



wwPDB EM Validation Summary Report ⓘ

Jul 26, 2026 – 05:16 PM JST

PDB ID : 9W0N / pdb_00009w0n
EMDB ID : EMD-65509
Title : Escherichia coli transcription-translation coupled complex class B (TTC-B) that ribosome walking for 4 codons to a 9 codon mRNA spacer, and fMet-tRNAs in E-site and P-site of the ribosome
Authors : Zhang, J.; Wang, C.
Deposited on : 2025-07-24
Resolution : 3.50 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.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

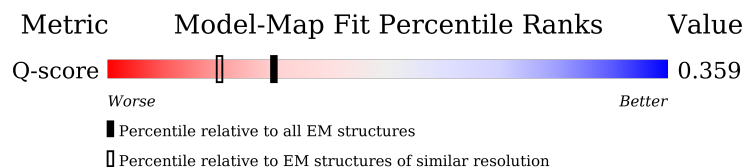
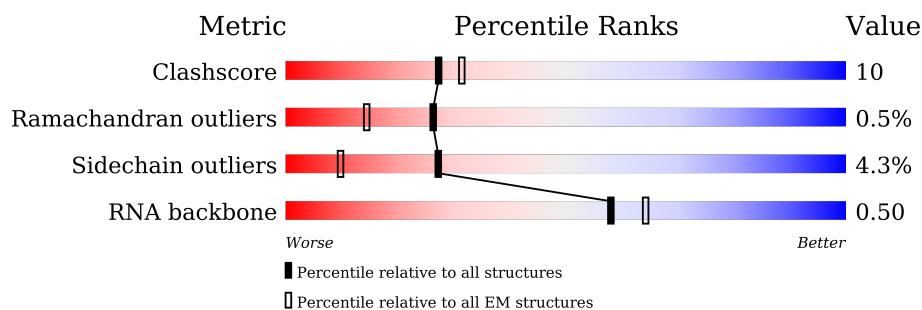
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



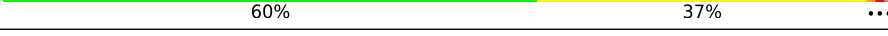
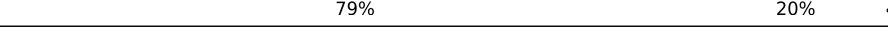
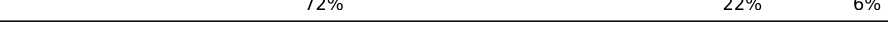
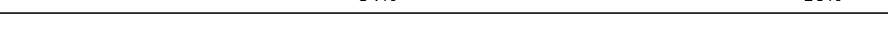
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	1	2904	 43% 51% 6%
2	2	120	 76% 19% 5%
3	3	1542	 69% 29% 2%

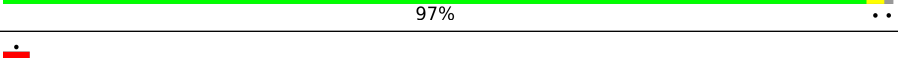
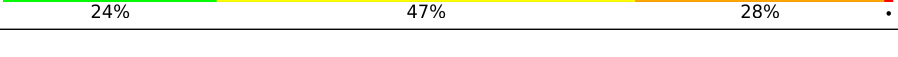
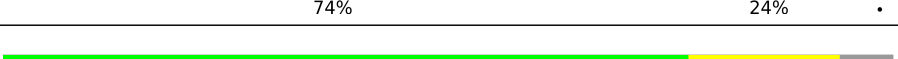
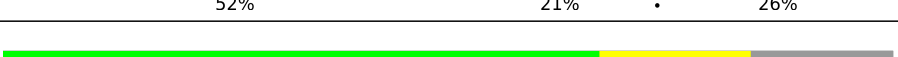
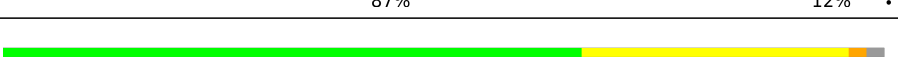
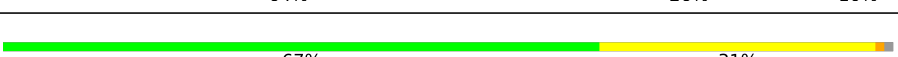
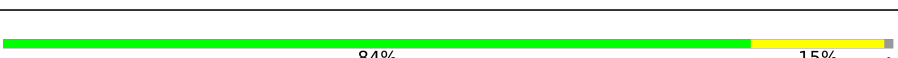
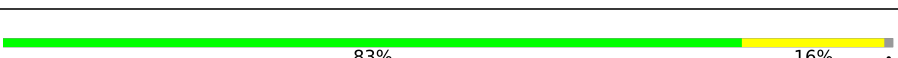
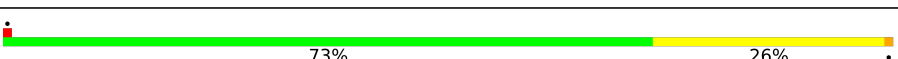
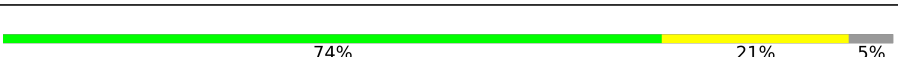
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Mol	Chain	Length	Quality of chain
4	0	704	
5	6	77	
6	b	273	
7	c	209	
8	d	201	
9	e	179	
10	f	177	
11	g	149	
12	i	142	
13	j	142	
14	k	123	
15	l	144	
16	m	136	
17	n	127	
18	o	117	
19	p	115	
20	q	118	
21	r	103	
22	s	110	
23	t	100	
24	u	104	
25	v	94	
26	w	85	
27	x	78	
28	y	63	

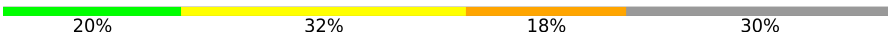
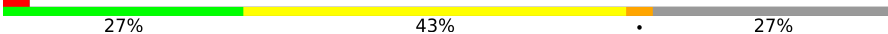
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Mol	Chain	Length	Quality of chain
29	z	59	
30	A	70	
31	B	57	
32	C	55	
33	D	46	
34	E	65	
35	F	38	
36	NA	495	
37	5	76	
38	G	241	
39	H	233	
40	I	206	
41	J	167	
42	K	135	
43	L	179	
44	M	130	
45	N	130	
46	O	103	
47	P	129	
48	Q	124	
49	R	118	
50	S	101	
51	T	89	
52	U	82	
53	V	84	

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Mol	Chain	Length	Quality of chain
54	W	75	
55	X	92	
56	Y	87	
57	Z	71	
58	4	56	
59	B2	1342	
60	9	37	
61	8	37	
62	a	325	
62	h	325	
63	7	176	
64	AA	82	
65	BA	1358	

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 181400 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 RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

- Molecule 3 is a RNA chain called 16S rRNA.

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

- Molecule 4 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	0	673	Total	C	N	O	S	0	0
			5212	3289	900	1000	23		

- Molecule 5 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 6 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 7 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 8 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	e	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 10 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 11 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	g	52	Total	C	N	O	S	0	0
			400	256	73	70	1		

- Molecule 12 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 14 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 15 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 16 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 17 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 18 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	o	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 19 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 20 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 21 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 22 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 23 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 25 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	v	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 26 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 27 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 28 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 29 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 30 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	A	66	Total	C	N	O	S	0	0
			521	323	98	94	6		

- Molecule 31 is a protein called Large ribosomal subunit protein bL32.

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

- Molecule 32 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	C	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 33 is a protein called Large ribosomal subunit protein bL34.

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

- Molecule 34 is a protein called Large ribosomal subunit protein bL35.

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

- Molecule 35 is a protein called Large ribosomal subunit protein bL36A.

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

- Molecule 36 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	NA	492	Total	C	N	O		0	0
			2432	1448	492	492			

- Molecule 37 is a RNA chain called tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	5	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 38 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	G	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 39 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	H	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 40 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 41 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	J	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 42 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	K	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 43 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 44 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 45 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 46 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	O	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 47 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	P	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 48 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 49 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	R	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 50 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 51 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 52 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	V	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 54 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	W	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 55 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	X	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 56 is a protein called Small ribosomal subunit protein bS20.

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

- Molecule 57 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 58 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	4	39	Total	C	N	O	P	0	0
			809	362	113	295	39		

- Molecule 59 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B2	1340	Total	C	N	O	S	0	0
			10546	6616	1839	2048	43		

- Molecule 60 is a DNA chain called non-templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	9	20	Total	C	N	O	P	0	0
			417	195	84	118	20		

- Molecule 61 is a DNA chain called templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	8	27	Total	C	N	O	P	0	0
			539	257	88	167	27		

- Molecule 62 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	a	301	Total	C	N	O	S	0	0
			2088	1293	380	409	6		
62	h	221	Total	C	N	O	S	0	0
			1698	1060	299	333	6		

- Molecule 63 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	7	154	Total	C	N	O	0	0
			758	450	154	154		

- Molecule 64 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AA	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 65 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BA	1335	Total	C	N	O	S	0	0
			10353	6509	1842	1955	47		

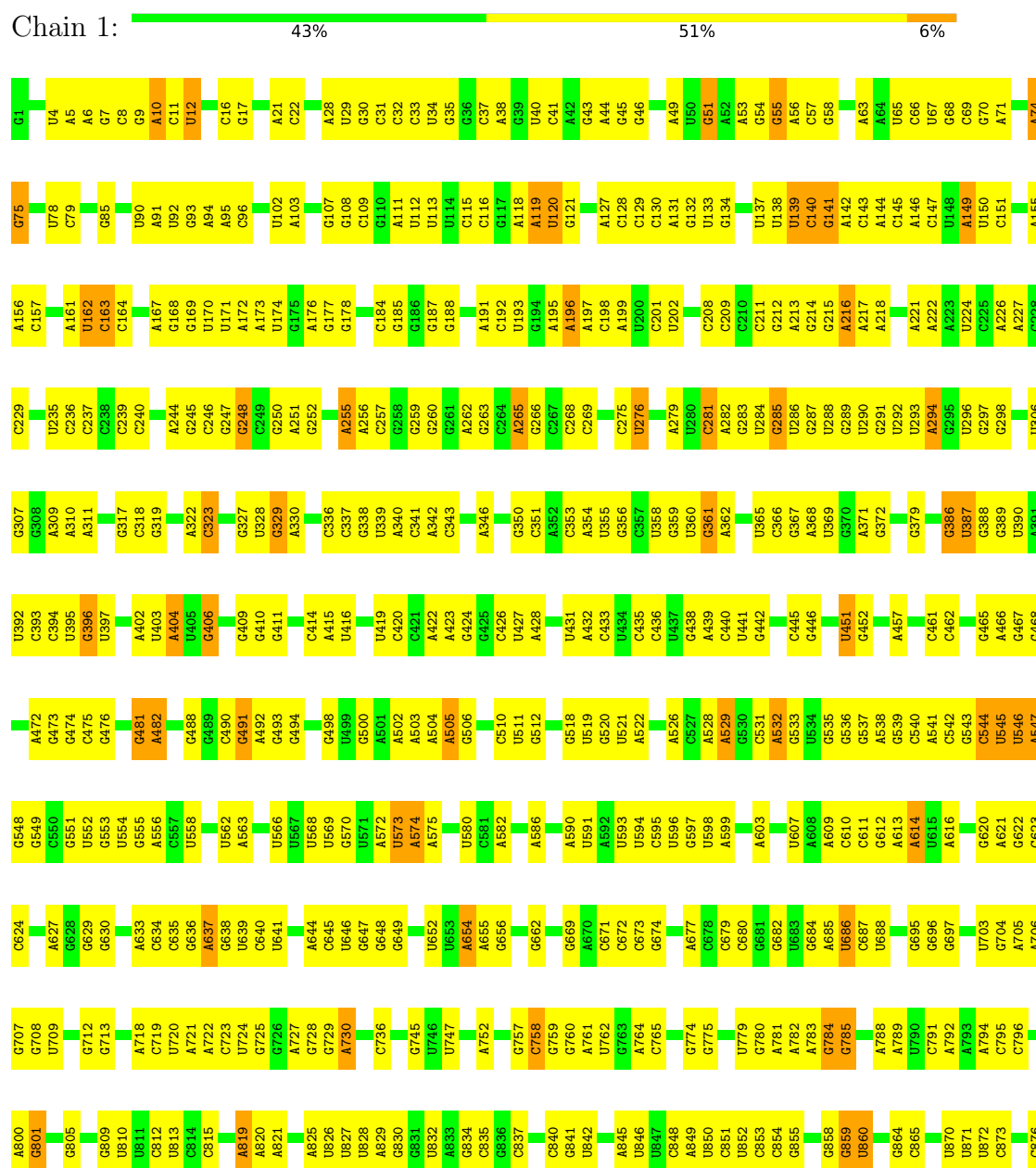
- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
66	BA	1	Total	Mg	0
			1	1	

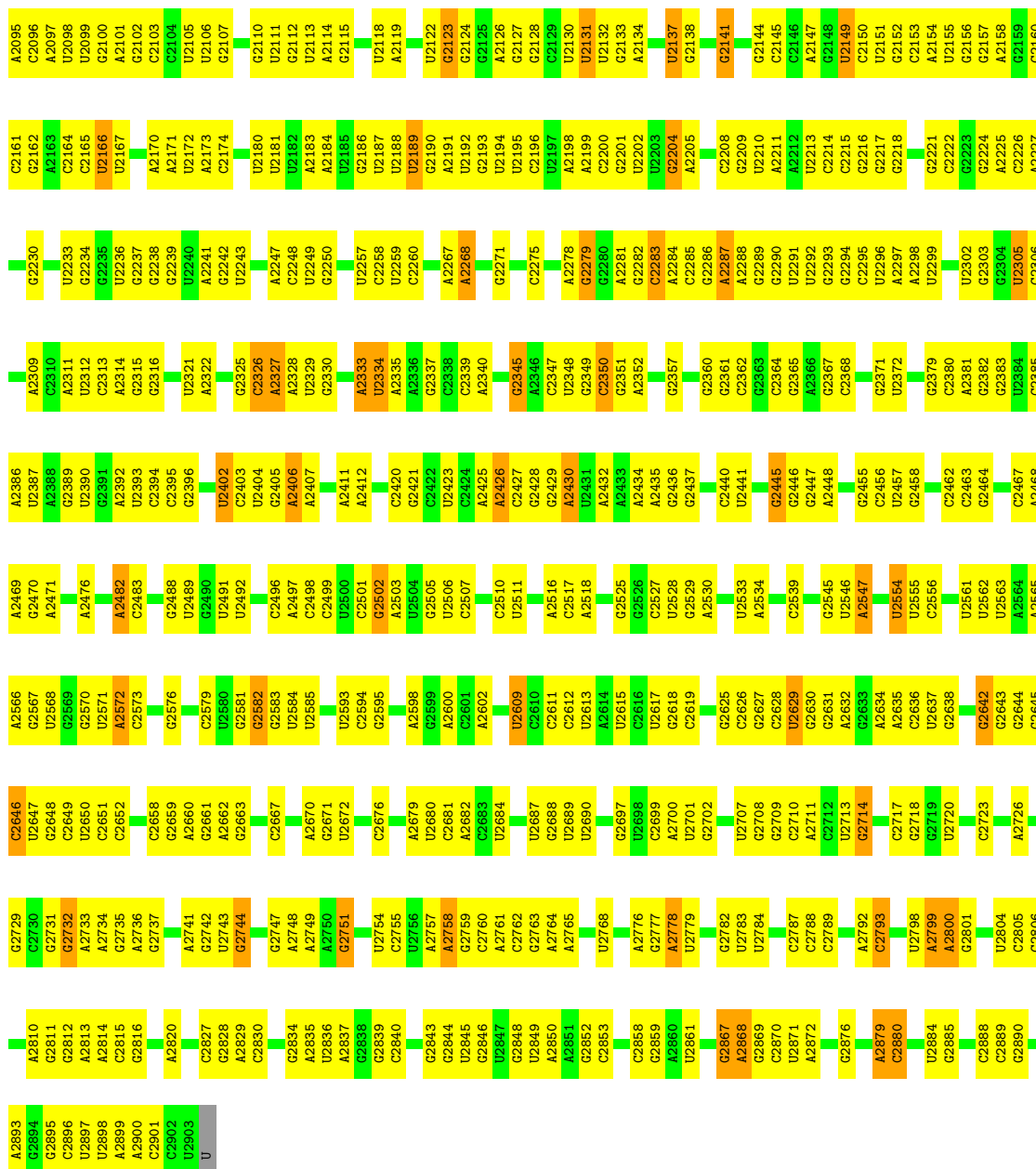
3 Residue-property plots

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: 23S rRNA

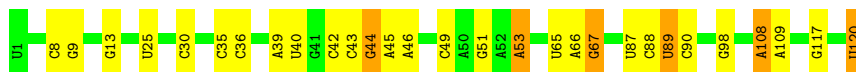


U1993	A1912	A1829	A1754	A1672	G1573	C1507	G1429	A1336	G1266	U1174	A1103	G1043	U955	A877
A1997	A1913	C1832	A1755	G1673	C1574	A1508	G1430	G1337	U1267	A1175	C1104	G1042	G956	A878
C1999	C1914	C1833	U1758	C1675	C1575	A1509	A1431	G1338	C1270	U1176	U1105	C1043	C957	G879
	U1917	U1834		G1676	A1578	G1510	A1432	G1339	G1271	U1177	G1106	C1044	U958	
	A1916		G1761	A1677	A1579	G1512	A1433	G1343	A1272	C1178	U1108	C1045	A969	C885
	A1918	G1845	A1762	A1678	A1580	A1515	G1435	U1344	U1273	U1180	C1109	A1046	A960	A866
A2013	A1919	G1846	G1763	A1679	A1583	G1516	G1436	C1345	U1274	U1181	G1110	G1047	C961	U887
A2014	C1920	A1847	C1764	U1680		G1517	G1437	U1348	A1275	U1182	A1048	C1049	C888	C889
A2015	G1921	A1848	U1765	G1681	A1583	G1518	U1438	C1349	A1276	U1183	C1049	C890	C891	C890
U2016	G1922		G1766			C1518	A1439			U1184	A1050		C969	G891
	U1923	U1851	G1767	G1696	G1588	G1519	U1440		C1278	G1185	G1114	A1054	A972	A892
A2020	C1924	U1852	C1768	G1697	A1589	U1520	G1441	U1352	G1279	G1186	G1115	G1055	A973	A893
C2021		A1853		A1698	A1591	G1521	U1442		G1281	G1187	G1116	G1056	G974	C993
U2022	A1927	A1854	A1772	G1699	C1592	U1522		A1365	U1282	U1188	C1117	G1057	A975	U894
C2023	A1928	U1855	A1773		A1593	U1523	G1448	A1366	G1283		C1118	A1057	A979	U895
G2024	G1929	C1774		G1702	U1594	G1524	A1449	A1367	A1284	G1193	U1119	U1058	A980	C897
C2025	G1930	G1857	U1775	G1703	C1595	A1526	G1450	G1368	A1285	A1194	U1120	U1060	A981	C898
U2026	U1931	A1858	G1776		A1596	C1526	G1451	A1286	U1287	G1195	G1121	U1061	C982	A899
G2027				G1710	A1597	G1527	G1452	G1377	A1287	G1196	C1121	G1062	A983	A900
		G1863	A1780	A1711	A1598	A1528	A1453	A1378	G1288	G1197	U1130	G1063	A984	C901
A2030	A1936	U1864	U1781		U1599	G1529	C1454	G1379		U1198	G1131	C1064	C985	C902
A2031	A1937	U1865	U1782	G1715	C1600	G1530		G1380	C1289	U1199	U1132	U1065		C903
G2032	A1938	A1866	A1783	U1716	G1601		G1461	G1381	G1292	A1204	A1133	U1066	G989	G904
A2033	U1939	G1867	A1784	A1717	G1602	G1533	C1462	G1382	C1293	A1205	C1135	U1067		A905
U2034		A1785	A1786	G1718	A1603	U1534	C1463	A1383	U1294		G1136	G1068	G993	U906
G2035	C1942	G1869	A1786		C1604	A1535	G1464		C1295	A1205	G1137	A1069	C994	G907
C2036	U1943	C1870	A1787	G1721	C1605	G1536	G1465	C1386	G1296	U1209	G1138	A1070	C995	C908
A2037	U1944	C1788		A1722	G1606	G1537	U1466	G1387	G1297	U1210	G1139	G1071	A996	A909
G2038	G1945	A1872	G1789	G1723	C1607	G1538	U1467	G1388	G1298	G1212	C1140	C1072		A910
U2039		C1873	G1790	U1724	A1608	U1539	U1468	G1389	G1299	G1211	U1141	A1073	C1005	A911
	G1948	C1874		U1725		G1540	U1469	U1390	G1300	G1212	U1142	G1074		
		G1875	A1794	C1726	A1614	C1541	A1470		A1301	A1213	A1143	C1075	A1009	G914
C2043			C1795	C1727	C1615	U1542		U1394	A1302		A1143	C1076	A1010	C915
C2047	A1952	G1878	U1796	C1728	A1616	U1543	G1480	U1400		U1219	A1144	C1077	G1011	
G2048	U1955	C1879	G1797	U1729		A1544	G1481	G1401	C1306	G1220	C1145	U1078	U1012	A918
C2050	U1956		U1798	C1730	C1625	A1545	G1482	U1402			C1146	C1079	C1013	U919
A2051		U1882	G1799	G1731	A1626	G1546	G1483	U1403	G1309	G1225	A1147	A1080	A1014	
U1963		G1883	C1800	C1732			U1484	A1403	G1310		U1148	U1081	U1015	G923
G1964		G1884	A1801	G1733	A1634	C1550	U1485	C1404	G1311	A1230	G1149	U1082	U1019	G924
C1965		A1885	A1802	G1734		A1551	U1486	U1405		U1231	C1150	U1083	A1020	A925
A2054		U1886		U1735	G1642	A1552	U1487	U1406	C1314	G1232	A1151	A1084	G926	G926
C2055	G1966	C1887	G1807	U1736	G1643	U1553	U1488		G1315	C1233	C1152	A1085	A1021	A927
G2056	C1967	G1888	A1808	G1737	C1644	U1554	C1489	U1409	G1316	A1237	C1153	A1086	G1022	A928
	G1968	A1889	A1809	G1738	G1645	G1555	U1490	G1410	G1317	G1238	G1154	G1087	U1023	U929
A2060	A1969	A1890		A1739	C1646		G1491	U1411	U1318	G1239	A1156	A1088	G1024	
C2061	U1970		U1812	G1740	U1647	C1558	U1492	U1412	C1319	U1240	G1157	A1090	G1026	U932
	U1971	C1893	G1813	C1741	U1648	U1559	C1493	A1413	C1320			G1091	A1027	
G2069	G1972	C1894		U1742		G1560	A1494	C1414	A1321	A1246	G1160	C1092		C935
			C1816	G1743	G1651	C1561	A1495	U1415	A1322	A1247	C1161	G1093	A1031	A936
C2073	A1978	A1901	G1817	A1744	U1662	U1562	A1496	G1416	C1323		G1162	U1094	G1032	C937
U2074		C1902	U1818	A1745	G1663		U1497	C1417	G1324	A1253	A1163	C1095	U1033	G938
	G1983		A1819	U1746		A1566		A1418	U1325	A1254	C1164	A1096	G939	G939
U2085	G1984	C1905	U1820	U1747		G1567	G1500	A1419	U1326	U1255	G1165	A1097	U1035	G940
U2086	C1985	G1906	A1821	C1748	G1666	G1567	A1501	A1420	A1327	U1256		A1098	G941	A941
	C1986	G1907	G1822	G1749	G1667	G1568	A1502		A1328	G1257	G1170	G1099	G1036	G942
C2091		G1823		G1750	A1668	A1569	A1503	G1425		C1257	C1171	C1100	G1037	C946
U2092	C1990			U1751	A1669	A1570	A1504	G1426	G1333	U1258	G1172	C1101	G1038	A947
G2093	U1991		U1827	C1670	C1670	A1571	A1505	A1427	G1334	G1259	C1173	C1102	A1039	
A2094	G1992	U1911	G1828	G1753	U1671	A1572	U1506	C1428	C1335		U1173		A1040	



• Molecule 2: 5S rRNA

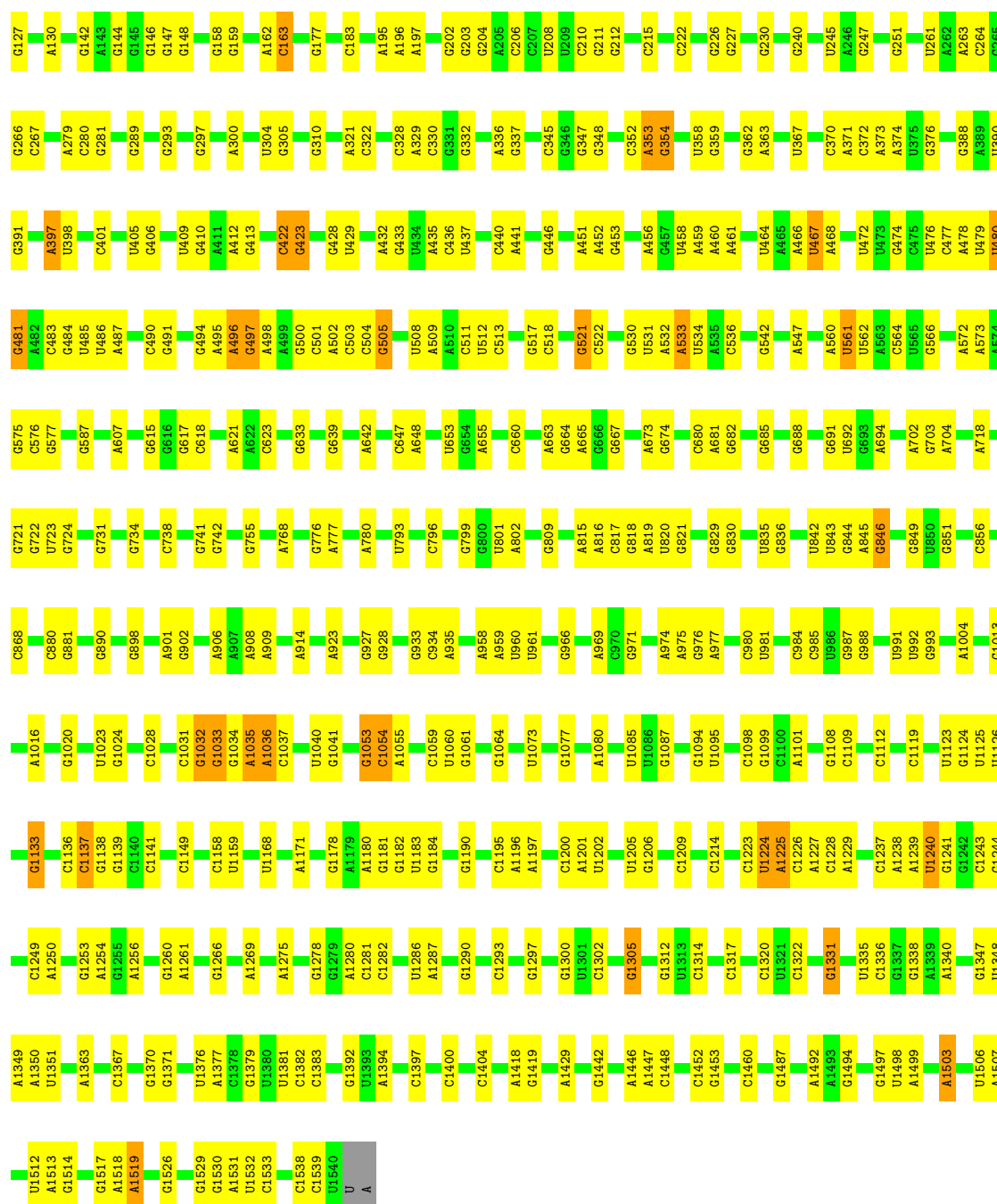
Chain 2: 76% 19% 5%



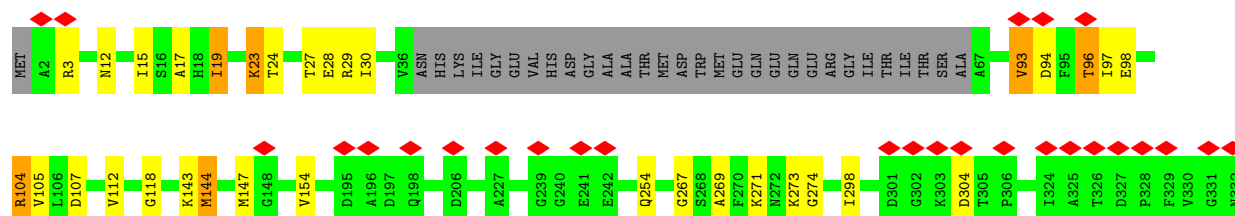
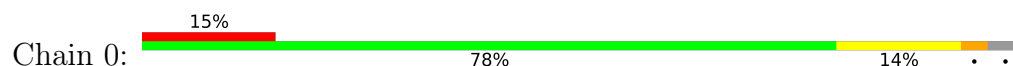
• Molecule 3: 16S rRNA

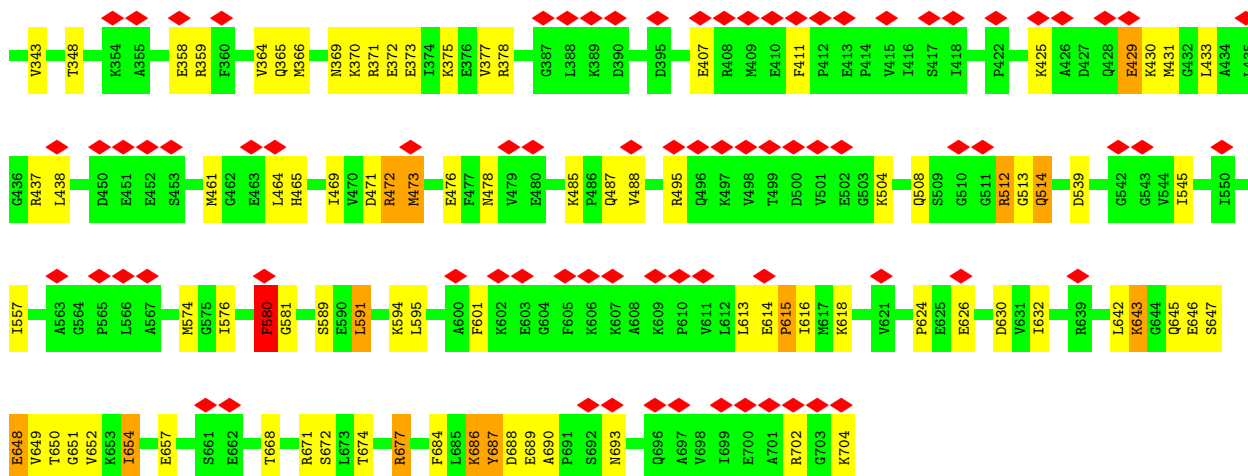
Chain 3: 69% 29% 2%



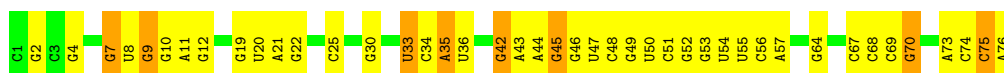


• Molecule 4: Elongation factor G

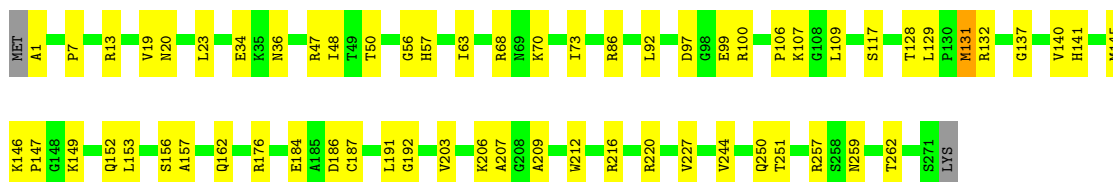
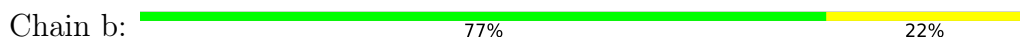




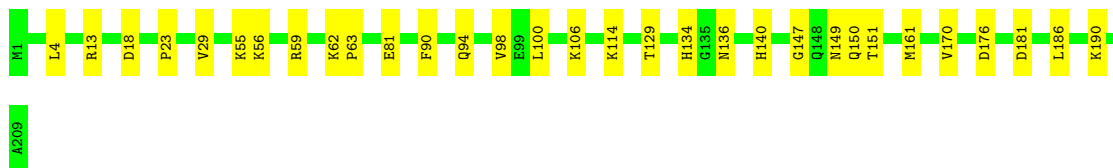
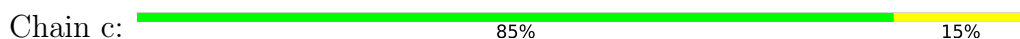
• Molecule 5: tRNA(fMet)



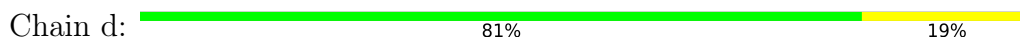
• Molecule 6: Large ribosomal subunit protein uL2

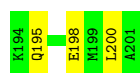


• Molecule 7: Large ribosomal subunit protein uL3



• Molecule 8: Large ribosomal subunit protein uL4





- Molecule 9: Large ribosomal subunit protein uL5

Chain e: 82% 17%



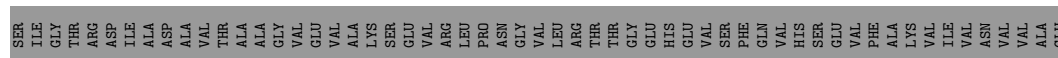
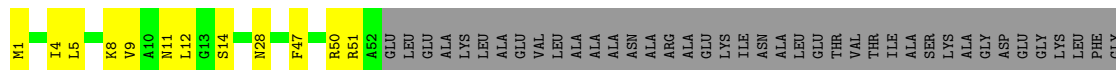
- Molecule 10: Large ribosomal subunit protein uL6

Chain f: 73% 25%



- Molecule 11: Large ribosomal subunit protein bL9

Chain g: 27% 8% 65%



- Molecule 12: Large ribosomal subunit protein uL11

Chain i: 60% 37%



- Molecule 13: Large ribosomal subunit protein uL13

Chain j: 85% 15%



- Molecule 14: Large ribosomal subunit protein uL14

Chain k:  79% 20%



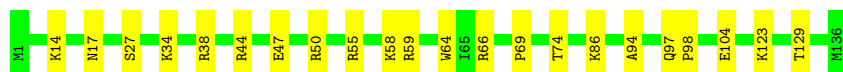
- Molecule 15: Large ribosomal subunit protein uL15

Chain l:  85% 15%



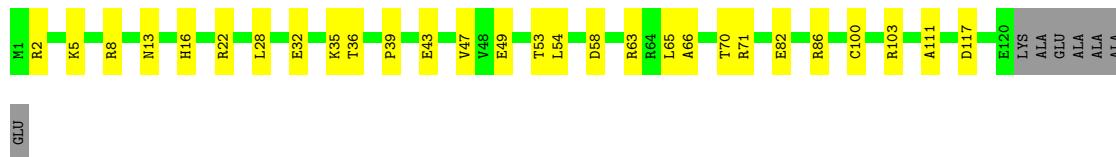
- Molecule 16: Large ribosomal subunit protein uL16

Chain m:  84% 16%



- Molecule 17: Large ribosomal subunit protein bL17

Chain n:  72% 22% 6%



- Molecule 18: Large ribosomal subunit protein uL18

Chain o:  82% 17%



- Molecule 19: Large ribosomal subunit protein bL19

Chain p:  86% 12%



- Molecule 20: Large ribosomal subunit protein bL20

Chain q:  81% 18%



- Molecule 21: Large ribosomal subunit protein bL21

Chain r:  74% 26%



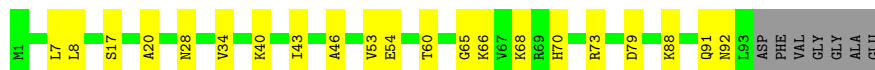
- Molecule 22: Large ribosomal subunit protein uL22

Chain s:  84% 16%



- Molecule 23: Large ribosomal subunit protein uL23

Chain t:  72% 21% 7%



- Molecule 24: Large ribosomal subunit protein uL24

Chain u:  72% 26% 2%



- Molecule 25: Large ribosomal subunit protein bL25

Chain v:  86% 14%



- Molecule 26: Large ribosomal subunit protein bL27

Chain w:  73% 15% 12%



- Molecule 27: Large ribosomal subunit protein bL28

Chain x:  74% 23% 3%



- Molecule 28: Large ribosomal subunit protein uL29

Chain y:  76% 24%



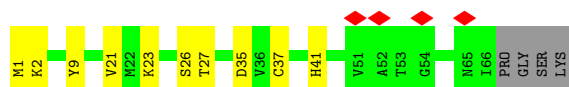
- Molecule 29: Large ribosomal subunit protein uL30

Chain z:  76% 22%



- Molecule 30: Large ribosomal subunit protein bL31

Chain A:  6% 80% 14% 6%



- Molecule 31: Large ribosomal subunit protein bL32

Chain B:  81% 18%



- Molecule 32: Large ribosomal subunit protein bL33

Chain C:  78% 13% 9%



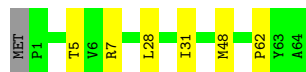
- Molecule 33: Large ribosomal subunit protein bL34

Chain D:  76% 22%



- Molecule 34: Large ribosomal subunit protein bL35

Chain E:  89% 9%



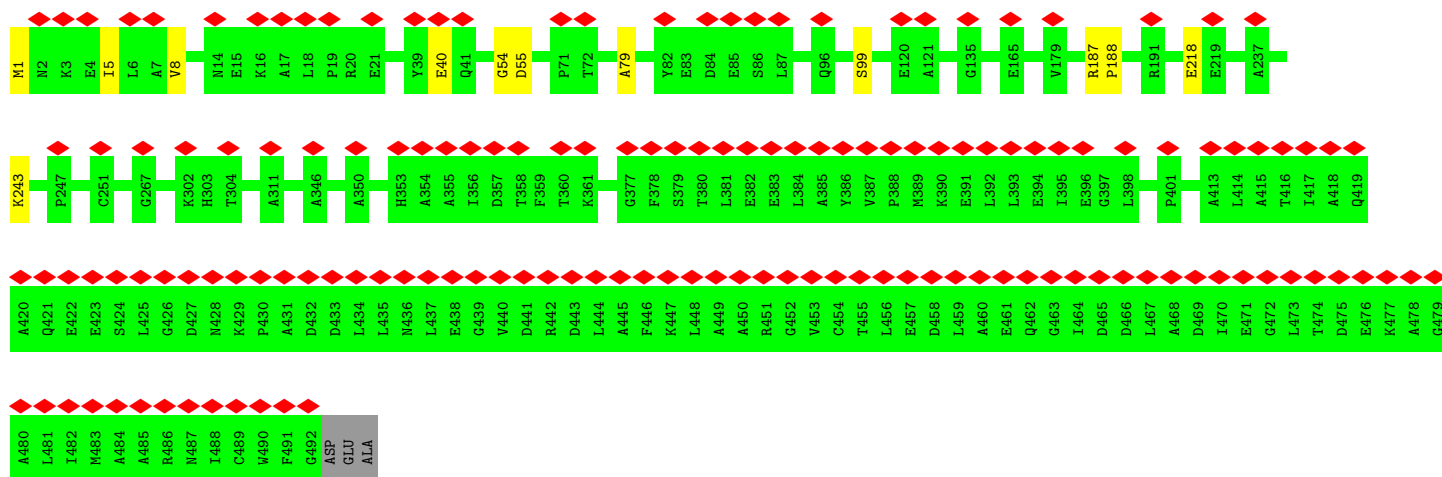
- Molecule 35: Large ribosomal subunit protein bL36A

Chain F:  76% 24%



- Molecule 36: Transcription termination/antitermination protein NusA

Chain NA:  30% 97%



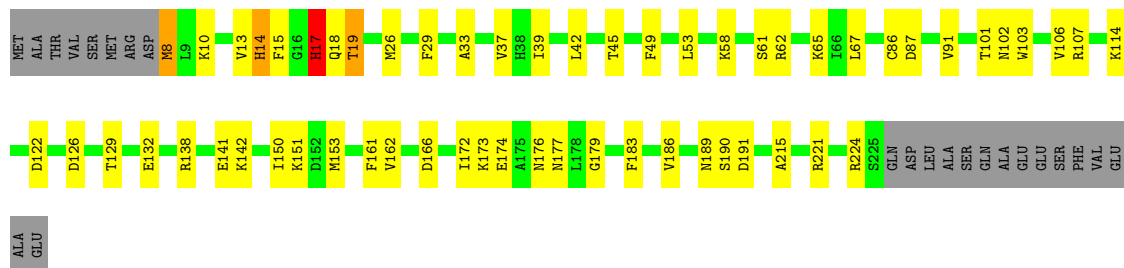
- Molecule 37: tRNA(Phe)

Chain 5:  24% 47% 28%



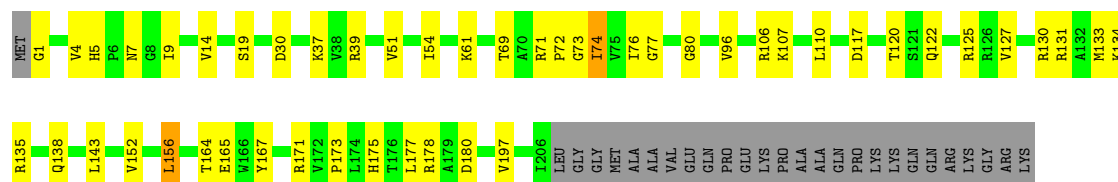
- Molecule 38: Small ribosomal subunit protein uS2

Chain G:  66% 22% 10%



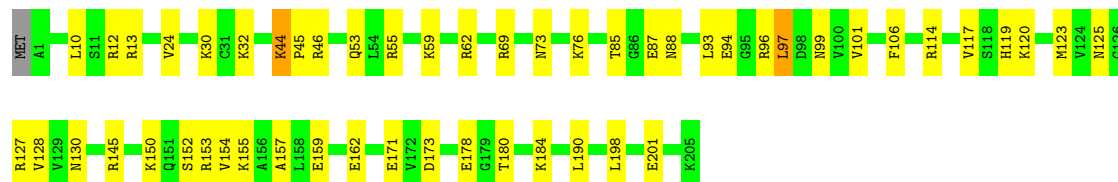
- Molecule 39: Small ribosomal subunit protein uS3

Chain H:  67% 20% 12%



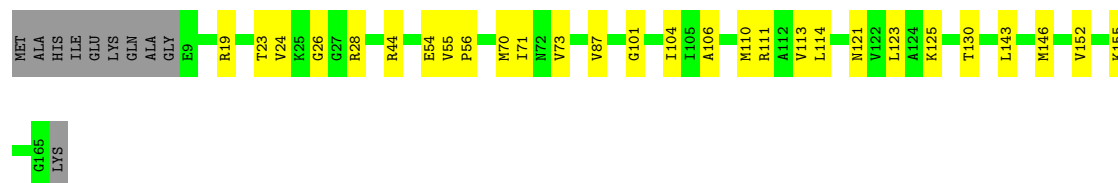
- Molecule 40: Small ribosomal subunit protein uS4

Chain I: 74% 24% .



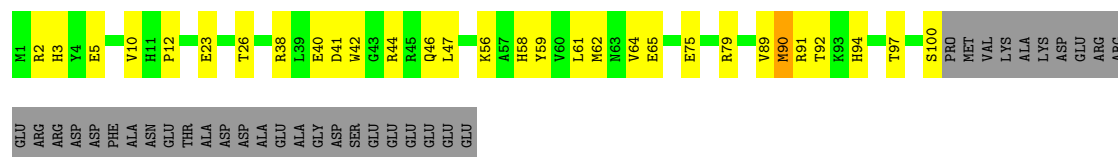
- Molecule 41: Small ribosomal subunit protein uS5

Chain J: 77% 17% 6%



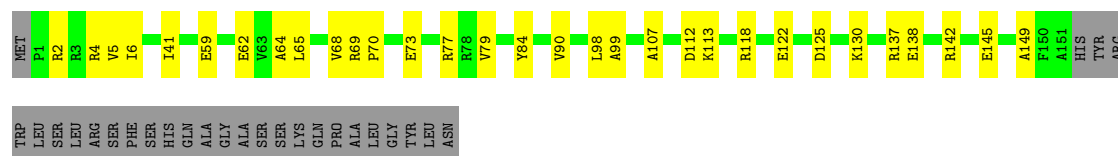
- Molecule 42: Small ribosomal subunit protein bS6, fully modified isoform

Chain K: 52% 21% 26%



- Molecule 43: Small ribosomal subunit protein uS7

Chain L: 67% 17% 16%



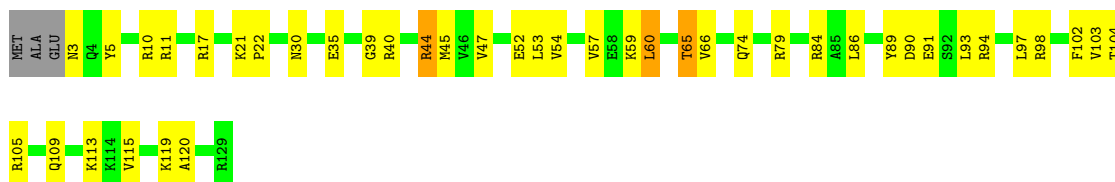
- Molecule 44: Small ribosomal subunit protein uS8

Chain M: 87% 12%



- Molecule 45: Small ribosomal subunit protein uS9

Chain N: 65% 30% ..



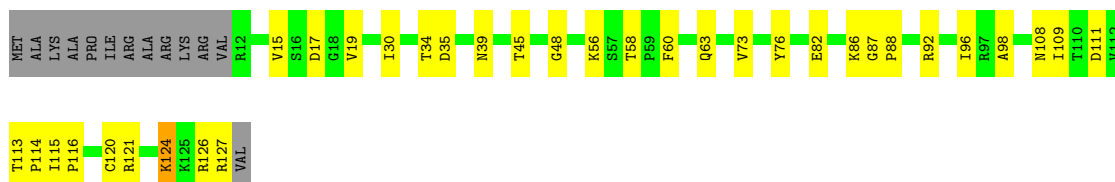
- Molecule 46: Small ribosomal subunit protein uS10

Chain O: 64% 22% 9% 5%



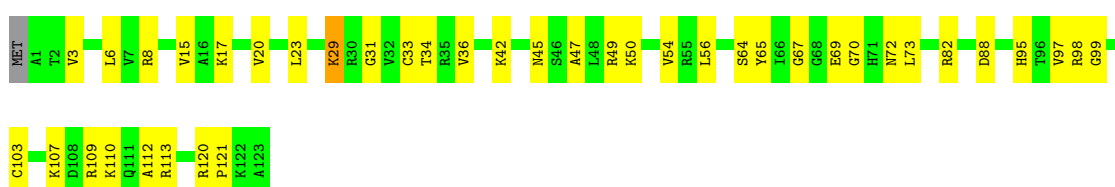
- Molecule 47: Small ribosomal subunit protein uS11

Chain P: 64% 26% • 10%



- Molecule 48: Small ribosomal subunit protein uS12

Chain Q: 67% 31% ..



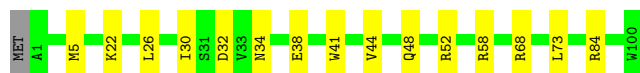
- Molecule 49: Small ribosomal subunit protein uS13

Chain R: 72% 25% •



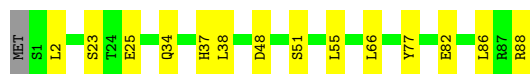
- Molecule 50: Small ribosomal subunit protein uS14

Chain S:  84% 15% .



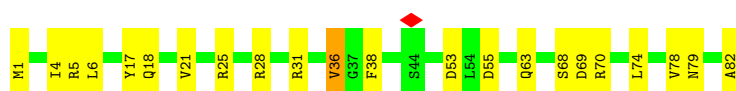
- Molecule 51: Small ribosomal subunit protein uS15

Chain T:  83% 16% .



- Molecule 52: Small ribosomal subunit protein bS16

Chain U:  73% 26% .



- Molecule 53: Small ribosomal subunit protein uS17

Chain V:  74% 21% 5%



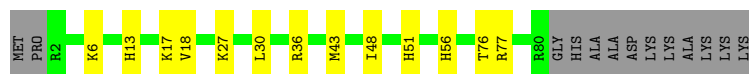
- Molecule 54: Small ribosomal subunit protein bS18

Chain W:  65% 20% 13%



- Molecule 55: Small ribosomal subunit protein uS19

Chain X:  72% 14% 14%

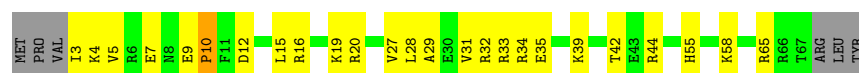


- Molecule 56: Small ribosomal subunit protein bS20

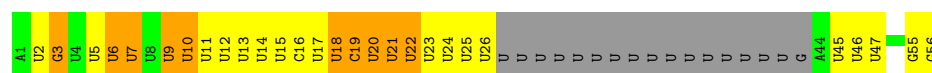
Chain Y:  76% 22% .



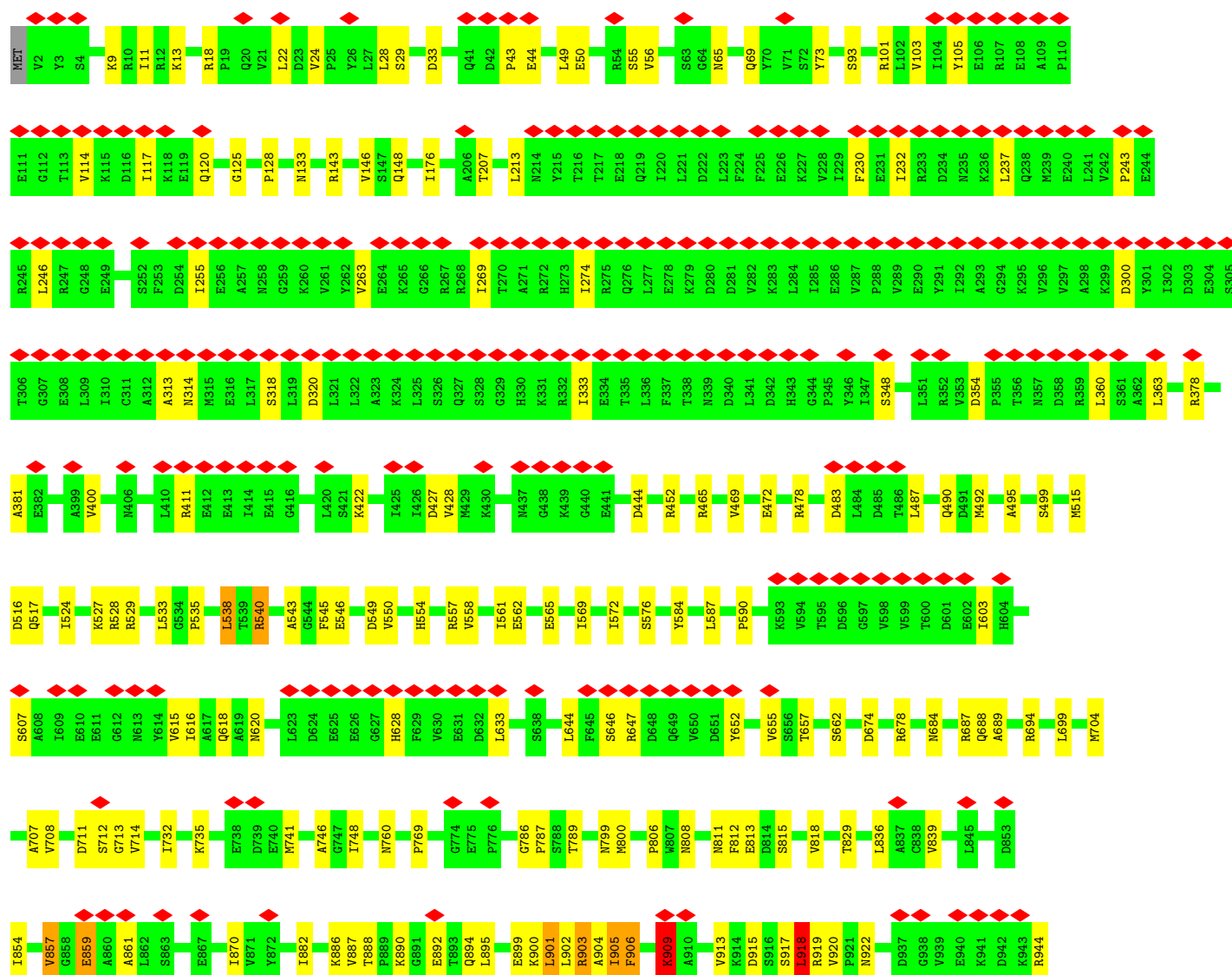
- Molecule 57: Small ribosomal subunit protein bS21

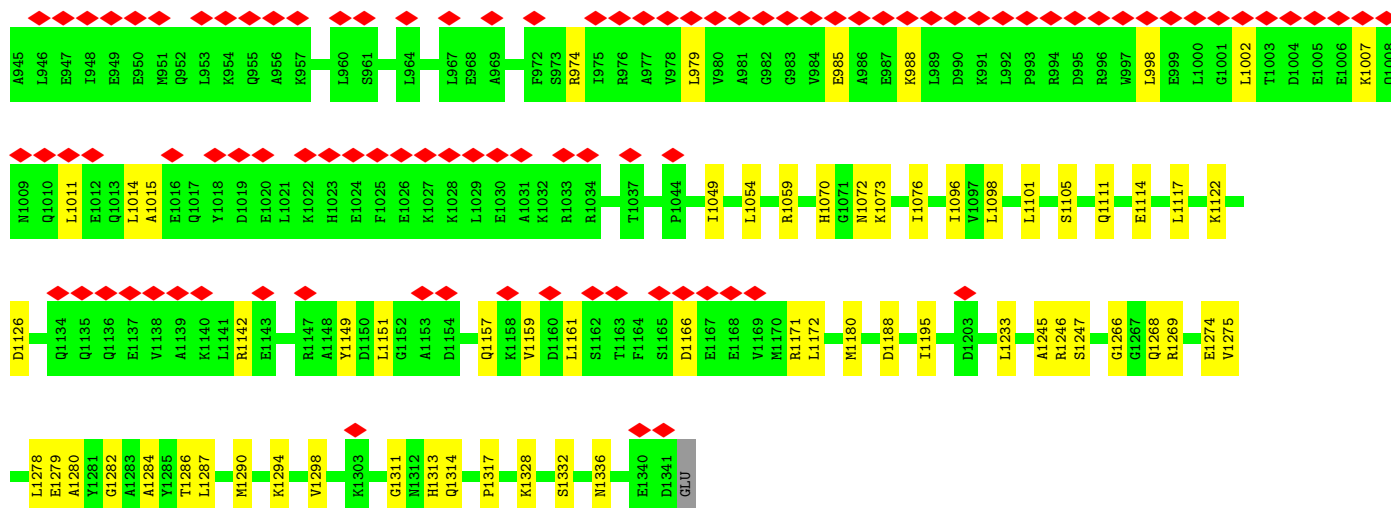


Chain 4:

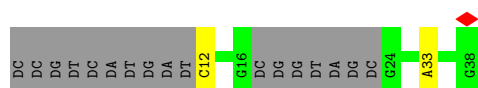


Chain B2:

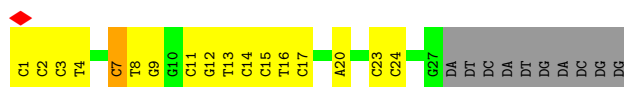




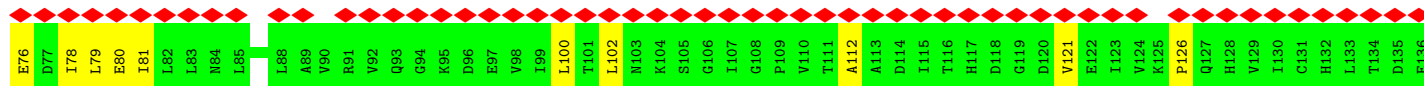
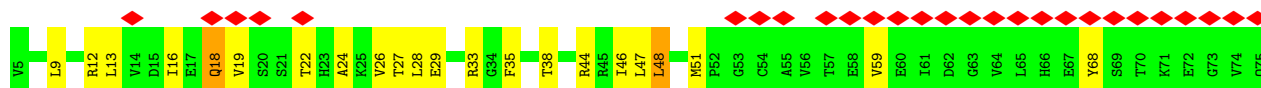
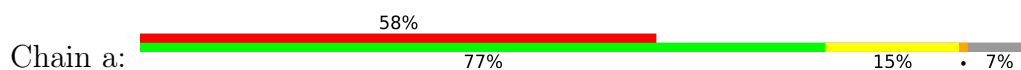
- Molecule 60: non-templated DNA strand

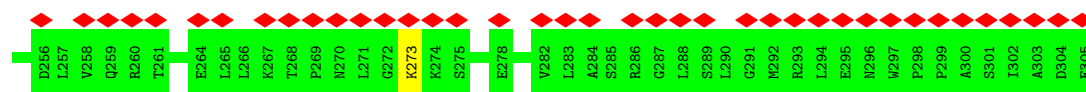


- Molecule 61: templated DNA strand

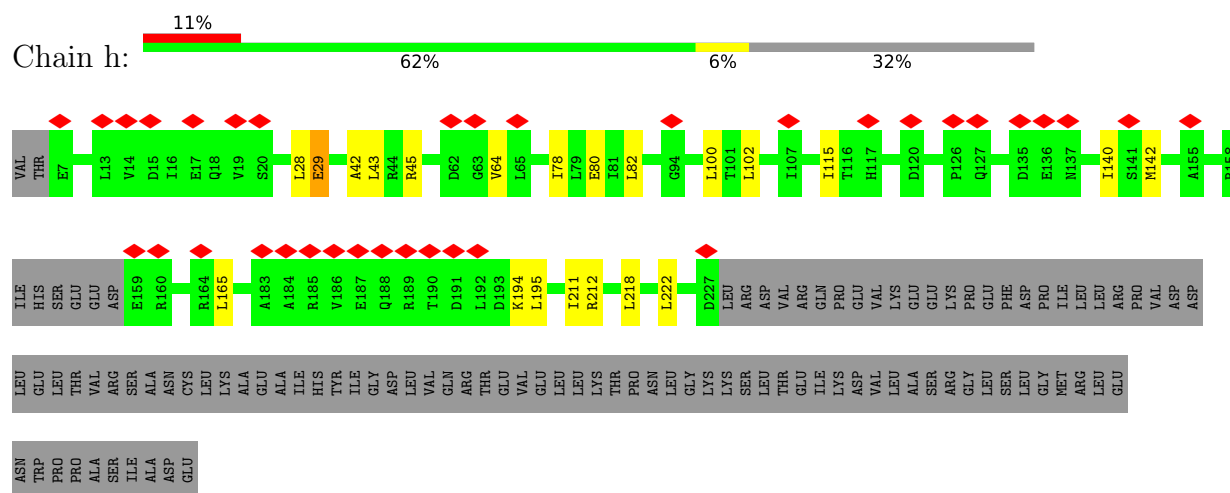


- Molecule 62: DNA-directed RNA polymerase subunit alpha

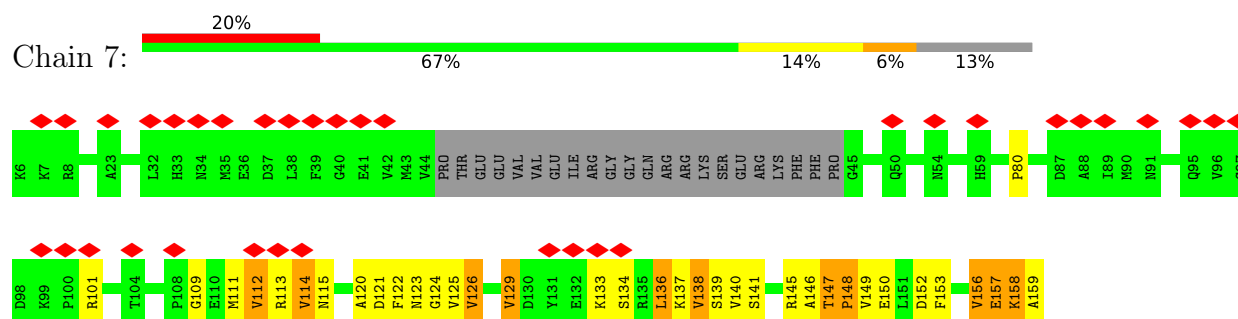




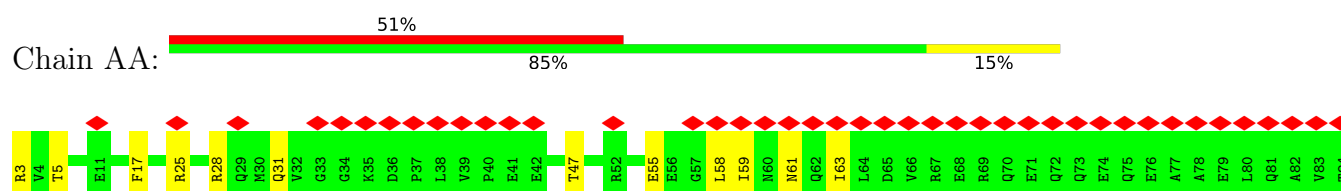
- Molecule 62: DNA-directed RNA polymerase subunit alpha



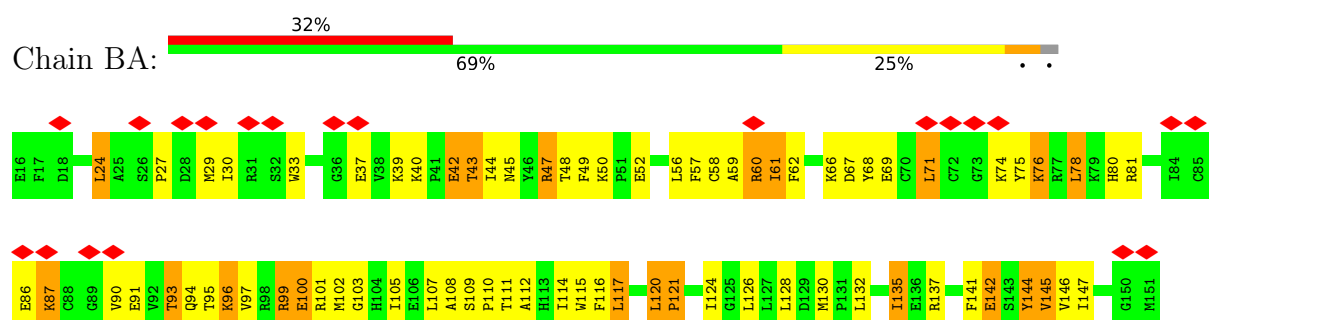
- Molecule 63: Transcription termination/antitermination protein NusG

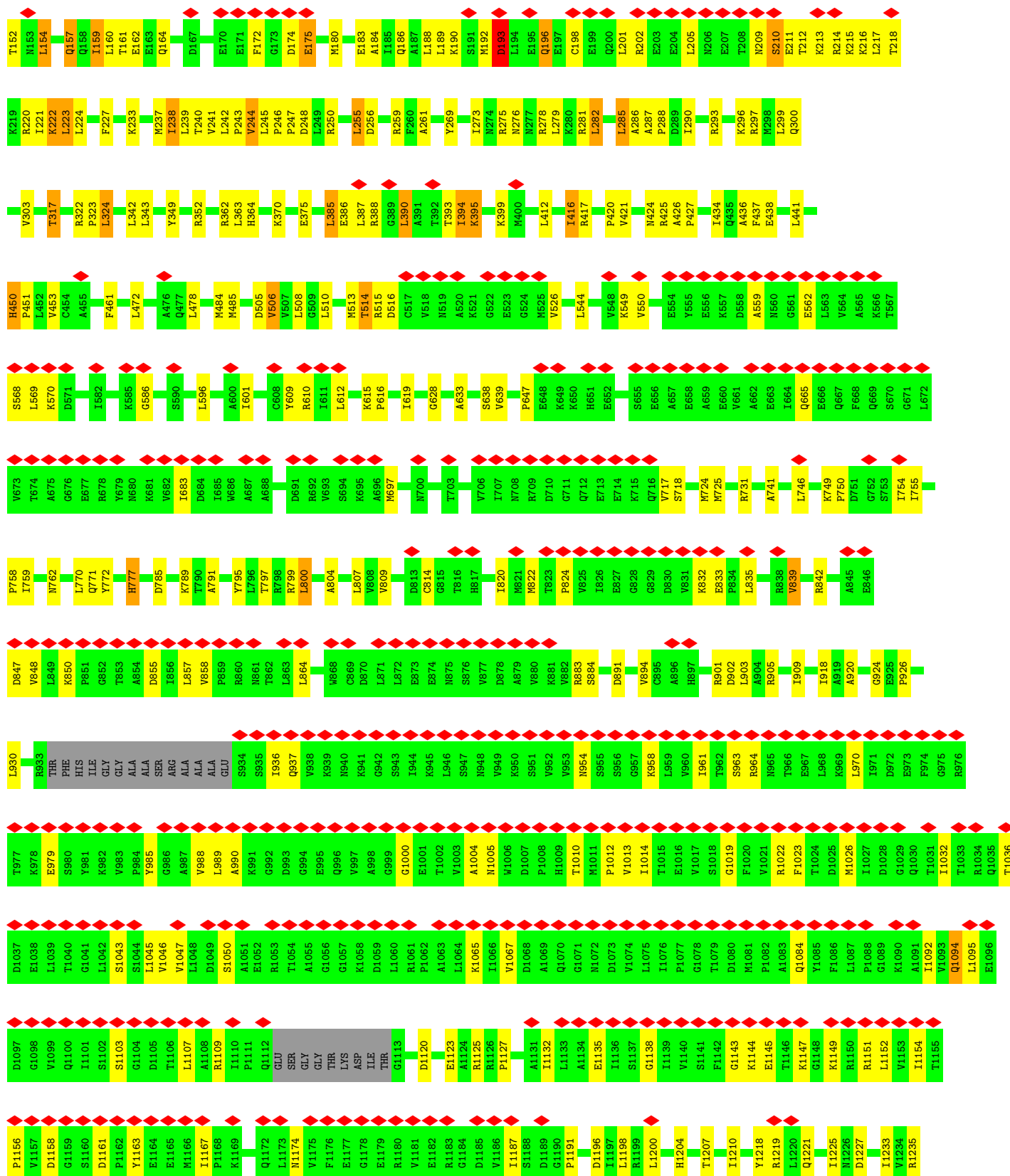


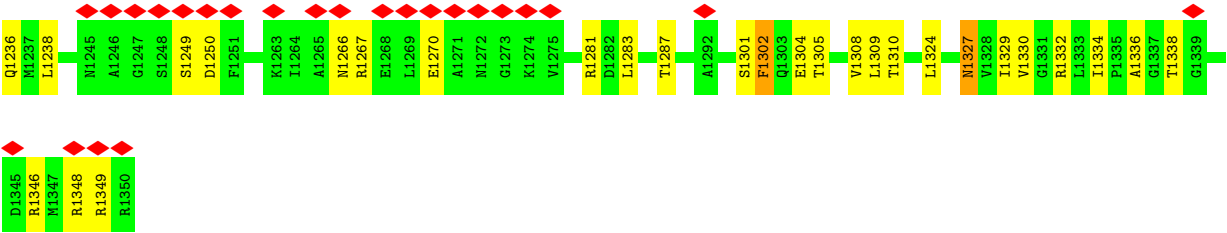
- Molecule 64: DNA-directed RNA polymerase subunit omega



- Molecule 65: DNA-directed RNA polymerase subunit beta'







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1717500	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.034	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.002	Depositor
Map size ($\text{\AA}$)	502.64, 502.64, 502.64	wwPDB
Map dimensions	610, 610, 610	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.824, 0.824, 0.824	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	1	0.51	0/69796	0.62	21/108888 (0.0%)
2	2	0.45	1/2869 (0.0%)	0.47	0/4474
3	3	0.42	0/36963	0.43	0/57662
4	0	0.84	0/5309	1.17	6/7181 (0.1%)
5	6	0.40	0/1832	0.57	1/2855 (0.0%)
6	b	0.49	0/2121	0.64	0/2852
7	c	0.42	0/1586	0.59	2/2134 (0.1%)
8	d	0.44	0/1571	0.62	0/2113
9	e	0.43	0/1434	0.65	2/1926 (0.1%)
10	f	0.35	0/1343	0.56	0/1816
11	g	0.32	0/405	0.75	0/544
12	i	0.51	0/1046	0.87	3/1410 (0.2%)
13	j	0.42	0/1152	0.55	1/1551 (0.1%)
14	k	0.45	0/947	0.66	0/1268
15	l	0.40	0/1054	0.63	0/1403
16	m	0.56	0/1093	0.74	0/1460
17	n	0.46	0/973	0.72	1/1301 (0.1%)
18	o	0.32	0/902	0.51	0/1209
19	p	0.42	0/929	0.63	0/1242
20	q	0.52	0/960	0.62	1/1278 (0.1%)
21	r	0.46	0/829	0.70	0/1107
22	s	0.44	0/864	0.58	0/1156
23	t	0.34	0/744	0.53	0/994
24	u	0.46	0/787	0.75	0/1051
25	v	0.34	0/766	0.51	0/1025
26	w	0.41	0/582	0.52	0/769
27	x	0.43	0/635	0.63	1/848 (0.1%)
28	y	0.29	0/510	0.63	0/677
29	z	0.41	0/453	0.53	0/605
30	A	0.27	0/530	0.54	0/707
31	B	0.41	0/450	0.60	0/599
32	C	0.28	0/416	0.52	0/554

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	D	0.47	0/380	0.76	2/498 (0.4%)
34	E	0.53	0/513	0.60	0/676
35	F	0.58	0/303	0.66	0/397
36	NA	0.79	0/2431	1.22	0/3385
37	5	0.57	0/1812	0.85	1/2823 (0.0%)
38	G	0.38	0/1735	0.64	0/2338
39	H	0.34	0/1651	0.55	0/2225
40	I	0.35	0/1665	0.71	0/2227
41	J	0.38	0/1169	0.68	2/1573 (0.1%)
42	K	0.46	0/835	0.77	0/1128
43	L	0.31	0/1195	0.66	3/1602 (0.2%)
44	M	0.35	0/989	0.53	0/1326
45	N	0.47	0/1034	0.77	0/1375
46	O	0.46	0/796	0.76	2/1077 (0.2%)
47	P	0.45	0/885	0.64	1/1195 (0.1%)
48	Q	0.50	0/969	0.86	2/1300 (0.2%)
49	R	0.33	0/892	0.73	4/1193 (0.3%)
50	S	0.33	0/817	0.61	0/1088
51	T	0.49	0/722	0.64	0/964
52	U	0.30	0/659	0.71	2/884 (0.2%)
53	V	0.44	0/657	0.71	0/881
54	W	0.55	0/544	0.74	1/731 (0.1%)
55	X	0.29	0/652	0.55	0/877
56	Y	0.29	0/671	0.52	0/888
57	Z	0.66	0/550	1.01	2/728 (0.3%)
58	4	0.53	0/896	0.69	0/1387
59	B2	0.46	0/10714	0.67	0/14459
60	9	0.49	0/468	0.53	0/719
61	8	0.56	0/599	0.71	1/919 (0.1%)
62	a	0.56	0/2106	0.82	0/2868
62	h	0.43	0/1718	0.63	0/2328
63	7	0.62	0/756	0.92	1/1048 (0.1%)
64	AA	0.31	0/652	0.60	0/879
65	BA	0.57	4/10510 (0.0%)	0.75	8/14196 (0.1%)
All	All	0.49	5/194796 (0.0%)	0.64	71/286841 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	120	U	C1'-N1	6.12	1.57	1.48
65	BA	1327	ASN	CG-ND2	-5.25	1.22	1.33
65	BA	1094	GLN	CD-OE1	5.19	1.33	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	BA	424	ASN	CG-ND2	-5.18	1.22	1.33
65	BA	665	GLN	CD-OE1	5.09	1.33	1.23

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	0	580	PHE	CA-CB-CG	9.56	123.36	113.80
47	P	73	VAL	N-CA-C	-9.02	104.54	113.20
20	q	33	VAL	N-CA-C	-8.78	104.75	112.12
43	L	64	ALA	N-CA-C	-7.68	105.07	114.75
1	1	1130	U	C2'-C3'-O3'	7.57	120.86	109.50

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	1	62317	0	31345	1457	0
2	2	2566	0	1302	15	0
3	3	33012	0	16618	187	0
4	0	5212	0	5200	64	0
5	6	1640	0	837	23	0
6	b	2082	0	2157	50	0
7	c	1565	0	1616	28	0
8	d	1552	0	1619	28	0
9	e	1410	0	1447	17	0
10	f	1323	0	1374	26	0
11	g	400	0	423	6	0
12	i	1032	0	1088	37	0
13	j	1129	0	1162	21	0
14	k	938	0	1012	19	0
15	l	1045	0	1117	17	0
16	m	1074	0	1157	11	0
17	n	960	0	1000	20	0
18	o	892	0	923	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	p	917	0	965	13	0
20	q	947	0	1022	13	0
21	r	816	0	839	17	0
22	s	857	0	922	12	0
23	t	738	0	807	12	0
24	u	779	0	834	14	0
25	v	753	0	780	8	0
26	w	575	0	592	9	0
27	x	625	0	655	11	0
28	y	509	0	543	12	0
29	z	449	0	491	8	0
30	A	521	0	520	8	0
31	B	444	0	461	8	0
32	C	409	0	440	5	0
33	D	377	0	418	9	0
34	E	504	0	574	3	0
35	F	302	0	343	4	0
36	NA	2432	0	1171	26	0
37	5	1622	0	821	39	0
38	G	1704	0	1732	39	0
39	H	1624	0	1699	67	0
40	I	1643	0	1710	31	0
41	J	1156	0	1199	19	0
42	K	817	0	808	16	0
43	L	1181	0	1240	19	0
44	M	979	0	1034	10	0
45	N	1022	0	1070	23	0
46	O	786	0	828	51	0
47	P	869	0	878	22	0
48	Q	955	0	1019	25	0
49	R	883	0	944	15	0
50	S	805	0	847	11	0
51	T	714	0	737	8	0
52	U	649	0	666	18	0
53	V	648	0	691	9	0
54	W	535	0	552	8	0
55	X	637	0	665	9	0
56	Y	665	0	714	12	0
57	Z	544	0	579	13	0
58	4	809	0	405	83	0
59	B2	10546	0	10550	181	0
60	9	417	0	224	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	8	539	0	305	28	0
62	a	2088	0	1895	28	0
62	h	1698	0	1718	14	0
63	7	758	0	334	48	0
64	AA	650	0	658	10	0
65	BA	10353	0	10548	348	0
66	BA	1	0	0	0	0
All	All	181400	0	130844	2994	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 2994 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)
36:NA:1:MET:CB	59:B2:903:ARG:HH11	0.96	1.60
4:0:512:ARG:CZ	58:4:7:U:H5''	1.44	1.46
39:H:73:GLY:HA3	58:4:22:U:C4'	1.52	1.39
36:NA:1:MET:CB	59:B2:903:ARG:NH1	1.81	1.37
36:NA:1:MET:CA	59:B2:903:ARG:HB3	1.59	1.32

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	
4	0	669/704 (95%)	625 (93%)	43 (6%)	1 (0%)	48	79
6	b	269/273 (98%)	244 (91%)	25 (9%)	0	100	100
7	c	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
8	d	199/201 (99%)	186 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	e	175/179 (98%)	157 (90%)	18 (10%)	0	100	100
10	f	174/177 (98%)	160 (92%)	14 (8%)	0	100	100
11	g	50/149 (34%)	44 (88%)	5 (10%)	1 (2%)	6	32
12	i	139/142 (98%)	110 (79%)	26 (19%)	3 (2%)	5	30
13	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
14	k	120/123 (98%)	106 (88%)	14 (12%)	0	100	100
15	l	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
16	m	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
17	n	118/127 (93%)	103 (87%)	15 (13%)	0	100	100
18	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
19	p	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
20	q	115/118 (98%)	110 (96%)	3 (3%)	2 (2%)	7	35
21	r	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
22	s	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
23	t	91/100 (91%)	82 (90%)	9 (10%)	0	100	100
24	u	100/104 (96%)	84 (84%)	15 (15%)	1 (1%)	12	44
25	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
26	w	73/85 (86%)	67 (92%)	6 (8%)	0	100	100
27	x	75/78 (96%)	72 (96%)	2 (3%)	1 (1%)	9	39
28	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
29	z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
30	A	64/70 (91%)	59 (92%)	5 (8%)	0	100	100
31	B	54/57 (95%)	48 (89%)	4 (7%)	2 (4%)	2	21
32	C	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
33	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
34	E	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
35	F	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
36	NA	490/495 (99%)	471 (96%)	17 (4%)	2 (0%)	30	62
38	G	216/241 (90%)	187 (87%)	27 (12%)	2 (1%)	14	47
39	H	204/233 (88%)	195 (96%)	9 (4%)	0	100	100
40	I	203/206 (98%)	172 (85%)	30 (15%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	J	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
42	K	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
43	L	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
44	M	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
45	N	125/130 (96%)	104 (83%)	21 (17%)	0	100	100
46	O	96/103 (93%)	85 (88%)	10 (10%)	1 (1%)	12	44
47	P	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	14	47
48	Q	121/124 (98%)	94 (78%)	27 (22%)	0	100	100
49	R	112/118 (95%)	98 (88%)	13 (12%)	1 (1%)	14	47
50	S	98/101 (97%)	83 (85%)	15 (15%)	0	100	100
51	T	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
52	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
53	V	78/84 (93%)	69 (88%)	8 (10%)	1 (1%)	9	39
54	W	63/75 (84%)	56 (89%)	5 (8%)	2 (3%)	3	24
55	X	77/92 (84%)	71 (92%)	6 (8%)	0	100	100
56	Y	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
57	Z	63/71 (89%)	44 (70%)	18 (29%)	1 (2%)	7	36
59	B2	1338/1342 (100%)	1206 (90%)	127 (10%)	5 (0%)	30	62
62	a	295/325 (91%)	273 (92%)	21 (7%)	1 (0%)	36	67
62	h	217/325 (67%)	207 (95%)	10 (5%)	0	100	100
63	7	150/176 (85%)	108 (72%)	29 (19%)	13 (9%)	0	7
64	AA	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
65	BA	1329/1358 (98%)	1203 (90%)	122 (9%)	4 (0%)	36	67
All	All	10188/10862 (94%)	9193 (90%)	949 (9%)	46 (0%)	26	57

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	x	25	LYS
36	NA	187	ARG
36	NA	188	PRO
63	7	80	PRO
63	7	101	ARG

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	
4	0	553/578 (96%)	482 (87%)	71 (13%)	4	21
6	b	216/218 (99%)	212 (98%)	4 (2%)	50	68
7	c	164/164 (100%)	164 (100%)	0	100	100
8	d	165/165 (100%)	162 (98%)	3 (2%)	51	69
9	e	148/150 (99%)	142 (96%)	6 (4%)	27	53
10	f	137/138 (99%)	132 (96%)	5 (4%)	31	57
11	g	41/114 (36%)	38 (93%)	3 (7%)	13	38
12	i	109/110 (99%)	100 (92%)	9 (8%)	10	34
13	j	116/116 (100%)	116 (100%)	0	100	100
14	k	103/104 (99%)	103 (100%)	0	100	100
15	l	102/103 (99%)	101 (99%)	1 (1%)	68	75
16	m	109/109 (100%)	103 (94%)	6 (6%)	19	46
17	n	100/103 (97%)	99 (99%)	1 (1%)	68	75
18	o	86/87 (99%)	86 (100%)	0	100	100
19	p	99/100 (99%)	98 (99%)	1 (1%)	68	75
20	q	89/90 (99%)	86 (97%)	3 (3%)	32	57
21	r	84/84 (100%)	82 (98%)	2 (2%)	43	64
22	s	93/93 (100%)	92 (99%)	1 (1%)	65	74
23	t	80/84 (95%)	80 (100%)	0	100	100
24	u	83/85 (98%)	79 (95%)	4 (5%)	23	49
25	v	78/78 (100%)	77 (99%)	1 (1%)	61	72
26	w	57/63 (90%)	57 (100%)	0	100	100
27	x	67/68 (98%)	67 (100%)	0	100	100
28	y	55/55 (100%)	55 (100%)	0	100	100
29	z	48/49 (98%)	46 (96%)	2 (4%)	26	52
30	A	58/62 (94%)	57 (98%)	1 (2%)	53	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	B	47/48 (98%)	47 (100%)	0	100	100
32	C	45/49 (92%)	44 (98%)	1 (2%)	45	65
33	D	38/38 (100%)	37 (97%)	1 (3%)	40	62
34	E	51/52 (98%)	49 (96%)	2 (4%)	28	54
35	F	34/34 (100%)	30 (88%)	4 (12%)	5	23
38	G	180/199 (90%)	174 (97%)	6 (3%)	33	58
39	H	170/190 (90%)	167 (98%)	3 (2%)	51	69
40	I	172/173 (99%)	168 (98%)	4 (2%)	44	64
41	J	119/126 (94%)	117 (98%)	2 (2%)	53	70
42	K	87/116 (75%)	82 (94%)	5 (6%)	18	45
43	L	124/147 (84%)	124 (100%)	0	100	100
44	M	104/105 (99%)	103 (99%)	1 (1%)	68	75
45	N	105/107 (98%)	95 (90%)	10 (10%)	8	31
46	O	86/90 (96%)	76 (88%)	10 (12%)	5	24
47	P	89/99 (90%)	86 (97%)	3 (3%)	32	57
48	Q	103/104 (99%)	98 (95%)	5 (5%)	22	48
49	R	92/96 (96%)	91 (99%)	1 (1%)	65	74
50	S	83/84 (99%)	83 (100%)	0	100	100
51	T	76/77 (99%)	73 (96%)	3 (4%)	28	54
52	U	65/65 (100%)	64 (98%)	1 (2%)	57	71
53	V	74/78 (95%)	72 (97%)	2 (3%)	39	62
54	W	56/65 (86%)	52 (93%)	4 (7%)	13	38
55	X	70/79 (89%)	70 (100%)	0	100	100
56	Y	65/66 (98%)	64 (98%)	1 (2%)	57	71
57	Z	55/61 (90%)	47 (86%)	8 (14%)	3	17
59	B2	1150/1157 (99%)	1118 (97%)	32 (3%)	38	61
62	a	185/283 (65%)	174 (94%)	11 (6%)	18	44
62	h	186/283 (66%)	185 (100%)	1 (0%)	81	80
64	AA	70/70 (100%)	69 (99%)	1 (1%)	59	71
65	BA	1110/1134 (98%)	1017 (92%)	93 (8%)	10	34
All	All	7931/8445 (94%)	7592 (96%)	339 (4%)	27	51

5 of 339 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	B2	1076	ILE
65	BA	174	ASP
62	a	22	THR
65	BA	80	HIS
65	BA	238	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 139 such sidechains are listed below:

Mol	Chain	Res	Type
59	B2	1313	HIS
62	a	117	HIS
65	BA	450	HIS
27	x	16	ASN
26	w	53	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2904 (99%)	398 (13%)	15 (0%)
2	2	119/120 (99%)	17 (14%)	1 (0%)
3	3	1538/1542 (99%)	253 (16%)	4 (0%)
37	5	75/76 (98%)	39 (52%)	6 (8%)
5	6	76/77 (98%)	27 (35%)	2 (2%)
58	4	37/56 (66%)	21 (56%)	2 (5%)
All	All	4747/4775 (99%)	755 (15%)	30 (0%)

5 of 755 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	12	U
1	1	34	U
1	1	35	G
1	1	46	G

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2326	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
37	5	60	U
3	3	1035	A
58	4	19	C
37	5	39	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

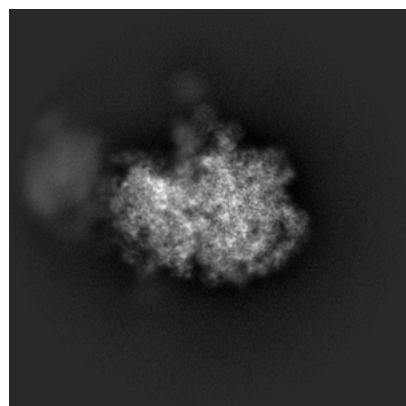
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65509. These allow visual inspection of the internal detail of the map and identification of artifacts.

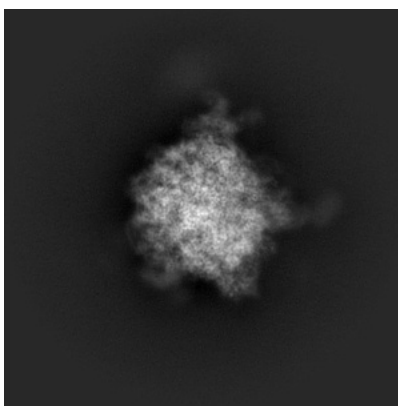
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

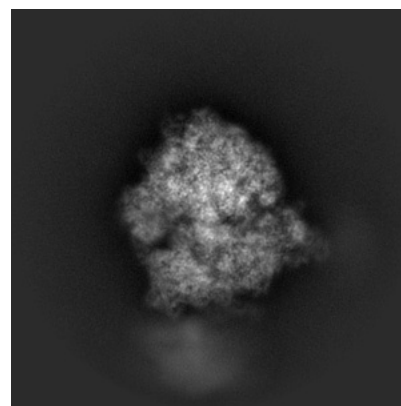
6.1.1 Primary map



X

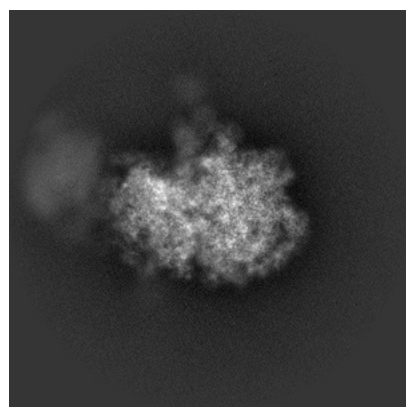


Y

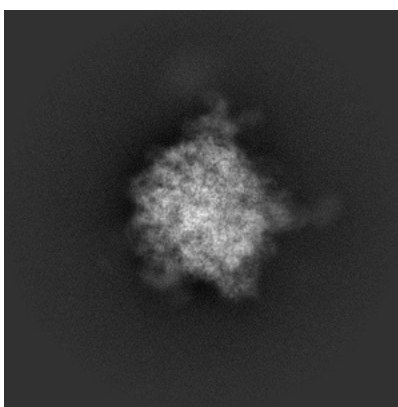


Z

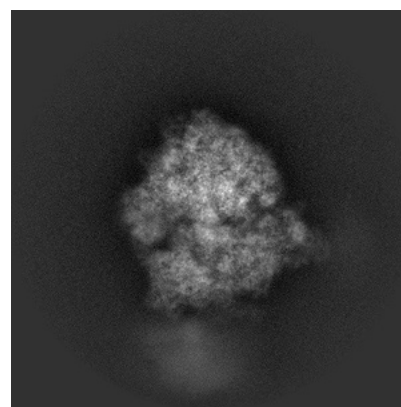
6.1.2 Raw map



X



Y

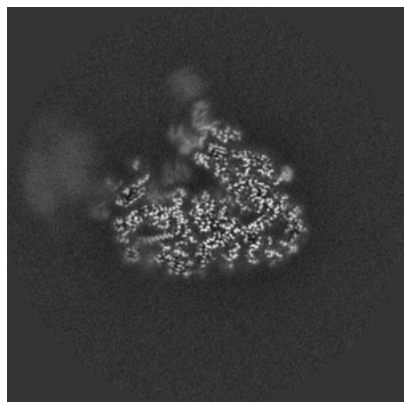


Z

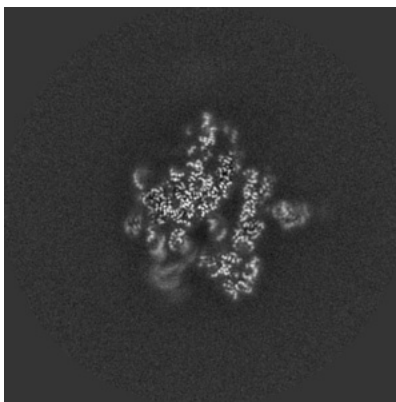
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

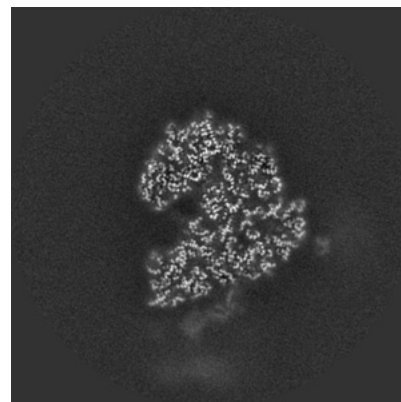
6.2.1 Primary map



X Index: 305

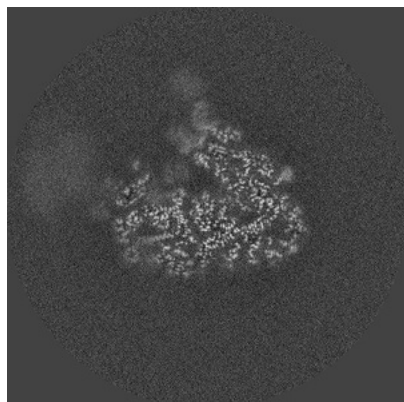


Y Index: 305

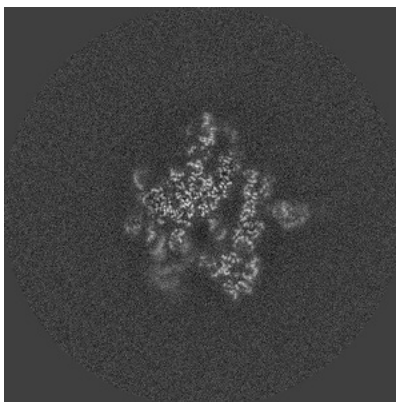


Z Index: 305

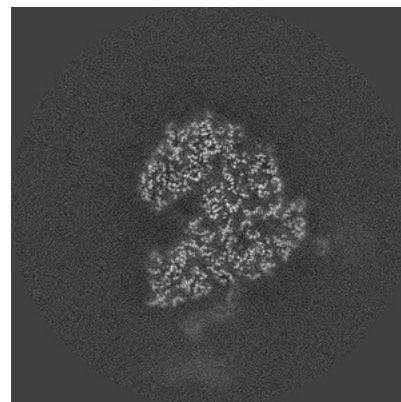
6.2.2 Raw map



X Index: 305



Y Index: 305

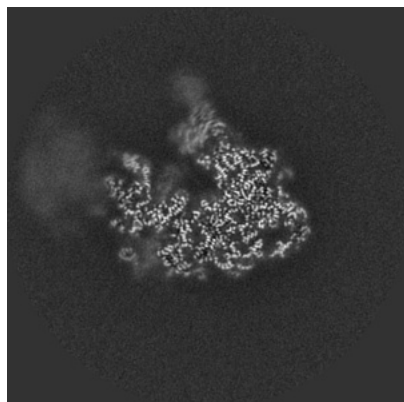


Z Index: 305

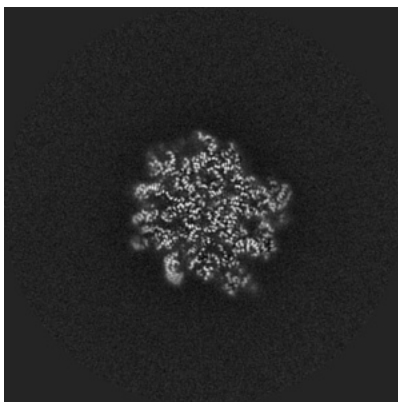
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

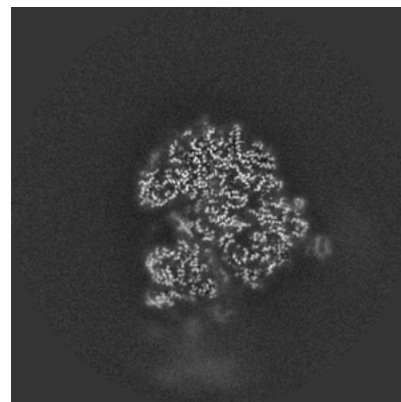
6.3.1 Primary map



X Index: 297

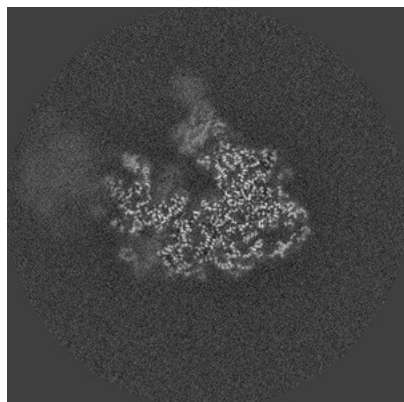


Y Index: 335

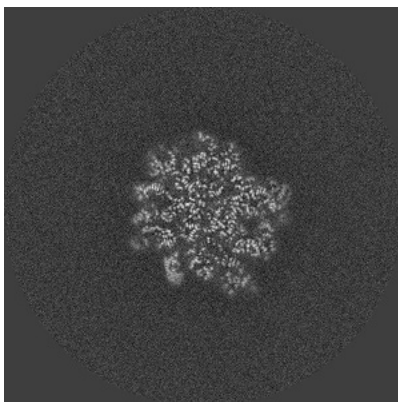


Z Index: 313

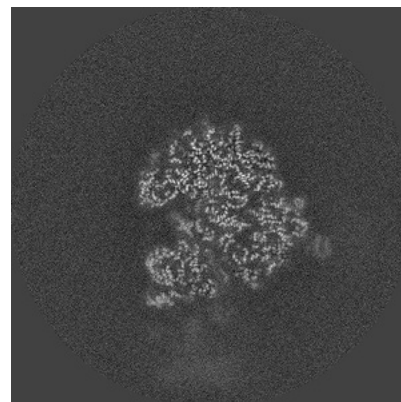
6.3.2 Raw map



X Index: 297



Y Index: 334



Z Index: 313

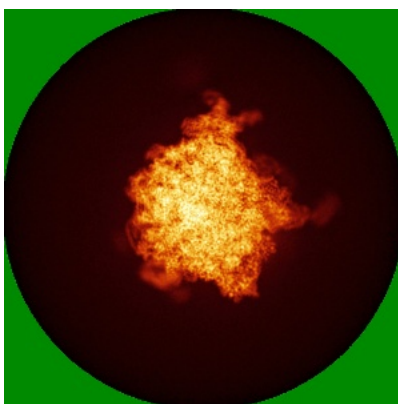
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

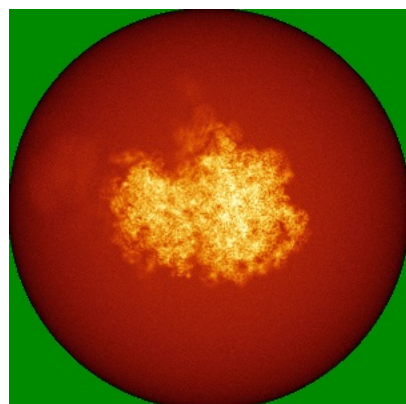


Y

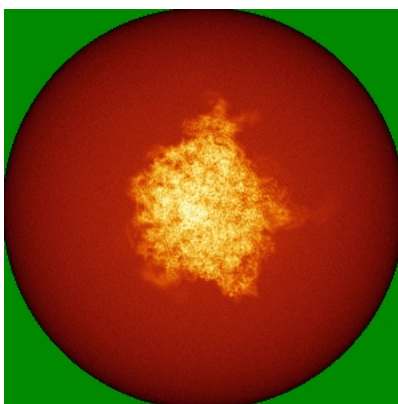


Z

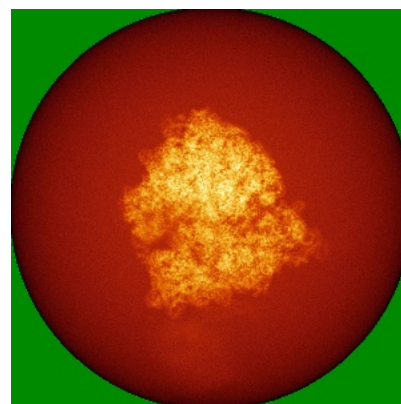
6.4.2 Raw map



X



Y

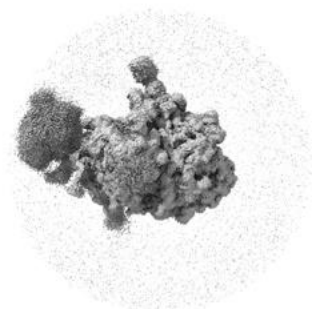


Z

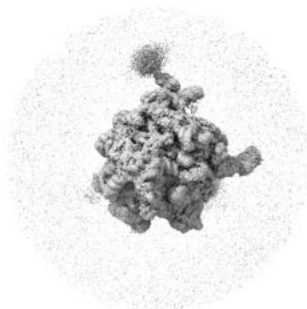
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



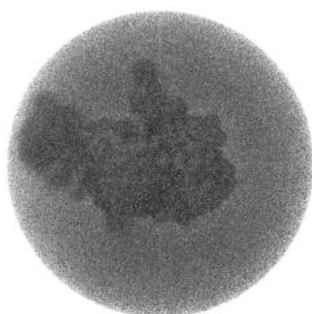
Y



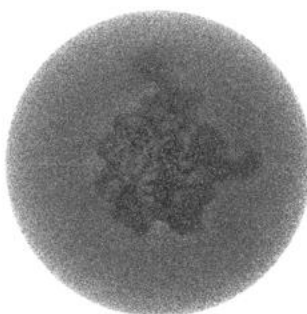
Z

The images above show the 3D surface view of the map at the recommended contour level 0.002. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

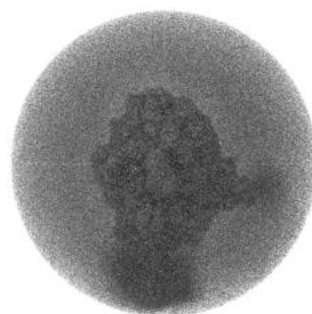
6.5.2 Raw map



X



Y



Z

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.

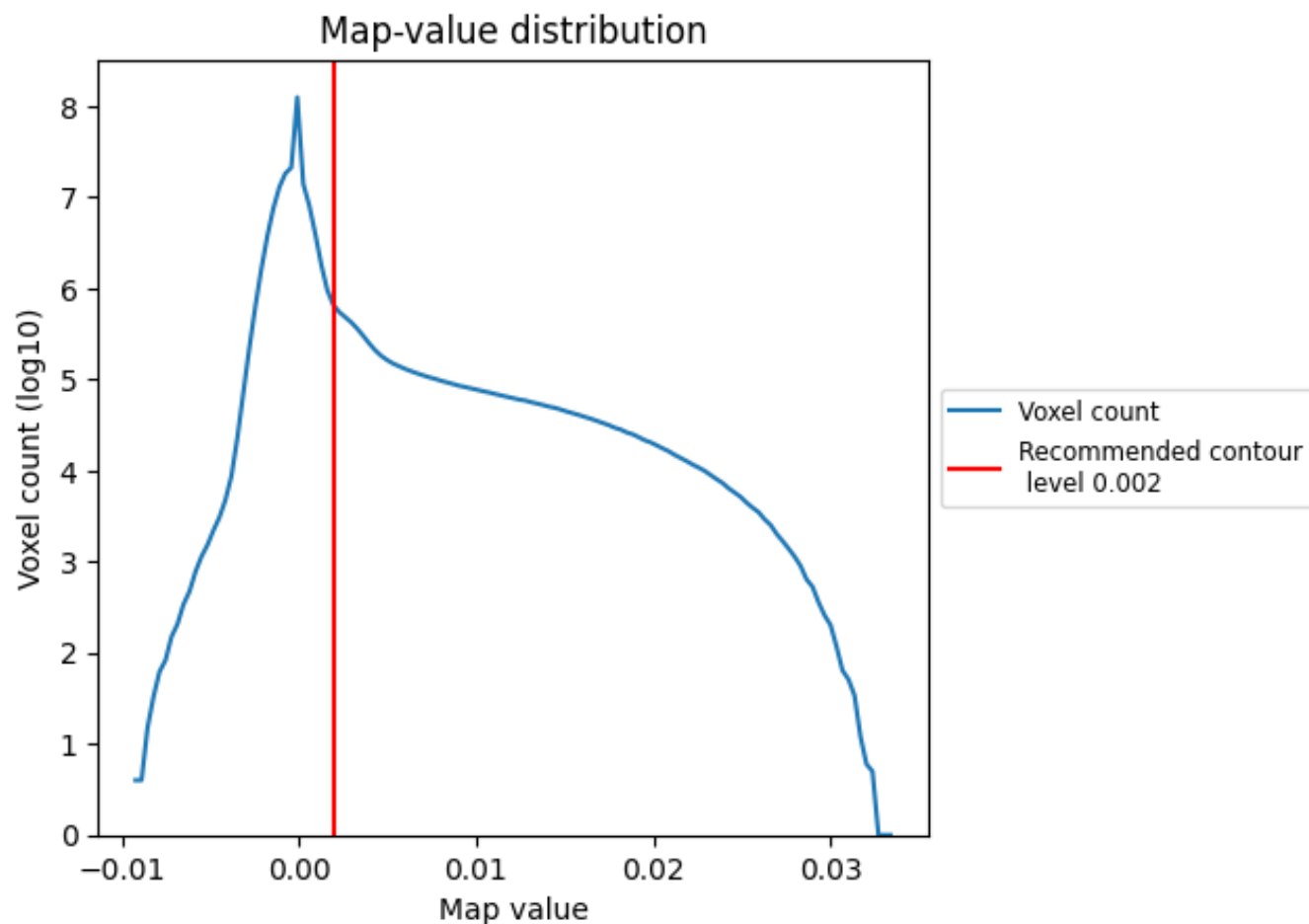
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

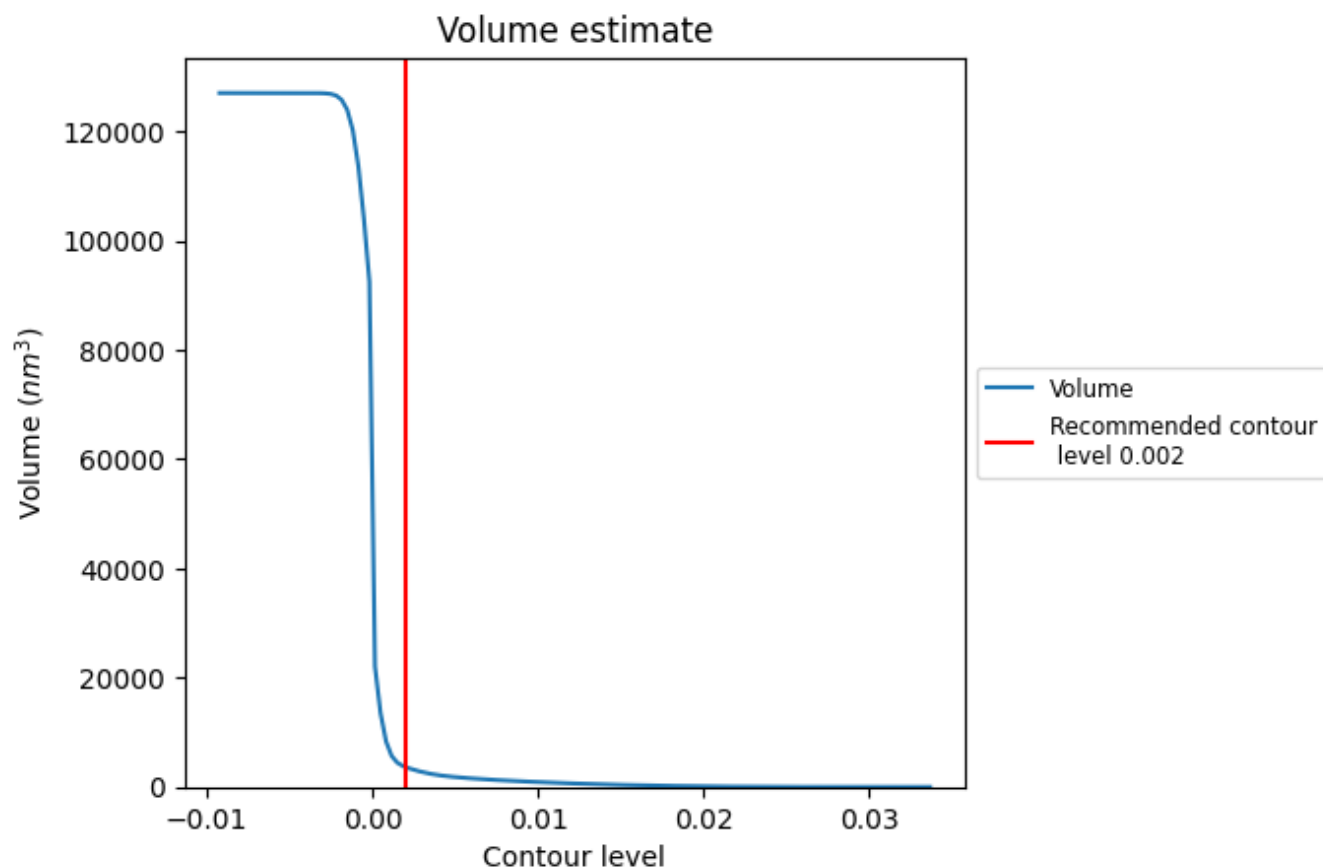
This section contains the results of statistical analysis of the map.

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.

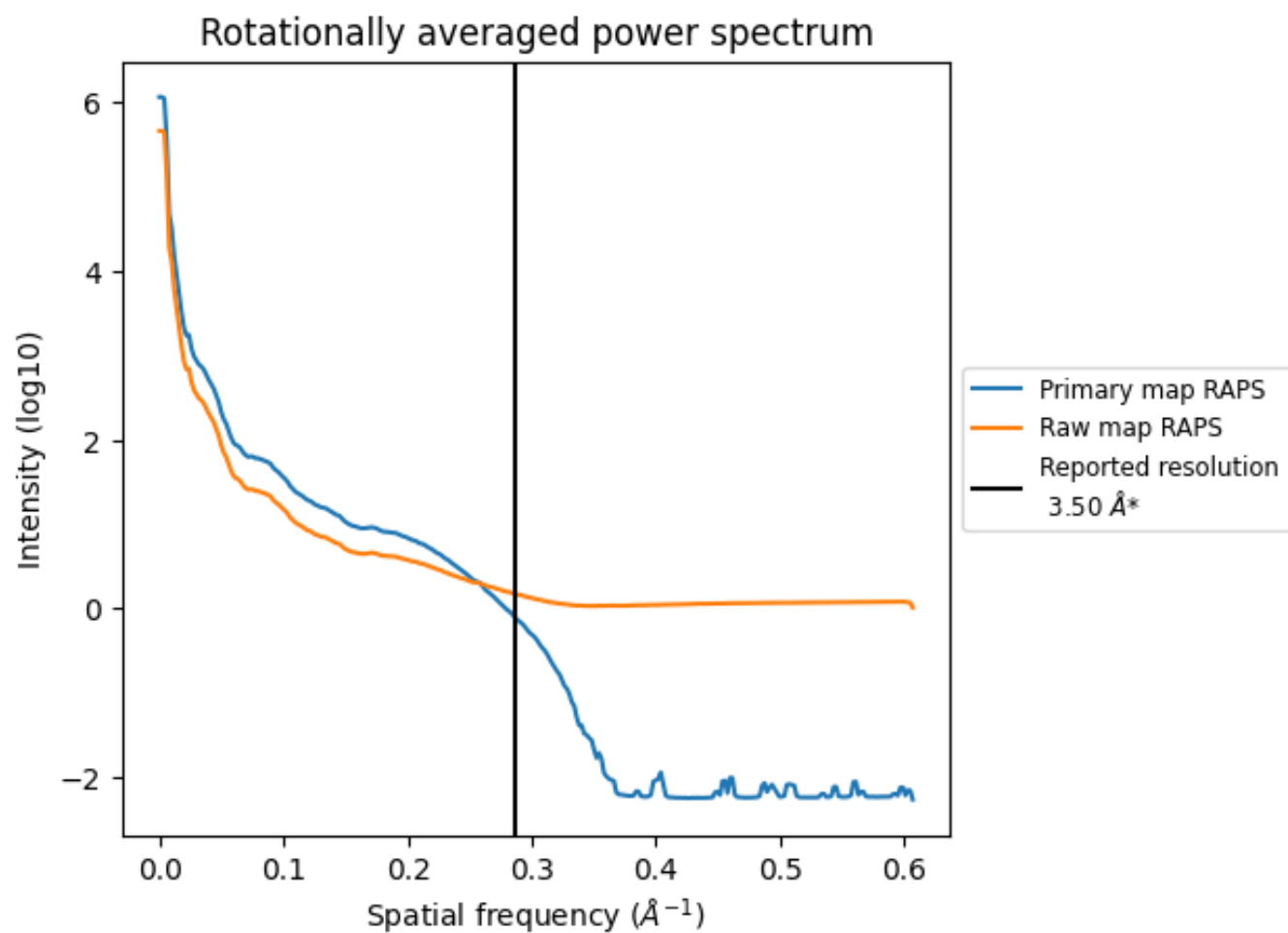
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3664 nm³; this corresponds to an approximate mass of 3309 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 ⓘ

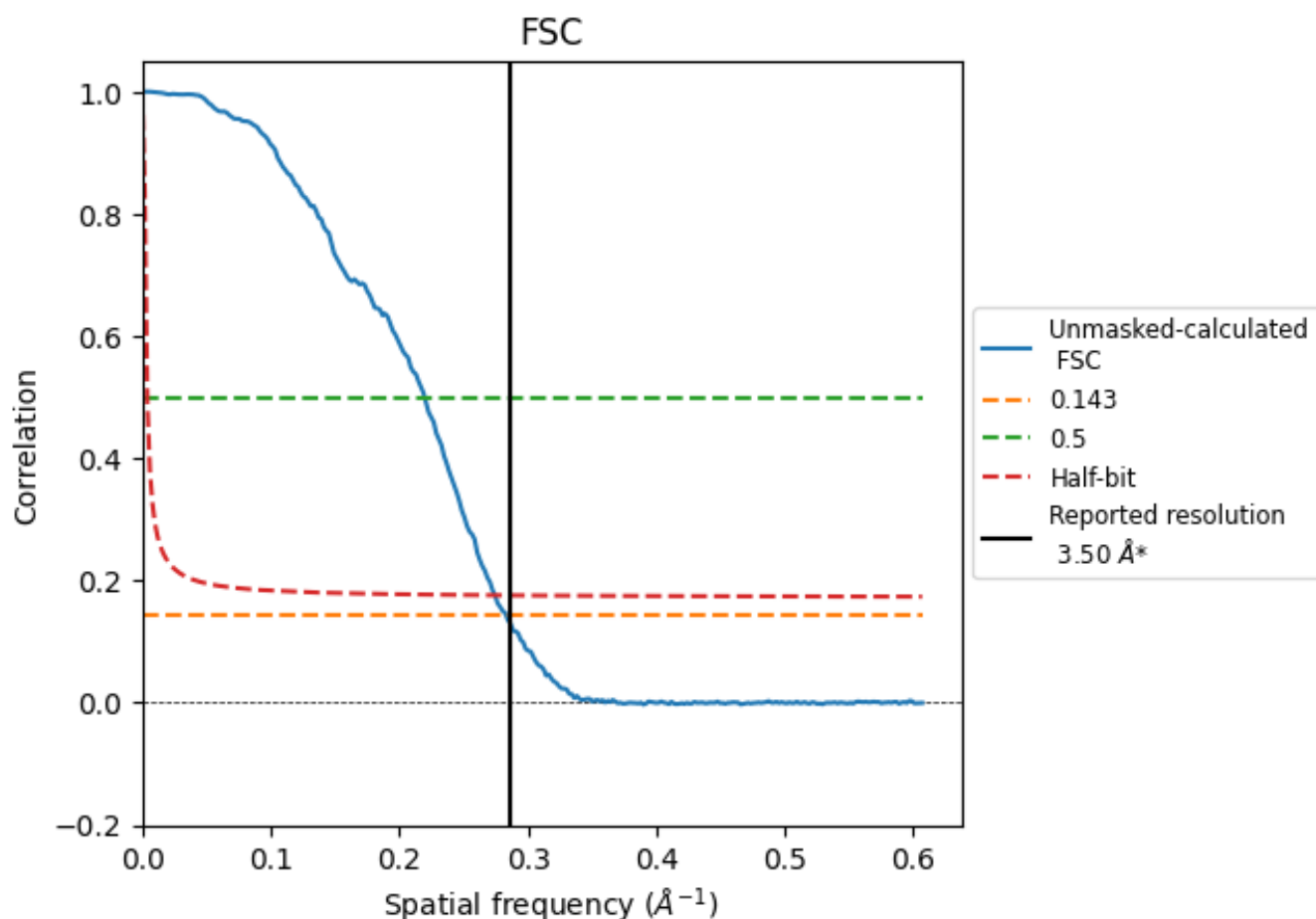


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

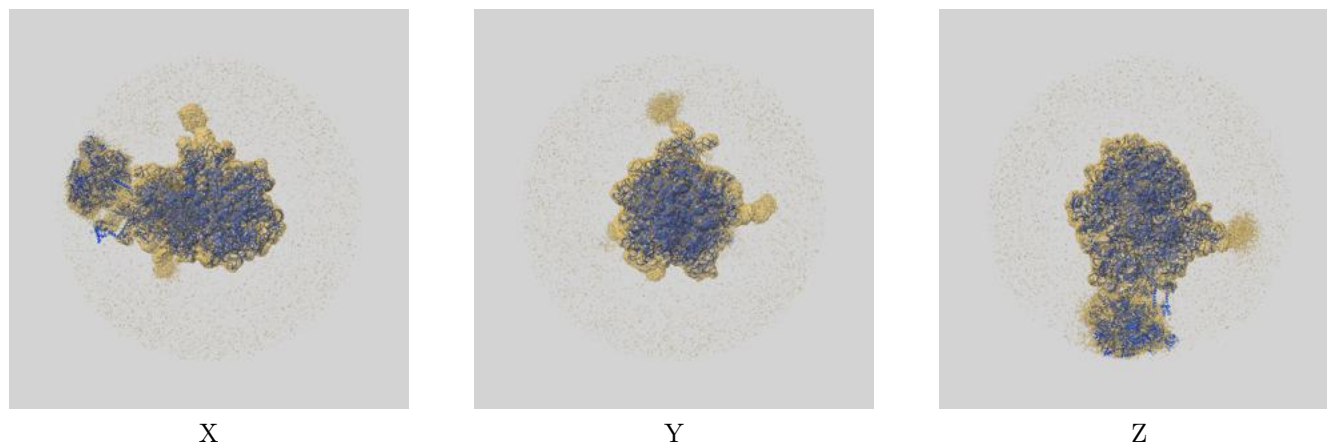
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.53	4.55	3.64

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

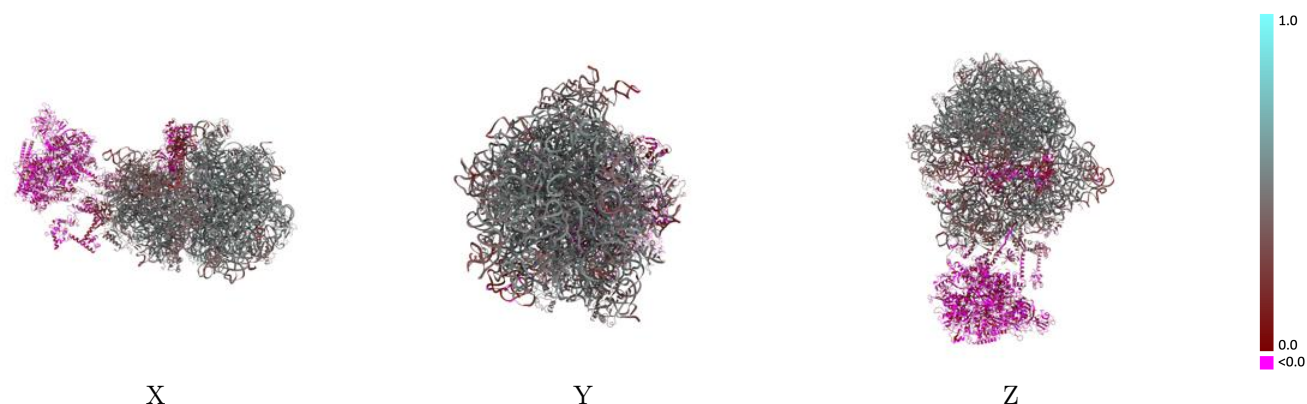
This section contains information regarding the fit between EMDB map EMD-65509 and PDB model 9W0N. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



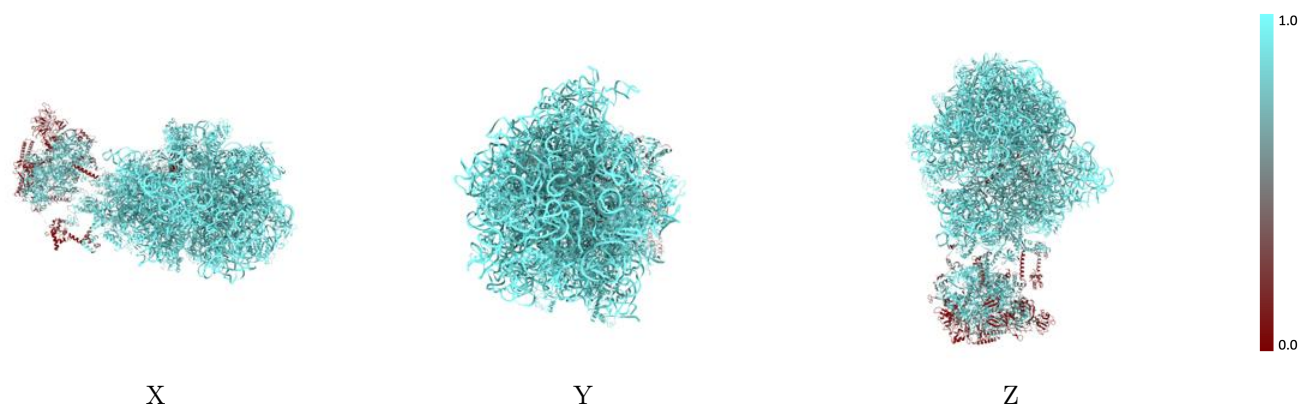
The images above show the 3D surface view of the map at the recommended contour level 0.002 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



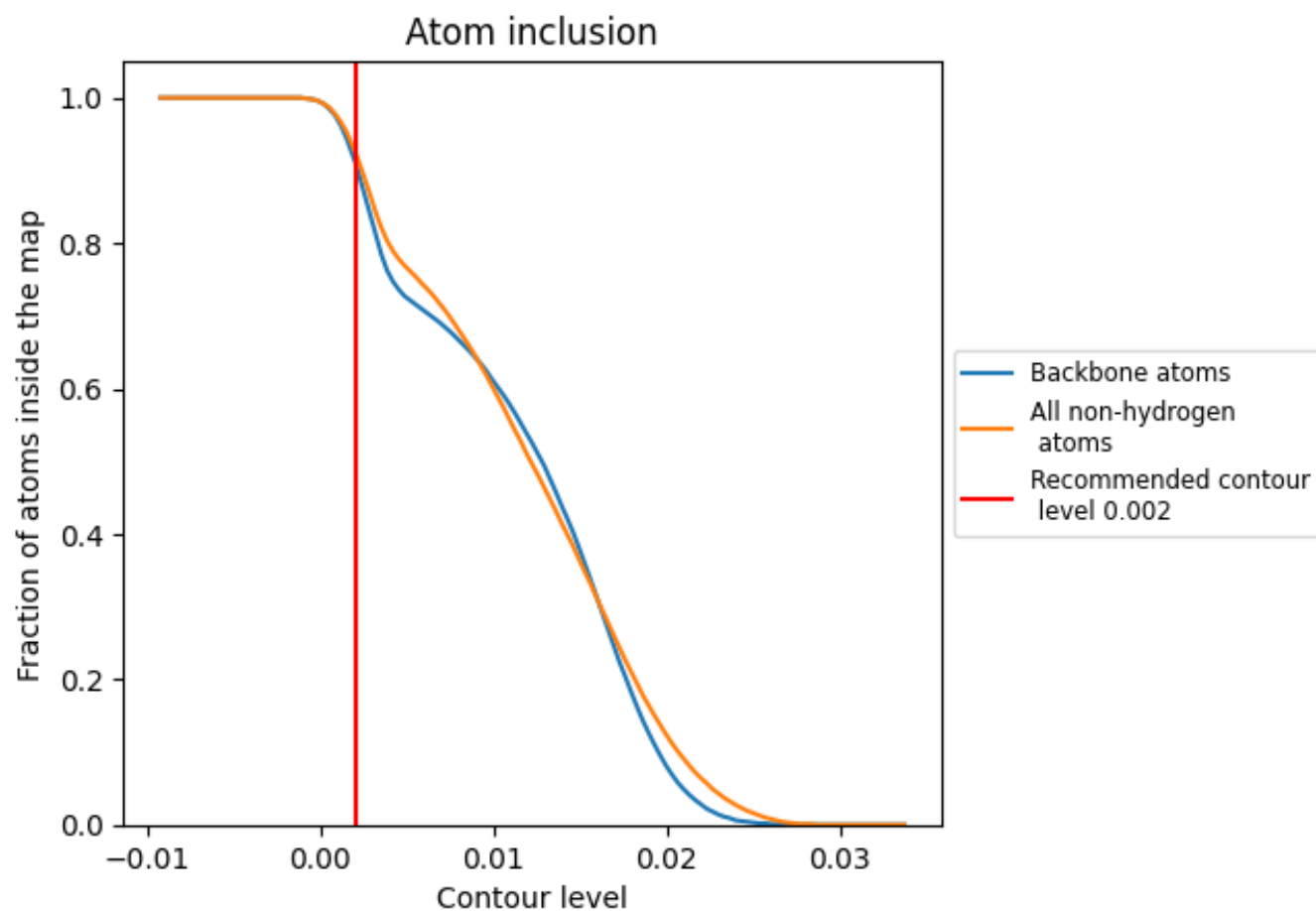
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.002).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.002) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9260	 0.3590
0	 0.7290	 0.1150
1	 0.9990	 0.4630
2	 0.9990	 0.4360
3	 0.9990	 0.4440
4	 0.9100	 0.0710
5	 0.9250	 0.1350
6	 0.9460	 0.2030
7	 0.7410	 0.0440
8	 0.8870	 0.0450
9	 0.9160	 -0.0060
A	 0.8690	 0.2560
AA	 0.4040	 -0.0150
B	 0.9860	 0.4880
B2	 0.6850	 0.0090
BA	 0.6300	 0.0170
C	 0.9730	 0.4350
D	 0.9750	 0.5000
E	 0.9820	 0.5060
F	 0.9760	 0.4440
G	 0.9680	 0.3890
H	 0.9580	 0.3990
I	 0.9740	 0.3480
J	 0.9780	 0.4580
K	 0.9650	 0.3950
L	 0.9700	 0.3910
M	 0.9660	 0.4590
N	 0.9860	 0.4040
NA	 0.6740	 0.0900
O	 0.9490	 0.3430
P	 0.9720	 0.4230
Q	 0.9300	 0.3130
R	 0.9850	 0.3920
S	 0.9720	 0.3810
T	 0.9750	 0.4240



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Chain	Atom inclusion	Q-score
U	 0.9570	 0.3940
V	 0.9670	 0.4050
W	 0.9770	 0.4150
X	 0.9790	 0.3360
Y	 0.9630	 0.3850
Z	 0.8960	 0.2530
a	 0.3710	 0.0130
b	 0.9850	 0.5110
c	 0.9820	 0.4930
d	 0.9690	 0.4440
e	 0.9710	 0.3520
f	 0.9670	 0.3910
g	 0.9850	 0.3820
h	 0.7510	 0.0140
i	 0.9370	 0.0390
j	 0.9800	 0.4850
k	 0.9750	 0.4850
l	 0.9810	 0.4780
m	 0.9800	 0.4730
n	 0.9960	 0.4870
o	 0.9870	 0.4150
p	 0.9740	 0.4810
q	 0.9810	 0.4910
r	 0.9670	 0.4650
s	 0.9700	 0.4710
t	 0.9610	 0.4350
u	 0.9800	 0.4400
v	 0.9770	 0.4450
w	 0.9930	 0.4860
x	 0.9770	 0.4850
y	 0.9740	 0.3870
z	 0.9840	 0.4760