



wwPDB EM Validation Summary Report ⓘ

Apr 21, 2025 – 12:28 PM EDT

PDB ID : 9B0O / pdb_00009b0o
EMDB ID : EMD-44048
Title : In situ human Post-eEF1A-A/T-P-Z state 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2024-03-12
Resolution : 2.83 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.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

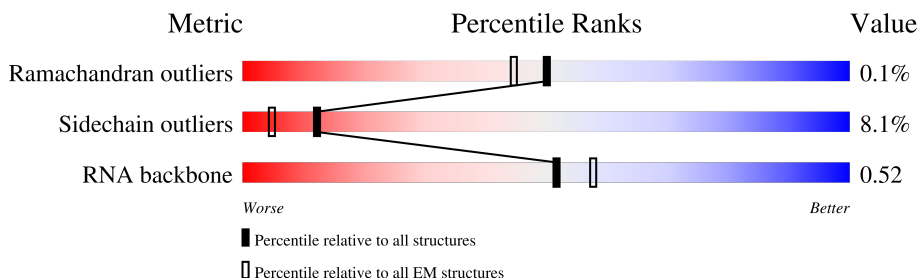
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.83 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	AT	77	<div> <div>45%</div> <div>43%</div> <div>53%</div> <div>..</div> </div>
2	CF	441	<div> <div>83%</div> <div>93%</div> <div>7%</div> <div>.</div> </div>
3	LW	118	<div> <div>25%</div> <div>94%</div> <div>6%</div> </div>
4	SE	262	<div> <div>93%</div> <div>7%</div> </div>
5	SI	206	<div> <div>6%</div> <div>93%</div> <div>7%</div> </div>
6	SL	153	<div> <div>12%</div> <div>92%</div> <div>8%</div> </div>
7	SX	141	<div> <div>89%</div> <div>11%</div> </div>
8	SG	237	<div> <div>16%</div> <div>89%</div> <div>10%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
9	SJ	185	
10	SY	131	
11	Se	58	
12	SA	221	
13	SB	214	
14	SH	186	
15	SV	83	
16	Sa	102	
17	SC	222	
18	SN	150	
19	SO	140	
20	SW	129	
21	Sb	83	
22	L5	3740	
23	L7	120	
24	L8	156	
25	LA	248	
26	LB	402	
27	LC	368	
28	LD	293	
29	LE	236	
30	LF	225	
31	LG	241	
32	LH	190	
33	LI	202	



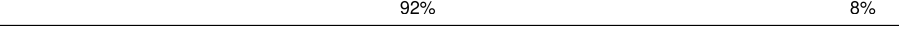
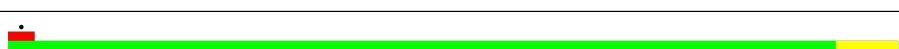

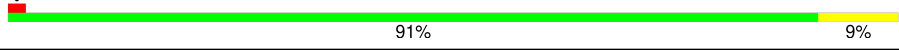
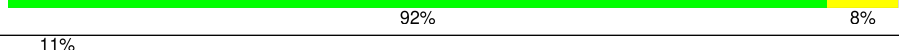
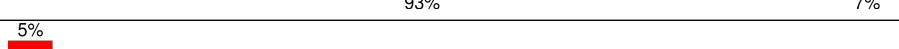



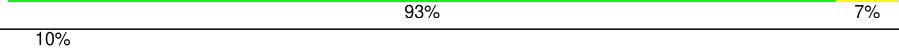
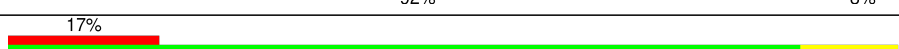
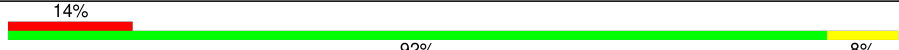


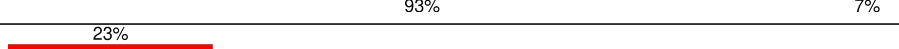



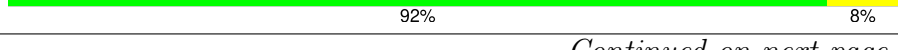



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Mol	Chain	Length	Quality of chain
34	LJ	176	
35	LL	210	
36	LM	139	
37	LN	203	
38	LO	201	
39	LP	153	
40	LQ	187	
41	LR	187	
42	LS	175	
43	LT	159	
44	LU	101	
45	LV	131	
46	LX	120	
47	LY	134	
48	LZ	135	
49	La	147	
50	Lb	109	
51	Lc	98	
52	Ld	107	
53	Le	128	
54	Lf	109	
55	Lg	114	
56	Lh	122	
57	Li	102	
58	Lj	86	

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Mol	Chain	Length	Quality of chain
59	Lk	69	
60	Ll	50	
61	Lm	52	
62	Ln	24	
63	Lo	105	
64	Lp	91	
65	Lr	125	
66	SR	135	
67	SD	227	
68	SF	189	
69	SK	98	
70	SP	121	
71	SQ	144	
72	SS	145	
73	ST	143	
74	SU	104	
75	Sc	64	
76	Sd	55	
77	Sg	313	
78	SM	122	
79	SZ	75	
80	Sf	67	
81	S2	1740	
82	Pt	76	
83	Lz	217	

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Mol	Chain	Length	Quality of chain
84	Ls	196	<div><div></div><div>77%</div><div></div><div>92%</div><div></div><div>7%</div><div></div><div></div></div>
85	Lt	141	<div><div></div><div>94%</div><div></div><div>96%</div><div></div><div></div><div></div><div></div></div>
86	Zt	75	<div><div></div><div>80%</div><div></div><div>39%</div><div></div><div>60%</div><div></div><div></div></div>

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 227757 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called A/T site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AT	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 2 is a protein called Elongation factor 1-alpha 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	CF	441	Total	C	N	O	P	S	0	0
			3383	2148	581	636	1	17		

- Molecule 3 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		

- Molecule 4 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 5 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 6 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 7 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 8 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 9 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 10 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 11 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 12 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 13 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 14 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 15 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 16 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 17 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 18 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 20 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 21 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 22 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L5	3740	Total	C	N	O	P	0	0
			79860	35549	14585	25987	3739		

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 24 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 25 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 26 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 27 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 28 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 29 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 30 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 31 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 32 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 33 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 34 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 35 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 36 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 37 is a protein called 60S ribosomal protein L15.

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

- Molecule 38 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 39 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 40 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 41 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 42 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 43 is a protein called 60S ribosomal protein L21.

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

- Molecule 44 is a protein called Heparin-binding protein HBp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 45 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 46 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 47 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 48 is a protein called 60S ribosomal protein L27.

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

- Molecule 49 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 50 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 51 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 52 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 53 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 54 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 55 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 56 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 57 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 58 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 59 is a protein called 60S ribosomal protein L38.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 61 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 62 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 63 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 64 is a protein called 60S ribosomal protein L37a.

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

- Molecule 65 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 66 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 67 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 68 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 69 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 70 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 71 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 72 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 73 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 74 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 75 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 76 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 77 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 78 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 79 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 81 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

- Molecule 82 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Pt	76	Total	C	N	O	P	0	0
			1620	725	296	524	75		

- Molecule 83 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 84 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 85 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 86 is a RNA chain called Z site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Zt	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
87	SG	1	Total	Mg	0
			1	1	
87	L5	212	Total	Mg	0
			212	212	
87	L7	3	Total	Mg	0
			3	3	
87	L8	4	Total	Mg	0
			4	4	
87	LA	1	Total	Mg	0
			1	1	
87	LI	1	Total	Mg	0
			1	1	
87	LP	1	Total	Mg	0
			1	1	
87	LV	1	Total	Mg	0
			1	1	
87	Le	2	Total	Mg	0
			2	2	
87	Lg	1	Total	Mg	0
			1	1	
87	S2	28	Total	Mg	0
			28	28	

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by

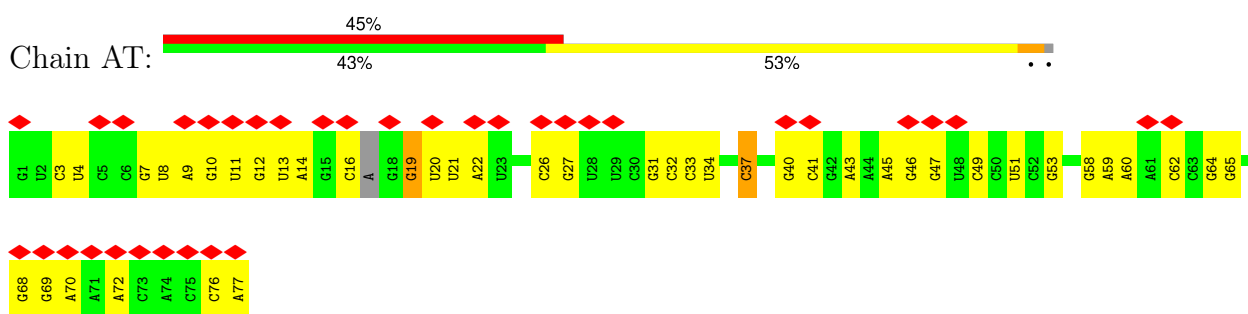
depositor).

Mol	Chain	Residues	Atoms		AltConf
88	Sa	1	Total 1	Zn 1	0
88	Lg	1	Total 1	Zn 1	0
88	Lj	1	Total 1	Zn 1	0
88	Lm	1	Total 1	Zn 1	0
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0

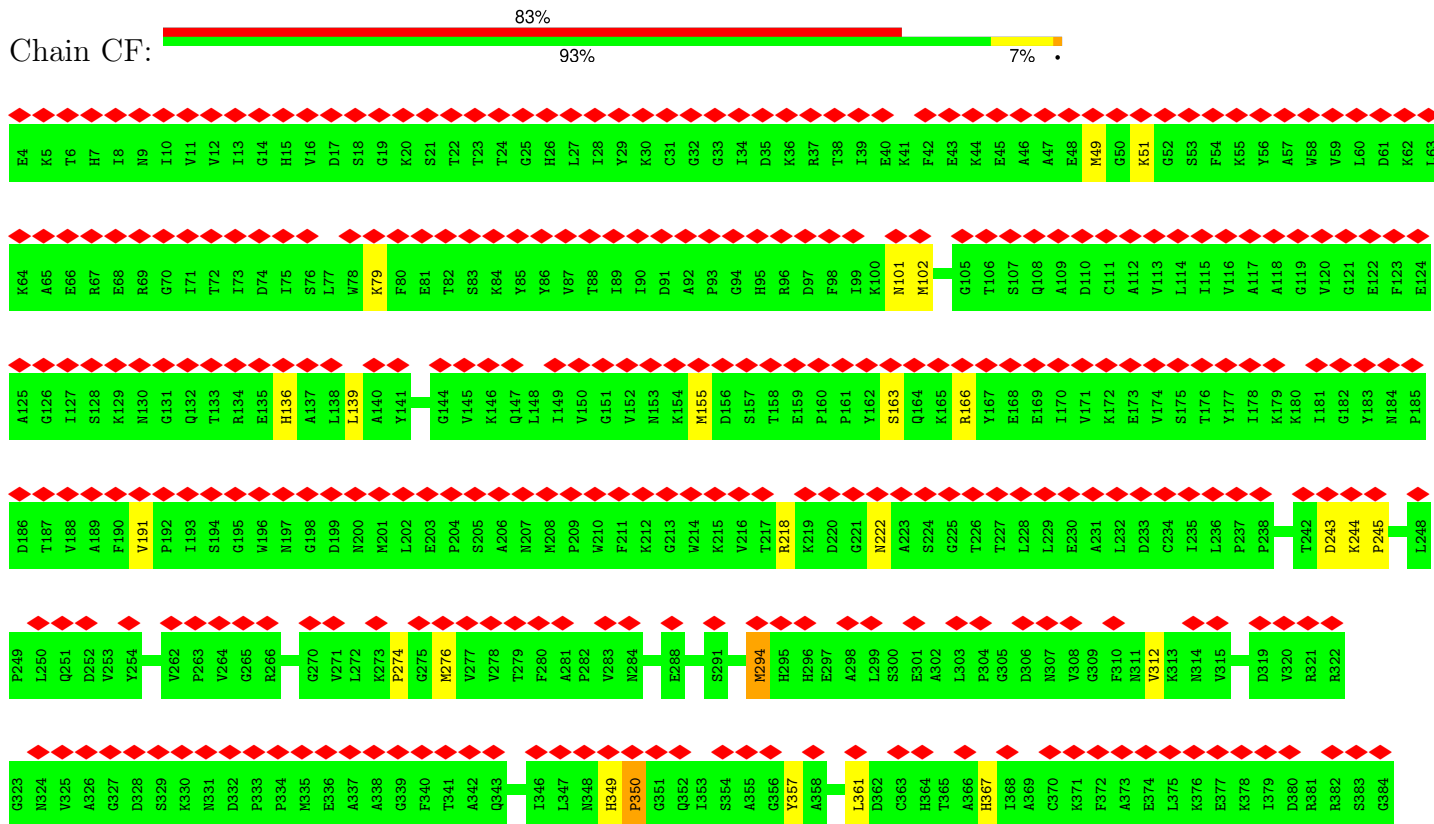
3 Residue-property plots

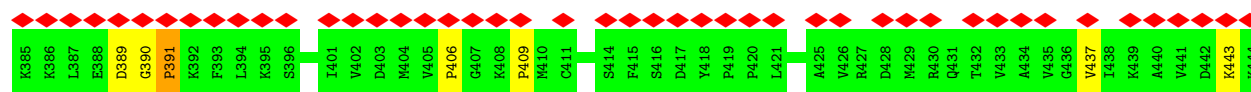
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

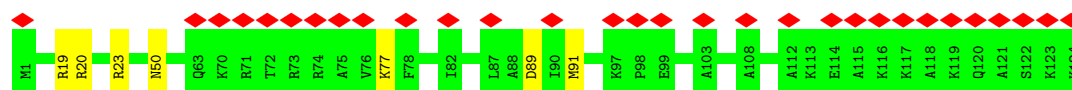


• Molecule 2: Elongation factor 1-alpha 1

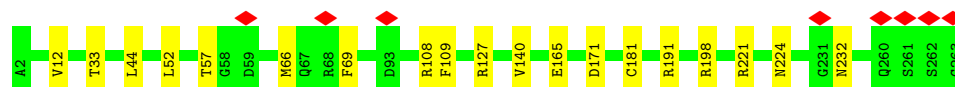




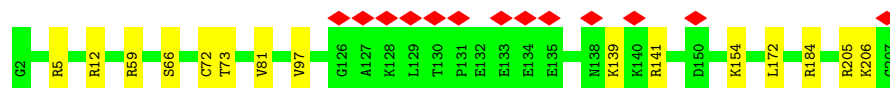
- Molecule 3: 60S ribosomal protein L24



- Molecule 4: Small ribosomal subunit protein eS4, X isoform



- Molecule 5: 40S ribosomal protein S8



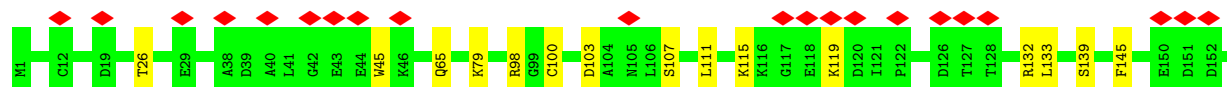
- Molecule 6: 40S ribosomal protein S11

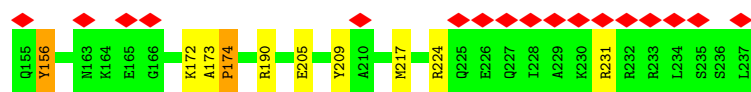


- Molecule 7: 40S ribosomal protein S23



- Molecule 8: 40S ribosomal protein S6

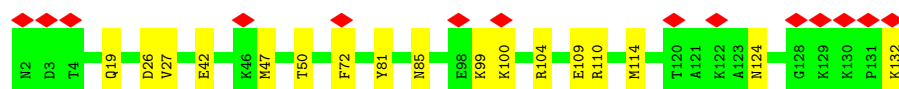




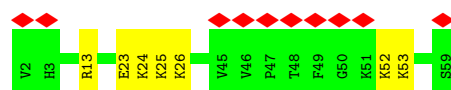
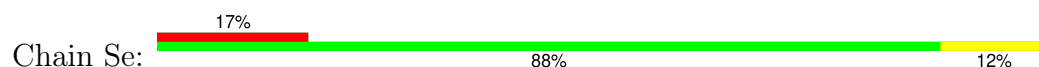
- Molecule 9: 40S ribosomal protein S9



- Molecule 10: 40S ribosomal protein S24



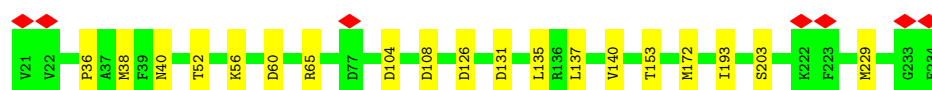
- Molecule 11: Small ribosomal subunit protein eS30



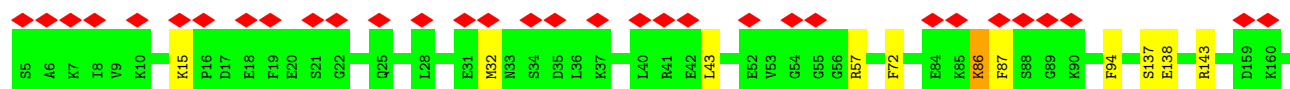
- Molecule 12: 40S ribosomal protein SA

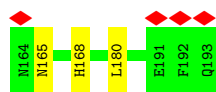


- Molecule 13: 40S ribosomal protein S3a



- Molecule 14: 40S ribosomal protein S7

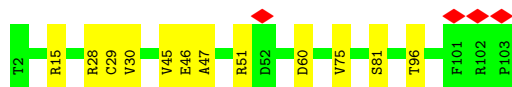




- Molecule 15: 40S ribosomal protein S21



- Molecule 16: 40S ribosomal protein S26



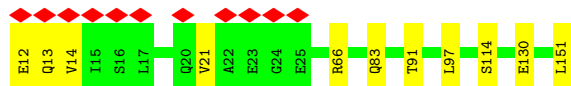
- Molecule 17: 40S ribosomal protein S2



- Molecule 18: 40S ribosomal protein S13



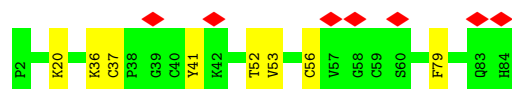
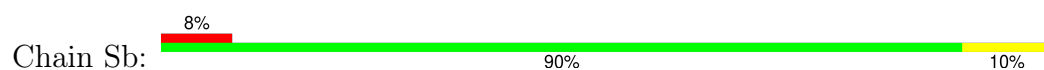
- Molecule 19: Small ribosomal subunit protein uS11



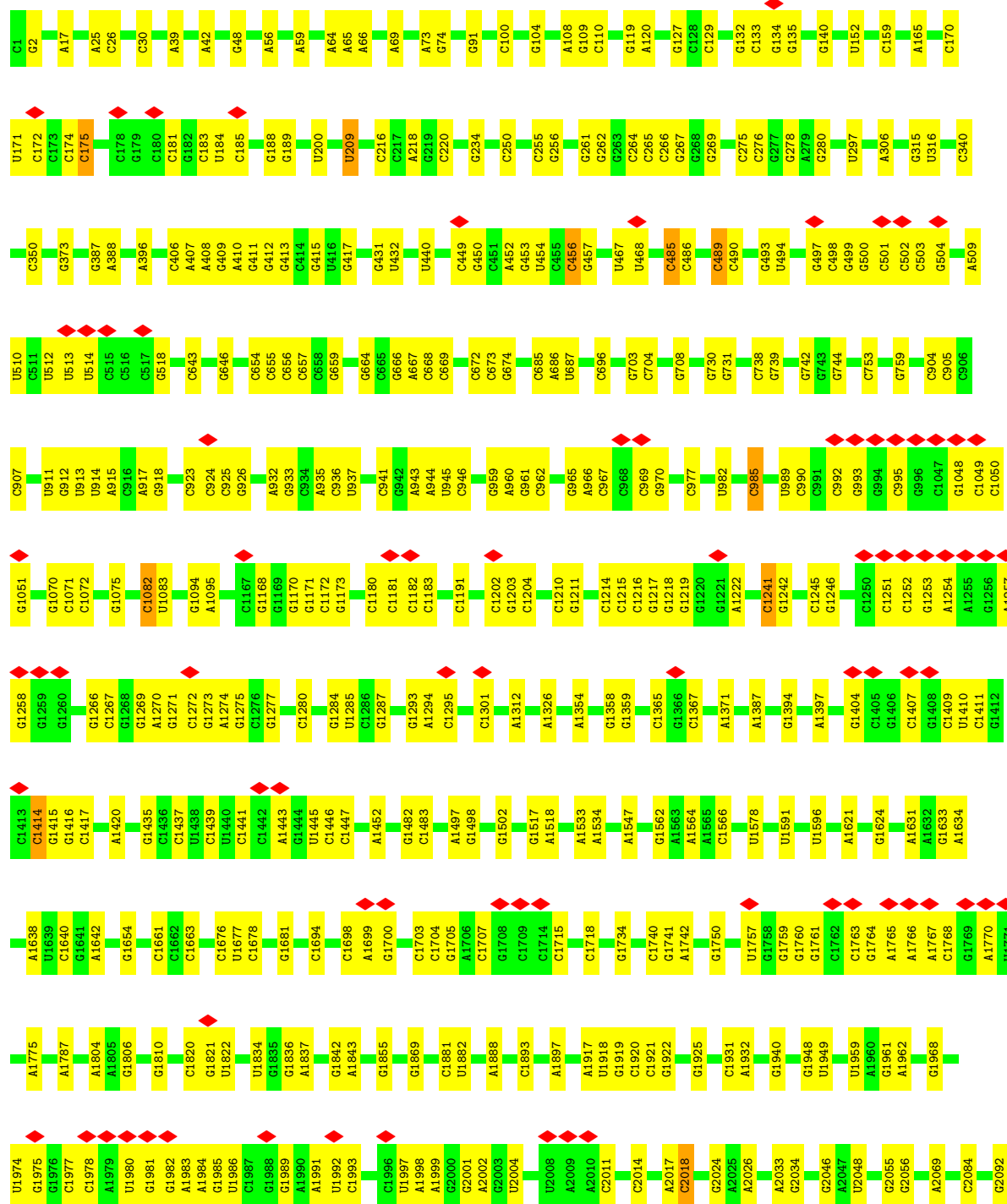
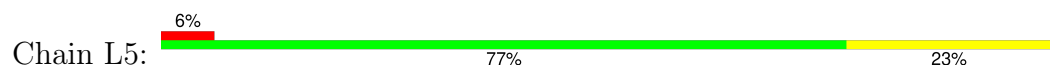
- Molecule 20: 40S ribosomal protein S15a



- Molecule 21: Small ribosomal subunit protein eS27



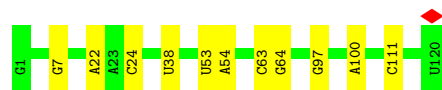
• Molecule 22: 28S rRNA






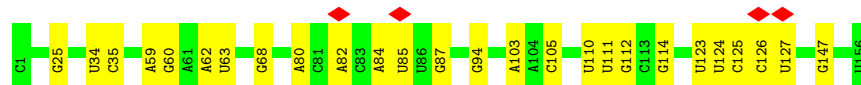
- Molecule 23: 5S rRNA

Chain L7: 



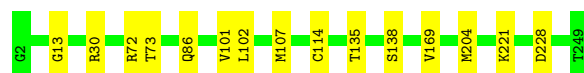
- Molecule 24: 5.8S rRNA

Chain L8: 



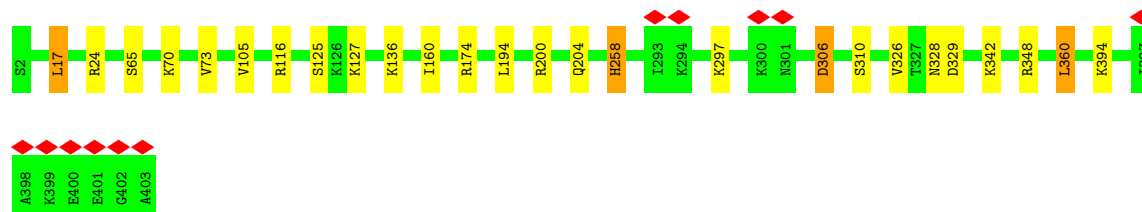
- Molecule 25: 60S ribosomal protein L8

Chain LA: 



- Molecule 26: Large ribosomal subunit protein uL3

Chain LB: 



- Molecule 27: 60S ribosomal protein L4

Chain LC: 

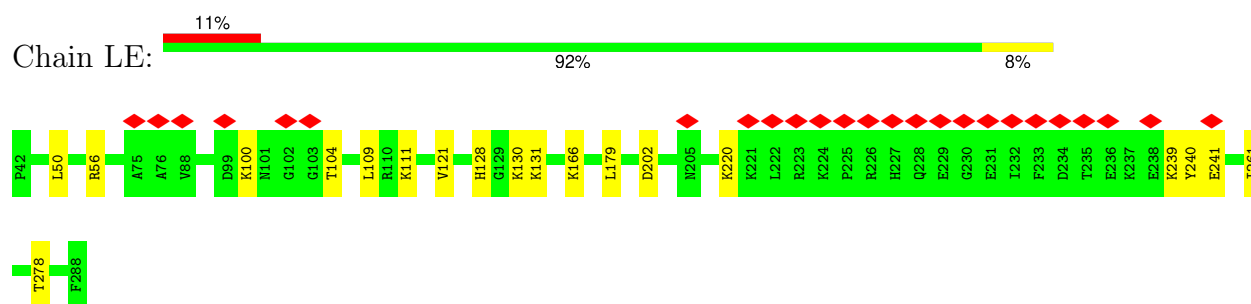


- Molecule 28: Large ribosomal subunit protein uL18

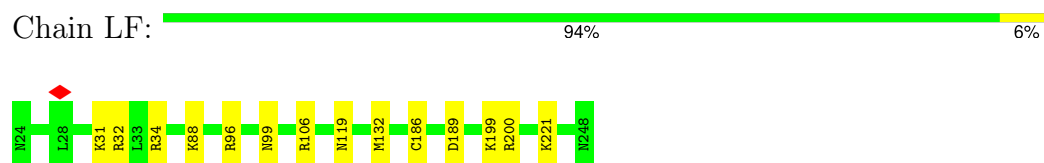
Chain LD: 



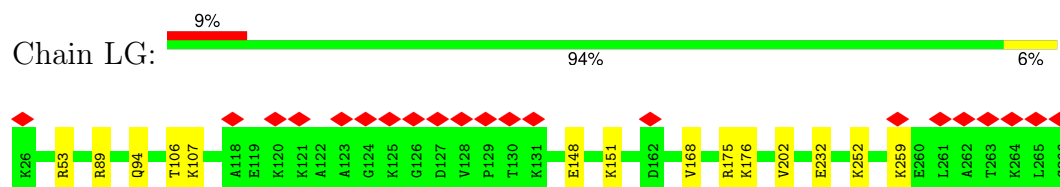
- Molecule 29: 60S ribosomal protein L6



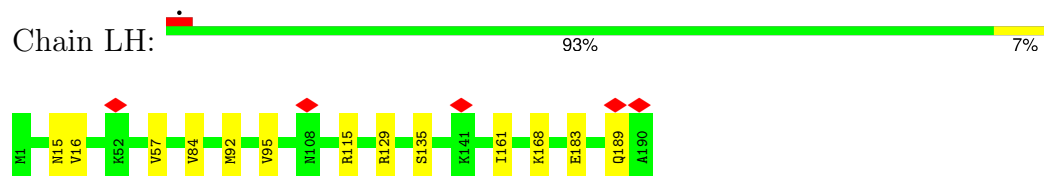
- Molecule 30: 60S ribosomal protein L7



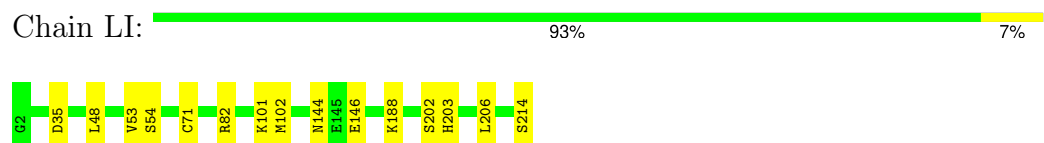
- Molecule 31: 60S ribosomal protein L7a



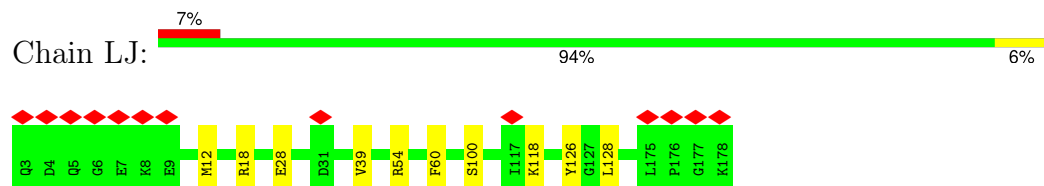
- Molecule 32: 60S ribosomal protein L9



- Molecule 33: 60S ribosomal protein L10-like

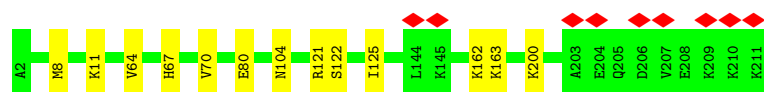


- Molecule 34: 60S ribosomal protein L11



- Molecule 35: Large ribosomal subunit protein eL13





- Molecule 36: 60S ribosomal protein L14



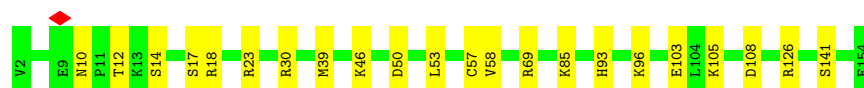
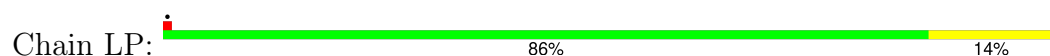
- Molecule 37: 60S ribosomal protein L15



- Molecule 38: 60S ribosomal protein L13a



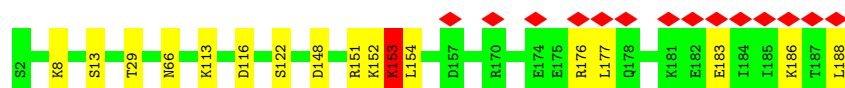
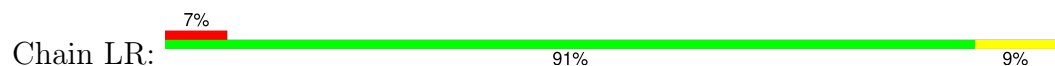
- Molecule 39: 60S ribosomal protein L17



- Molecule 40: 60S ribosomal protein L18



- Molecule 41: 60S ribosomal protein L19



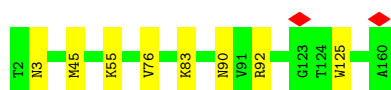
- Molecule 42: 60S ribosomal protein L18a

Chain LS:  92% 8%




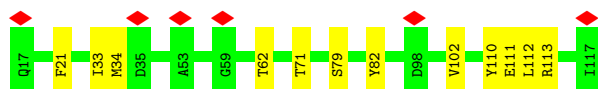
- Molecule 43: 60S ribosomal protein L21

Chain LT:  95% 5%



- Molecule 44: Heparin-binding protein HBp15

Chain LU:  6% 88% 12%



- Molecule 45: 60S ribosomal protein L23

Chain LV:  98% 2%



- Molecule 46: 60S ribosomal protein L23a

Chain LX:  94% 6%



- Molecule 47: 60S ribosomal protein L26

Chain LY:  94% 6%

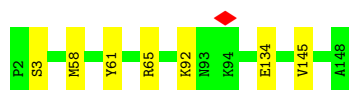


- Molecule 48: 60S ribosomal protein L27

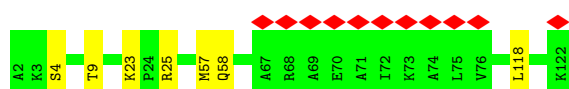
Chain LZ:  94% 6%



• Molecule 49: 60S ribosomal protein L27a

Chain La:  95% 5%

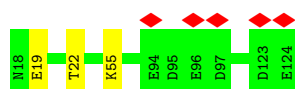
• Molecule 50: 60S ribosomal protein L29

Chain Lb:  10% 94% 6%

• Molecule 51: 60S ribosomal protein L30

Chain Lc:  95% 5%

• Molecule 52: 60S ribosomal protein L31

Chain Ld:  5% 97% .

• Molecule 53: 60S ribosomal protein L32

Chain Le:  95% 5%

• Molecule 54: 60S ribosomal protein L35a

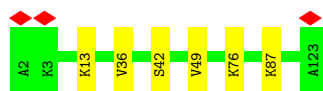
Chain Lf:  92% 8%

• Molecule 55: 60S ribosomal protein L34

Chain Lg:  93% 7%



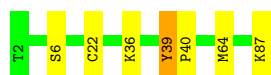
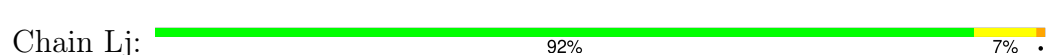
- Molecule 56: 60S ribosomal protein L35



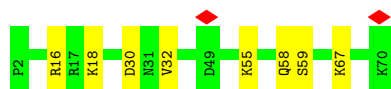
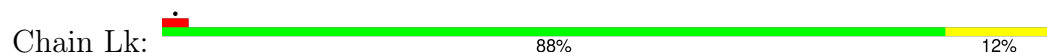
- Molecule 57: 60S ribosomal protein L36



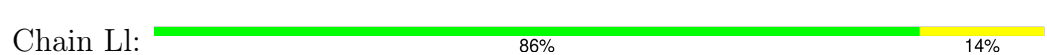
- Molecule 58: 60S ribosomal protein L37



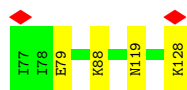
- Molecule 59: 60S ribosomal protein L38




- Molecule 60: 60S ribosomal protein L39



- Molecule 61: Large ribosomal subunit protein eL40



- Molecule 62: 60S ribosomal protein L41

Chain Ln:  79% 21%



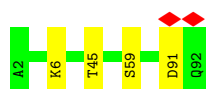
- Molecule 63: 60S ribosomal protein L36a

Chain Lo:  93% 7%



- Molecule 64: 60S ribosomal protein L37a

Chain Lp:  96% 4%



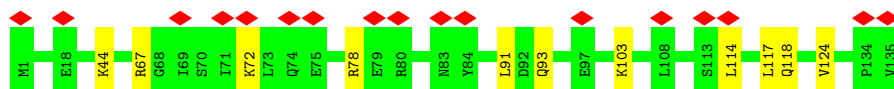
- Molecule 65: 60S ribosomal protein L28

Chain Lr:  91% 9%



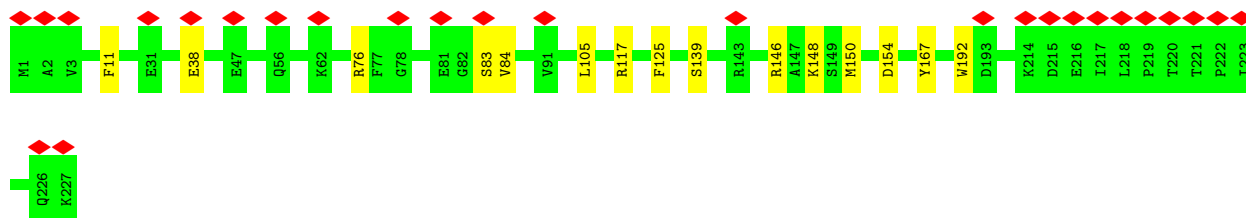
- Molecule 66: 40S ribosomal protein S17

Chain SR:  13% 92% 8%



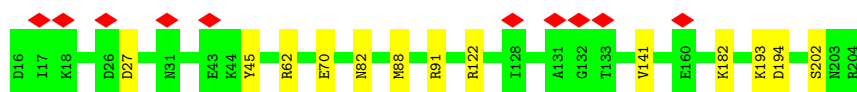
- Molecule 67: Small ribosomal subunit protein uS3

Chain SD:  11% 93% 7%

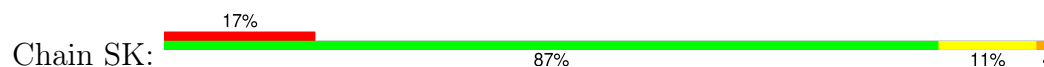


- Molecule 68: 40S ribosomal protein S5

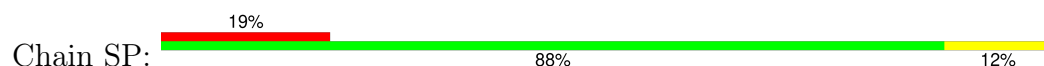
Chain SF:  5% 93% 7%



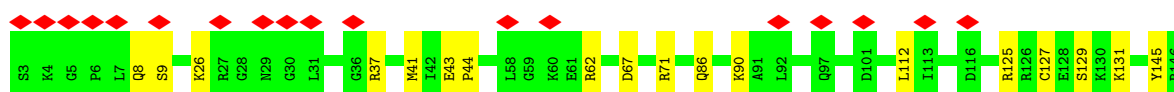
- Molecule 69: 40S ribosomal protein S10



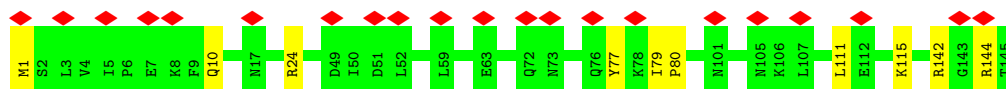
- Molecule 70: Small ribosomal subunit protein uS19



- Molecule 71: Small ribosomal subunit protein uS9



- Molecule 72: 40S ribosomal protein S18



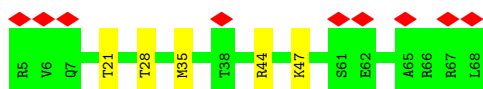
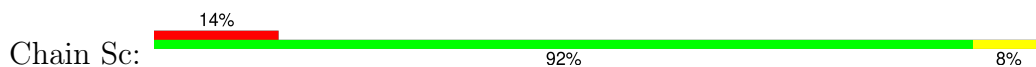
- Molecule 73: 40S ribosomal protein S19



- Molecule 74: 40S ribosomal protein S20



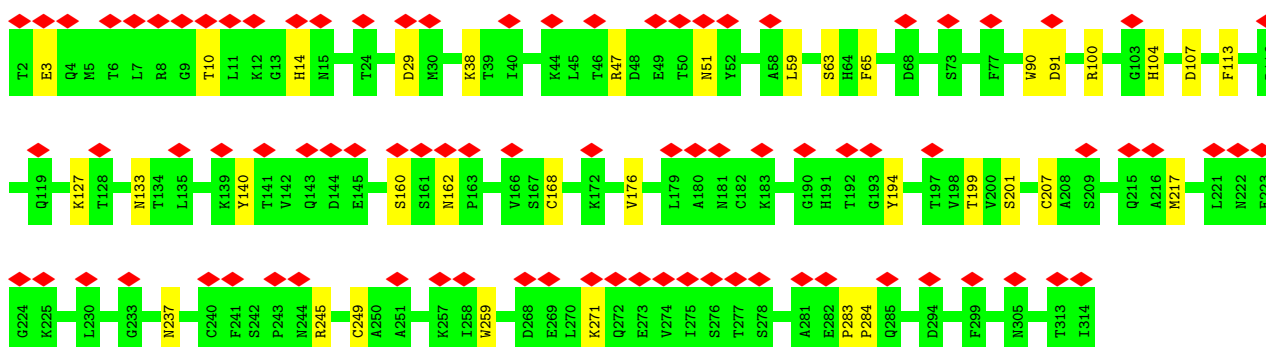
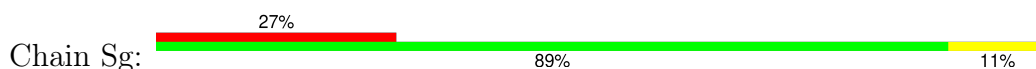
- Molecule 75: 40S ribosomal protein S28



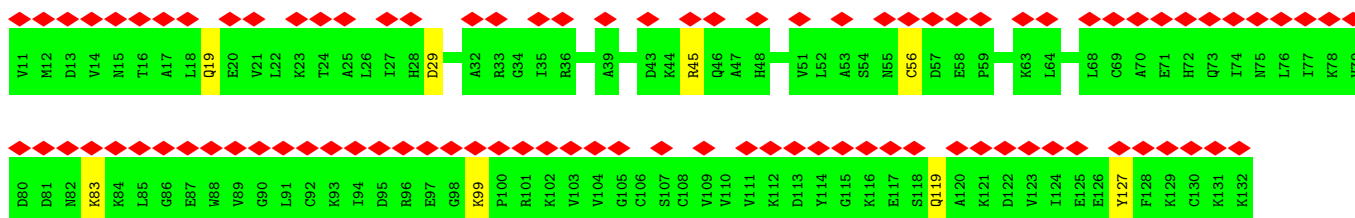
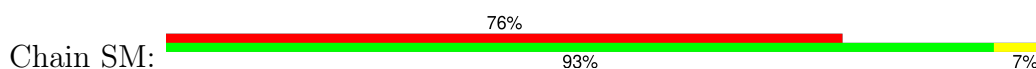
- Molecule 76: 40S ribosomal protein S29



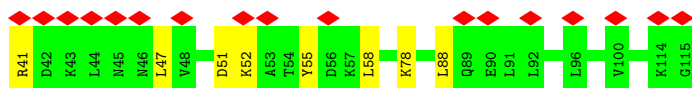
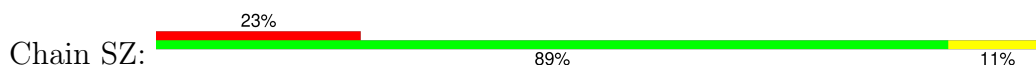
- Molecule 77: Receptor of activated protein C kinase 1



- Molecule 78: Small ribosomal subunit protein eS12

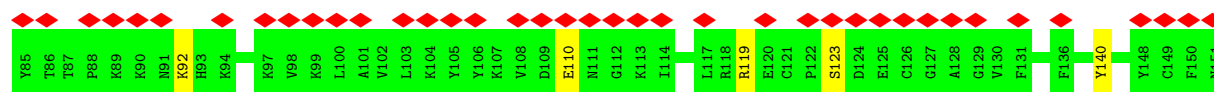


- Molecule 79: Small ribosomal subunit protein eS25

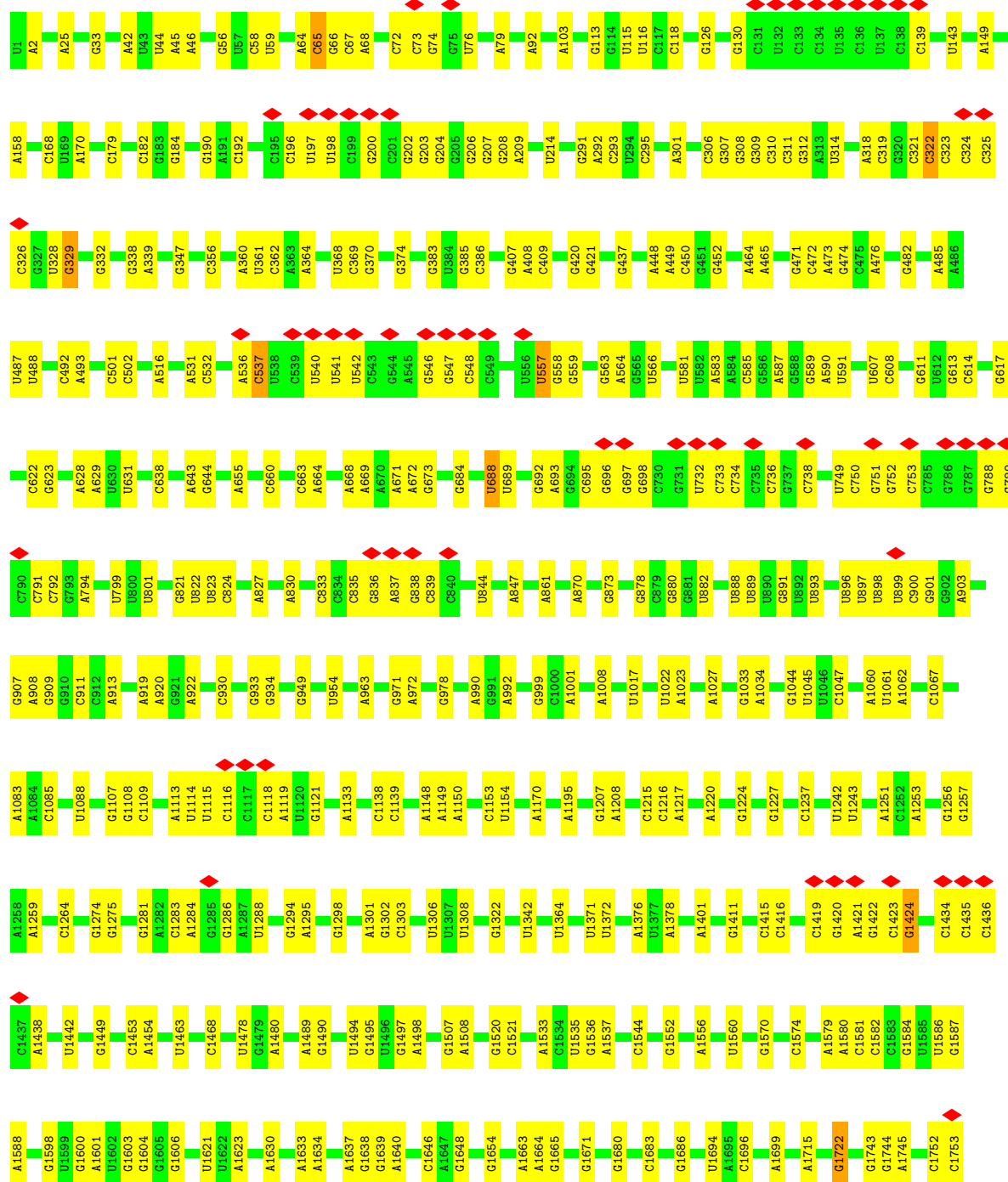
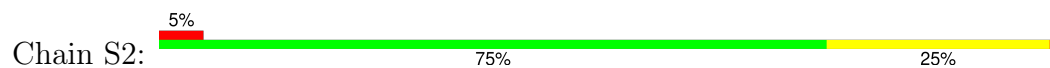


- Molecule 80: Ubiquitin-40S ribosomal protein S27a

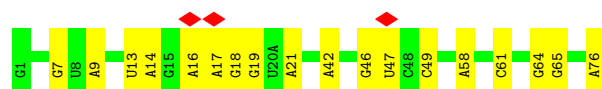
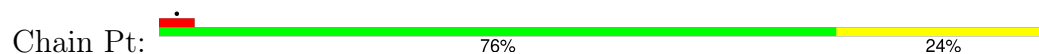




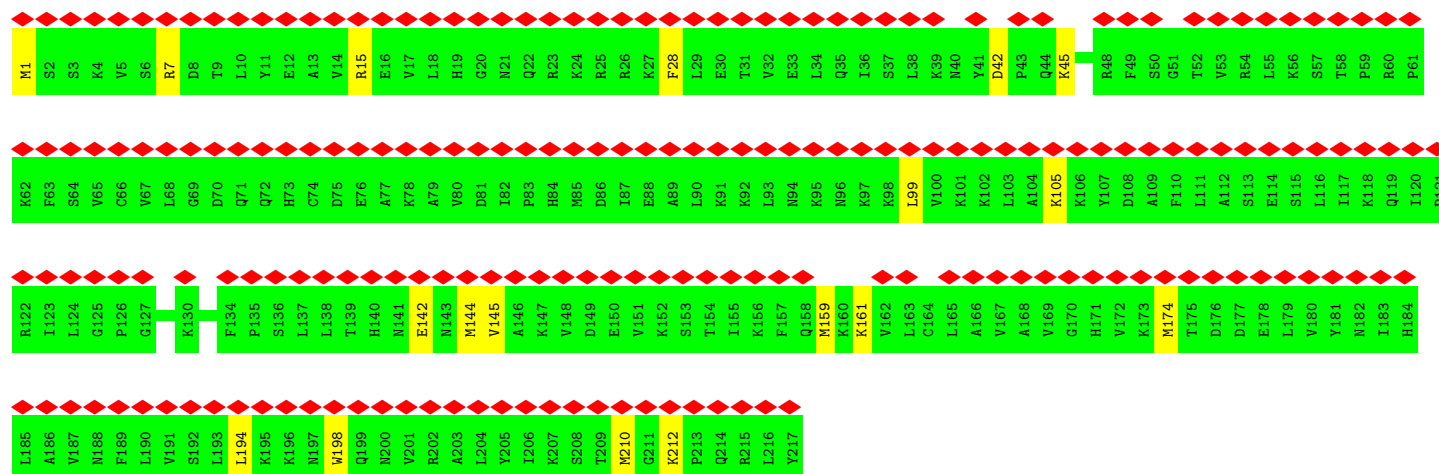
• Molecule 81: 18S rRNA



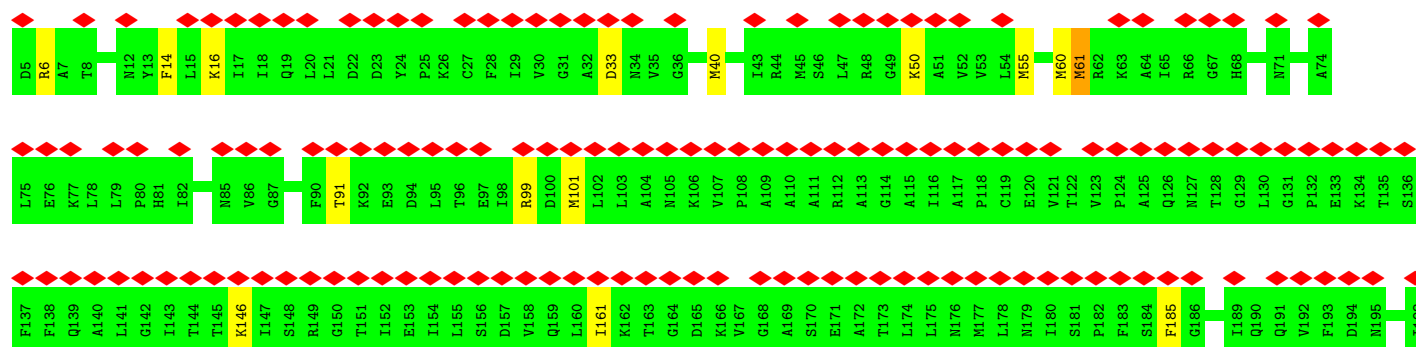
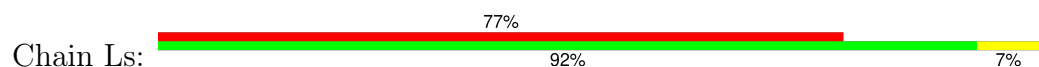
- Molecule 82: P site tRNA



- Molecule 83: 60S ribosomal protein L10a

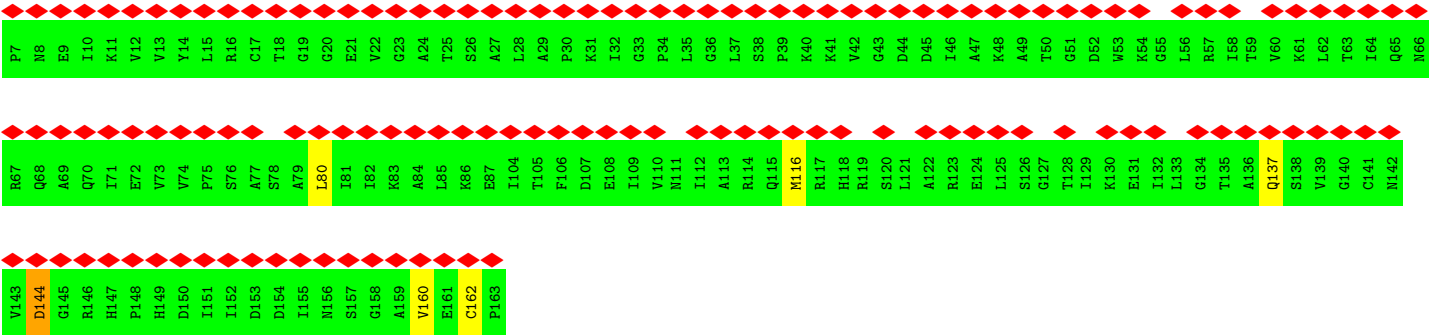
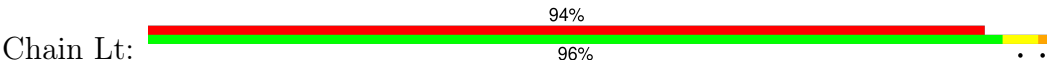


- Molecule 84: 60S acidic ribosomal protein P0

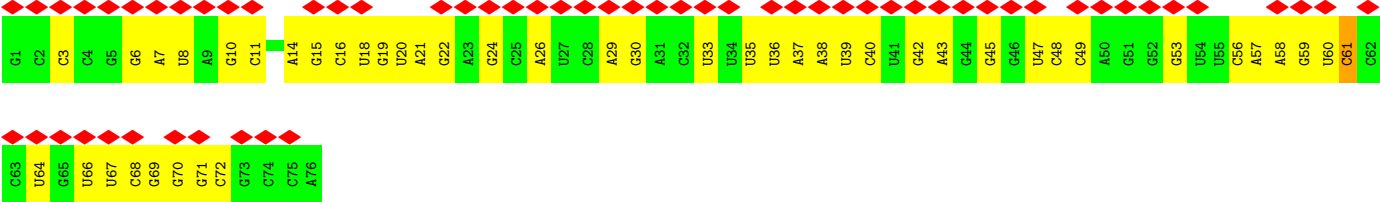
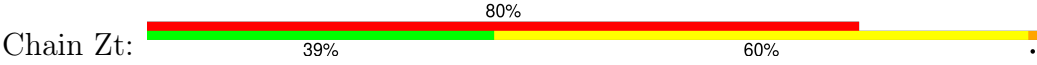




• Molecule 85: 60S ribosomal protein L12



• Molecule 86: Z site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	50321	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.294	Depositor
Minimum map value	-0.122	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.0291	Depositor
Map size (\AA)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

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	AT	0.27	0/1805	0.90	2/2809 (0.1%)
2	CF	0.59	6/3442 (0.2%)	0.88	18/4656 (0.4%)
3	LW	0.32	0/979	0.60	0/1295
4	SE	0.28	0/2118	0.55	0/2849
5	SI	0.29	0/1715	0.61	1/2287 (0.0%)
6	SL	0.29	0/1268	0.57	0/1696
7	SX	0.30	0/1116	0.56	0/1490
8	SG	0.53	3/1946 (0.2%)	0.85	7/2590 (0.3%)
9	SJ	0.28	0/1550	0.60	0/2069
10	SY	0.31	0/1083	0.62	0/1438
11	Se	0.35	0/465	0.61	0/612
12	SA	0.39	1/1778 (0.1%)	0.66	2/2416 (0.1%)
13	SB	0.46	2/1765 (0.1%)	0.81	4/2362 (0.2%)
14	SH	0.45	2/1519 (0.1%)	0.63	2/2033 (0.1%)
15	SV	0.29	0/643	0.57	0/860
16	Sa	0.32	0/836	0.61	0/1121
17	SC	0.31	0/1762	0.56	1/2381 (0.0%)
18	SN	0.30	0/1232	0.56	0/1656
19	SO	0.29	0/1062	0.61	1/1425 (0.1%)
20	SW	0.31	0/1051	0.56	0/1406
21	Sb	0.29	0/665	0.57	0/891
22	L5	0.58	0/89311	0.85	70/139283 (0.1%)
23	L7	0.55	0/2861	0.80	0/4459
24	L8	0.58	0/3701	0.79	0/5766
25	LA	0.37	0/1936	0.60	0/2596
26	LB	0.33	0/3306	0.57	2/4424 (0.0%)
27	LC	0.32	0/2981	0.56	1/4002 (0.0%)
28	LD	0.37	1/2428 (0.0%)	0.53	0/3252
29	LE	0.31	0/1942	0.59	1/2606 (0.0%)
30	LF	0.35	0/1905	0.54	0/2539
31	LG	0.31	0/1960	0.54	0/2637
32	LH	0.32	0/1537	0.57	0/2066

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LI	0.34	0/1673	0.57	0/2233
34	LJ	0.30	0/1433	0.59	0/1915
35	LL	0.31	0/1732	0.58	0/2315
36	LM	0.32	0/1161	0.54	0/1554
37	LN	0.35	0/1746	0.59	0/2338
38	LO	0.33	0/1682	0.54	0/2250
39	LP	0.33	0/1268	0.53	0/1701
40	LQ	0.33	0/1537	0.60	0/2052
41	LR	0.34	1/1582 (0.1%)	1.26	4/2091 (0.2%)
42	LS	0.37	0/1493	0.56	0/2003
43	LT	0.33	0/1326	0.55	0/1770
44	LU	0.46	1/839 (0.1%)	0.63	1/1126 (0.1%)
45	LV	0.33	0/993	0.53	0/1332
46	LX	0.31	0/1002	0.53	0/1345
47	LY	0.32	0/1132	0.58	0/1504
48	LZ	0.35	0/1130	0.57	0/1507
49	La	0.33	0/1191	0.52	0/1591
50	Lb	0.28	0/889	0.61	1/1175 (0.1%)
51	Lc	0.32	0/774	0.50	0/1038
52	Ld	0.33	0/903	0.59	0/1216
53	Le	0.33	0/1071	0.54	0/1429
54	Lf	0.34	0/895	0.58	0/1198
55	Lg	0.35	0/916	0.58	0/1220
56	Lh	0.28	0/1023	0.54	0/1351
57	Li	0.32	0/843	0.61	0/1115
58	Lj	0.43	0/720	1.03	2/952 (0.2%)
59	Lk	0.32	0/575	0.60	0/761
60	Ll	0.29	0/454	0.59	0/599
61	Lm	0.31	0/435	0.55	0/575
62	Ln	0.28	0/231	0.72	0/294
63	Lo	0.33	0/876	0.56	0/1156
64	Lp	0.34	0/718	0.52	0/953
65	Lr	0.31	0/1017	0.56	0/1364
66	SR	0.29	0/1105	0.62	0/1484
67	SD	0.30	0/1793	0.59	0/2414
68	SF	0.27	0/1516	0.57	0/2037
69	SK	0.46	1/851 (0.1%)	0.96	3/1147 (0.3%)
70	SP	0.34	0/1003	0.65	0/1342
71	SQ	0.29	0/1160	0.60	0/1553
72	SS	0.35	0/1216	0.68	4/1628 (0.2%)
73	ST	0.29	0/1131	0.57	0/1515
74	SU	0.28	0/831	0.60	0/1115
75	Sc	0.28	0/508	0.67	0/680

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sd	0.29	0/470	0.60	0/623
77	Sg	0.82	11/2493 (0.4%)	0.99	8/3394 (0.2%)
78	SM	0.29	0/950	0.58	0/1275
79	SZ	0.34	0/604	0.66	0/810
80	Sf	0.26	0/560	0.58	0/745
81	S2	0.40	1/41242 (0.0%)	0.83	46/64255 (0.1%)
82	Pt	0.32	0/1812	0.78	0/2823
83	Lz	0.28	0/1769	0.56	0/2371
84	Ls	0.38	1/1519 (0.1%)	0.55	0/2052
85	Lt	0.25	0/1058	0.56	0/1430
86	Zt	0.35	0/1779	1.03	2/2771 (0.1%)
All	All	0.46	31/244298 (0.0%)	0.77	183/358459 (0.1%)

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
7	SX	0	1
12	SA	0	1
14	SH	0	1
25	LA	0	1
26	LB	0	2
36	LM	0	1
38	LO	0	1
41	LR	0	1
54	Lf	0	2
58	Lj	0	1
70	SP	0	1
71	SQ	0	1
79	SZ	0	1
All	All	0	15

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
77	Sg	284	PRO	CG-CD	-26.02	0.64	1.50
2	CF	391	PRO	CG-CD	-20.15	0.84	1.50
8	SG	174	PRO	CG-CD	-13.86	1.04	1.50
2	CF	245	PRO	CG-CD	-13.06	1.07	1.50
77	Sg	284	PRO	N-CD	11.53	1.64	1.47

The worst 5 of 183 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	LR	153	LYS	O-C-N	-46.16	48.85	122.70
77	Sg	284	PRO	CA-N-CD	-23.00	79.30	111.50
77	Sg	284	PRO	N-CD-CG	-22.19	69.92	103.20
77	Sg	284	PRO	CB-CG-CD	-21.22	23.73	106.50
58	Lj	40	PRO	CA-N-CD	-20.65	82.59	111.50

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
25	LA	13	GLY	Peptide
26	LB	17	LEU	Peptide
12	SA	18	PHE	Sidechain
14	SH	15	LYS	Peptide
7	SX	126	ALA	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
2	CF	438/441 (99%)	423 (97%)	14 (3%)	1 (0%)	44	63
3	LW	114/118 (97%)	107 (94%)	7 (6%)	0	100	100
4	SE	260/262 (99%)	240 (92%)	20 (8%)	0	100	100
5	SI	204/206 (99%)	199 (98%)	5 (2%)	0	100	100
6	SL	151/153 (99%)	141 (93%)	10 (7%)	0	100	100
7	SX	139/141 (99%)	127 (91%)	11 (8%)	1 (1%)	19	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	SG	235/237 (99%)	219 (93%)	15 (6%)	1 (0%)	30	49
9	SJ	183/185 (99%)	170 (93%)	13 (7%)	0	100	100
10	SY	129/131 (98%)	120 (93%)	9 (7%)	0	100	100
11	Se	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
12	SA	219/221 (99%)	200 (91%)	19 (9%)	0	100	100
13	SB	212/214 (99%)	203 (96%)	9 (4%)	0	100	100
14	SH	182/186 (98%)	163 (90%)	19 (10%)	0	100	100
15	SV	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
16	Sa	100/102 (98%)	91 (91%)	8 (8%)	1 (1%)	13	25
17	SC	220/222 (99%)	198 (90%)	22 (10%)	0	100	100
18	SN	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
19	SO	138/140 (99%)	125 (91%)	13 (9%)	0	100	100
20	SW	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
21	Sb	81/83 (98%)	69 (85%)	12 (15%)	0	100	100
25	LA	246/248 (99%)	224 (91%)	22 (9%)	0	100	100
26	LB	400/402 (100%)	374 (94%)	26 (6%)	0	100	100
27	LC	366/368 (100%)	341 (93%)	25 (7%)	0	100	100
28	LD	291/293 (99%)	279 (96%)	12 (4%)	0	100	100
29	LE	232/236 (98%)	212 (91%)	20 (9%)	0	100	100
30	LF	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
31	LG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
32	LH	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
33	LI	198/202 (98%)	185 (93%)	13 (7%)	0	100	100
34	LJ	174/176 (99%)	162 (93%)	12 (7%)	0	100	100
35	LL	208/210 (99%)	194 (93%)	14 (7%)	0	100	100
36	LM	137/139 (99%)	129 (94%)	7 (5%)	1 (1%)	19	36
37	LN	201/203 (99%)	191 (95%)	9 (4%)	1 (0%)	25	44
38	LO	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
39	LP	151/153 (99%)	141 (93%)	10 (7%)	0	100	100
40	LQ	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
41	LR	185/187 (99%)	178 (96%)	5 (3%)	2 (1%)	12	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	LS	173/175 (99%)	160 (92%)	13 (8%)	0	100	100
43	LT	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
44	LU	99/101 (98%)	81 (82%)	18 (18%)	0	100	100
45	LV	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
46	LX	118/120 (98%)	116 (98%)	2 (2%)	0	100	100
47	LY	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
48	LZ	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
49	La	145/147 (99%)	135 (93%)	10 (7%)	0	100	100
50	Lb	105/109 (96%)	96 (91%)	9 (9%)	0	100	100
51	Lc	96/98 (98%)	91 (95%)	5 (5%)	0	100	100
52	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
53	Le	126/128 (98%)	120 (95%)	6 (5%)	0	100	100
54	Lf	107/109 (98%)	99 (92%)	7 (6%)	1 (1%)	14	28
55	Lg	112/114 (98%)	112 (100%)	0	0	100	100
56	Lh	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
57	Li	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
58	Lj	84/86 (98%)	79 (94%)	5 (6%)	0	100	100
59	Lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
60	Ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
61	Lm	50/52 (96%)	50 (100%)	0	0	100	100
62	Ln	22/24 (92%)	22 (100%)	0	0	100	100
63	Lo	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
64	Lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
65	Lr	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
66	SR	133/135 (98%)	119 (90%)	13 (10%)	1 (1%)	16	32
67	SD	225/227 (99%)	207 (92%)	18 (8%)	0	100	100
68	SF	187/189 (99%)	168 (90%)	19 (10%)	0	100	100
69	SK	96/98 (98%)	84 (88%)	11 (12%)	1 (1%)	13	25
70	SP	119/121 (98%)	105 (88%)	14 (12%)	0	100	100
71	SQ	142/144 (99%)	126 (89%)	15 (11%)	1 (1%)	19	36
72	SS	143/145 (99%)	138 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	ST	141/143 (99%)	129 (92%)	11 (8%)	1 (1%)	19	36
74	SU	102/104 (98%)	97 (95%)	5 (5%)	0	100	100
75	Sc	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
76	Sd	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
77	Sg	311/313 (99%)	277 (89%)	34 (11%)	0	100	100
78	SM	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
79	SZ	73/75 (97%)	60 (82%)	13 (18%)	0	100	100
80	Sf	65/67 (97%)	56 (86%)	9 (14%)	0	100	100
83	Lz	215/217 (99%)	172 (80%)	43 (20%)	0	100	100
84	Ls	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
85	Lt	137/141 (97%)	108 (79%)	28 (20%)	1 (1%)	19	36
All	All	12301/12472 (99%)	11413 (93%)	874 (7%)	14 (0%)	50	69

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
41	LR	153	LYS
41	LR	154	LEU
73	ST	39	LEU
7	SX	127	ASN
8	SG	174	PRO

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	
2	CF	365/366 (100%)	342 (94%)	23 (6%)	15	30
3	LW	97/97 (100%)	90 (93%)	7 (7%)	12	25
4	SE	224/224 (100%)	205 (92%)	19 (8%)	8	19
5	SI	178/178 (100%)	164 (92%)	14 (8%)	10	21
6	SL	137/137 (100%)	125 (91%)	12 (9%)	8	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	SX	113/113 (100%)	100 (88%)	13 (12%)	4	9
8	SG	207/207 (100%)	185 (89%)	22 (11%)	5	11
9	SJ	161/161 (100%)	151 (94%)	10 (6%)	15	30
10	SY	113/113 (100%)	96 (85%)	17 (15%)	2	4
11	Se	47/47 (100%)	40 (85%)	7 (15%)	2	4
12	SA	183/183 (100%)	165 (90%)	18 (10%)	6	13
13	SB	195/195 (100%)	177 (91%)	18 (9%)	7	15
14	SH	166/166 (100%)	154 (93%)	12 (7%)	12	25
15	SV	67/67 (100%)	61 (91%)	6 (9%)	8	16
16	Sa	89/89 (100%)	78 (88%)	11 (12%)	4	7
17	SC	188/188 (100%)	172 (92%)	16 (8%)	8	19
18	SN	130/130 (100%)	117 (90%)	13 (10%)	6	13
19	SO	110/110 (100%)	100 (91%)	10 (9%)	7	16
20	SW	112/112 (100%)	102 (91%)	10 (9%)	8	16
21	Sb	75/75 (100%)	67 (89%)	8 (11%)	5	11
25	LA	190/190 (100%)	176 (93%)	14 (7%)	11	24
26	LB	348/348 (100%)	322 (92%)	26 (8%)	11	24
27	LC	306/306 (100%)	291 (95%)	15 (5%)	21	42
28	LD	246/247 (100%)	230 (94%)	16 (6%)	14	29
29	LE	209/209 (100%)	191 (91%)	18 (9%)	8	18
30	LF	194/194 (100%)	180 (93%)	14 (7%)	12	25
31	LG	203/205 (99%)	189 (93%)	14 (7%)	13	26
32	LH	169/169 (100%)	156 (92%)	13 (8%)	10	23
33	LI	172/172 (100%)	157 (91%)	15 (9%)	8	17
34	LJ	148/148 (100%)	138 (93%)	10 (7%)	13	27
35	LL	176/176 (100%)	163 (93%)	13 (7%)	11	24
36	LM	118/118 (100%)	114 (97%)	4 (3%)	32	57
37	LN	171/171 (100%)	164 (96%)	7 (4%)	26	50
38	LO	173/173 (100%)	167 (96%)	6 (4%)	31	56
39	LP	134/134 (100%)	112 (84%)	22 (16%)	2	2
40	LQ	164/164 (100%)	152 (93%)	12 (7%)	11	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	LR	166/166 (100%)	152 (92%)	14 (8%)	9	19
42	LS	156/156 (100%)	142 (91%)	14 (9%)	8	16
43	LT	139/139 (100%)	131 (94%)	8 (6%)	17	34
44	LU	91/91 (100%)	81 (89%)	10 (11%)	5	10
45	LV	101/101 (100%)	98 (97%)	3 (3%)	36	61
46	LX	108/108 (100%)	101 (94%)	7 (6%)	14	29
47	LY	124/124 (100%)	116 (94%)	8 (6%)	14	29
48	LZ	117/117 (100%)	109 (93%)	8 (7%)	13	27
49	La	120/120 (100%)	113 (94%)	7 (6%)	17	34
50	Lb	88/90 (98%)	82 (93%)	6 (7%)	13	27
51	Lc	83/83 (100%)	78 (94%)	5 (6%)	16	32
52	Ld	98/98 (100%)	95 (97%)	3 (3%)	35	60
53	Le	114/114 (100%)	107 (94%)	7 (6%)	15	31
54	Lf	88/88 (100%)	82 (93%)	6 (7%)	13	27
55	Lg	98/98 (100%)	90 (92%)	8 (8%)	9	20
56	Lh	109/109 (100%)	103 (94%)	6 (6%)	18	36
57	Li	86/86 (100%)	80 (93%)	6 (7%)	12	26
58	Lj	73/73 (100%)	68 (93%)	5 (7%)	13	27
59	Lk	64/64 (100%)	56 (88%)	8 (12%)	3	7
60	Ll	47/47 (100%)	40 (85%)	7 (15%)	2	4
61	Lm	48/48 (100%)	44 (92%)	4 (8%)	9	20
62	Ln	23/23 (100%)	18 (78%)	5 (22%)	1	0
63	Lo	93/93 (100%)	86 (92%)	7 (8%)	11	24
64	Lp	74/74 (100%)	70 (95%)	4 (5%)	18	37
65	Lr	109/109 (100%)	98 (90%)	11 (10%)	6	12
66	SR	122/122 (100%)	112 (92%)	10 (8%)	9	20
67	SD	190/190 (100%)	175 (92%)	15 (8%)	10	21
68	SF	159/159 (100%)	146 (92%)	13 (8%)	9	20
69	SK	89/89 (100%)	76 (85%)	13 (15%)	2	5
70	SP	107/107 (100%)	94 (88%)	13 (12%)	4	8
71	SQ	119/119 (100%)	103 (87%)	16 (13%)	3	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	SS	126/126 (100%)	118 (94%)	8 (6%)	15	30
73	ST	113/113 (100%)	102 (90%)	11 (10%)	6	13
74	SU	94/94 (100%)	83 (88%)	11 (12%)	4	9
75	Sc	57/57 (100%)	52 (91%)	5 (9%)	8	17
76	Sd	48/48 (100%)	43 (90%)	5 (10%)	5	11
77	Sg	272/272 (100%)	242 (89%)	30 (11%)	5	10
78	SM	102/104 (98%)	94 (92%)	8 (8%)	10	22
79	SZ	66/66 (100%)	59 (89%)	7 (11%)	5	11
80	Sf	60/60 (100%)	55 (92%)	5 (8%)	9	20
83	Lz	195/196 (100%)	177 (91%)	18 (9%)	7	15
84	Ls	162/164 (99%)	147 (91%)	15 (9%)	7	15
85	Lt	112/115 (97%)	106 (95%)	6 (5%)	18	37
All	All	10688/10702 (100%)	9817 (92%)	871 (8%)	12	20

5 of 871 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	LP	58	VAL
51	Lc	94	LEU
77	Sg	160	SER
40	LQ	95	VAL
39	LP	57	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
45	LV	135	ASN
77	Sg	15	ASN
47	LY	43	ASN
66	SR	121	GLN
78	SM	19	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AT	74/77 (96%)	41 (55%)	2 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	L5	3703/3740 (99%)	841 (22%)	20 (0%)
23	L7	119/120 (99%)	11 (9%)	0
24	L8	155/156 (99%)	26 (16%)	0
81	S2	1715/1740 (98%)	429 (25%)	7 (0%)
82	Pt	75/76 (98%)	18 (24%)	0
86	Zt	74/75 (98%)	45 (60%)	0
All	All	5915/5984 (98%)	1411 (23%)	29 (0%)

5 of 1411 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AT	3	C
1	AT	4	U
1	AT	8	U
1	AT	9	A
1	AT	10	G

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	L5	2760	G
81	S2	1434	C
22	L5	3673	C
81	S2	531	A
22	L5	3614	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	$\# Z > 2$
2	SEP	CF	163	2	8,9,10	1.58	1 (12%)	7,12,14	1.36	1 (14%)

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
2	SEP	CF	163	2	-	6/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	CF	163	SEP	P-O1P	3.47	1.61	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	CF	163	SEP	OG-CB-CA	2.95	111.01	108.14

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	CF	163	SEP	C-CA-CB-OG
2	CF	163	SEP	CA-CB-OG-P
2	CF	163	SEP	CB-OG-P-O1P
2	CF	163	SEP	CB-OG-P-O2P
2	CF	163	SEP	CB-OG-P-O3P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 261 ligands modelled in this entry, 261 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
22	L5	13
81	S2	6
50	Lb	1
29	LE	1
3	LW	1
14	SH	1
85	Lt	1
33	LI	1

The worst 5 of 25 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lb	76:VAL	C	89:VAL	N	34.67
1	S2	753:C	O3'	785:C	P	28.21
1	LE	76:ALA	C	88:VAL	N	24.08
1	L5	2910:G	O3'	3584:C	P	20.02
1	L5	760:G	O3'	903:C	P	16.64

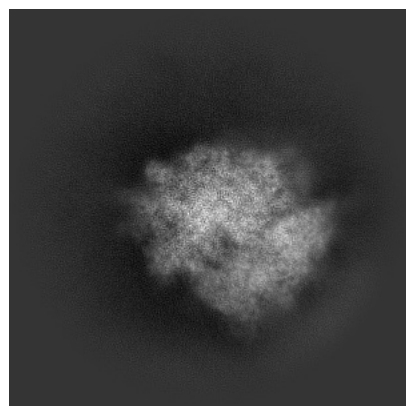
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44048. These allow visual inspection of the internal detail of the map and identification of artifacts.

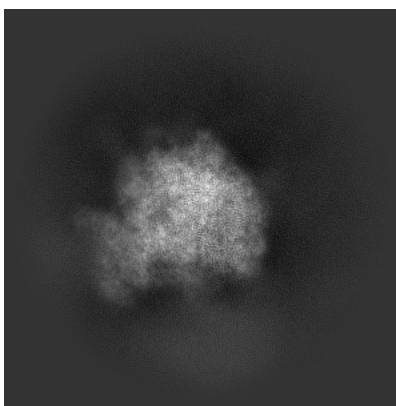
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

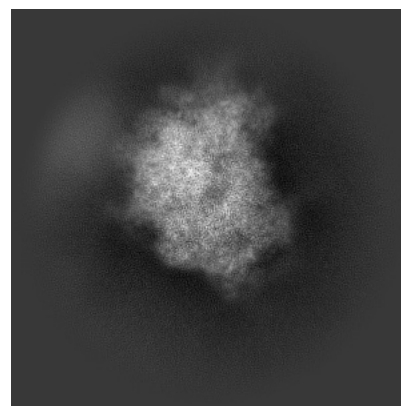
6.1.1 Primary map



X

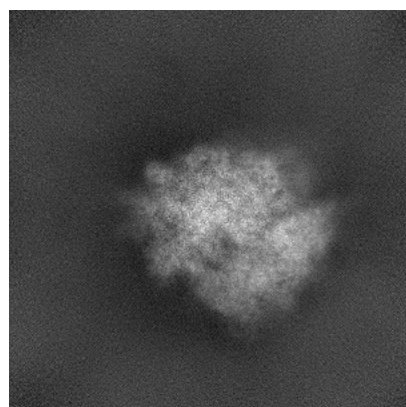


Y

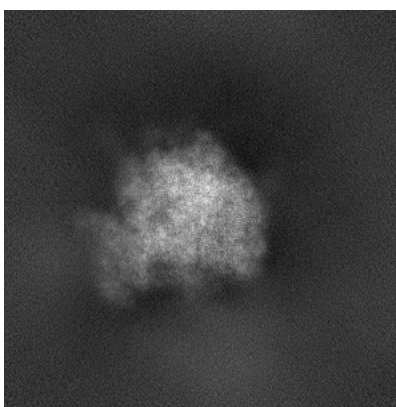


Z

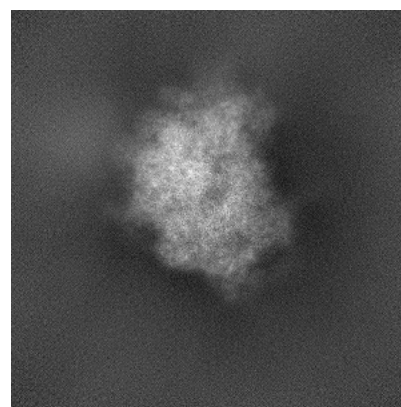
6.1.2 Raw map



X



Y

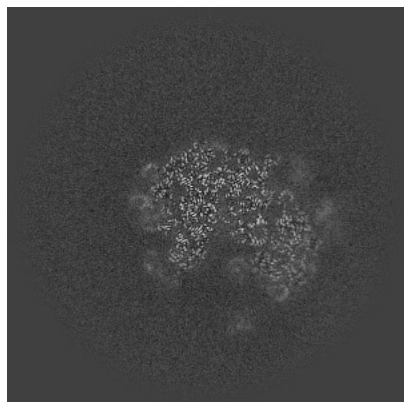


Z

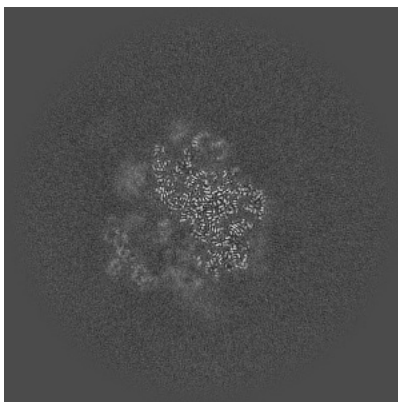
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

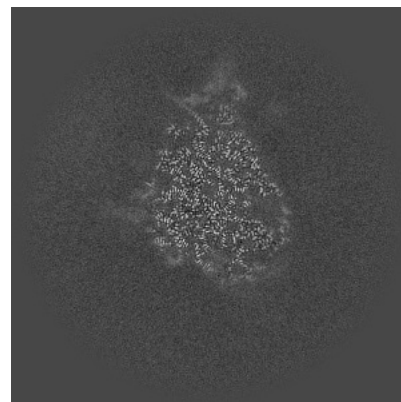
6.2.1 Primary map



X Index: 256

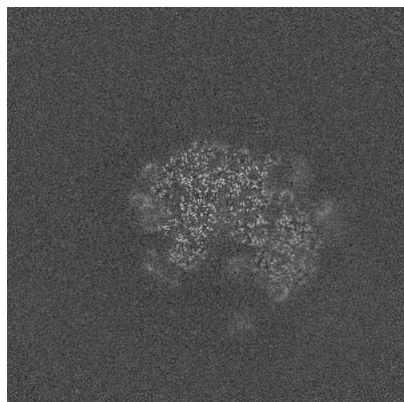


Y Index: 256

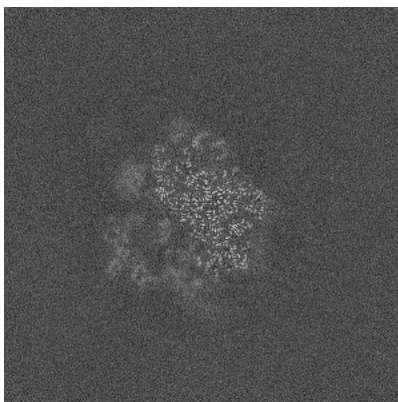


Z Index: 256

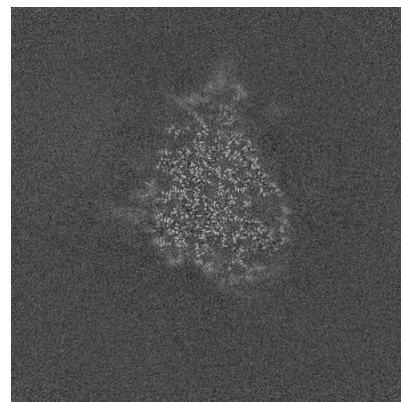
6.2.2 Raw map



X Index: 256



Y Index: 256

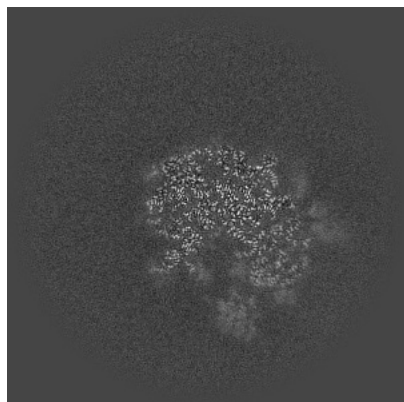


Z Index: 256

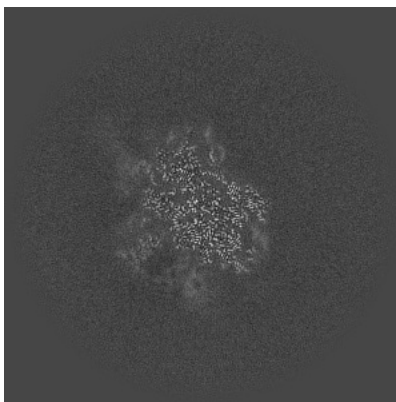
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

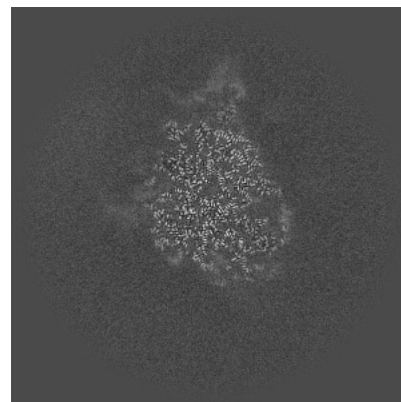
6.3.1 Primary map



X Index: 243

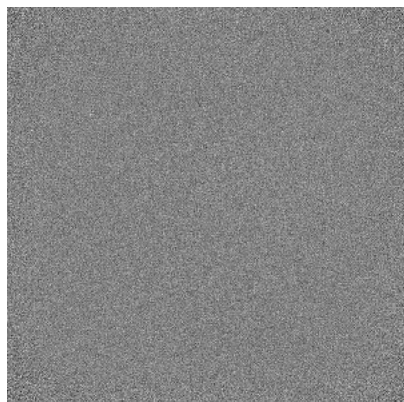


Y Index: 243

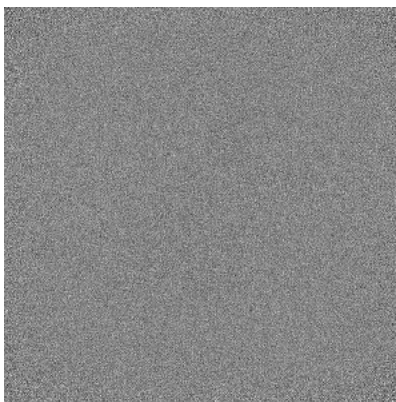


Z Index: 258

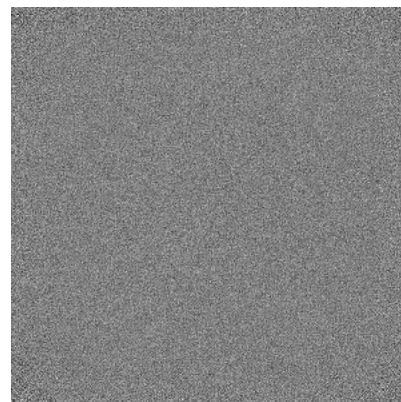
6.3.2 Raw map



X Index: 0



Y Index: 0

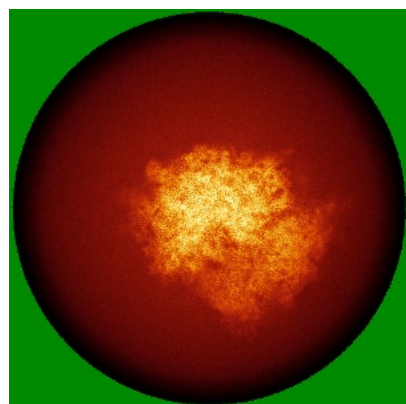


Z Index: 0

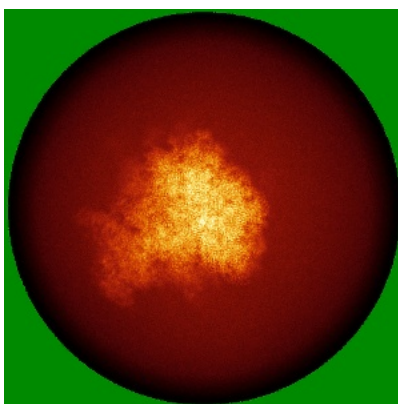
The images above show the largest variance slices of the map in three orthogonal directions.

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

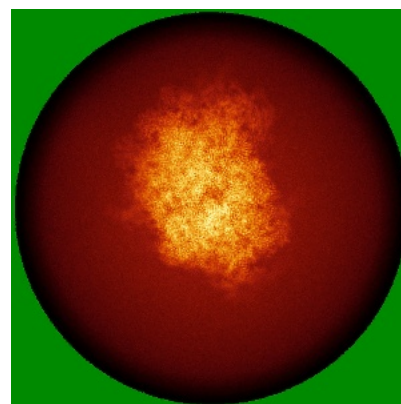
6.4.1 Primary map



X

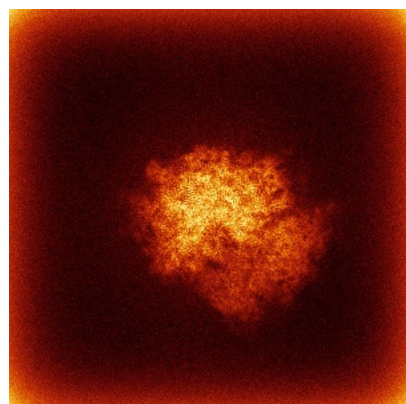


Y

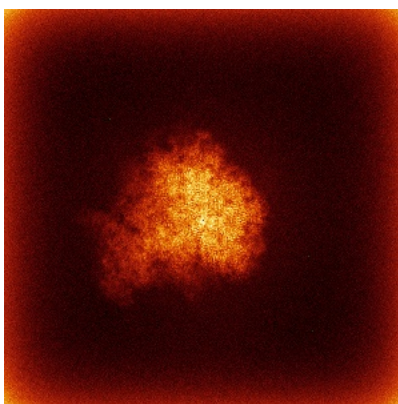


Z

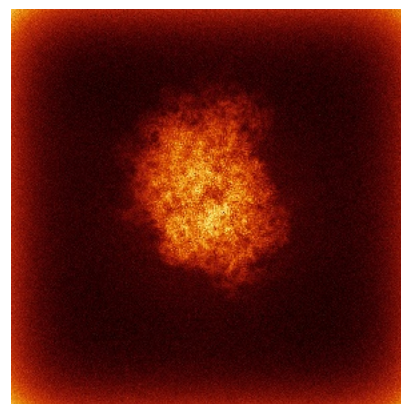
6.4.2 Raw map



X



Y

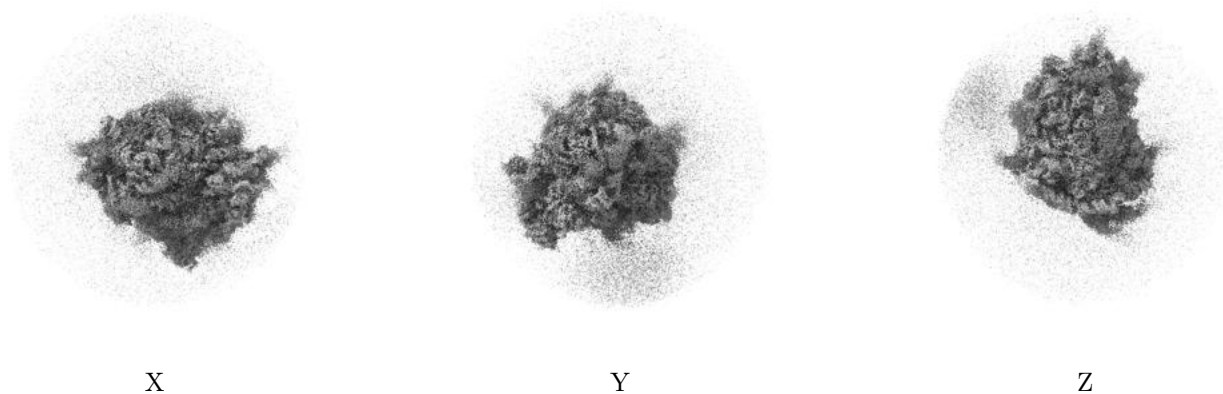


Z

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

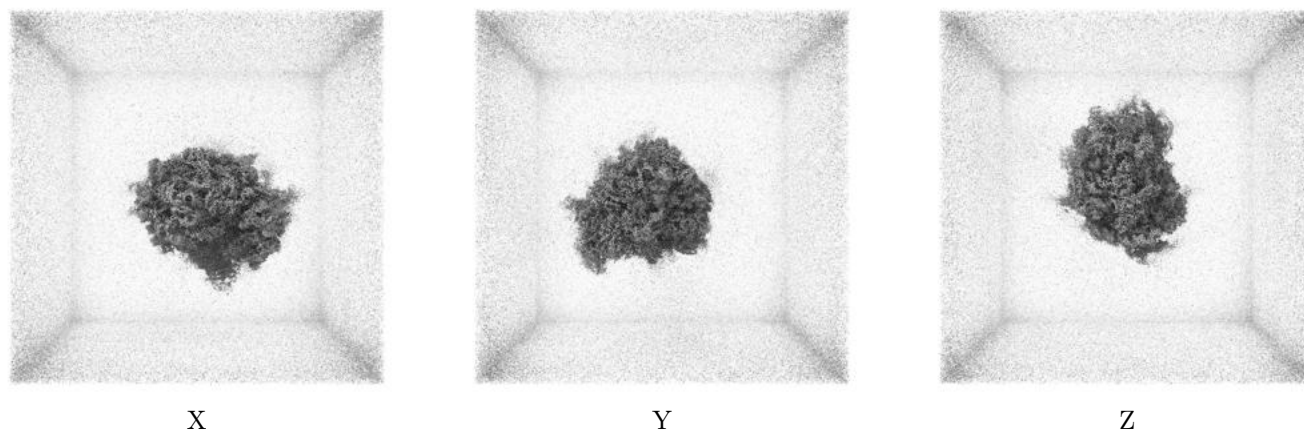
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0291. 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.

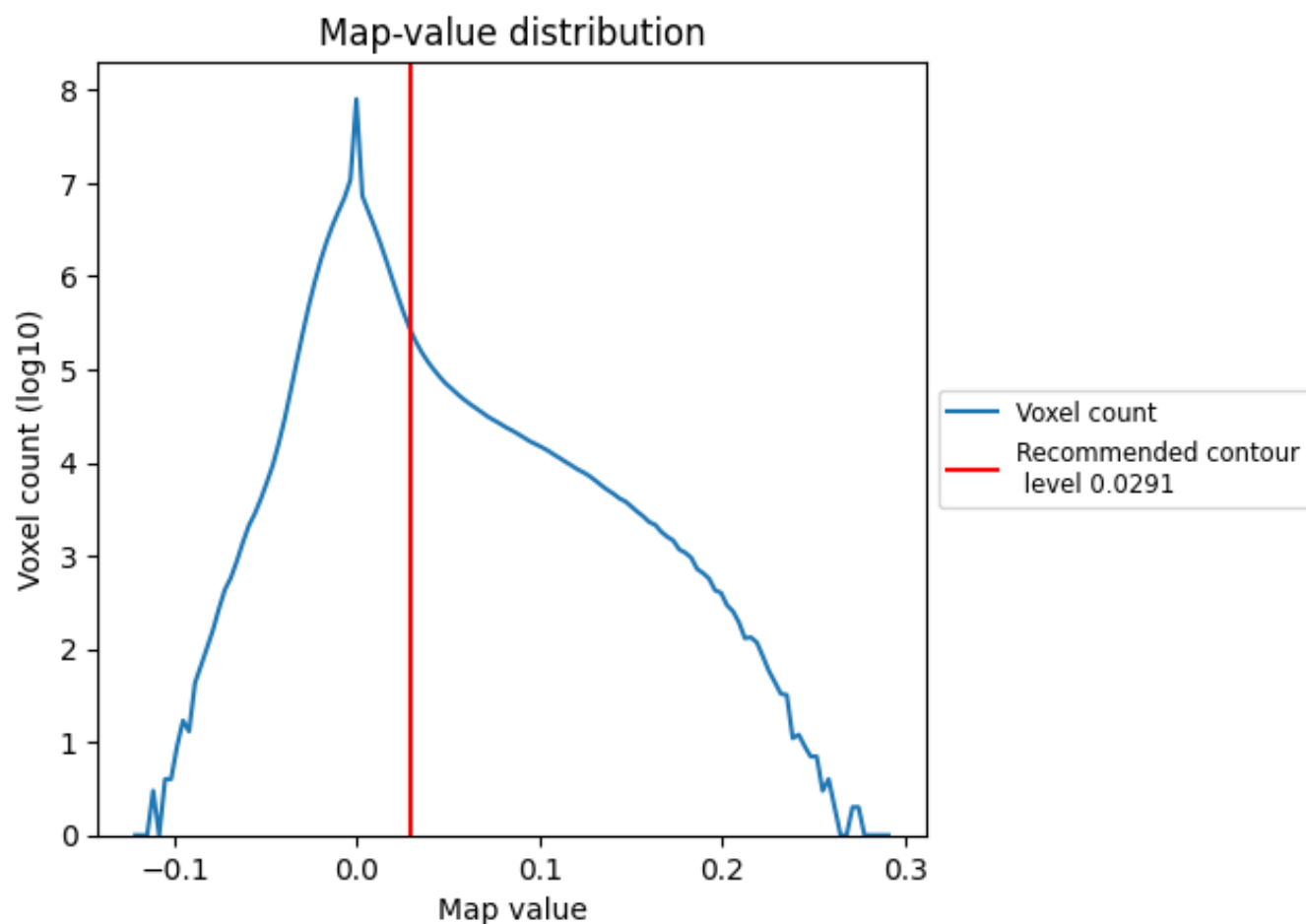
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

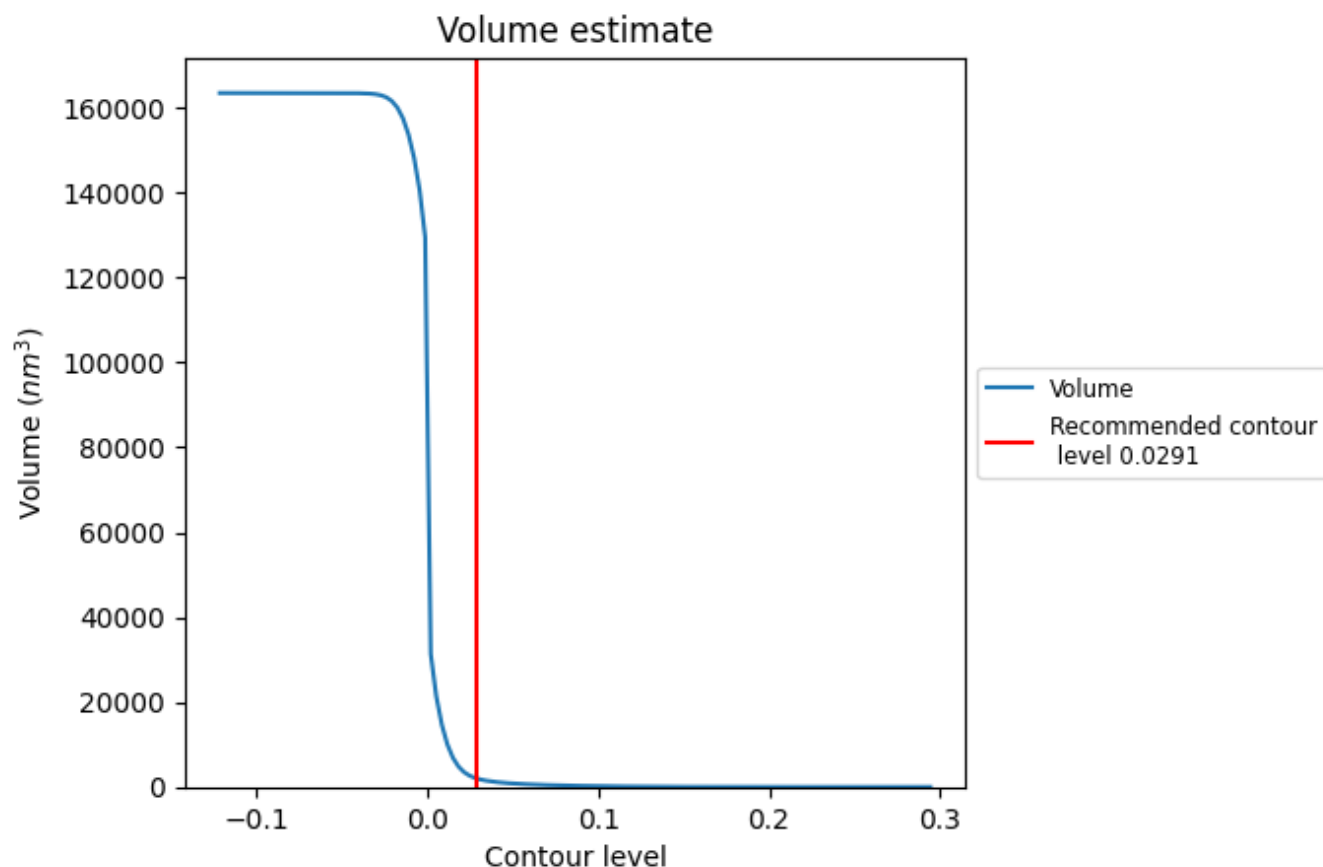
This section contains the results of statistical analysis of the map.

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.

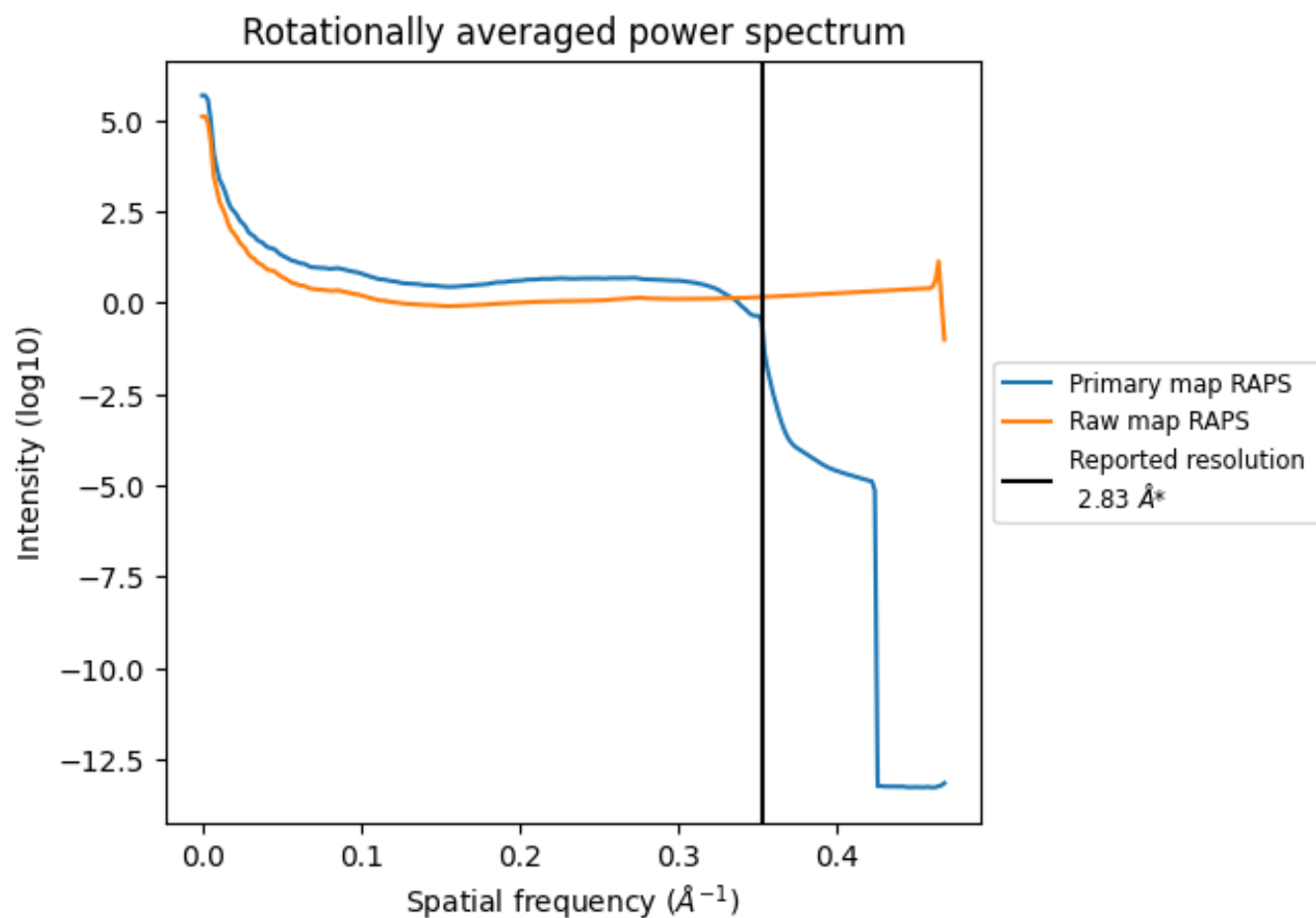
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1975 nm^3 ; this corresponds to an approximate mass of 1784 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 ⓘ

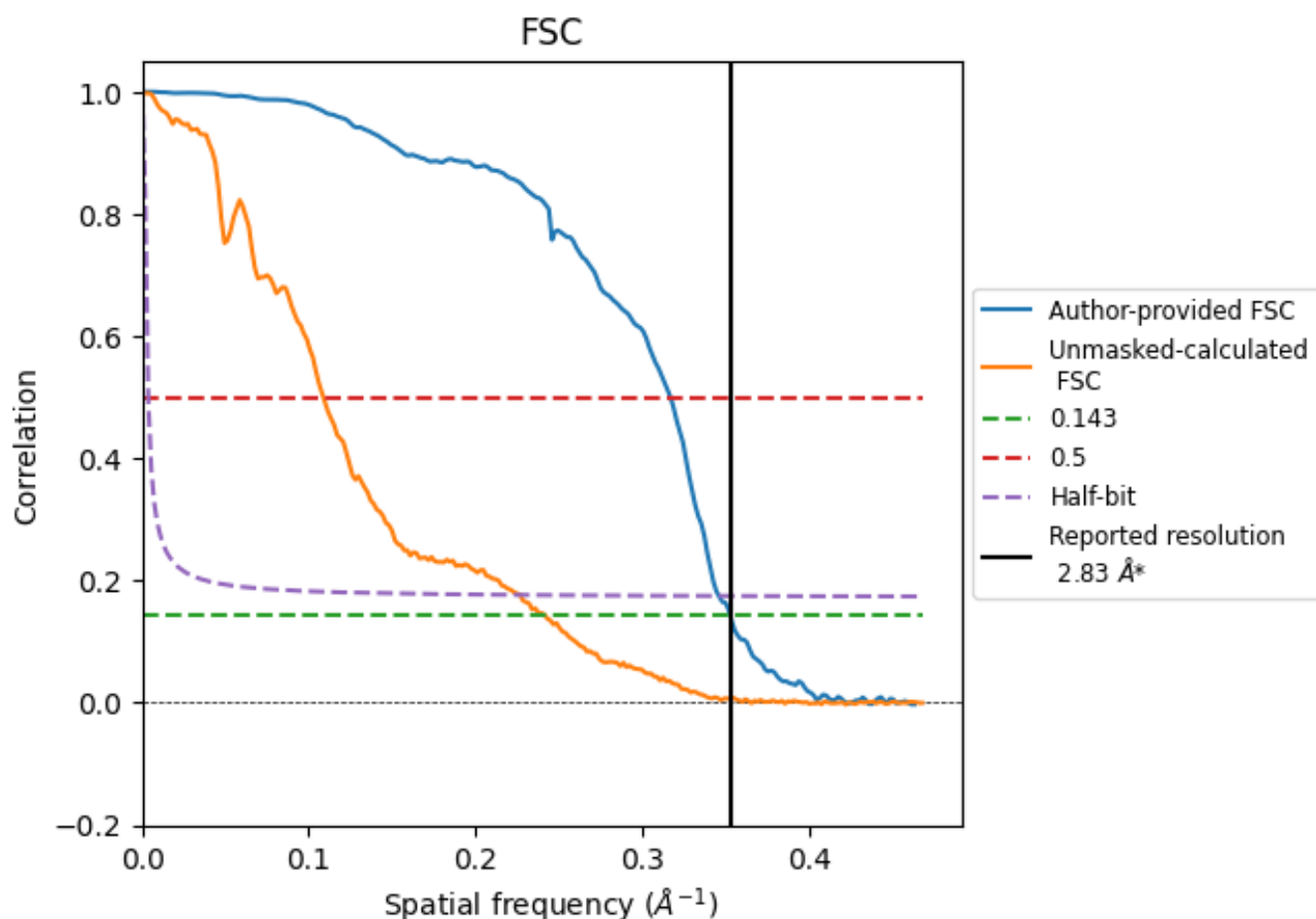


*Reported resolution corresponds to spatial frequency of 0.353 Å⁻¹

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 0.353 Å⁻¹

8.2 Resolution estimates

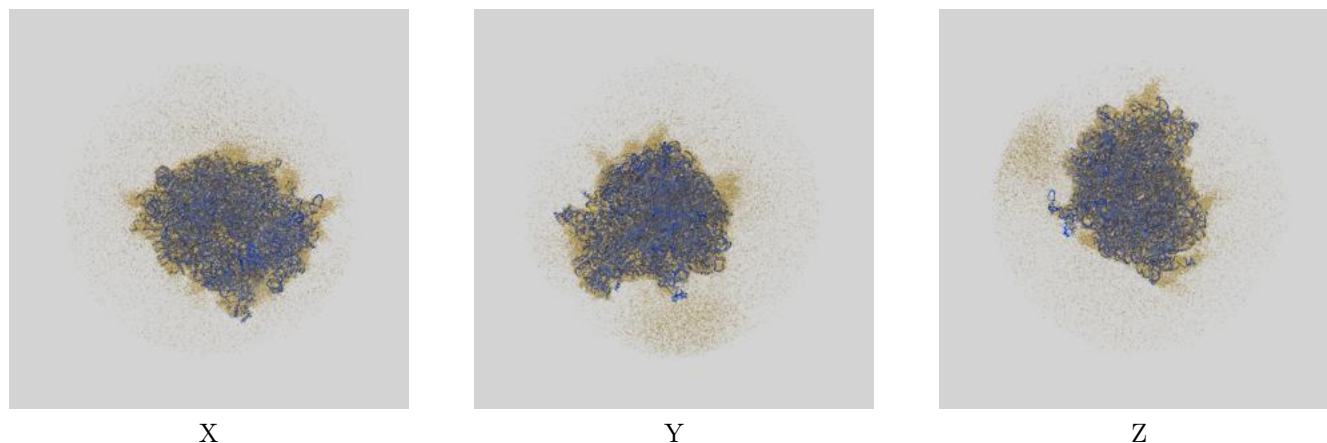
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.83	-	-
Author-provided FSC curve	2.83	3.15	2.89
Unmasked-calculated*	4.14	9.20	4.41

*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 4.14 differs from the reported value 2.83 by more than 10 %

9 Map-model fit [i](#)

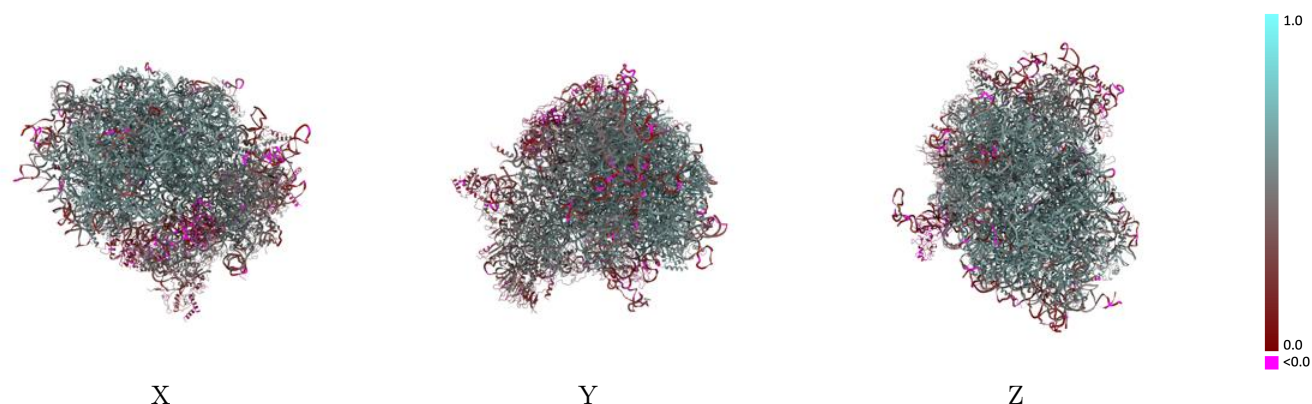
This section contains information regarding the fit between EMDB map EMD-44048 and PDB model 9B0O. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



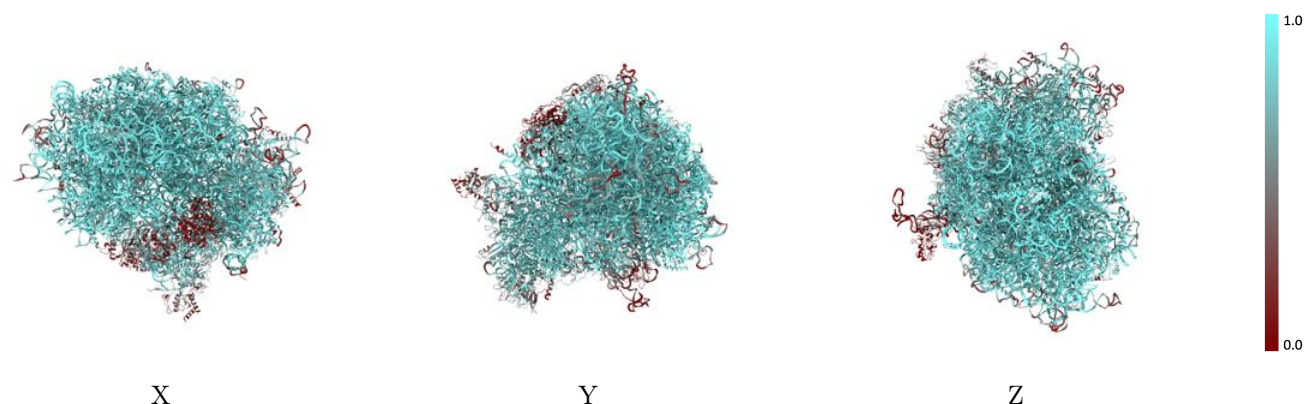
The images above show the 3D surface view of the map at the recommended contour level 0.0291 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



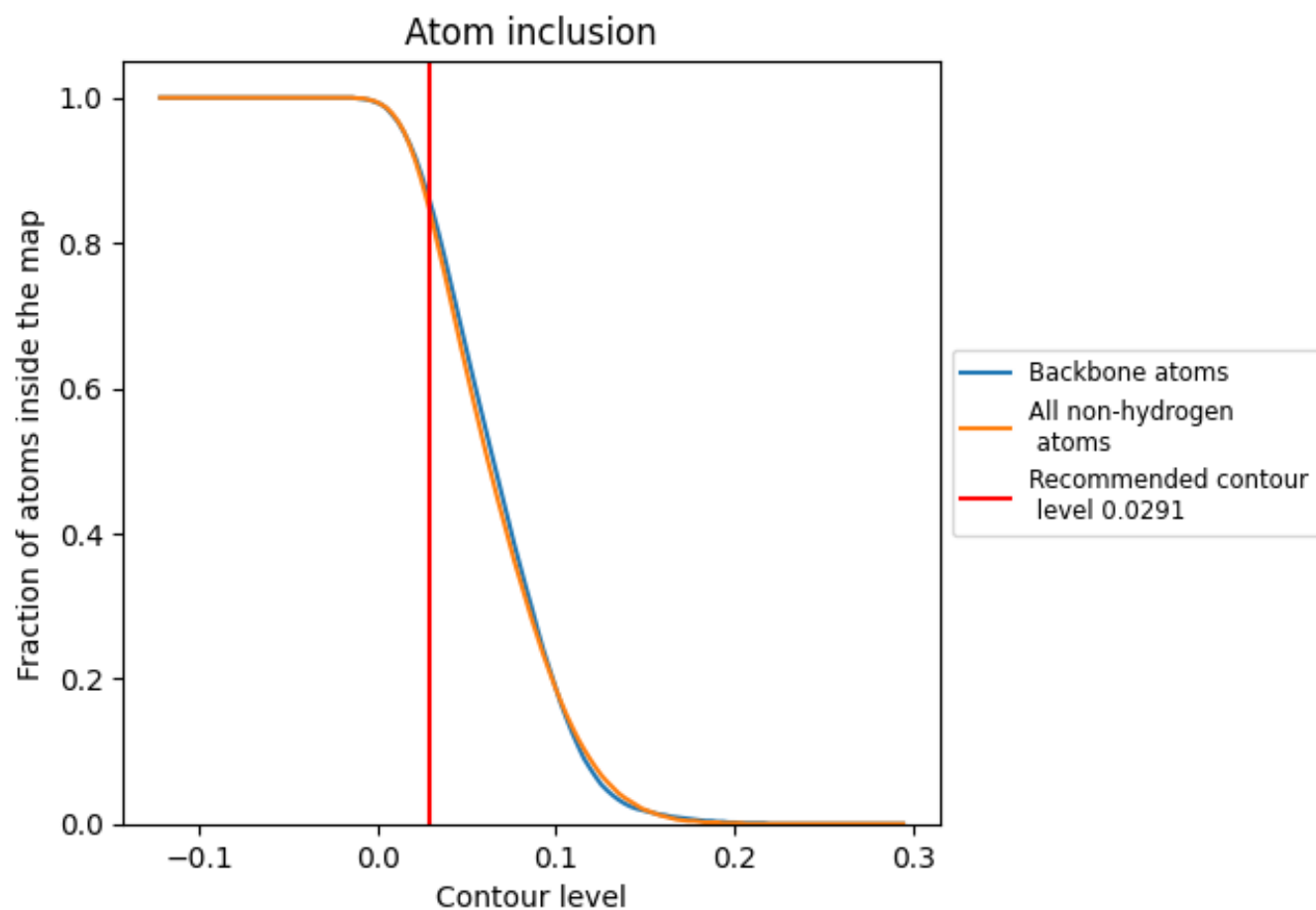
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0291).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 86% of all backbone atoms, 85% 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 (0.0291) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.4900
AT	 0.4640	 0.1450
CF	 0.1710	 0.1070
L5	 0.9050	 0.5210
L7	 0.9790	 0.5900
L8	 0.9450	 0.5610
LA	 0.9660	 0.6060
LB	 0.9260	 0.5900
LC	 0.9230	 0.5830
LD	 0.8850	 0.5520
LE	 0.8280	 0.5150
LF	 0.9440	 0.5950
LG	 0.8460	 0.5310
LH	 0.9020	 0.5650
LI	 0.9300	 0.5860
LJ	 0.8150	 0.4960
LL	 0.8840	 0.5600
LM	 0.9200	 0.5720
LN	 0.9770	 0.6130
LO	 0.9490	 0.5970
LP	 0.9450	 0.6050
LQ	 0.9570	 0.6130
LR	 0.8540	 0.5230
LS	 0.9620	 0.6040
LT	 0.9180	 0.5790
LU	 0.8080	 0.4790
LV	 0.9430	 0.5980
LW	 0.6670	 0.3950
LX	 0.9160	 0.5780
LY	 0.8960	 0.5740
LZ	 0.9260	 0.5730
La	 0.9640	 0.6090
Lb	 0.8360	 0.5160
Lc	 0.9020	 0.5590
Ld	 0.8950	 0.5630























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Chain	Atom inclusion	Q-score
Le	 0.9650	 0.6050
Lf	 0.9680	 0.6130
Lg	 0.9120	 0.5790
Lh	 0.9110	 0.5790
Li	 0.8880	 0.5660
Lj	 0.9640	 0.6080
Lk	 0.8100	 0.5170
Ll	 0.9550	 0.6000
Lm	 0.9060	 0.5860
Ln	 0.9760	 0.6110
Lo	 0.9040	 0.5710
Lp	 0.9290	 0.5890
Lr	 0.9430	 0.5890
Ls	 0.2370	 0.1630
Lt	 0.1380	 0.1070
Lz	 0.0680	 0.0910
Pt	 0.8780	 0.4350
S2	 0.9010	 0.4700
SA	 0.7980	 0.4820
SB	 0.8280	 0.5150
SC	 0.8690	 0.5120
SD	 0.6960	 0.3960
SE	 0.8190	 0.4720
SF	 0.7790	 0.4310
SG	 0.6850	 0.3780
SH	 0.6670	 0.3900
SI	 0.8210	 0.4930
SJ	 0.8090	 0.4650
SK	 0.6660	 0.3480
SL	 0.8230	 0.5050
SM	 0.2660	 0.1870
SN	 0.8900	 0.5540
SO	 0.8390	 0.5170
SP	 0.6770	 0.4000
SQ	 0.7400	 0.4140
SR	 0.6930	 0.4070
SS	 0.6820	 0.4070
ST	 0.7470	 0.4230
SU	 0.6880	 0.3780
SV	 0.8140	 0.4810
SW	 0.8820	 0.5390
SX	 0.8730	 0.5310

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Chain	Atom inclusion	Q-score
SY	 0.7120	 0.3770
SZ	 0.6360	 0.3640
Sa	 0.8820	 0.5340
Sb	 0.8230	 0.4850
Sc	 0.7080	 0.4080
Sd	 0.8530	 0.4530
Se	 0.7120	 0.4010
Sf	 0.3790	 0.1680
Sg	 0.5450	 0.3070
Zt	 0.2470	 0.0700