W	 0.9570	 0.4250
X	 0.9730	 0.4150
Y	 0.9180	 0.3690
Z	 0.8900	 0.3690
a	 0.9000	 0.2040
b	 0.9690	 0.5250



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Chain	Atom inclusion	Q-score
c	 0.9750	 0.5170
d	 0.9600	 0.4770
e	 0.9670	 0.3740
f	 0.9620	 0.4120
g	 0.8240	 0.3180
h	 0.6940	 0.1510
i	 0.7370	 0.1490
j	 0.9610	 0.5040
k	 0.9660	 0.5050
l	 0.9660	 0.4920
m	 0.9580	 0.5050
n	 0.9730	 0.5110
o	 0.9650	 0.4340
p	 0.9630	 0.4980
q	 0.9660	 0.5150
r	 0.9560	 0.4750
s	 0.9570	 0.4990
t	 0.9520	 0.4770
u	 0.9530	 0.4430
v	 0.9580	 0.4680
w	 0.9710	 0.5310
x	 0.9730	 0.5020
y	 0.9380	 0.4050
z	 0.9750	 0.5070