



wwPDB EM Validation Summary Report ⓘ

Sep 6, 2026 – 06:32 PM EDT

PDB ID : 11HV / pdb_000011hv
EMDB ID : EMD-75704
Title : Rabbit 60S ribosomal subunit with eEF2 domain IV open
Authors : Seraj, Z.; Zottig, X.; Huang, C.H.; Loveland, A.B.; Diggs, S.; Sholi, E.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2026-02-25
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

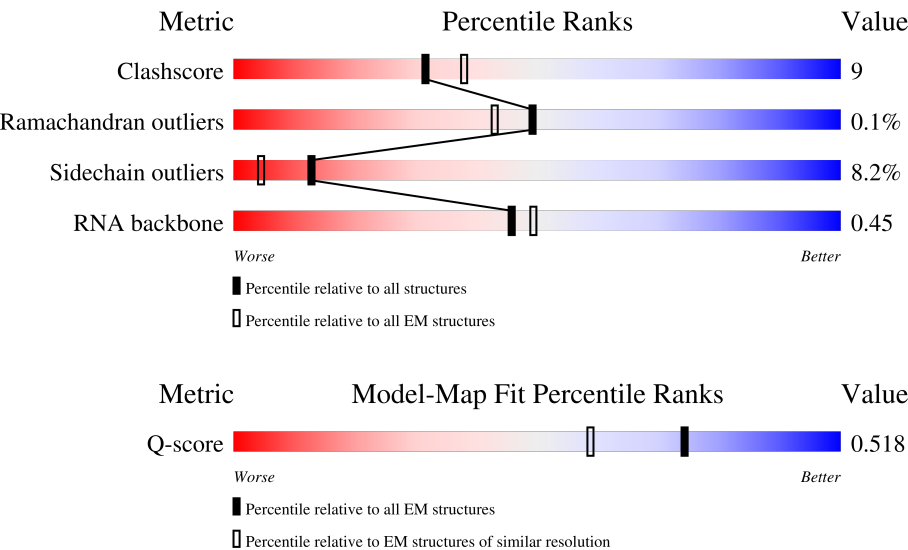
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.



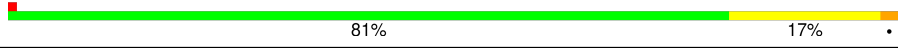
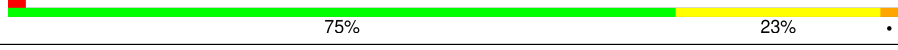
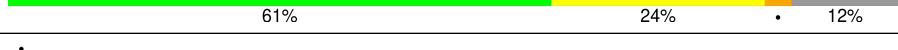
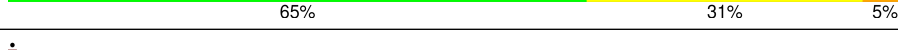
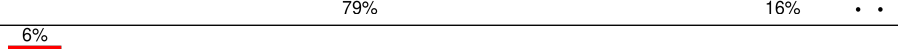
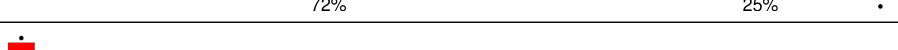
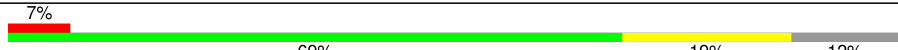
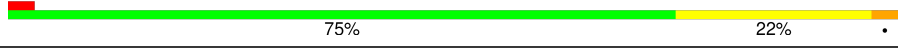
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	v	858	74% 60%30%6%
2	58	156	5% 46%42%9%
3	5	120	65%32%

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Mol	Chain	Length	Quality of chain
4	L8	248	
5	L3	394	
6	L4	362	
7	L5	293	
8	L6	251	
9	L7	225	
10	aa	266	
11	L9	190	
12	10	213	
13	11	170	
14	13	261	
15	14	138	
16	15	203	
17	bb	199	
18	17	153	
19	19	180	
20	20	176	
21	21	159	
22	22	99	
23	24	63	
24	cc	118	
25	26	134	
26	27	135	
27	dd	147	
28	29	245	

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Mol	Chain	Length	Quality of chain
29	30	98	
30	31	107	
31	32	128	
32	ee	109	
33	34	114	
34	35	122	
35	36	102	
36	37	86	
37	38	69	
38	39	50	
39	40	52	
40	42	104	
41	ff	91	
42	gg	124	
43	s	196	
44	t	153	
45	EB	375	
46	u	206	
47	Q	187	
48	ES	5070	
49	28	4807	
50	25	139	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 147582 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 Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	v	810	Total	C	N	O	S	0	0
			6323	4027	1082	1171	43		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L8	248	Total	C	N	O	S	0	0
			1899	1189	389	315	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L3	394	Total	C	N	O	S	0	0
			3173	2020	597	543	13		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L4	362	Total	C	N	O	S	0	0
			2884	1812	577	481	14		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L5	293	Total	C	N	O	S	0	0
			2392	1512	438	428	14		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L6	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L7	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 10 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	aa	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L9	190	Total	C	N	O	S	0	0
			1517	954	284	273	6		

- Molecule 12 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	10	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	11	170	Total	C	N	O	S	0	0
			1363	861	254	242	6		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	13	210	Total	C	N	O	S	0	0
			1701	1065	354	278	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	14	138	Total	C	N	O	S	0	0
			1138	727	221	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	bb	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	17	153	Total	C	N	O	S	0	0
			1243	777	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	19	159	Total	C	N	O	S	0	0
			1325	825	283	208	9		

- Molecule 20 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	20	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 21 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 22 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	22	99	Total	C	N	O	S	0	0
			810	519	141	148	2		

- Molecule 23 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	24	63	Total	C	N	O	S	0	0
			529	337	103	86	3		

- Molecule 24 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	cc	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 25 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	26	134	Total	C	N	O	S	0	0
			1116	700	226	187	3		

- Molecule 26 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 27 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	dd	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 28 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	30	98	Total	C	N	O	S	0	0
			762	481	134	141	6		

- Molecule 30 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	31	107	Total	C	N	O	S	0	0
			889	560	171	156	2		

- Molecule 31 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	32	128	Total	C	N	O	S	0	0
			1054	667	216	166	5		

- Molecule 32 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	ee	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 33 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	34	114	Total	C	N	O	S	0	0
			907	566	187	148	6		

- Molecule 34 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 35 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	36	102	Total	C	N	O	S	0	0
			831	520	176	130	5		

- Molecule 36 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	37	86	Total	C	N	O	S	0	0
			706	434	155	112	5		

- Molecule 37 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 38 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 39 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	42	104	Total	C	N	O	S	0	0
			852	533	174	139	6		

- Molecule 41 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	ff	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	gg	124	Total	C	N	O	S	0	0
			991	615	202	168	6		

- Molecule 43 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1508	959	263	277	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1161	722	218	218	3		

- Molecule 45 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	EB	375	Total	C	N	O	S	0	0
			2932	1844	509	562	17		

- Molecule 46 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	206	Total	C	N	O	S	0	0
			1655	1058	297	292	8		

- Molecule 47 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 48 is a RNA chain called ES27L.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	ES	67	Total	C	N	O	P	0	0
			1444	639	266	472	67		

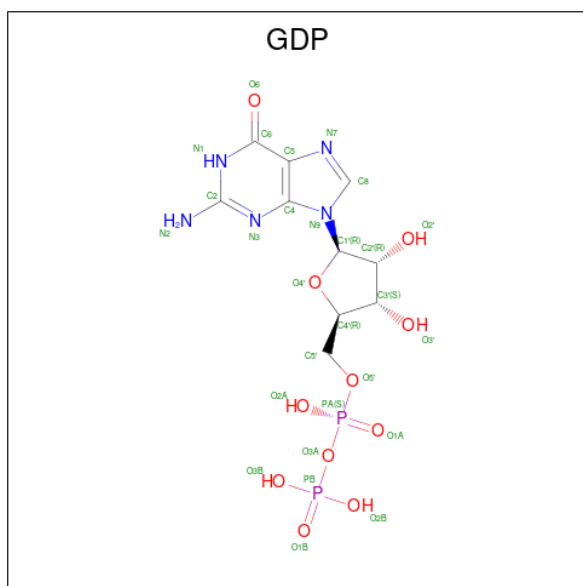
- Molecule 49 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	28	3486	Total	C	N	O	P	0	0
			74767	33297	13700	24284	3486		

- Molecule 50 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	25	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

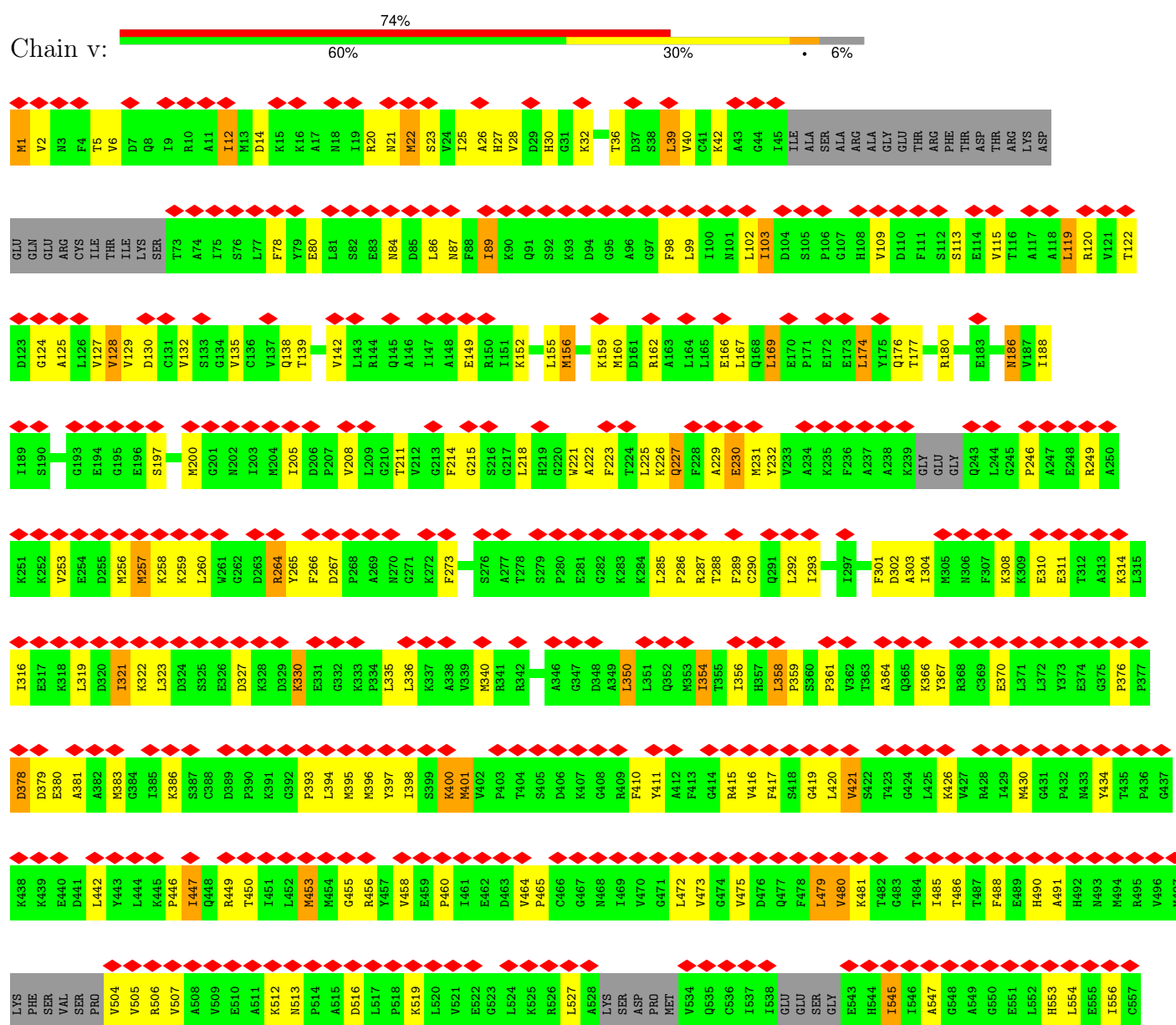
- Molecule 51 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

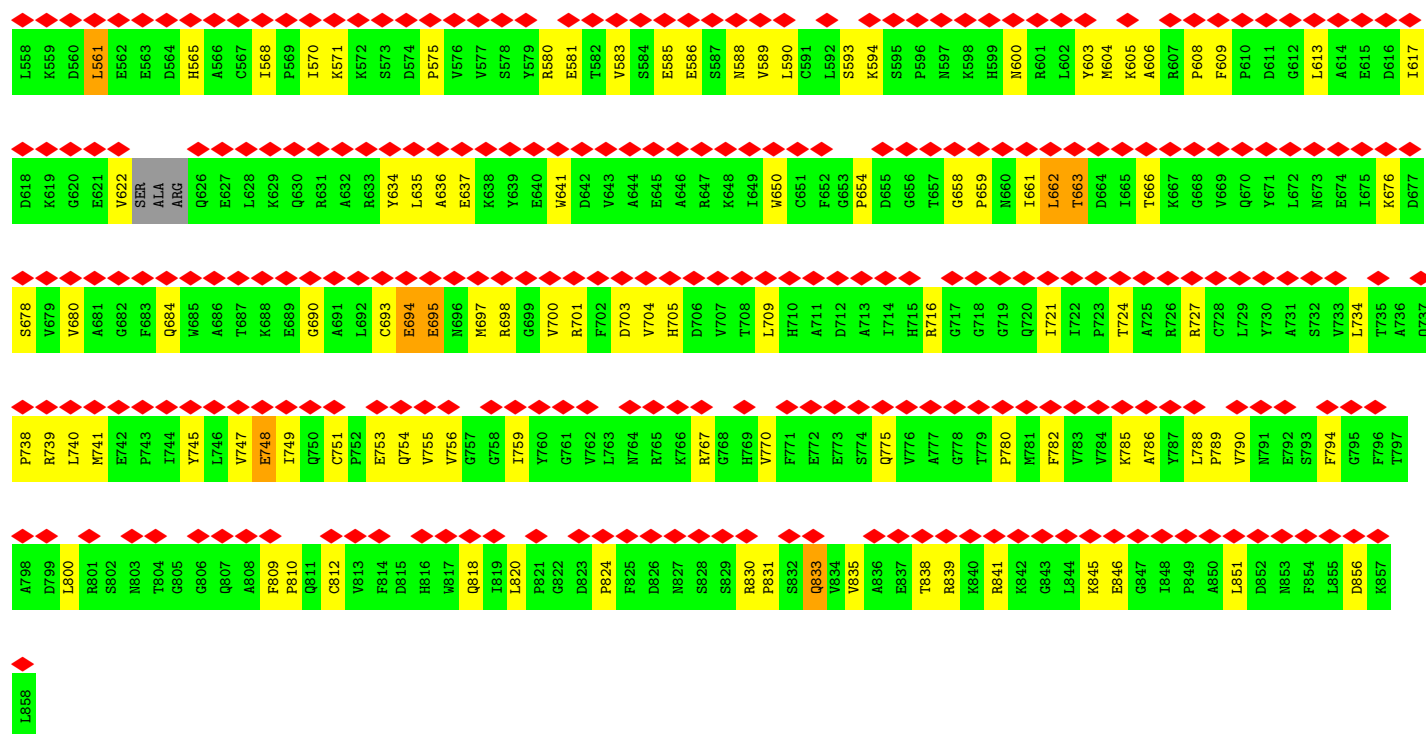


3 Residue-property plots

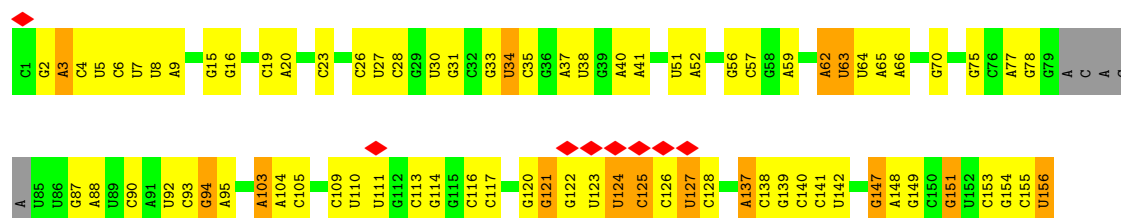
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Elongation factor 2

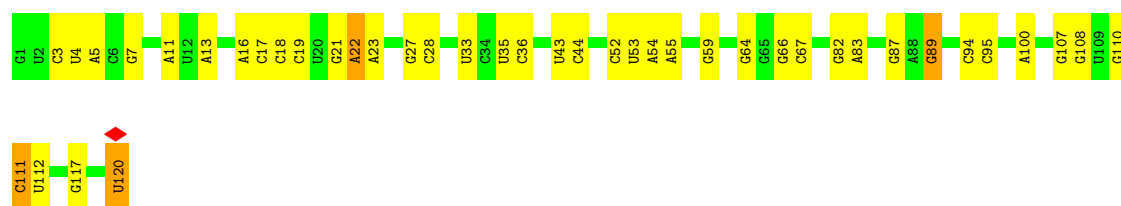




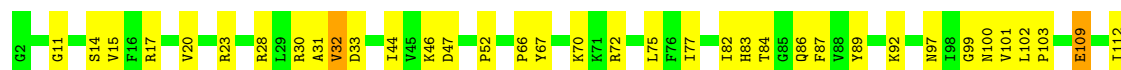
• Molecule 2: 5.8S rRNA

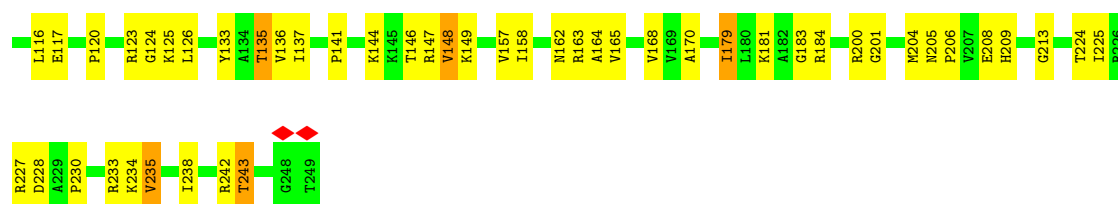


• Molecule 3: 5S rRNA

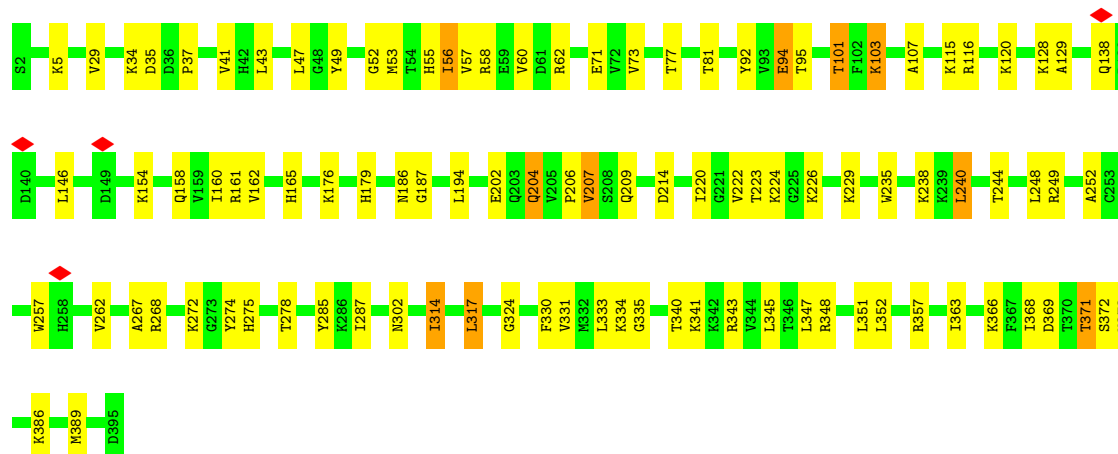
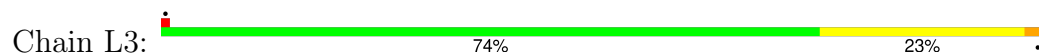


• Molecule 4: 60S ribosomal protein L8

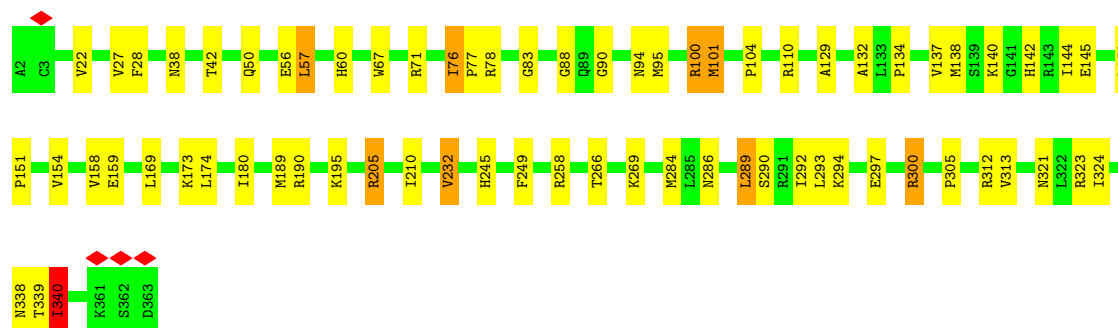
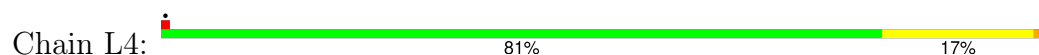




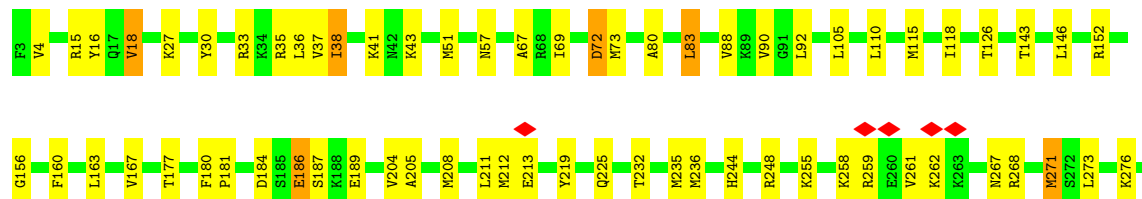
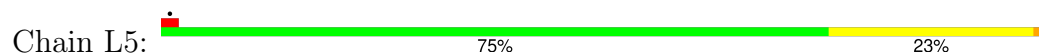
• Molecule 5: 60S ribosomal protein L3



• Molecule 6: 60S ribosomal protein L4

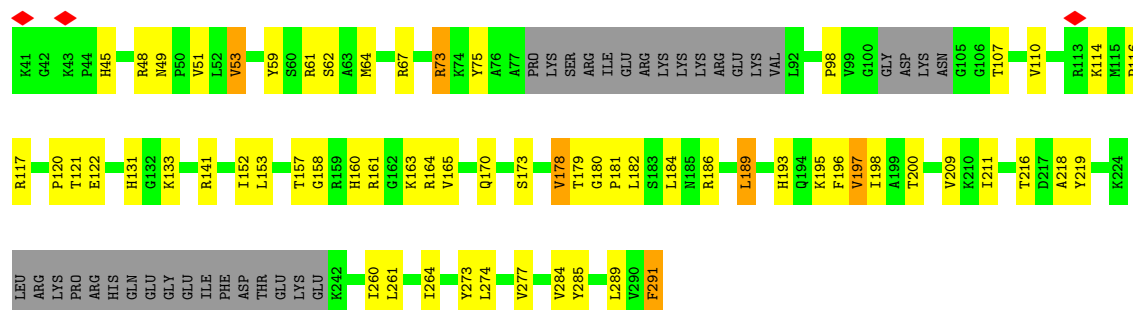


• Molecule 7: 60S ribosomal protein L5

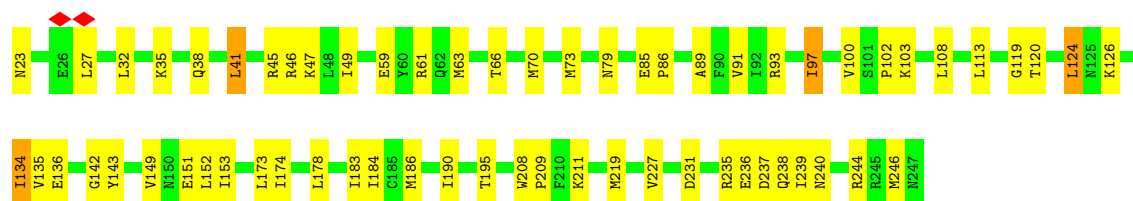




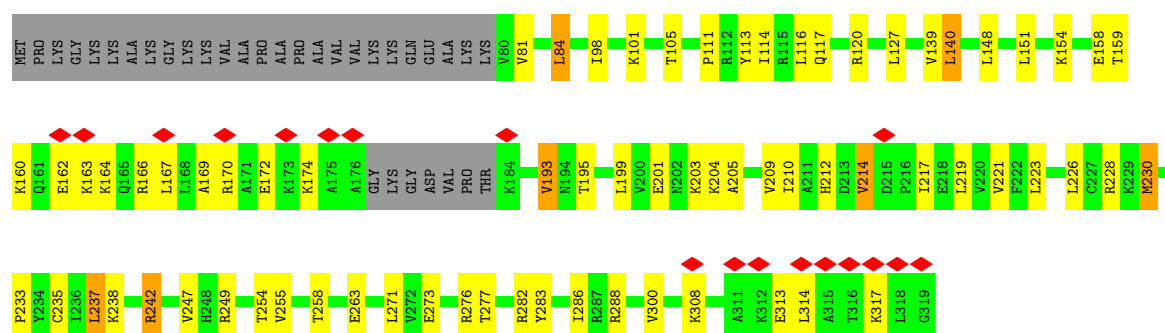
• Molecule 8: Large ribosomal subunit protein eL6



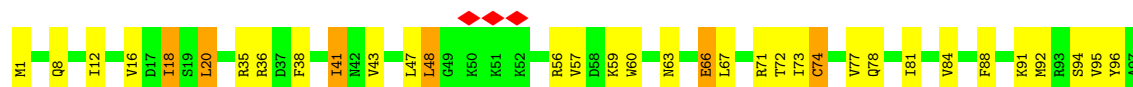
• Molecule 9: 60S ribosomal protein L7

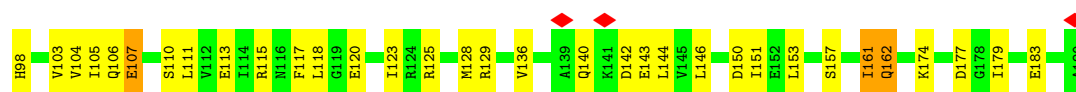


• Molecule 10: Large ribosomal subunit protein eL8

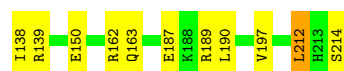
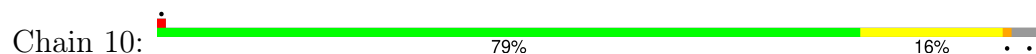


• Molecule 11: 60S ribosomal protein L9

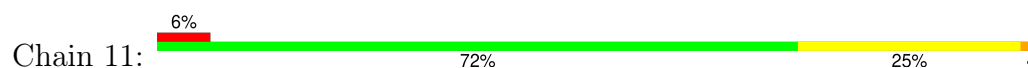




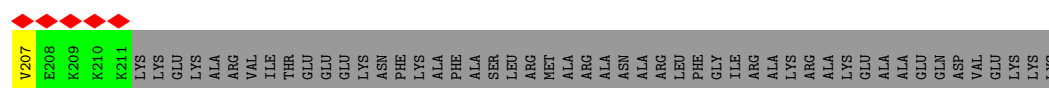
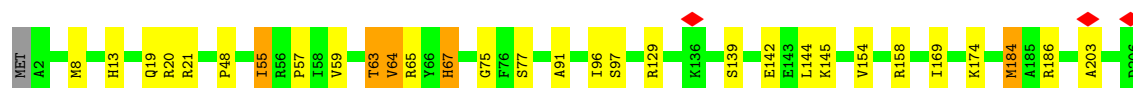
• Molecule 12: Ribosomal protein L10



• Molecule 13: 60S ribosomal protein L11



• Molecule 14: Large ribosomal subunit protein eL13

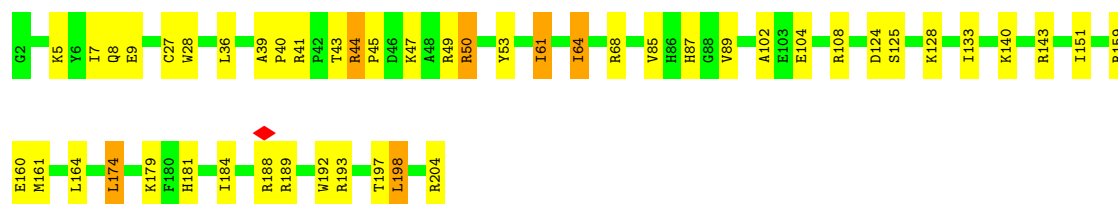


• Molecule 15: 60S ribosomal protein L14



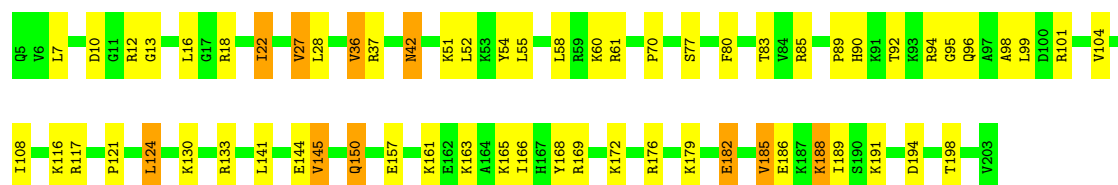
• Molecule 16: 60S ribosomal protein L15

Chain 15: 



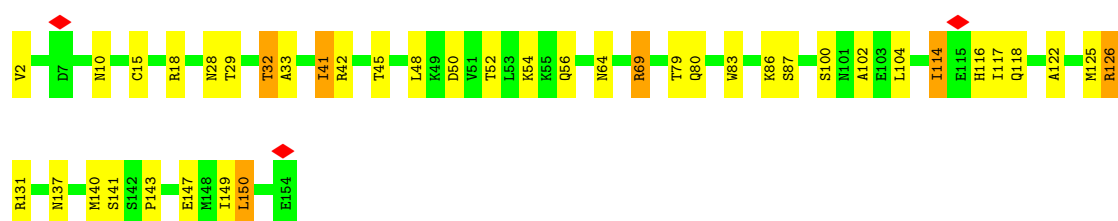
- Molecule 17: Large ribosomal subunit protein uL13

Chain bb: 



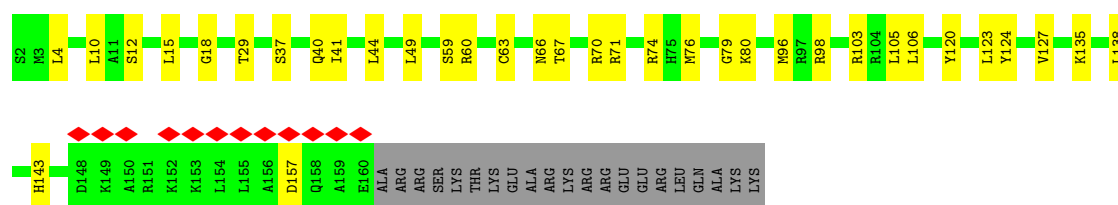
- Molecule 18: 60S ribosomal protein L17

Chain 17: 



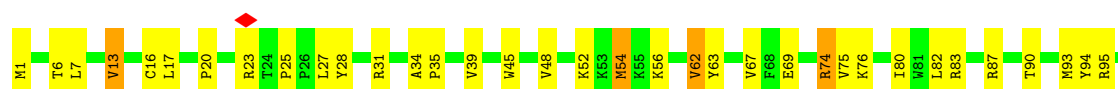
- Molecule 19: 60S ribosomal protein L19

Chain 19: 



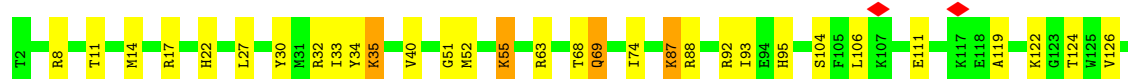
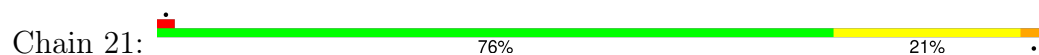
- Molecule 20: Large ribosomal subunit protein eL20

Chain 20: 

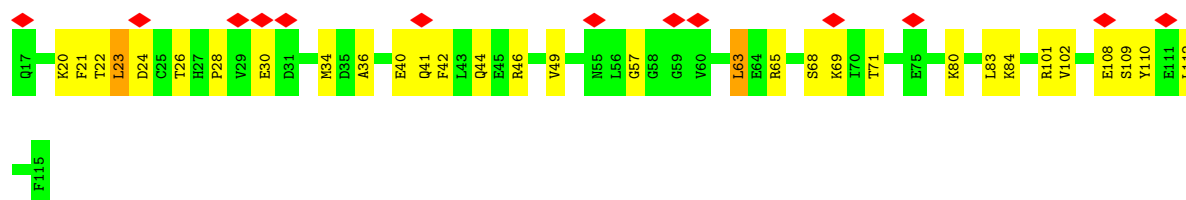




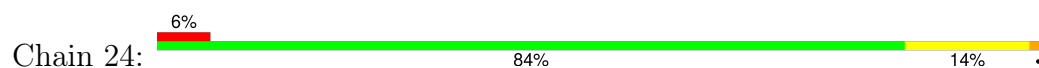
- Molecule 21: 60S ribosomal protein L21



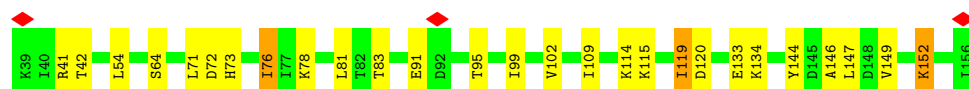
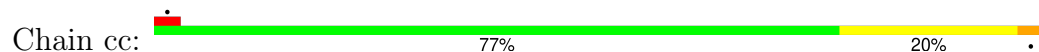
- Molecule 22: Large ribosomal subunit protein eL22



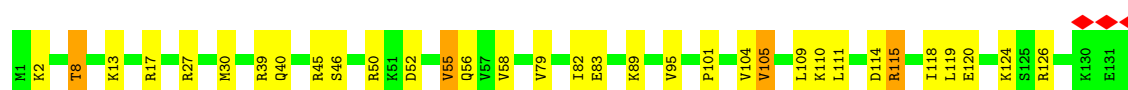
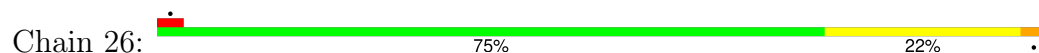
- Molecule 23: Ribosomal protein L24



- Molecule 24: Large ribosomal subunit protein uL23



- Molecule 25: 60S ribosomal protein L26



Chain 31:  72% 26%



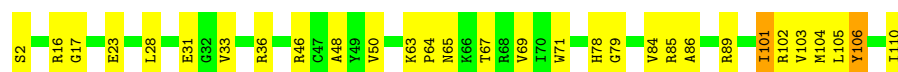
- Molecule 31: Large ribosomal subunit protein eL32

Chain 32:  70% 30%



- Molecule 32: Large ribosomal subunit protein eL33

Chain ee:  72% 26%



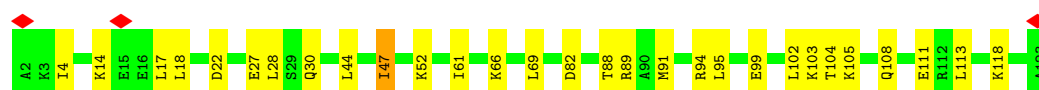
- Molecule 33: 60S ribosomal protein L34

Chain 34:  6% 76% 22%



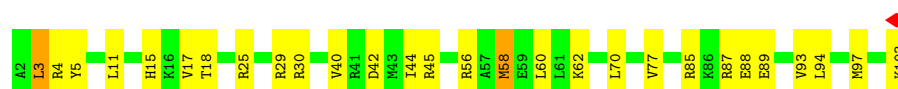
- Molecule 34: 60S ribosomal protein L35

Chain 35:  76% 23%



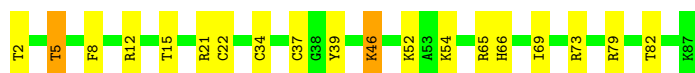
- Molecule 35: 60S ribosomal protein L36

Chain 36:  73% 25%



- Molecule 36: 60S ribosomal protein L37

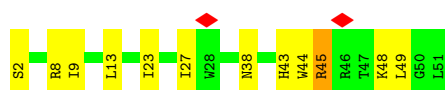
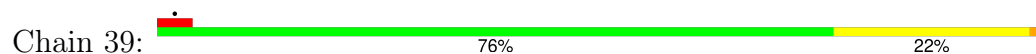
Chain 37:  78% 20%



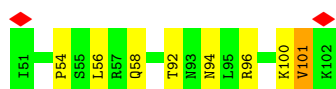
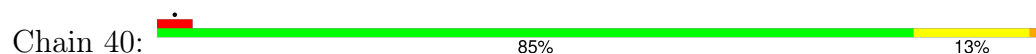
- Molecule 37: Large ribosomal subunit protein eL38



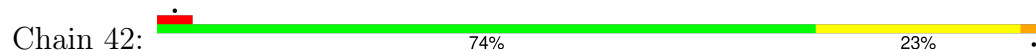
- Molecule 38: 60S ribosomal protein L39



- Molecule 39: Large ribosomal subunit protein eL40



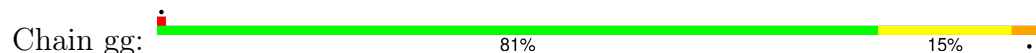
- Molecule 40: eL42



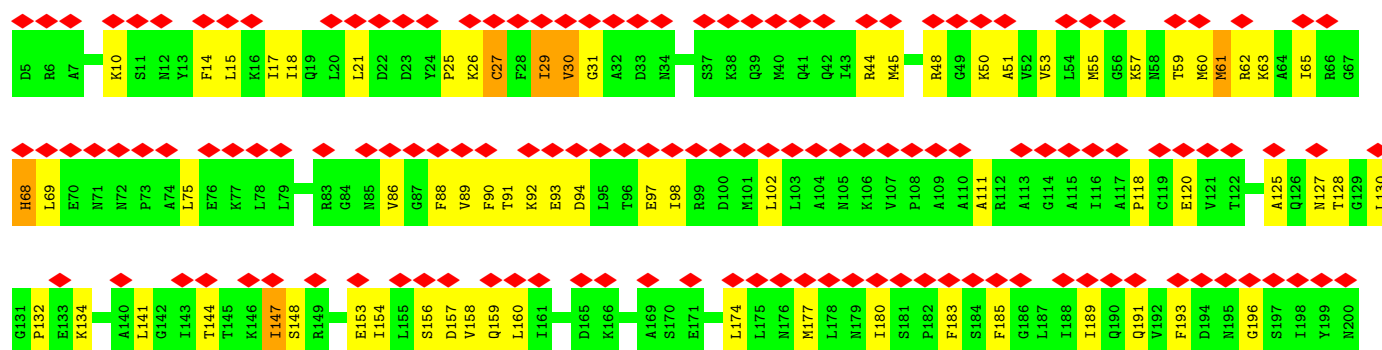
- Molecule 41: 60S ribosomal protein L37a



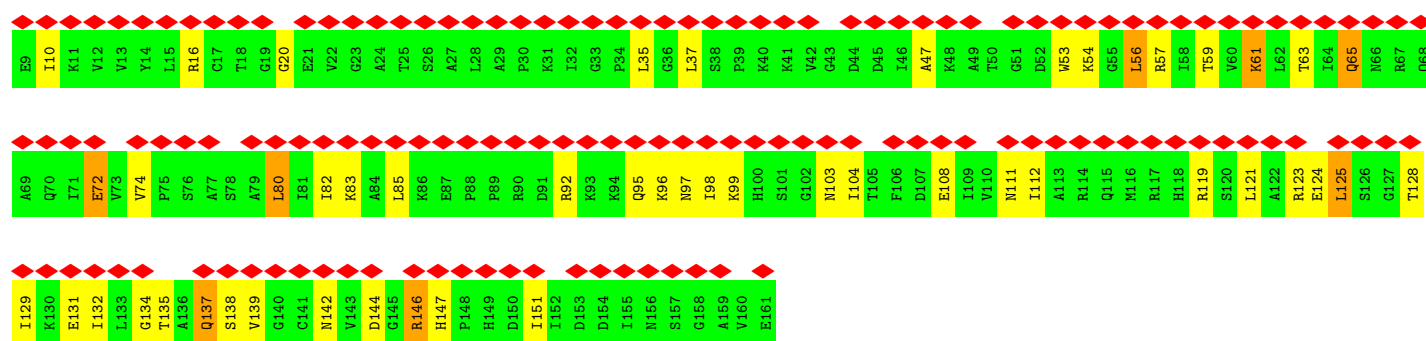
- Molecule 42: 60S ribosomal protein L28



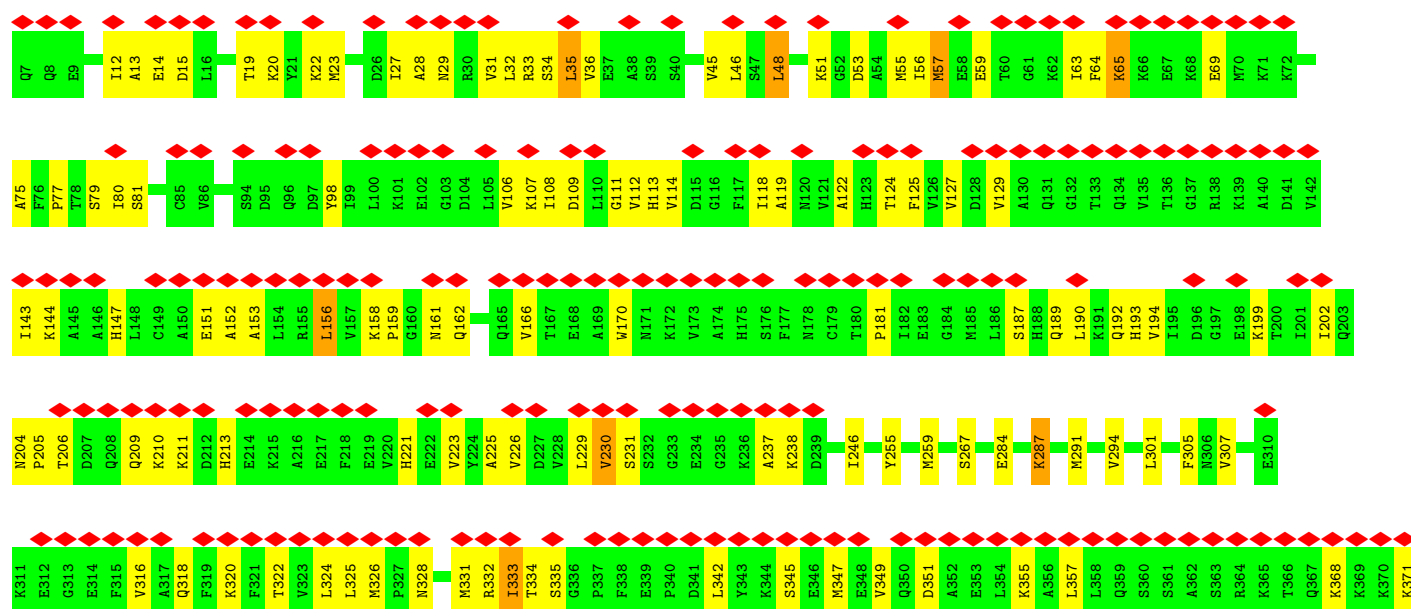
- Molecule 43: 60S acidic ribosomal protein P0

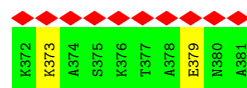


• Molecule 44: uL11

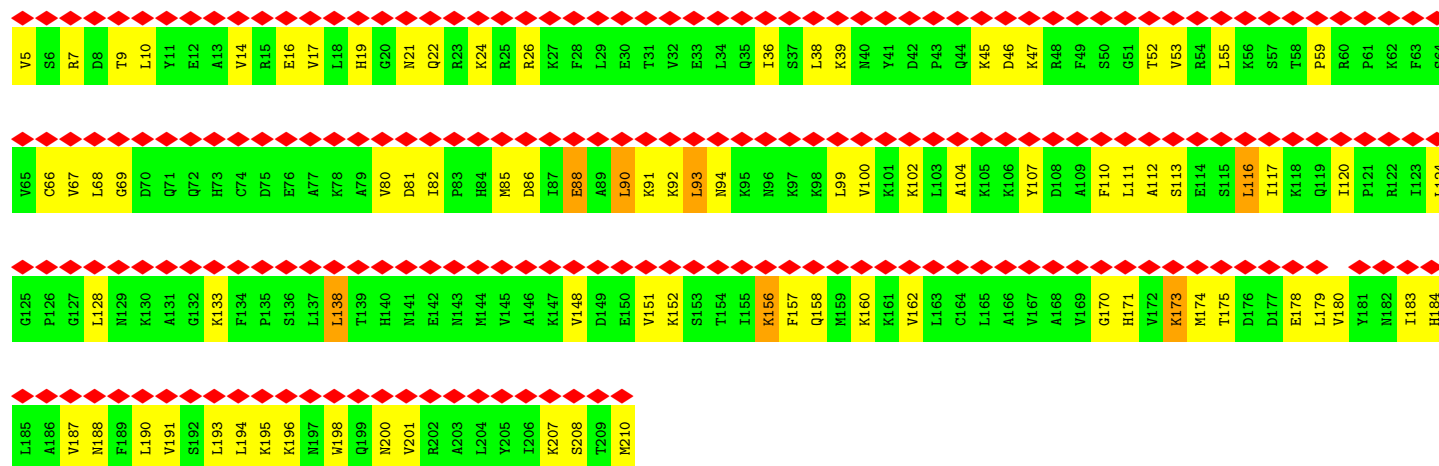


• Molecule 45: Proliferation-associated protein 2G4

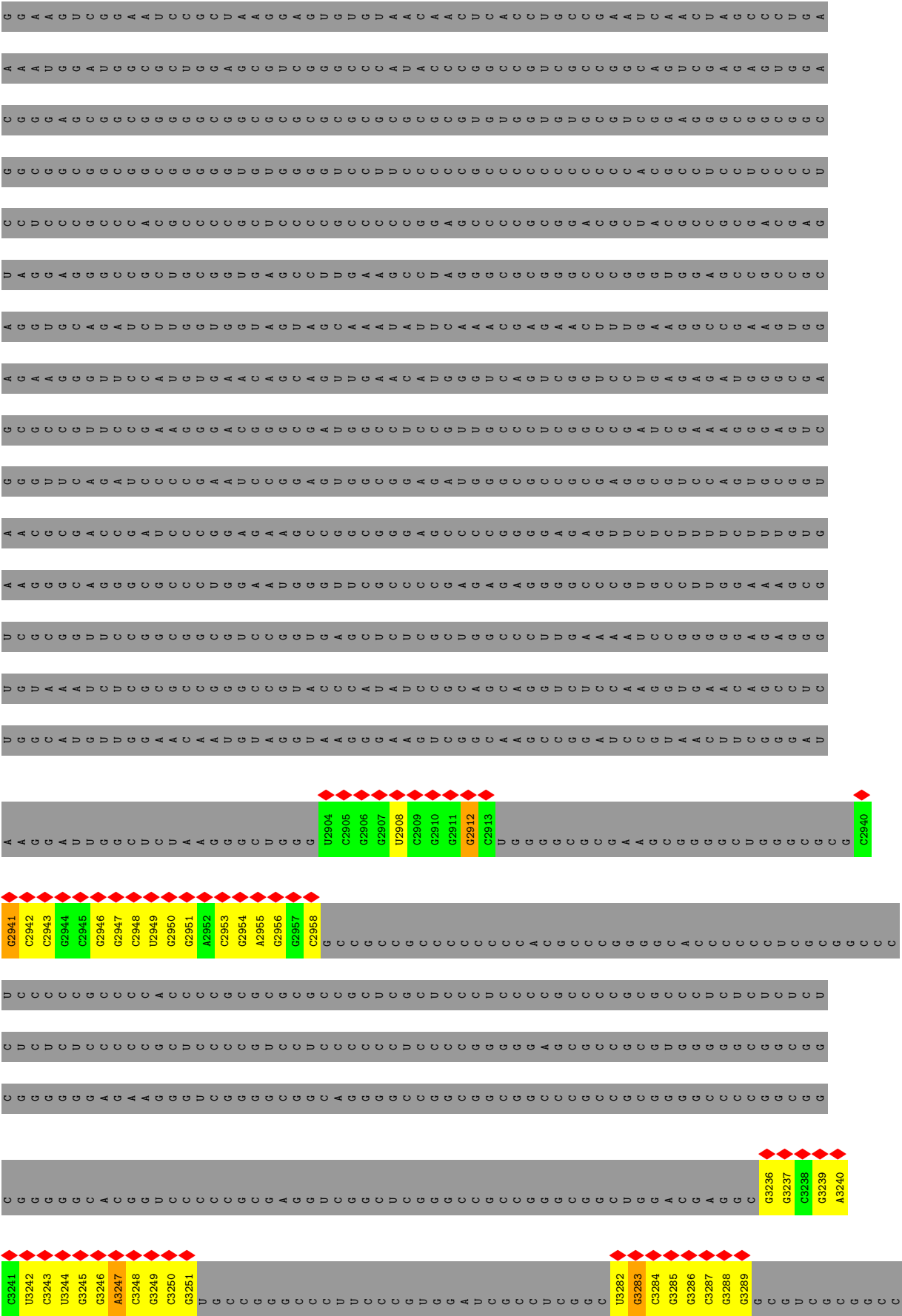




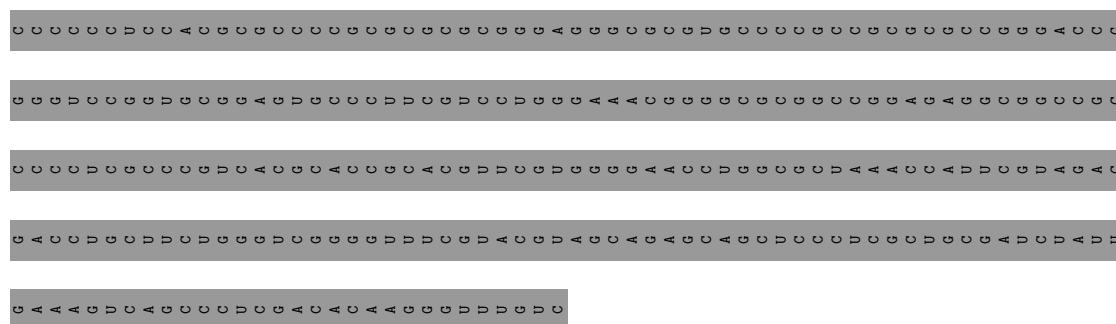
• Molecule 46: 60S ribosomal protein L10a



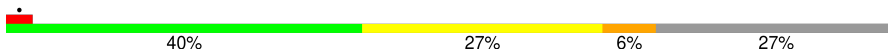


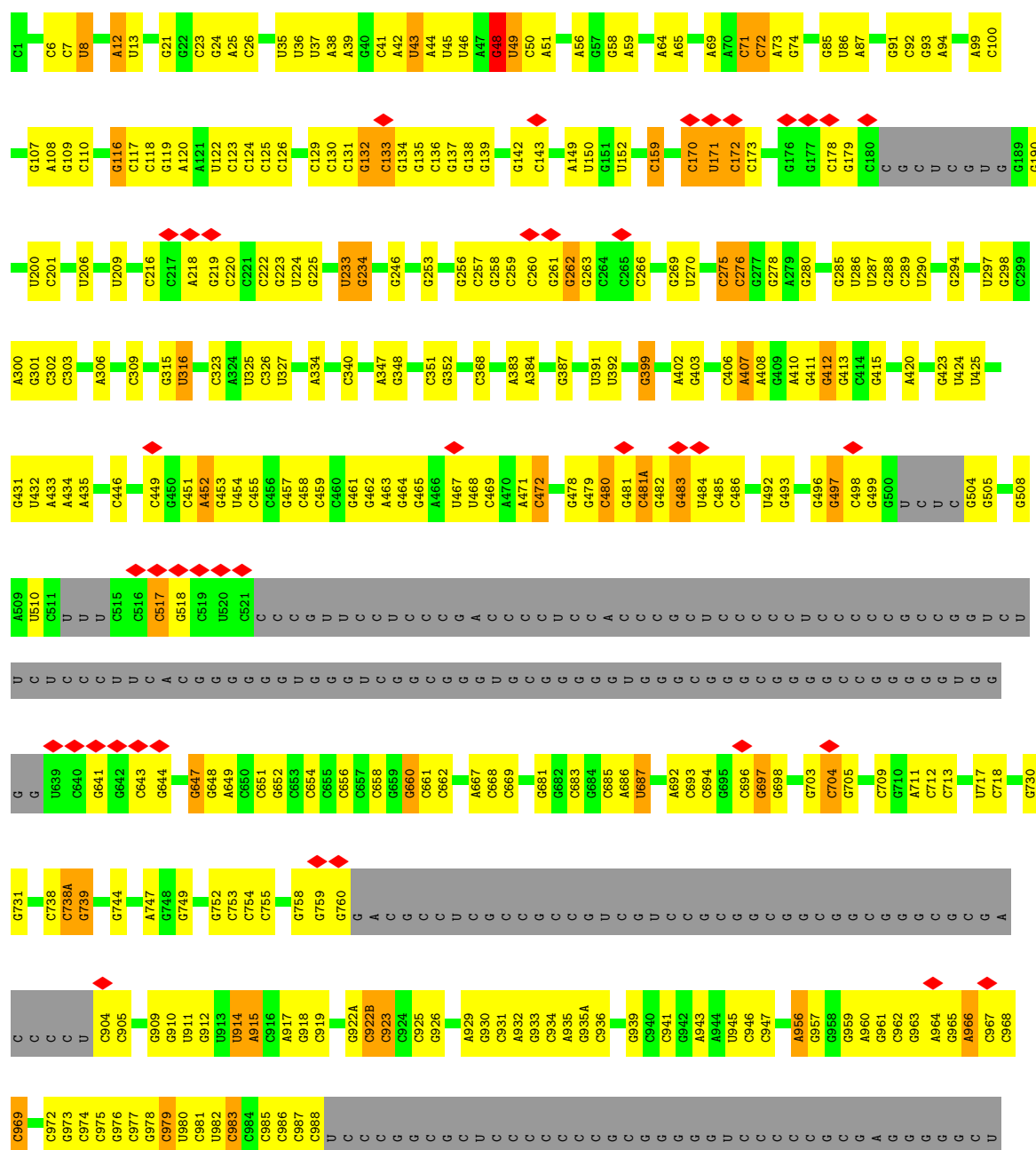






• Molecule 49: 28S rRNA

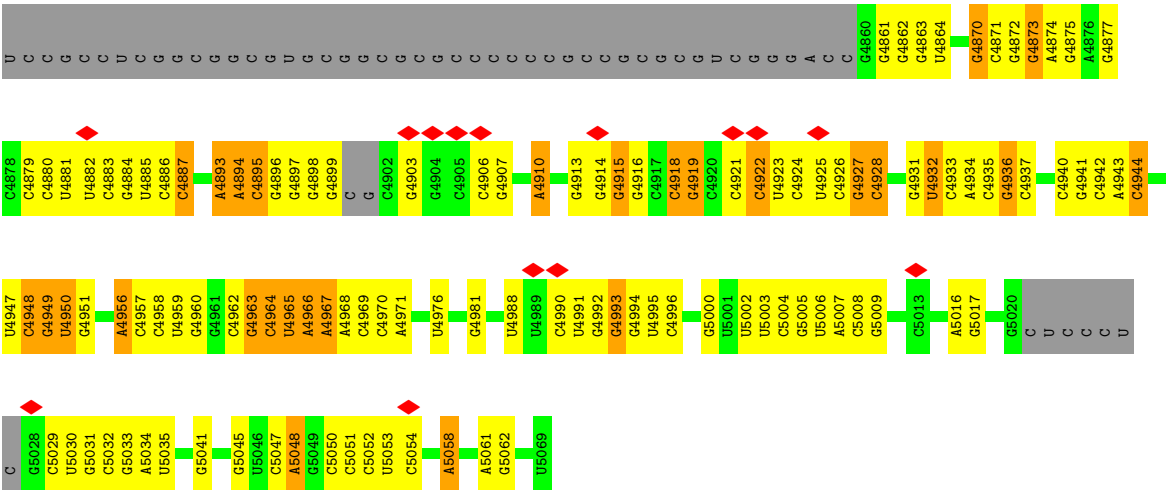
Chain 28:  40% 27% 6% 27%



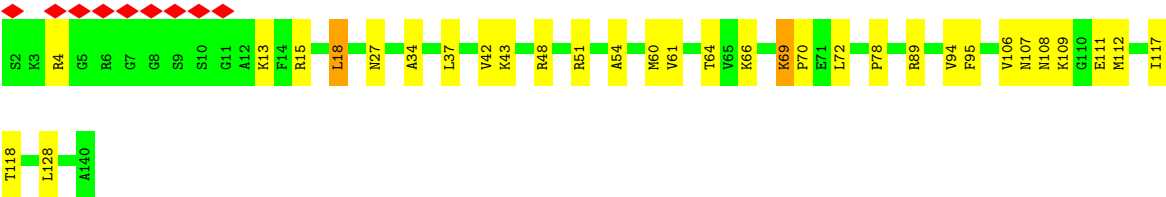
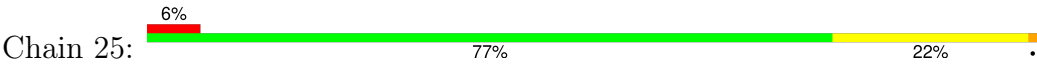




G4740	A	G4637	A4548	U4459	C4349	C4261	C4162	C	G	G	A3908	A3817	U3713	A3604
A	U4638	U4639	G4549	U4460	C4350	C4262	U4163	G	G	G	C3909	U3818	G3714	C3605
G	C4461	C4462	U4557	C4461	U4351	C4263	C4164	C	C	A	C3910	C3819	U3715	
	U4642	G4643	C4560	U4463	U4352	U4264	G4165	C	C	G	C3911	C3716	C3716	A3611
				U4464	U4353	U4265	G4166	C	C	G	U3912	A3821	A3717	
				U4465	U4354	U4266	G4167	C	C	G	U3915	U3822	G3615	G3615
				U4466	U4355	U4267	G4168	C	C	C	G3916	G3623	U3616	U3616
				U4467	U4356	U4268	G4169	C	C	C	A3917	A3824	G3617	G3617
				U4471	U4357	U4271	U4170	C	C	C	G3918	A3830	G3618	G3618
				U4472	U4358	U4272	U4171	C	C	C	U3920	A3831	G3619	G3619
				U4473	U4359	U4273	U4172	C	C					



● Molecule 50: Large ribosomal subunit protein uL14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15960	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	OTHER	Depositor
Maximum map value	29.413	Depositor
Minimum map value	-17.059	Depositor
Average map value	0.003	Depositor
Map value standard deviation	1.135	Depositor
Recommended contour level	4	Depositor
Map size ($\text{\AA}$)	664.0, 664.0, 664.0	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	v	0.25	0/6444	0.48	0/8699
2	58	0.53	0/3581	0.41	0/5577
3	5	0.50	0/2858	0.38	0/4455
4	L8	0.51	0/1937	0.53	0/2596
5	L3	0.49	0/3241	0.52	0/4339
6	L4	0.51	0/2938	0.54	1/3946 (0.0%)
7	L5	0.41	0/2438	0.46	0/3264
8	L6	0.43	0/1762	0.51	0/2362
9	L7	0.49	0/1911	0.50	0/2549
10	aa	0.43	0/1910	0.50	0/2569
11	L9	0.44	0/1536	0.50	0/2063
12	10	0.45	0/1702	0.50	0/2272
13	11	0.37	0/1386	0.51	0/1852
14	13	0.44	0/1732	0.47	0/2316
15	14	0.45	0/1159	0.50	0/1547
16	15	0.55	0/1746	0.55	0/2338
17	bb	0.50	0/1662	0.50	0/2222
18	17	0.51	0/1269	0.53	0/1700
19	19	0.43	0/1341	0.47	0/1776
20	20	0.50	0/1501	0.51	0/2012
21	21	0.48	0/1326	0.50	0/1770
22	22	0.33	0/824	0.52	0/1104
23	24	0.45	0/542	0.45	0/720
24	cc	0.46	0/984	0.48	0/1323
25	26	0.46	0/1133	0.49	0/1504
26	27	0.44	0/1130	0.50	1/1507 (0.1%)
27	dd	0.51	0/1191	0.52	0/1590
28	29	0.38	0/861	0.46	0/1138
29	30	0.39	0/772	0.41	0/1034
30	31	0.48	0/904	0.51	0/1216
31	32	0.53	0/1072	0.52	0/1429
32	ee	0.54	0/895	0.56	2/1198 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	34	0.45	0/917	0.49	0/1220
34	35	0.44	0/1021	0.51	0/1348
35	36	0.42	0/842	0.47	0/1112
36	37	0.50	0/721	0.50	0/952
37	38	0.36	0/575	0.47	0/761
38	39	0.48	0/459	0.49	0/608
39	40	0.40	0/435	0.48	0/575
40	42	0.46	0/865	0.49	0/1140
41	ff	0.47	0/718	0.54	0/953
42	gg	0.46	0/1007	0.47	0/1349
43	s	0.24	0/1531	0.47	0/2064
44	t	0.21	0/1175	0.48	0/1582
45	EB	0.26	0/2979	0.41	0/4000
46	u	0.21	0/1681	0.47	0/2255
47	Q	0.53	0/1539	0.59	0/2054
48	ES	0.19	0/1609	0.39	0/2502
49	28	0.53	5/83635 (0.0%)	0.44	5/130433 (0.0%)
50	25	0.51	0/1048	0.51	0/1402
All	All	0.49	5/158445 (0.0%)	0.46	9/232297 (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
49	28	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	28	3945	A	O3'-P	22.43	1.94	1.61
49	28	3940	U	O3'-P	-20.84	1.29	1.61
49	28	2024	G	O3'-P	8.16	1.73	1.61
49	28	3715	U	C5-C6	6.08	1.46	1.34
49	28	2026	A	O3'-P	-5.14	1.53	1.61

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L4	340	ILE	N-CA-C	-9.03	104.48	111.62
49	28	2024	G	P-O3'-C3'	-6.91	109.84	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	27	26	VAL	N-CA-C	-6.71	106.96	113.53
49	28	2024	G	OP2-P-O3'	5.95	125.85	108.00
32	ee	106	TYR	CA-C-N	-5.52	111.39	120.88

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
49	28	3941	G	Sidechain
49	28	3944	G	Sidechain
49	28	3945	A	Sidechain

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	v	6323	0	6409	184	0
2	58	3208	0	1629	52	0
3	5	2558	0	1296	28	0
4	L8	1899	0	1993	55	0
5	L3	3173	0	3310	70	0
6	L4	2884	0	3053	56	0
7	L5	2392	0	2424	50	0
8	L6	1729	0	1887	50	0
9	L7	1875	0	1995	38	0
10	aa	1879	0	2027	45	0
11	L9	1517	0	1597	44	0
12	10	1664	0	1712	24	0
13	11	1363	0	1399	30	0
14	13	1701	0	1820	25	0
15	14	1138	0	1211	33	0
16	15	1701	0	1749	39	0
17	bb	1630	0	1778	48	0
18	17	1243	0	1274	25	0
19	19	1325	0	1457	18	0
20	20	1462	0	1508	39	0
21	21	1298	0	1366	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	22	810	0	833	18	0
23	24	529	0	541	7	0
24	cc	967	0	1040	15	0
25	26	1116	0	1205	13	0
26	27	1107	0	1182	23	0
27	dd	1162	0	1209	33	0
28	29	848	0	920	11	0
29	30	762	0	794	13	0
30	31	889	0	930	18	0
31	32	1054	0	1147	27	0
32	ee	876	0	912	20	0
33	34	907	0	998	16	0
34	35	1013	0	1147	18	0
35	36	831	0	916	19	0
36	37	706	0	737	13	0
37	38	569	0	637	28	0
38	39	447	0	480	7	0
39	40	429	0	469	5	0
40	42	852	0	924	20	0
41	ff	708	0	756	17	0
42	gg	991	0	1044	14	0
43	s	1508	0	1564	44	0
44	t	1161	0	1218	36	0
45	EB	2932	0	2967	71	0
46	u	1655	0	1760	62	0
47	Q	1515	0	1634	42	0
48	ES	1444	0	735	45	0
49	28	74767	0	37769	906	0
50	25	1034	0	1097	17	0
51	v	28	0	12	4	0
52	34	1	0	0	0	0
52	37	1	0	0	0	0
52	ff	1	0	0	0	0
All	All	147582	0	110471	2255	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 9.

The worst 5 of 2255 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)
41:ff:42:CYS:HB3	41:ff:60:CYS:SG	1.82	1.19
49:28:2638:G:H1	49:28:2697:A:N6	1.48	1.11
49:28:2007:G:N2	49:28:2012:A:H62	1.53	1.04
49:28:2007:G:H21	49:28:2012:A:N6	1.54	1.03
49:28:1398:A:H62	49:28:1419:G:N2	1.58	0.99

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	v	796/858 (93%)	771 (97%)	25 (3%)	0	100	100
4	L8	246/248 (99%)	232 (94%)	14 (6%)	0	100	100
5	L3	392/394 (100%)	379 (97%)	13 (3%)	0	100	100
6	L4	360/362 (99%)	348 (97%)	12 (3%)	0	100	100
7	L5	291/293 (99%)	273 (94%)	16 (6%)	2 (1%)	18	48
8	L6	208/251 (83%)	198 (95%)	10 (5%)	0	100	100
9	L7	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
10	aa	229/266 (86%)	221 (96%)	8 (4%)	0	100	100
11	L9	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
12	10	201/213 (94%)	193 (96%)	8 (4%)	0	100	100
13	11	168/170 (99%)	163 (97%)	5 (3%)	0	100	100
14	13	208/261 (80%)	199 (96%)	7 (3%)	2 (1%)	12	39
15	14	136/138 (99%)	130 (96%)	6 (4%)	0	100	100
16	15	201/203 (99%)	194 (96%)	7 (4%)	0	100	100
17	bb	197/199 (99%)	192 (98%)	5 (2%)	0	100	100
18	17	151/153 (99%)	148 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	19	157/180 (87%)	153 (98%)	4 (2%)	0	100	100
20	20	174/176 (99%)	167 (96%)	6 (3%)	1 (1%)	21	51
21	21	157/159 (99%)	151 (96%)	6 (4%)	0	100	100
22	22	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
23	24	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
24	cc	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
25	26	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
26	27	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
27	dd	145/147 (99%)	134 (92%)	11 (8%)	0	100	100
28	29	100/245 (41%)	96 (96%)	4 (4%)	0	100	100
29	30	96/98 (98%)	96 (100%)	0	0	100	100
30	31	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
31	32	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
32	ee	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
33	34	112/114 (98%)	112 (100%)	0	0	100	100
34	35	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
35	36	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
36	37	84/86 (98%)	80 (95%)	4 (5%)	0	100	100
37	38	67/69 (97%)	64 (96%)	3 (4%)	0	100	100
38	39	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
39	40	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
40	42	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
41	ff	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
42	gg	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
43	s	194/196 (99%)	181 (93%)	13 (7%)	0	100	100
44	t	151/153 (99%)	135 (89%)	16 (11%)	0	100	100
45	EB	373/375 (100%)	358 (96%)	15 (4%)	0	100	100
46	u	204/206 (99%)	183 (90%)	21 (10%)	0	100	100
47	Q	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
50	25	137/139 (99%)	135 (98%)	2 (2%)	0	100	100
All	All	8039/8492 (95%)	7712 (96%)	322 (4%)	5 (0%)	49	77

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	13	64	VAL
7	L5	36	LEU
14	13	63	THR
20	20	165	PRO
7	L5	37	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	v	690/730 (94%)	615 (89%)	75 (11%)	6	20
4	L8	190/190 (100%)	172 (90%)	18 (10%)	8	26
5	L3	342/342 (100%)	318 (93%)	24 (7%)	14	40
6	L4	302/302 (100%)	285 (94%)	17 (6%)	19	50
7	L5	247/247 (100%)	229 (93%)	18 (7%)	13	38
8	L6	190/223 (85%)	171 (90%)	19 (10%)	7	24
9	L7	196/196 (100%)	182 (93%)	14 (7%)	13	40
10	aa	200/224 (89%)	177 (88%)	23 (12%)	5	18
11	L9	169/169 (100%)	155 (92%)	14 (8%)	10	32
12	10	175/180 (97%)	165 (94%)	10 (6%)	18	49
13	11	143/143 (100%)	135 (94%)	8 (6%)	19	50
14	13	175/215 (81%)	166 (95%)	9 (5%)	21	53
15	14	117/117 (100%)	104 (89%)	13 (11%)	6	20
16	15	171/171 (100%)	158 (92%)	13 (8%)	12	36
17	bb	171/171 (100%)	158 (92%)	13 (8%)	12	36
18	17	134/134 (100%)	121 (90%)	13 (10%)	8	25
19	19	141/159 (89%)	131 (93%)	10 (7%)	13	40
20	20	157/157 (100%)	140 (89%)	17 (11%)	6	21
21	21	139/139 (100%)	127 (91%)	12 (9%)	10	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	22	89/89 (100%)	85 (96%)	4 (4%)	24	58
23	24	55/55 (100%)	52 (94%)	3 (6%)	19	50
24	cc	106/106 (100%)	98 (92%)	8 (8%)	12	37
25	26	124/124 (100%)	109 (88%)	15 (12%)	5	16
26	27	117/117 (100%)	108 (92%)	9 (8%)	12	35
27	dd	119/119 (100%)	114 (96%)	5 (4%)	26	60
28	29	84/184 (46%)	78 (93%)	6 (7%)	13	40
29	30	84/84 (100%)	80 (95%)	4 (5%)	23	55
30	31	98/98 (100%)	91 (93%)	7 (7%)	13	40
31	32	114/114 (100%)	107 (94%)	7 (6%)	17	46
32	ee	88/88 (100%)	82 (93%)	6 (7%)	14	42
33	34	98/98 (100%)	88 (90%)	10 (10%)	7	23
34	35	109/109 (100%)	104 (95%)	5 (5%)	24	57
35	36	86/86 (100%)	76 (88%)	10 (12%)	5	18
36	37	73/73 (100%)	70 (96%)	3 (4%)	27	61
37	38	64/64 (100%)	62 (97%)	2 (3%)	35	69
38	39	47/47 (100%)	44 (94%)	3 (6%)	16	44
39	40	48/48 (100%)	46 (96%)	2 (4%)	26	60
40	42	92/92 (100%)	86 (94%)	6 (6%)	15	44
41	ff	74/74 (100%)	71 (96%)	3 (4%)	27	61
42	gg	107/108 (99%)	95 (89%)	12 (11%)	6	19
43	s	164/164 (100%)	145 (88%)	19 (12%)	5	18
44	t	126/126 (100%)	109 (86%)	17 (14%)	4	12
45	EB	321/321 (100%)	290 (90%)	31 (10%)	8	25
46	u	186/186 (100%)	173 (93%)	13 (7%)	14	40
47	Q	164/164 (100%)	146 (89%)	18 (11%)	6	20
50	25	106/106 (100%)	99 (93%)	7 (7%)	15	43
All	All	6992/7253 (96%)	6417 (92%)	575 (8%)	13	32

5 of 575 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	gg	78	VAL

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Mol	Chain	Res	Type
50	25	94	VAL
43	s	61	MET
42	gg	75	THR
45	EB	156	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 148 such sidechains are listed below:

Mol	Chain	Res	Type
42	gg	70	GLN
47	Q	93	GLN
43	s	159	GLN
45	EB	193	HIS
11	L9	189	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	58	149/156 (95%)	36 (24%)	1 (0%)
3	5	119/120 (99%)	12 (10%)	0
48	ES	63/5070 (1%)	16 (25%)	1 (1%)
49	28	3461/4807 (71%)	778 (22%)	49 (1%)
All	All	3792/10153 (37%)	842 (22%)	51 (1%)

5 of 842 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	58	2	G
2	58	3	A
2	58	16	G
2	58	23	C
2	58	34	U

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	28	2502	A
49	28	3625	G
49	28	4936	G
49	28	2513	A
49	28	2639	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
51	GDP	v	900	-	29,30,30	3.51	13 (44%)	45,47,47	1.83	11 (24%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
51	GDP	v	900	-	-	3/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	v	900	GDP	O6-C6	9.38	1.41	1.23
51	v	900	GDP	C2'-C3'	-8.43	1.30	1.53
51	v	900	GDP	O4'-C4'	-7.01	1.29	1.45
51	v	900	GDP	O4'-C1'	5.34	1.54	1.42
51	v	900	GDP	C2-N2	4.74	1.45	1.34

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	v	900	GDP	C5-C4-N3	-5.65	119.39	128.39
51	v	900	GDP	C2-N3-C4	4.86	120.67	112.30
51	v	900	GDP	N9-C4-N3	3.88	133.71	125.95
51	v	900	GDP	C3'-C2'-C1'	3.05	107.23	101.46
51	v	900	GDP	C6-C5-N7	2.83	135.44	130.29

There are no chirality outliers.

All (3) torsion outliers are listed below:

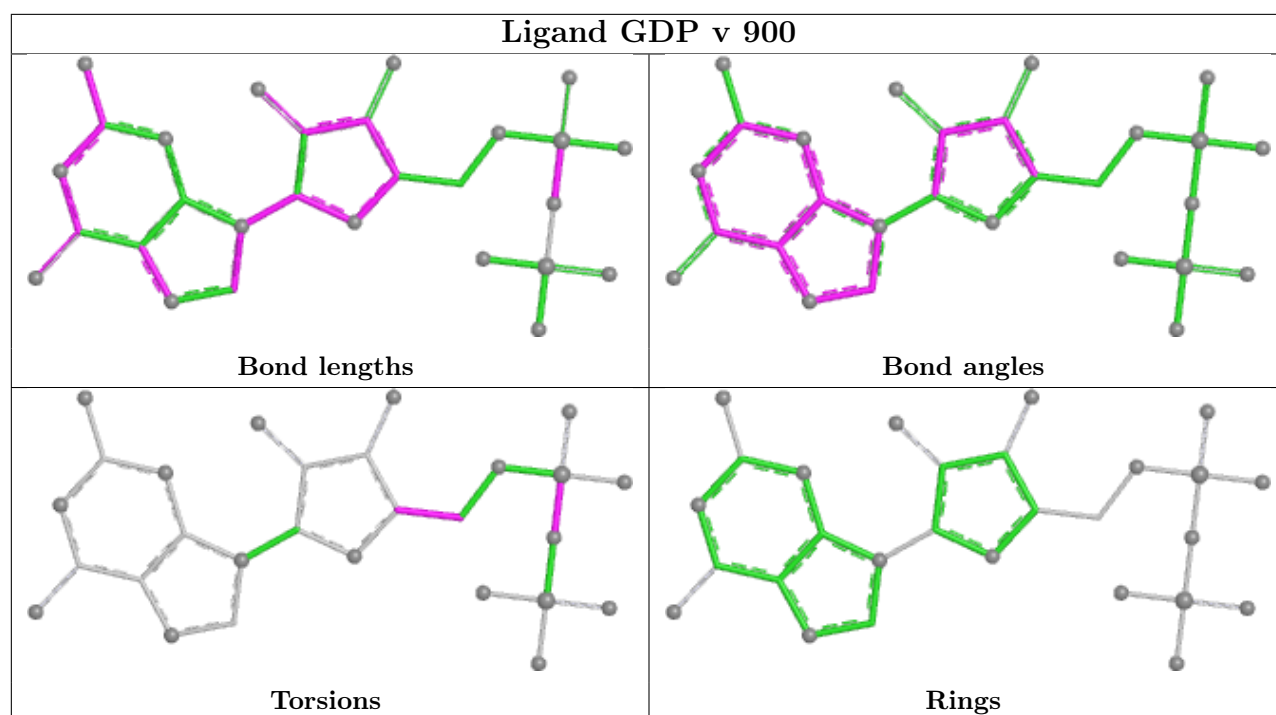
Mol	Chain	Res	Type	Atoms
51	v	900	GDP	C3'-C4'-C5'-O5'
51	v	900	GDP	O4'-C4'-C5'-O5'
51	v	900	GDP	PB-O3A-PA-O2A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
51	v	900	GDP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
49	28	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	28	3945:A	O3'	3946:G	P	1.94
1	28	3940:U	O3'	3941:G	P	1.29

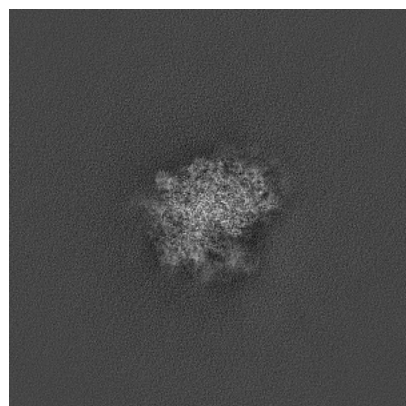
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75704. These allow visual inspection of the internal detail of the map and identification of artifacts.

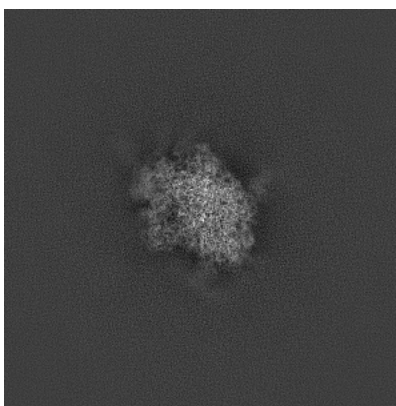
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

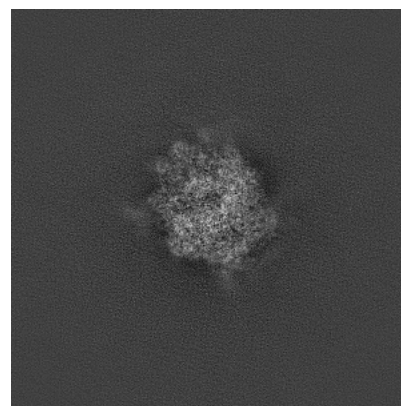
6.1.1 Primary map



X

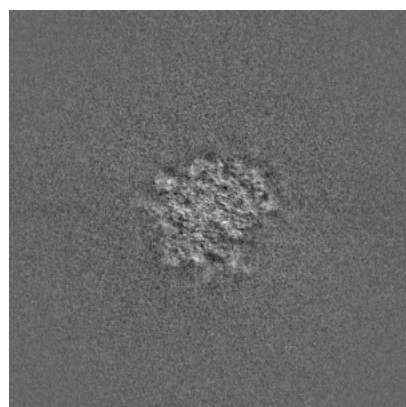


Y

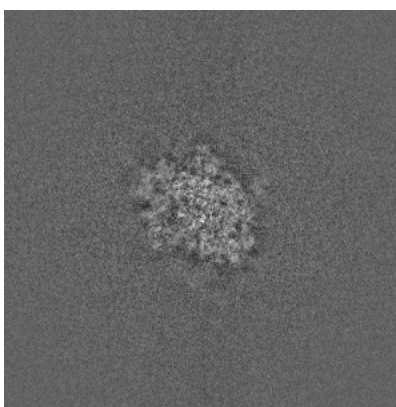


Z

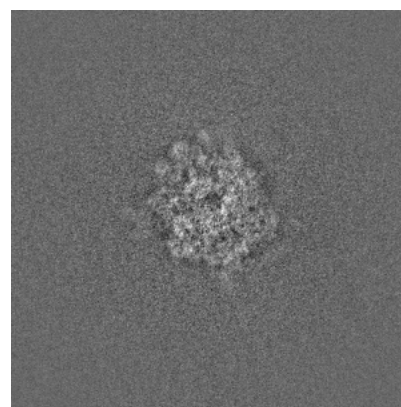
6.1.2 Raw map



X



Y

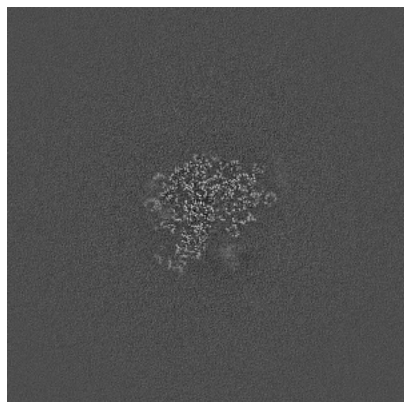


Z

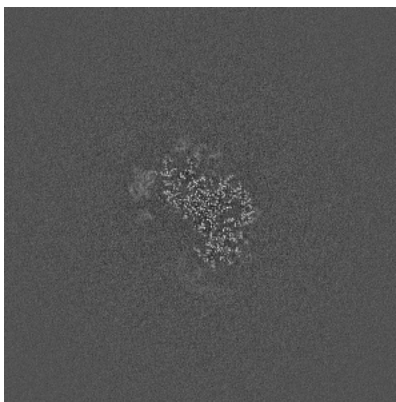
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

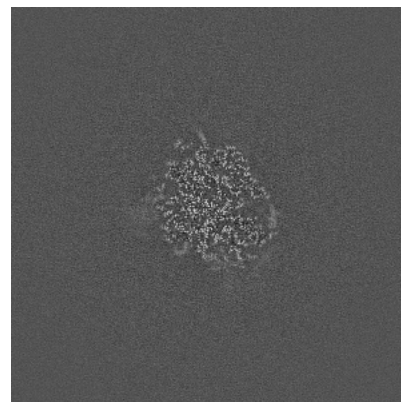
6.2.1 Primary map



X Index: 400

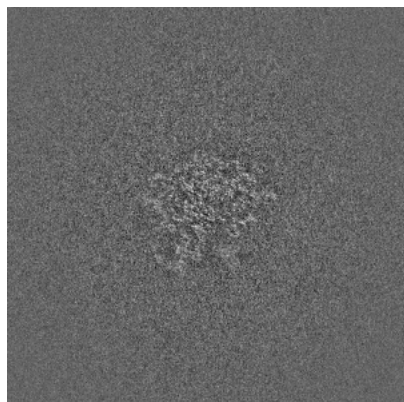


Y Index: 400

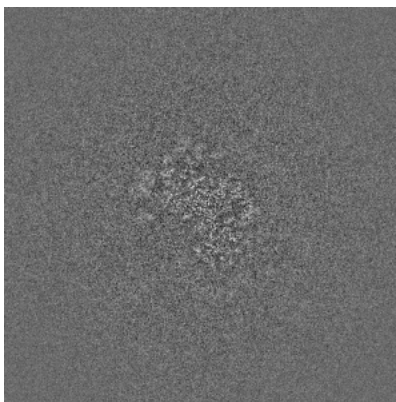


Z Index: 400

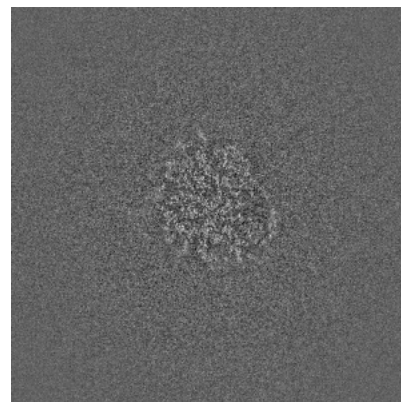
6.2.2 Raw map



X Index: 400



Y Index: 400

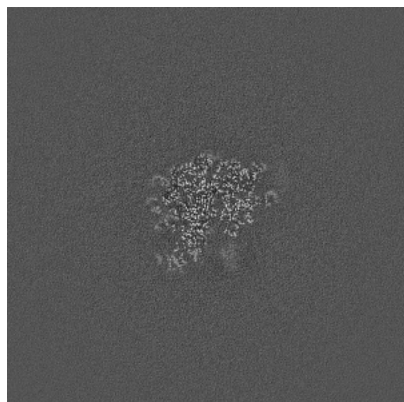


Z Index: 400

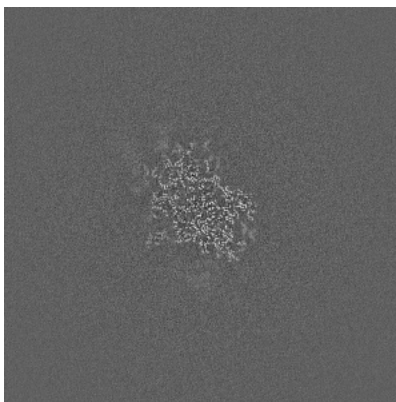
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

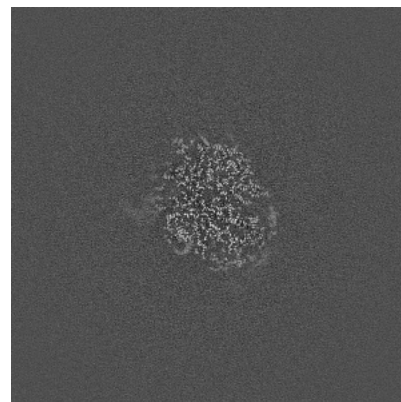
6.3.1 Primary map



X Index: 396

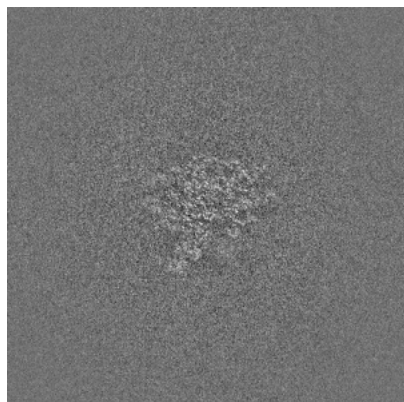


Y Index: 380

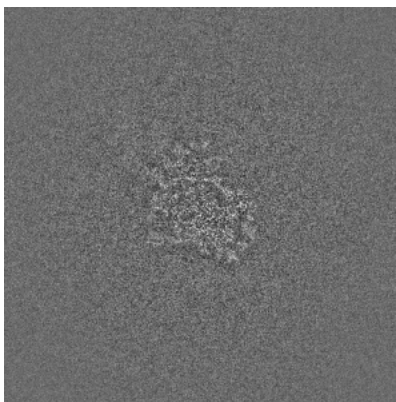


Z Index: 403

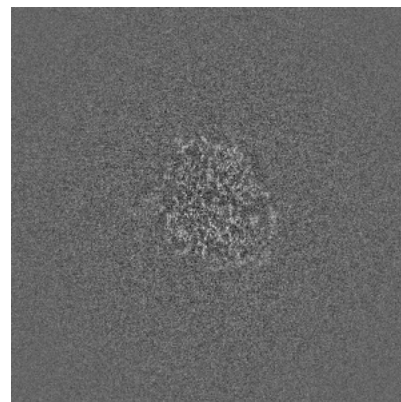
6.3.2 Raw map



X Index: 398



Y Index: 380

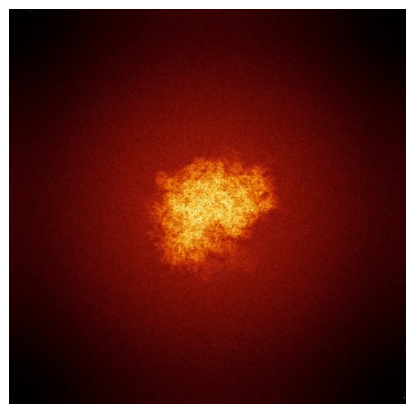


Z Index: 403

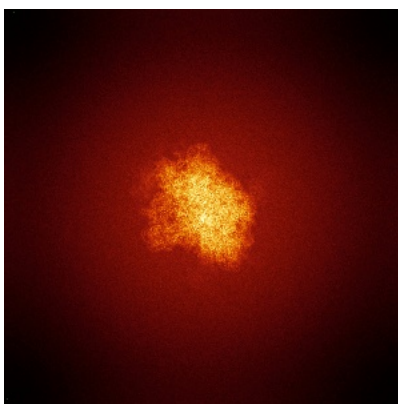
The images above show the largest variance slices of the map in three orthogonal directions.

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

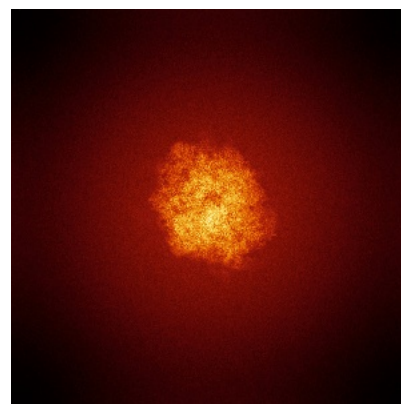
6.4.1 Primary map



X

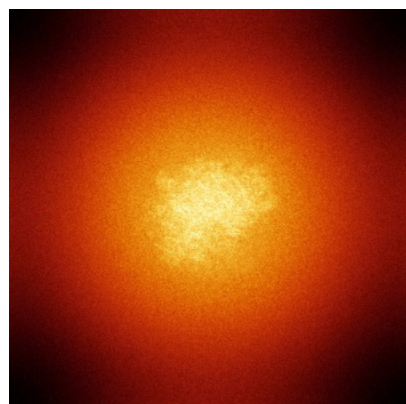


Y

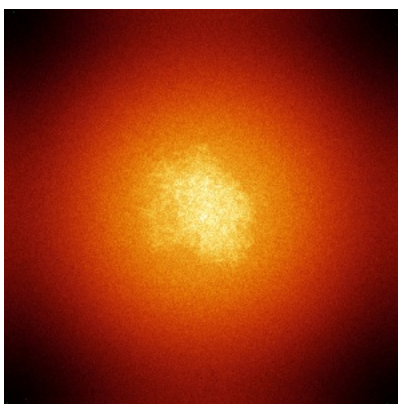


Z

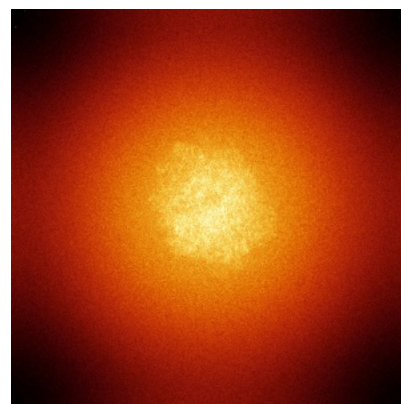
6.4.2 Raw map



X



Y

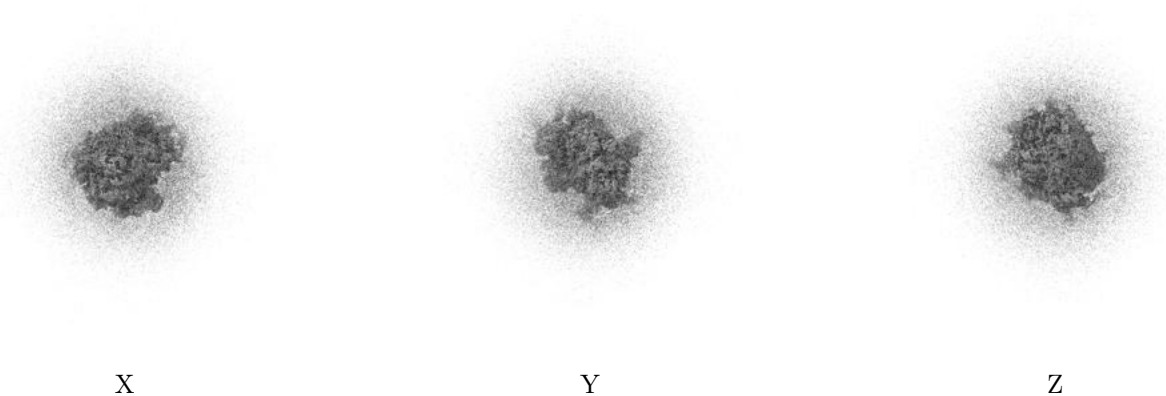


Z

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.

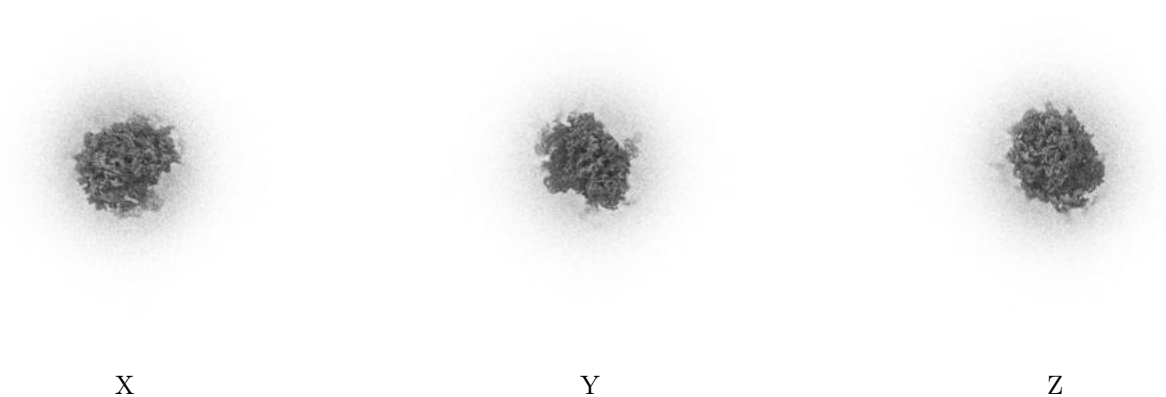
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

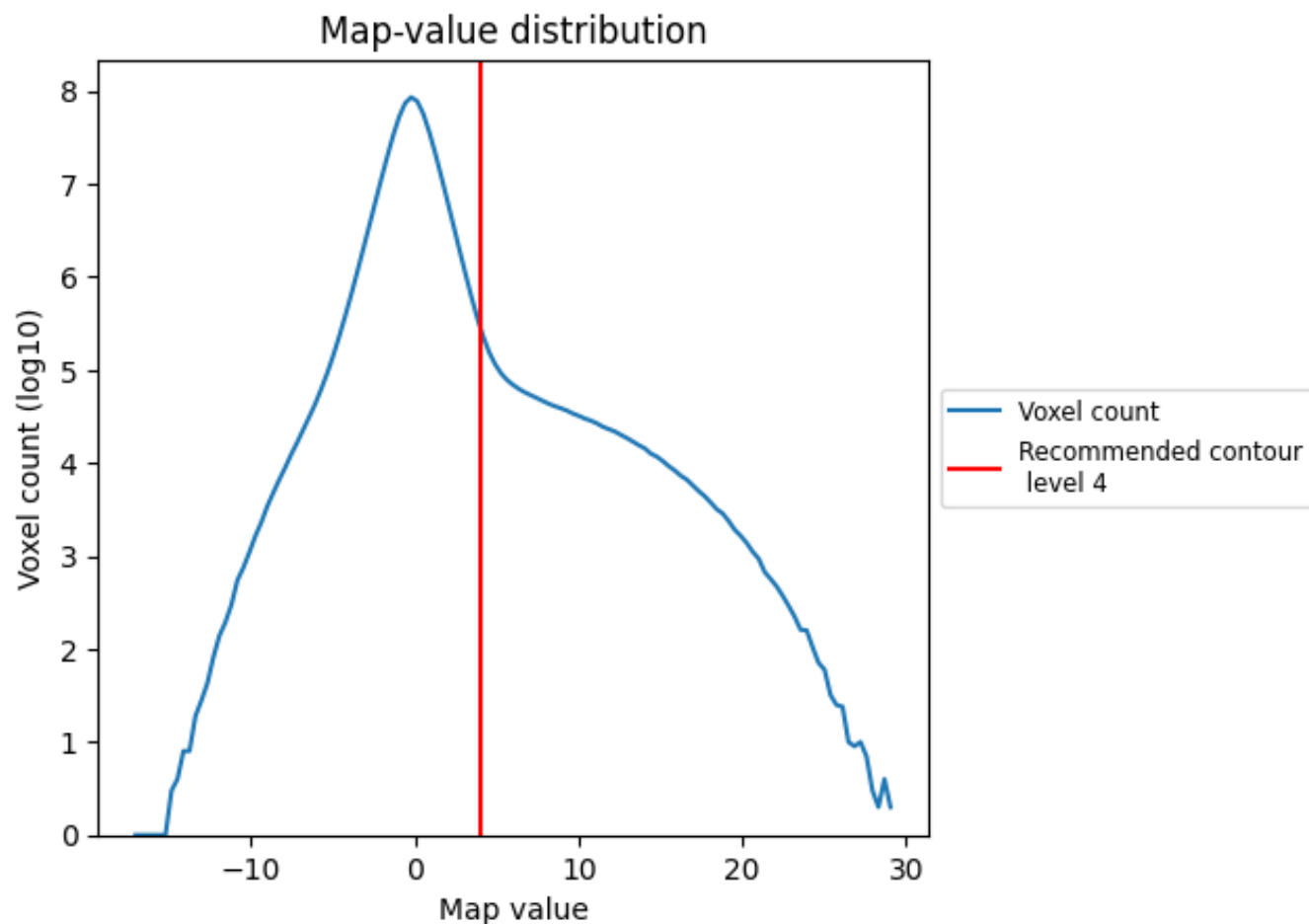
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

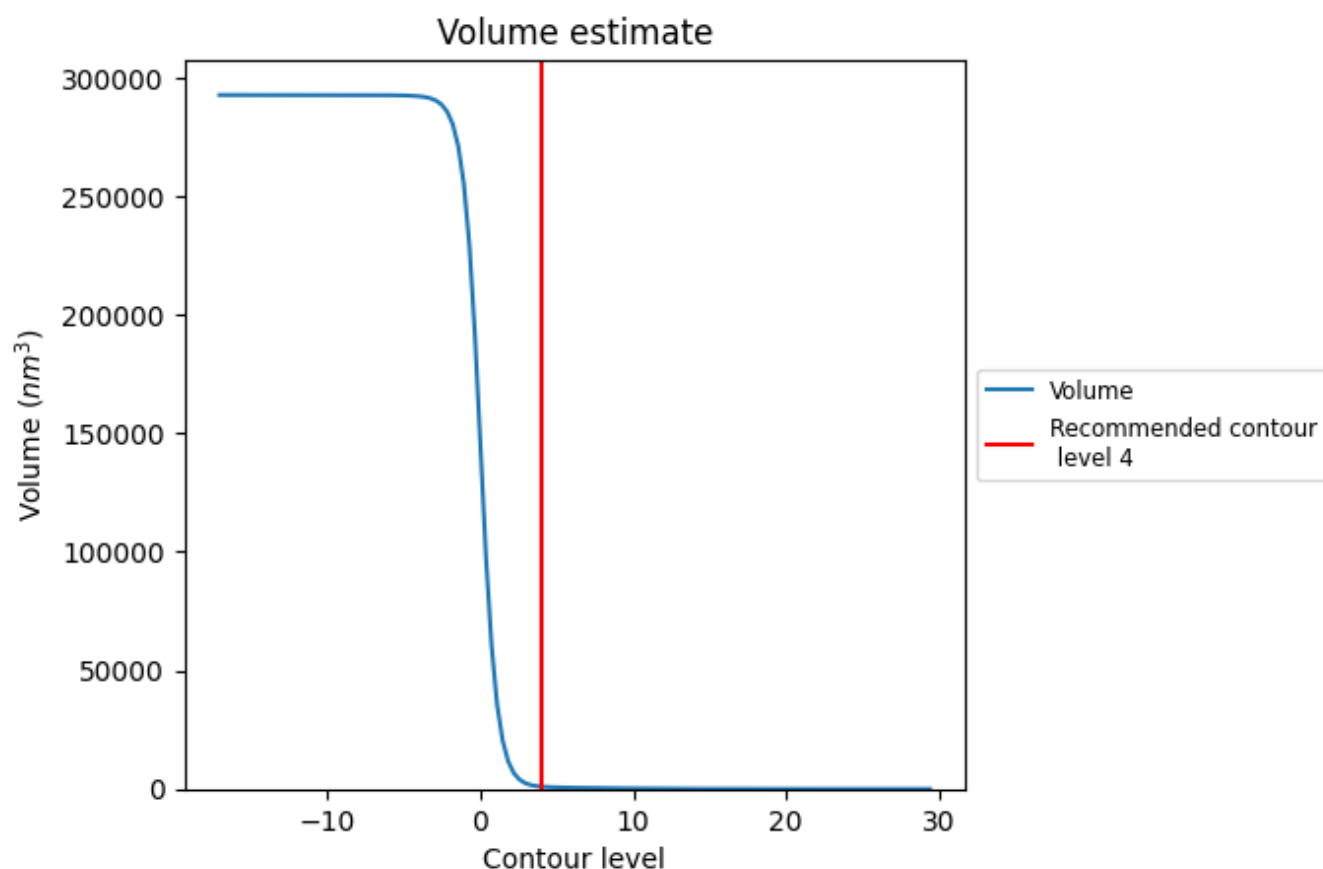
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

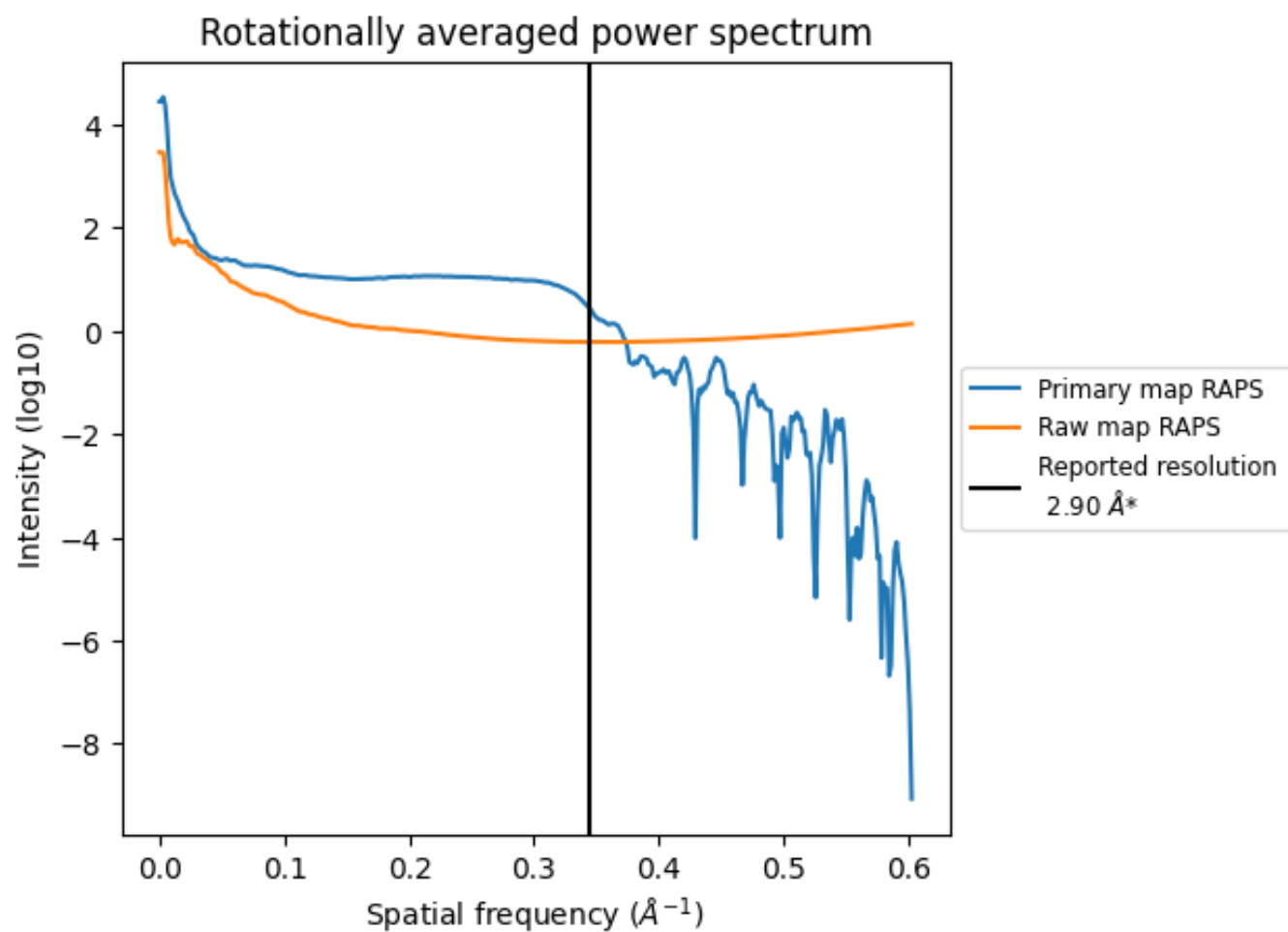
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 986 nm³; this corresponds to an approximate mass of 891 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 ⓘ

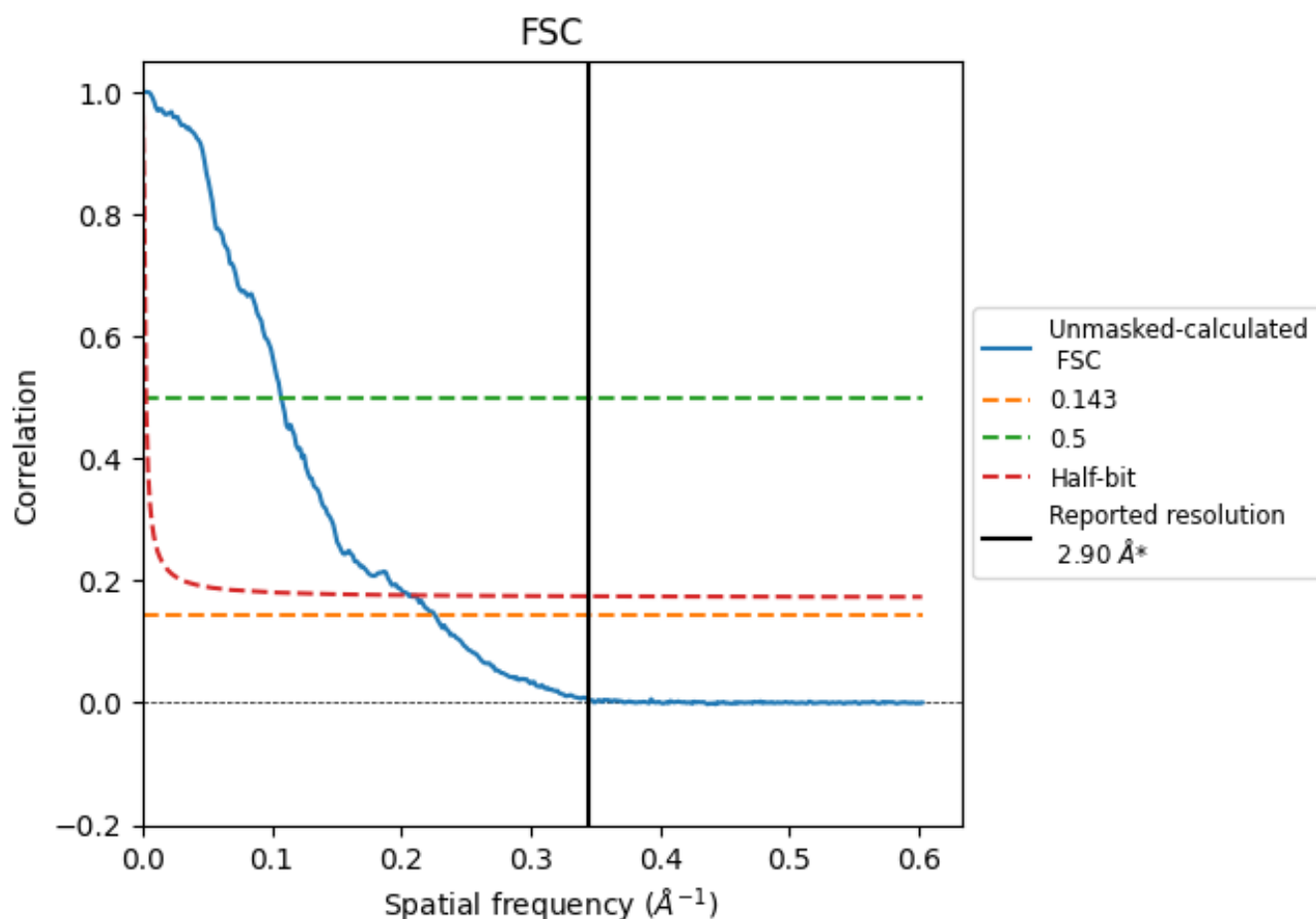


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

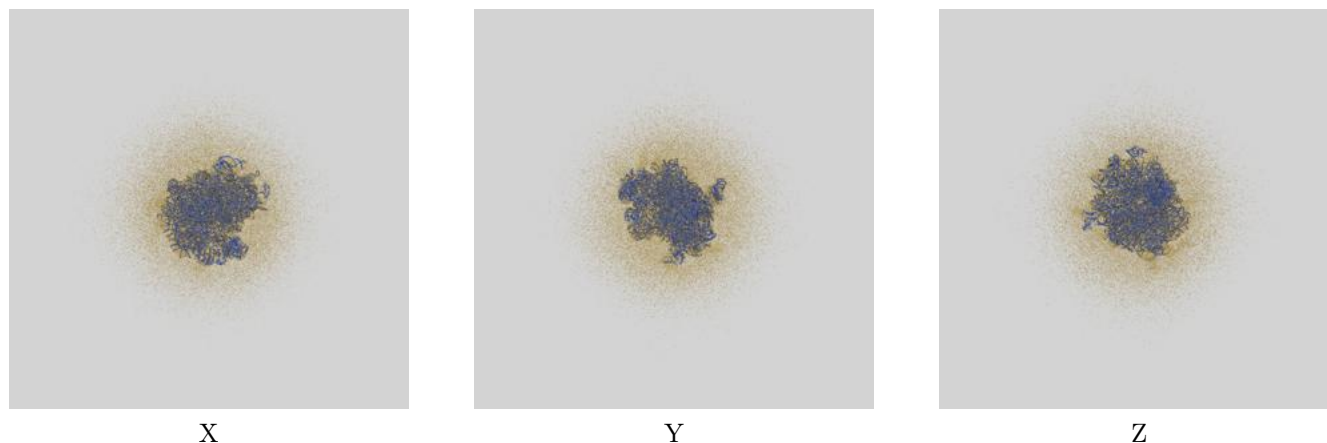
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.42	9.33	4.86

*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 4.42 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

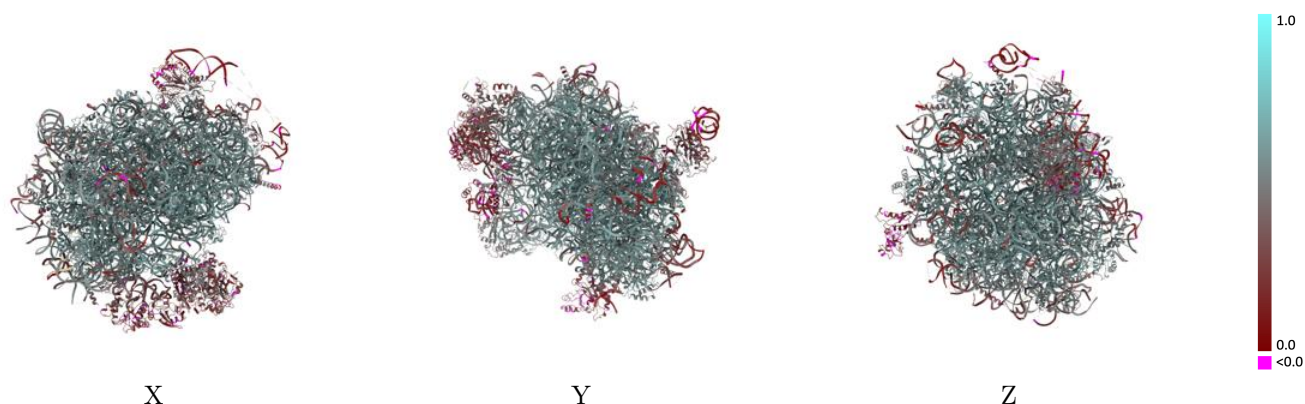
This section contains information regarding the fit between EMDB map EMD-75704 and PDB model 11HV. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



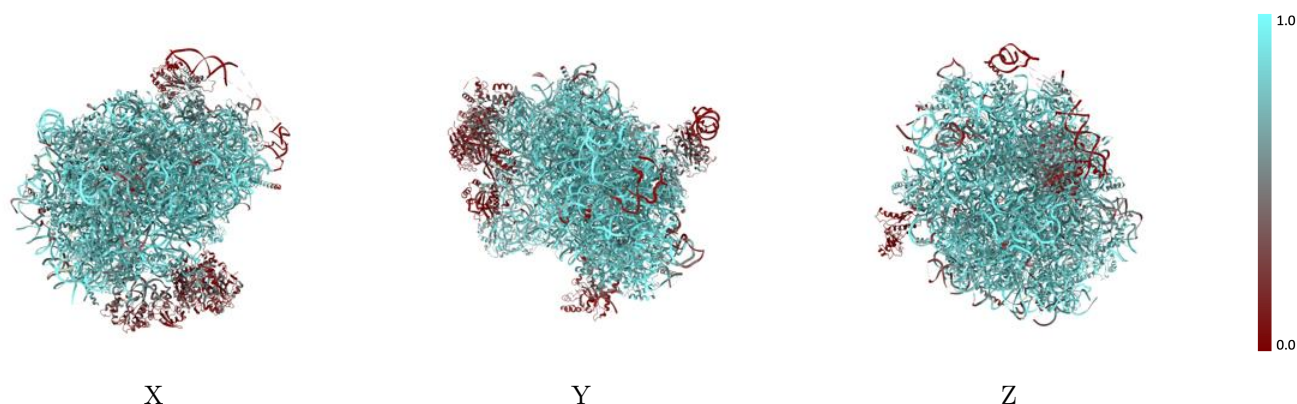
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



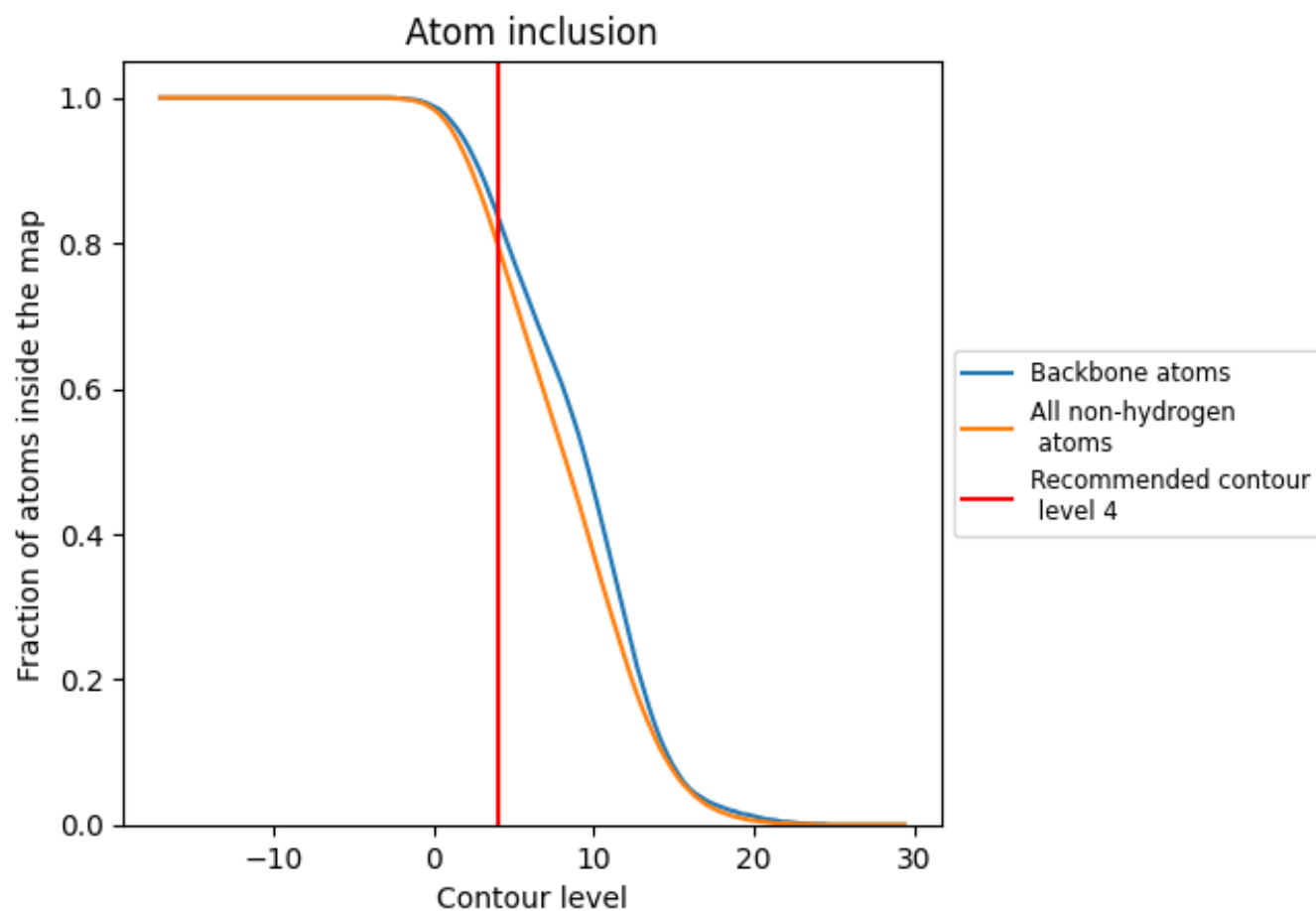
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7980	 0.5180
10	 0.8430	 0.5600
11	 0.7050	 0.4760
13	 0.8180	 0.5450
14	 0.8250	 0.5480
15	 0.8940	 0.6010
17	 0.8600	 0.5870
19	 0.7910	 0.5260
20	 0.8710	 0.5780
21	 0.8330	 0.5590
22	 0.6540	 0.4420
24	 0.7920	 0.5530
25	 0.8060	 0.5640
26	 0.8280	 0.5570
27	 0.8130	 0.5490
28	 0.8810	 0.5400
29	 0.7070	 0.4810
30	 0.7450	 0.5030
31	 0.7970	 0.5430
32	 0.8840	 0.5910
34	 0.7980	 0.5530
35	 0.8010	 0.5500
36	 0.8160	 0.5400
37	 0.8950	 0.5990
38	 0.7070	 0.4920
39	 0.8450	 0.5680
40	 0.8170	 0.5580
42	 0.8230	 0.5610
5	 0.9480	 0.5830
58	 0.8990	 0.5580
EB	 0.3880	 0.3420
ES	 0.0670	 0.1190
L3	 0.8530	 0.5770
L4	 0.8580	 0.5780
L5	 0.8010	 0.5350



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Chain	Atom inclusion	Q-score
L6	 0.8340	 0.5450
L7	 0.8630	 0.5840
L8	 0.8740	 0.5900
L9	 0.7860	 0.5500
Q	 0.8790	 0.5870
aa	 0.7650	 0.5190
bb	 0.8690	 0.5730
cc	 0.8070	 0.5610
dd	 0.8860	 0.5970
ee	 0.8990	 0.6050
ff	 0.8160	 0.5590
gg	 0.8720	 0.5820
s	 0.3190	 0.2860
t	 0.1320	 0.1730
u	 0.0450	 0.1410
v	 0.2400	 0.2810