



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 11:20 AM UTC

PDB ID : 6WD1 / pdb_00006wd1
EMDB ID : EMD-21620
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure I-B)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

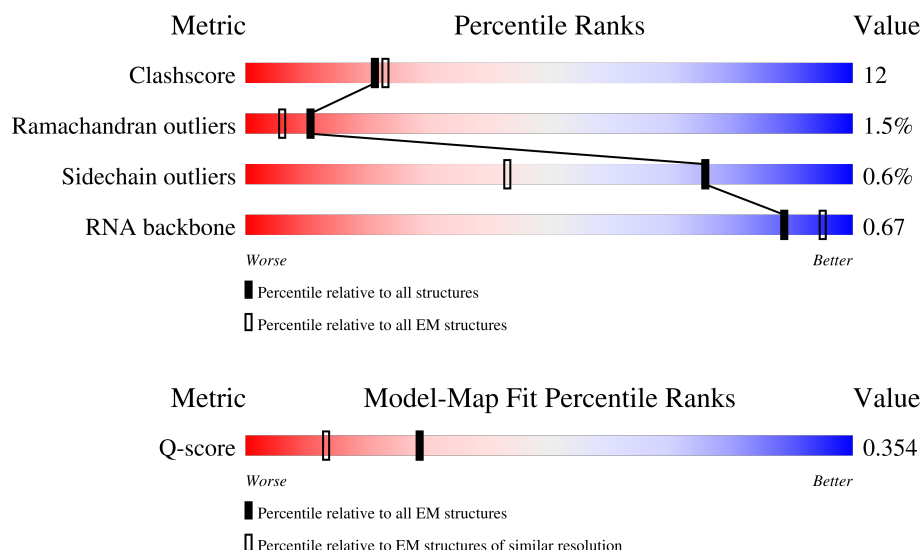
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 Å.

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



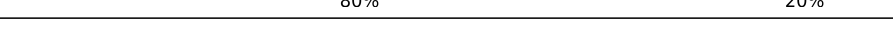
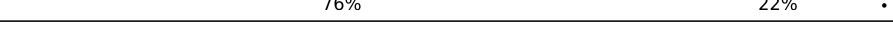
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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

Mol	Chain	Length	Quality of chain
1	b	271	
2	c	209	
3	d	201	

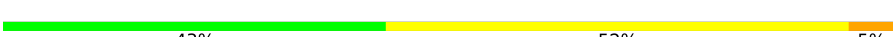
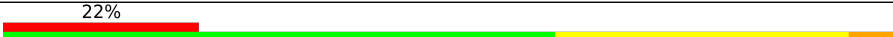
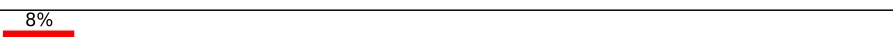
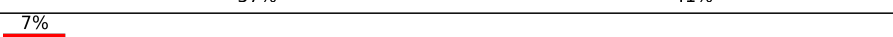
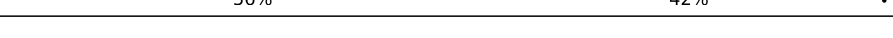
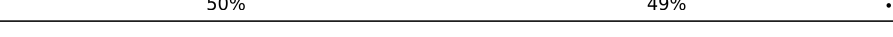
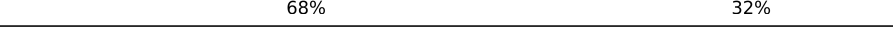
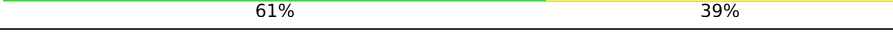
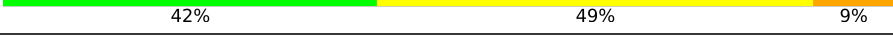
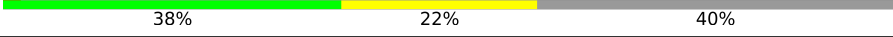
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56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

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

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Mol	Chain	Length	Quality of chain
54	2	120	61% 35%
55	5	77	43% 38% 18%
56	4	18	17% 56% 33% 6% 6%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 146942 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	variant	GB 1036415628

- 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 1370526515

- Molecule 55 is a RNA chain called tRNAfMet.

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

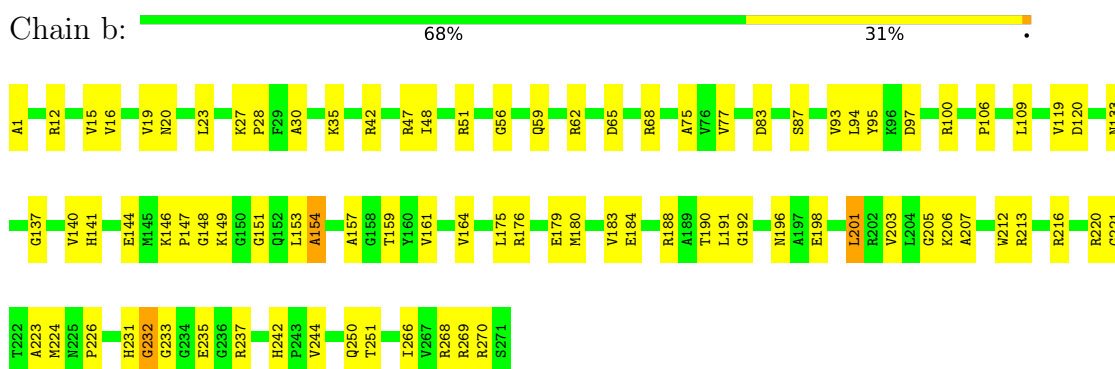
- Molecule 56 is a RNA chain called mRNA.

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

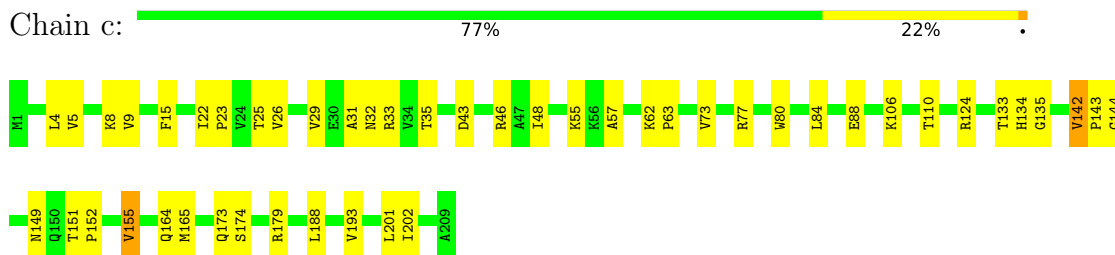
3 Residue-property plots

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.

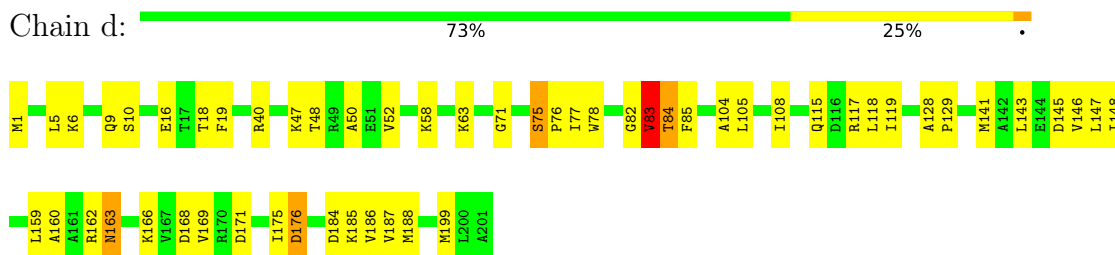
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

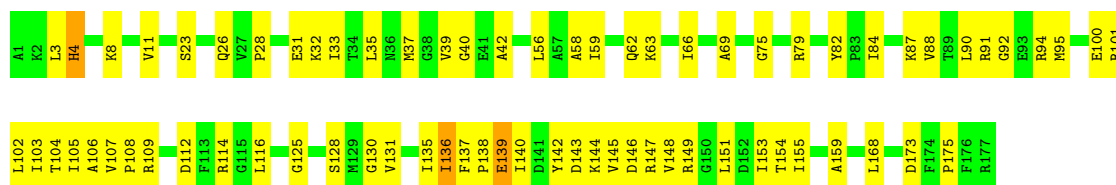


• Molecule 3: 50S ribosomal protein L4

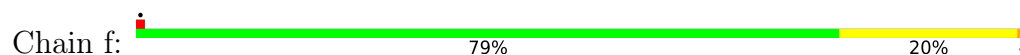


• Molecule 4: 50S ribosomal protein L5

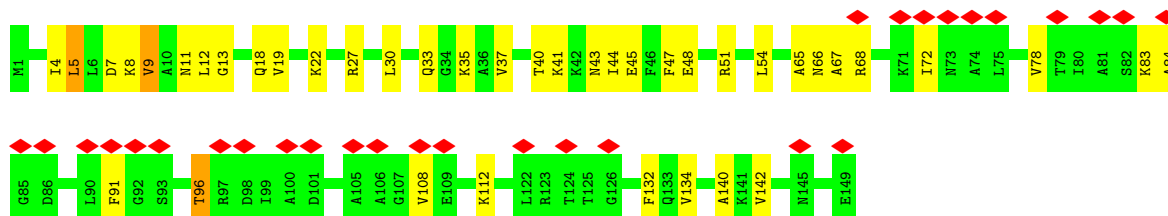




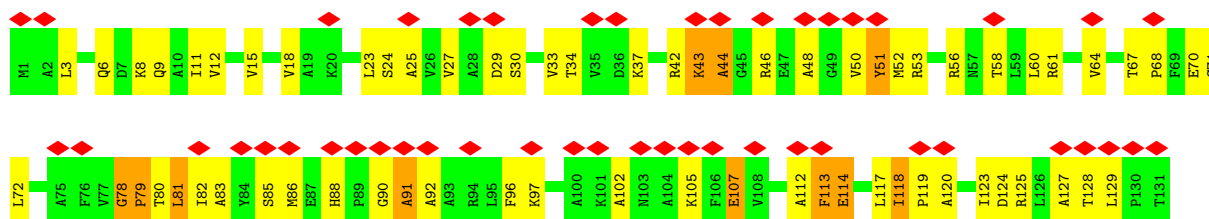
• Molecule 5: 50S ribosomal protein L6



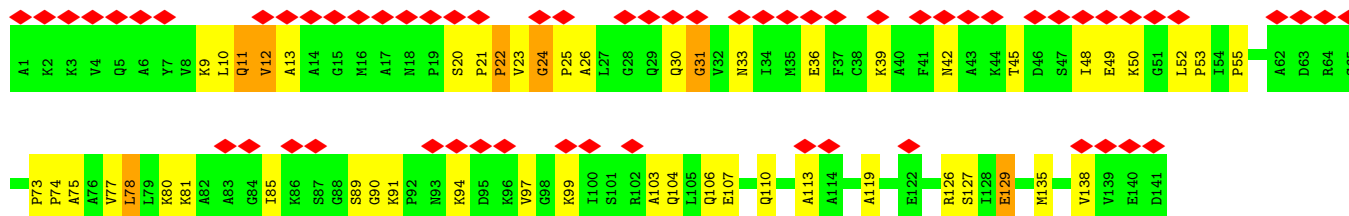
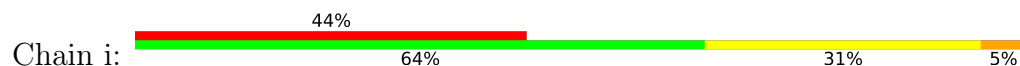
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10



• Molecule 8: 50S ribosomal protein L11



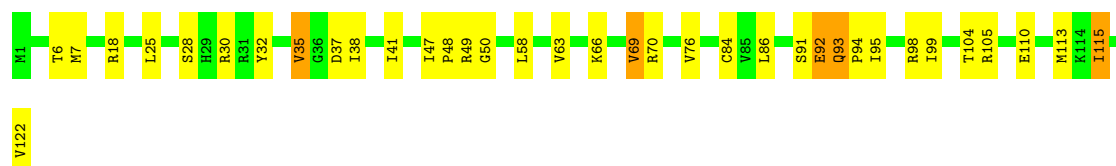
• Molecule 9: 50S ribosomal protein L13

Chain j:  76% 21%



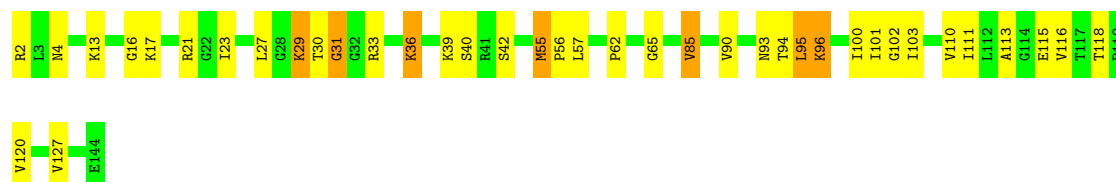
- Molecule 10: 50S ribosomal protein L14

Chain k:  70% 25%



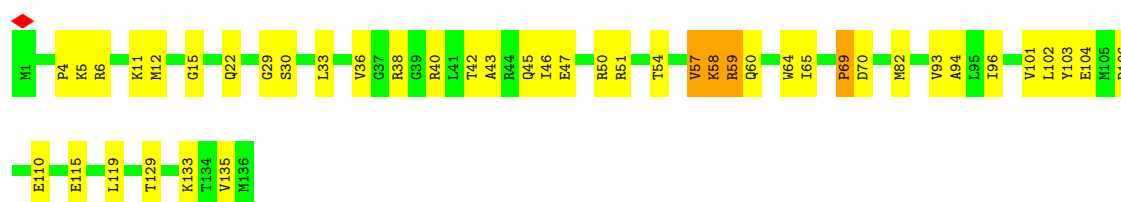
- Molecule 11: 50S ribosomal protein L15

Chain l:  73% 22% 5%



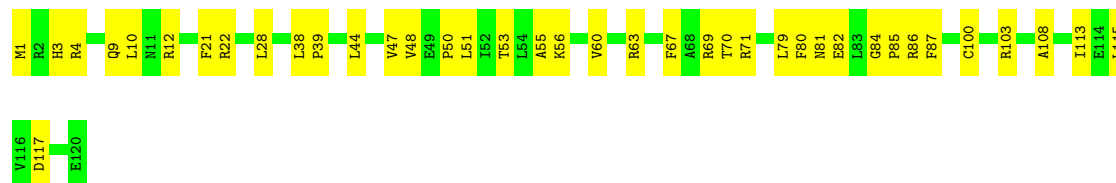
- Molecule 12: 50S ribosomal protein L16

Chain m:  68% 29%



- Molecule 13: 50S ribosomal protein L17

Chain n:  68% 32%

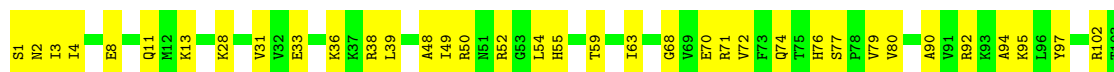


- Molecule 14: 50S ribosomal protein L18

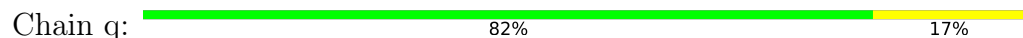
Chain o:  79% 20%



- Molecule 15: 50S ribosomal protein L19



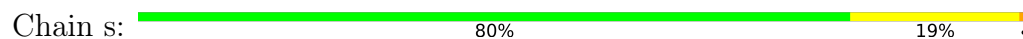
- Molecule 16: 50S ribosomal protein L20



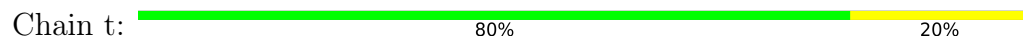
- Molecule 17: 50S ribosomal protein L21



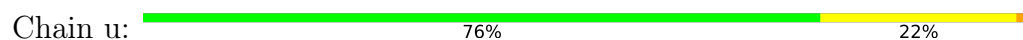
- Molecule 18: 50S ribosomal protein L22



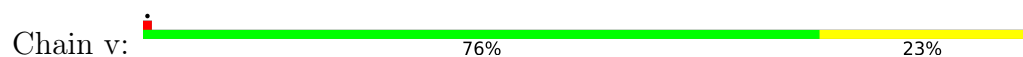
- Molecule 19: 50S ribosomal protein L23



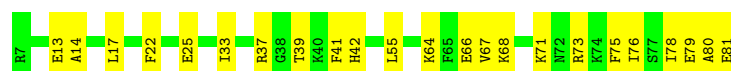
- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25



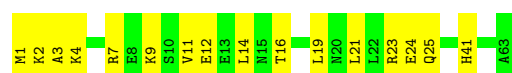
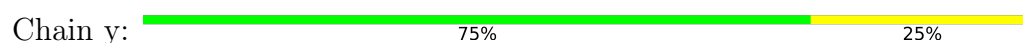
- Molecule 22: 50S ribosomal protein L27



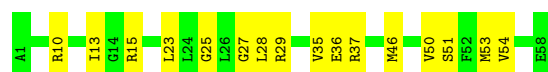
- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29



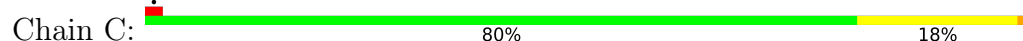
- Molecule 25: 50S ribosomal protein L30



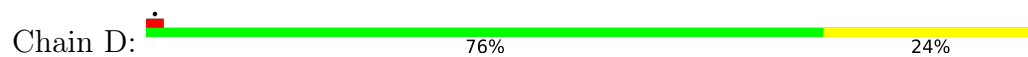
- Molecule 26: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L33



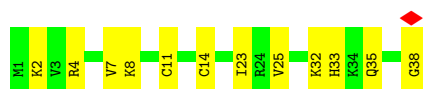
- Molecule 28: 50S ribosomal protein L34



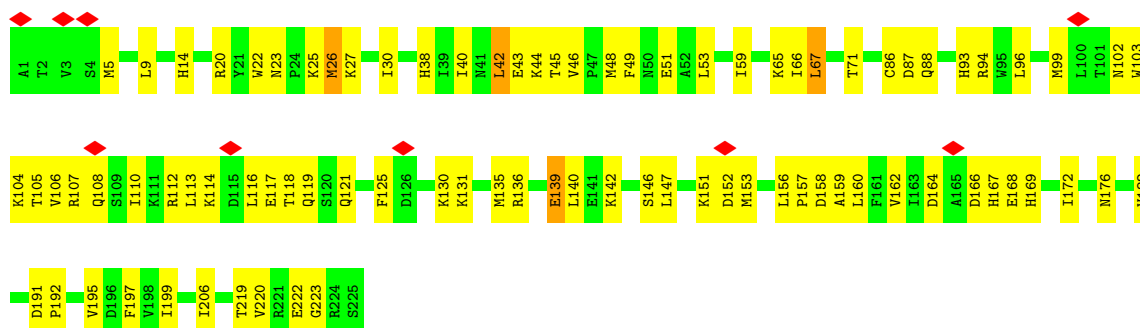
- Molecule 29: 50S ribosomal protein L35



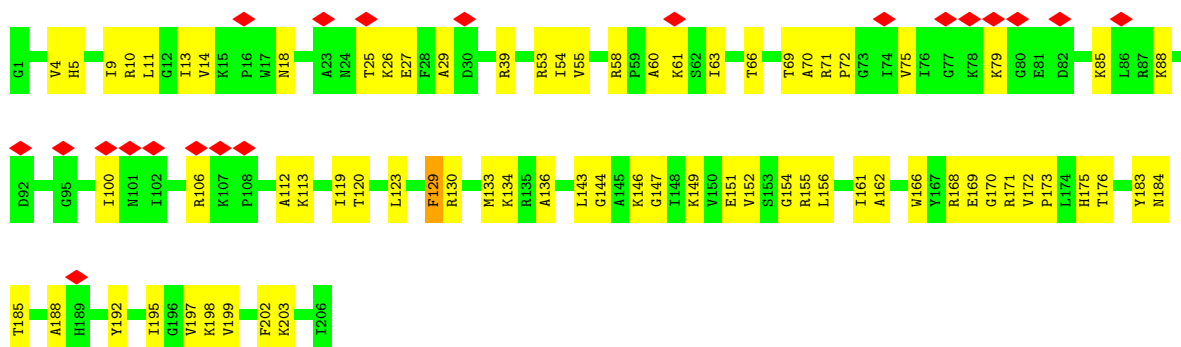
- Molecule 30: 50S ribosomal protein L36



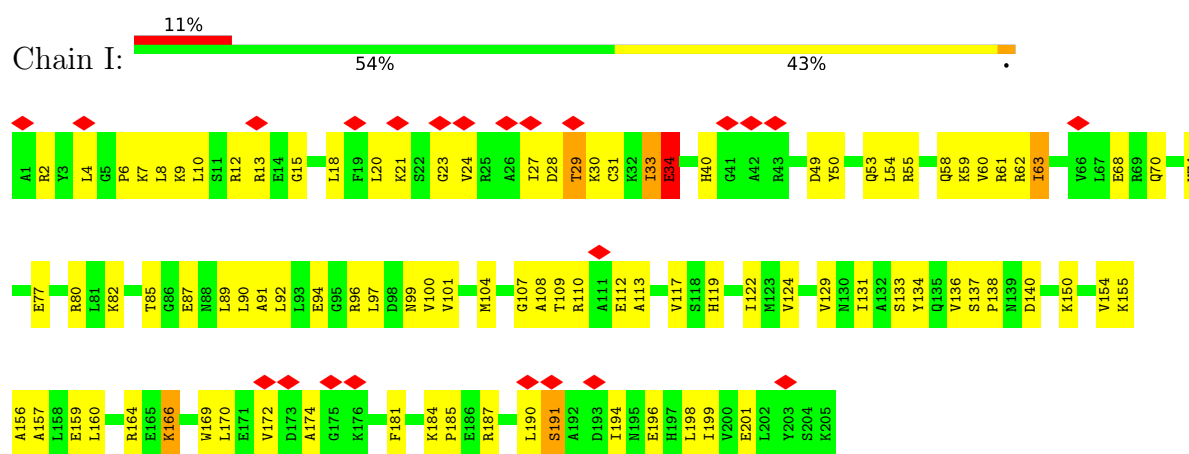
- Molecule 31: 30S ribosomal protein S2



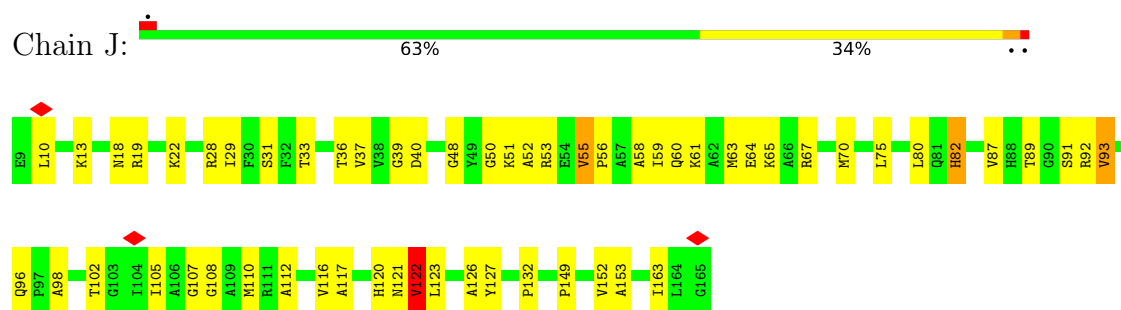
- Molecule 32: 30S ribosomal protein S3



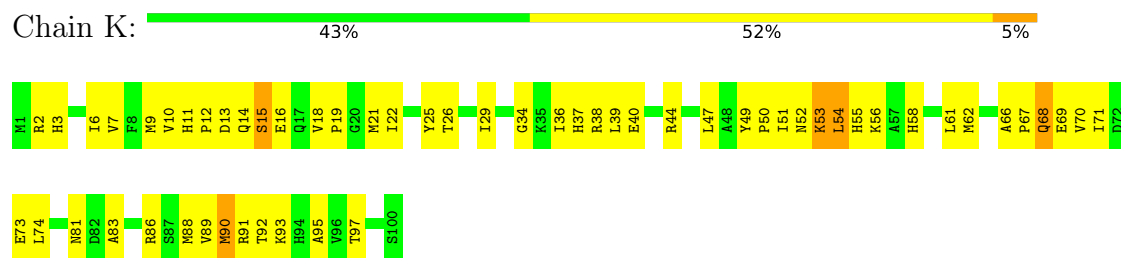
- Molecule 33: 30S ribosomal protein S4



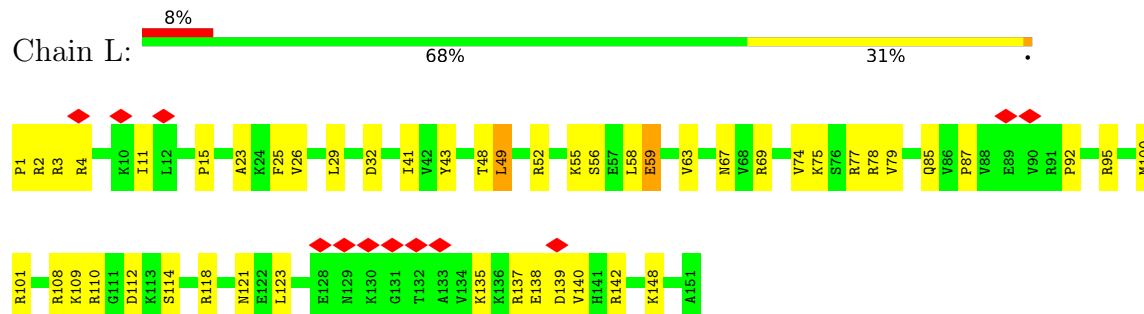
- Molecule 34: 30S ribosomal protein S5



- Molecule 35: 30S ribosomal protein S6

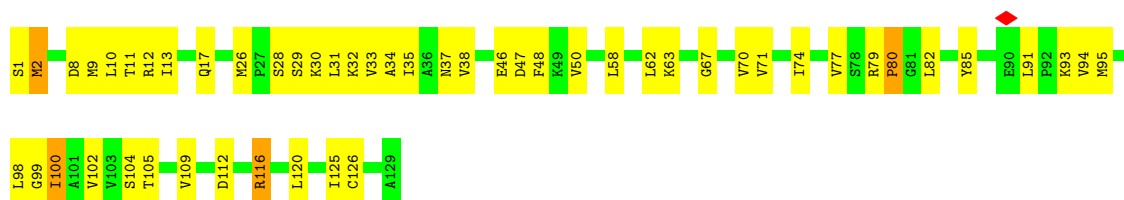


- Molecule 36: 30S ribosomal protein S7

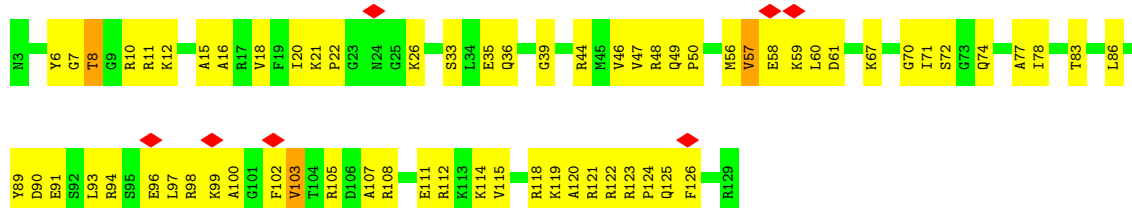


- Molecule 37: 30S ribosomal protein S8

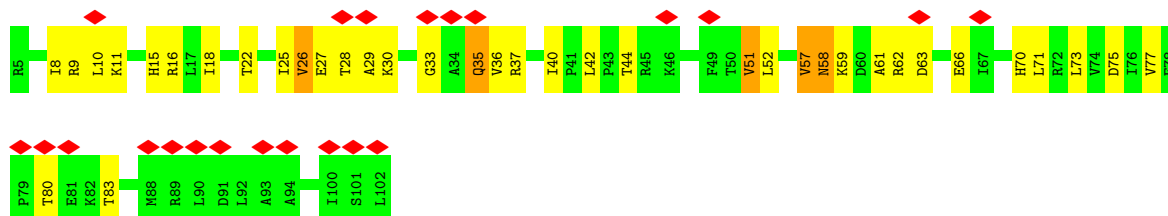




• Molecule 38: 30S ribosomal protein S9



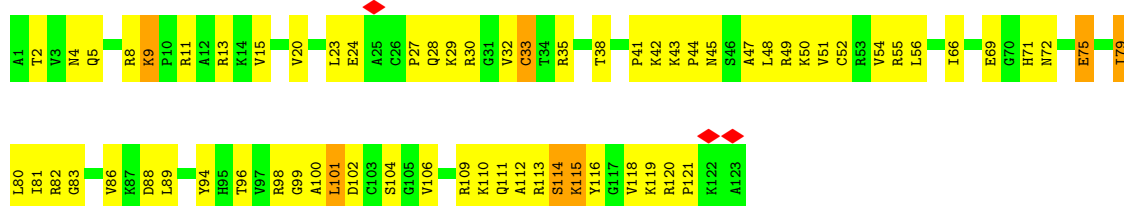
• Molecule 39: 30S ribosomal protein S10



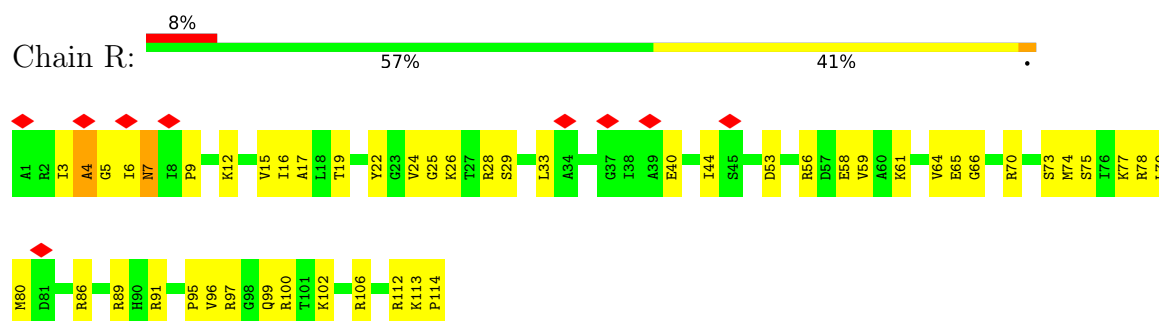
• Molecule 40: 30S ribosomal protein S11



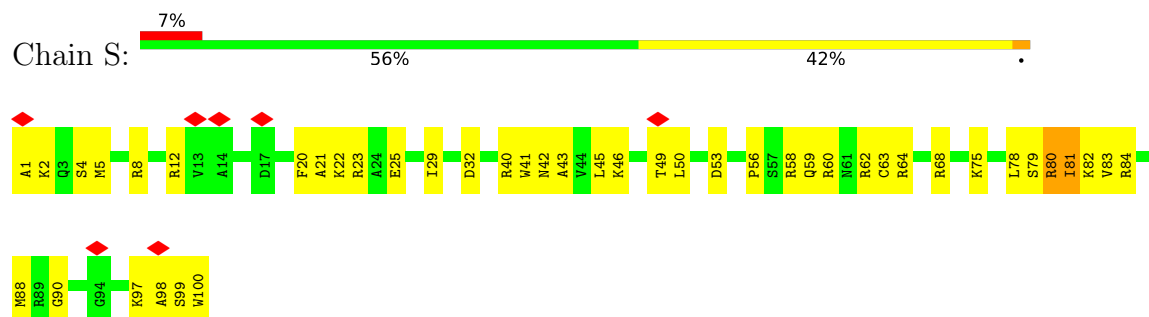
• Molecule 41: 30S ribosomal protein S12



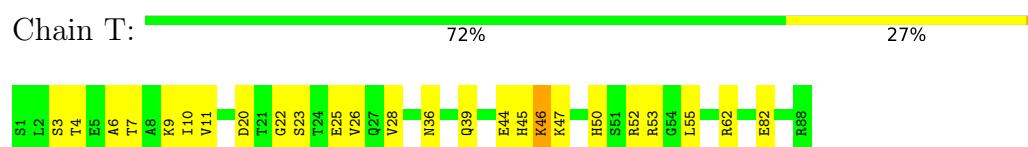
• Molecule 42: 30S ribosomal protein S13



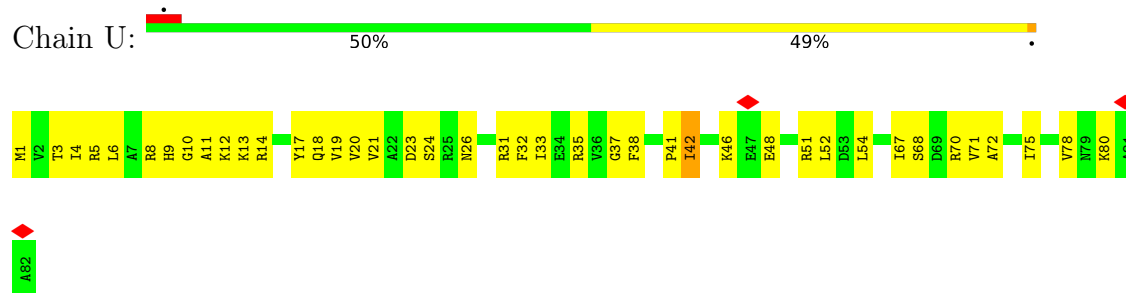
- Molecule 43: 30S ribosomal protein S14



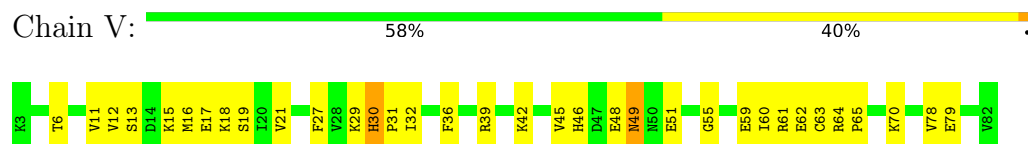
- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16

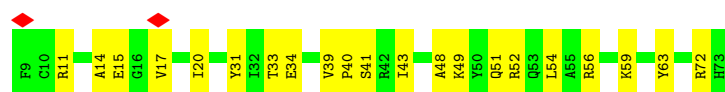


- Molecule 46: 30S ribosomal protein S17

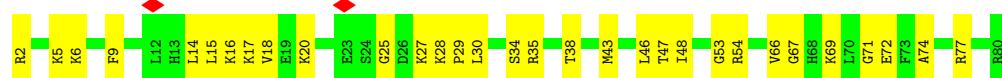


- Molecule 47: 30S ribosomal protein S18





- Molecule 48: 30S ribosomal protein S19



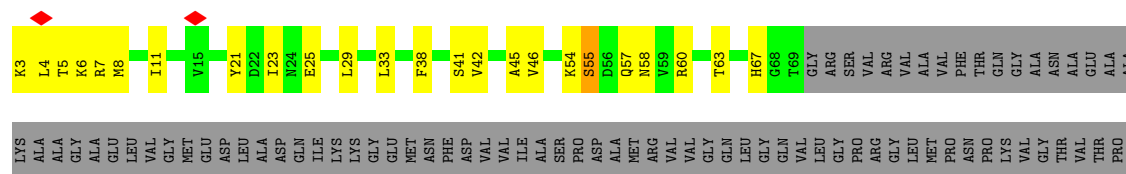
- Molecule 49: 30S ribosomal protein S20



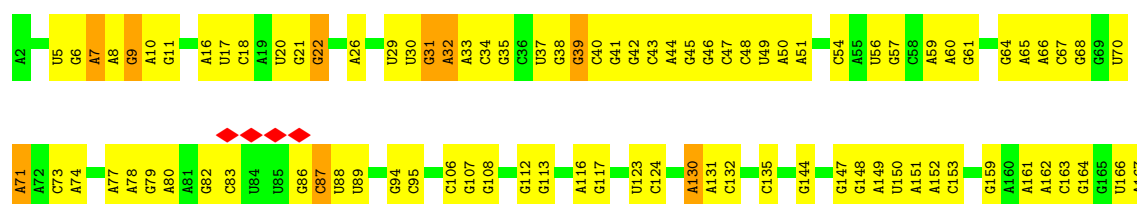
- Molecule 50: 30S ribosomal protein S21



- Molecule 51: 50S ribosomal protein L1



- Molecule 52: 16S ribosomal RNA

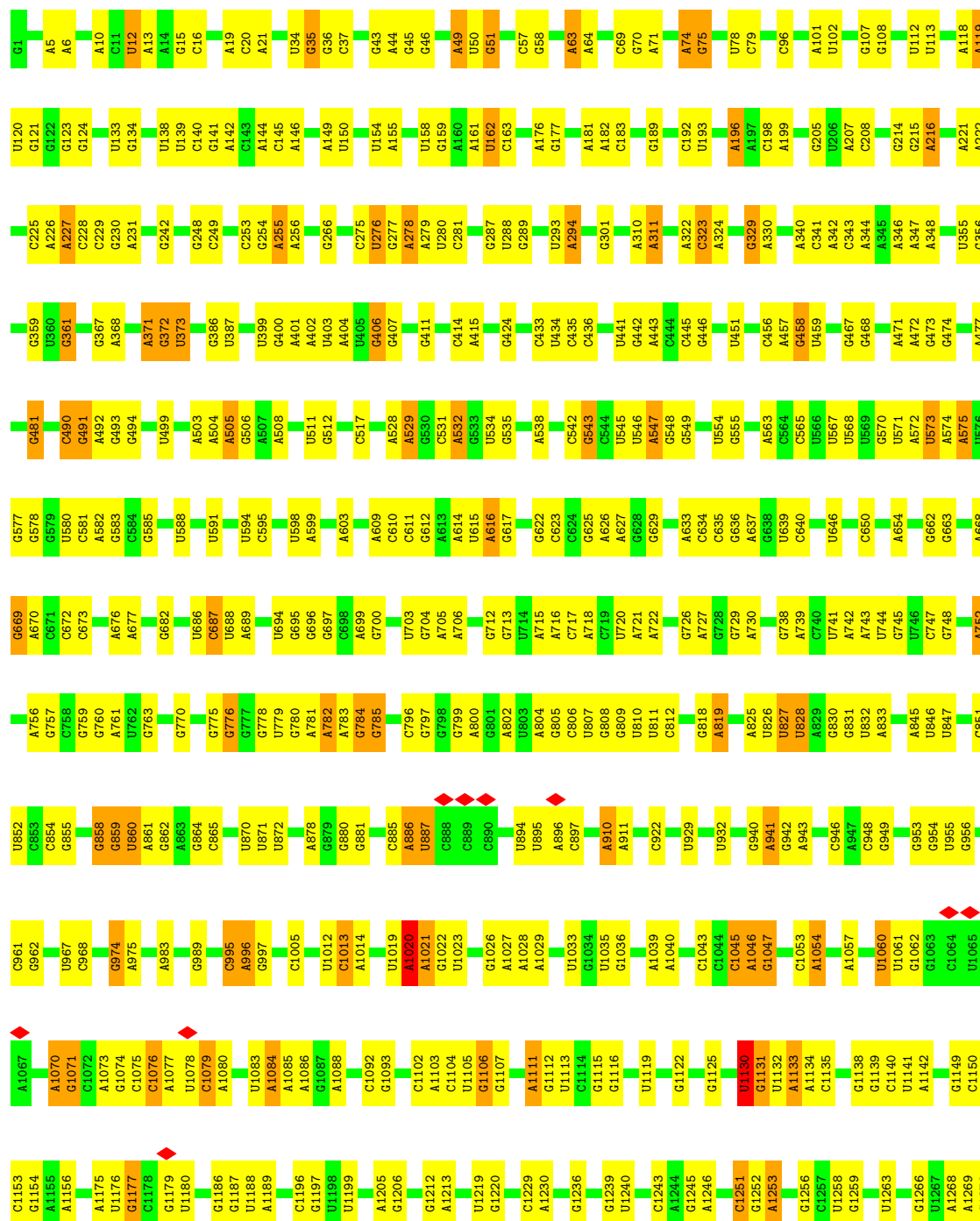


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G1392	U1313	A1236	A1146	U1062	U870	G765	U686	U594	U515	G413	G346	G265	A171
U1393	C1314	C1237	U1147	G1063	U871	A766	A687	U594	U516	C418	G347	G266	
A1394	U1315	U1237	U1148	G1064		A767	A688	A595	C518	C419		C267	C175
C1395	A1238	A1239	G1153	C1071	U874	A768	G689	A596	C519	C422	G350	U268	C176
C1396	C1317	U1239	U1158	G1072	C876	G769	G690	A597	A520	C423	G351	C269	C183
C1397	A1318	U1240	U1159	U1073	A877	G773	G691	G597	A521	G424	C352	C270	G184
	C1320	G1241	U1160	G1074	A878		G692	G598	C522	G425	A353	C271	U185
C1400	C1325	A1245	C1162	U1075	C879	A777	G693	A600	A523	G426	C354	C272	C186
G1401	U1326	C1246	A1163	C880	C881	C779	A694	G601	C528	U427	C355	C273	G187
C1402				G881			A695	A602	G529	G428	A356	A279	
C1403							A696	U603	G530	U429	G357	C280	C193
C1404							U697	A607	G531	A430	U358	G281	C194
G1405							G698	A608	U531	A431	G359	C282	A195
U1406								A609	A532	A432	C360	C286	A196
									A533	U434	G361	C287	A197
C1412									U534	U435	G362	G289	A205
C1413									A535	A436	A363	C290	C206
									C536	C437	A364	U291	C207
									G537	U438	A365	G292	U208
									A539	A439	U367	C295	U209
									G540	A440	U368	C296	C210
									G541	G449		U296	G211
									G542	G450	A371	C297	G212
									U543	U458	C372	A303	
									G544	A459	U375	U304	C222
									C545	A460	U376	G305	A223
									A546	A461	G377	U306	U224
									A547		C378	C308	C225
											C379	C309	G226
											G380	A309	U229
											C381	G310	G230
											C382	C311	U231
											U387	C312	G232
												A313	C233
												C314	C234
												A315	C235
												C316	A236
												C392	G237
												A393	A238
												A321	A243
												C322	U244
												G324	U245
												A246	A247
												C327	G247
												C328	
												G331	G251
												A253	U252
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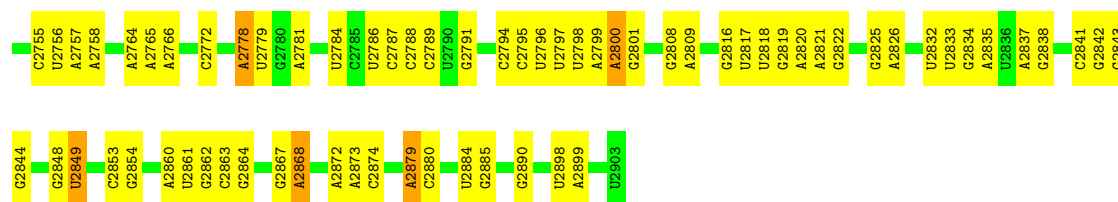


• Molecule 53: 23S ribosomal RNA

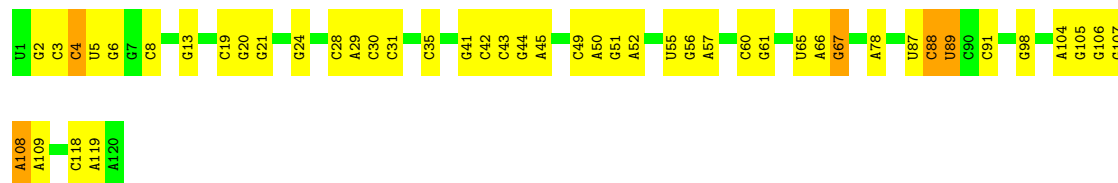
Chain 1: 58% 37% 5%



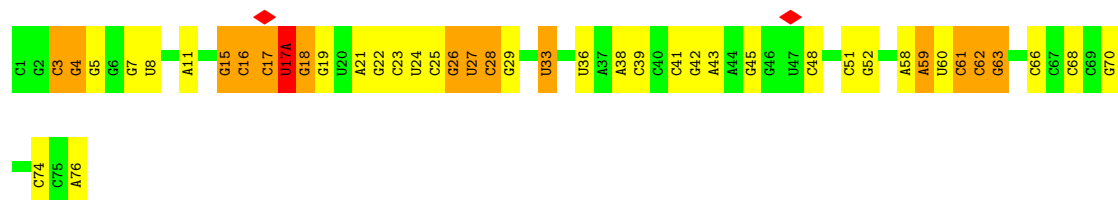
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C2465	C2466	A2566	C2465	A2378	U2292	A2199	G2125	A2033	U1931	G1828	A1744	U1636	G1517	A1378	A1272
C2467	C2468	C2567	C2466	A2381	G2293	U2203	G2126	U2034	G1932	A1829	A1745	U1637	G1524	A1379	A1275
A2469	C2470	A2572	A2469	G2383	U2296	G2204	G2129	C2036	A1936	C1833	G1748	G1645	A1528	A1383	C1278
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C2474	C2475	C2574	C2474	C2389	G2303	C2214	U2131	G2041	A1938	C1842	G1753	U1648	C1533	A1386	A1285
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G2481	G2482	U2585	G2481	G2399	C2310	A2227	G2140	A2054	U1955	C1857	A1759	U1667	G1540	G1416	C1296
G2484	G2485	C2590	G2484	U2402	U2312	A2228	G2141	G2056	U1956	A1858	G1760	U1667	U1541	G1417	C1297
C2486	C2487	C2591	C2486	G2403	C2313	U2243	G2142	G2057	U1957	A1871	G1764	U1668	C1547	A1420	G1300
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C2490	C2491	C2593	C2490	U2405	G2315	U2245	C2146	A2061	G1964	C1874	A1773	U1670	A1549	G1437	C1302
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C2502	C2503	C2599	C2502	U2411	U2321	U2251	U2155	U2067	A1971	U1880	U1779	U1676	C1555	A1443	C1308
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C2562	C2563	C2629	C2562	U2441	U2351	U2281	G2175	C2101	C1999	C1910	U1809	U1706	C1585	A1473	C1338
C2564	C2565	C2630	C2564	G2442	U2352	U2282	G2176	U2102	C1999	C1911	U1810	U1707	C1586	A1474	C1339
C2566	C2567	C2631	C2566	U2443	U2353	U2283	G2177	U2103	C1999	C1912	U1811	U1708	C1587	A1475	C1340
C2568	C2569	C2632	C2568	G2444	U2354	U2284	G2178	U2104	C1999	C1913	U1812	U1709	C1588	A1476	C1341
C2570	C2571	C2633	C2570	U2445	U2355	U2285	G2179	U2105	C1999	C1914	U1813	U1710	C1589	A1477	C1342
C2572	C2573	C2634	C2572	G2446	U2356	U2286	G2180	U2106	C1999	C1915	U1814	U1711	C1590	A1478	C1343
C2574	C2575	C2635	C2574	U2447	U2357	U2287	G2181	U2107	C1999	C1916	U1815	U1712	C1591	A1479	C1344
C2576	C2577	C2636	C2576	G2448	U2358	U2288	G2182	U2108	C1999	C1917	U1816	U1713	C1592	A1480	C1345
C2578	C2579	C2637	C2578	U2449	U2359	U2289	G2183	U2109	C1999	C1918	U1817	U1714	C1593	A1481	C1346
C2580	C2581	C2638	C2580	G2450	U2360	U2290	G2184	U2110	C1999	C1919	U1818	U1715	C1594	A1482	C1347
C2582	C2583	C2639	C2582	U2451	U2361	U2291	G2185	U2111	C1999	C1920	U1819	U1716	C1595	A1483	C1348
C2584	C2585	C2640	C2584	G2452	U2362	U2292	G2186	U2112	C1999	C1921	U1820	U1717	C1596	A1484	C1349
C2586	C2587	C2641	C2586	U2453	U2363	U2293	G2187	U2113	C1999	C1922	U1821	U1718	C1597	A1485	C1350
C2588	C2589	C2642	C2588	G2454	U2364	U2294	G2188	U2114	C1999	C1923	U1822	U1719	C1598	A1486	C1351
C2590	C2591	C2643	C2590	U2455	U2365	U2295	G2189	U2115	C1999	C1924	U1823	U1720	C1599	A1487	C1352
C2592	C2593	C2644	C2592	G2456	U2366	U2296	G2190	U2116	C1999	C1925	U1824	U1721	C1600	A1488	C1353
C2594	C2595	C2645	C2594	U2457	U2367	U2297	G2191	U2117	C1999	C1926	U1825	U1722	C1601	A1489	C1354
C2596	C2597	C2646	C2596	G2458	U2368	U2298	G2192	U2118	C1999	C1927	U1826	U1723	C1602	A1490	C1355
C2598	C2599	C2647	C2598	U2459	U2369	U2299	G2193	U2119	C1999	C1928	U1827	U1724	C1603	A1491	C1356
C2600	C2601	C2648	C2600	G2460	U2370	U2300	G2194	U2120	C1999	C1929	U1828	U1725	C1604	A1492	C1357
C2602	C2603	C2649	C2602	U2461	U2371	U2301	G2195	U2121	C1999	C1930	U1829	U1726	C1605	A1493	C1358
C2604	C2605	C2650	C2604	G2462	U2372	U2302	G2196	U2122	C1999	C1931	U1830	U1727	C1606	A1494	C1359
C2606	C2607	C2651	C2606	U2463	U2373	U2303	G2197	U2123	C1999	C1932	U1831	U1728	C1607	A1495	C1360
C2608	C2609	C2652	C2608	G2464	U2374	U2304	G2198	U2124	C1999	C1933	U1832	U1729	C1608	A1496	C1361
C2610	C2611	C2653	C2610	U2465	U2375	U2305	G2199	U2125	C1999	C1934	U1833	U1730	C1609	A1497	C1362
C2612	C2613	C2654	C2612	G2466	U2376	U2306	G2200	U2126	C1999	C1935	U1834	U1731	C1610	A1498	C1363
C2614	C2615	C2655	C2614	U2467	U2377	U2307	G2201	U2127	C1999	C1936	U1835	U1732	C1611	A1499	C1364
C2616	C2617	C2656	C2616	G2468	U2378	U2308	G2202	U2128	C1999	C1937	U1836	U1733	C1612	A1500	C1365
C2618	C2619	C2657	C2618	U2469	U2379	U2309	G2203	U2129	C1999	C1938	U1837	U1734	C1613	A1501	C1366
C2620	C2621	C2658	C2620	G2470	U2380	U2310	G2204	U2130	C1999	C1939	U1838	U1735	C1614	A1502	C1367
C2622	C2623	C2659													



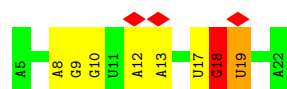
• Molecule 54: 5S ribosomal RNA



• Molecule 55: tRNA^{fMet}



• Molecule 56: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	22656	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	23.417	Depositor
Minimum map value	-11.898	Depositor
Average map value	0.109	Depositor
Map value standard deviation	0.889	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	0.29	0/2122	0.95	8/2852 (0.3%)
2	c	0.30	0/1586	0.83	0/2134
3	d	0.30	0/1571	0.84	6/2113 (0.3%)
4	e	0.31	0/1435	0.92	8/1926 (0.4%)
5	f	0.30	0/1343	0.84	1/1816 (0.1%)
6	g	0.32	0/1122	0.96	4/1515 (0.3%)
7	h	0.36	0/1002	1.03	8/1350 (0.6%)
8	i	0.37	0/1046	1.00	8/1410 (0.6%)
9	j	0.28	0/1152	0.89	7/1551 (0.5%)
10	k	0.28	0/948	0.94	6/1268 (0.5%)
11	l	0.30	0/1054	0.94	6/1403 (0.4%)
12	m	0.33	0/1093	0.87	3/1460 (0.2%)
13	n	0.31	0/974	0.94	4/1301 (0.3%)
14	o	0.29	0/902	0.86	1/1209 (0.1%)
15	p	0.29	0/929	0.79	0/1242
16	q	0.28	0/960	0.89	1/1278 (0.1%)
17	r	0.29	0/829	0.89	2/1107 (0.2%)
18	s	0.28	0/864	0.90	2/1156 (0.2%)
19	t	0.30	0/745	0.84	1/994 (0.1%)
20	u	0.29	0/788	0.85	0/1051
21	v	0.28	0/766	0.89	2/1025 (0.2%)
22	w	0.29	0/582	0.80	0/769
23	x	0.28	0/635	0.82	0/848
24	y	0.28	0/510	0.82	1/677 (0.1%)
25	z	0.28	0/453	0.84	0/605
26	B	0.26	0/450	0.87	2/599 (0.3%)
27	C	0.32	0/417	0.93	3/554 (0.5%)
28	D	0.30	0/380	0.80	0/498
29	E	0.30	0/513	0.95	2/676 (0.3%)
30	F	0.33	0/303	0.83	0/397
31	G	0.32	0/1788	0.93	8/2408 (0.3%)
32	H	0.36	0/1652	0.84	1/2225 (0.0%)
33	I	0.33	0/1665	0.94	9/2227 (0.4%)
34	J	0.34	0/1170	0.95	6/1573 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	K	0.33	0/836	1.03	10/1128 (0.9%)
36	L	0.31	0/1196	0.87	3/1602 (0.2%)
37	M	0.33	0/989	0.98	4/1326 (0.3%)
38	N	0.35	0/1034	0.92	3/1375 (0.2%)
39	O	0.35	0/797	0.92	5/1077 (0.5%)
40	P	0.35	0/886	0.93	1/1195 (0.1%)
41	Q	0.37	0/969	1.00	7/1300 (0.5%)
42	R	0.35	0/893	0.90	0/1193
43	S	0.33	0/817	0.94	3/1088 (0.3%)
44	T	0.30	0/722	0.89	2/964 (0.2%)
45	U	0.34	0/659	0.82	0/884
46	V	0.34	0/658	0.92	4/881 (0.5%)
47	W	0.33	0/545	0.81	0/731
48	X	0.35	0/653	0.92	1/877 (0.1%)
49	Y	0.31	0/671	0.95	2/888 (0.2%)
50	Z	0.34	0/551	1.09	5/728 (0.7%)
51	a	0.32	0/1034	0.81	2/1387 (0.1%)
52	3	0.44	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	0.48	0/4479
55	5	0.43	0/1832	0.52	1/2855 (0.0%)
56	4	0.45	0/436	0.54	1/679 (0.1%)
All	All	0.39	0/159558	0.62	170/238404 (0.1%)

There are no bond length outliers.

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	E	61	LEU	CA-C-N	8.91	128.56	118.85
29	E	61	LEU	C-N-CA	8.91	128.56	118.85
1	b	12	ARG	N-CA-C	-8.38	103.50	114.31
43	S	49	THR	N-CA-C	-8.37	103.06	113.18
17	r	50	GLY	N-CA-C	-8.34	102.40	112.49

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	36	0
3	d	1552	0	1619	49	0
4	e	1411	0	1447	56	0
5	f	1323	0	1374	30	0
6	g	1111	0	1148	33	0
7	h	989	0	1025	54	0
8	i	1032	0	1088	40	0
9	j	1129	0	1162	32	0
10	k	939	0	1012	31	0
11	l	1045	0	1117	36	0
12	m	1074	0	1157	32	0
13	n	961	0	1000	26	0
14	o	892	0	923	22	0
15	p	917	0	965	31	0
16	q	947	0	1022	19	0
17	r	816	0	839	25	0
18	s	857	0	922	19	0
19	t	739	0	807	17	0
20	u	780	0	834	18	0
21	v	753	0	780	22	0
22	w	575	0	592	18	0
23	x	625	0	655	15	0
24	y	509	0	543	12	0
25	z	449	0	491	13	0
26	B	444	0	461	13	0
27	C	410	0	440	7	0
28	D	377	0	418	8	0
29	E	504	0	574	18	0
30	F	302	0	343	12	0
31	G	1757	0	1787	61	0
32	H	1625	0	1699	61	0
33	I	1643	0	1710	96	0
34	J	1157	0	1199	48	0
35	K	818	0	808	40	0
36	L	1182	0	1240	37	0
37	M	979	0	1034	45	0
38	N	1022	0	1070	60	0
39	O	787	0	828	37	0
40	P	870	0	878	27	0
41	Q	955	0	1019	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	R	884	0	944	39	0
43	S	805	0	847	43	0
44	T	714	0	737	24	0
45	U	649	0	666	38	0
46	V	649	0	691	28	0
47	W	536	0	552	16	0
48	X	638	0	665	29	0
49	Y	665	0	714	30	0
50	Z	545	0	579	36	0
51	a	1027	0	1092	43	0
52	3	33012	0	16618	726	0
53	1	62317	0	31346	903	0
54	2	2568	0	1303	50	0
55	5	1640	0	837	40	0
56	4	388	0	196	9	0
All	All	146942	0	99590	2915	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 12.

The worst 5 of 2915 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'	1.32	1.10
50:Z:25:ALA:HB3	56:4:9:G:H4'	1.36	1.07
55:5:62:C:H2'	55:5:63:G:H5''	1.37	1.05
44:T:39:GLN:HE22	53:1:715:A:H4'	1.22	1.04
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.27	0.98

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	238 (88%)	28 (10%)	3 (1%)	11	39
2	c	207/209 (99%)	191 (92%)	15 (7%)	1 (0%)	24	55
3	d	199/201 (99%)	179 (90%)	18 (9%)	2 (1%)	12	40
4	e	175/177 (99%)	157 (90%)	16 (9%)	2 (1%)	11	39
5	f	174/176 (99%)	158 (91%)	15 (9%)	1 (1%)	21	52
6	g	147/149 (99%)	124 (84%)	21 (14%)	2 (1%)	9	33
7	h	129/131 (98%)	97 (75%)	26 (20%)	6 (5%)	2	12
8	i	139/141 (99%)	122 (88%)	13 (9%)	4 (3%)	3	21
9	j	140/142 (99%)	130 (93%)	8 (6%)	2 (1%)	9	33
10	k	120/122 (98%)	103 (86%)	14 (12%)	3 (2%)	4	23
11	l	141/143 (99%)	122 (86%)	14 (10%)	5 (4%)	3	18
12	m	134/136 (98%)	120 (90%)	9 (7%)	5 (4%)	2	17
13	n	118/120 (98%)	98 (83%)	19 (16%)	1 (1%)	16	45
14	o	114/116 (98%)	105 (92%)	8 (7%)	1 (1%)	14	43
15	p	112/114 (98%)	95 (85%)	16 (14%)	1 (1%)	14	43
16	q	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
17	r	101/103 (98%)	85 (84%)	15 (15%)	1 (1%)	12	40
18	s	108/110 (98%)	96 (89%)	11 (10%)	1 (1%)	14	43
19	t	91/93 (98%)	85 (93%)	6 (7%)	0	100	100
20	u	100/102 (98%)	82 (82%)	15 (15%)	3 (3%)	3	20
21	v	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	w	73/75 (97%)	62 (85%)	10 (14%)	1 (1%)	9	33
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	7	31
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
26	B	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
27	C	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
28	D	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
29	E	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	31
30	F	36/38 (95%)	29 (81%)	7 (19%)	0	100	100
31	G	223/225 (99%)	205 (92%)	18 (8%)	0	100	100
32	H	204/206 (99%)	192 (94%)	11 (5%)	1 (0%)	24	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	I	203/205 (99%)	174 (86%)	25 (12%)	4 (2%)	6	27
34	J	155/157 (99%)	133 (86%)	17 (11%)	5 (3%)	3	19
35	K	98/100 (98%)	84 (86%)	11 (11%)	3 (3%)	3	20
36	L	149/151 (99%)	131 (88%)	18 (12%)	0	100	100
37	M	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	7	31
38	N	125/127 (98%)	104 (83%)	18 (14%)	3 (2%)	4	24
39	O	96/98 (98%)	83 (86%)	10 (10%)	3 (3%)	3	20
40	P	114/116 (98%)	95 (83%)	15 (13%)	4 (4%)	3	18
41	Q	121/123 (98%)	94 (78%)	20 (16%)	7 (6%)	1	9
42	R	112/114 (98%)	98 (88%)	11 (10%)	3 (3%)	4	22
43	S	98/100 (98%)	83 (85%)	15 (15%)	0	100	100
44	T	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	37
45	U	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
46	V	78/80 (98%)	65 (83%)	11 (14%)	2 (3%)	4	23
47	W	63/65 (97%)	60 (95%)	2 (3%)	1 (2%)	7	31
48	X	77/79 (98%)	67 (87%)	9 (12%)	1 (1%)	9	35
49	Y	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
50	Z	63/65 (97%)	41 (65%)	19 (30%)	3 (5%)	2	12
51	a	130/223 (58%)	123 (95%)	7 (5%)	0	100	100
All	All	5919/6112 (97%)	5204 (88%)	625 (11%)	90 (2%)	11	32

5 of 90 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
3	d	83	VAL
3	d	84	THR
6	g	9	VAL
7	h	81	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	215 (100%)	1 (0%)	81	83
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	75
3	d	165/165 (100%)	163 (99%)	2 (1%)	63	75
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%)	98 (98%)	2 (2%)	48	68
8	i	109/109 (100%)	108 (99%)	1 (1%)	70	78
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	76
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	76
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%)	86 (100%)	0	100	100
15	p	99/99 (100%)	99 (100%)	0	100	100
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	76
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
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	46 (98%)	1 (2%)	47	67
27	C	45/45 (100%)	44 (98%)	1 (2%)	45	66
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	G	186/186 (100%)	183 (98%)	3 (2%)	55	72
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	81
33	I	172/172 (100%)	171 (99%)	1 (1%)	78	81
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	79
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	76
36	L	124/124 (100%)	123 (99%)	1 (1%)	73	79
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	76
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	66
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%)	92 (100%)	0	100	100
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	72
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%)	64 (98%)	1 (2%)	57	72
50	Z	55/55 (100%)	55 (100%)	0	100	100
51	a	110/174 (63%)	109 (99%)	1 (1%)	70	78
All	All	4908/4972 (99%)	4881 (99%)	27 (1%)	76	81

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	G	67	LEU
33	I	124	VAL
45	U	42	ILE
32	H	169	GLU
34	J	55	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 116 such sidechains are listed below:

Mol	Chain	Res	Type
22	w	72	ASN
49	Y	20	ASN
31	G	119	GLN
49	Y	19	HIS
41	Q	72	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	139 (9%)	3 (0%)
53	1	2902/2903 (99%)	322 (11%)	11 (0%)
54	2	119/120 (99%)	10 (8%)	1 (0%)
55	5	76/77 (98%)	24 (31%)	1 (1%)
56	4	17/18 (94%)	3 (17%)	1 (5%)
All	All	4652/4657 (99%)	498 (10%)	17 (0%)

5 of 498 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	7	A
52	3	9	G
52	3	22	G
52	3	31	G

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	2	88	C
56	4	18	G
53	1	1020	A
53	1	1130	U
53	1	1475	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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.

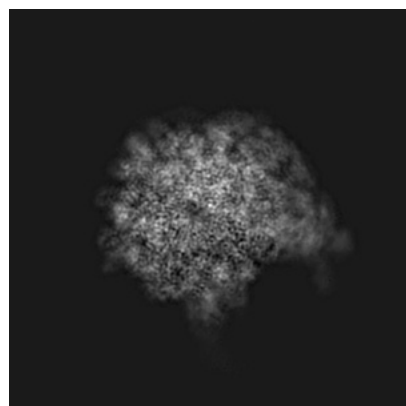
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21620. These allow visual inspection of the internal detail of the map and identification of artifacts.

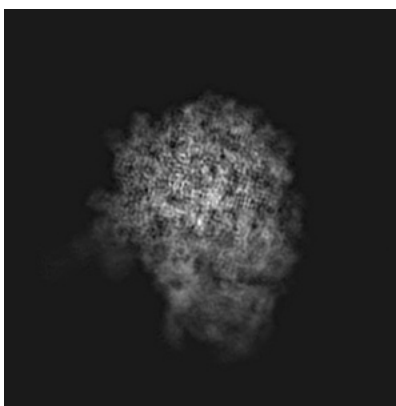
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

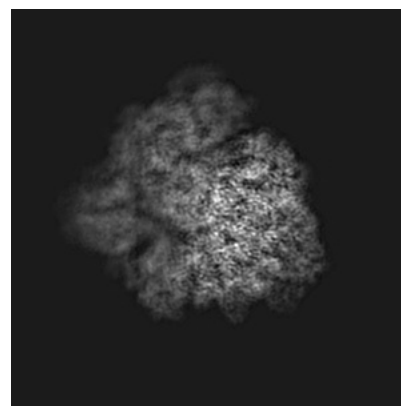
6.1.1 Primary map



X

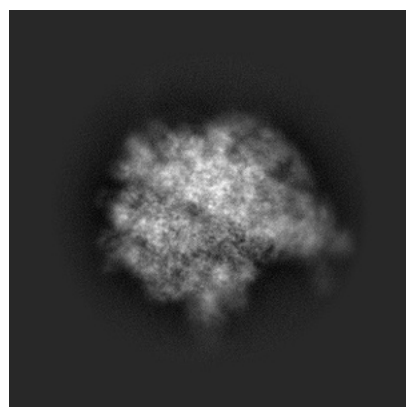


Y

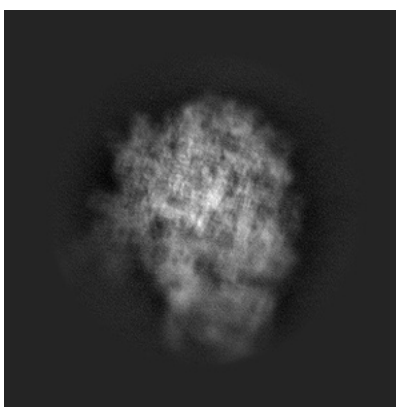


Z

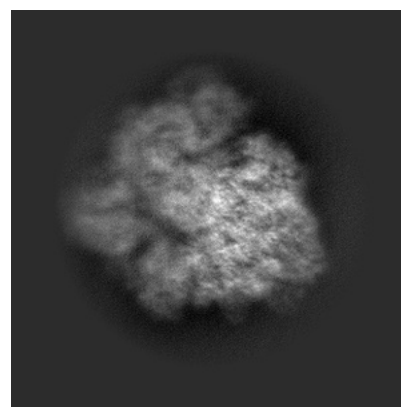
6.1.2 Raw map



X



Y

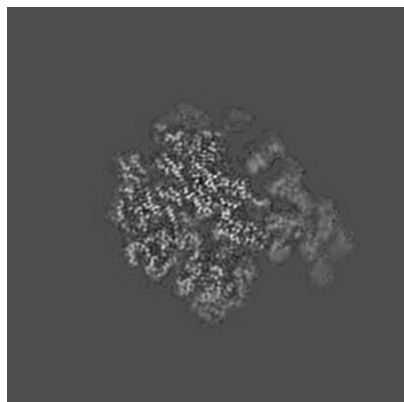


Z

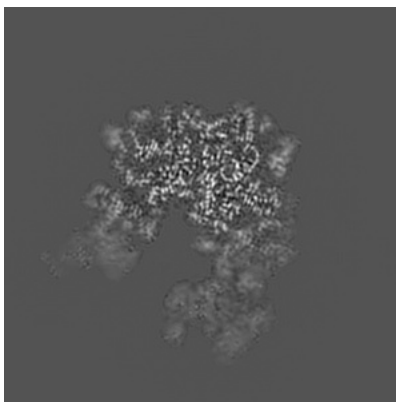
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

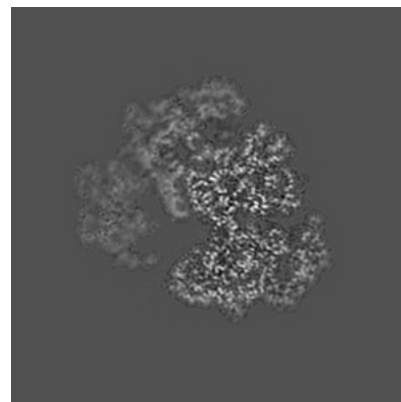
6.2.1 Primary map



X Index: 144

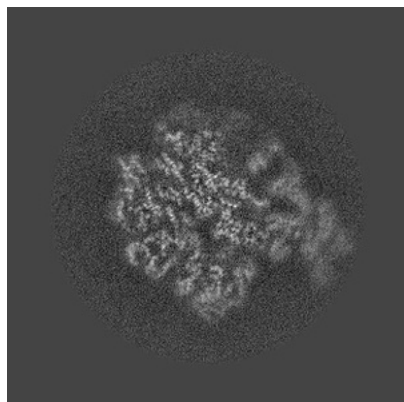


Y Index: 144

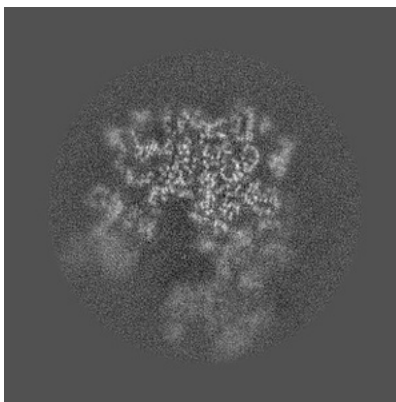


Z Index: 144

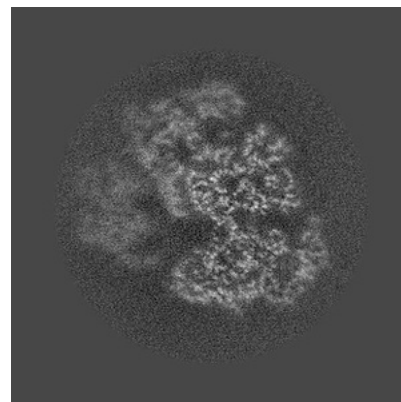
6.2.2 Raw map



X Index: 144



Y Index: 144

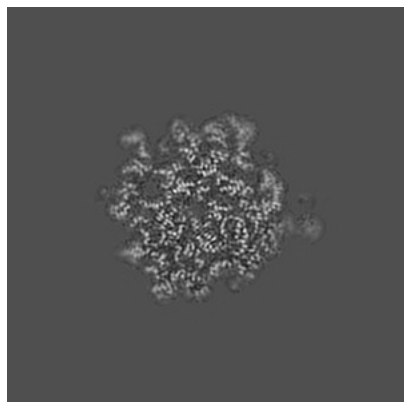


Z Index: 144

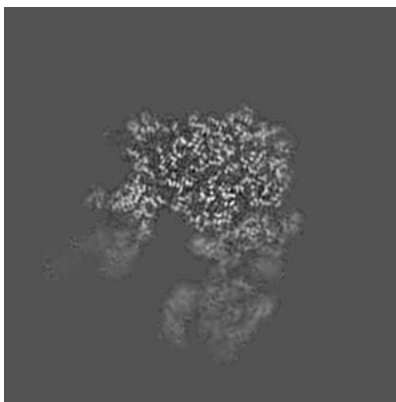
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

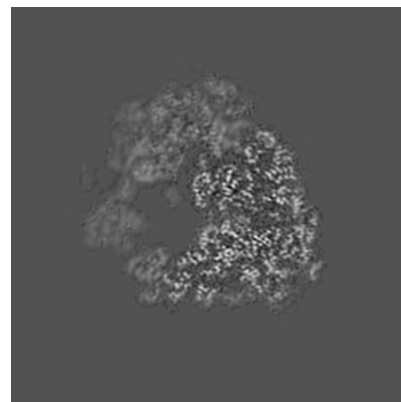
6.3.1 Primary map



X Index: 171

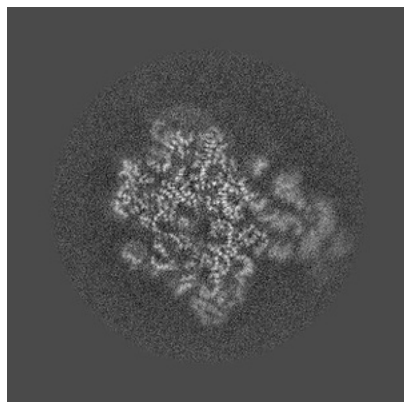


Y Index: 151

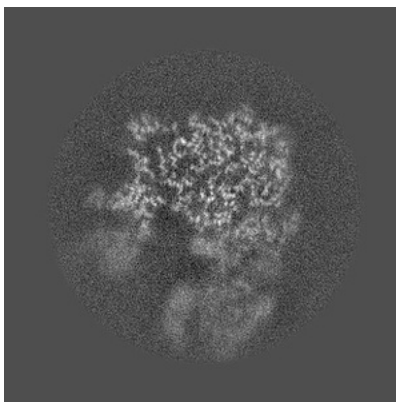


Z Index: 135

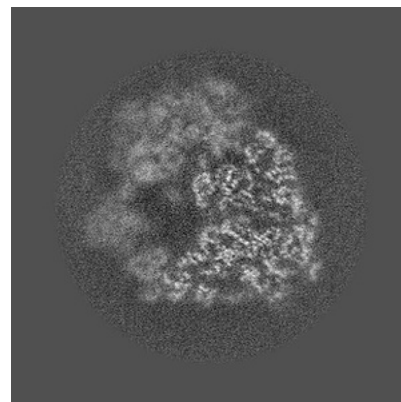
6.3.2 Raw map



X Index: 148



Y Index: 151

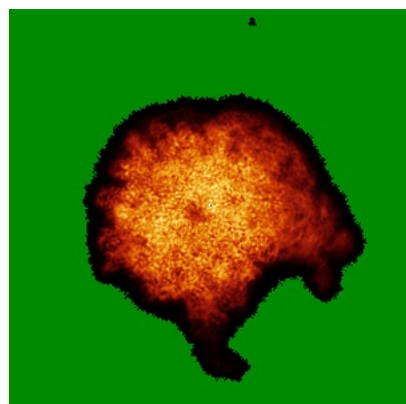


Z Index: 135

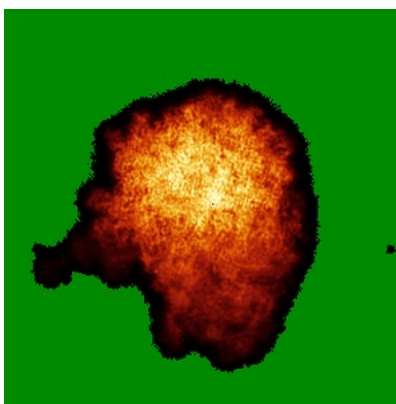
The images above show the largest variance slices of the map in three orthogonal directions.

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

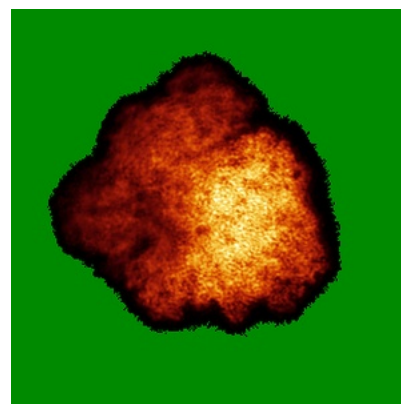
6.4.1 Primary map



X

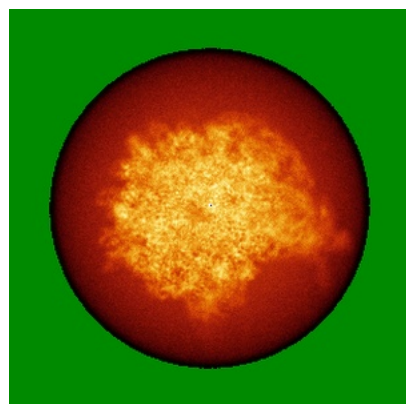


Y

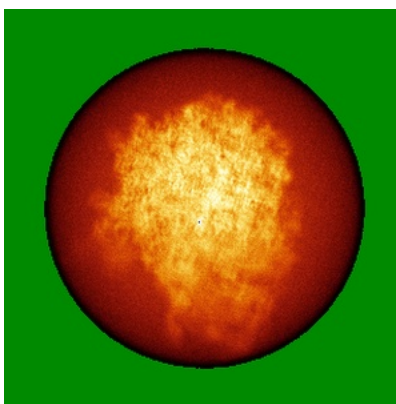


Z

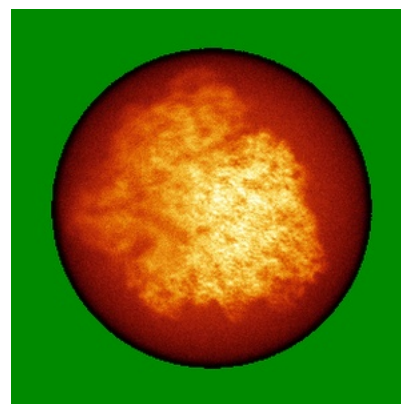
6.4.2 Raw map



X



Y

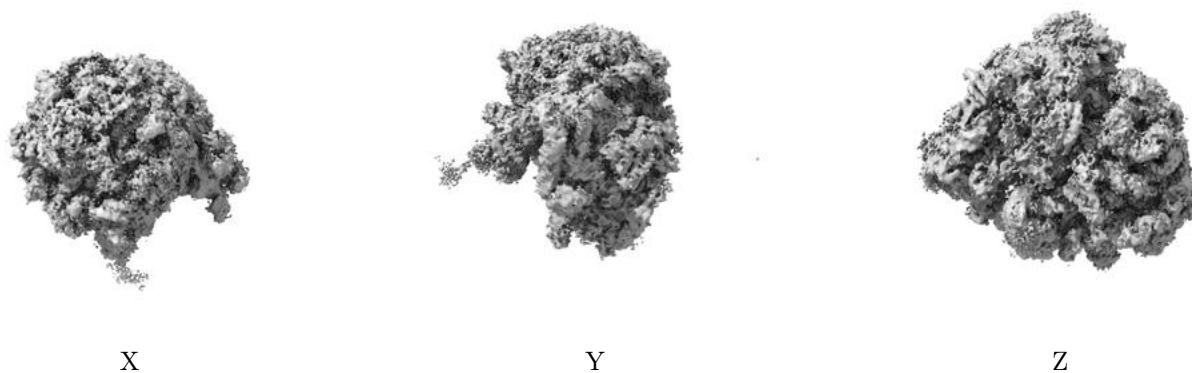


Z

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

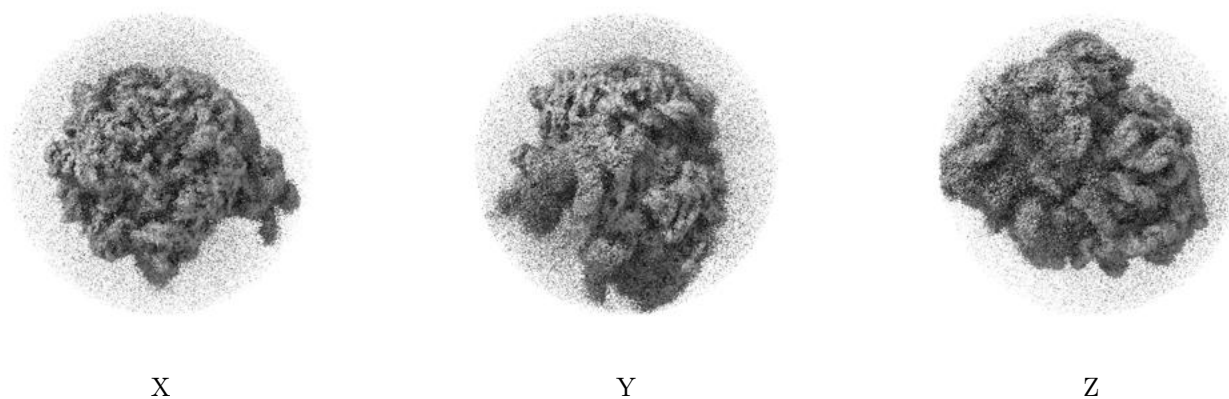
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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

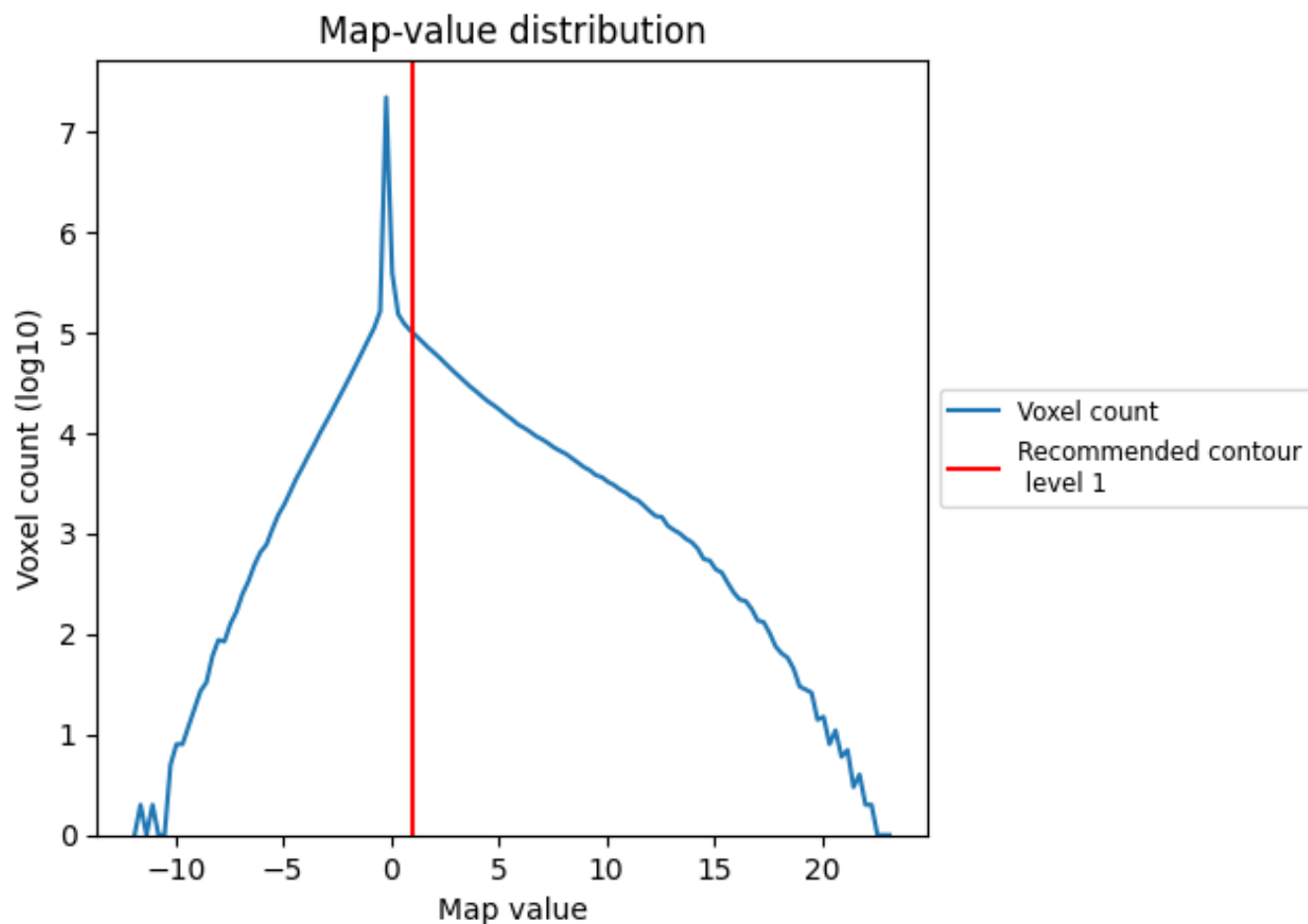
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

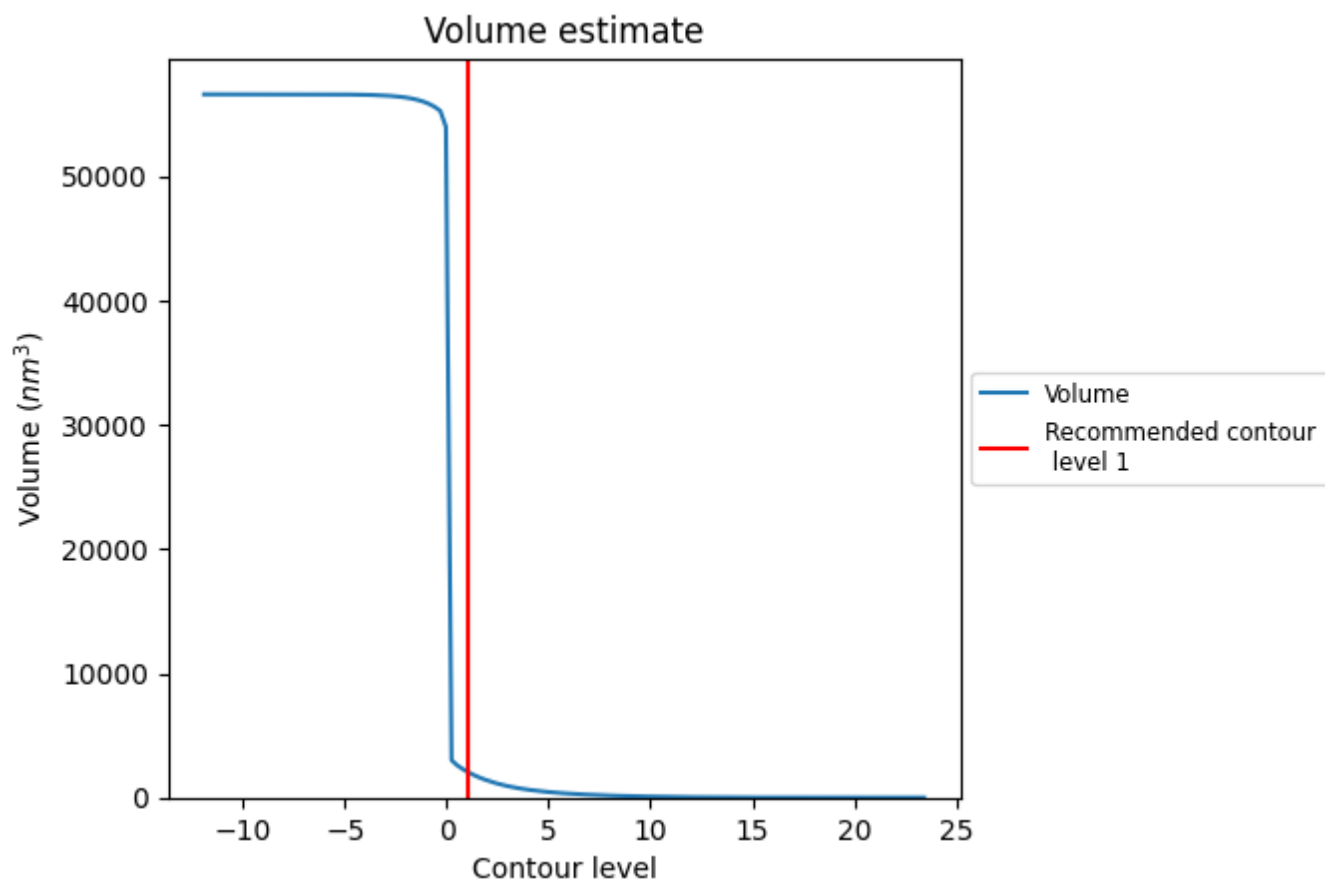
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

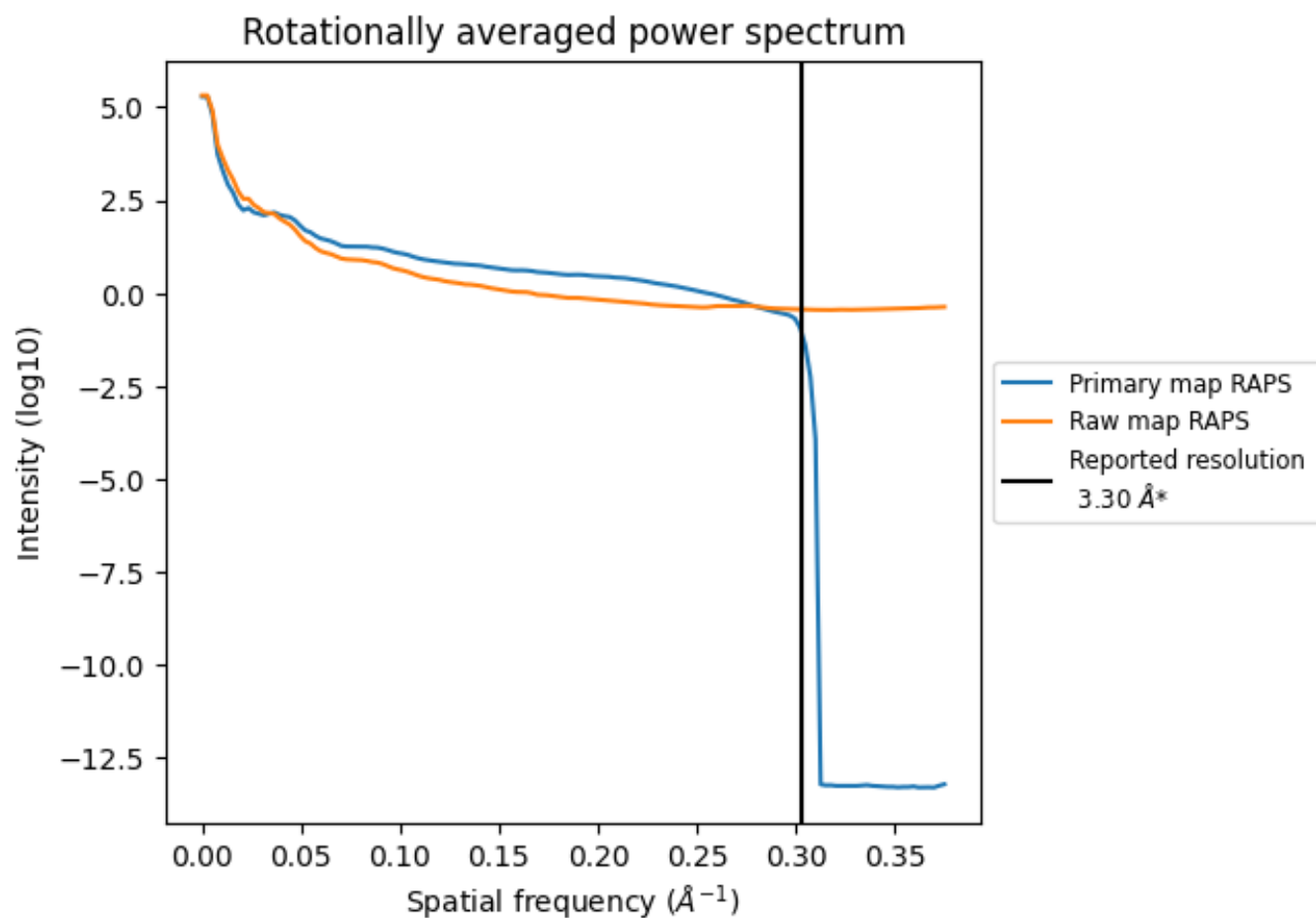
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2097 nm³; this corresponds to an approximate mass of 1894 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

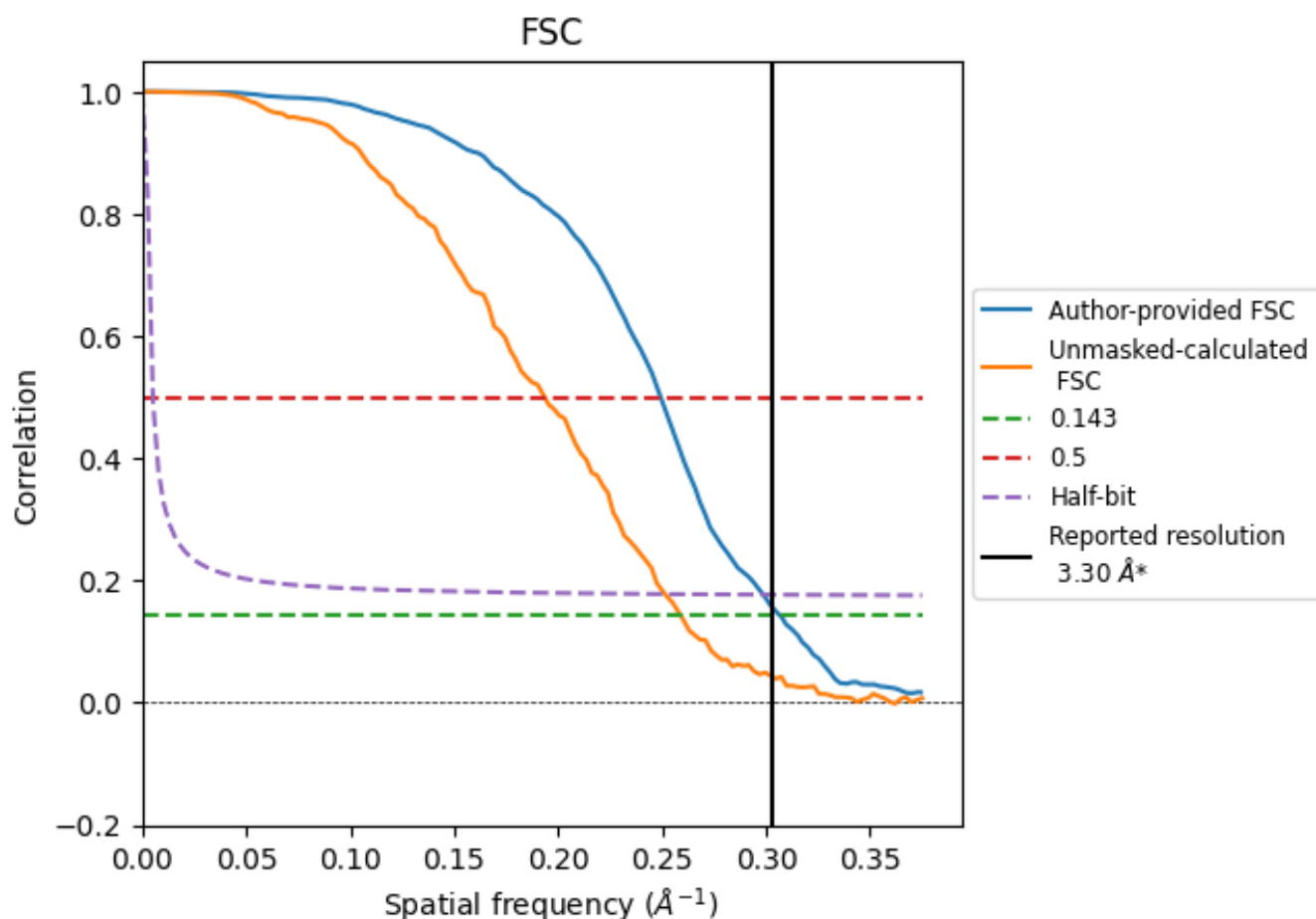


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

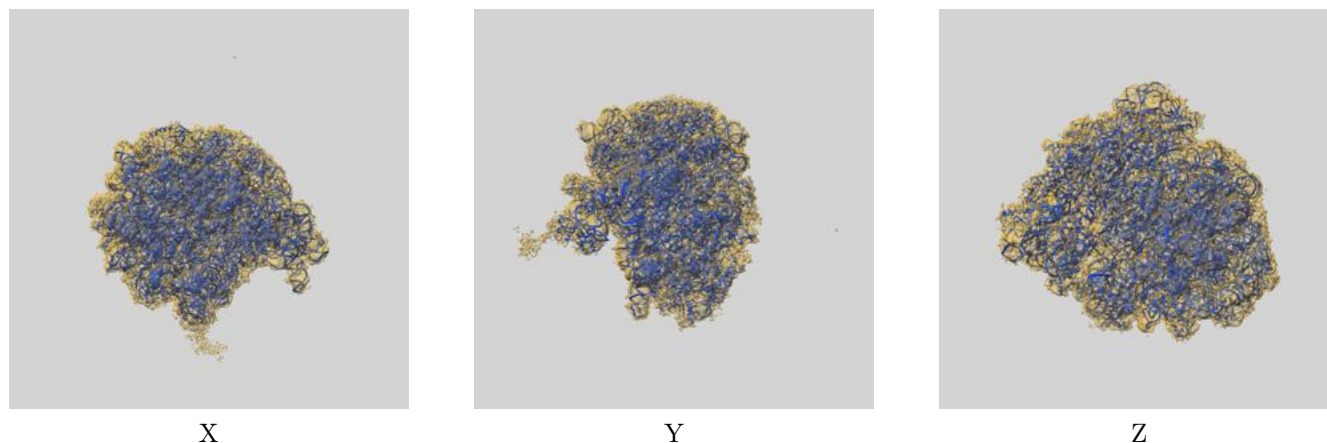
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.26	4.01	3.35
Unmasked-calculated*	3.86	5.17	3.98

*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 3.86 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21620 and PDB model 6WD1. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



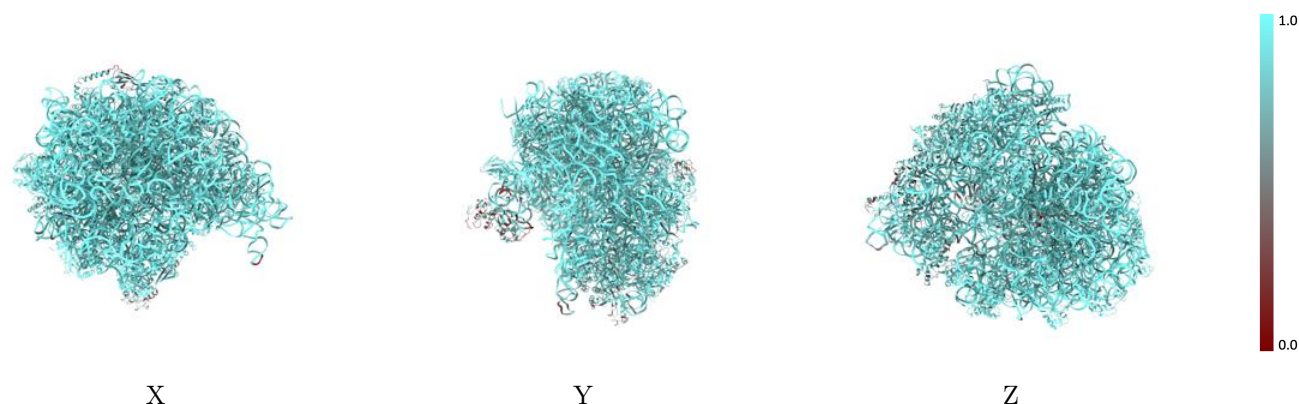
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



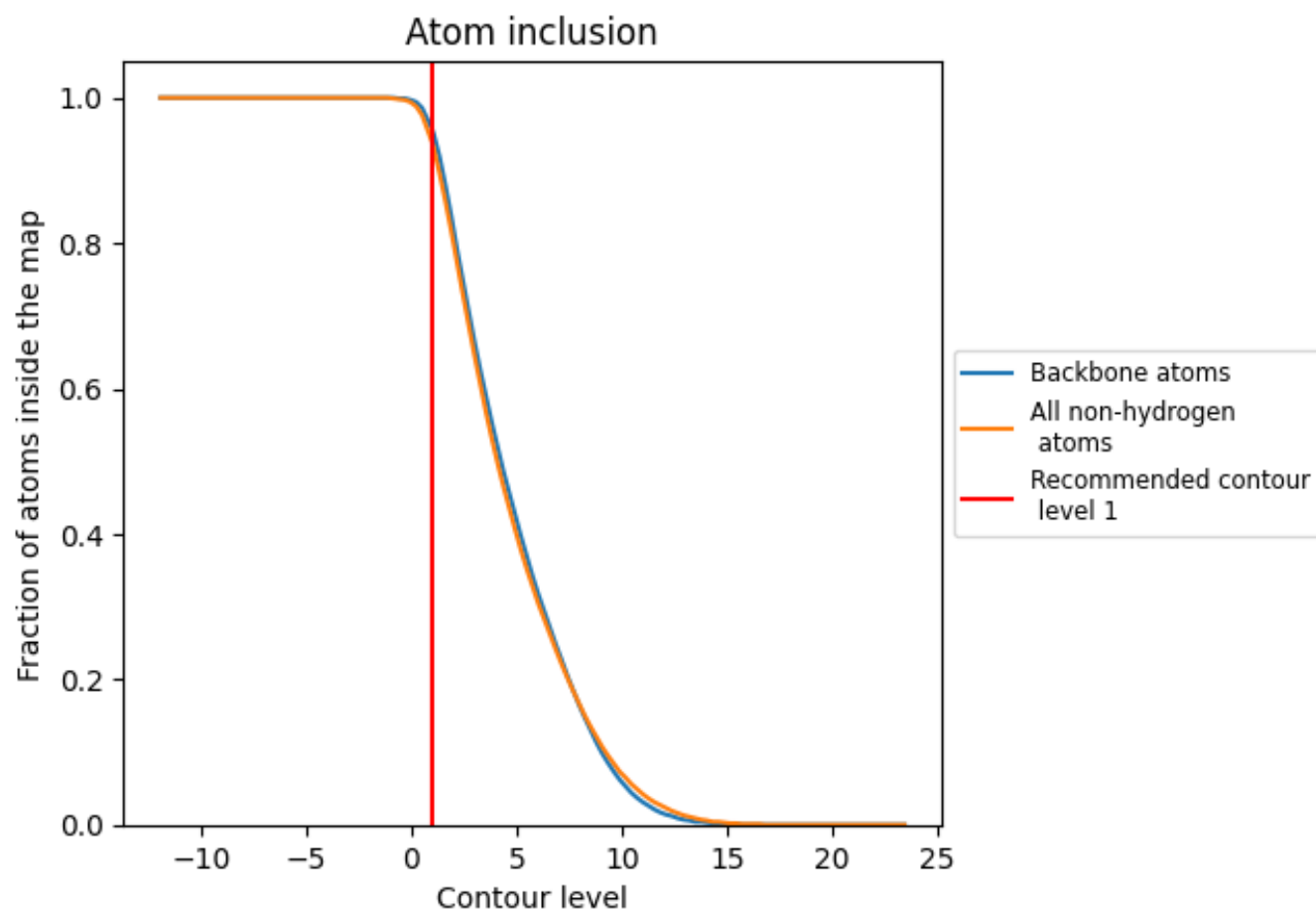
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 96% of all backbone atoms, 94% 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	 0.9380	 0.3540
1	 0.9790	 0.4230
2	 0.9770	 0.3550
3	 0.9450	 0.2470
4	 0.6910	 0.1060
5	 0.9320	 0.1990
B	 0.9560	 0.4920
C	 0.8230	 0.4000
D	 0.9470	 0.5150
E	 0.9550	 0.5180
F	 0.8870	 0.4530
G	 0.7950	 0.2370
H	 0.7740	 0.2190
I	 0.8020	 0.1910
J	 0.8770	 0.2750
K	 0.9310	 0.3240
L	 0.7850	 0.1880
M	 0.9050	 0.3350
N	 0.8080	 0.1930
O	 0.6780	 0.1800
P	 0.9350	 0.3160
Q	 0.9390	 0.3300
R	 0.8040	 0.2020
S	 0.7870	 0.1830
T	 0.9290	 0.3620
U	 0.8640	 0.2830
V	 0.9160	 0.2940
W	 0.9070	 0.3350
X	 0.8840	 0.1820
Y	 0.8650	 0.2380
Z	 0.8210	 0.2350
a	 0.8980	 0.1610
b	 0.9670	 0.4970
c	 0.9570	 0.4920
d	 0.9410	 0.4380



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Chain	Atom inclusion	Q-score
e	 0.9250	 0.2860
f	 0.9580	 0.3750
g	 0.7180	 0.2790
h	 0.5550	 0.1410
i	 0.4970	 0.1320
j	 0.9620	 0.4930
k	 0.9440	 0.4760
l	 0.9550	 0.4730
m	 0.8840	 0.4360
n	 0.9600	 0.4910
o	 0.9370	 0.3960
p	 0.9530	 0.4650
q	 0.9530	 0.4860
r	 0.9640	 0.4590
s	 0.9320	 0.4830
t	 0.9520	 0.4600
u	 0.9320	 0.4290
v	 0.9360	 0.4280
w	 0.9590	 0.4960
x	 0.9730	 0.4810
y	 0.9190	 0.3980
z	 0.9570	 0.4600