



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:23 AM UTC

PDB ID : 8VIO / pdb_00008vio
EMDB ID : EMD-43267
Title : Structure of Mycobacterium smegmatis HflX bound to a 70S ribosome
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.;
Agrawal, R.K.
Deposited on : 2024-01-05
Resolution : 3.26 Å (reported)
Based on initial models : 5O61, 6DZI

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

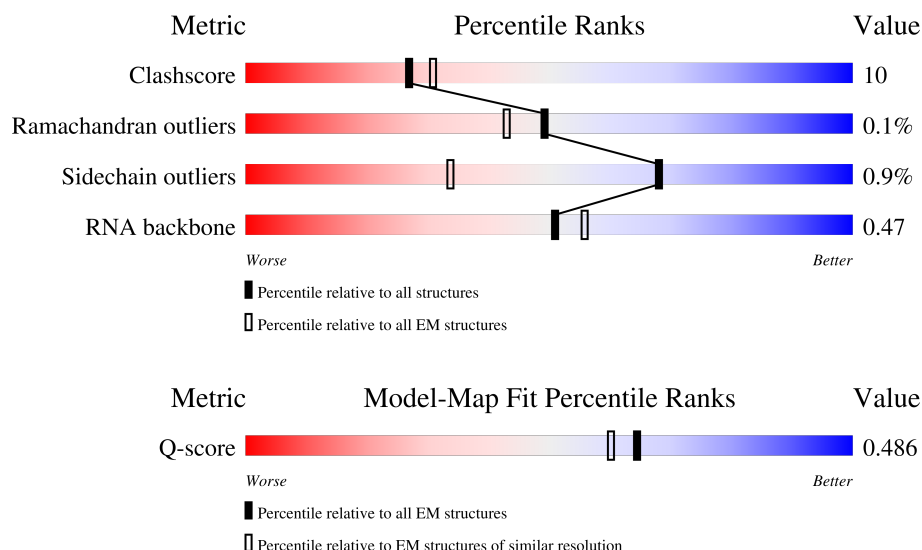
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.26 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.



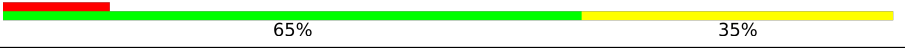
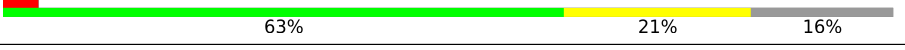
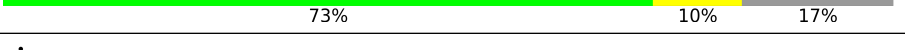
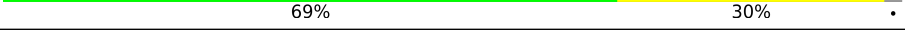
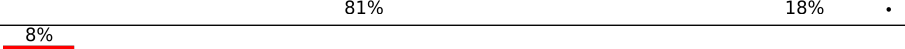
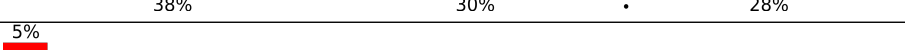
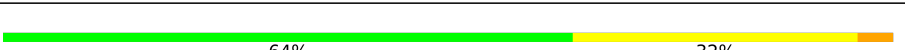
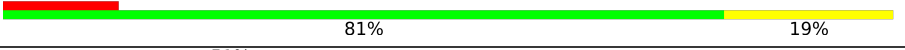
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14557 (2.76 - 3.76)

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	Y	64	
2	c	55	
3	g	75	

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Mol	Chain	Length	Quality of chain
4	r	84	
5	l	33	
6	j	201	
7	k	214	
8	l	96	
9	n	132	
10	q	138	
11	s	124	
12	v	89	
13	w	156	
14	x	98	
15	z	86	
16	h	277	
17	3	24	
18	A	3120	
19	B	118	
20	C	278	
21	D	217	
22	E	215	
23	F	187	
24	G	179	
25	H	151	
26	I	175	
27	J	142	
28	K	147	

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Mol	Chain	Length	Quality of chain
29	L	122	
30	M	147	
31	N	138	
32	O	199	
33	P	127	
34	Q	113	
35	R	129	
36	S	103	
37	T	153	
38	U	100	
39	V	105	
40	W	215	
41	X	88	
42	Z	77	
43	2	61	
44	b	57	
45	d	47	
46	e	64	
47	f	37	
48	5	77	
49	a	1528	
50	i	275	
51	m	156	
52	o	150	
53	p	101	

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Mol	Chain	Length	Quality of chain
54	t	124	23%49%38%13%
55	y	93	13%53%35%12%
56	4	470	55%40%17%43%
57	u	61	34%57%7%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 152629 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 L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 2 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 3 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 4 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	r	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 5 is a protein called Conserved domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	j	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 7 is a protein called 30S Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	k	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	l	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 9 is a protein called 30S Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	n	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	q	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	s	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 12 is a protein called 30S Ribosomal Protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	v	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 13 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	w	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 14 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	x	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 15 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	z	85	Total	C	N	O		0	0
			660	402	139	119			

- Molecule 16 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 17 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	3	23	Total	C	N	O		0	0
			189	111	50	28			

- Molecule 18 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 19 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 20 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 21 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 22 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 23 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 24 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 25 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 26 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 27 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 28 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	K	145	Total	C	N	O	S	0	0
			1125	719	206	199	1		

- Molecule 29 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 30 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 31 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 32 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 33 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	P	126	Total	C	N	O	S	0	0
			956	586	199	171			

- Molecule 34 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 35 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	R	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 36 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	S	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 37 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 38 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 39 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 40 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 41 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 44 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 45 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 46 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	e	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 47 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 48 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 49 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	a	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 50 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	i	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 51 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	m	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 52 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	o	126	Total	C	N	O		0	0
			994	630	194	170			

- Molecule 53 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	p	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 54 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	t	108	Total	C	N	O	S	0	0
			877	535	180	159	3		

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 56 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	267	Total	C	N	O	S	0	0
			2058	1275	383	397	3		

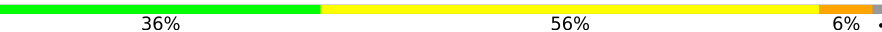
- Molecule 57 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	u	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

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 L28

Chain Y: 



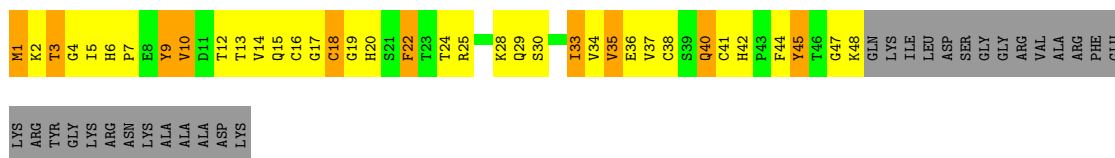
- Molecule 2: 50S Ribosomal Protein L33

Chain c: 



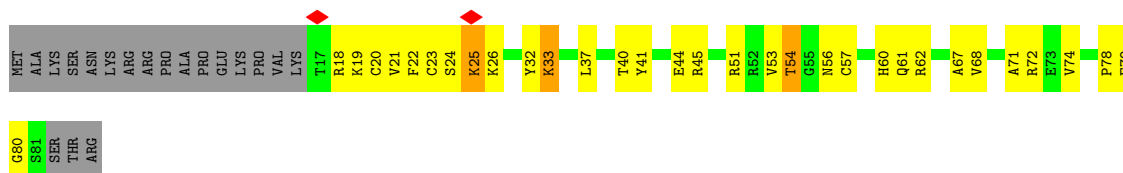
- Molecule 3: 50S Ribosomal Protein L31

Chain g: 



- Molecule 4: 30S Ribosomal Protein S18

Chain r: 



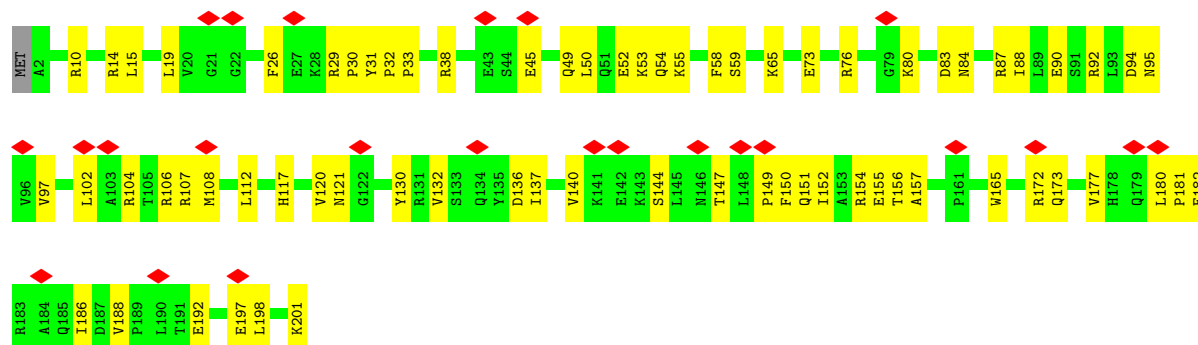
- Molecule 5: Conserved domain protein

Chain 1: 

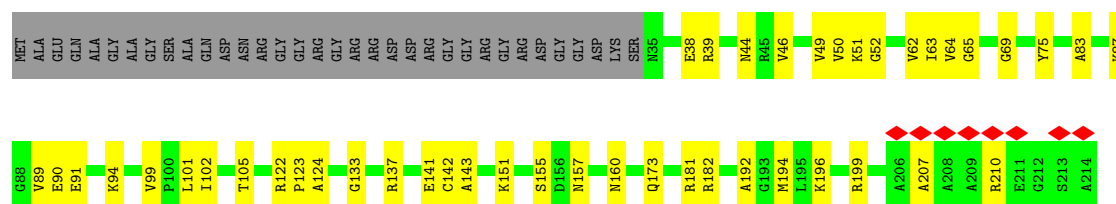




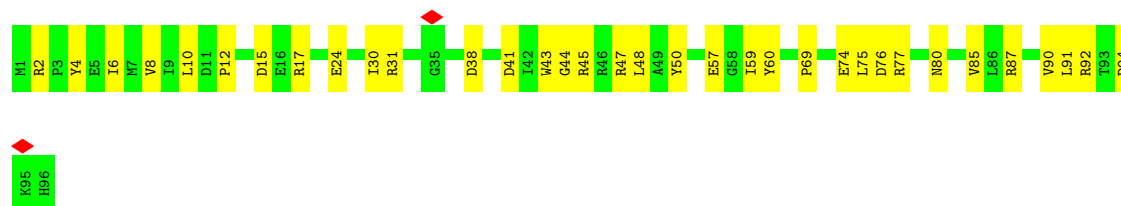
- Molecule 6: 30S ribosomal protein S4



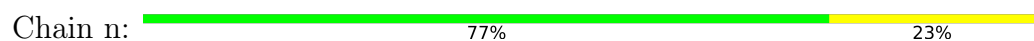
- Molecule 7: 30S Ribosomal Protein S5



- Molecule 8: 30S ribosomal protein S6



- Molecule 9: 30S Ribosomal Protein S8

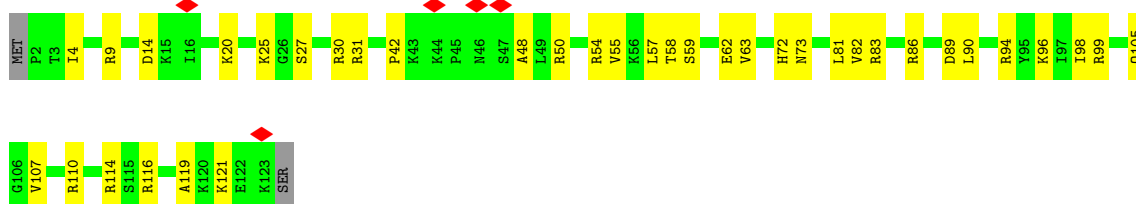


- Molecule 10: 30S ribosomal protein S11

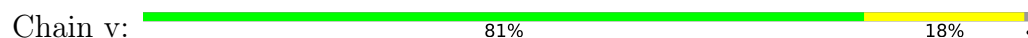




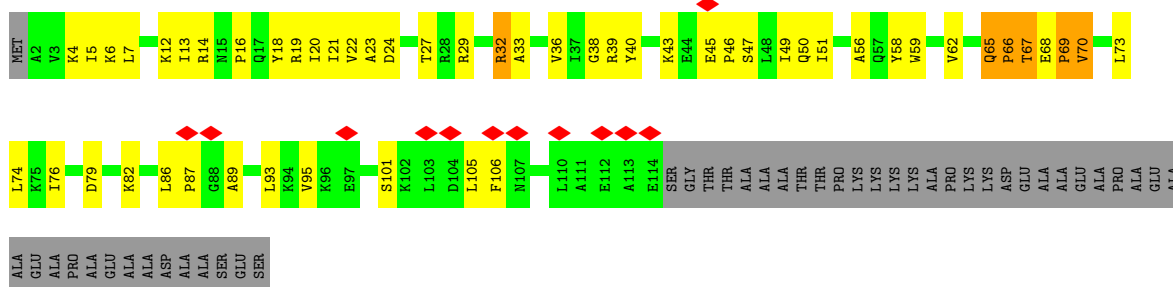
• Molecule 11: 30S ribosomal protein S12



• Molecule 12: 30S Ribosomal Protein S15



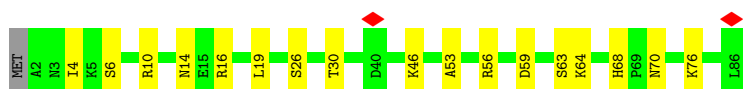
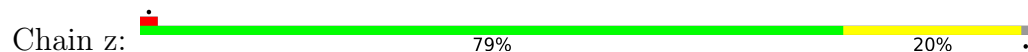
• Molecule 13: 30S ribosomal protein S16



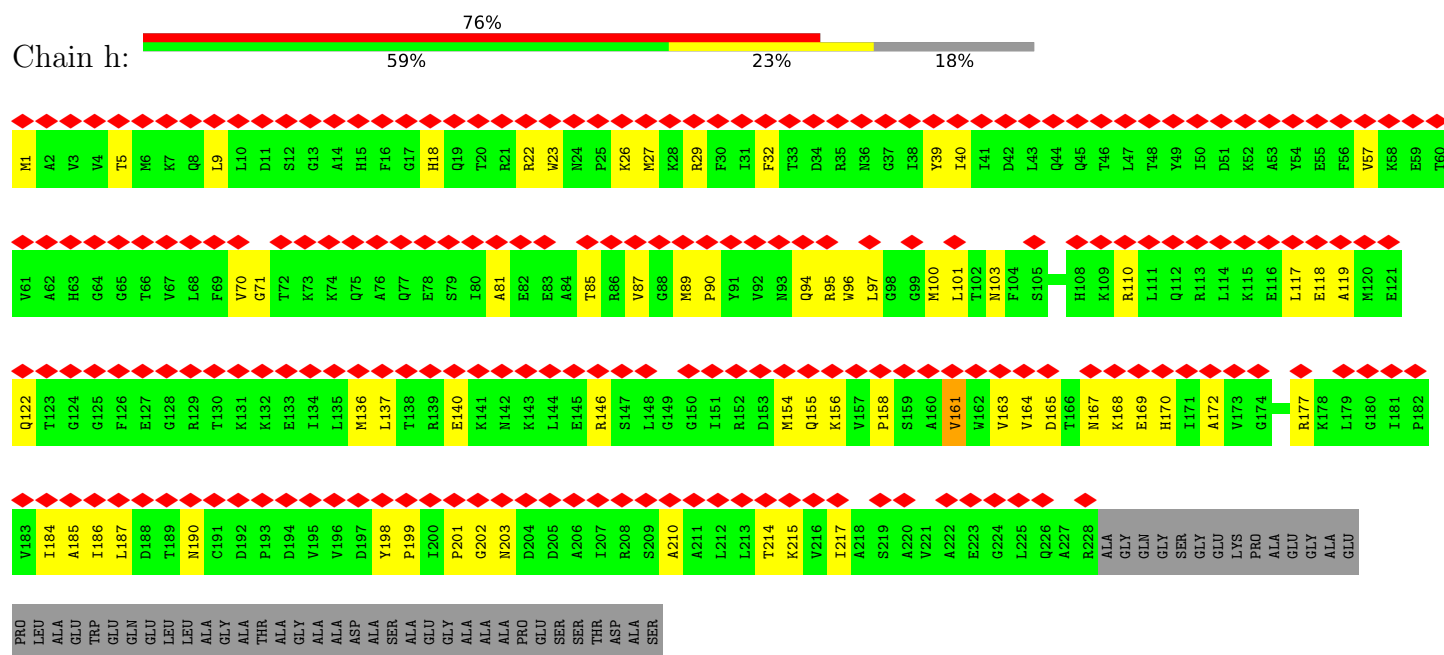
• Molecule 14: 30S ribosomal protein S17



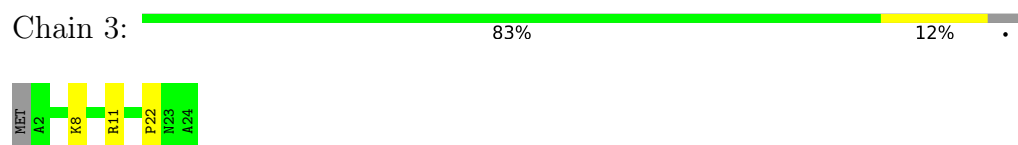
• Molecule 15: 30S ribosomal protein S20



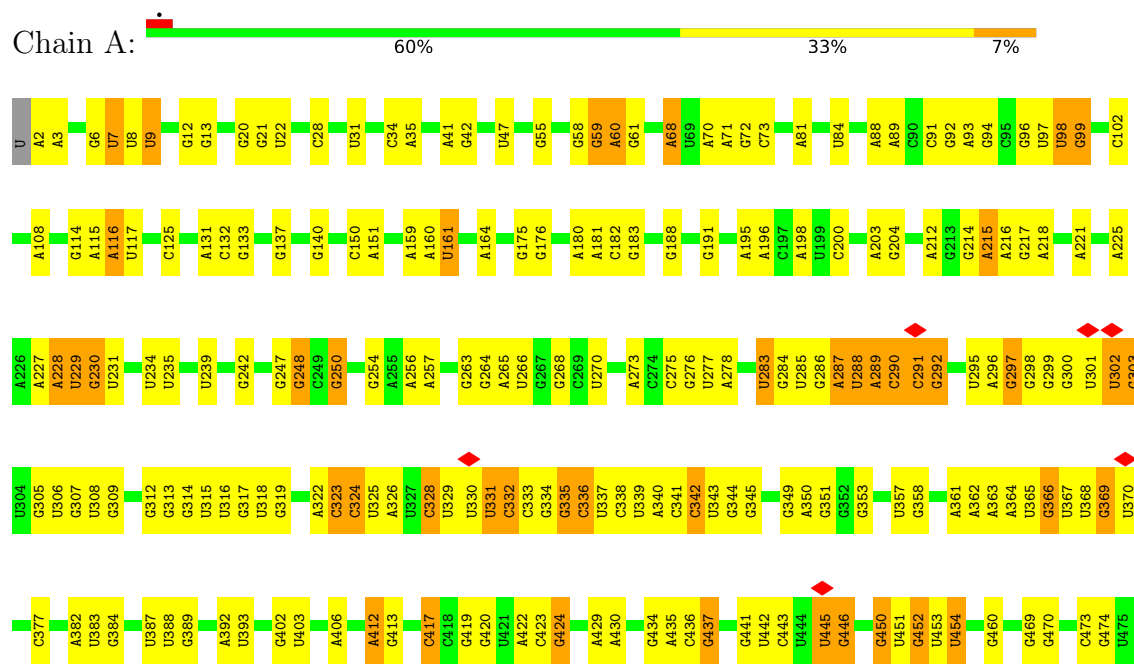
- Molecule 16: 30S Ribosomal Protein S2



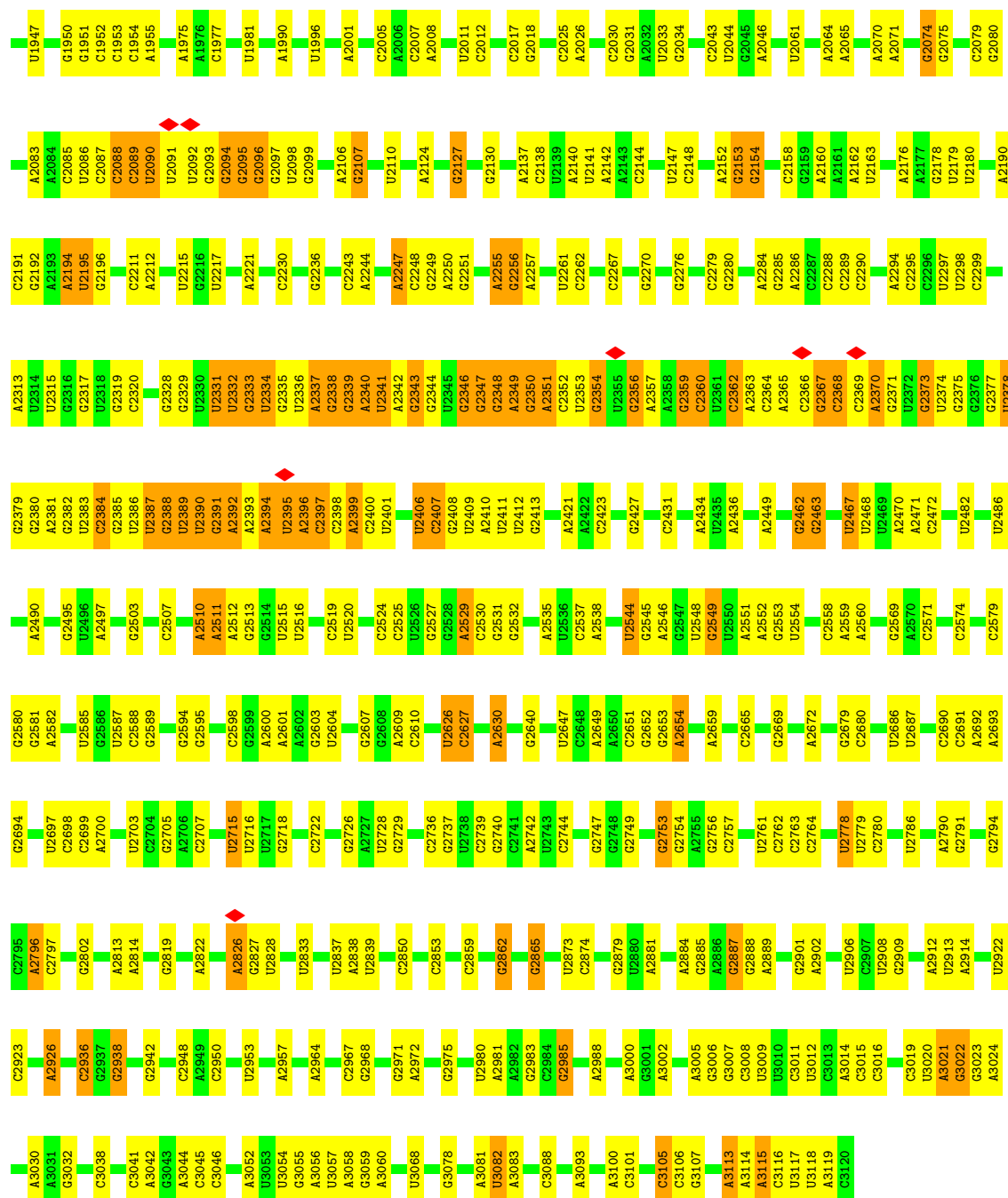
- Molecule 17: 50S Ribosomal Protein L37



- Molecule 18: 23S ribosomal RNA



U1798	G1696	U1608	C1548	C1465	G1339	U1223	C1159	G1083	U947	A800	C692	G608	C476
G1803	A1803	G1609	G1549	C1466	G1343	G1224	G1160	G1063	G948	U801	C696	G609	C481
G1804	C1610	C1610	U1467	U1467	G1344	G1225	C1161	C1068	C949	A808	A696	C610	U482
G1805	U1611	U1611	A1468	A1468	G1345	C1227	A1163	G1072	A950	G815	U699	U617	G483
U1809	C1705	G1613	C1552	C1472	U1349	A1228	A1164	U1076	A958	C705	C618	C619	C484
A1810	A1706	A1616	U1554	G1473	G1350	A1229	G1165	A1076	U959	A830	C706	G620	A489
C1811	G1707	C1617	A1555	A1474	G1351	U1231	A1166	A1077	G960	A831	G707	U621	A490
G1815	A1714	G1621	A1556	G1475	G1352	G1232	A1168	G1078	G967	G832	U709	C622	C492
U1816	C1715	G1622	C1557	C1476	G1353	A1233	U1171	C1079	C968	U839	G716	U493	U494
C1818	A1716	G1623	A1558	C1477	A1362	U1234	C1171	U1080	G974	C845	G717	A633	G499
G1819	U1717	U1624	A1559	A1478	G1363	G1236	G1173	C1082	U975	C718	C718	C634	G498
C1825	C1718	G1625	C1561	A1480	U1364	U1237	A1174	U1083	U976	U857	A721	G635	G499
A1826	G1719	G1626	G1486	G1477	G1365	G1238	G1175	A1084	G977	A858	G728	U636	C502
A1834	G1720	U1627	U1487	U1487	A1366	C1239	G1177	C1086	A978	G729	G742	G637	A503
U1723	U1723	A1628	A1493	A1493	G1367	G1240	U1178	G1087	G979	U862	U734	U641	G504
A1727	U1728	U1629	U1494	U1494	A1368	U1245	U1179	U1088	C980	G863	G735	G642	C505
G1840	U1729	A1630	U1499	U1499	A1369	U1250	G1180	A1091	U981	A731	U735	G643	A511
G1849	G1632	G1632	A1500	A1500	U1370	A1251	C1181	G1092	A982	G872	A738	G644	G512
A1850	U1730	U1633	C1501	C1501	G1371	G1252	U1183	A1093	G986	C879	A739	G645	A517
C1851	C1634	C1634	G1502	G1502	A1377	G1253	U1184	G1094	C992	A879	A740	U644	A520
A1852	A1635	A1635	U1506	U1506	G1378	G1254	A1185	A1101	C993	G880	A746	G645	A517
A1853	A1636	A1636	G1507	G1507	A1380	G1255	G1186	G1102	G994	U888	U739	U646	A520
C1854	G1637	G1637	A1508	A1508	G1381	G1256	A1187	G1103	U995	A898	A748	G665	A554
A1855	G1638	G1638	U1509	U1509	U1382	G1257	A1188	C1105	G996	G890	G741	G666	G555
C1856	A1639	A1639	A1510	A1510	G1386	C1258	G1189	G1112	C997	G891	G742	U654	U544
U1864	G1640	G1640	U1511	U1511	A1387	U1259	C1190	G1113	G998	G745	G745	G655	G551
U1865	U1641	U1641	A1514	A1514	U1388	G1260	A1191	G1114	A896	A747	U748	A663	A567
A1866	G1642	G1642	C1515	C1515	A1389	A1261	G1192	G1115	C1000	A897	A753	A664	A568
C1867	A1648	A1648	A1518	A1518	C1410	G1270	C1193	A1118	C1001	A898	A754	G670	G569
G1868	G1649	G1649	G1522	G1522	A1415	G1273	C1194	A1119	C1002	G900	A755	G671	A571
A1869	G1650	G1650	U1529	U1529	A1416	A1274	A1195	G1143	A1003	A908	A756	C672	U570
C1870	C1651	C1651	G1530	G1530	G1425	G1281	C1198	A1144	C1004	G920	A757	U674	G587
G1871	A1652	A1652	U1531	U1531	U1428	C1282	U1199	A1145	A1005	C927	A758	A588	A588
U1872	A1656	A1656	G1532	G1532	A1429	A1283	U1200	U1151	G1006	U928	U767	A590	A599
U1877	G1657	G1657	U1533	U1533	C1430	G1284	G1201	U1152	G1007	C929	G768	C681	G591
A1886	G1664	G1664	G1534	G1534	U1431	U1292	A1203	U1153	G1008	A917	A768	A682	A592
A1887	A1673	A1673	C1535	C1535	C1435	G1293	A1204	G1154	U1009	G932	G771	G683	G593
C1888	G1674	G1674	U1536	U1536	C1436	U1294	G1205	A1144	U1010	G933	U772	G684	U594
G1892	U1675	U1675	U1537	U1537	C1440	U1295	G1207	U1155	A1011	A934	G773	G685	A595
U1900	G1676	G1676	G1538	G1538	U1444	C1298	U1208	G1157	C1012	A935	G774	A688	C596
C1901	G1677	G1677	U1539	U1539	U1445	G1302	G1211	U1158	U1013	U941	G784	G690	G605
G1905	A1681	A1681	U1540	U1540	G1456	U1303	U1212	U1159	G1014	U942		U691	
G1920	C1684	C1684	A1542	A1542	G1457	C1318	A1213	C1037	A1025	C927	G765	A678	
G1933	G1685	G1685	A1543	A1543	G1458	U1318	U1214	U1159	A1026	U928	G766	U680	
U1937	A1690	A1690	U1544	U1544	U1459	G1326	A1215	U1154	C1037	C929	U767	C681	
	A1791	A1791	C1545	C1545	G1462	G1335	A1216	G1154	U1044	A935	G774	A688	
G1938	G1692	G1692	U1546	U1546	G1462		U1219	U1157	A1047	U942		G690	
			G1547	G1547			A1221	C1220	A1048			U691	
							C1222		G1049				



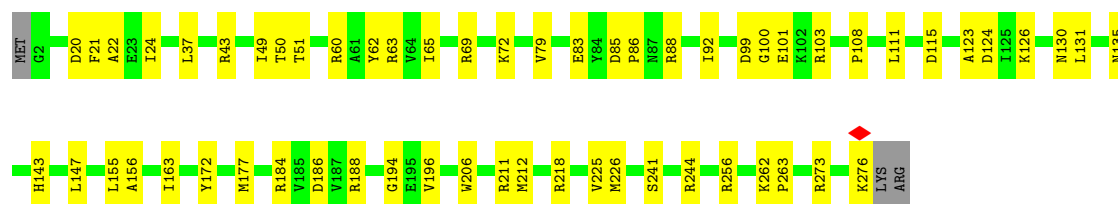
• Molecule 19: 5S ribosomal RNA

Chain B: 64% 32%



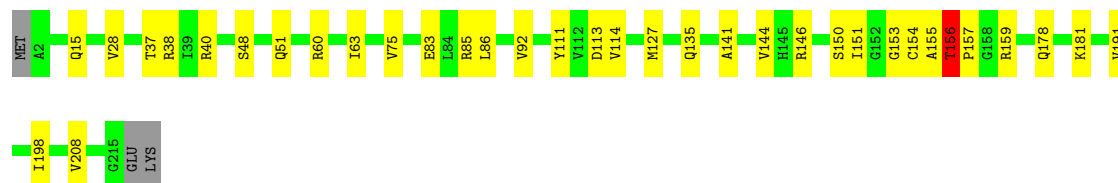
• Molecule 20: 50S ribosomal protein L2

Chain C:  78% 21% .



- Molecule 21: 50S ribosomal protein L3

Chain D:  82% 16% .



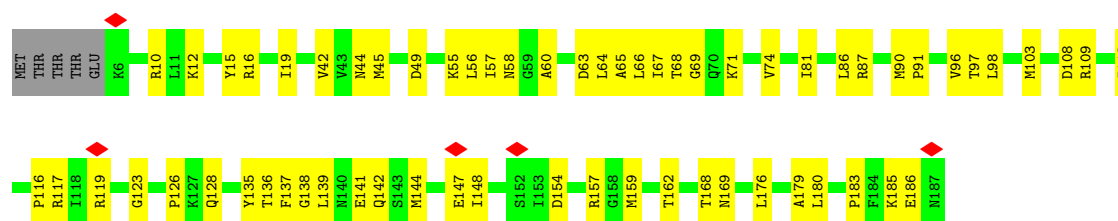
- Molecule 22: 50S Ribosomal Protein L4

Chain E:  85% 13% .



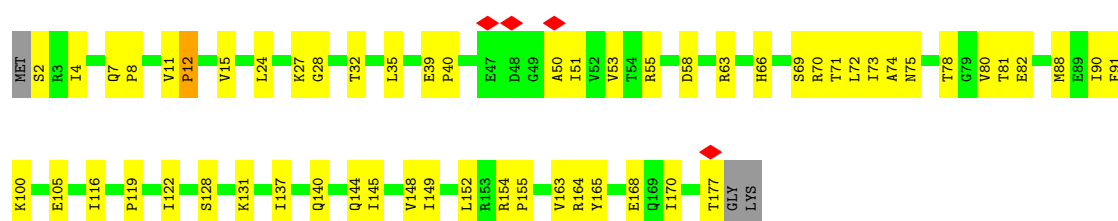
- Molecule 23: 50S Ribosomal Protein L5

Chain F:  64% 34% .

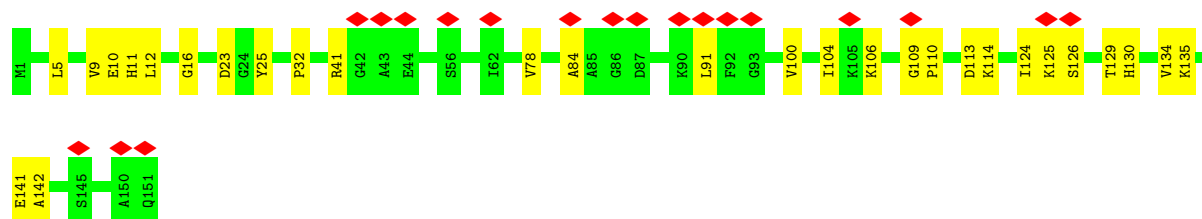
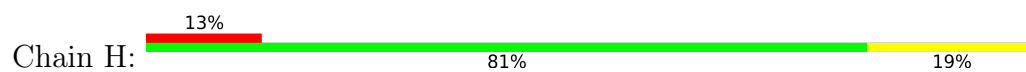


- Molecule 24: 50S ribosomal protein L6

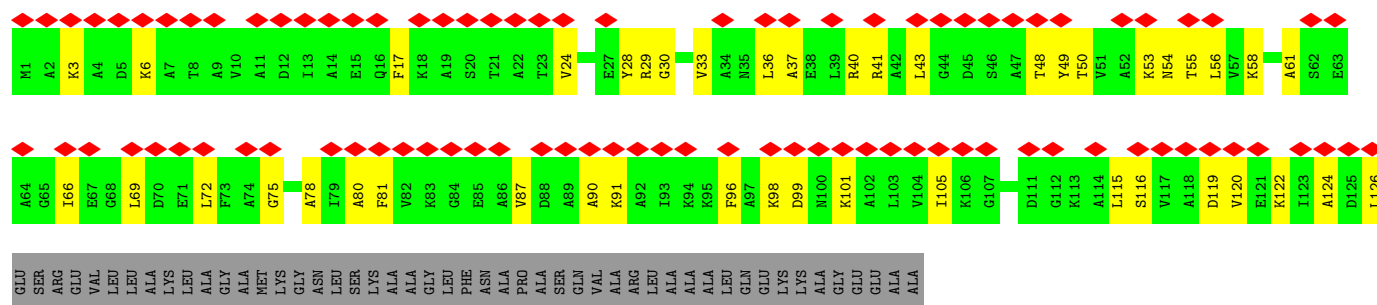
Chain G:  66% 31% .



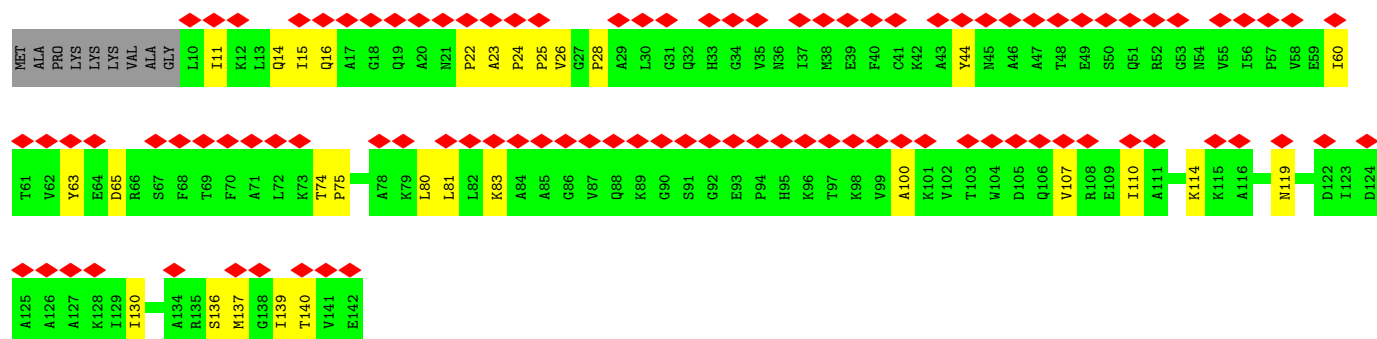
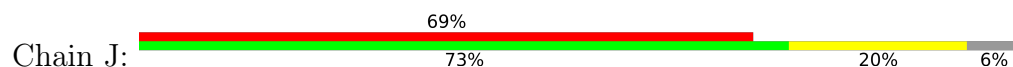
- Molecule 25: 50S ribosomal protein L9



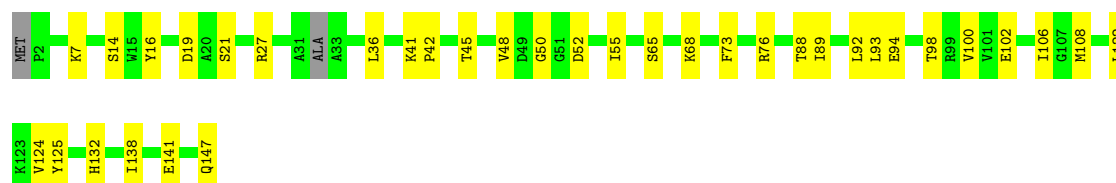
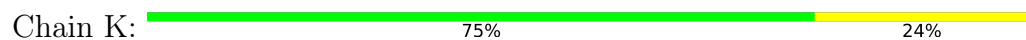
- Molecule 26: 50S ribosomal protein L10



- Molecule 27: 50S ribosomal protein L11



- Molecule 28: 50S Ribosomal Protein L13



- Molecule 29: 50S ribosomal protein L14

M1	L2	L8	D12	I22	R23	V24	R30	R31	Y32	A33	D37	K59	Y76	I77	K78	F79	N82	P93	R107	M112	K113	I114	V115	V121	L122
----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------

- | |
|------|
| MET |
| SER |
| V3 |
| H7 |
| R21 |
| V22 |
| G23 |
| R24 |
| S28 |
| K29 |
| T32 |
| E51 |
| G52 |
| G53 |
| Q54 |
| M55 |
| M59 |
| R60 |
| L61 |
| K65 |
| Q76 |
| V80 |
| N84 |
| G94 |
| V95 |
| D96 |
| E97 |
| L98 |
| V99 |
| V104 |
| S108 |
| L109 |
| V110 |
| L113 |
| L118 |
| N127 |
| S130 |
| |
| |

- | | | | | | | | | | |
|----|------|------|------|------|------|------|------|-----|-----|
| K1 | L20 | G30 | I42 | S49 | A50 | I58 | K59 | R60 | K63 | V64 | W65 | I66 | N67 | P70 | D71 | M83 | K87 | E91 | Y92 | A95 | N96 | V97 | E105 | R120 | A121 | K124 | R134 | E135 | I136 | G1N | P1F |
|----|------|------|------|------|------|------|------|-----|-----|

- | | | |
|-----|-----|------|
| ALA | ARG | MET |
| GLU | ARG | P2 |
| GLU | ALA | K3 |
| SER | ALA | P4 |
| GLU | ALA | |
| ALA | SER | G7 |
| LYS | GLN | P6 |
| ASP | ALA | R9 |
| ASP | LYS | L10 |
| THR | ALA | |
| LYS | ASP | S14 |
| | GLU | |
| | ARG | T37 |
| | ALA | E38 |
| | ASP | P39 |
| | GLU | K40 |
| | LYS | A41 |
| | ALA | R42 |
| | ASP | |
| | GLU | R45 |
| | LYS | |
| | ALA | E49 |
| | GLU | |
| | GLU | K57 |
| | THR | |
| | VAL | N62 |
| | GLU | |
| | GLU | I70 |
| | THR | R71 |
| | THR | D72 |
| | GLU | K73 |
| | ALA | |
| | PRO | V76 |
| | ALA | |
| | GLU | Y87 |
| | GLU | A88 |
| | SER | D89 |
| | THR | |
| | GLU | T95 |
| | ALA | |
| | ALA | R103 |
| | ALA | |
| | GLU | D106 |
| | GLU | |
| | THR | M110 |
| | VAL | |
| | GLU | L115 |
| | GLU | V116 |
| | THR | R117 |
| | THR | E118 |
| | GLU | K119 |
| | ALA | THR |
| | PRO | VAL |
| | ALA | THR |
| | GLU | ASP |
| | GLU | GLU |
| | SER | ALA |
| | THR | ASN |
| | GLU | ARG |
| | ALA | |

-
- | Amino Acid | Count |
|------------|-------|
| MET | 1 |
| A2 | 2 |
| H3 | 3 |
| N9 | 9 |
| I10 | 10 |
| S11 | 11 |
| E12 | 12 |
| L19 | 19 |
| R20 | 20 |
| R24 | 24 |
| L25 | 25 |
| R26 | 26 |
| V40 | 40 |
| S43 | 43 |
| A44 | 44 |
| R45 | 45 |
| H46 | 46 |
| I47 | 47 |
| H48 | 48 |
| N56 | 56 |
| S64 | 64 |
| S65 | 65 |
| D69 | 69 |
| V70 | 70 |
| I73 | 73 |
| B74 | 74 |
| G75 | 75 |
| D76 | 76 |
| K77 | 77 |
| K78 | 78 |
| S81 | 81 |
| V82 | 82 |
| R83 | 83 |
| V100 | 100 |
| V101 | 101 |
| R112 | 112 |
| I113 | 113 |
| R121 | 121 |
| L125 | 125 |
| K126 | 126 |

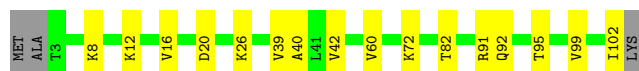
-
- | Category | Count (approx.) |
|----------|-----------------|
| M1 | 100 |
| T2 | 100 |
| M3 | 100 |
| L4 | 100 |
| D5 | 100 |
| L12 | 100 |
| P17 | 100 |
| T18 | 100 |
| F19 | 100 |
| E33 | 100 |
| R48 | 100 |
| R49 | 100 |
| Q50 | 100 |
| G51 | 100 |
| S55 | 100 |
| E56 | 100 |
| T57 | 100 |
| F58 | 100 |
| T59 | 100 |
| V60 | 100 |
| R61 | 100 |
| V69 | 100 |
| E70 | 100 |
| R71 | 100 |
| T72 | 100 |
| F73 | 100 |
| H76 | 100 |
| L83 | 100 |
| K95 | 100 |
| P113 | 100 |

- Chain R:  83% 13% .



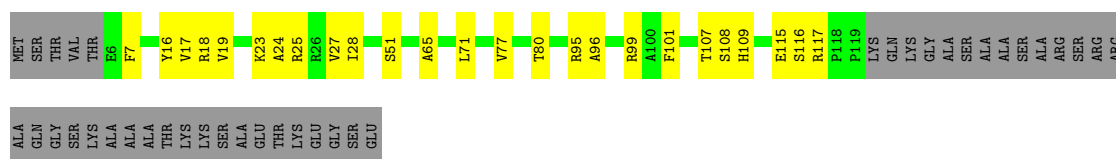
- Molecule 36: 50S Ribosomal Protein L21

Chain S: 82% 16% .



- Molecule 37: 50S Ribosomal Protein L22

Chain T: 58% 16% 25%



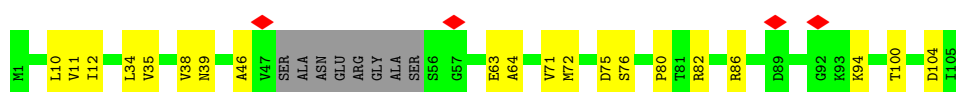
- Molecule 38: 50S Ribosomal Protein L23

Chain U: 83% 14% .



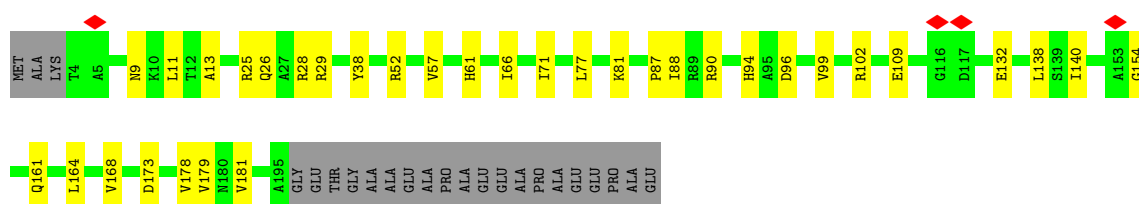
- Molecule 39: 50S ribosomal protein L24

Chain V: 73% 19% 8%



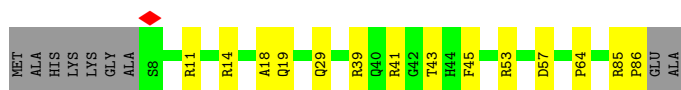
- Molecule 40: 50S ribosomal protein L25

Chain W: 73% 16% 11%



- Molecule 41: 50S ribosomal protein L27

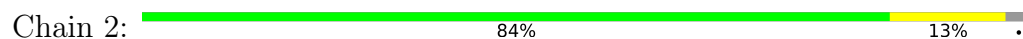
Chain X: 74% 16% 10%



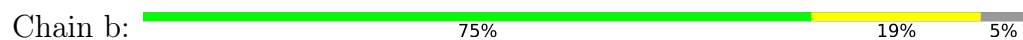
- Molecule 42: 50S ribosomal protein L29



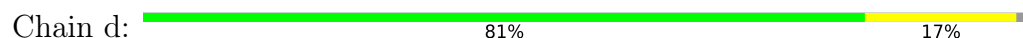
- Molecule 43: 50S ribosomal protein L30



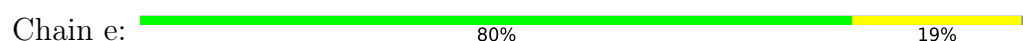
- Molecule 44: 50S ribosomal protein L32



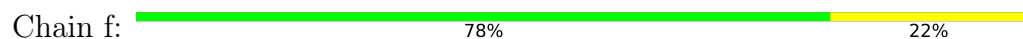
- Molecule 45: 50S ribosomal protein L34



- Molecule 46: 50S ribosomal protein L35



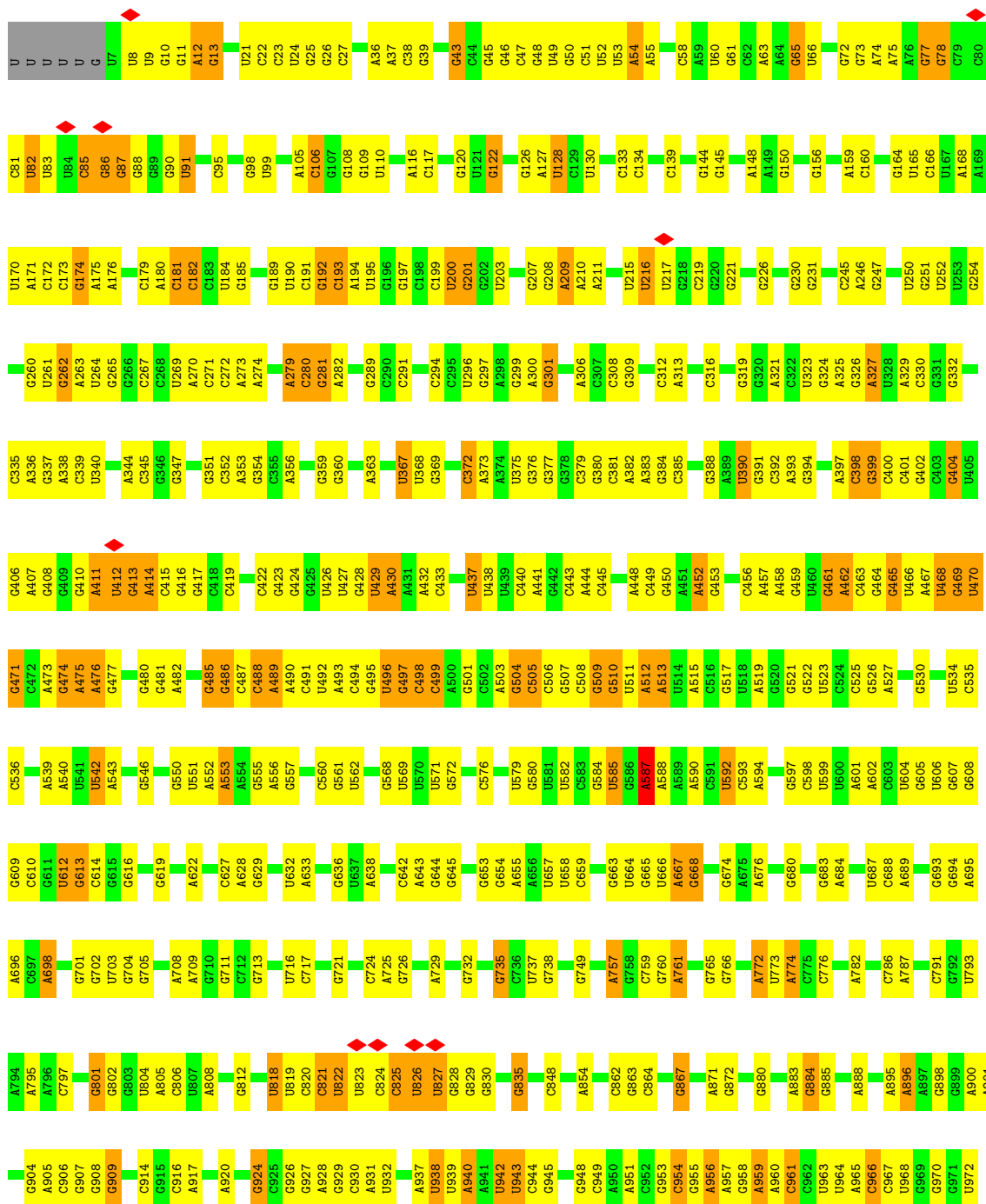
- Molecule 47: 50S ribosomal protein L36

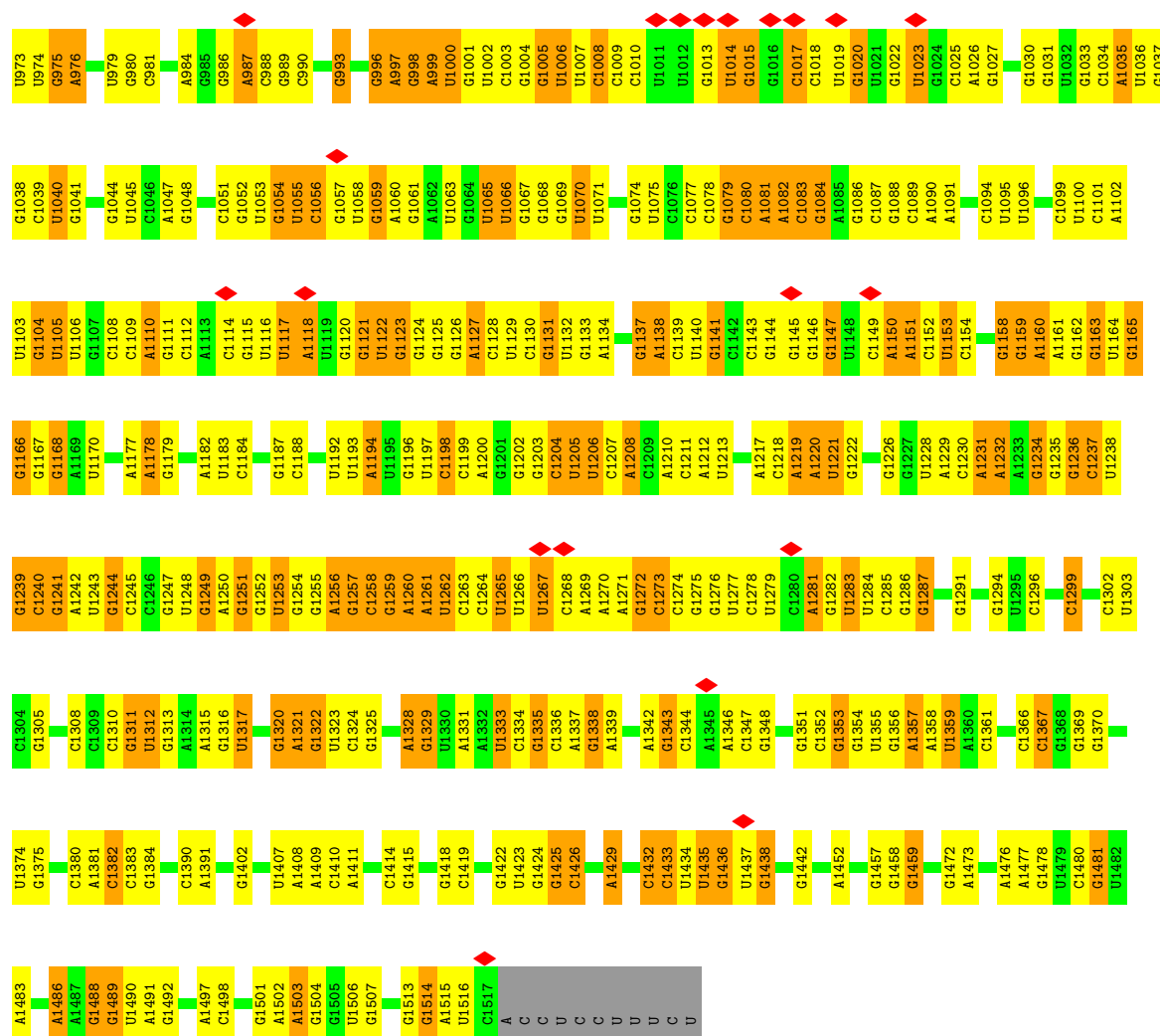


- Molecule 48: E-tRNA

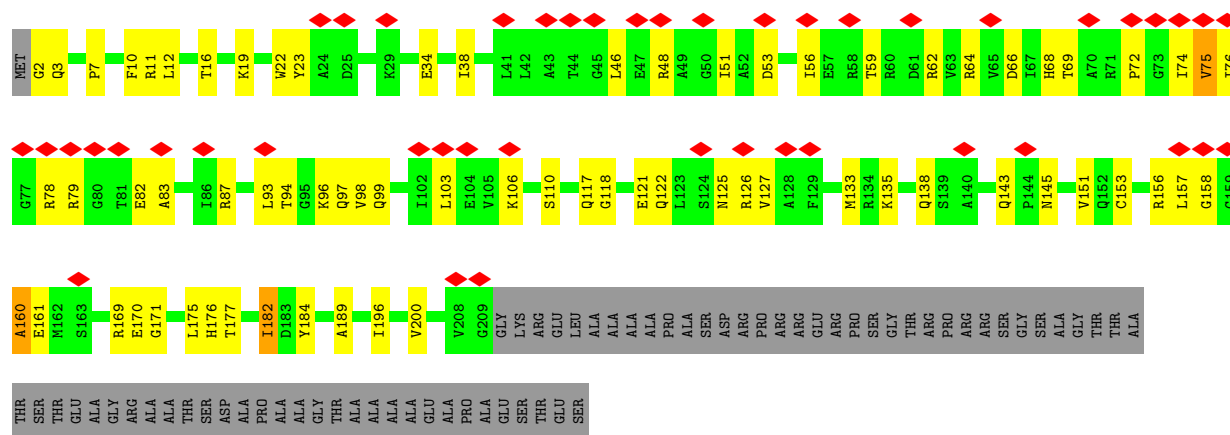


- Molecule 49: 16S ribosomal RNA

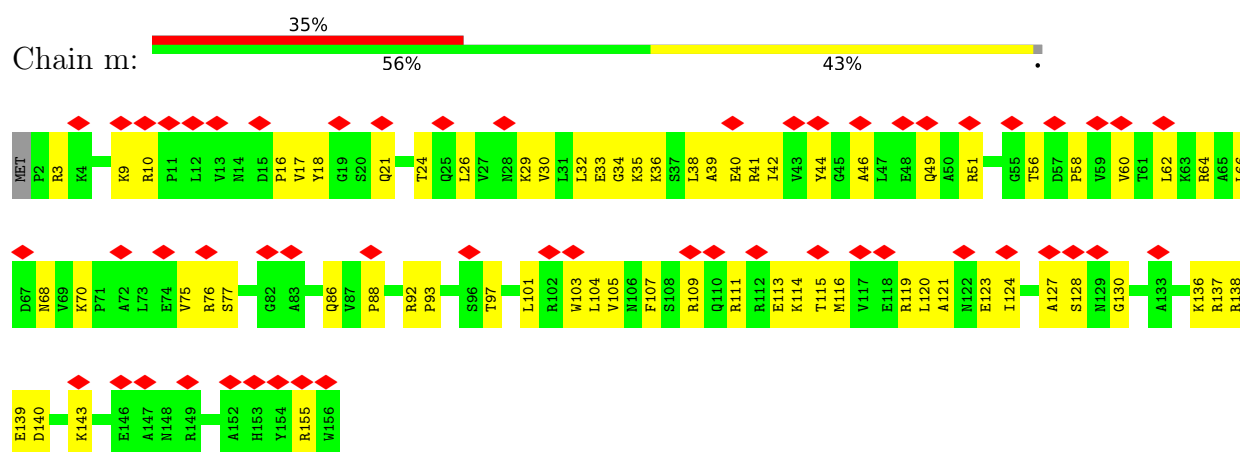




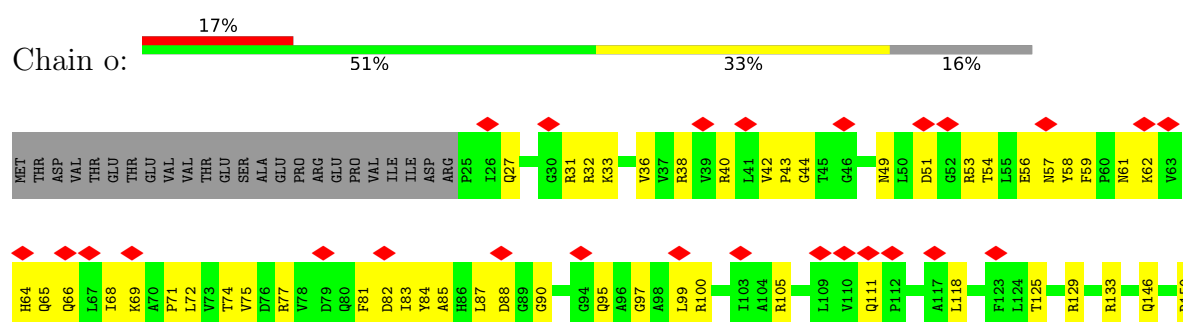
• Molecule 50: 30S ribosomal protein S3



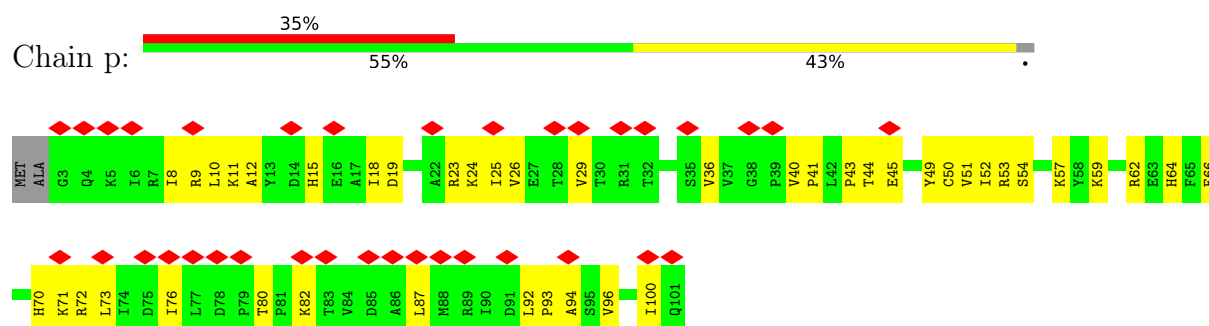
• Molecule 51: 30S ribosomal protein S7



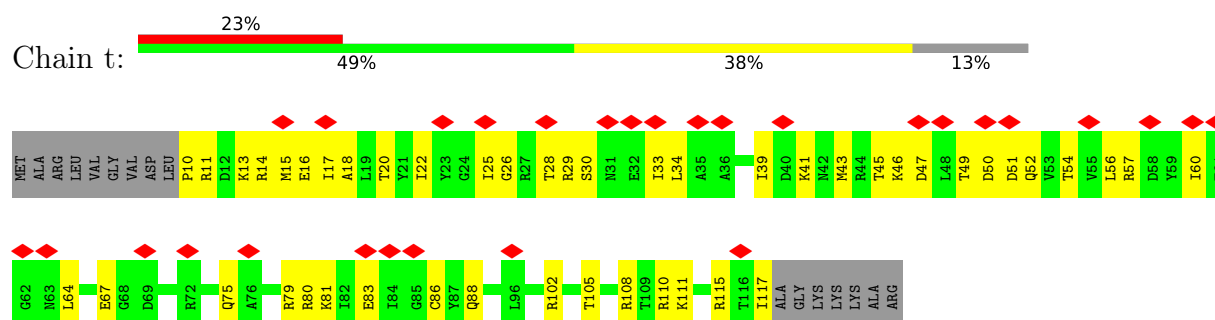
• Molecule 52: 30S ribosomal protein S9



• Molecule 53: 30S ribosomal protein S10

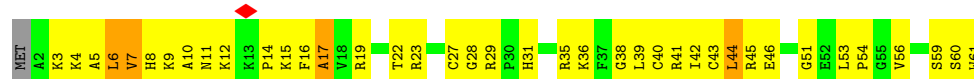


• Molecule 54: 30S ribosomal protein S13



• Molecule 55: 30S ribosomal protein S19





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	48443	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 ($e^-/\text{\AA}^2$)	51.22	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.845	Depositor
Minimum map value	-1.224	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.083	Depositor
Recommended contour level	0.2	Depositor
Map size ($\text{\AA}$)	433.19998, 433.19998, 433.19998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.083, 1.083, 1.083	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	Y	1.25	0/478	1.26	5/641 (0.8%)
2	c	0.99	0/413	1.08	2/553 (0.4%)
3	g	0.63	0/372	1.07	2/503 (0.4%)
4	r	0.96	0/518	1.11	5/693 (0.7%)
5	l	0.19	0/280	0.32	0/359
6	j	0.16	0/1672	0.39	0/2251
7	k	0.20	0/1312	0.39	0/1772
8	l	0.22	0/782	0.33	0/1059
9	n	0.21	0/1025	0.33	0/1385
10	q	0.18	0/873	0.31	0/1180
11	s	0.20	0/969	0.42	0/1294
12	v	0.21	0/729	0.28	0/977
13	w	0.92	3/908 (0.3%)	1.10	4/1226 (0.3%)
14	x	0.17	0/759	0.37	0/1016
15	z	0.15	0/663	0.31	0/882
16	h	0.14	0/1822	0.41	1/2457 (0.0%)
17	3	0.24	0/191	0.31	0/247
18	A	0.28	0/75001	0.32	0/117027
19	B	0.21	0/2821	0.28	0/4396
20	C	0.29	0/2153	0.35	0/2895
21	D	0.36	0/1609	0.48	2/2165 (0.1%)
22	E	0.26	0/1592	0.36	0/2153
23	F	0.43	2/1467 (0.1%)	0.86	5/1973 (0.3%)
24	G	0.27	0/1369	0.53	2/1848 (0.1%)
25	H	0.17	0/1027	0.39	0/1398
26	I	0.12	0/925	0.29	0/1246
27	J	0.15	0/1006	0.44	0/1364
28	K	0.29	0/1151	0.35	0/1557
29	L	0.29	0/946	0.35	0/1268
30	M	0.27	0/1091	0.43	0/1457
31	N	0.23	0/1118	0.33	0/1506
32	O	0.29	0/945	0.37	0/1267
33	P	0.20	0/966	0.30	0/1298
34	Q	0.63	2/921 (0.2%)	0.50	0/1236

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	R	0.31	0/1000	0.31	0/1341
36	S	0.27	0/764	0.32	0/1030
37	T	0.30	0/887	0.34	0/1204
38	U	0.26	0/766	0.33	0/1030
39	V	0.21	0/738	0.36	0/987
40	W	0.18	0/1443	0.30	0/1970
41	X	0.27	0/595	0.32	0/798
42	Z	0.23	0/534	0.30	0/713
43	2	0.28	0/477	0.27	0/640
44	b	0.29	0/427	0.33	0/572
45	d	0.31	0/380	0.40	0/500
46	e	0.28	0/507	0.33	0/672
47	f	0.24	0/303	0.29	0/401
48	5	0.16	0/1835	0.33	0/2859
49	a	0.33	6/36309 (0.0%)	0.32	2/56657 (0.0%)
50	i	0.16	0/1684	0.43	0/2261
51	m	0.16	0/1252	0.43	0/1690
52	o	0.16	0/1012	0.42	0/1362
53	p	0.17	0/802	0.43	0/1086
54	t	0.16	0/884	0.47	0/1180
55	y	0.16	0/680	0.43	0/915
56	4	0.14	0/2085	0.35	0/2829
57	u	0.67	0/488	1.07	5/650 (0.8%)
All	All	0.31	13/165726 (0.0%)	0.37	35/247896 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
34	Q	0	1
50	i	0	3
All	All	0	4

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	a	587	A	N3-C4	23.33	1.81	1.34
49	a	587	A	C6-N1	22.68	1.80	1.35
49	a	587	A	N1-C2	22.54	1.79	1.34
49	a	587	A	C2-N3	21.88	1.77	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	w	32	ARG	CD-NE	19.57	1.73	1.46

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	w	32	ARG	CD-NE-CZ	19.90	152.26	124.40
23	F	116	PRO	CA-CB-CG	-19.30	67.83	104.50
23	F	116	PRO	N-CD-CG	-18.93	74.80	103.20
23	F	116	PRO	CB-CG-CD	17.47	162.00	106.10
13	w	65	GLN	CA-C-N	16.80	136.82	119.85

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	Q	4	LEU	Mainchain
50	i	158	GLY	Peptide
50	i	160	ALA	Peptide
50	i	75	VAL	Peptide

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	Y	470	0	484	36	0
2	c	405	0	411	17	0
3	g	364	0	352	47	0
4	r	513	0	540	38	0
5	l	280	0	342	11	0
6	j	1641	0	1668	52	0
7	k	1296	0	1360	30	0
8	l	771	0	797	20	0
9	n	1010	0	1046	24	0
10	q	855	0	863	10	0
11	s	958	0	1045	30	0
12	v	720	0	760	10	0
13	w	891	0	935	76	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	x	748	0	795	24	0
15	z	660	0	712	12	0
16	h	1793	0	1839	48	0
17	3	189	0	205	4	0
18	A	66981	0	33700	733	0
19	B	2522	0	1285	27	0
20	C	2110	0	2165	46	0
21	D	1587	0	1630	29	0
22	E	1569	0	1607	21	0
23	F	1445	0	1476	48	0
24	G	1348	0	1399	39	0
25	H	1018	0	988	20	0
26	I	918	0	959	37	0
27	J	990	0	1021	22	0
28	K	1125	0	1161	23	0
29	L	938	0	1000	14	0
30	M	1078	0	1151	22	0
31	N	1092	0	1128	16	0
32	O	928	0	972	20	0
33	P	956	0	991	20	0
34	Q	907	0	938	19	0
35	R	988	0	1038	14	0
36	S	754	0	802	11	0
37	T	873	0	909	14	0
38	U	756	0	802	10	0
39	V	732	0	782	15	0
40	W	1428	0	1443	26	0
41	X	586	0	601	12	0
42	Z	531	0	541	9	0
43	2	474	0	500	7	0
44	b	423	0	463	8	0
45	d	377	0	411	5	0
46	e	502	0	541	9	0
47	f	299	0	324	6	0
48	5	1643	0	836	29	0
49	a	32439	0	16321	663	0
50	i	1660	0	1707	54	0
51	m	1232	0	1282	60	0
52	o	994	0	1050	47	0
53	p	788	0	819	41	0
54	t	877	0	922	44	0
55	y	662	0	677	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	4	2058	0	2093	59	0
57	u	477	0	503	50	0
All	All	152629	0	103092	2485	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 2485 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)
13:w:32:ARG:NE	49:a:587:A:C2	1.73	1.53
49:a:587:A:C2	49:a:587:A:N3	1.77	1.53
13:w:32:ARG:NE	49:a:587:A:C6	1.78	1.51
49:a:587:A:C2	49:a:587:A:N1	1.79	1.50
13:w:32:ARG:NE	13:w:32:ARG:CD	1.73	1.48

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	Y	61/64 (95%)	49 (80%)	12 (20%)	0	100	100
2	c	47/55 (86%)	46 (98%)	1 (2%)	0	100	100
3	g	46/75 (61%)	33 (72%)	10 (22%)	3 (6%)	1	7
4	r	63/84 (75%)	53 (84%)	10 (16%)	0	100	100
5	1	30/33 (91%)	30 (100%)	0	0	100	100
6	j	198/201 (98%)	167 (84%)	31 (16%)	0	100	100
7	k	178/214 (83%)	168 (94%)	10 (6%)	0	100	100
8	l	94/96 (98%)	90 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	n	129/132 (98%)	124 (96%)	5 (4%)	0	100	100
10	q	113/138 (82%)	103 (91%)	10 (9%)	0	100	100
11	s	120/124 (97%)	106 (88%)	14 (12%)	0	100	100
12	v	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
13	w	111/156 (71%)	91 (82%)	20 (18%)	0	100	100
14	x	92/98 (94%)	85 (92%)	7 (8%)	0	100	100
15	z	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
16	h	226/277 (82%)	204 (90%)	22 (10%)	0	100	100
17	3	21/24 (88%)	21 (100%)	0	0	100	100
20	C	273/278 (98%)	258 (94%)	15 (6%)	0	100	100
21	D	212/217 (98%)	195 (92%)	16 (8%)	1 (0%)	24	55
22	E	207/215 (96%)	203 (98%)	4 (2%)	0	100	100
23	F	180/187 (96%)	165 (92%)	15 (8%)	0	100	100
24	G	174/179 (97%)	165 (95%)	9 (5%)	0	100	100
25	H	149/151 (99%)	141 (95%)	8 (5%)	0	100	100
26	I	124/175 (71%)	115 (93%)	9 (7%)	0	100	100
27	J	131/142 (92%)	112 (86%)	19 (14%)	0	100	100
28	K	141/147 (96%)	133 (94%)	8 (6%)	0	100	100
29	L	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
30	M	143/147 (97%)	127 (89%)	16 (11%)	0	100	100
31	N	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
32	O	116/199 (58%)	110 (95%)	6 (5%)	0	100	100
33	P	124/127 (98%)	120 (97%)	4 (3%)	0	100	100
34	Q	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
35	R	122/129 (95%)	117 (96%)	5 (4%)	0	100	100
36	S	98/103 (95%)	94 (96%)	4 (4%)	0	100	100
37	T	112/153 (73%)	107 (96%)	5 (4%)	0	100	100
38	U	95/100 (95%)	89 (94%)	6 (6%)	0	100	100
39	V	93/105 (89%)	84 (90%)	9 (10%)	0	100	100
40	W	190/215 (88%)	182 (96%)	8 (4%)	0	100	100
41	X	77/88 (88%)	74 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	Z	62/77 (80%)	62 (100%)	0	0	100	100
43	2	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
44	b	52/57 (91%)	52 (100%)	0	0	100	100
45	d	44/47 (94%)	44 (100%)	0	0	100	100
46	e	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
47	f	35/37 (95%)	35 (100%)	0	0	100	100
50	i	206/275 (75%)	173 (84%)	33 (16%)	0	100	100
51	m	153/156 (98%)	131 (86%)	22 (14%)	0	100	100
52	o	124/150 (83%)	103 (83%)	21 (17%)	0	100	100
53	p	97/101 (96%)	89 (92%)	8 (8%)	0	100	100
54	t	106/124 (86%)	88 (83%)	18 (17%)	0	100	100
55	y	80/93 (86%)	67 (84%)	13 (16%)	0	100	100
56	4	265/470 (56%)	250 (94%)	15 (6%)	0	100	100
57	u	58/61 (95%)	48 (83%)	10 (17%)	0	100	100
All	All	6224/7149 (87%)	5721 (92%)	499 (8%)	4 (0%)	49	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	g	4	GLY
3	g	3	THR
21	D	156	THR
3	g	10	VAL

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	Y	50/51 (98%)	47 (94%)	3 (6%)	17	44
2	c	47/52 (90%)	44 (94%)	3 (6%)	16	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	g	43/63 (68%)	36 (84%)	7 (16%)	2	10
4	r	55/72 (76%)	51 (93%)	4 (7%)	13	38
5	1	30/31 (97%)	30 (100%)	0	100	100
6	j	175/176 (99%)	175 (100%)	0	100	100
7	k	127/147 (86%)	125 (98%)	2 (2%)	55	70
8	l	85/85 (100%)	85 (100%)	0	100	100
9	n	107/108 (99%)	107 (100%)	0	100	100
10	q	89/105 (85%)	89 (100%)	0	100	100
11	s	103/105 (98%)	102 (99%)	1 (1%)	68	75
12	v	76/77 (99%)	75 (99%)	1 (1%)	61	73
13	w	92/118 (78%)	88 (96%)	4 (4%)	26	52
14	x	80/83 (96%)	79 (99%)	1 (1%)	61	73
15	z	69/70 (99%)	68 (99%)	1 (1%)	59	72
16	h	191/218 (88%)	191 (100%)	0	100	100
17	3	18/19 (95%)	18 (100%)	0	100	100
20	C	215/218 (99%)	215 (100%)	0	100	100
21	D	160/163 (98%)	160 (100%)	0	100	100
22	E	169/173 (98%)	169 (100%)	0	100	100
23	F	151/156 (97%)	151 (100%)	0	100	100
24	G	148/150 (99%)	147 (99%)	1 (1%)	76	79
25	H	90/116 (78%)	89 (99%)	1 (1%)	65	75
26	I	89/120 (74%)	89 (100%)	0	100	100
27	J	102/108 (94%)	102 (100%)	0	100	100
28	K	119/120 (99%)	118 (99%)	1 (1%)	73	78
29	L	100/100 (100%)	99 (99%)	1 (1%)	68	75
30	M	112/114 (98%)	111 (99%)	1 (1%)	70	76
31	N	114/116 (98%)	113 (99%)	1 (1%)	70	76
32	O	97/158 (61%)	97 (100%)	0	100	100
33	P	93/94 (99%)	92 (99%)	1 (1%)	65	75
34	Q	100/100 (100%)	98 (98%)	2 (2%)	48	66
35	R	97/99 (98%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	S	81/83 (98%)	81 (100%)	0	100	100
37	T	90/117 (77%)	89 (99%)	1 (1%)	65	75
38	U	83/85 (98%)	83 (100%)	0	100	100
39	V	81/86 (94%)	81 (100%)	0	100	100
40	W	155/168 (92%)	154 (99%)	1 (1%)	78	81
41	X	58/63 (92%)	58 (100%)	0	100	100
42	Z	58/66 (88%)	57 (98%)	1 (2%)	53	69
43	2	52/54 (96%)	52 (100%)	0	100	100
44	b	43/46 (94%)	43 (100%)	0	100	100
45	d	35/36 (97%)	35 (100%)	0	100	100
46	e	53/54 (98%)	53 (100%)	0	100	100
47	f	35/35 (100%)	35 (100%)	0	100	100
50	i	170/212 (80%)	168 (99%)	2 (1%)	63	74
51	m	131/132 (99%)	131 (100%)	0	100	100
52	o	102/125 (82%)	102 (100%)	0	100	100
53	p	89/90 (99%)	88 (99%)	1 (1%)	65	75
54	t	93/104 (89%)	92 (99%)	1 (1%)	65	75
55	y	73/84 (87%)	73 (100%)	0	100	100
56	4	220/372 (59%)	220 (100%)	0	100	100
57	u	49/50 (98%)	46 (94%)	3 (6%)	17	44
All	All	5144/5747 (90%)	5098 (99%)	46 (1%)	68	76

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	H	129	THR
34	Q	3	THR
28	K	94	GLU
31	N	49	SER
40	W	140	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
41	X	19	GLN
53	p	47	ASN
43	2	19	GLN
51	m	14	ASN
56	4	344	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
18	A	3118/3120 (99%)	610 (19%)	25 (0%)
19	B	117/118 (99%)	15 (12%)	1 (0%)
48	5	76/77 (98%)	21 (27%)	2 (2%)
49	a	1510/1528 (98%)	448 (29%)	0
All	All	4821/4843 (99%)	1094 (22%)	28 (0%)

5 of 1094 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
18	A	7	U
18	A	9	U
18	A	12	G
18	A	20	G
18	A	31	U

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	A	1186	G
48	5	75	C
18	A	1629	G
18	A	2626	U
18	A	1573	U

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 [i](#)

There are no ligands in this entry.

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.

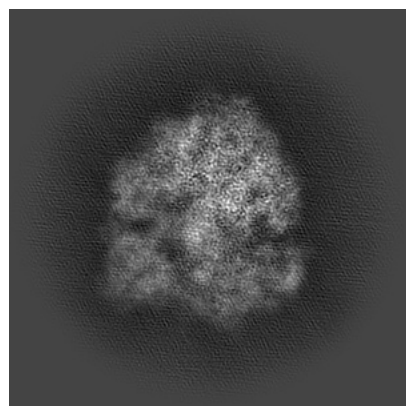
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43267. These allow visual inspection of the internal detail of the map and identification of artifacts.

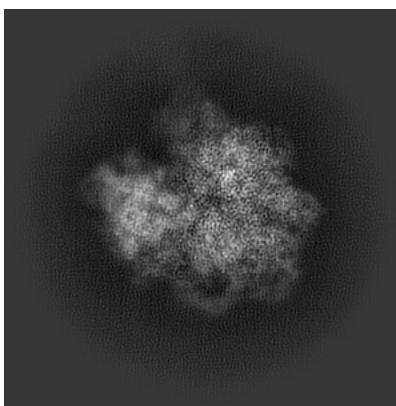
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

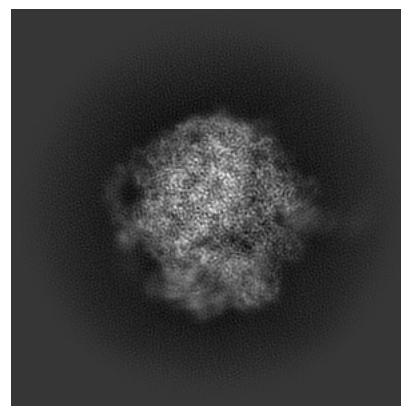
6.1.1 Primary map



X

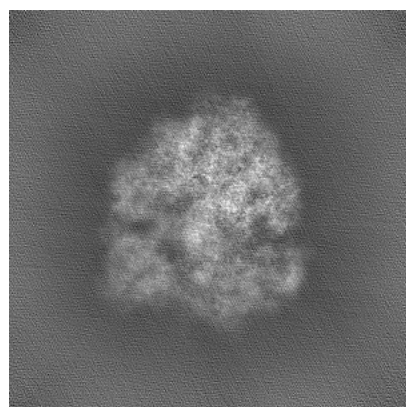


Y

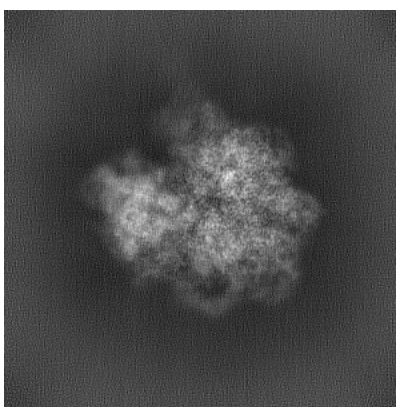


Z

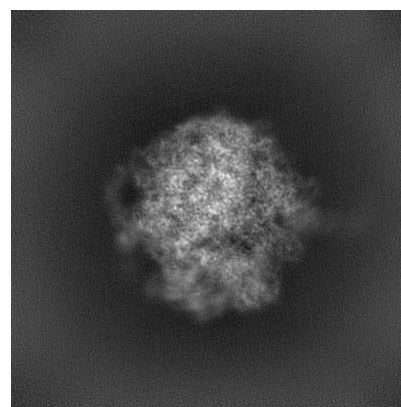
6.1.2 Raw map



X



Y

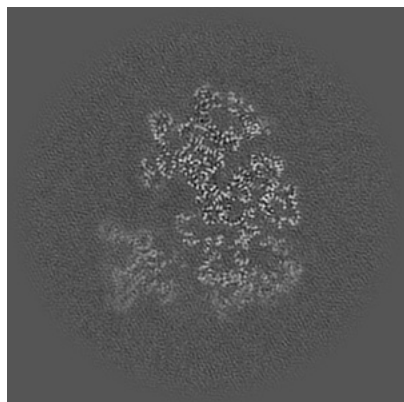


Z

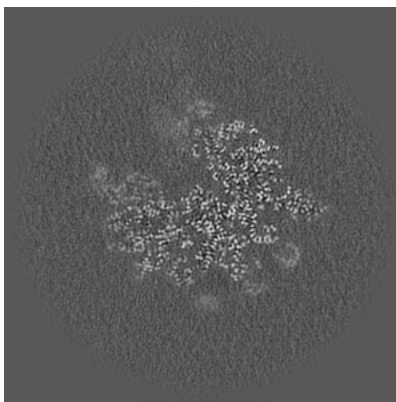
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

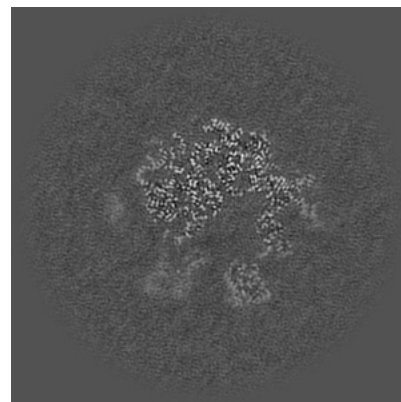
6.2.1 Primary map



X Index: 200

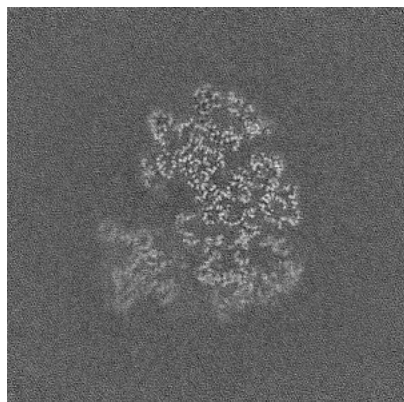


Y Index: 200

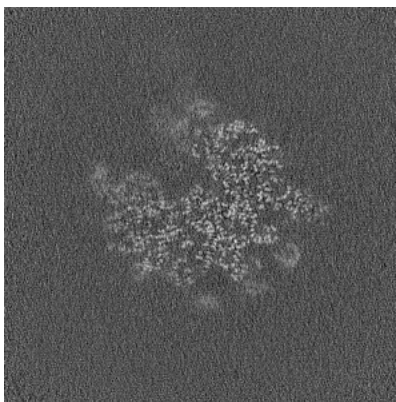


Z Index: 200

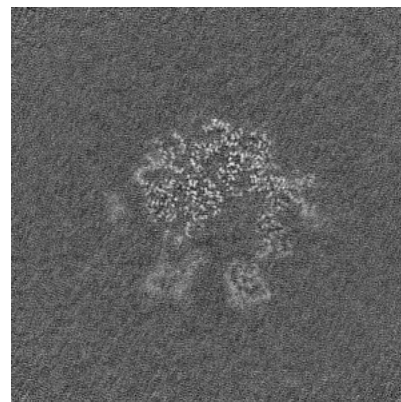
6.2.2 Raw map



X Index: 200



Y Index: 200

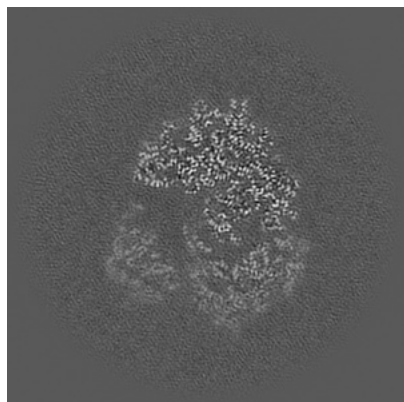


Z Index: 200

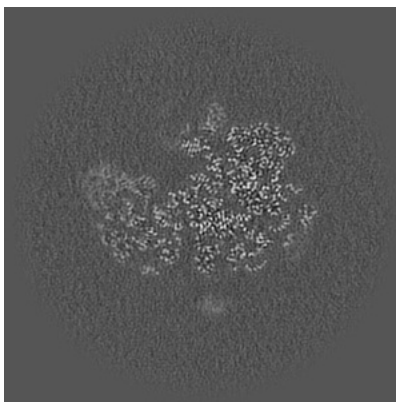
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

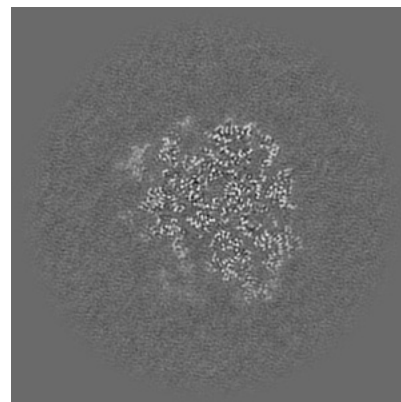
6.3.1 Primary map



X Index: 214

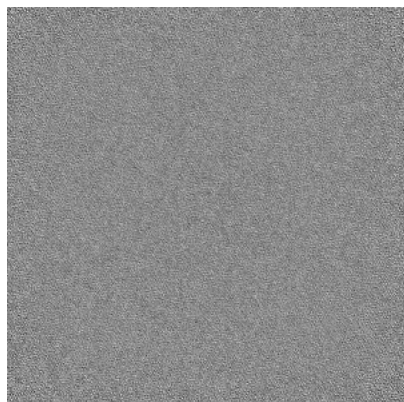


Y Index: 213

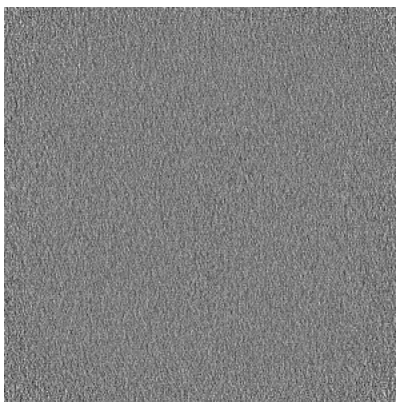


Z Index: 230

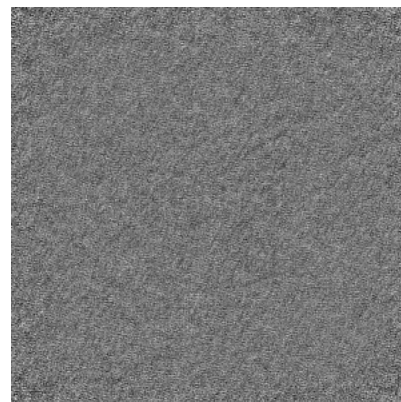
6.3.2 Raw map



X Index: 0



Y Index: 0

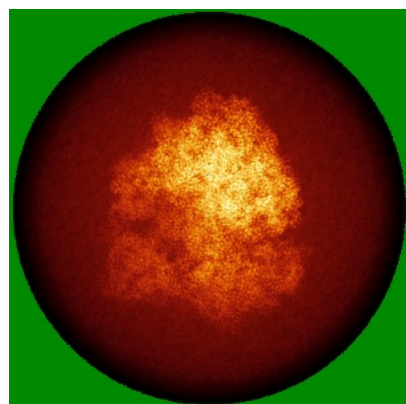


Z Index: 0

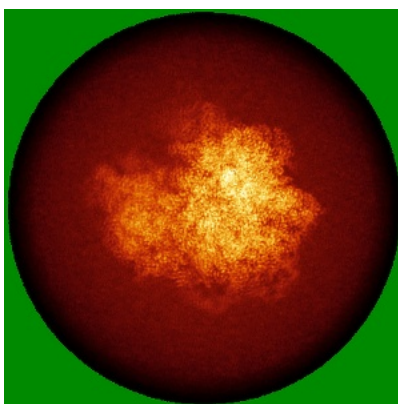
The images above show the largest variance slices of the map in three orthogonal directions.

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

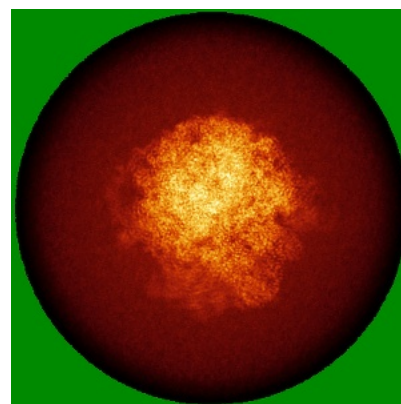
6.4.1 Primary map



X

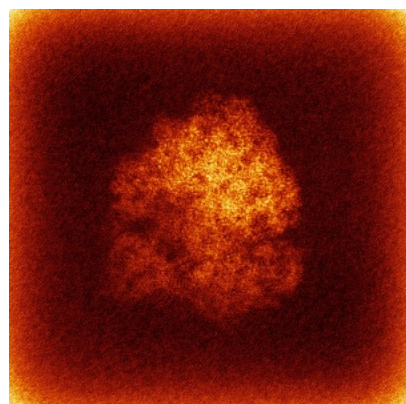


Y

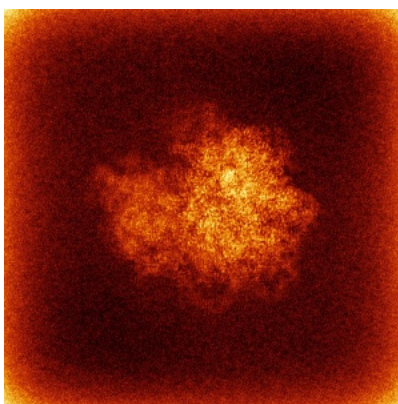


Z

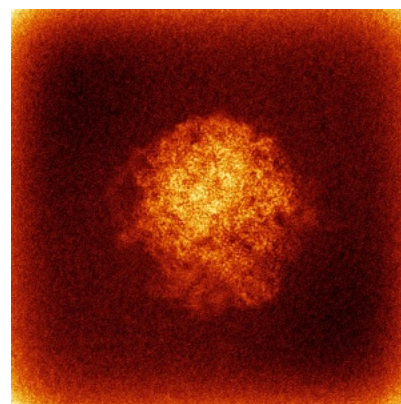
6.4.2 Raw map



X



Y

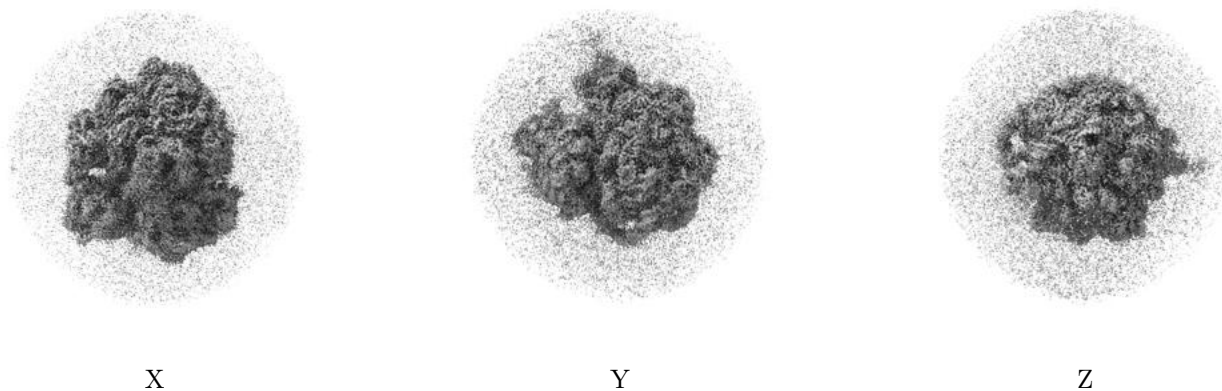


Z

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.

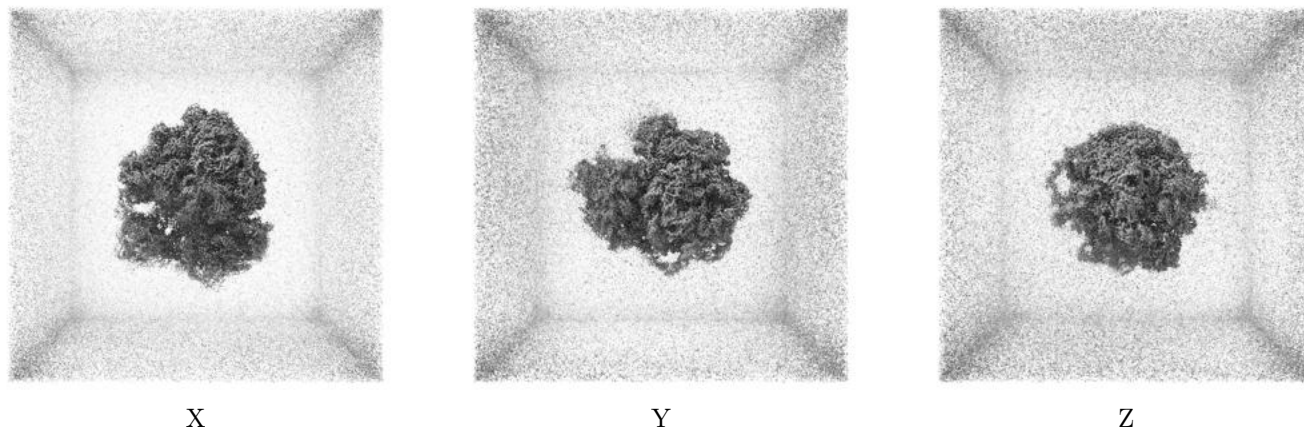
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. 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.

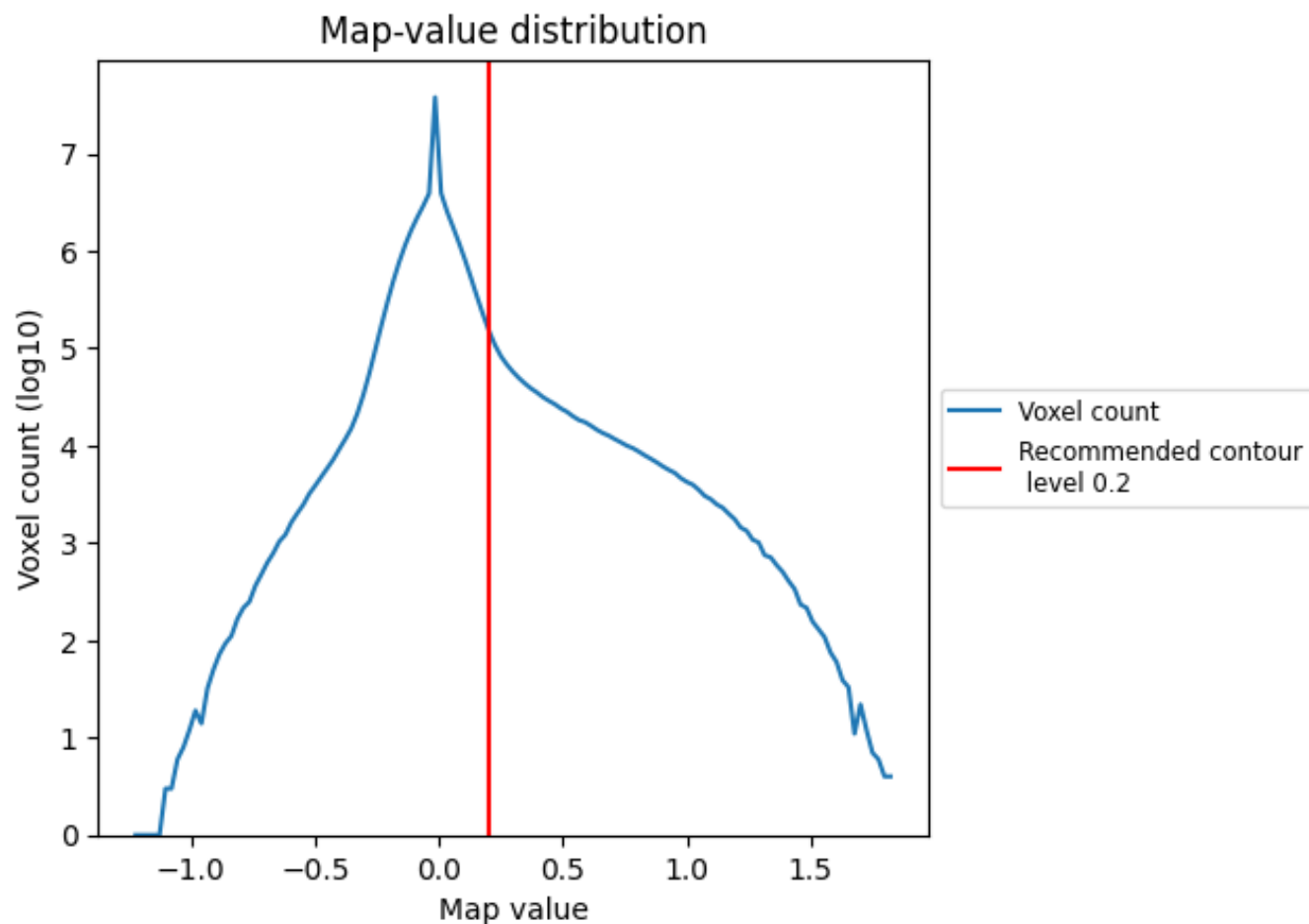
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

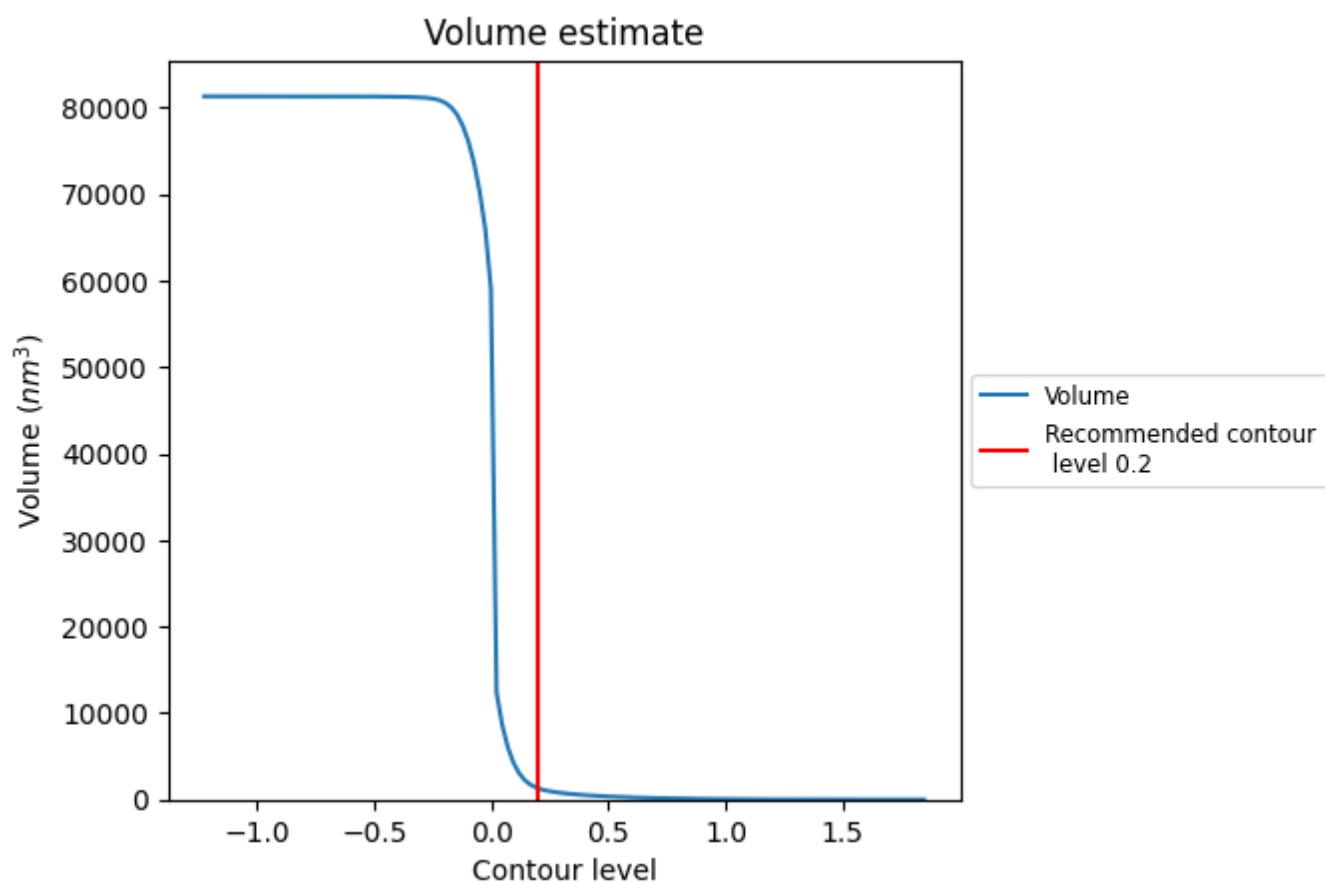
This section contains the results of statistical analysis of the map.

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.

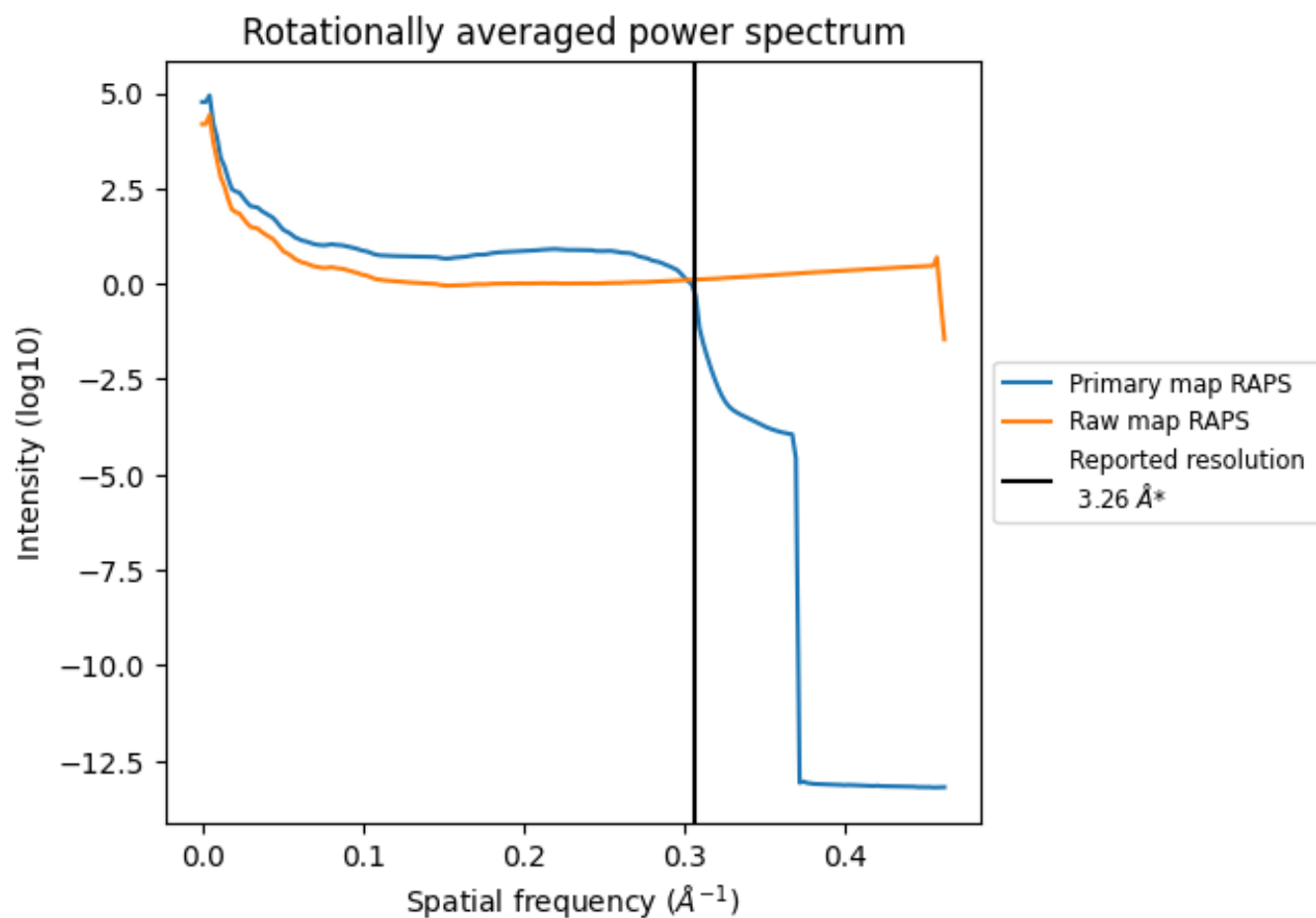
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1311 nm³; this corresponds to an approximate mass of 1184 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 ⓘ

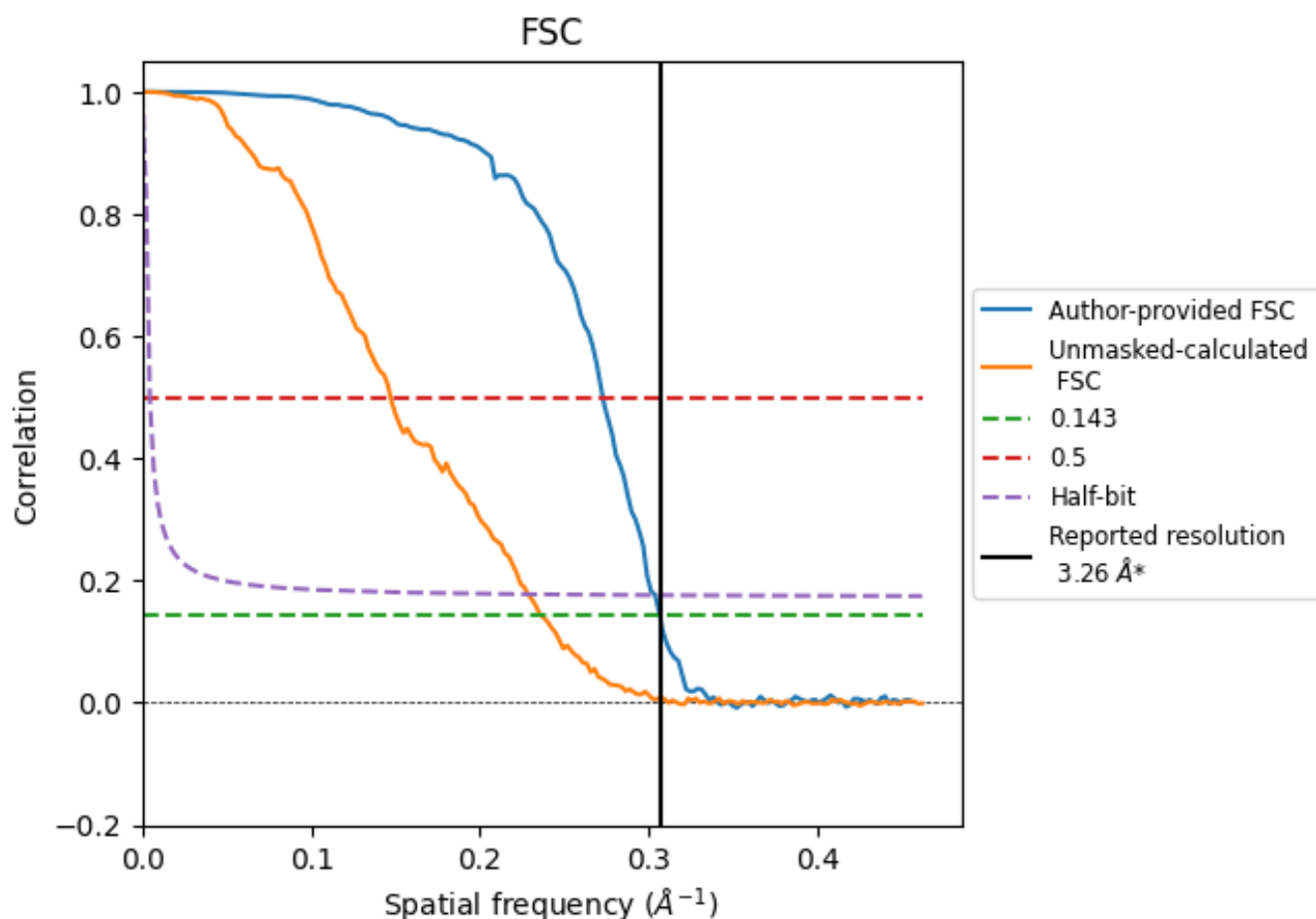


*Reported resolution corresponds to spatial frequency of 0.307 Å⁻¹

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 0.307 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.26	-	-
Author-provided FSC curve	3.26	3.67	3.29
Unmasked-calculated*	4.24	6.80	4.38

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.24 differs from the reported value 3.26 by more than 10 %

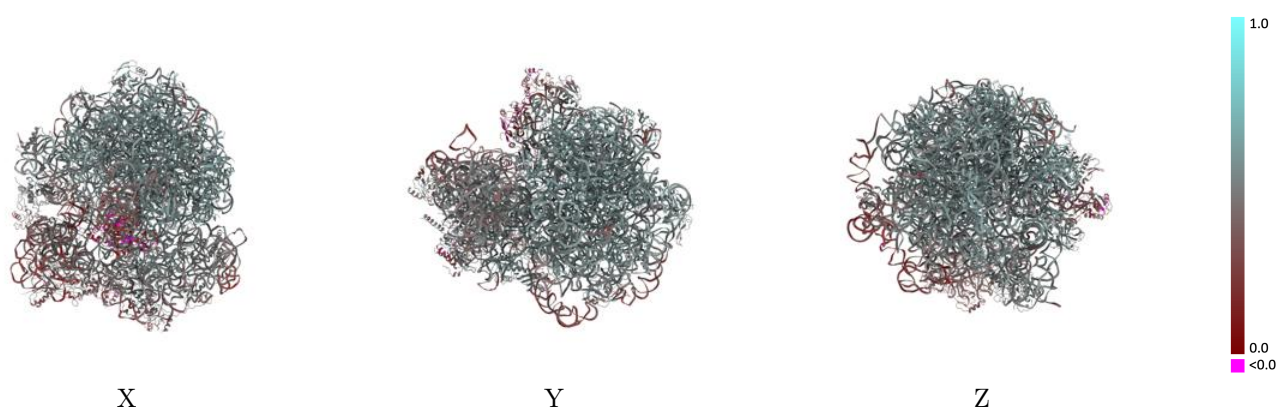
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43267 and PDB model 8VIO. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

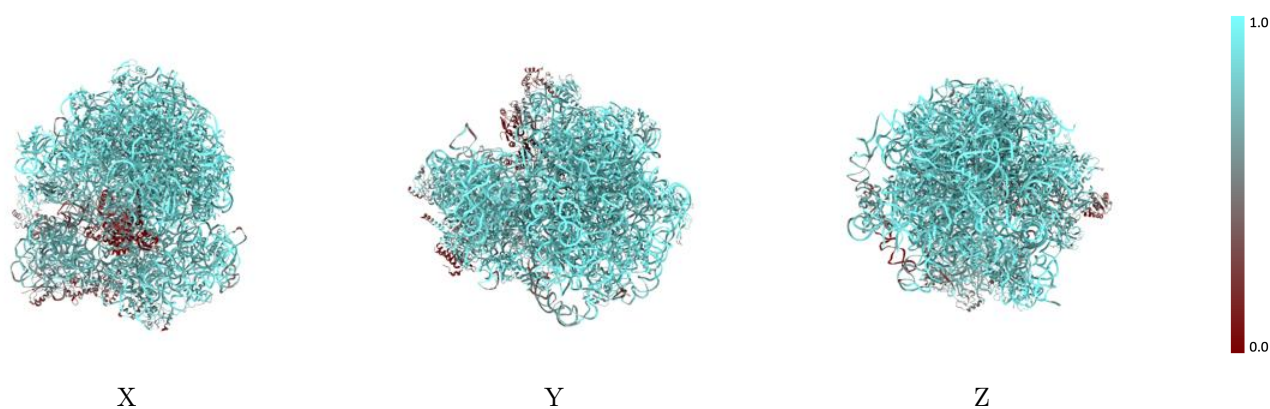
This section was not generated.

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



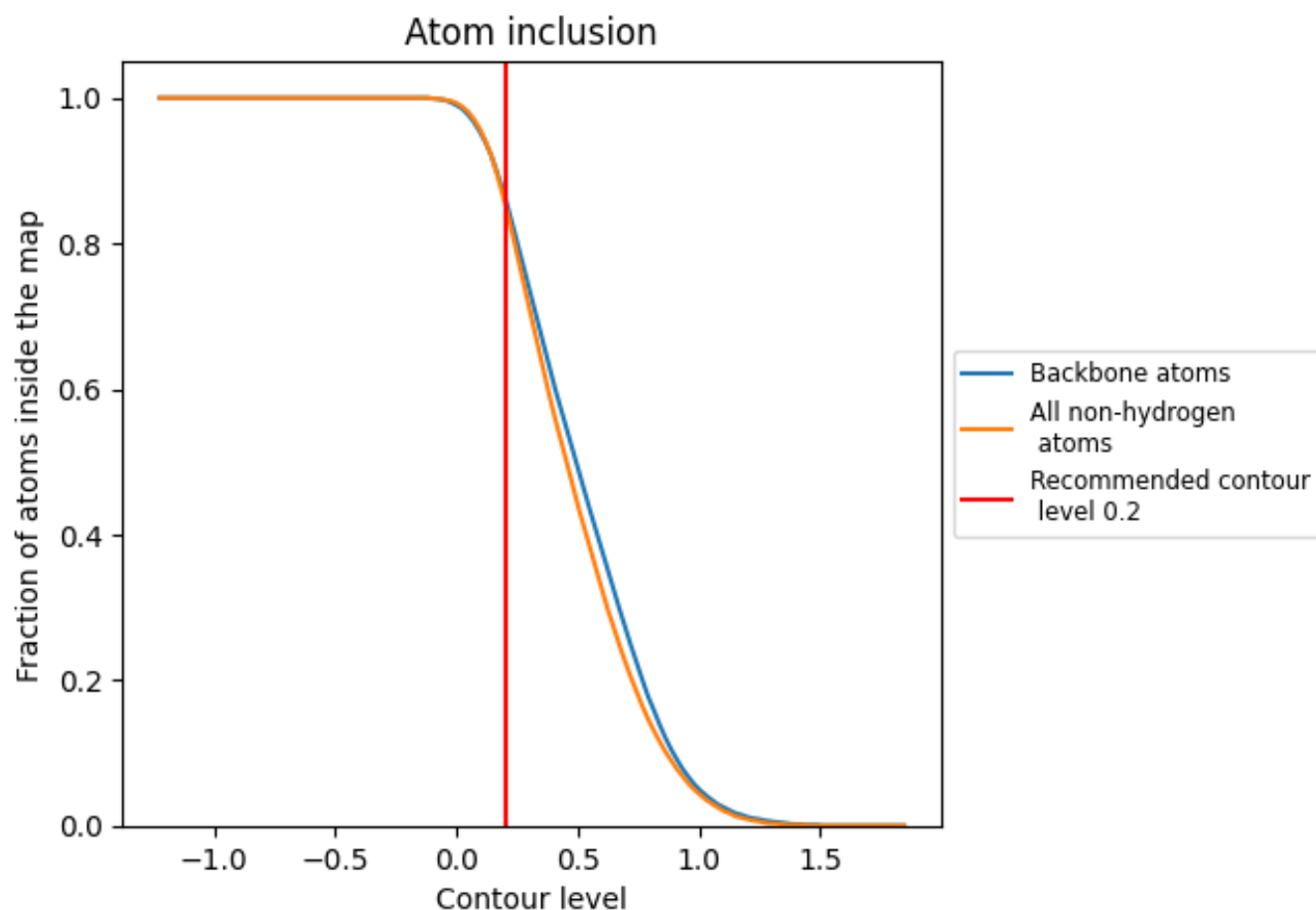
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8550	 0.4860
1	 0.8320	 0.5550
2	 0.9480	 0.5780
3	 0.9610	 0.5920
4	 0.0800	 0.3100
5	 0.8090	 0.4030
A	 0.9170	 0.5050
B	 0.9460	 0.4970
C	 0.9320	 0.5780
D	 0.9440	 0.5770
E	 0.9130	 0.5590
F	 0.8260	 0.4890
G	 0.8320	 0.4940
H	 0.7040	 0.4630
I	 0.3060	 0.2700
J	 0.2460	 0.2590
K	 0.9440	 0.5730
L	 0.9100	 0.5690
M	 0.9240	 0.5640
N	 0.8990	 0.5690
O	 0.9440	 0.5720
P	 0.8940	 0.5230
Q	 0.9140	 0.5720
R	 0.9390	 0.5750
S	 0.9310	 0.5770
T	 0.9230	 0.5690
U	 0.9050	 0.5560
V	 0.8400	 0.5230
W	 0.8030	 0.5200
X	 0.9220	 0.5760
Y	 0.9120	 0.5660
Z	 0.9180	 0.5600
a	 0.8800	 0.4460
b	 0.9450	 0.5710
c	 0.8930	 0.5680



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Chain	Atom inclusion	Q-score
d	 0.9510	 0.5870
e	 0.9480	 0.5860
f	 0.9200	 0.5790
g	 0.8000	 0.4580
h	 0.1200	 0.2780
i	 0.6000	 0.4120
j	 0.6850	 0.4460
k	 0.8260	 0.5240
l	 0.8640	 0.5170
m	 0.5080	 0.3380
n	 0.8950	 0.5450
o	 0.6040	 0.3900
p	 0.5290	 0.4030
q	 0.8900	 0.5400
r	 0.8320	 0.5140
s	 0.7800	 0.5060
t	 0.5420	 0.3710
u	 0.7830	 0.4640
v	 0.9060	 0.5430
w	 0.7340	 0.4770
x	 0.7990	 0.4900
y	 0.6340	 0.4000
z	 0.8080	 0.4710