



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:18 AM UTC

PDB ID : 7PAJ / pdb_00007paj
EMDB ID : EMD-13274
Title : 70S ribosome with EF-Tu-tRNA, P- and E-site tRNAs in Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 7.30 Å (reported)
Based on initial models : 4V7C, 7OOC, 7OOD, 4V5L

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:

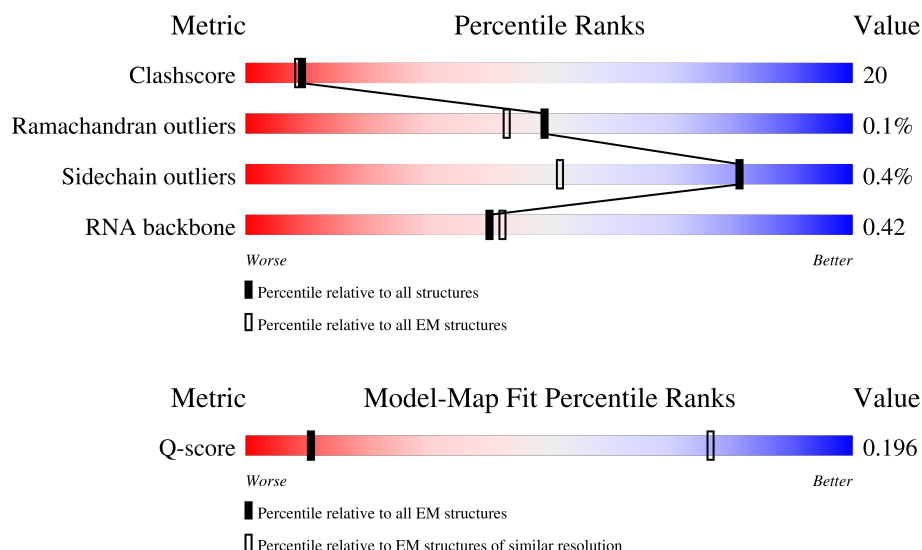
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 7.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	436 (6.80 - 7.80)

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

Mol	Chain	Length	Quality of chain
1	0	48	
2	1	59	
3	2	37	

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Mol	Chain	Length	Quality of chain
4	9	394	
5	A	294	
6	B	273	
7	C	205	
8	D	219	
9	E	215	
10	F	155	
11	G	142	
12	H	132	
13	I	108	
14	J	121	
15	K	139	
16	L	124	
17	M	61	
18	N	86	
19	O	94	
20	P	85	
21	Q	104	
22	R	87	
23	S	87	
24	T	60	
25	a	287	
26	b	287	
27	c	212	
28	d	180	

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Mol	Chain	Length	Quality of chain
29	e	184	
30	f	149	
31	g	161	
32	h	137	
33	i	146	
34	j	122	
35	k	151	
36	l	139	
37	m	124	
38	n	116	
39	o	119	
40	p	127	
41	q	100	
42	r	159	
43	s	237	
44	t	111	
45	u	104	
46	v	65	
47	w	111	
48	x	97	
49	y	57	
50	z	53	
51	3	2907	
52	4	108	
53	5	1520	

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Mol	Chain	Length	Quality of chain
54	6	76	25% 29% 58% 13%
54	7	76	32% 54% 14%
54	8	76	36% 29% 57% 14%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 150759 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 L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	393	Total	C	N	O	S	0	0
			3021	1892	533	583	13		

- Molecule 5 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	240	Total	C	N	O	S	0	0
			1921	1226	334	352	9		

- Molecule 6 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	215	Total	C	N	O	S	0	0
			1698	1073	313	307	5		

- Molecule 7 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

- Molecule 8 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

- Molecule 9 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 10 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

- Molecule 11 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

- Molecule 13 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

- Molecule 14 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 15 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 16 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	118	Total	C	N	O		0	0
			951	594	191	166			

- Molecule 17 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 18 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	83	Total	C	N	O		0	0
			673	428	125	120			

- Molecule 19 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 20 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	83	Total	C	N	O		0	0
			675	425	135	115			

- Molecule 21 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 22 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 23 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	77	Total	C	N	O		0	0
			629	383	135	111			

- Molecule 24 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	176	Total	C	N	O	S	0	0
			1396	899	247	250			

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	145	Total	C	N	O	S	0	0
			1160	746	204	207	3		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	126	Total	C	N	O	S	0	0
			960	612	167	178	3		

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	k	148	Total	C	N	O	0	0
			1153	731	226	196		

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 45 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 46 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 47 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	100	Total	C	N	O	S	0	0
			818	517	153	148			

- Molecule 48 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 50 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

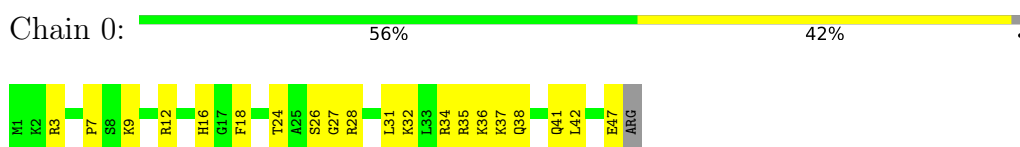
- Molecule 54 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
54	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
54	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

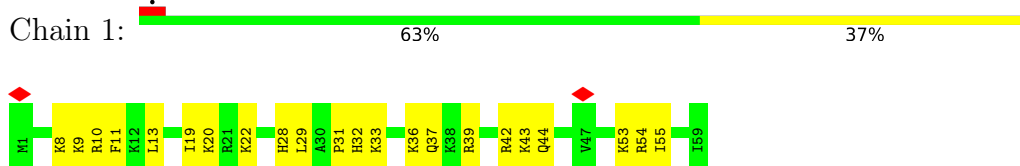
3 Residue-property plots [i](#)

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

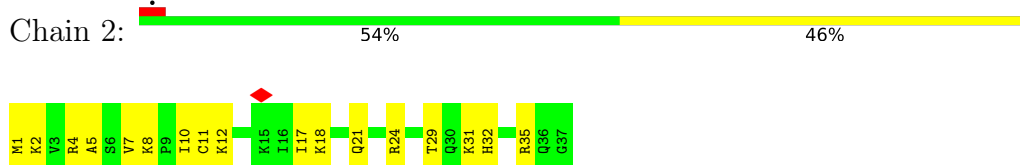
- Molecule 1: 50S ribosomal protein L34



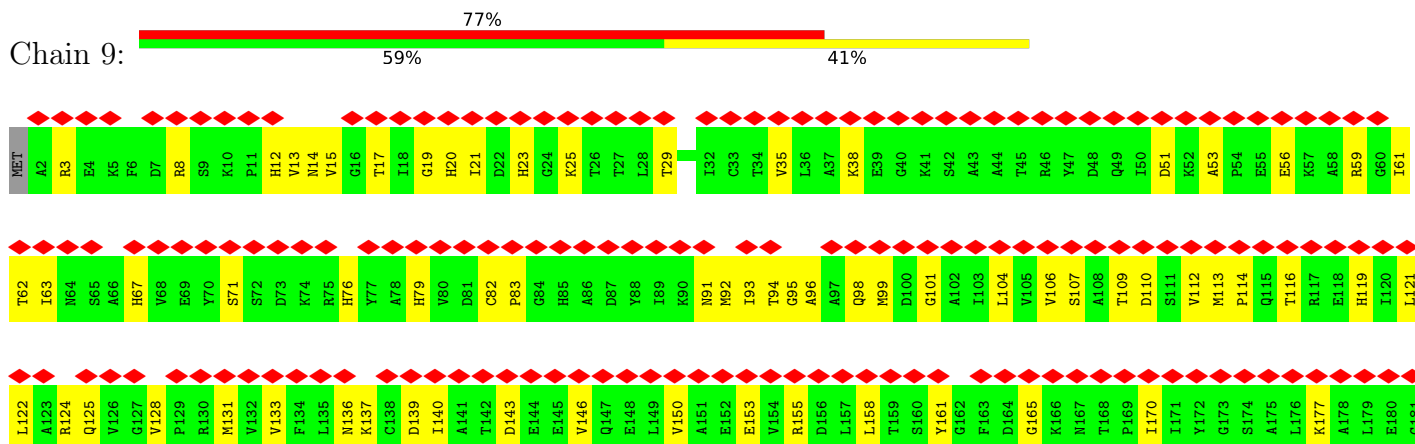
- Molecule 2: 50S ribosomal protein L35

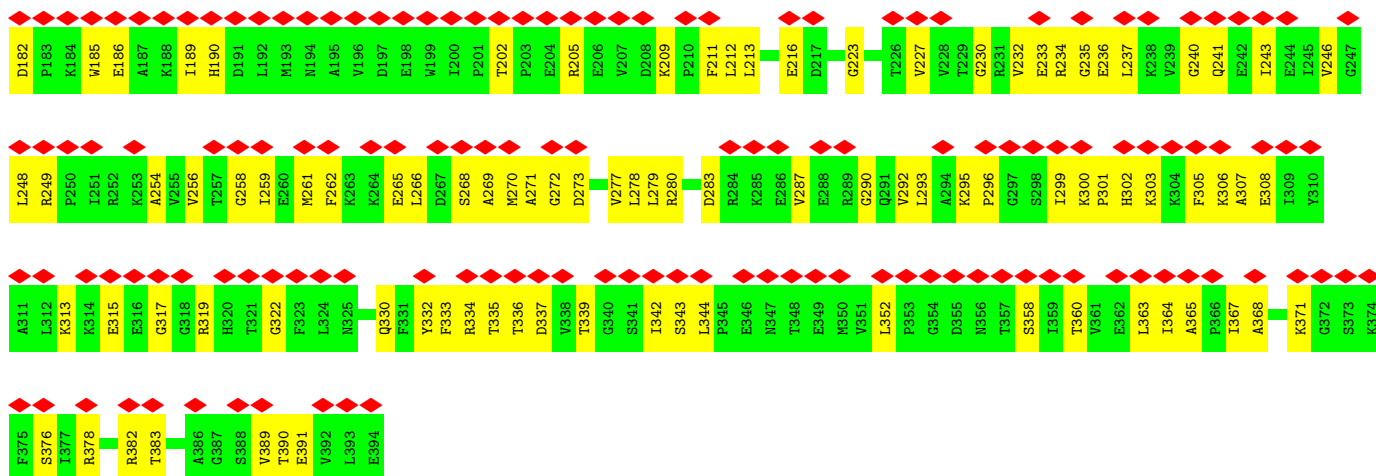


- Molecule 3: 50S ribosomal protein L36

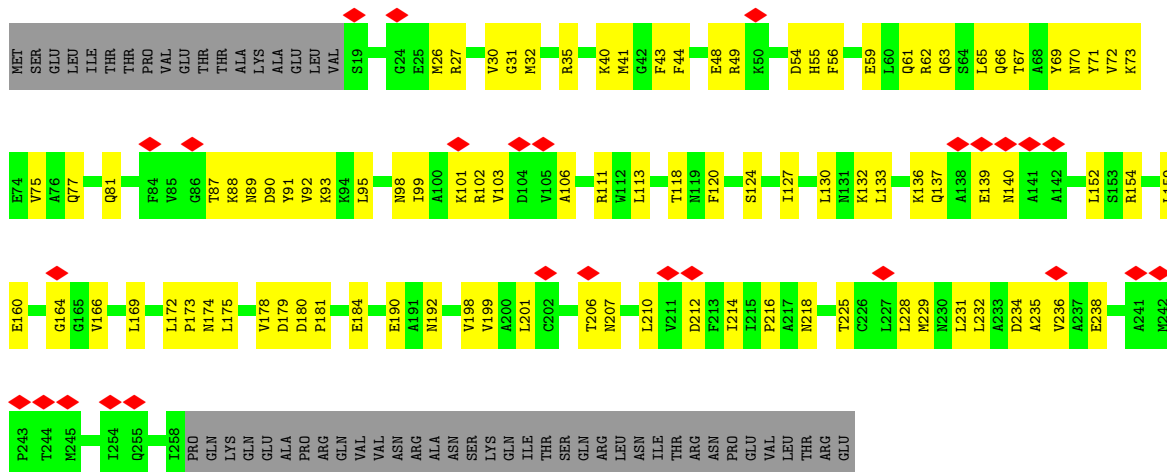


- Molecule 4: Elongation factor Tu

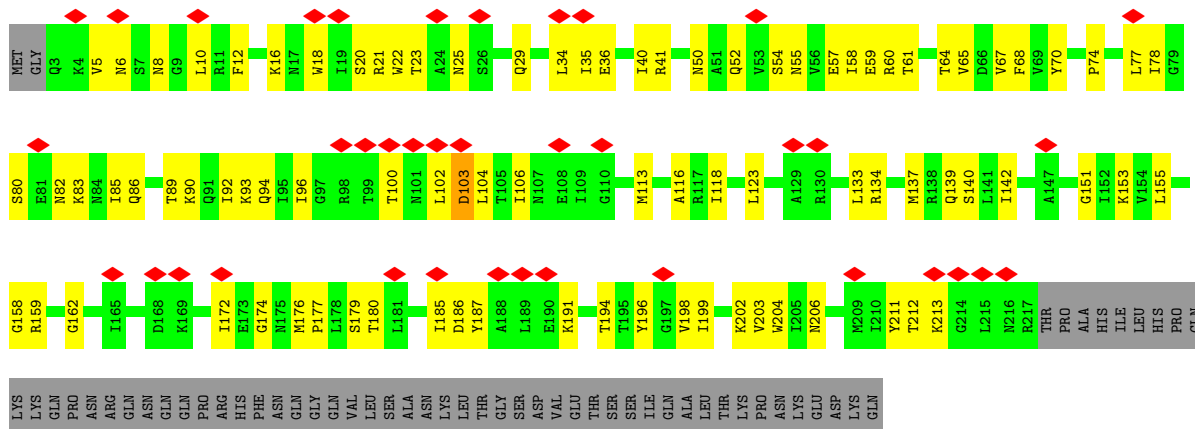




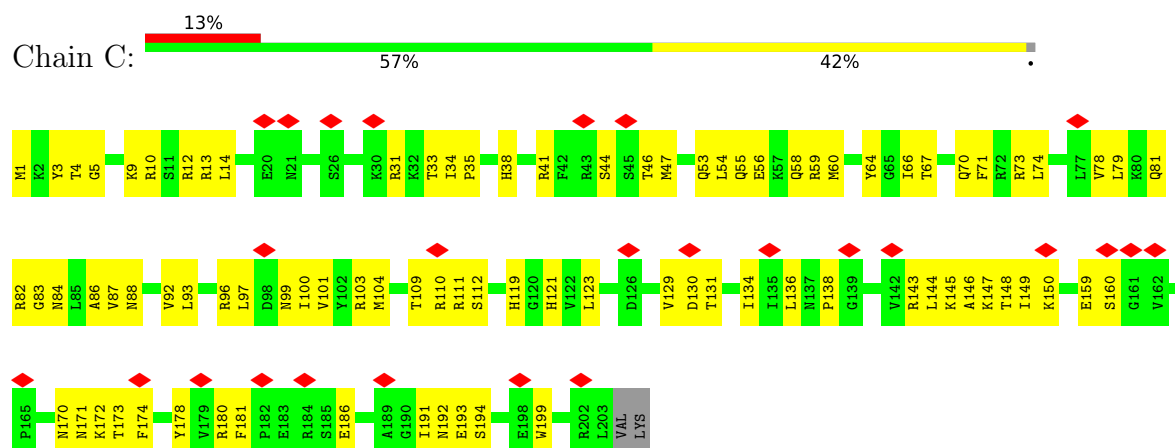
• Molecule 5: 30S ribosomal protein S2



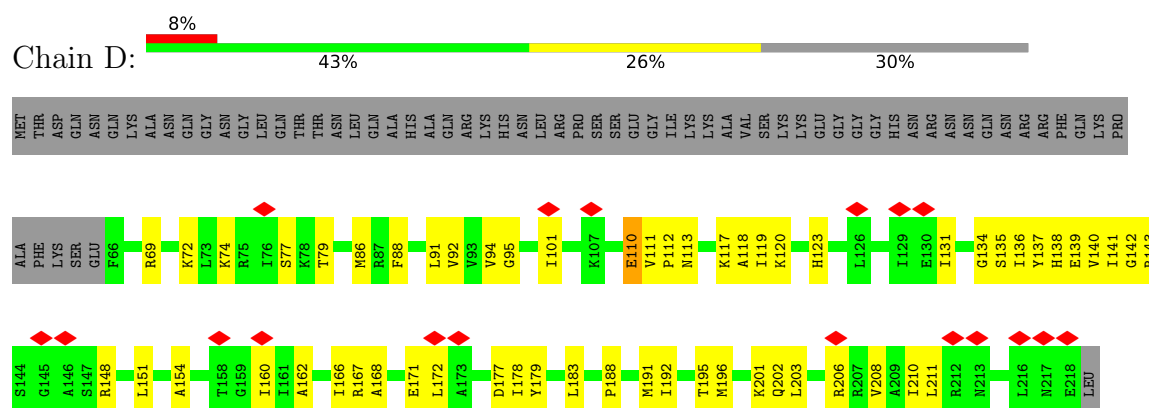
• Molecule 6: 30S ribosomal protein S3



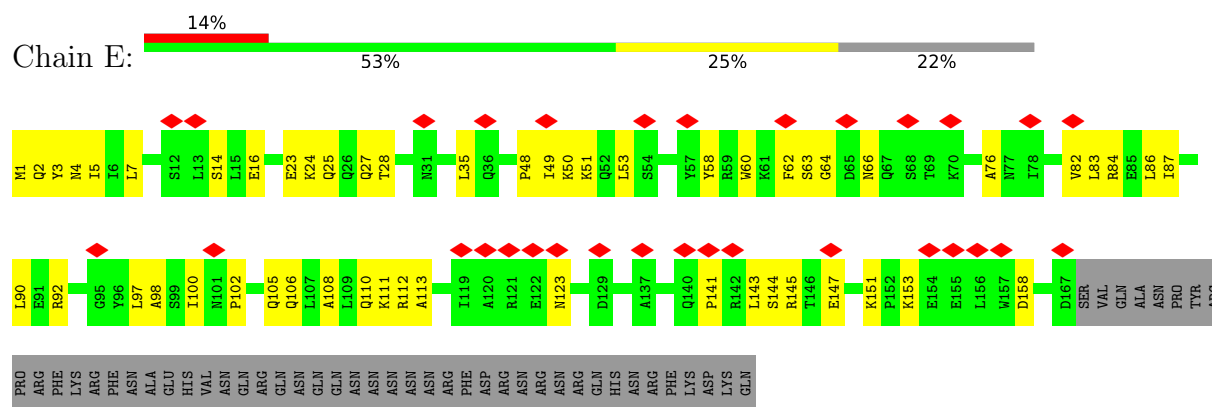
- Molecule 7: 30S ribosomal protein S4



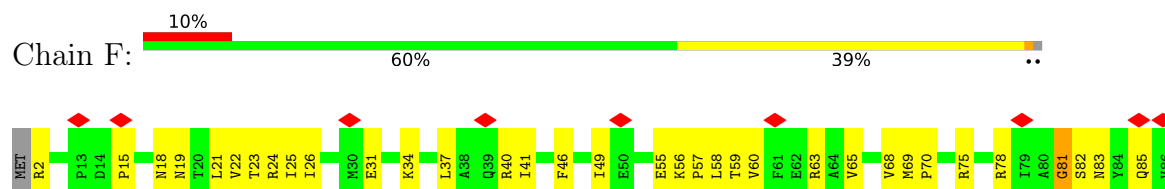
- Molecule 8: 30S ribosomal protein S5



- Molecule 9: 30S ribosomal protein S6



- Molecule 10: 30S ribosomal protein S7

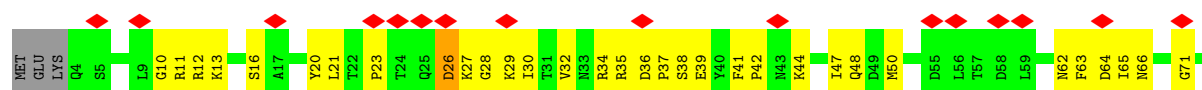




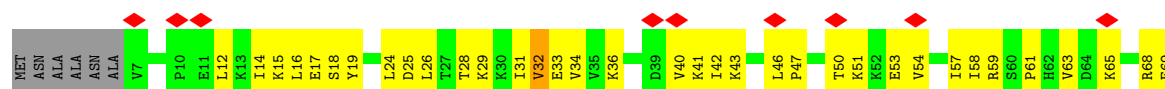
- Molecule 11: 30S ribosomal protein S8



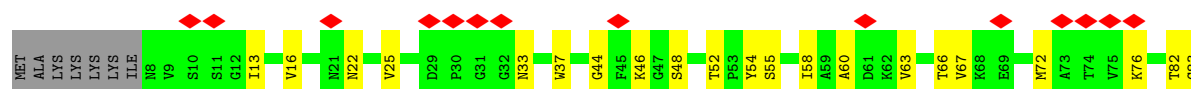
- Molecule 12: 30S ribosomal protein S9



- Molecule 13: 30S ribosomal protein S10

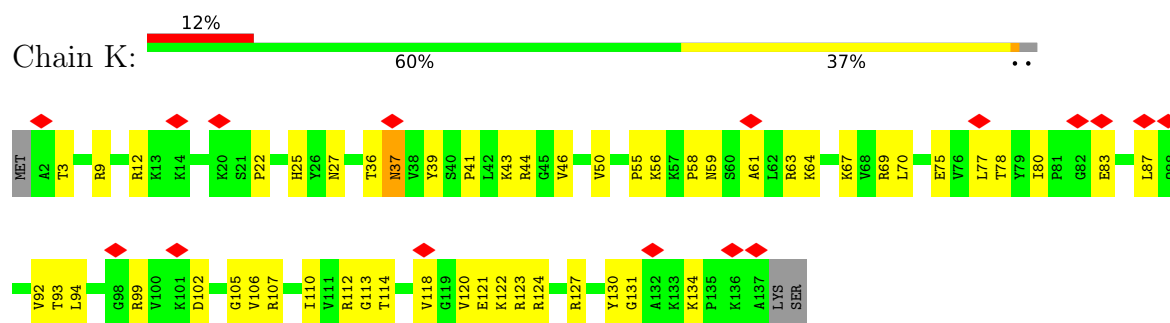


- Molecule 14: 30S ribosomal protein S11

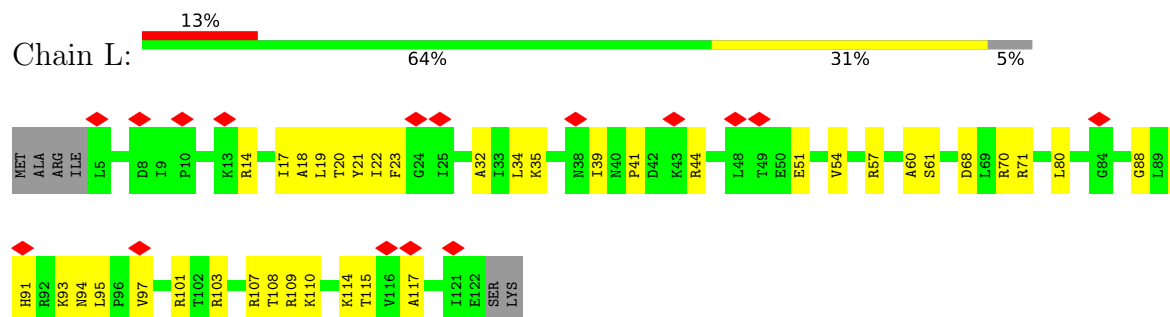


- Molecule 15: 30S ribosomal protein S12

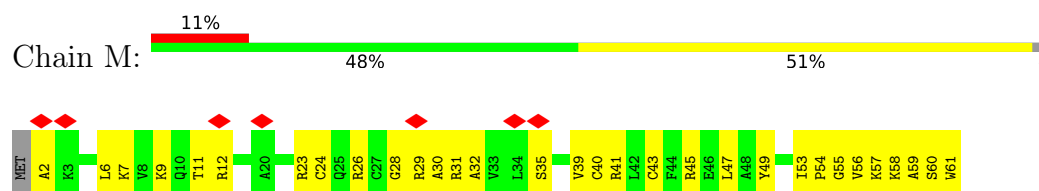




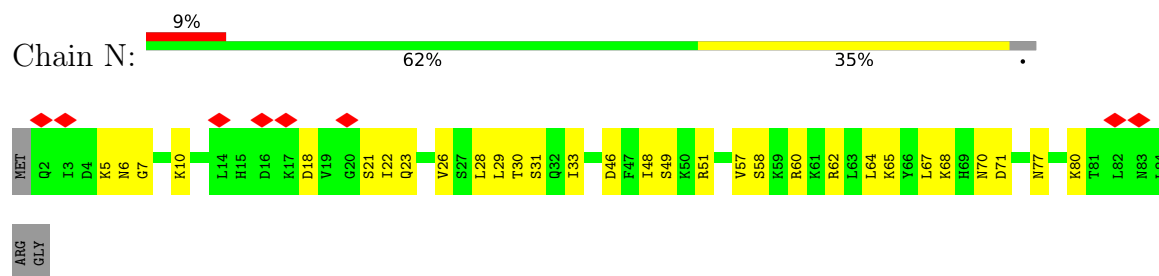
- Molecule 16: 30S ribosomal protein S13



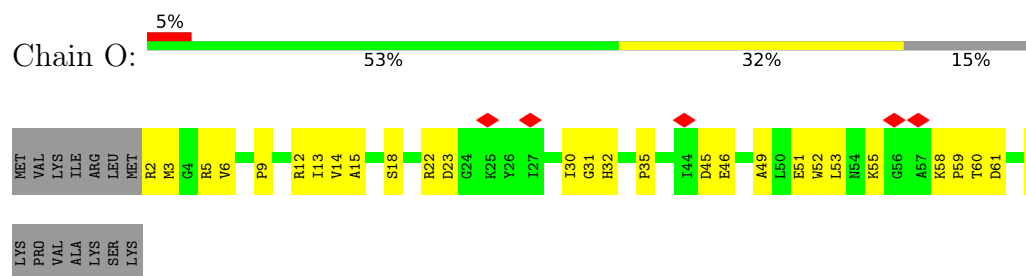
- Molecule 17: 30S ribosomal protein S14 type Z



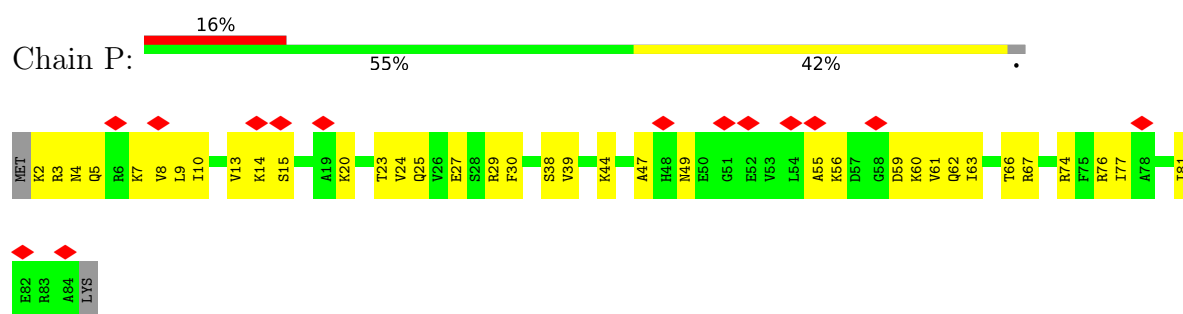
- Molecule 18: 30S ribosomal protein S15



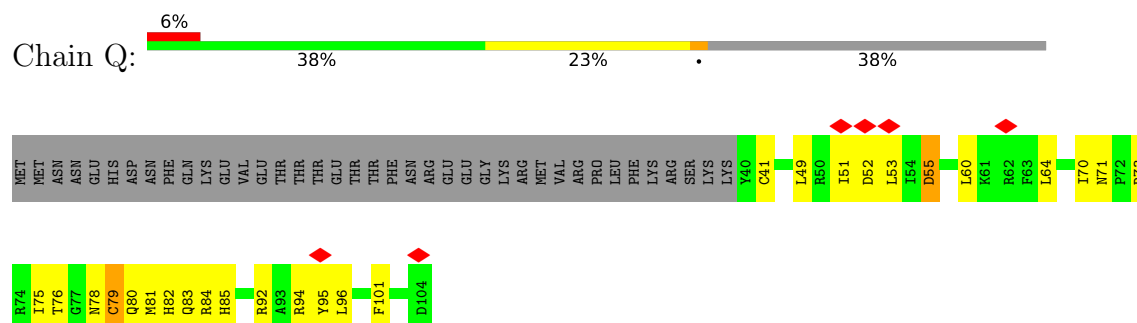
- Molecule 19: 30S ribosomal protein S16



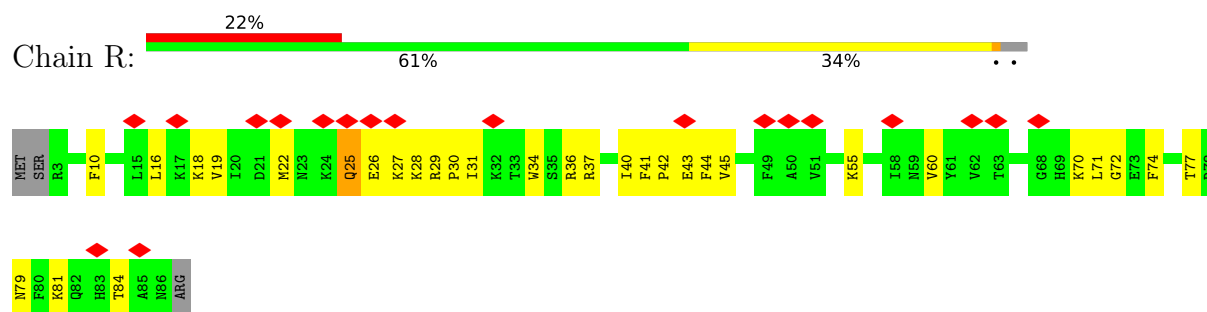
- Molecule 20: 30S ribosomal protein S17



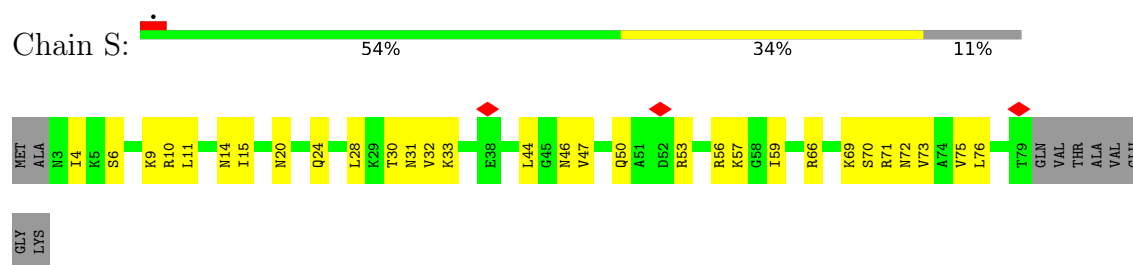
- Molecule 21: 30S ribosomal protein S18



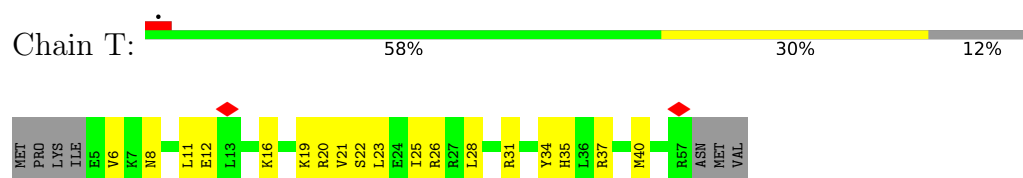
- Molecule 22: 30S ribosomal protein S19



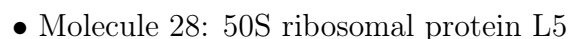
- Molecule 23: 30S ribosomal protein S20

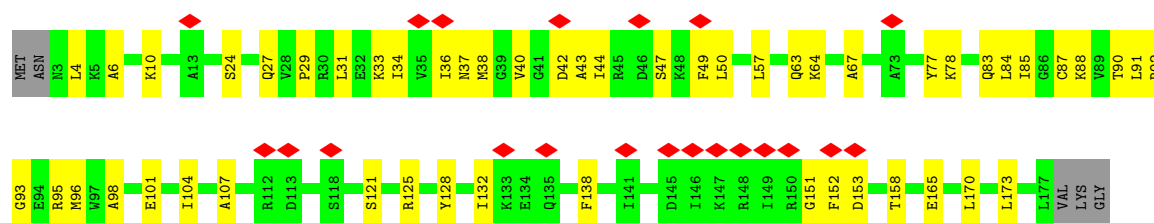


- Molecule 24: 30S ribosomal protein S21

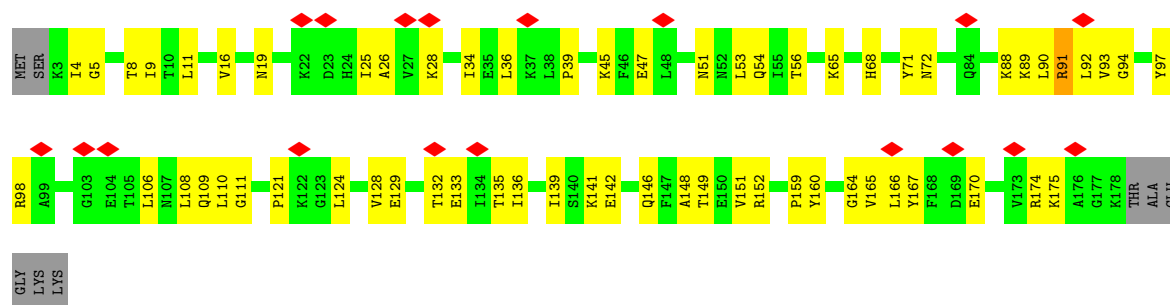


- Molecule 25: 50S ribosomal protein L2

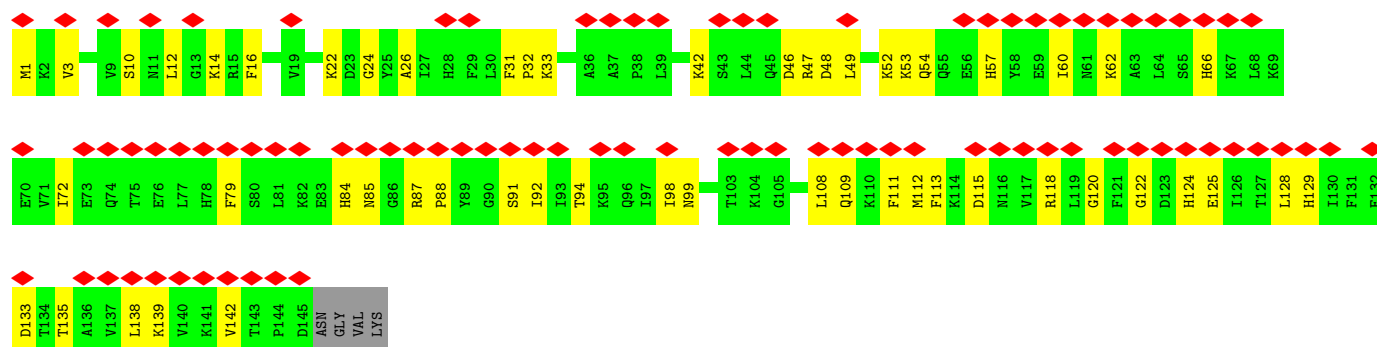




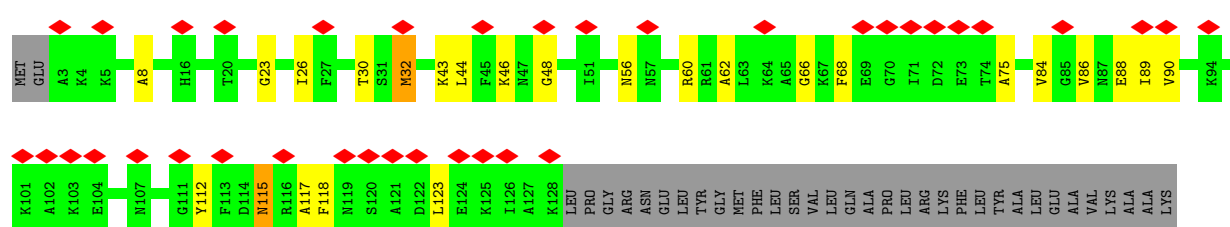
• Molecule 29: 50S ribosomal protein L6



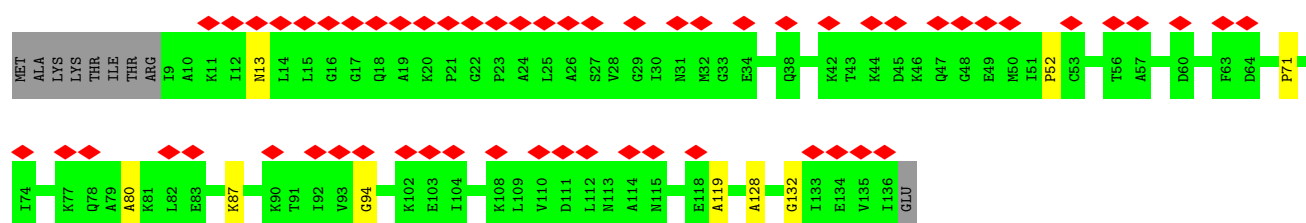
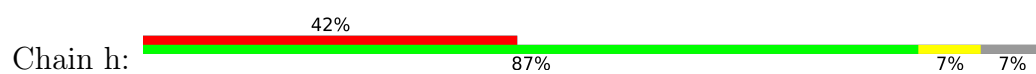
• Molecule 30: 50S ribosomal protein L9



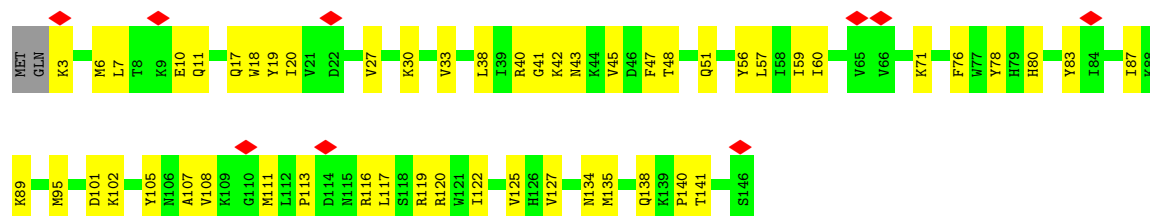
• Molecule 31: 50S ribosomal protein L10



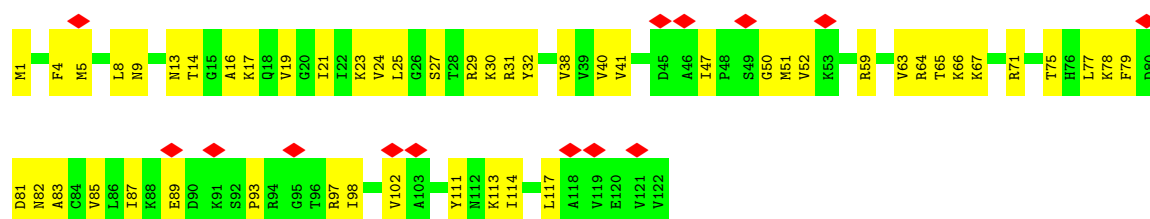
• Molecule 32: 50S ribosomal protein L11



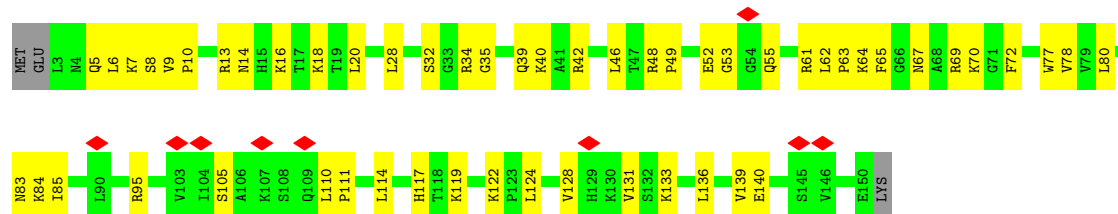
• Molecule 33: 50S ribosomal protein L13



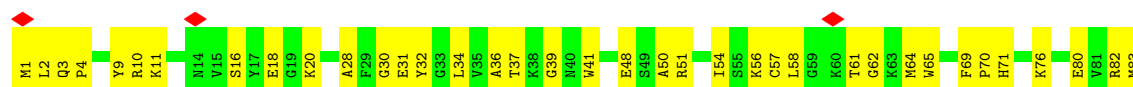
• Molecule 34: 50S ribosomal protein L14

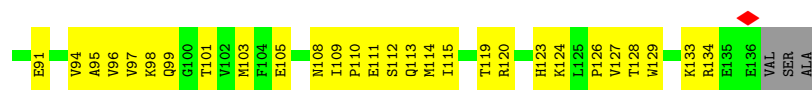


• Molecule 35: 50S ribosomal protein L15



• Molecule 36: 50S ribosomal protein L16





- Molecule 37: 50S ribosomal protein L17

Chain m: 53% 43%



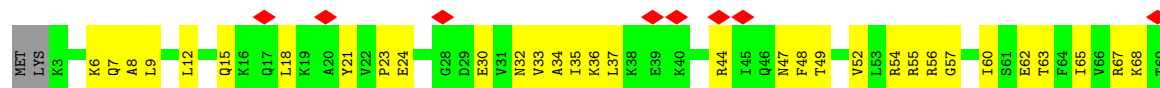
- Molecule 38: 50S ribosomal protein L18

Chain n: 8% 61% 35%



- Molecule 39: 50S ribosomal protein L19

Chain o: 10% 53% 44%

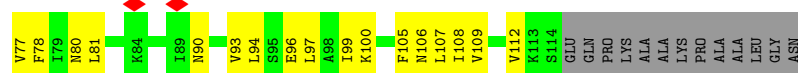


- Molecule 40: 50S ribosomal protein L20

Chain p: 48% 42% 10%



- Molecule 41: 50S ribosomal protein L21

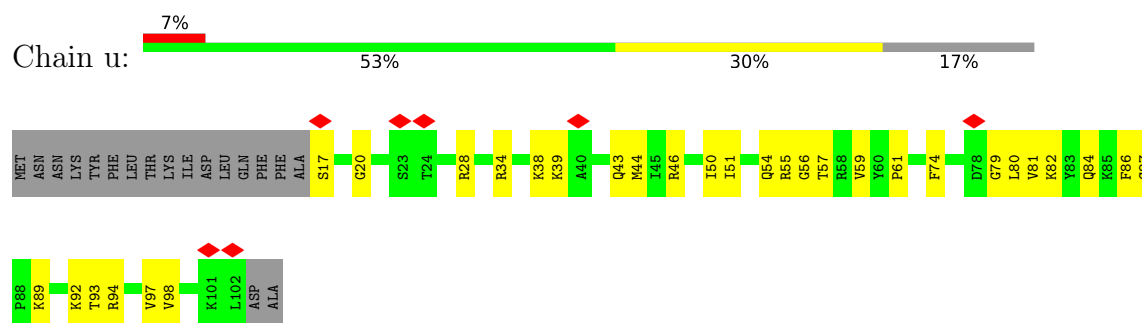


- Molecule 42: 50S ribosomal protein L22

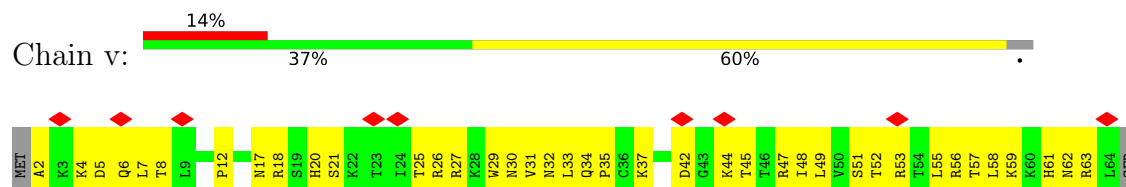
- Molecule 43: 50S ribosomal protein L23

- Molecule 44: 50S ribosomal protein L24

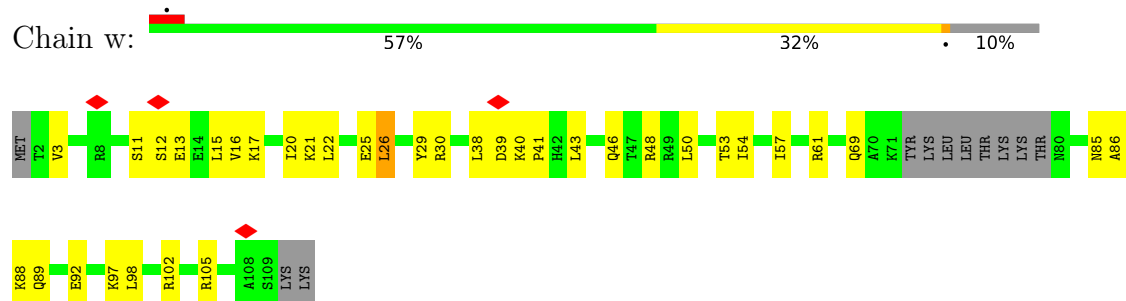
- Molecule 45: 50S ribosomal protein L27



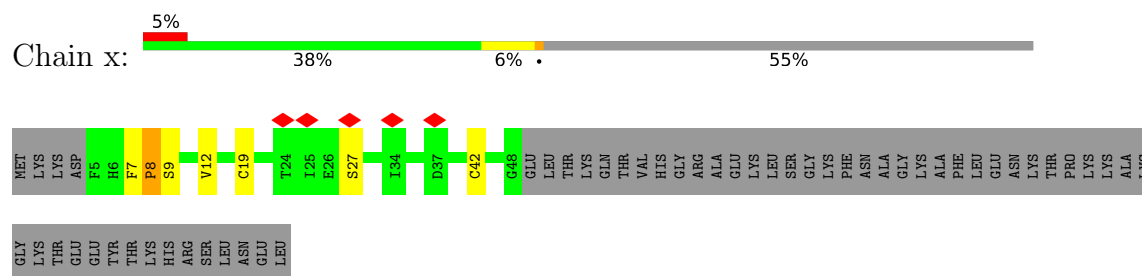
- Molecule 46: 50S ribosomal protein L28



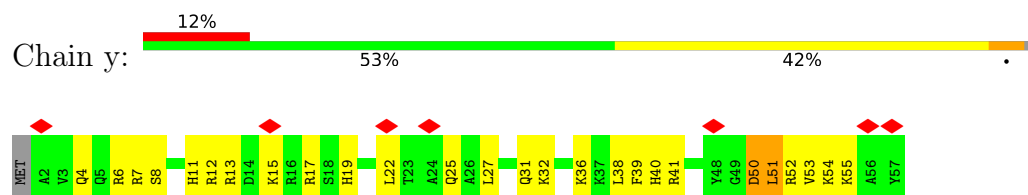
- Molecule 47: 50S ribosomal protein L29



- Molecule 48: 50S ribosomal protein L31

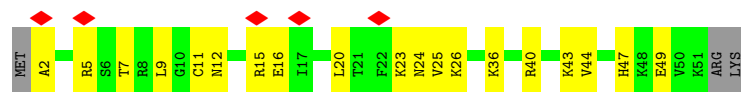


- Molecule 49: 50S ribosomal protein L32

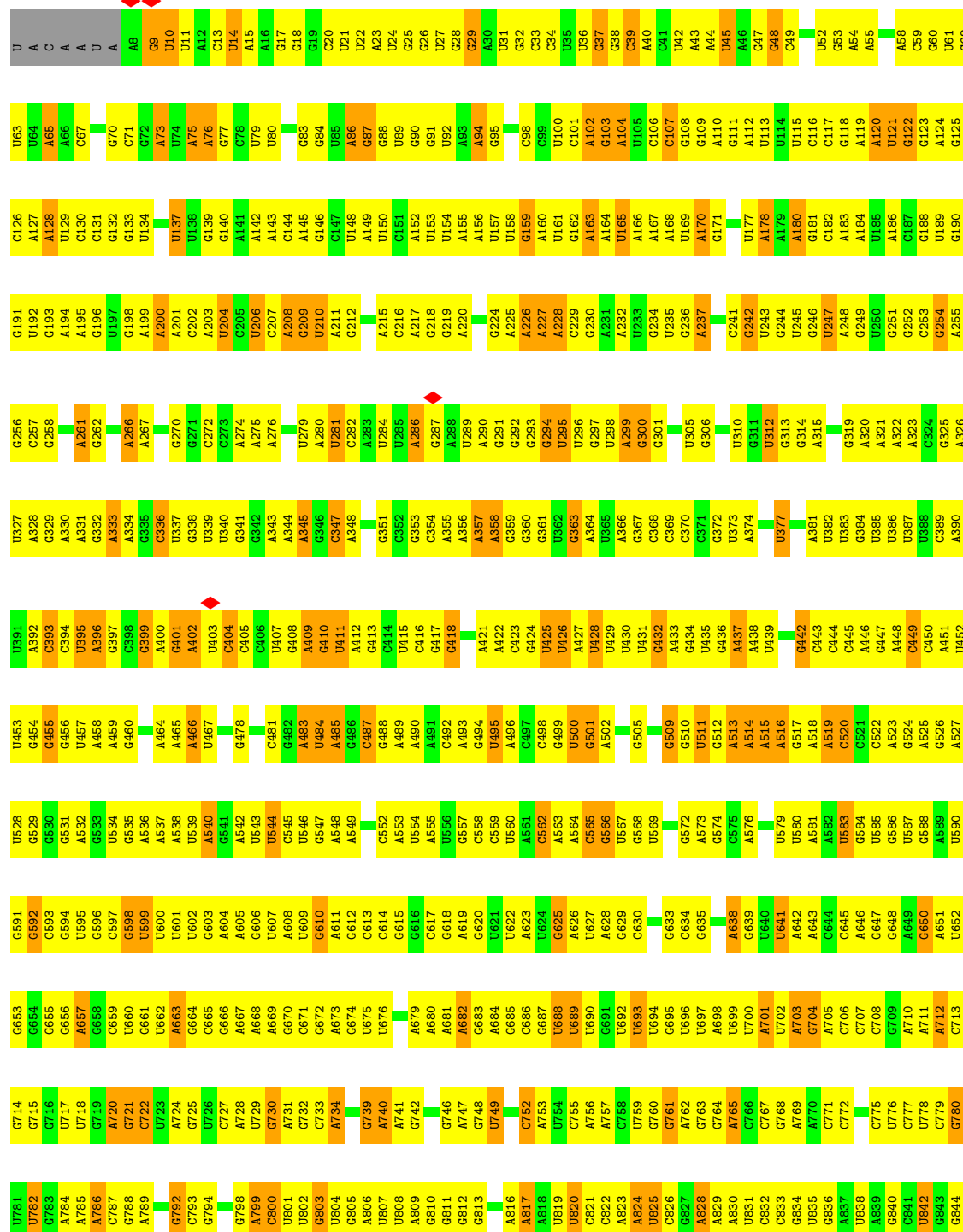


- Molecule 50: 50S ribosomal protein L33 1



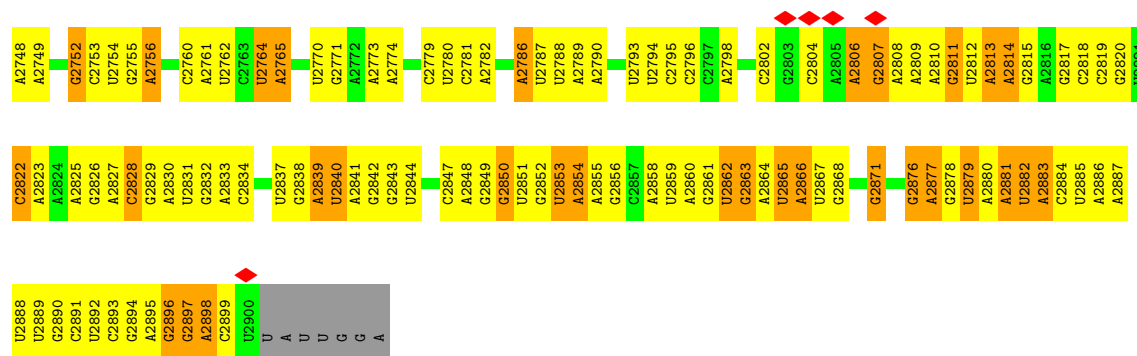


• Molecule 51: 23S ribosomal RNA



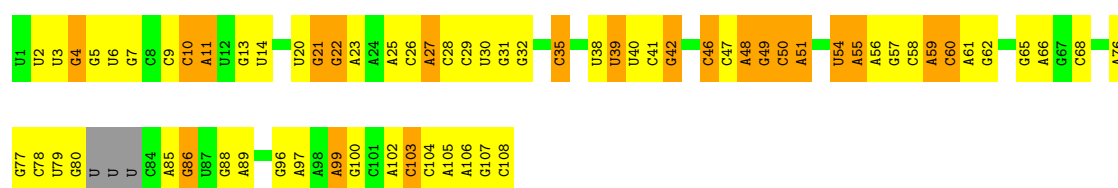






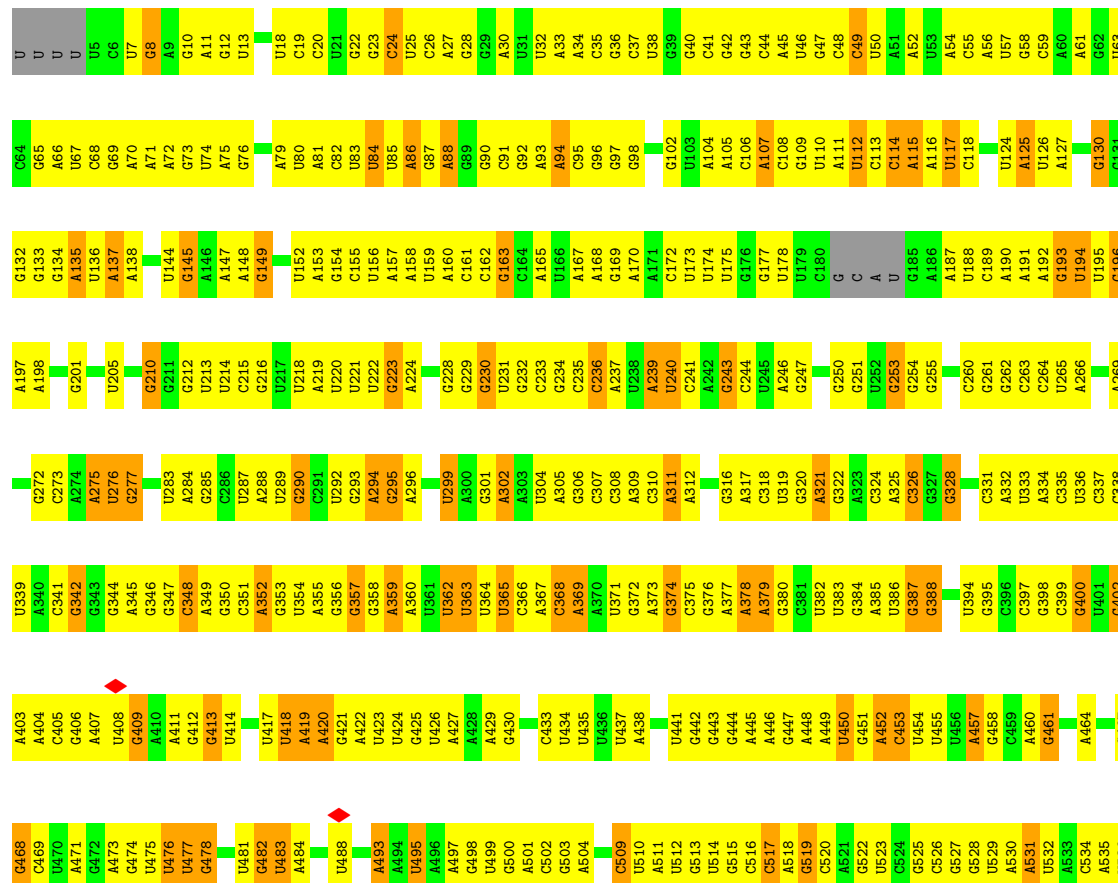
• Molecule 52: 5S ribosomal RNA

Chain 4: 35% 43% 19% .



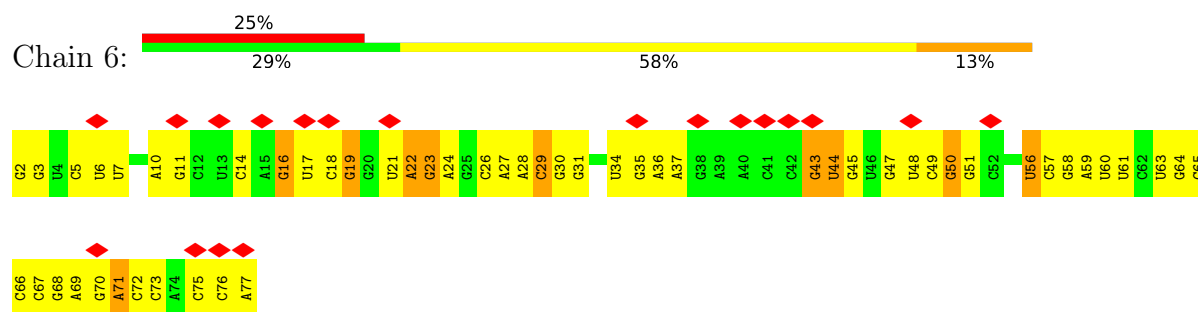
• Molecule 53: 16S ribosomal RNA

Chain 5: 26% 57% 15% .

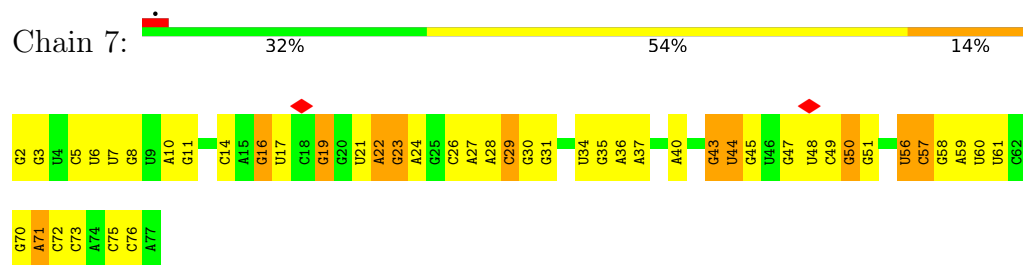


A1474	A1408	U1339	A1204	A1140	A1071	G1008	A941	A870	C805	A731	G665	G599	A537
A1477	A1409	G1340	C1205	U1141	G1072	G1009	G942	U871	A806	A732	U666	G600	G538
A1478	A1410	G1343	G1206	G1142	U1073	A1010	C943	C872	C807	A733	U667	U601	U539
G1479	G1413	G1344	G1209	C1143	U1074	A1011	A944	U873	C808	A734	G602	G602	U540
G1480	G1414	G1345	C1210	A1144	G1075	A1012	U945	C874	G809	C735	U669	U603	C541
U1481	G1415	G1346	A1211	A1145	U1076	C1013	G946	U875	U810	U736	G670	U604	G542
A1482	U1416	G1347	A1212	A1146	U1077	A1014	U947	C876	A811	U737	G671	A605	C543
C1483	U1417	G1348	C1213	U1147	U1081	U1015	U948	C877	A812	A738	A606	A606	A544
C1484	G1418	U1281	A1214	U1148	U1082	A1016	G949	C878	A813	A672	A607	A607	A545
C1485	U1282	G1283	C1215	A1149	U1083	A1017	C950	G879	C814	U674	G608	G608	C547
C1486	G1283	U1284	U1215	G1150	A1084	U1018	U951	G880	G815	U675	G609	G609	C547
U1487	G1216	G1285	G1216	G1151	A1085	G1019	U952	G881	A816	U745	C610	C610	G548
A1421	A1220	G1286	A1220	G1152	U1086	G	A953	U882	U817	A746	A611	A611	U549
C1422	A1221	G1287	A1221	G1153	U1087	A	A954	A883	A818	C747	U550	U550	U550
C1423	U1222	U1288	U1222	A1154	C1087	G	U955	G884	G819	A673	A608	A608	A551
C1424	A1223	U1289	A1223	A1155	U1088	G	U956	U885	A820	U674	U674	U674	U552
G1429	A1224	G1290	A1224	G1156	C1089	U	G	A886	A821	U675	G609	G609	C553
G1430	U1358	C1291	C1224	G1157	G1090	U	G611	C887	A822	A750	U681	U681	C554
A1431	G1359	A1292	A1225	A1158	C1091	A	G962	U888	C823	G752	G683	U618	G555
A1432	G1360	A1293	A1226	A1159	A1092	A	U963	U824	U824	C753	A684	A619	G556
G1433	G1361	U1294	A1227	G1160	C1093	C1028	A964	C891	A825	U754	A685	A620	A557
C1434	U1295	U1295	C1228	G1161	C1094	G1029	C965	G892	G826	U755	C621	C621	U558
G1435	G1229	U1296	A1229	G1162	U1099	G1030	A966	C893	A827	A756	A622	A622	U559
C1436	G1230	G1297	G1230	G1165	G1099	U1033	C967	A894	G829	U760	G623	G623	U560
U1437	U1298	U1298	G1233	G1166	A1102	U1037	G968	A895	U830	U761	U624	U624	A561
U1438	C1299	C1299	C1234	G1168	C1103	A1037	A969	G896	C831	U762	U625	U625	U562
G1439	U1304	U1304	C1235	U1169	C1104	G1038	A971	A897	G832	A763	A628	A628	U563
U1503	G1305	G1305	A1236	C1170	C1105	G1039	A972	U905	G833	G764	U629	U629	G564
G1504	A1306	A1306	G1237	C1171	U1106	U1040	A973	U906	G834	A765	G630	G630	G565
G1505	G1376	A1307	G1241	A1172	U1107	G1041	C974	A908	G835	G766	G631	G631	G566
A1506	C1377	A1307	U1242	A1173	A1108	G1042	C975	A909	G836	U767	A632	A632	C567
U1507	G1378	G1310	U1243	U1174	U1109	U1043	C976	C910	A838	G773	U633	U633	G568
C1508	C1379	G1311	A1243	C1175	G1110	G1044	U977	G911	U839	A774	A637	A637	U569
C	U1380	G1312	A1244	A1176	C1111	G1045	A978	G912	C840	G775	A638	A638	A570
C	U1381	A1313	A1245	U1177	U1112	A1046	C979	A913	C841	G776	A639	A639	A571
U	A1384	A1314	A1246	C1178	U1113	U1047	C980	A914	G842	A705	G573	G573	A572
U	A1385	U1315	G1247	A1179	A1114	G1048	U981	U915	C843	U706	C574	C574	C574
C	C1386	C1316	U1248	U1180	G1115	G1049	A982	U916	U844	G707	A575	A575	A575
C	U1387	A1317	G1249	G1181	U1116	U1050	G983	G917	U847	A708	U643	U643	A576
U	A1388	U1318	A1250	C1182	U1117	U1051	A984	A918	U848	A709	U644	U644	G577
U	C1389	U1319	G1251	C1183	A1118	G1052	C985	C919	U849	A781	A645	A645	C578
U	U1390	A1320	C1252	C1184	C1119	U1053	U986	G920	A849	G711	A646	A646	G579
C	G1391	G1321	A1253	U1187	A1120	G1054	U987	G921	G850	A712	U647	U647	C580
U	A1391	U1322	A1254	U1188	U1121	G1055	G988	G922	U851	A784	C648	C648	A581
U	G1394	U1325	A1255	U1189	G1122	U1056	A989	G923	G852	A787	U649	U649	G582
G1395	C1326	C1326	U1258	C1192	U1124	G1059	U996	C927	A854	C715	A650	A650	C584
U1396	G1327	G1327	G1259	U1193	A1127	C1060	G997	G928	G855	G788	G653	G653	G585
G1397	C1328	C1328	U1260	A1194	G1128	U1061	G998	C929	A858	A718	U654	U654	G586
G1398	G1329	G1329	A1261	U1195	C1129	C1062	C999	A930	U790	C719	G655	G655	A587
U1399	A1330	A1330	A1262	G1196	U1129	U1063	A1000	A931	U720	G721	U656	U656	G590
A1400	U1266	U1266	G1197	G1197	A1133	U1064	A1001	A932	G722	G721	G657	G657	A591
U1402	G1267	G1267	U1198	C1194	C1134	G1065	A1002	A933	G723	G723	G658	G658	A592
A1403	C1332	C1332	U1199	U1199	U1135	U1066	G1003	U935	G724	G724	U659	U659	A593
G1404	G1335	G1335	G1200	G1200	G1136	C1067	U1004	G936	A866	A725	G661	G661	A594
U1470	C1336	C1336	C1270	C1201	C1137	U1068	U1005	G937	A867	C802	G662	G662	G595
C1471	U1337	U1337	A1201	U1069	C1138	U1069	A1006	G940	G868	C803	G663	G663	A596
U1473	A1203	A1203	A1272	A1203	A1139	G1070	U1007		U869	A804	A664	A664	U598

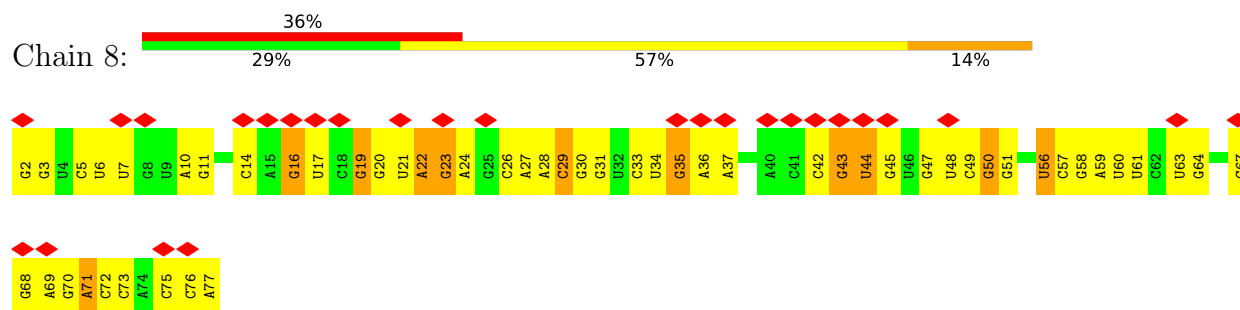
• Molecule 54: tRNA-Phe



- Molecule 54: tRNA-Phe



- Molecule 54: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	4634	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.676	Depositor
Minimum map value	-0.632	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.127	Depositor
Recommended contour level	0.47	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	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	0	0.18	0/383	0.43	0/504
2	1	0.14	0/484	0.47	0/637
3	2	0.22	0/306	0.67	0/401
4	9	0.19	0/3071	0.48	0/4147
5	A	0.18	0/1954	0.51	0/2642
6	B	0.17	0/1721	0.51	0/2323
7	C	0.17	0/1691	0.48	0/2267
8	D	0.15	0/1188	0.47	2/1593 (0.1%)
9	E	0.18	0/1384	0.49	0/1867
10	F	0.17	0/1266	0.52	0/1700
11	G	0.17	0/1126	0.52	1/1517 (0.1%)
12	H	0.19	0/1044	0.52	0/1395
13	I	0.23	0/820	0.72	2/1103 (0.2%)
14	J	0.16	0/844	0.45	0/1136
15	K	0.29	0/1094	0.61	0/1468
16	L	0.15	0/962	0.48	0/1289
17	M	0.25	0/483	0.53	0/643
18	N	0.17	0/679	0.47	0/907
19	O	0.16	0/659	0.48	0/885
20	P	0.18	0/684	0.48	0/913
21	Q	0.21	0/545	0.62	1/730 (0.1%)
22	R	0.18	0/698	0.57	0/936
23	S	0.20	0/631	0.51	0/838
24	T	0.20	0/475	0.56	0/621
25	a	0.17	0/2267	0.46	0/3044
26	b	0.15	0/1795	0.44	0/2412
27	c	0.14	0/1671	0.43	0/2246
28	d	0.17	0/1409	0.47	0/1894
29	e	0.24	0/1420	0.54	1/1912 (0.1%)
30	f	0.18	0/1183	0.50	1/1587 (0.1%)
31	g	0.50	0/969	0.87	1/1295 (0.1%)
32	h	0.14	0/968	0.46	0/1298
33	i	0.16	0/1186	0.46	0/1592
34	j	0.17	0/953	0.49	0/1275

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	k	0.17	0/1170	0.48	0/1559
36	l	0.18	0/1104	0.52	0/1481
37	m	0.16	0/973	0.50	0/1309
38	n	0.18	0/897	0.54	0/1198
39	o	0.16	0/948	0.46	0/1262
40	p	0.15	0/961	0.47	0/1278
41	q	0.19	0/828	0.64	2/1111 (0.2%)
42	r	0.20	0/1077	0.57	0/1441
43	s	0.19	0/732	0.56	1/988 (0.1%)
44	t	0.15	0/879	0.44	0/1165
45	u	0.15	0/665	0.46	0/884
46	v	0.32	0/519	0.63	0/695
47	w	0.18	0/826	0.55	1/1104 (0.1%)
48	x	0.17	0/353	0.46	1/474 (0.2%)
49	y	0.35	0/457	0.76	0/601
50	z	0.14	0/412	0.44	0/547
51	3	0.10	0/69073	0.26	0/107710
52	4	0.10	0/2505	0.26	0/3902
53	5	0.10	0/35768	0.24	0/55764
54	6	0.11	0/1808	0.31	0/2817
54	7	0.11	0/1808	0.31	0/2817
54	8	0.11	0/1808	0.31	0/2817
All	All	0.14	0/163584	0.35	14/243941 (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
11	G	0	1
12	H	0	1
22	R	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	I	32	VAL	CA-C-N	-6.45	109.65	121.52
13	I	32	VAL	C-N-CA	-6.45	109.65	121.52
30	f	3	VAL	N-CA-C	-6.24	106.65	112.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	e	91	ARG	CG-CD-NE	5.86	124.89	112.00
43	s	45	GLU	CA-CB-CG	5.76	125.62	114.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	G	108	LEU	Peptide
12	H	26	ASP	Peptide
22	R	25	GLN	Peptide

5.2 Too-close contacts [i](#)

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	0	380	0	429	21	0
2	1	477	0	530	24	0
3	2	304	0	350	13	0
4	9	3021	0	3050	131	0
5	A	1921	0	1973	74	0
6	B	1698	0	1768	69	0
7	C	1660	0	1719	72	0
8	D	1173	0	1267	48	0
9	E	1362	0	1377	54	0
10	F	1246	0	1308	56	0
11	G	1110	0	1226	50	0
12	H	1028	0	1094	47	0
13	I	809	0	894	57	0
14	J	829	0	855	32	0
15	K	1076	0	1170	47	0
16	L	951	0	1014	33	0
17	M	474	0	509	34	0
18	N	673	0	730	25	0
19	O	646	0	677	26	0
20	P	675	0	728	29	0
21	Q	535	0	562	26	0
22	R	682	0	691	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	S	629	0	681	27	0
24	T	471	0	522	25	0
25	a	2225	0	2301	99	0
26	b	1762	0	1808	70	0
27	c	1644	0	1731	67	0
28	d	1388	0	1469	43	0
29	e	1396	0	1481	51	0
30	f	1160	0	1172	47	0
31	g	960	0	1014	7	0
32	h	959	0	1039	7	0
33	i	1164	0	1192	47	0
34	j	944	0	1019	44	0
35	k	1153	0	1256	46	0
36	l	1079	0	1134	57	0
37	m	958	0	1011	40	0
38	n	889	0	952	33	0
39	o	938	0	1008	46	0
40	p	947	0	1028	59	0
41	q	811	0	858	50	0
42	r	1068	0	1150	32	0
43	s	720	0	803	30	0
44	t	872	0	972	31	0
45	u	657	0	695	28	0
46	v	513	0	560	41	0
47	w	818	0	870	30	0
48	x	344	0	333	3	0
49	y	452	0	472	29	0
50	z	408	0	440	15	0
51	3	61664	0	30954	2049	0
52	4	2239	0	1137	57	0
53	5	31943	0	16058	1061	0
54	6	1618	0	821	38	0
54	7	1618	0	821	38	0
54	8	1618	0	821	40	0
All	All	150759	0	103504	4828	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 20.

The worst 5 of 4828 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)
51:3:1310:U:C2	51:3:1314:A:N6	2.06	1.24
45:u:79:GLY:HA3	45:u:98:VAL:O	1.51	1.10
51:3:2483:C:N4	51:3:2537:G:H22	1.51	1.08
53:5:61:A:H62	53:5:95:C:N4	1.54	1.04
29:e:16:VAL:HA	29:e:28:LYS:O	1.59	1.03

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	0	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
2	1	57/59 (97%)	51 (90%)	6 (10%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	9	391/394 (99%)	367 (94%)	23 (6%)	1 (0%)	36	72
5	A	238/294 (81%)	223 (94%)	15 (6%)	0	100	100
6	B	213/273 (78%)	192 (90%)	20 (9%)	1 (0%)	24	63
7	C	201/205 (98%)	180 (90%)	21 (10%)	0	100	100
8	D	151/219 (69%)	144 (95%)	7 (5%)	0	100	100
9	E	165/215 (77%)	147 (89%)	18 (11%)	0	100	100
10	F	152/155 (98%)	136 (90%)	15 (10%)	1 (1%)	18	56
11	G	139/142 (98%)	122 (88%)	17 (12%)	0	100	100
12	H	126/132 (96%)	102 (81%)	23 (18%)	1 (1%)	16	54
13	I	99/108 (92%)	91 (92%)	8 (8%)	0	100	100
14	J	112/121 (93%)	107 (96%)	5 (4%)	0	100	100
15	K	134/139 (96%)	120 (90%)	14 (10%)	0	100	100
16	L	116/124 (94%)	100 (86%)	16 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	M	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
18	N	81/86 (94%)	81 (100%)	0	0	100	100
19	O	78/94 (83%)	73 (94%)	5 (6%)	0	100	100
20	P	81/85 (95%)	77 (95%)	4 (5%)	0	100	100
21	Q	63/104 (61%)	55 (87%)	7 (11%)	1 (2%)	7	38
22	R	82/87 (94%)	71 (87%)	11 (13%)	0	100	100
23	S	75/87 (86%)	75 (100%)	0	0	100	100
24	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
25	a	283/287 (99%)	256 (90%)	27 (10%)	0	100	100
26	b	227/287 (79%)	209 (92%)	18 (8%)	0	100	100
27	c	208/212 (98%)	197 (95%)	11 (5%)	0	100	100
28	d	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
29	e	174/184 (95%)	160 (92%)	14 (8%)	0	100	100
30	f	143/149 (96%)	130 (91%)	13 (9%)	0	100	100
31	g	124/161 (77%)	115 (93%)	7 (6%)	2 (2%)	7	38
32	h	126/137 (92%)	106 (84%)	20 (16%)	0	100	100
33	i	142/146 (97%)	133 (94%)	9 (6%)	0	100	100
34	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
35	k	146/151 (97%)	139 (95%)	7 (5%)	0	100	100
36	l	134/139 (96%)	129 (96%)	5 (4%)	0	100	100
37	m	117/124 (94%)	111 (95%)	6 (5%)	0	100	100
38	n	108/116 (93%)	98 (91%)	10 (9%)	0	100	100
39	o	113/119 (95%)	104 (92%)	9 (8%)	0	100	100
40	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
41	q	97/100 (97%)	79 (81%)	18 (19%)	0	100	100
42	r	137/159 (86%)	126 (92%)	11 (8%)	0	100	100
43	s	90/237 (38%)	81 (90%)	9 (10%)	0	100	100
44	t	109/111 (98%)	100 (92%)	9 (8%)	0	100	100
45	u	84/104 (81%)	79 (94%)	5 (6%)	0	100	100
46	v	61/65 (94%)	57 (93%)	4 (7%)	0	100	100
47	w	96/111 (86%)	90 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	x	42/97 (43%)	35 (83%)	6 (14%)	1 (2%)	4	27
49	y	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
50	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
All	All	6211/7064 (88%)	5704 (92%)	499 (8%)	8 (0%)	49	83

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	9	334	ARG
6	B	103	ASP
31	g	32	MET
12	H	27	LYS
21	Q	79	CYS

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	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	9	324/325 (100%)	324 (100%)	0	100	100
5	A	212/262 (81%)	212 (100%)	0	100	100
6	B	180/232 (78%)	180 (100%)	0	100	100
7	C	181/183 (99%)	180 (99%)	1 (1%)	78	83
8	D	123/178 (69%)	123 (100%)	0	100	100
9	E	150/196 (76%)	150 (100%)	0	100	100
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	123 (100%)	0	100	100
12	H	111/115 (96%)	111 (100%)	0	100	100
13	I	95/99 (96%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	113 (97%)	4 (3%)	32	54
16	L	100/105 (95%)	100 (100%)	0	100	100
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	74 (100%)	0	100	100
23	S	70/77 (91%)	70 (100%)	0	100	100
24	T	49/56 (88%)	49 (100%)	0	100	100
25	a	241/243 (99%)	241 (100%)	0	100	100
26	b	186/233 (80%)	186 (100%)	0	100	100
27	c	182/184 (99%)	182 (100%)	0	100	100
28	d	150/154 (97%)	150 (100%)	0	100	100
29	e	153/159 (96%)	153 (100%)	0	100	100
30	f	123/134 (92%)	123 (100%)	0	100	100
31	g	101/129 (78%)	89 (88%)	12 (12%)	5	18
32	h	102/110 (93%)	102 (100%)	0	100	100
33	i	126/128 (98%)	126 (100%)	0	100	100
34	j	103/103 (100%)	103 (100%)	0	100	100
35	k	123/126 (98%)	123 (100%)	0	100	100
36	l	113/115 (98%)	113 (100%)	0	100	100
37	m	105/109 (96%)	105 (100%)	0	100	100
38	n	96/99 (97%)	96 (100%)	0	100	100
39	o	101/105 (96%)	101 (100%)	0	100	100
40	p	100/108 (93%)	100 (100%)	0	100	100
41	q	90/91 (99%)	90 (100%)	0	100	100
42	r	116/132 (88%)	116 (100%)	0	100	100
43	s	82/208 (39%)	82 (100%)	0	100	100
44	t	96/96 (100%)	96 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	u	69/85 (81%)	69 (100%)	0	100	100
46	v	58/60 (97%)	58 (100%)	0	100	100
47	w	87/98 (89%)	87 (100%)	0	100	100
48	x	41/86 (48%)	41 (100%)	0	100	100
49	y	48/49 (98%)	45 (94%)	3 (6%)	16	37
50	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5417/6076 (89%)	5397 (100%)	20 (0%)	81	84

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

Mol	Chain	Res	Type
31	g	89	ILE
49	y	50	ASP
49	y	52	ARG
49	y	51	LEU
31	g	30	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
30	f	55	GLN
39	o	47	ASN
30	f	109	GLN
35	k	134	GLN
42	r	15	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	2875/2907 (98%)	806 (28%)	31 (1%)
52	4	103/108 (95%)	33 (32%)	3 (2%)
53	5	1490/1520 (98%)	354 (23%)	3 (0%)
54	6	75/76 (98%)	23 (30%)	2 (2%)
54	7	75/76 (98%)	23 (30%)	2 (2%)
54	8	75/76 (98%)	23 (30%)	2 (2%)
All	All	4693/4763 (98%)	1262 (26%)	43 (0%)

5 of 1262 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	9	G
51	3	10	U
51	3	14	U
51	3	15	A
51	3	29	G

5 of 43 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	3	2764	U
53	5	419	A
51	3	2862	U
52	4	54	U
54	6	16	G

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](#)

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.

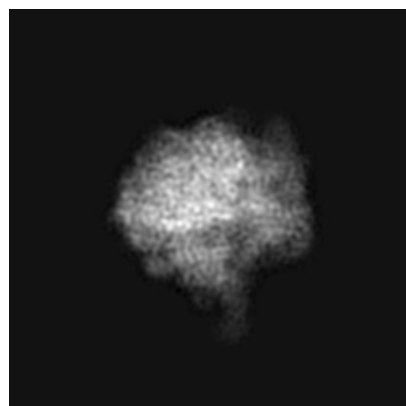
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13274. These allow visual inspection of the internal detail of the map and identification of artifacts.

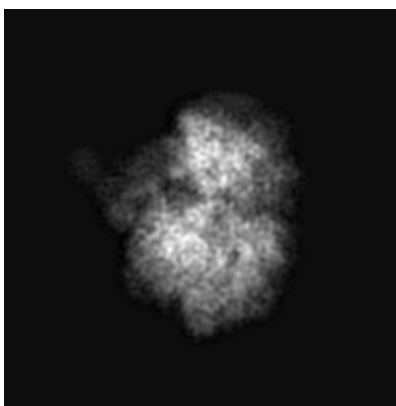
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

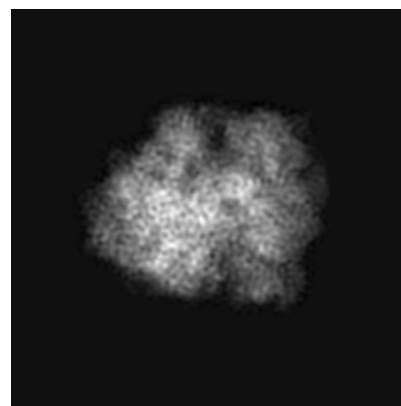
6.1.1 Primary map



X

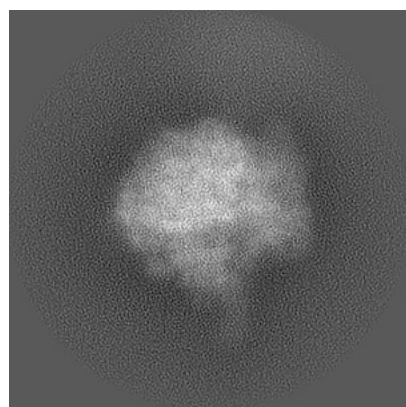


Y

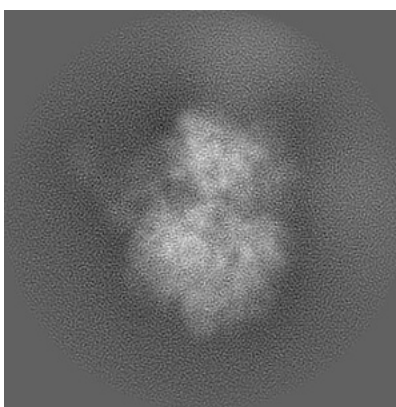


Z

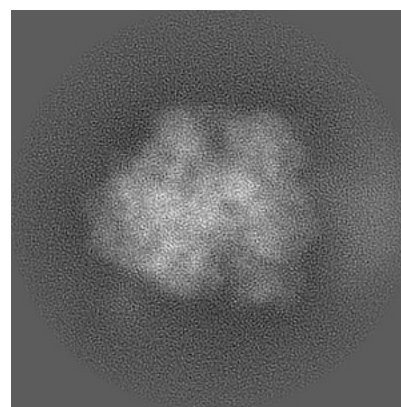
6.1.2 Raw map



X



Y

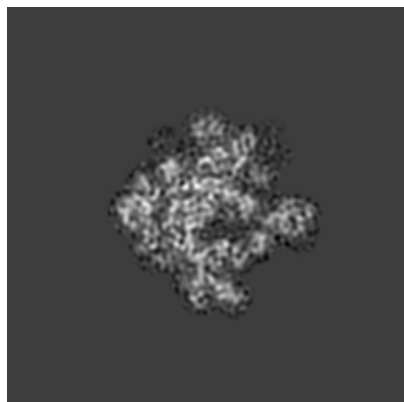


Z

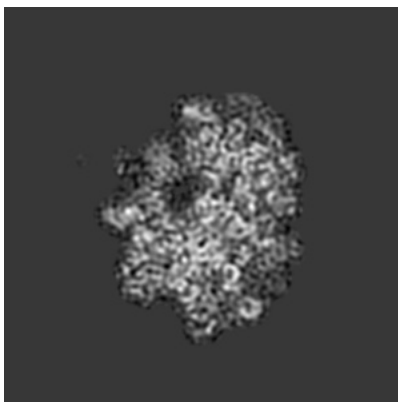
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

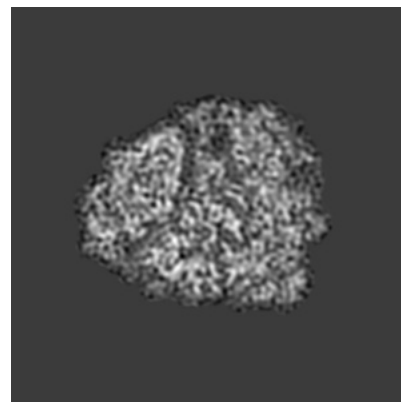
6.2.1 Primary map



X Index: 128

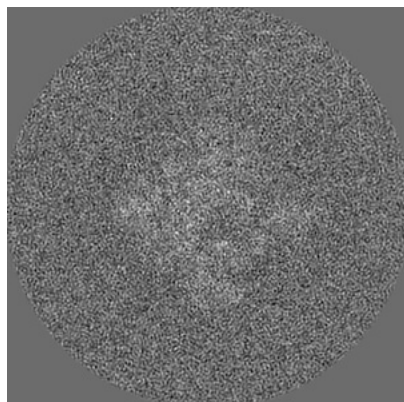


Y Index: 128

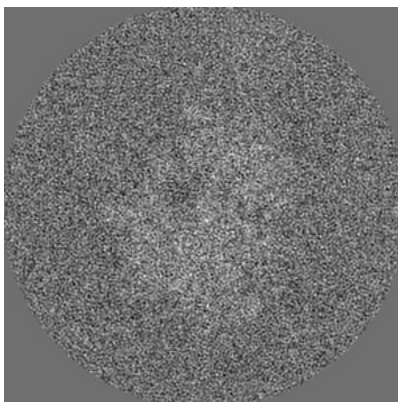


Z Index: 128

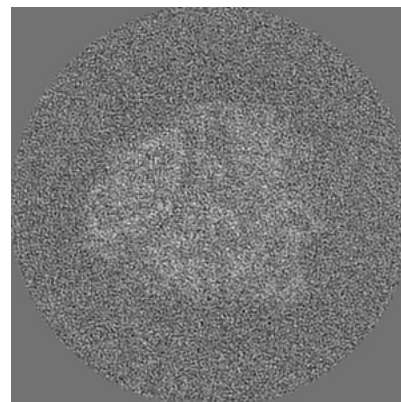
6.2.2 Raw map



X Index: 128



Y Index: 128

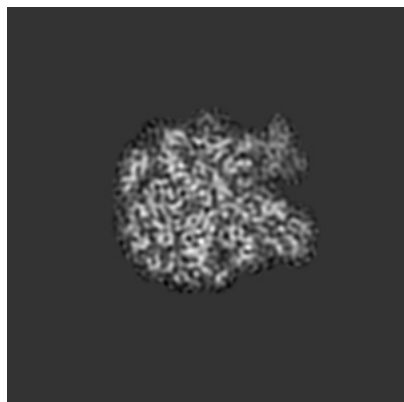


Z Index: 128

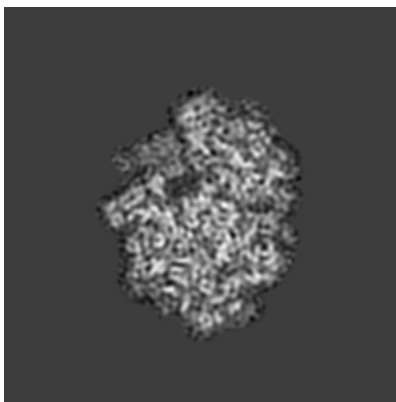
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

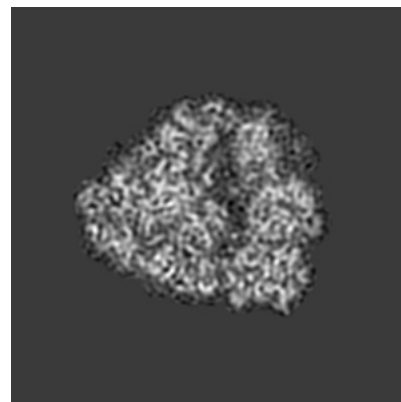
6.3.1 Primary map



X Index: 103

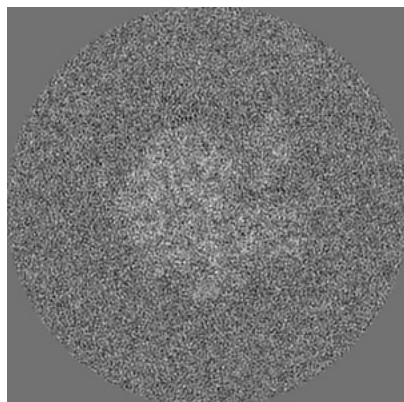


Y Index: 120

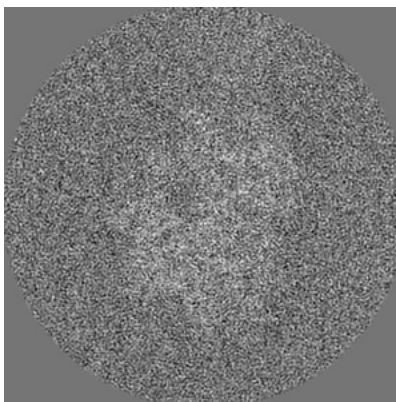


Z Index: 123

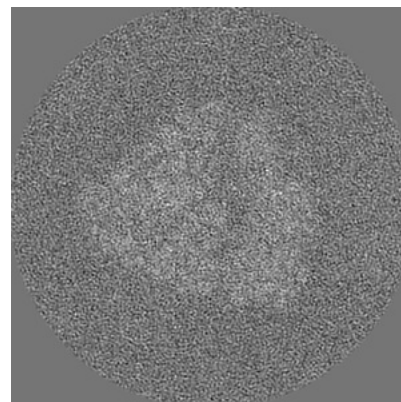
6.3.2 Raw map



X Index: 117



Y Index: 130

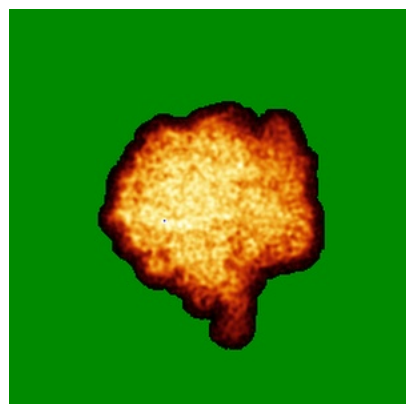


Z Index: 123

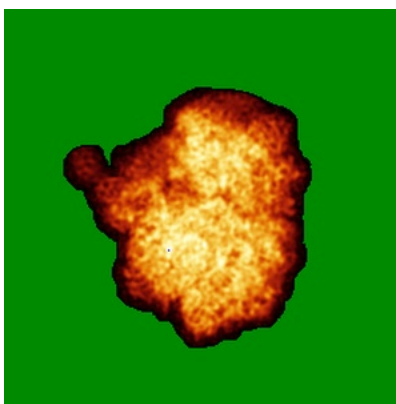
The images above show the largest variance slices of the map in three orthogonal directions.

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

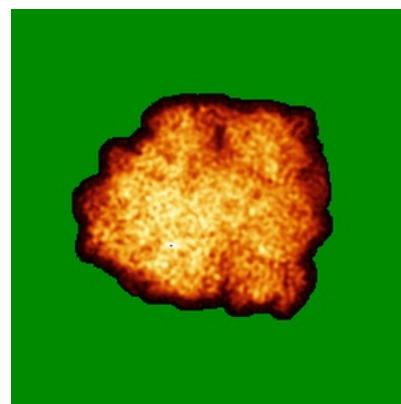
6.4.1 Primary map



X

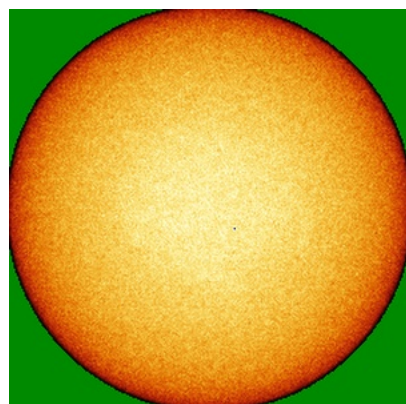


Y

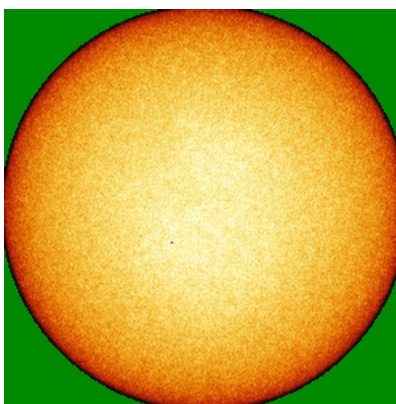


Z

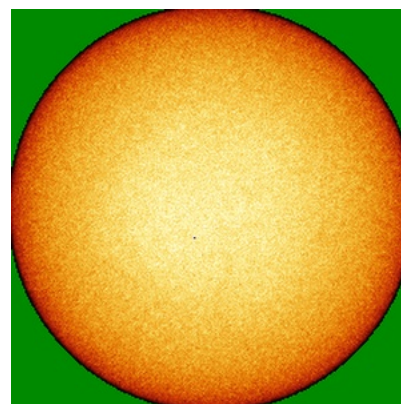
6.4.2 Raw map



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.

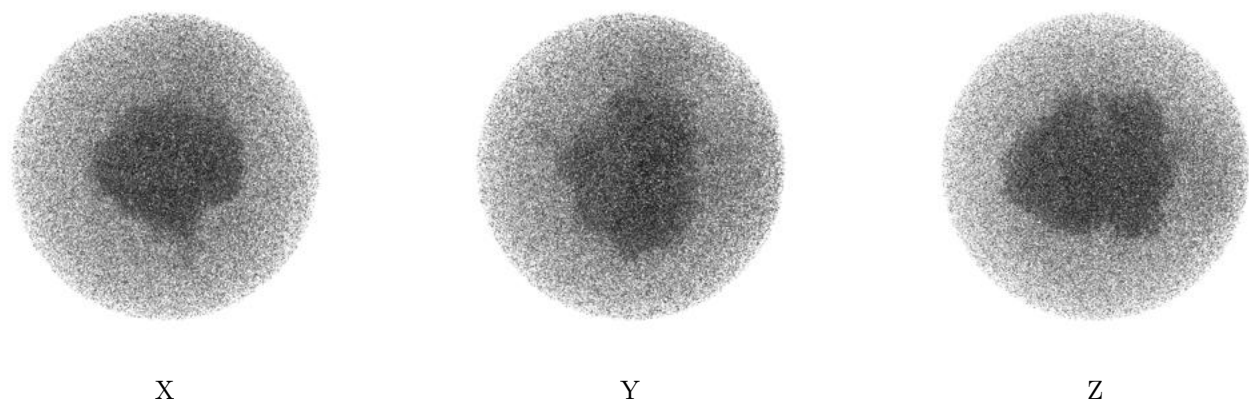
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.47. 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.

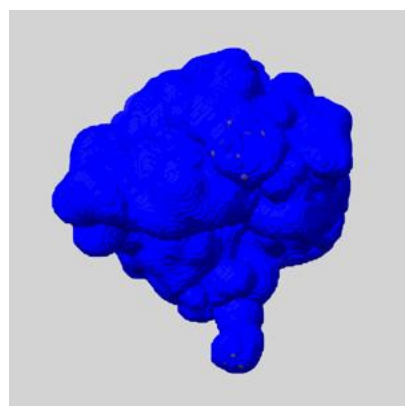
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

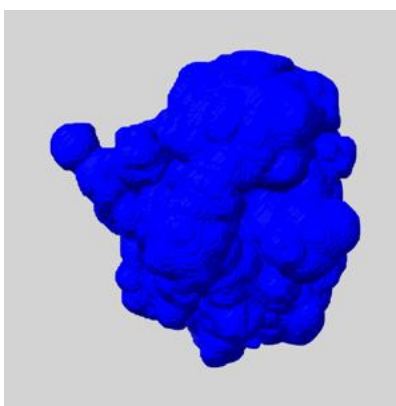
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

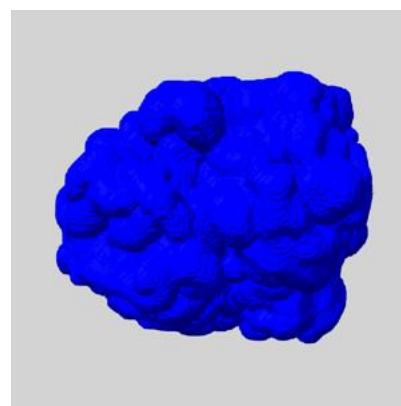
6.6.1 emd_13274_msk_1.map [i](#)



X



Y

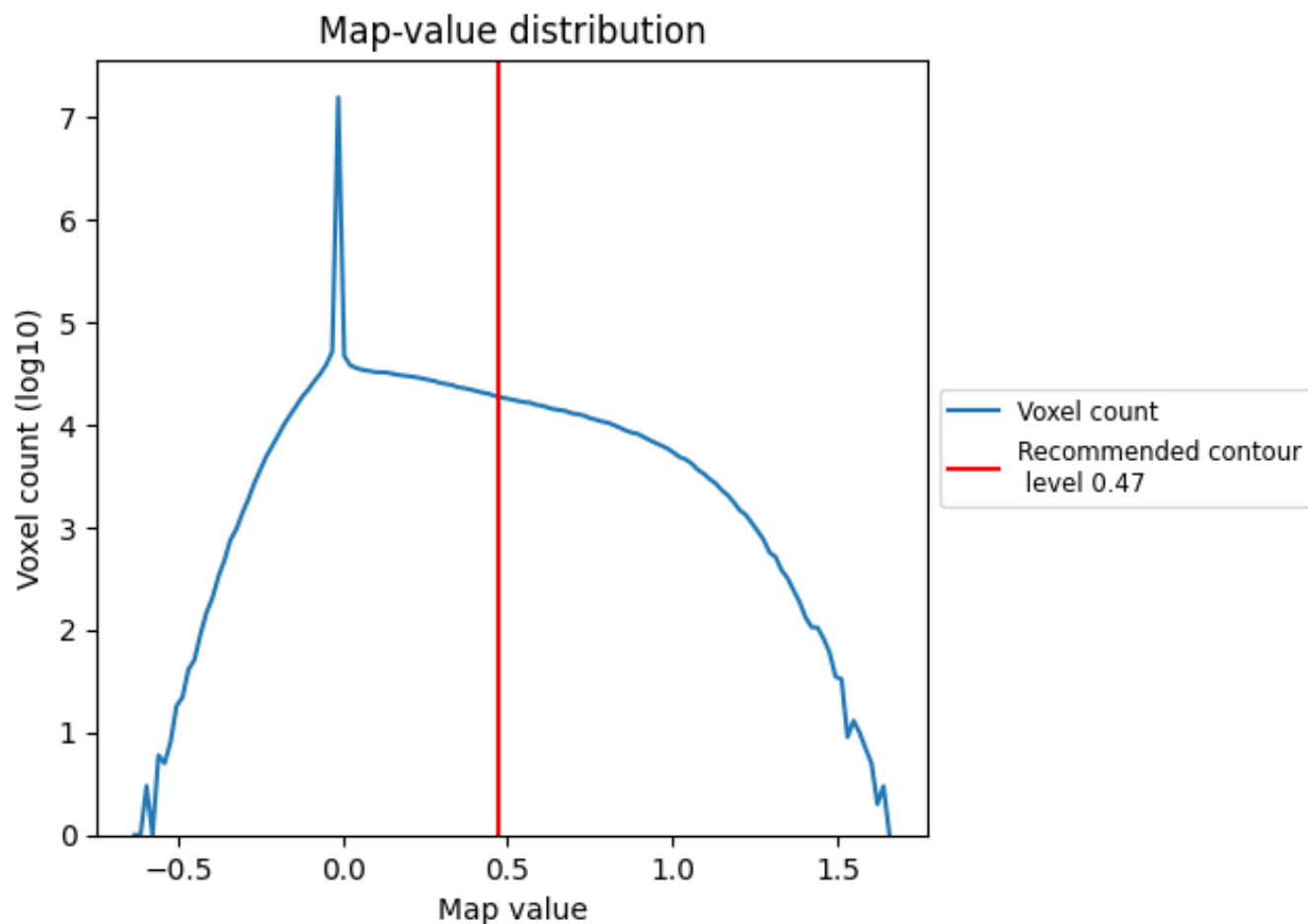


Z

7 Map analysis [i](#)

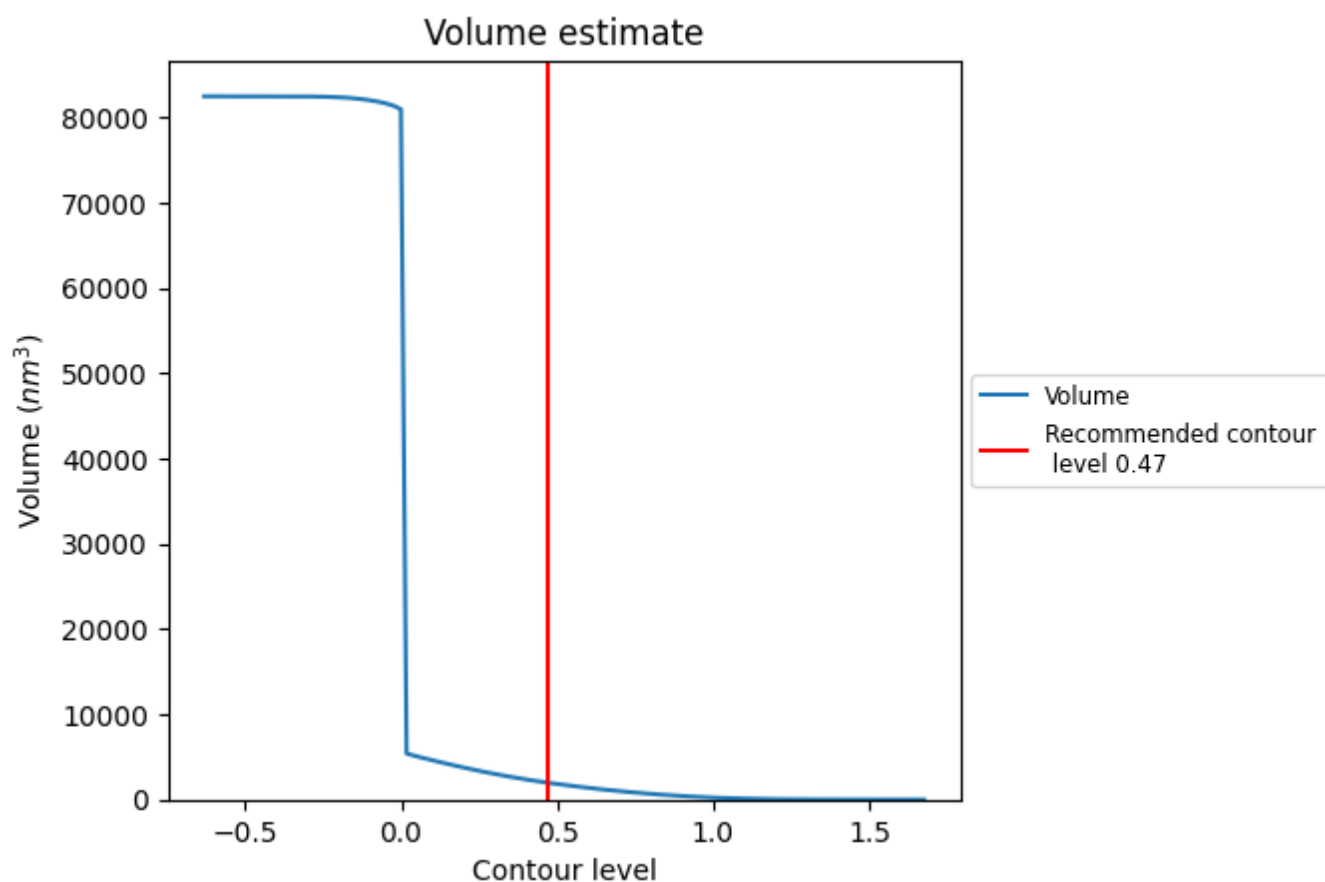
This section contains the results of statistical analysis of the map.

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.

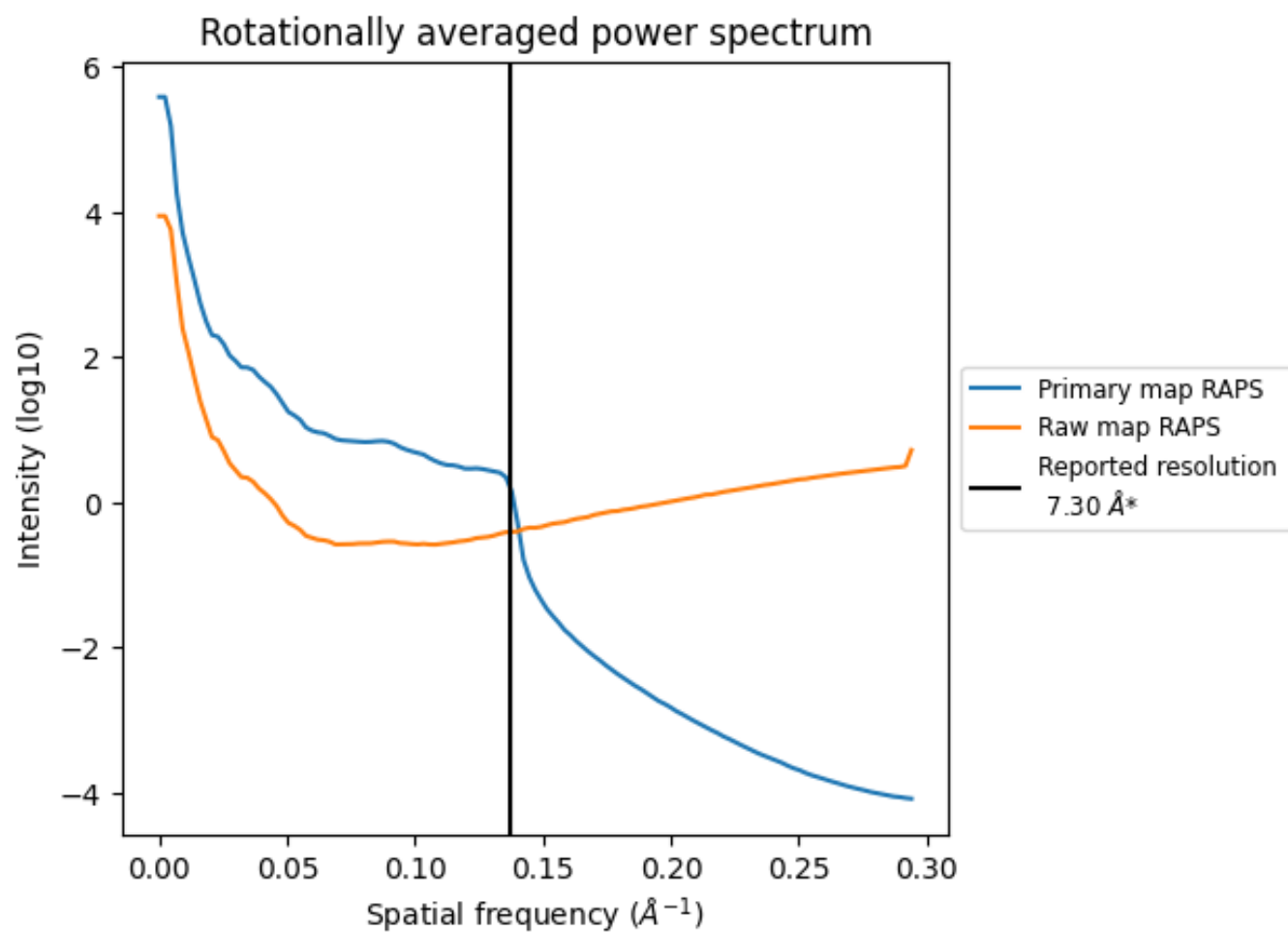
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1977 nm^3 ; this corresponds to an approximate mass of 1786 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 ⓘ

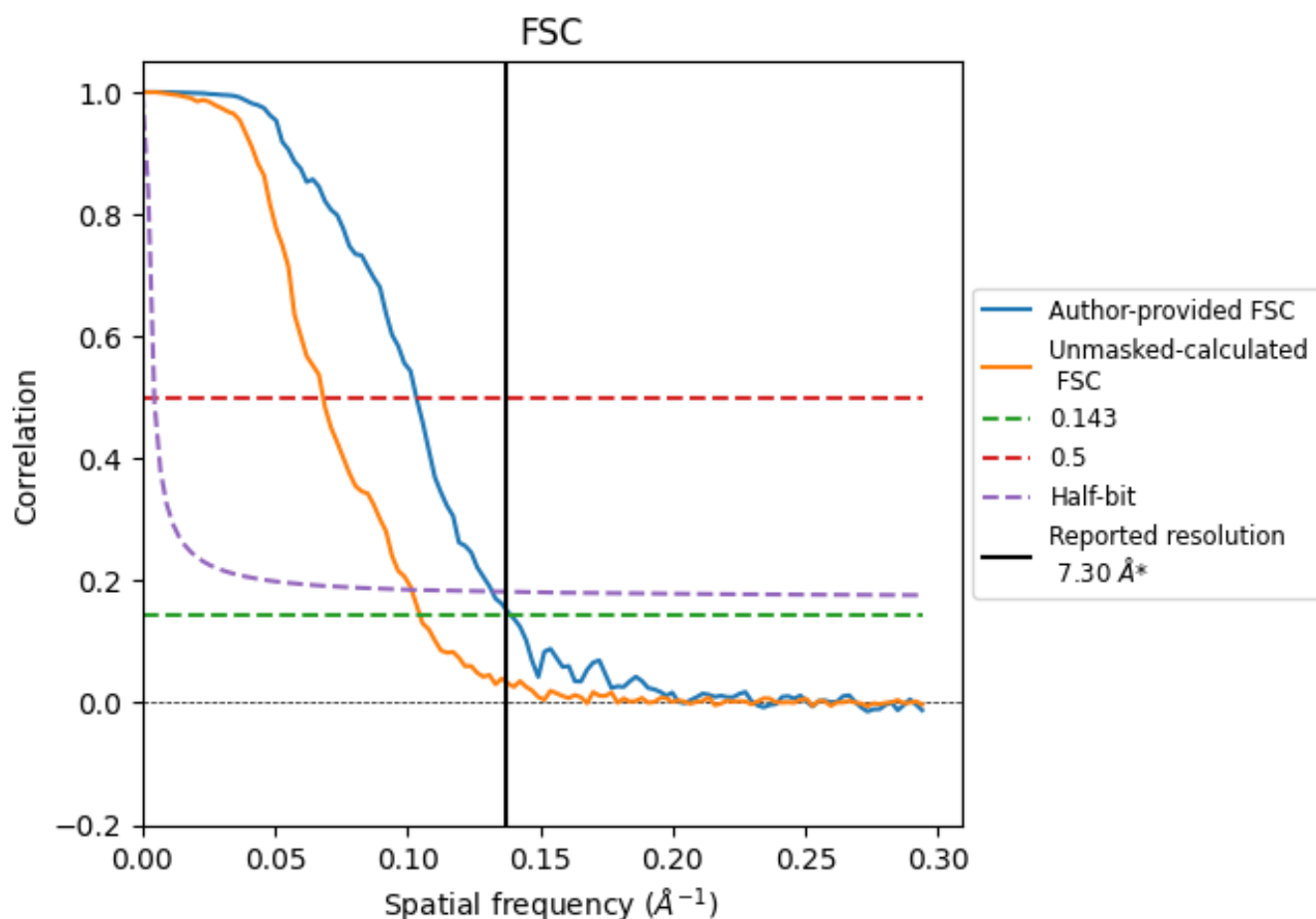


*Reported resolution corresponds to spatial frequency of 0.137 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.137 Å⁻¹

8.2 Resolution estimates [i](#)

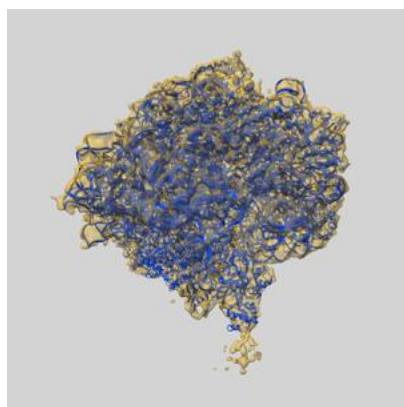
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.30	-	-
Author-provided FSC curve	7.19	9.68	7.58
Unmasked-calculated*	9.55	14.66	9.85

*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 9.55 differs from the reported value 7.3 by more than 10 %

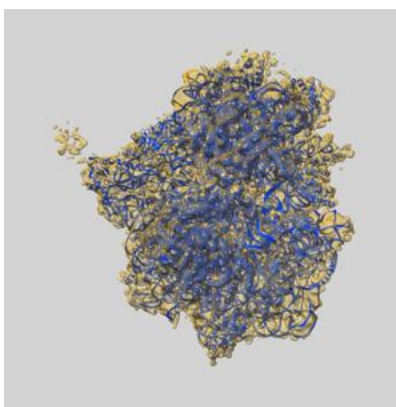
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13274 and PDB model 7PAJ. Per-residue inclusion information can be found in section [3](#) on page [14](#).

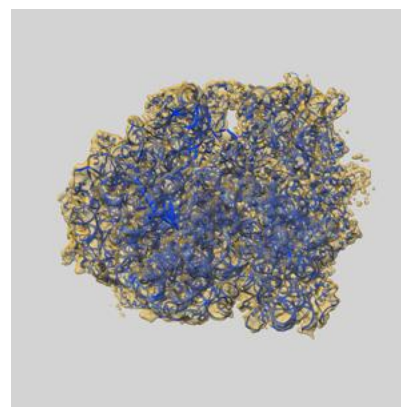
9.1 Map-model overlay [i](#)



X



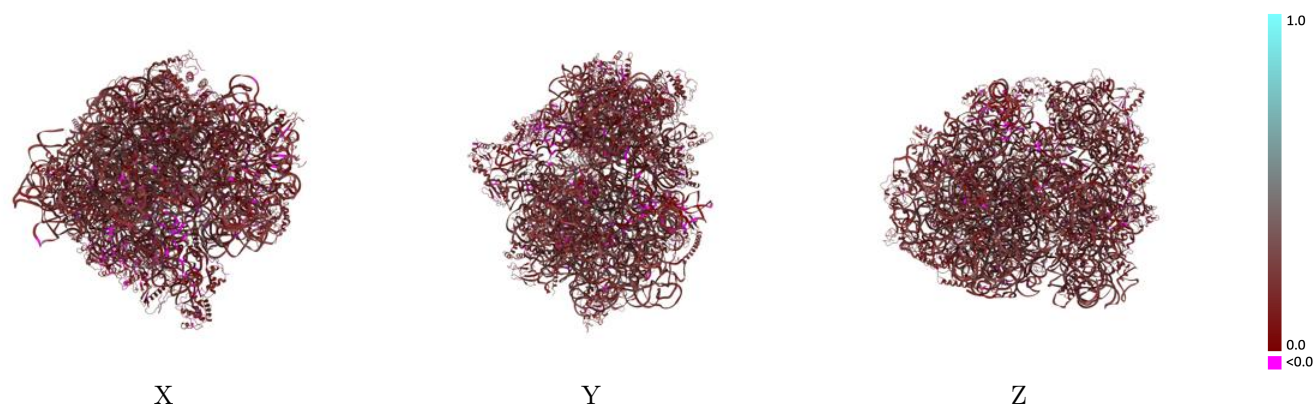
Y



Z

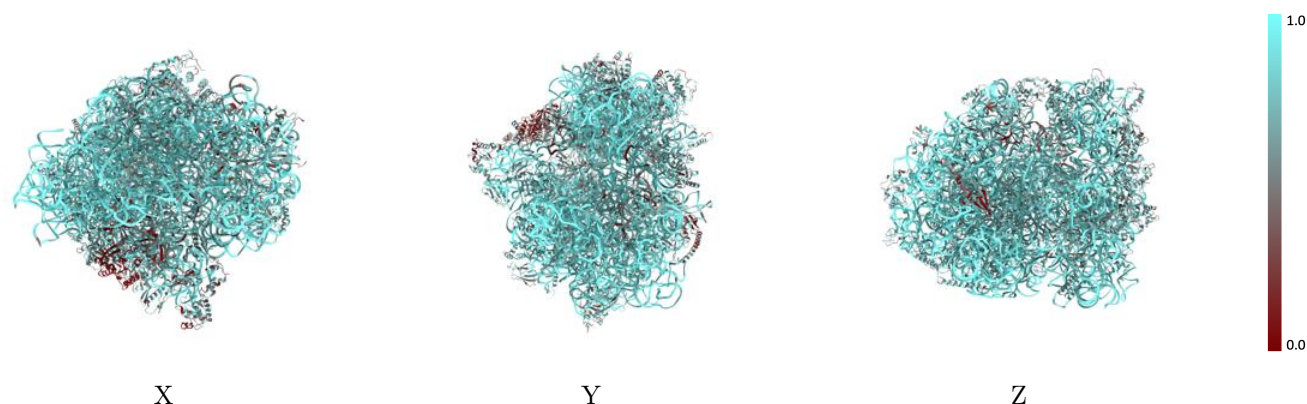
The images above show the 3D surface view of the map at the recommended contour level 0.47 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



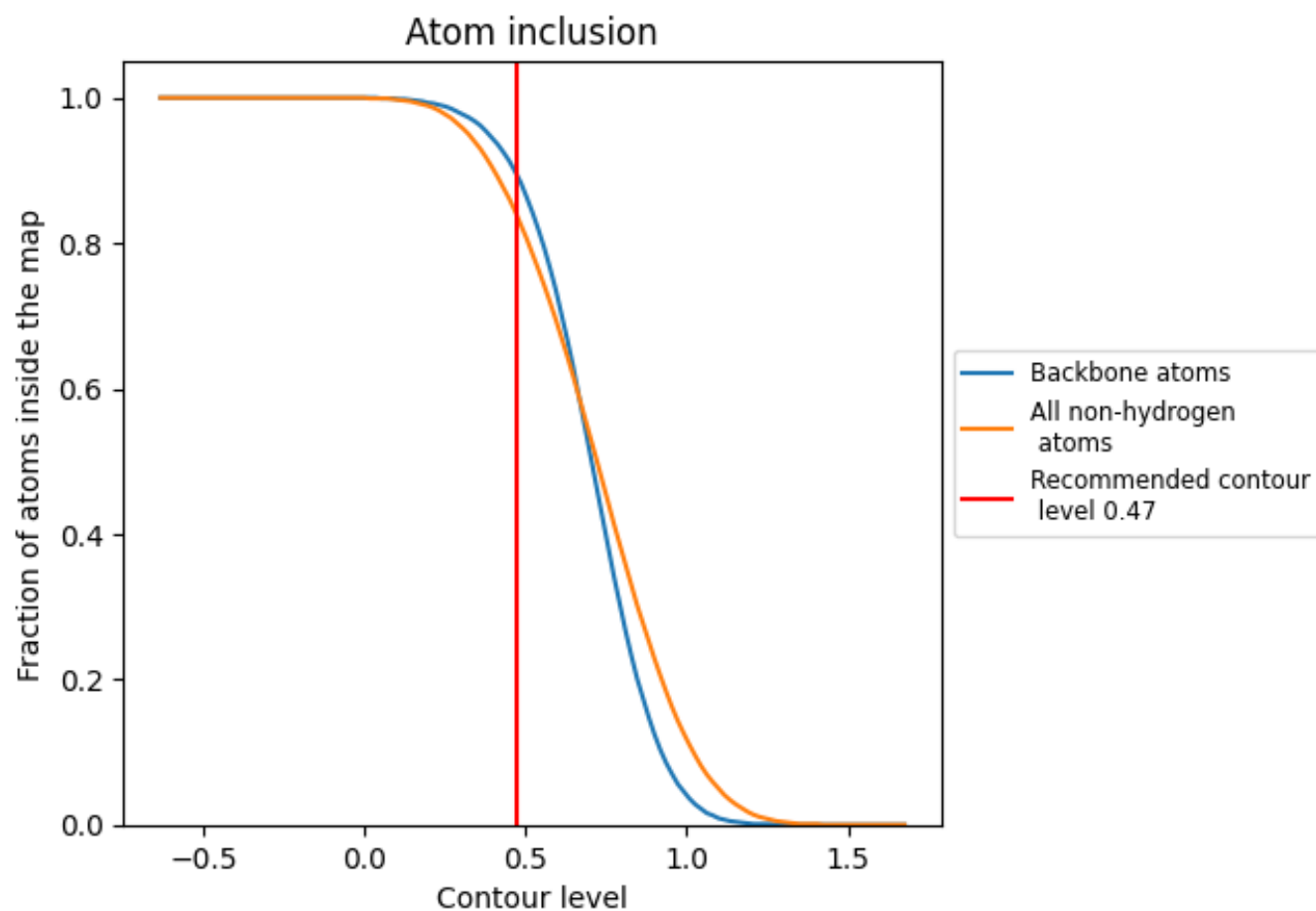
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.47).

9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 84% 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 (0.47) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8420	 0.1960
0	 0.7780	 0.1690
1	 0.7550	 0.1730
2	 0.7600	 0.1510
3	 0.9510	 0.2120
4	 0.9550	 0.2220
5	 0.9510	 0.2100
6	 0.5970	 0.0750
7	 0.8870	 0.1850
8	 0.4920	 0.0950
9	 0.1920	 0.1340
A	 0.6510	 0.1940
B	 0.6340	 0.1810
C	 0.6620	 0.1730
D	 0.6780	 0.1840
E	 0.6230	 0.2000
F	 0.6470	 0.1790
G	 0.6710	 0.1730
H	 0.6600	 0.1570
I	 0.6150	 0.1580
J	 0.6930	 0.1750
K	 0.6990	 0.1740
L	 0.6560	 0.1730
M	 0.6610	 0.1520
N	 0.6800	 0.1880
O	 0.7410	 0.1650
P	 0.6740	 0.1740
Q	 0.7210	 0.1780
R	 0.6540	 0.1550
S	 0.7620	 0.1860
T	 0.6940	 0.1860
a	 0.7350	 0.1660
b	 0.7110	 0.1740
c	 0.6980	 0.1860
d	 0.6830	 0.1660



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Chain	Atom inclusion	Q-score
e	 0.6810	 0.1940
f	 0.3300	 0.1680
g	 0.5540	 0.1750
h	 0.4260	 0.1440
i	 0.7600	 0.1900
j	 0.6620	 0.1870
k	 0.7420	 0.1890
l	 0.7710	 0.1920
m	 0.7580	 0.1820
n	 0.7070	 0.1700
o	 0.6660	 0.1910
p	 0.7560	 0.1650
q	 0.6670	 0.1810
r	 0.7480	 0.1800
s	 0.7090	 0.1870
t	 0.5920	 0.1810
u	 0.7530	 0.1680
v	 0.7290	 0.1510
w	 0.7180	 0.1990
x	 0.6620	 0.1810
y	 0.7010	 0.1700
z	 0.7030	 0.1750