



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2025 – 03:07 PM EDT

PDB ID : 9B0F
EMDB ID : EMD-44039
Title : In situ human Hibernating class3 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2024-03-12
Resolution : 2.78 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:

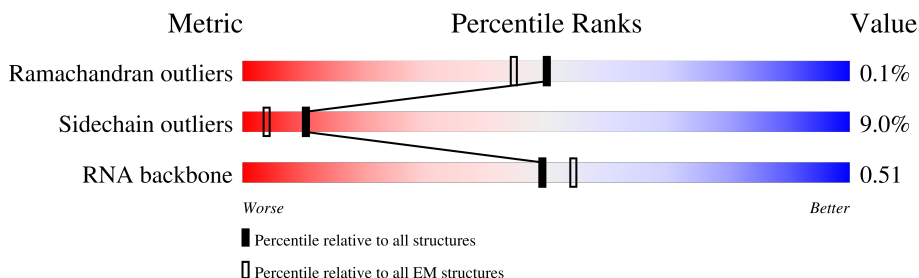
EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

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 2.78 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.





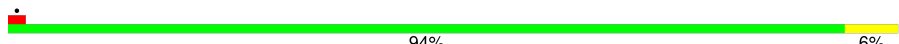
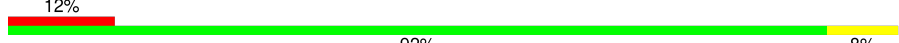

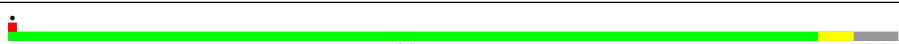


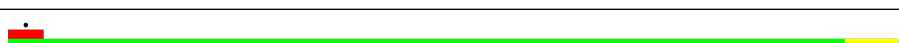
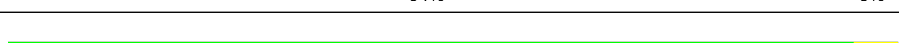
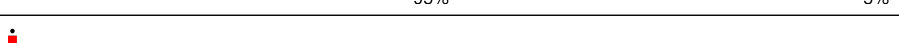
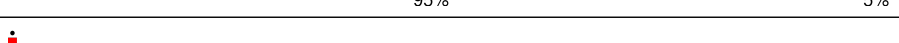
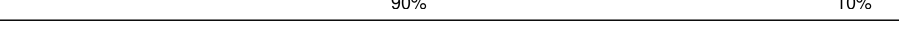
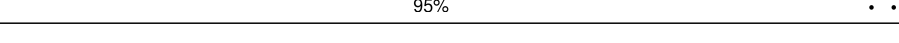
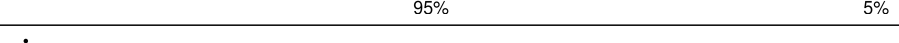
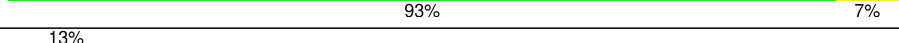

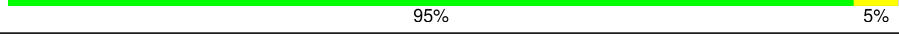
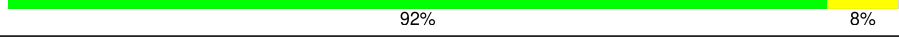
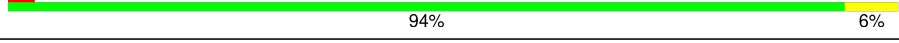
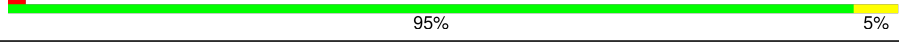
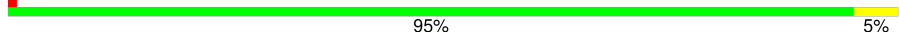


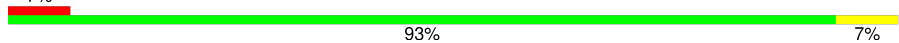
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	LR	187	<div> <div>12%</div> <div>90%</div> <div>10%</div> </div>
2	S2	1869	<div> <div>9%</div> <div>68%</div> <div>25%</div> <div>7%</div> </div>
3	L5	5070	<div> <div>7%</div> <div>56%</div> <div>18%</div> <div>26%</div> </div>
4	L7	120	<div> <div>88%</div> <div>12%</div> </div>
5	L8	156	<div> <div>5%</div> <div>81%</div> <div>19%</div> </div>
6	LA	248	<div> <div>93%</div> <div>6%</div> </div>
7	LB	402	<div> <div>94%</div> <div>6%</div> </div>
8	LC	368	<div> <div>95%</div> <div>5%</div> </div>

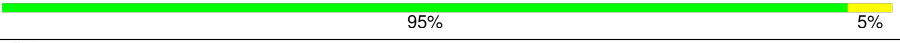
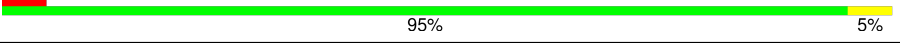
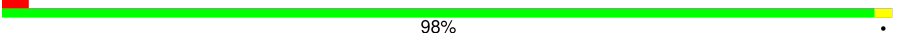
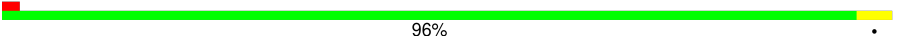
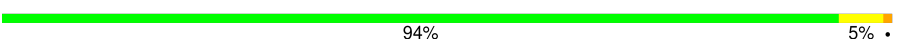


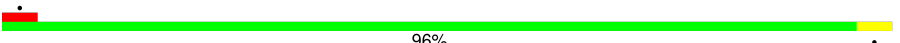



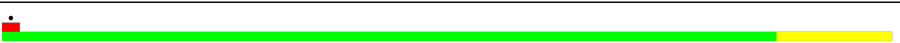
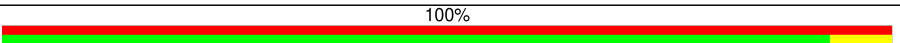

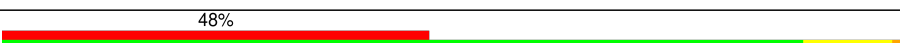

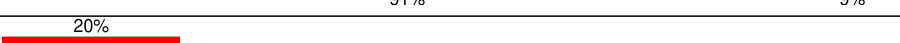
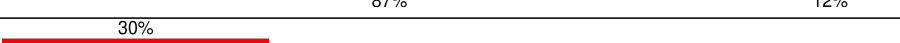
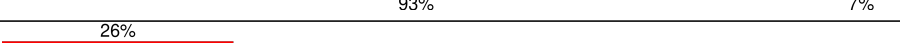

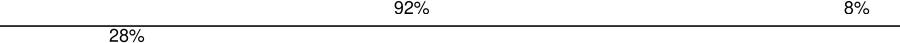
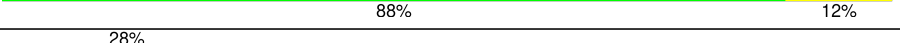


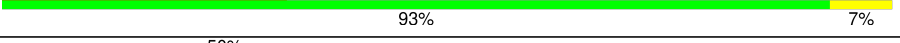
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	LD	293	
10	LE	247	
11	LF	225	
12	LG	241	
13	LH	190	
14	LI	213	
15	LJ	176	
16	LL	210	
17	LM	139	
18	LN	203	
19	LO	201	
20	LP	153	
21	LQ	187	
22	LS	175	
23	LT	159	
24	LU	101	
25	LV	131	
26	LX	120	
27	LY	134	
28	LZ	135	
29	La	147	
30	Lb	121	
31	Lc	98	
32	Ld	107	
33	Le	128	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	Lf	109	
35	Lg	114	
36	Lh	122	
37	Li	102	
38	Lj	86	
39	Lk	69	
40	Ll	50	
41	Lm	52	
42	Ln	24	
43	Lo	105	
44	Lp	91	
45	Lr	125	
46	Lz	217	
47	CA	356	
48	Ls	196	
49	Lt	141	
50	SD	227	
51	SF	189	
52	SK	98	
53	SP	121	
54	SQ	144	
55	SS	145	
56	ST	143	
57	SU	104	
58	Sc	64	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	Sd	55	
60	Sg	313	
61	SM	122	
62	SZ	75	
63	Sf	67	
64	CD	55	
65	LW	124	
66	SE	262	
67	SI	206	
68	SL	153	
69	SX	141	
70	SG	237	
71	SJ	185	
72	SY	131	
73	Se	58	
74	SA	221	
75	SB	214	
76	SH	189	
77	SV	83	
78	Sa	102	
79	SC	222	
80	SN	150	
81	SO	140	
82	SW	129	
83	Sb	83	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
84	CB	856	<div><div></div><div>29%</div><div></div><div>89%</div><div></div><div>9%</div><div></div></div>
85	Et	75	<div><div></div><div>27%</div><div></div><div>73%</div><div></div><div>68%</div><div></div><div>5%</div></div>

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 229857 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 60S ribosomal protein L19.

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

- Molecule 2 is a RNA chain called 18S rRNA.

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

- Molecule 3 is a RNA chain called 28S rRNA.

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

- Molecule 4 is a RNA chain called 5S rRNA.

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

- Molecule 5 is a RNA chain called 5.8S rRNA.

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

- Molecule 6 is a protein called 60S ribosomal protein L8.

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

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

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

- Molecule 8 is a protein called 60S ribosomal protein L4.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 10 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 11 is a protein called 60S ribosomal protein L7.

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

- Molecule 12 is a protein called 60S ribosomal protein L7a.

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

- Molecule 13 is a protein called 60S ribosomal protein L9.

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

- Molecule 14 is a protein called Ribosomal protein uL16-like.

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

- Molecule 15 is a protein called 60S ribosomal protein L11.

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

- Molecule 16 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 17 is a protein called 60S ribosomal protein L14.

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

- Molecule 18 is a protein called 60S ribosomal protein L15.

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

- Molecule 19 is a protein called 60S ribosomal protein L13a.

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

- Molecule 20 is a protein called 60S ribosomal protein L17.

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

- Molecule 21 is a protein called 60S ribosomal protein L18.

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

- Molecule 22 is a protein called 60S ribosomal protein L18a.

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

- Molecule 23 is a protein called 60S ribosomal protein L21.

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

- Molecule 24 is a protein called Heparin-binding protein HBp15.

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

- Molecule 25 is a protein called 60S ribosomal protein L23.

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

- Molecule 26 is a protein called 60S ribosomal protein L23a.

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

- Molecule 27 is a protein called 60S ribosomal protein L26.

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

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 31 is a protein called 60S ribosomal protein L30.

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

- Molecule 32 is a protein called 60S ribosomal protein L31.

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

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

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

- Molecule 36 is a protein called 60S ribosomal protein L35.

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

- Molecule 37 is a protein called 60S ribosomal protein L36.

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

- Molecule 38 is a protein called 60S ribosomal protein L37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 42 is a protein called 60S ribosomal protein L41.

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

- Molecule 43 is a protein called 60S ribosomal protein L36a.

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

- Molecule 44 is a protein called 60S ribosomal protein L37a.

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

- Molecule 45 is a protein called 60S ribosomal protein L28.

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

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

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

- Molecule 47 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	17		

- Molecule 48 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 49 is a protein called 60S ribosomal protein L12 [Homo sapiens].

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

- Molecule 50 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 51 is a protein called 40S ribosomal protein S5.

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

- Molecule 52 is a protein called 40S ribosomal protein S10.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 54 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 55 is a protein called 40S ribosomal protein S18.

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

- Molecule 56 is a protein called 40S ribosomal protein S19.

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

- Molecule 57 is a protein called 40S ribosomal protein S20.

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

- Molecule 58 is a protein called 40S ribosomal protein S28.

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

- Molecule 59 is a protein called 40S ribosomal protein S29.

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

- Molecule 60 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 61 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 62 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 63 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 64 is a protein called Serbp1.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	CD	55	Total	C	N	O	0	0
			440	263	87	90		

- Molecule 65 is a protein called Ribosomal protein L24.

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

- Molecule 66 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 67 is a protein called 40S ribosomal protein S8.

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

- Molecule 68 is a protein called 40S ribosomal protein S11.

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

- Molecule 69 is a protein called 40S ribosomal protein S23.

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

- Molecule 70 is a protein called 40S ribosomal protein S6.

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

- Molecule 71 is a protein called 40S ribosomal protein S9.

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

- Molecule 72 is a protein called 40S ribosomal protein S24.

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

- Molecule 73 is a protein called Small ribosomal subunit protein eS30.

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

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

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

- Molecule 75 is a protein called 40S ribosomal protein S3a.

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

- Molecule 76 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 77 is a protein called 40S ribosomal protein S21.

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

- Molecule 78 is a protein called 40S ribosomal protein S26.

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

- Molecule 79 is a protein called 40S ribosomal protein S2.

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

- Molecule 80 is a protein called 40S ribosomal protein S13.

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

- Molecule 81 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 82 is a protein called 40S ribosomal protein S15a.

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

- Molecule 83 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 84 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

- Molecule 85 is a RNA chain called E site tRNA [Homo sapiens].

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

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
86	S2	29	Total	Mg	0
			29	29	
86	L5	213	Total	Mg	0
			213	213	
86	L7	3	Total	Mg	0
			3	3	
86	L8	4	Total	Mg	0
			4	4	
86	LA	1	Total	Mg	0
			1	1	
86	LI	1	Total	Mg	0
			1	1	
86	LP	1	Total	Mg	0
			1	1	
86	LV	1	Total	Mg	0
			1	1	
86	Le	1	Total	Mg	0
			1	1	
86	Lg	1	Total	Mg	0
			1	1	

- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
87	Lg	1	Total	Zn	0
			1	1	
87	Lj	1	Total	Zn	0
			1	1	

Continued on next page...

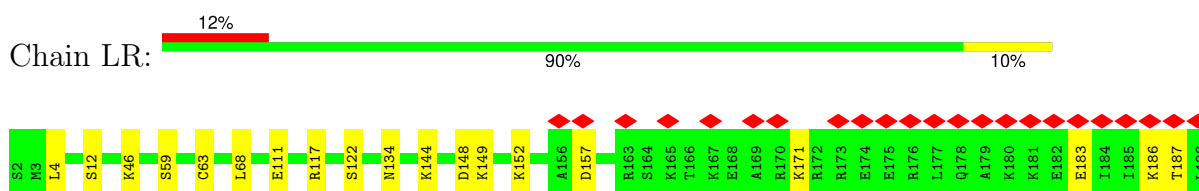
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
87	Lm	1	Total 1	Zn 1	0
87	Lo	1	Total 1	Zn 1	0
87	Lp	1	Total 1	Zn 1	0
87	Sa	1	Total 1	Zn 1	0

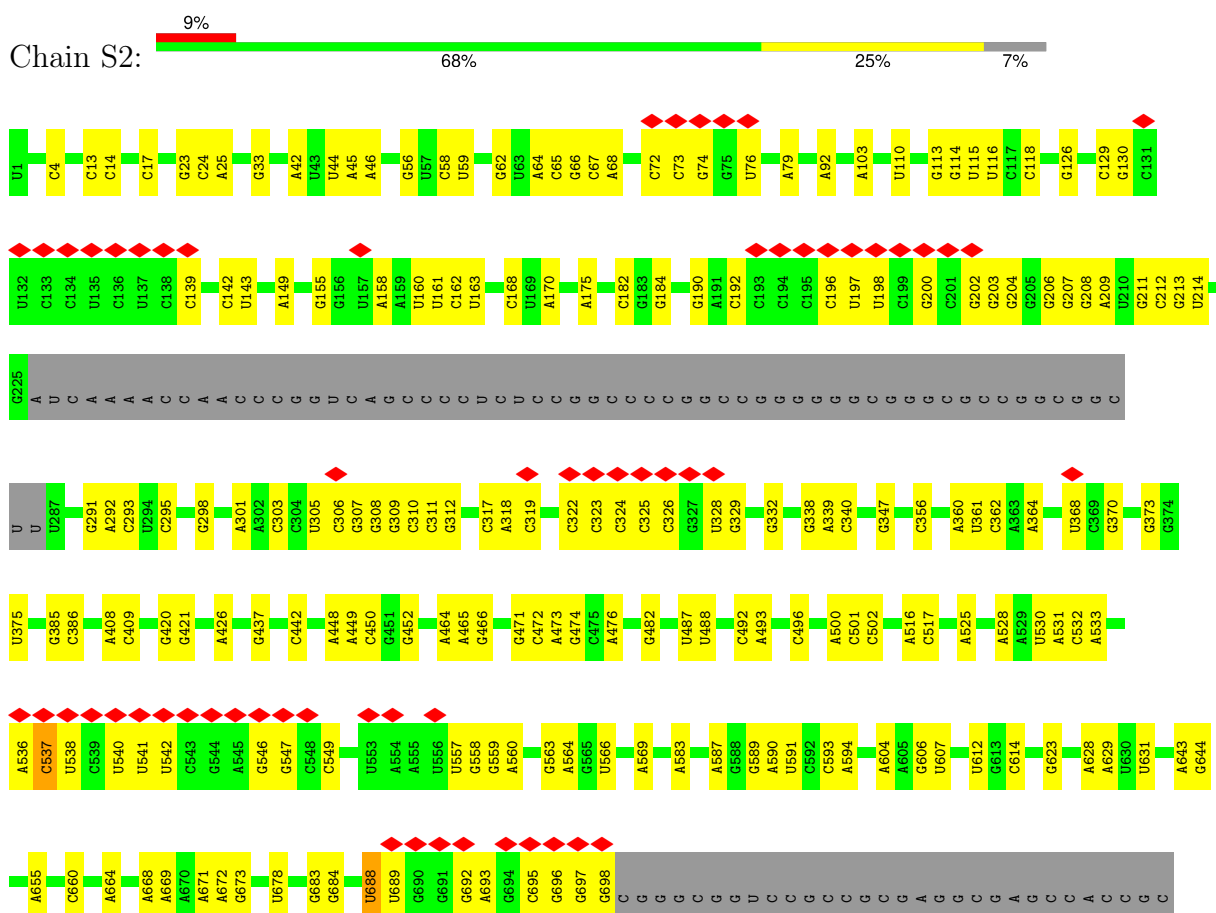
3 Residue-property plots

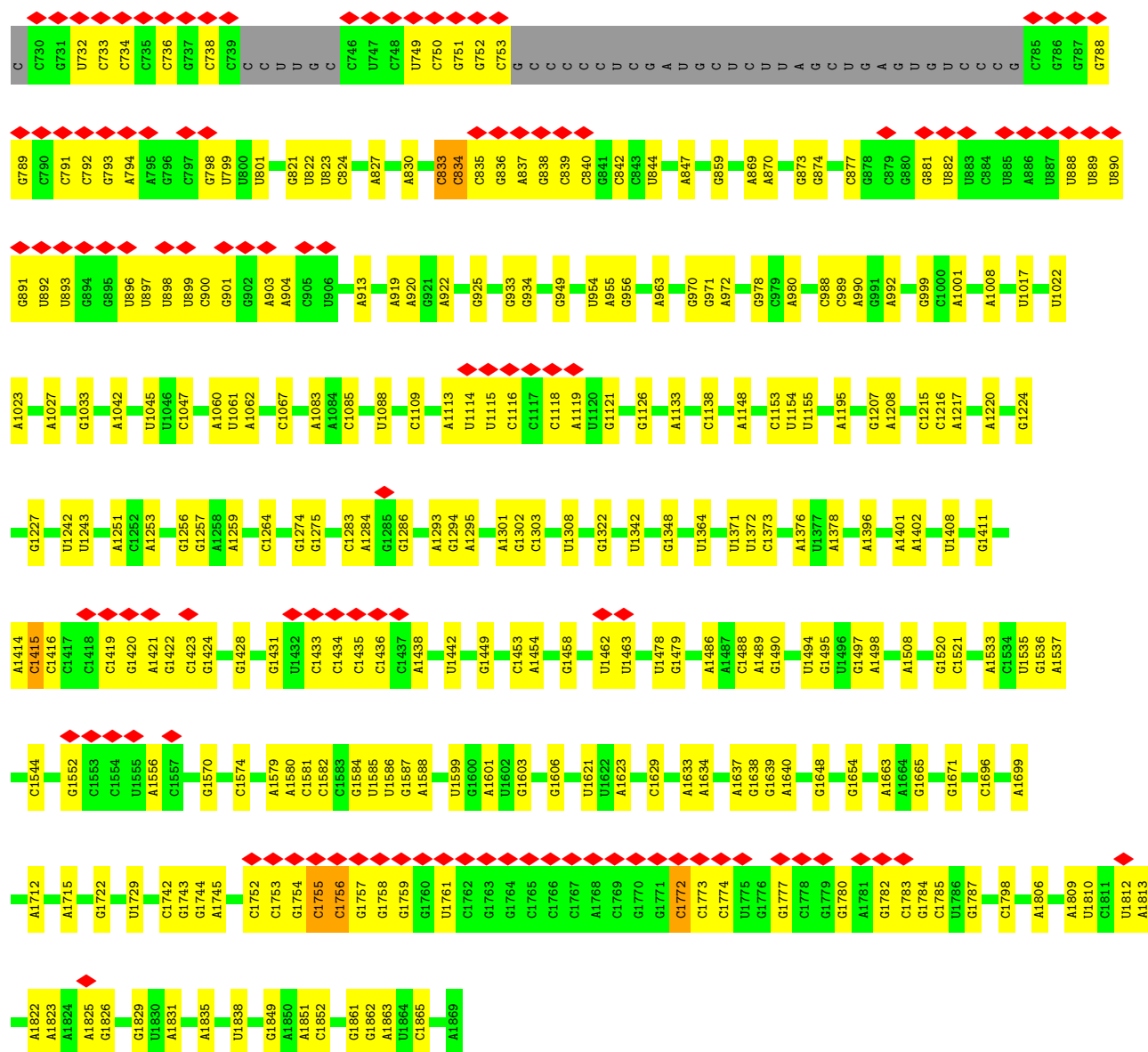
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 60S ribosomal protein L19

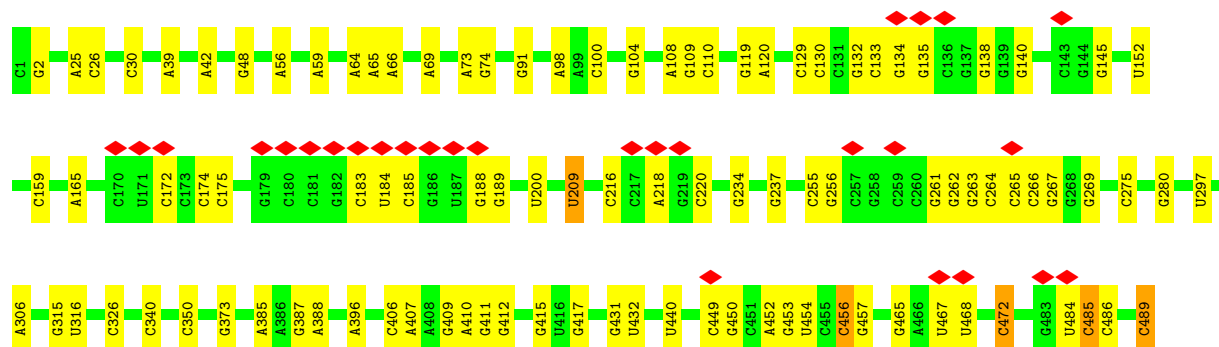


- Molecule 2: 18S rRNA



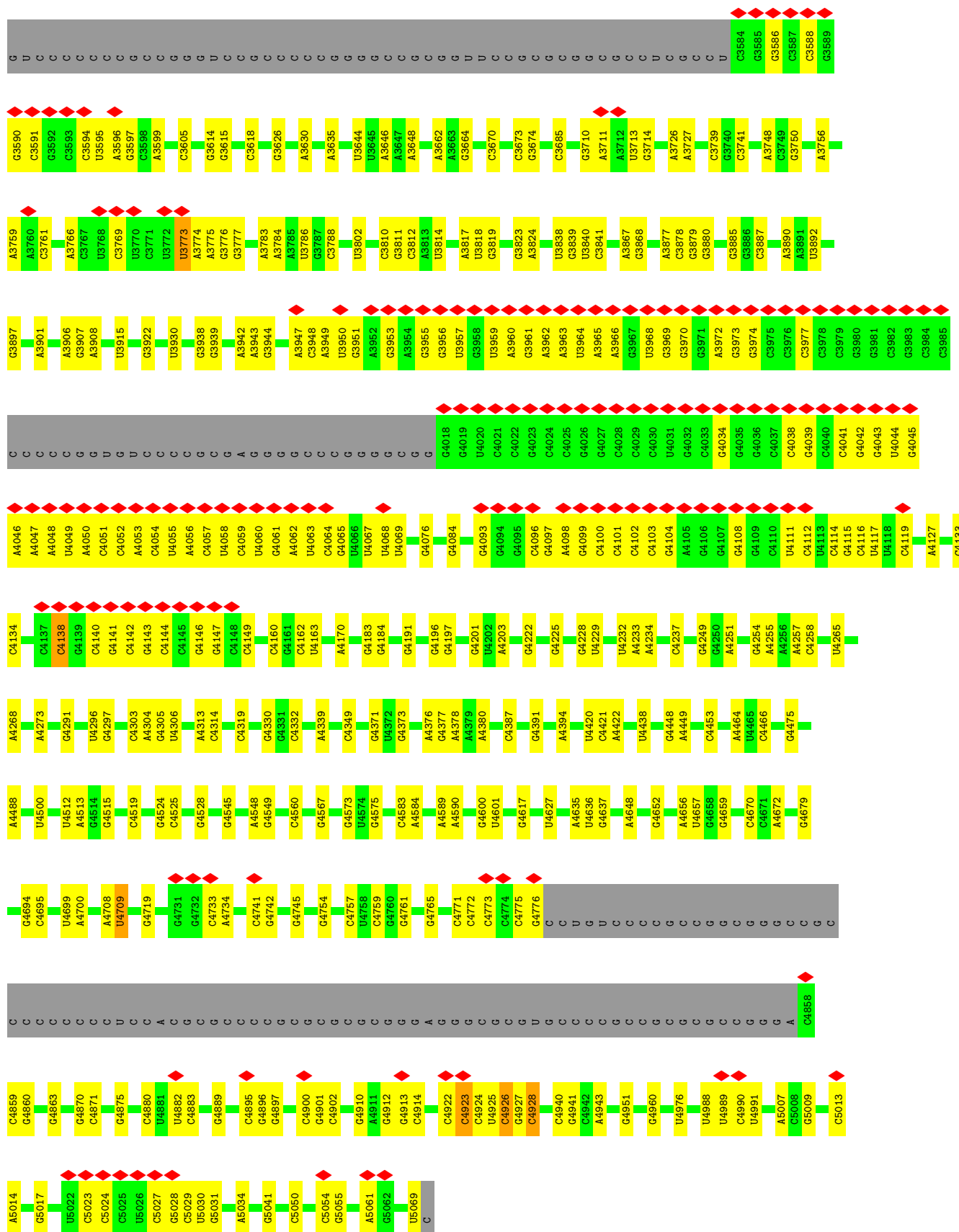


• Molecule 3: 28S rRNA

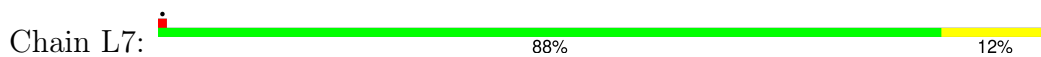




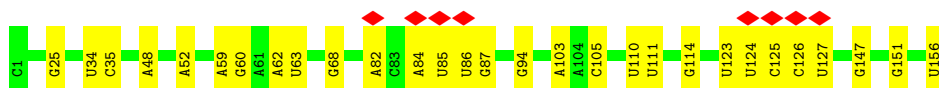
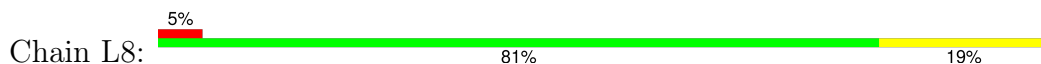




• Molecule 4: 5S rRNA



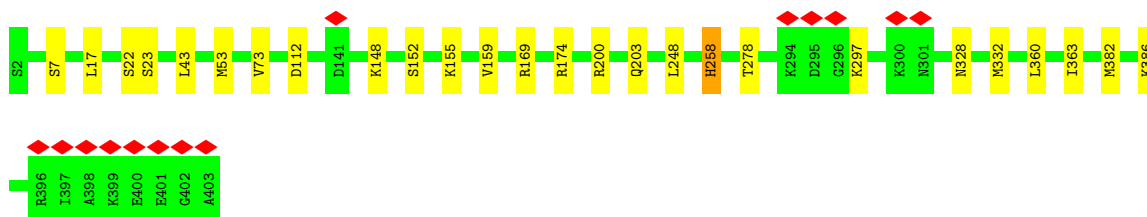
- Molecule 5: 5.8S rRNA



- Molecule 6: 60S ribosomal protein L8



- Molecule 7: Large ribosomal subunit protein uL3



- Molecule 8: 60S ribosomal protein L4

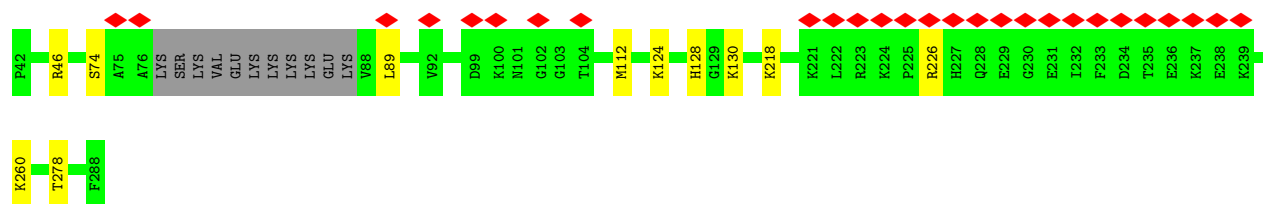


- Molecule 9: Large ribosomal subunit protein uL18



- Molecule 10: Large ribosomal subunit protein eL6

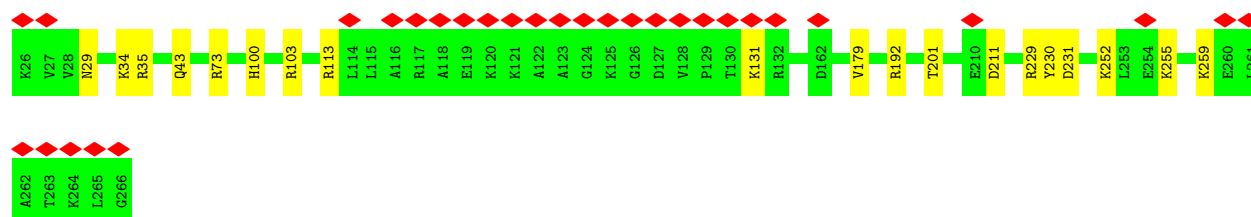




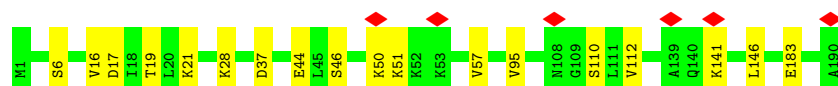
- Molecule 11: 60S ribosomal protein L7



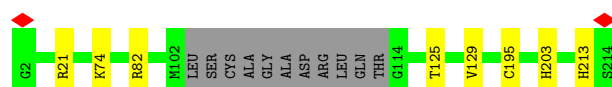
- Molecule 12: 60S ribosomal protein L7a



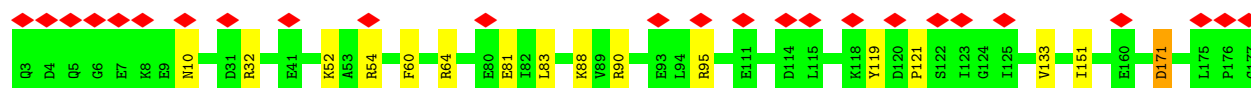
- Molecule 13: 60S ribosomal protein L9



- Molecule 14: Ribosomal protein uL16-like

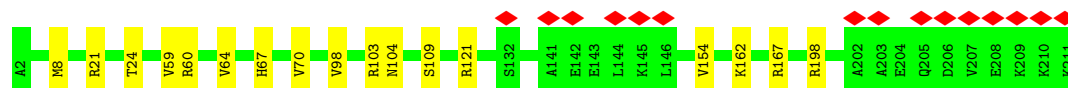
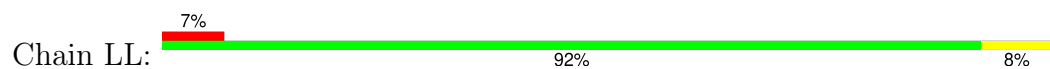


- Molecule 15: 60S ribosomal protein L11





- Molecule 16: Large ribosomal subunit protein eL13



- Molecule 17: 60S ribosomal protein L14



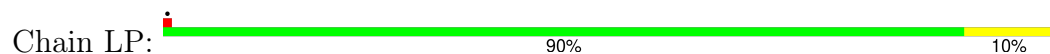
- Molecule 18: 60S ribosomal protein L15



- Molecule 19: 60S ribosomal protein L13a



- Molecule 20: 60S ribosomal protein L17

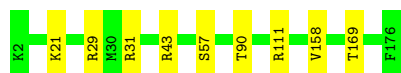


- Molecule 21: 60S ribosomal protein L18



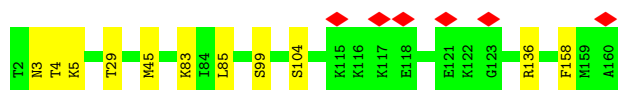
- Molecule 22: 60S ribosomal protein L18a

Chain LS:  95% 5%




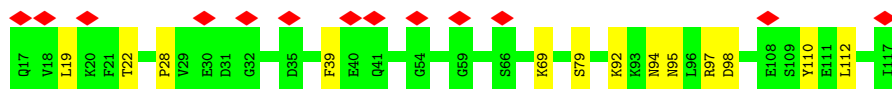
- Molecule 23: 60S ribosomal protein L21

Chain LT:  93% 7%



- Molecule 24: Heparin-binding protein HBp15

Chain LU:  13% 87% 13%



- Molecule 25: 60S ribosomal protein L23

Chain LV:  95% 5%



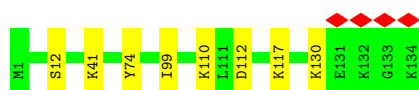
- Molecule 26: 60S ribosomal protein L23a

Chain LX:  92% 8%



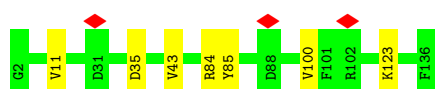
- Molecule 27: 60S ribosomal protein L26

Chain LY:  94% 6%



- Molecule 28: 60S ribosomal protein L27

Chain LZ:  95% 5%




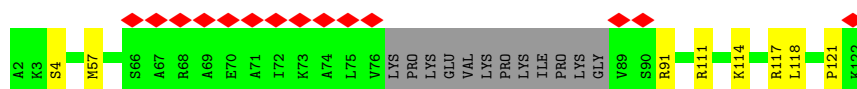
- Molecule 29: 60S ribosomal protein L27a

Chain La:  95% 5%

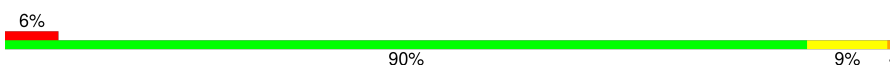


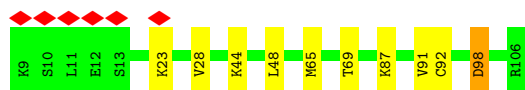
- Molecule 30: Large ribosomal subunit protein eL29

Chain Lb:  12% 83% 7% 10%



- Molecule 31: 60S ribosomal protein L30

Chain Lc:  6% 90% 9%



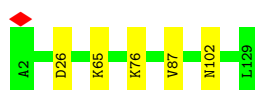
- Molecule 32: 60S ribosomal protein L31

Chain Ld:  7% 93% 7%



- Molecule 33: 60S ribosomal protein L32

Chain Le:  96%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf:  95% 5%



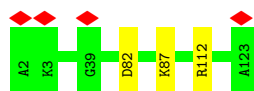
- Molecule 35: 60S ribosomal protein L34

Chain Lg:  5% 95% 5%



- Molecule 36: 60S ribosomal protein L35

Chain Lh: 98%



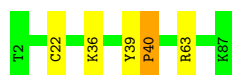
- Molecule 37: 60S ribosomal protein L36

Chain Li: 96%



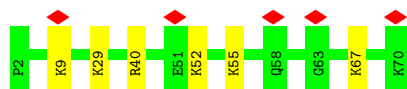
- Molecule 38: 60S ribosomal protein L37

Chain Lj: 94% 5%



- Molecule 39: 60S ribosomal protein L38

Chain Lk: 7% 91% 9%



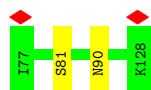
- Molecule 40: 60S ribosomal protein L39

Chain Ll: 94% 6%



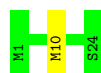
- Molecule 41: Large ribosomal subunit protein eL40

Chain Lm: 96%



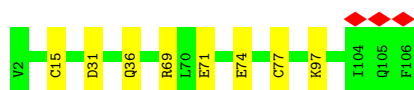
- Molecule 42: 60S ribosomal protein L41

Chain Ln:  96% .



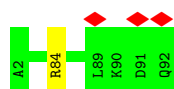
- Molecule 43: 60S ribosomal protein L36a

Chain Lo:  92% 8%




- Molecule 44: 60S ribosomal protein L37a

Chain Lp:  99% .



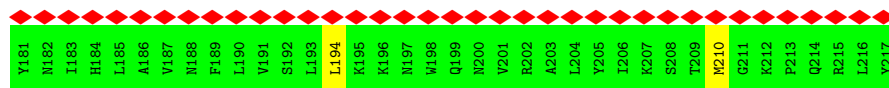
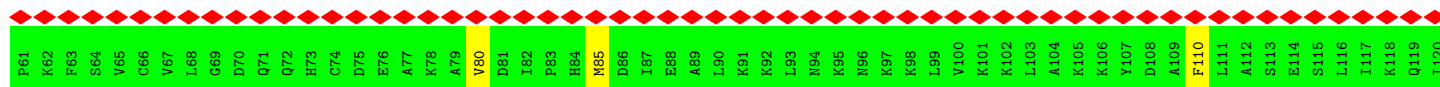
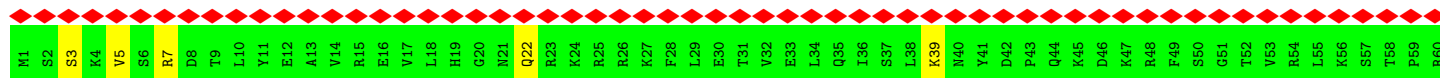
- Molecule 45: 60S ribosomal protein L28

Chain Lr:  87% 13%



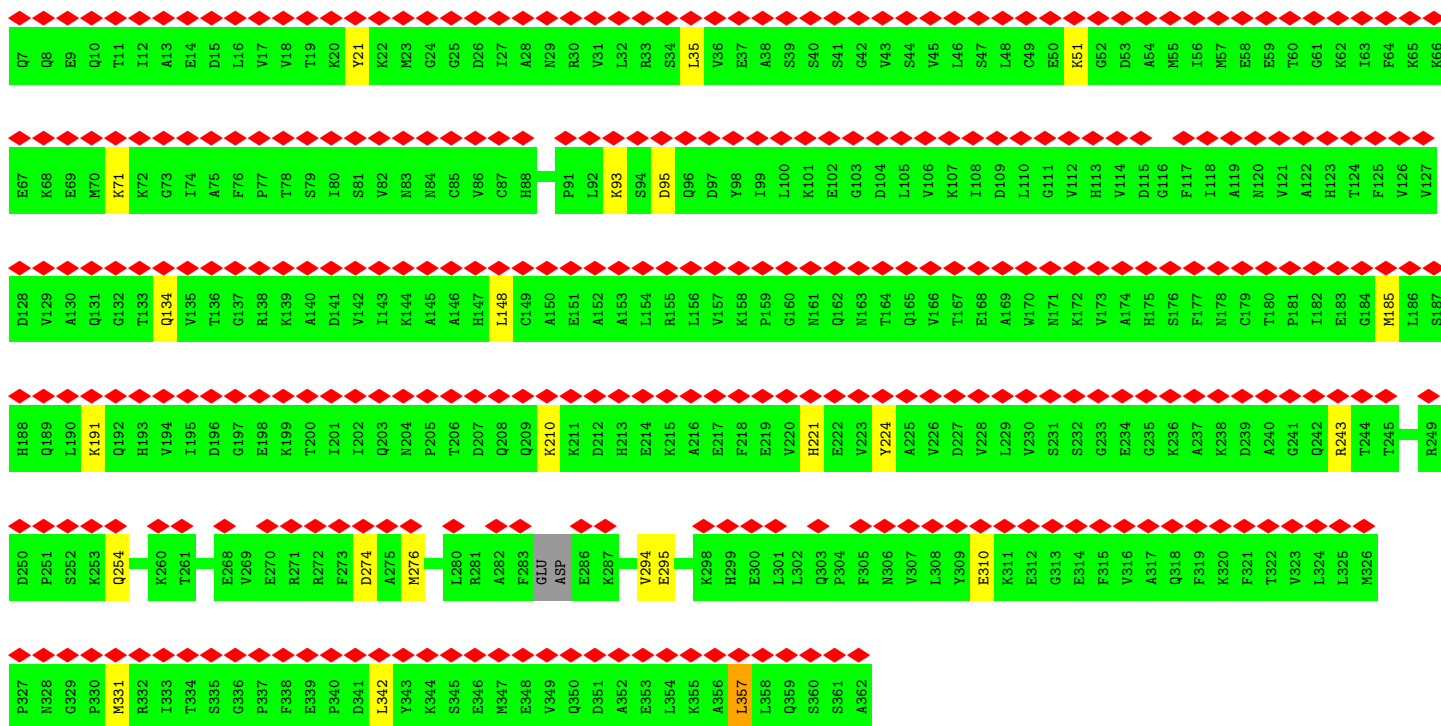
- Molecule 46: 60S ribosomal protein L10a

Chain Lz:  100% 93% 7%

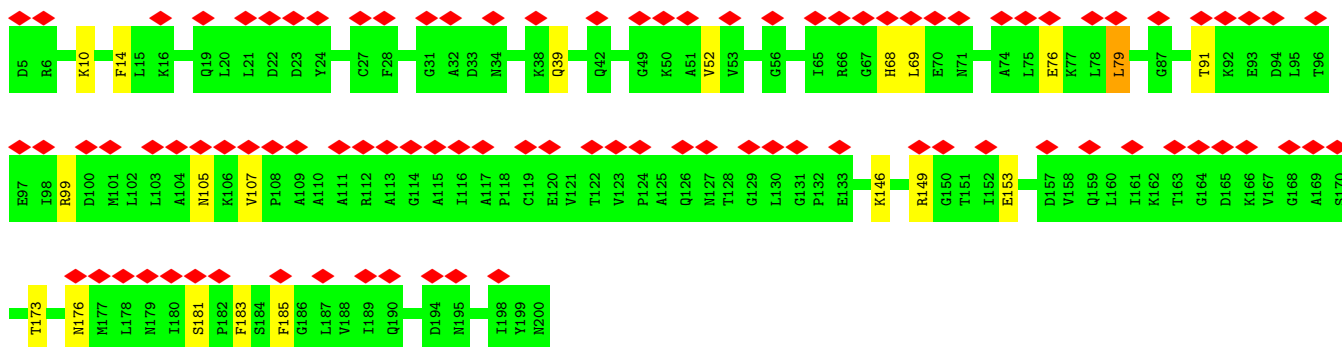
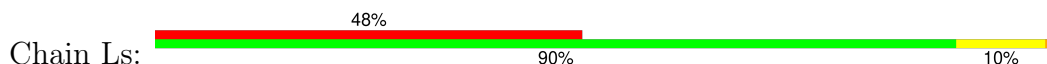


- Molecule 47: Proliferation-associated protein 2G4

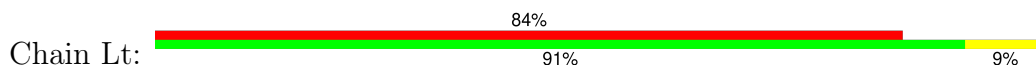
Chain CA:  90% 93% 6% .



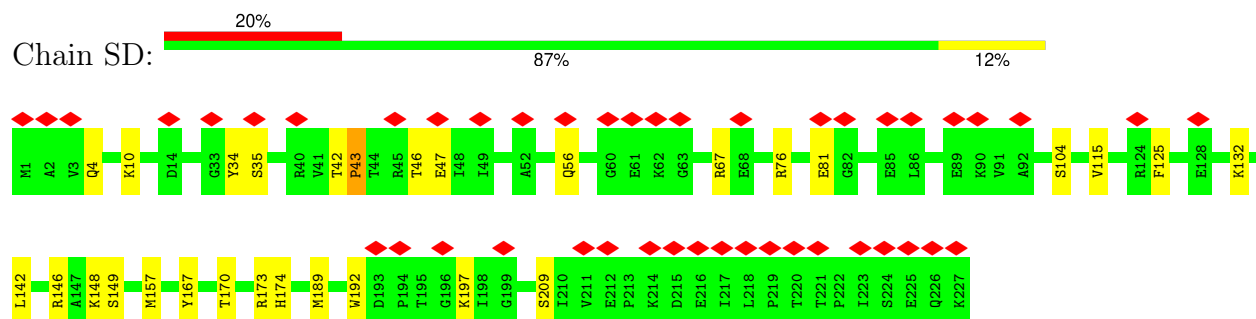
• Molecule 48: 60S acidic ribosomal protein P0



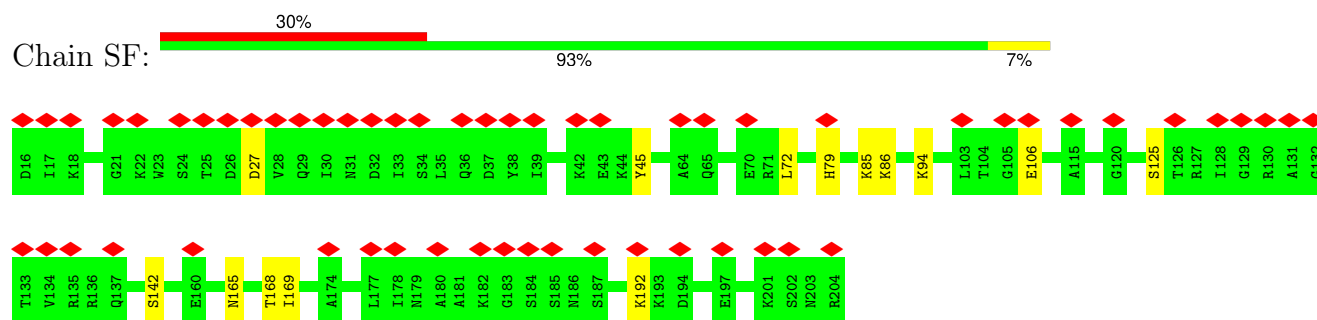
• Molecule 49: 60S ribosomal protein L12 [Homo sapiens]



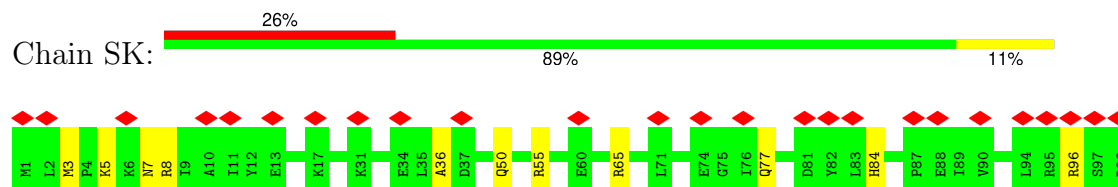
- Molecule 50: Small ribosomal subunit protein uS3



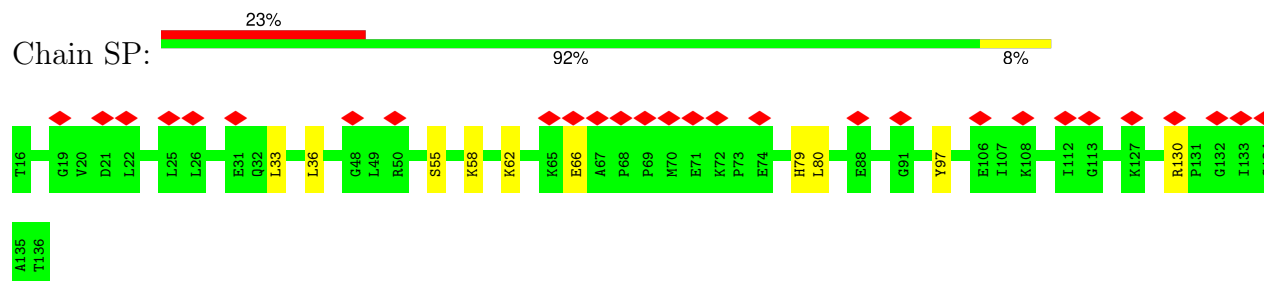
- Molecule 51: 40S ribosomal protein S5



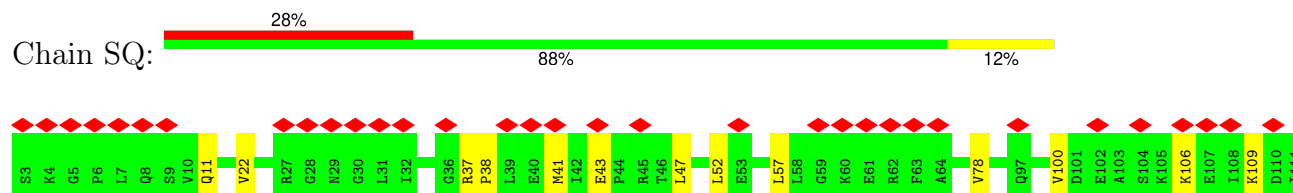
- Molecule 52: 40S ribosomal protein S10

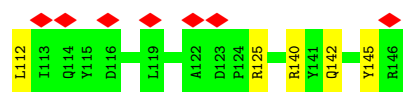


- Molecule 53: Small ribosomal subunit protein uS19

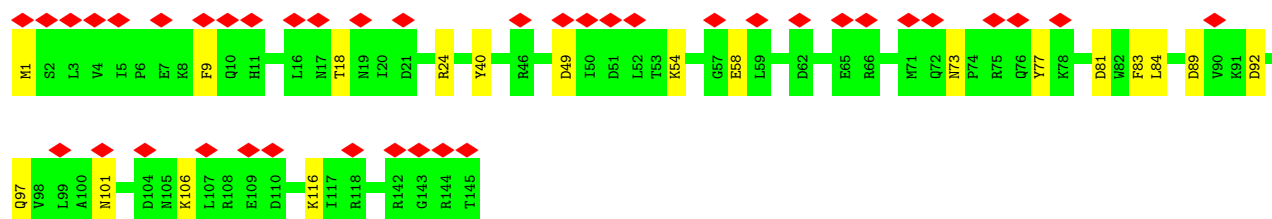
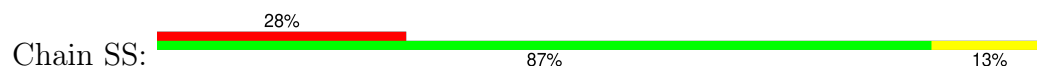


- Molecule 54: Small ribosomal subunit protein uS9

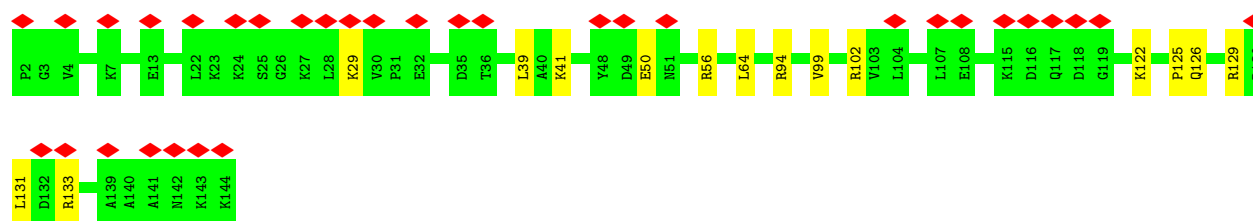
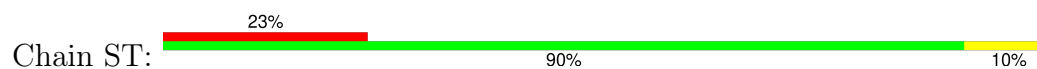




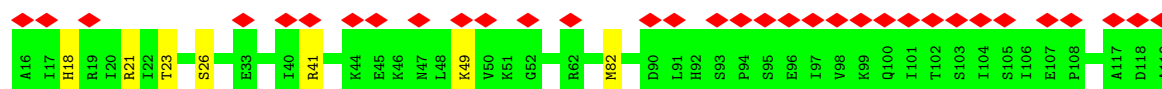
- Molecule 55: 40S ribosomal protein S18



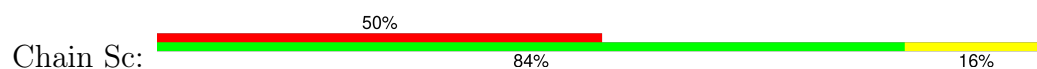
- Molecule 56: 40S ribosomal protein S19



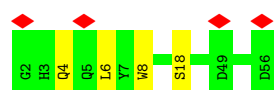
- Molecule 57: 40S ribosomal protein S20



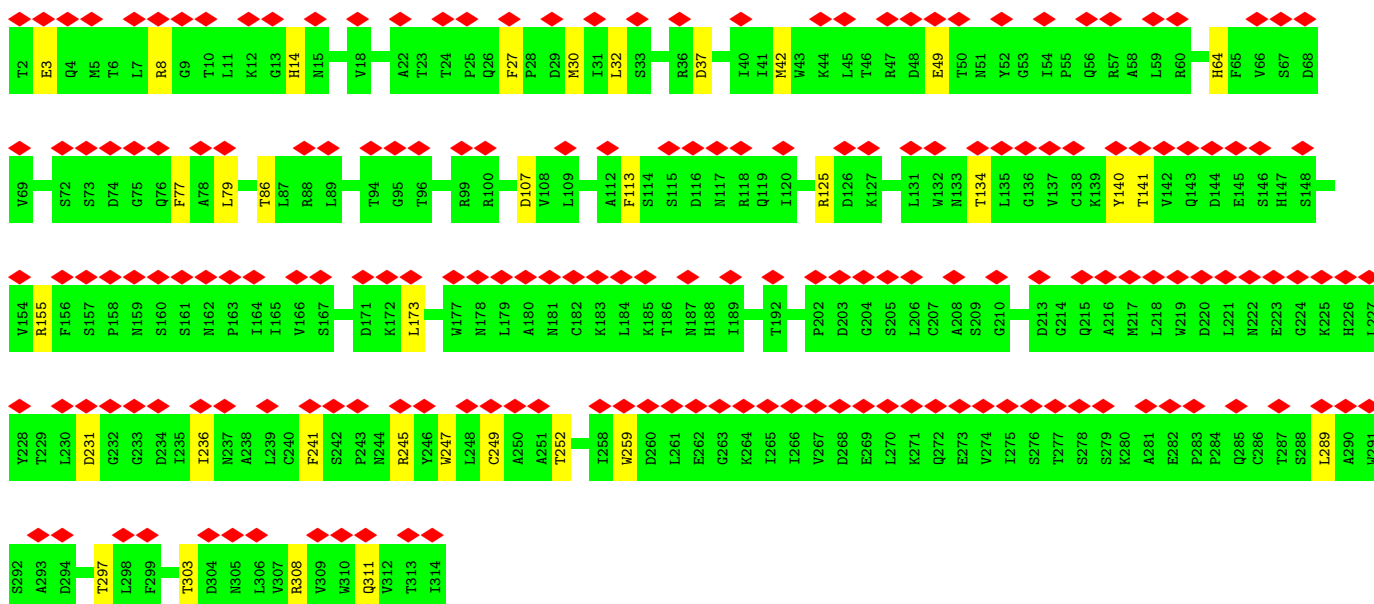
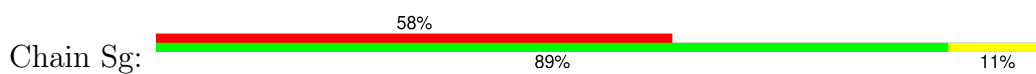
- Molecule 58: 40S ribosomal protein S28



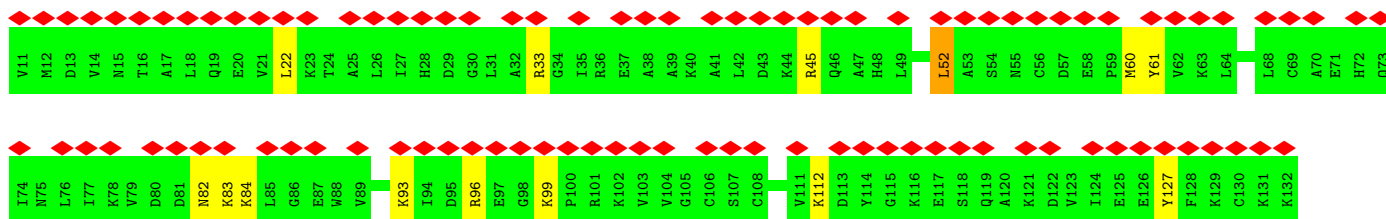
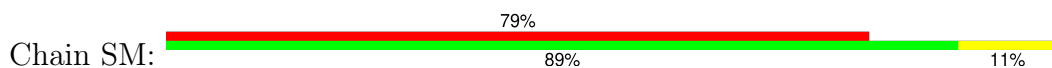
- Molecule 59: 40S ribosomal protein S29



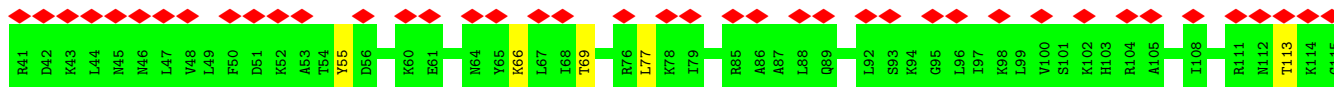
- Molecule 60: Receptor of activated protein C kinase 1



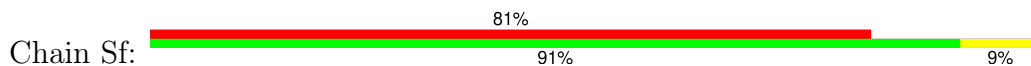
- Molecule 61: Small ribosomal subunit protein eS12



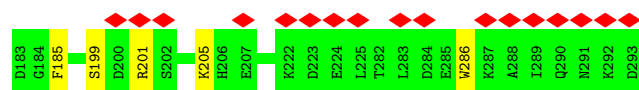
- Molecule 62: Small ribosomal subunit protein eS25



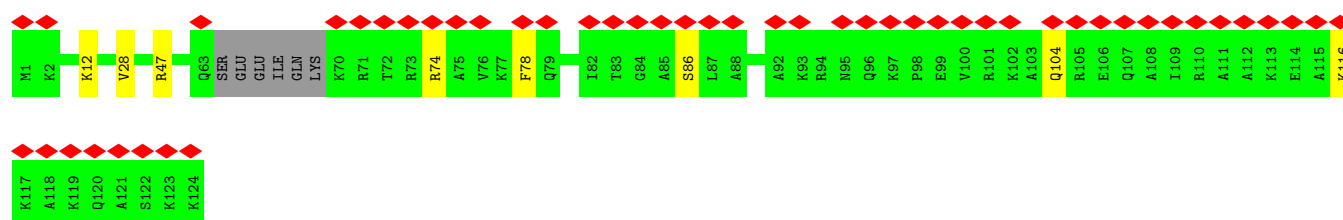
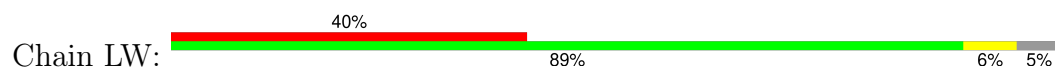
- Molecule 63: Ubiquitin-40S ribosomal protein S27a



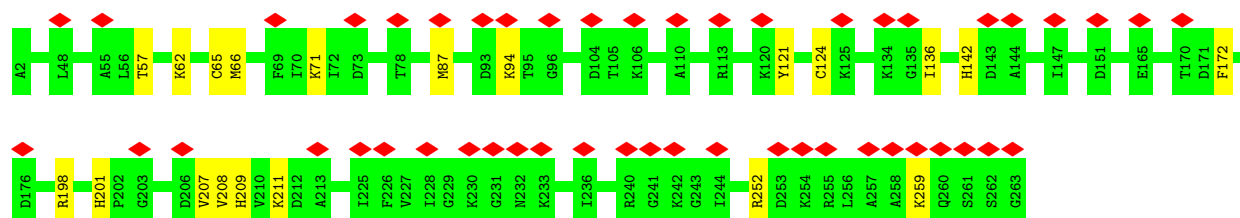
- Molecule 64: Serbp1



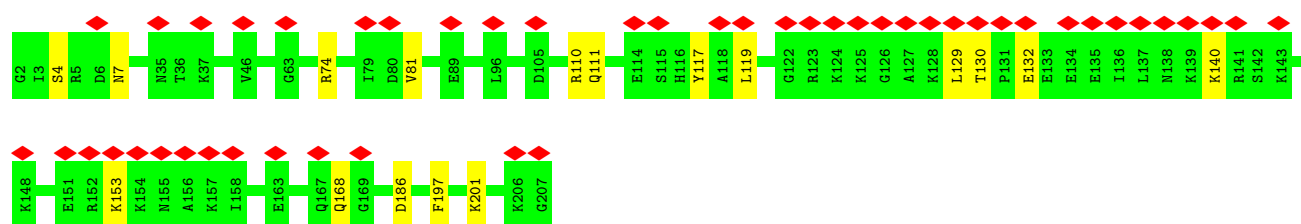
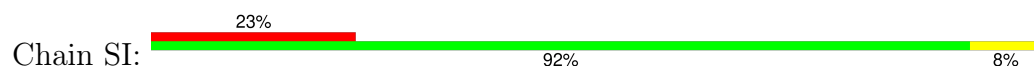
- Molecule 65: Ribosomal protein L24



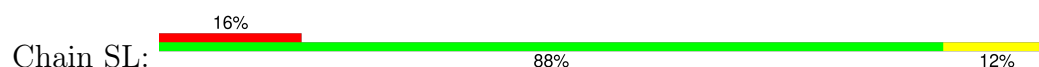
- Molecule 66: Small ribosomal subunit protein eS4, X isoform

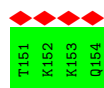


- Molecule 67: 40S ribosomal protein S8



- Molecule 68: 40S ribosomal protein S11

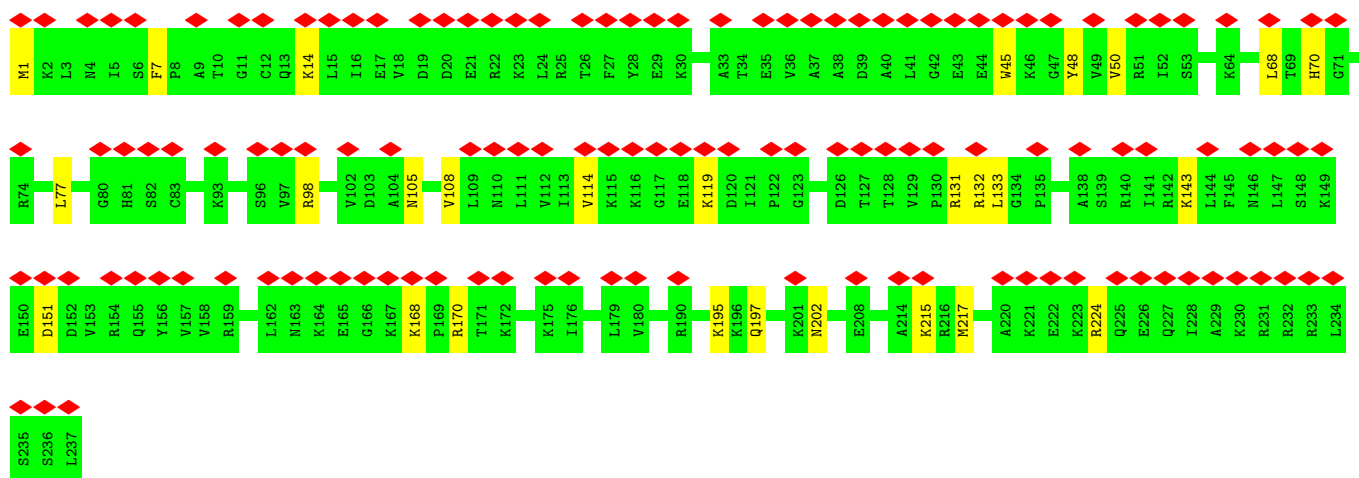
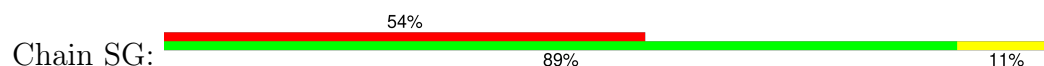




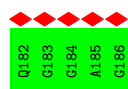
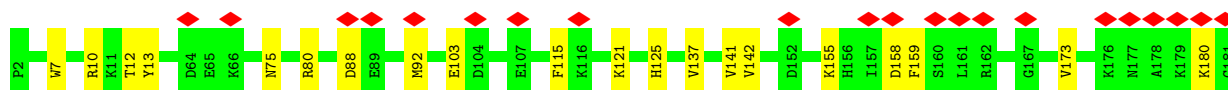
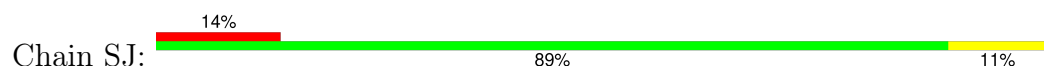
- Molecule 69: 40S ribosomal protein S23



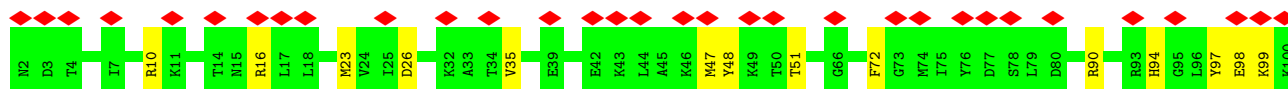
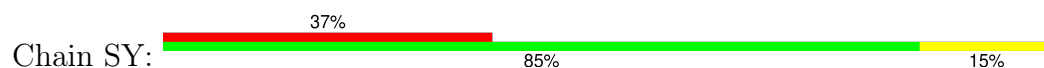
- Molecule 70: 40S ribosomal protein S6

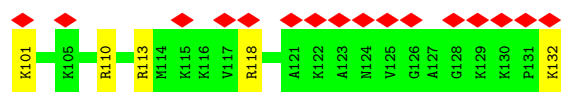


- Molecule 71: 40S ribosomal protein S9

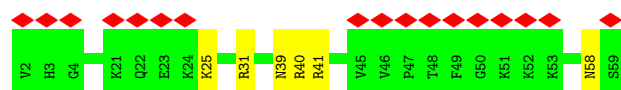
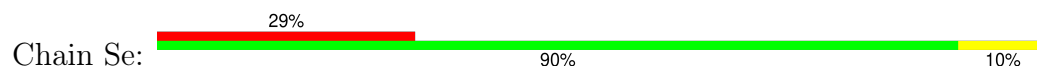


- Molecule 72: 40S ribosomal protein S24

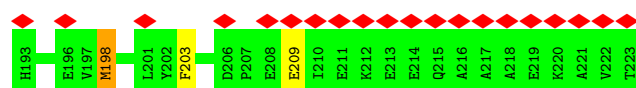
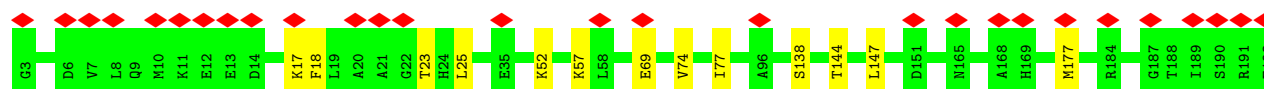




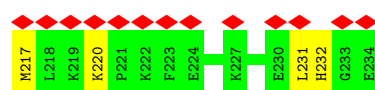
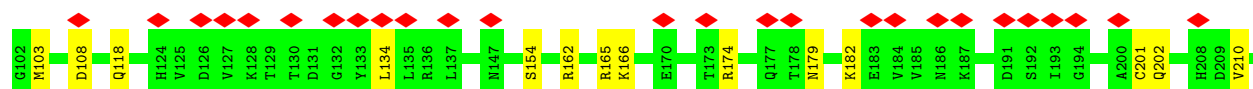
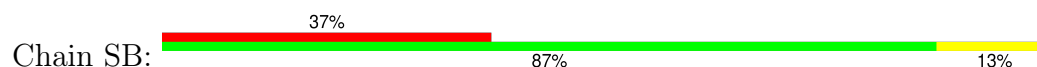
- Molecule 73: Small ribosomal subunit protein eS30



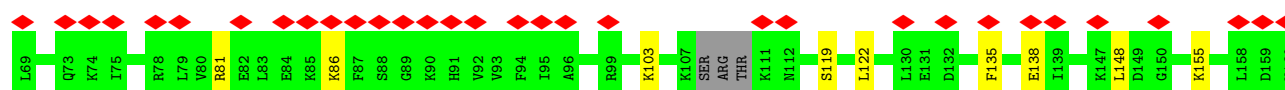
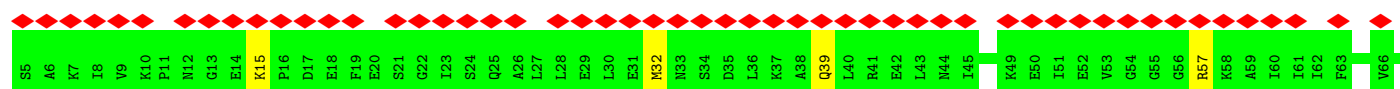
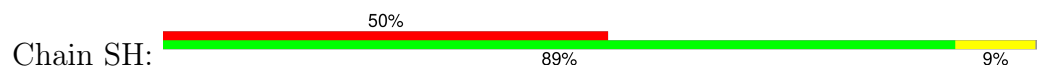
- Molecule 74: 40S ribosomal protein SA

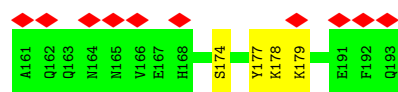


- Molecule 75: 40S ribosomal protein S3a

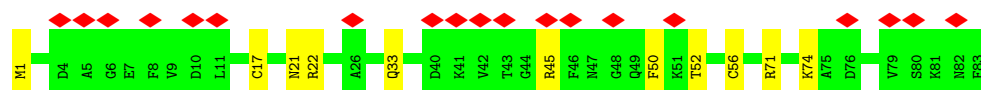
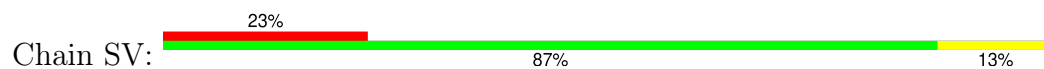


- Molecule 76: Small ribosomal subunit protein eS7

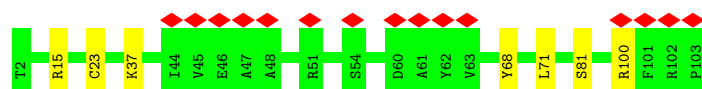




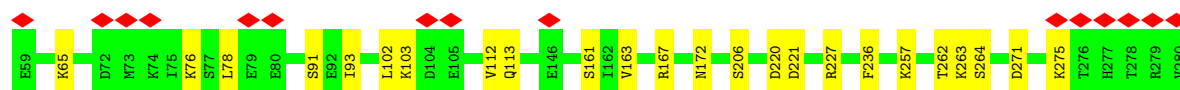
- Molecule 77: 40S ribosomal protein S21



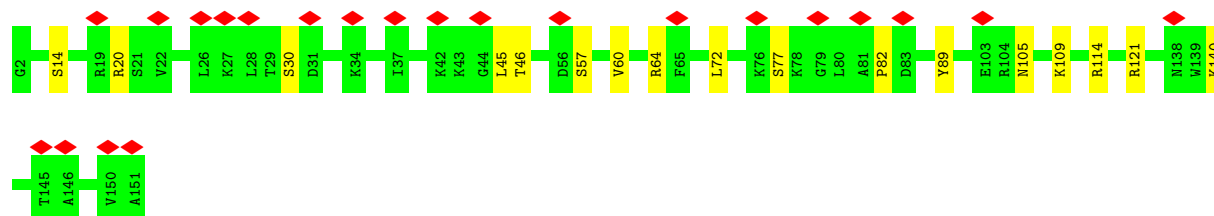
- Molecule 78: 40S ribosomal protein S26



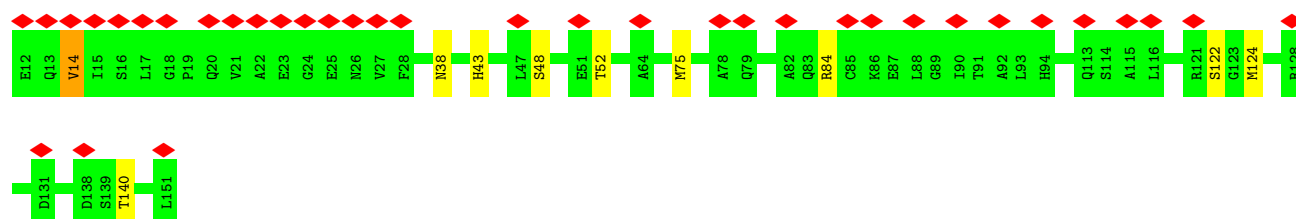
- Molecule 79: 40S ribosomal protein S2



- Molecule 80: 40S ribosomal protein S13

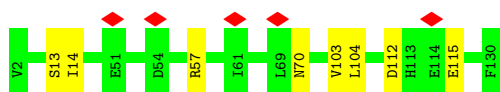


- Molecule 81: Small ribosomal subunit protein uS11




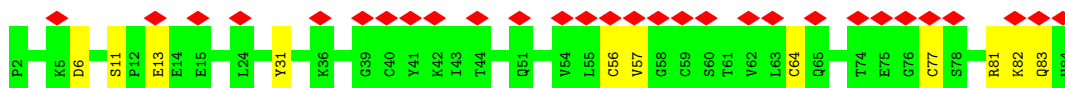
- Molecule 82: 40S ribosomal protein S15a

Chain SW:  94% 6%



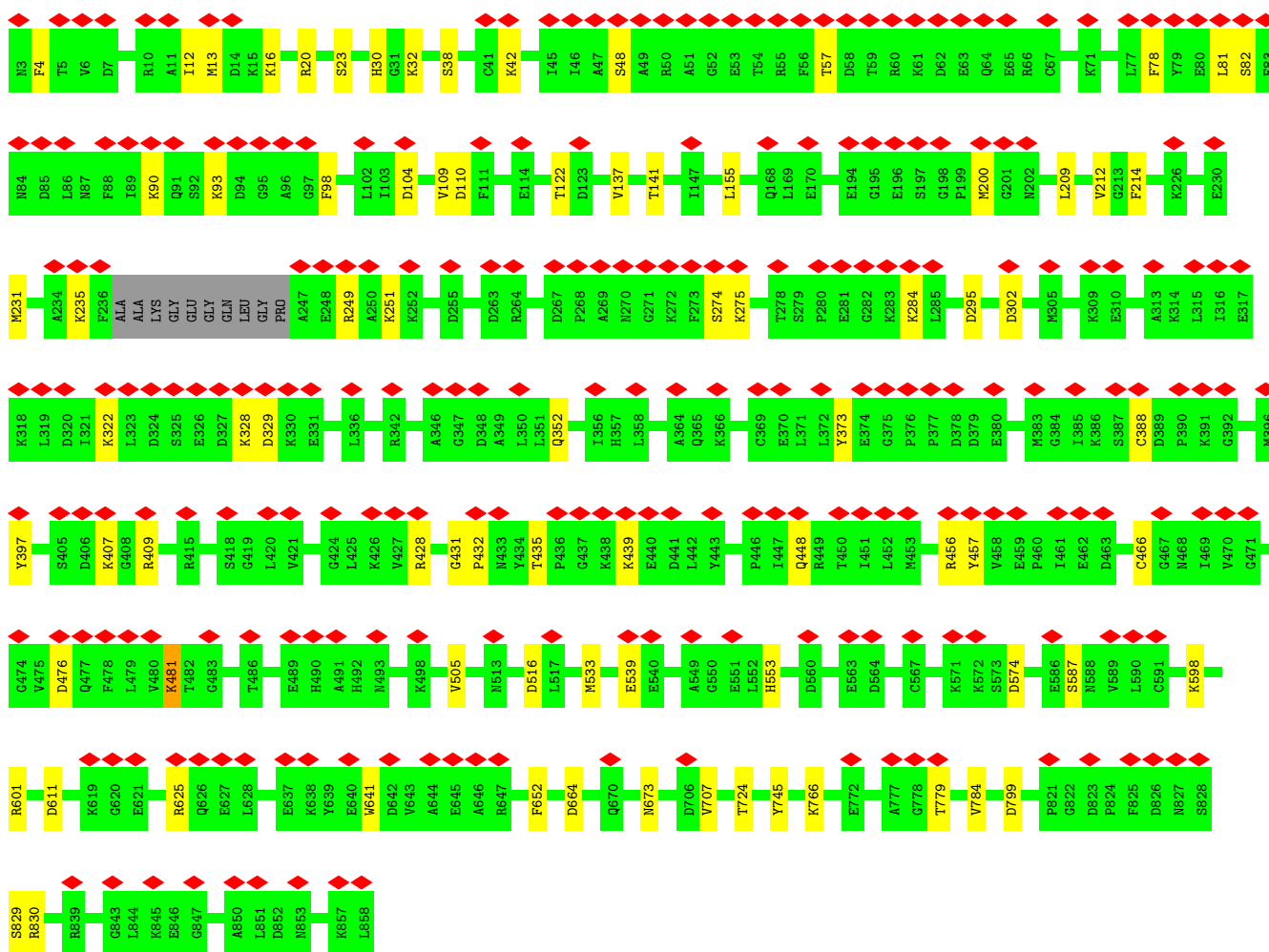
- Molecule 83: Small ribosomal subunit protein eS27

Chain Sb:  35% 87% 13%




- Molecule 84: Elongation factor 2

Chain CB:  29% 89% 9%



- Molecule 85: E site tRNA [Homo sapiens]

Chain Et:  27% 73% 68% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54480	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	0.495	Depositor
Minimum map value	-0.198	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.05	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: ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	LR	0.31	0/1582	0.58	0/2091
2	S2	0.41	0/41244	0.81	31/64263 (0.0%)
3	L5	0.64	0/89313	0.86	97/139291 (0.1%)
4	L7	0.62	0/2861	0.78	0/4459
5	L8	0.64	0/3701	0.78	0/5766
6	LA	0.40	0/1936	0.62	0/2596
7	LB	0.39	0/3306	0.59	0/4424
8	LC	0.36	0/2981	0.59	1/4002 (0.0%)
9	LD	0.36	0/2428	0.55	0/3252
10	LE	0.34	0/1942	0.58	0/2606
11	LF	0.38	0/1905	0.55	0/2539
12	LG	0.34	0/1960	0.57	0/2637
13	LH	0.36	0/1537	0.58	0/2066
14	LI	0.36	0/1673	0.56	0/2233
15	LJ	0.35	0/1433	0.68	2/1915 (0.1%)
16	LL	0.36	0/1732	0.59	0/2315
17	LM	0.36	0/1161	0.58	1/1554 (0.1%)
18	LN	0.39	0/1746	0.59	0/2338
19	LO	0.37	0/1682	0.56	0/2250
20	LP	0.37	0/1268	0.53	0/1701
21	LQ	0.37	0/1537	0.63	1/2052 (0.0%)
22	LS	0.39	0/1493	0.58	0/2003
23	LT	0.37	0/1326	0.56	0/1770
24	LU	0.38	0/839	0.66	2/1126 (0.2%)
25	LV	0.38	0/993	0.55	0/1332
26	LX	0.35	0/1002	0.58	0/1345
27	LY	0.37	0/1132	0.59	0/1504
28	LZ	0.36	0/1130	0.58	0/1507
29	La	0.38	0/1191	0.56	0/1591
30	Lb	0.34	0/889	0.65	2/1175 (0.2%)
31	Lc	0.35	0/774	0.58	1/1038 (0.1%)
32	Ld	0.35	0/903	0.61	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.39	0/1071	0.56	0/1429
34	Lf	0.41	0/895	0.63	0/1198
35	Lg	0.36	0/916	0.61	0/1220
36	Lh	0.32	0/1023	0.58	0/1351
37	Li	0.32	0/843	0.58	0/1115
38	Lj	1.03	3/720 (0.4%)	1.40	5/952 (0.5%)
39	Lk	0.31	0/575	0.60	0/761
40	Ll	0.33	0/454	0.59	0/599
41	Lm	0.34	0/435	0.56	0/575
42	Ln	0.28	0/231	0.74	0/294
43	Lo	0.38	0/876	0.61	0/1156
44	Lp	0.38	0/718	0.53	0/953
45	Lr	0.36	0/1017	0.59	0/1364
46	Lz	0.25	0/1769	0.57	1/2371 (0.0%)
47	CA	0.28	0/2810	0.53	1/3780 (0.0%)
48	Ls	0.29	0/1519	0.58	1/2052 (0.0%)
49	Lt	0.26	0/1058	0.64	1/1430 (0.1%)
50	SD	0.50	1/1793 (0.1%)	0.83	3/2414 (0.1%)
51	SF	0.29	0/1516	0.60	0/2037
52	SK	0.33	0/851	0.63	0/1147
53	SP	0.29	0/1003	0.67	2/1342 (0.1%)
54	SQ	0.30	0/1160	0.65	1/1553 (0.1%)
55	SS	0.28	0/1216	0.64	0/1628
56	ST	0.30	0/1131	0.62	1/1515 (0.1%)
57	SU	0.27	0/831	0.62	0/1115
58	Sc	0.28	0/508	0.66	0/680
59	Sd	0.31	0/470	0.58	0/623
60	Sg	0.28	0/2493	0.61	0/3394
61	SM	0.30	0/950	0.70	2/1275 (0.2%)
62	SZ	0.27	0/604	0.57	0/810
63	Sf	0.29	0/560	0.61	0/745
64	CD	0.28	0/447	0.57	0/592
65	LW	0.33	0/979	0.57	0/1295
66	SE	0.30	0/2118	0.59	0/2849
67	SI	0.29	0/1715	0.62	0/2287
68	SL	0.30	0/1268	0.60	0/1696
69	SX	0.32	0/1116	0.56	0/1490
70	SG	0.28	0/1946	0.66	0/2590
71	SJ	0.30	0/1550	0.59	0/2069
72	SY	0.28	0/1083	0.61	0/1438
73	Se	0.29	0/465	0.57	0/612
74	SA	0.28	0/1778	0.63	2/2416 (0.1%)
75	SB	0.29	0/1765	0.61	0/2362

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SH	0.27	0/1519	0.59	1/2033 (0.0%)
77	SV	0.30	0/643	0.61	0/860
78	Sa	0.33	0/836	0.64	0/1121
79	SC	0.31	0/1762	0.54	0/2381
80	SN	0.50	2/1232 (0.2%)	0.92	4/1656 (0.2%)
81	SO	0.28	0/1062	0.64	1/1425 (0.1%)
82	SW	0.31	0/1051	0.60	0/1406
83	Sb	0.28	0/665	0.55	0/891
84	CB	0.46	3/6734 (0.0%)	0.65	7/9094 (0.1%)
85	Et	0.37	0/1778	1.07	4/2767 (0.1%)
All	All	0.49	9/246128 (0.0%)	0.76	175/360165 (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
6	LA	0	2
7	LB	0	2
16	LL	0	1
17	LM	0	1
19	LO	0	1
23	LT	0	1
34	Lf	0	1
38	Lj	0	2
54	SQ	0	1
69	SX	0	1
76	SH	0	1
All	All	0	14

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	CB	432	PRO	CB-CG	19.48	2.47	1.50
38	Lj	40	PRO	CB-CG	19.12	2.45	1.50
84	CB	432	PRO	CG-CD	-17.08	0.94	1.50
50	SD	43	PRO	CG-CD	-15.46	0.99	1.50
38	Lj	40	PRO	CG-CD	-15.07	1.00	1.50

The worst 5 of 175 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	Lj	40	PRO	CB-CG-CD	-26.47	3.27	106.50
84	CB	432	PRO	CB-CG-CD	-23.04	16.63	106.50
50	SD	43	PRO	N-CD-CG	-19.95	73.28	103.20
38	Lj	40	PRO	CA-N-CD	-19.71	83.90	111.50
80	SN	82	PRO	CA-CB-CG	-18.40	69.04	104.00

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	LA	13	GLY	Peptide
6	LA	54	ARG	Peptide
7	LB	17	LEU	Peptide
7	LB	258	HIS	Peptide
16	LL	154	VAL	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	
1	LR	185/187 (99%)	180 (97%)	5 (3%)	0	100	100
6	LA	246/248 (99%)	222 (90%)	23 (9%)	1 (0%)	30	58
7	LB	400/402 (100%)	373 (93%)	27 (7%)	0	100	100
8	LC	366/368 (100%)	342 (93%)	24 (7%)	0	100	100
9	LD	291/293 (99%)	277 (95%)	14 (5%)	0	100	100
10	LE	232/247 (94%)	207 (89%)	25 (11%)	0	100	100
11	LF	223/225 (99%)	213 (96%)	10 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	LG	239/241 (99%)	225 (94%)	14 (6%)	0	100	100
13	LH	188/190 (99%)	173 (92%)	15 (8%)	0	100	100
14	LI	198/213 (93%)	184 (93%)	14 (7%)	0	100	100
15	LJ	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
16	LL	208/210 (99%)	192 (92%)	16 (8%)	0	100	100
17	LM	137/139 (99%)	130 (95%)	6 (4%)	1 (1%)	19	45
18	LN	201/203 (99%)	192 (96%)	8 (4%)	1 (0%)	25	52
19	LO	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
20	LP	151/153 (99%)	139 (92%)	12 (8%)	0	100	100
21	LQ	185/187 (99%)	180 (97%)	5 (3%)	0	100	100
22	LS	173/175 (99%)	163 (94%)	10 (6%)	0	100	100
23	LT	157/159 (99%)	146 (93%)	11 (7%)	0	100	100
24	LU	99/101 (98%)	81 (82%)	18 (18%)	0	100	100
25	LV	129/131 (98%)	125 (97%)	4 (3%)	0	100	100
26	LX	118/120 (98%)	116 (98%)	2 (2%)	0	100	100
27	LY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
28	LZ	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
29	La	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
30	Lb	105/121 (87%)	97 (92%)	8 (8%)	0	100	100
31	Lc	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
32	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
33	Le	126/128 (98%)	118 (94%)	8 (6%)	0	100	100
34	Lf	107/109 (98%)	96 (90%)	10 (9%)	1 (1%)	14	38
35	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
36	Lh	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
38	Lj	84/86 (98%)	80 (95%)	4 (5%)	0	100	100
39	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
40	Ll	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
41	Lm	50/52 (96%)	50 (100%)	0	0	100	100
42	Ln	22/24 (92%)	22 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	Lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
44	Lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
45	Lr	123/125 (98%)	115 (94%)	8 (6%)	0	100	100
46	Lz	215/217 (99%)	172 (80%)	43 (20%)	0	100	100
47	CA	350/356 (98%)	333 (95%)	17 (5%)	0	100	100
48	Ls	194/196 (99%)	185 (95%)	9 (5%)	0	100	100
49	Lt	137/141 (97%)	106 (77%)	29 (21%)	2 (2%)	8	25
50	SD	225/227 (99%)	200 (89%)	25 (11%)	0	100	100
51	SF	187/189 (99%)	169 (90%)	18 (10%)	0	100	100
52	SK	96/98 (98%)	80 (83%)	14 (15%)	2 (2%)	5	18
53	SP	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
54	SQ	142/144 (99%)	124 (87%)	18 (13%)	0	100	100
55	SS	143/145 (99%)	134 (94%)	9 (6%)	0	100	100
56	ST	141/143 (99%)	128 (91%)	11 (8%)	2 (1%)	9	27
57	SU	102/104 (98%)	92 (90%)	10 (10%)	0	100	100
58	Sc	62/64 (97%)	51 (82%)	11 (18%)	0	100	100
59	Sd	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
60	Sg	311/313 (99%)	274 (88%)	37 (12%)	0	100	100
61	SM	120/122 (98%)	108 (90%)	11 (9%)	1 (1%)	16	41
62	SZ	73/75 (97%)	62 (85%)	11 (15%)	0	100	100
63	Sf	65/67 (97%)	56 (86%)	9 (14%)	0	100	100
64	CD	51/55 (93%)	46 (90%)	5 (10%)	0	100	100
65	LW	114/124 (92%)	109 (96%)	5 (4%)	0	100	100
66	SE	260/262 (99%)	243 (94%)	17 (6%)	0	100	100
67	SI	204/206 (99%)	200 (98%)	4 (2%)	0	100	100
68	SL	151/153 (99%)	144 (95%)	7 (5%)	0	100	100
69	SX	139/141 (99%)	122 (88%)	16 (12%)	1 (1%)	19	45
70	SG	235/237 (99%)	219 (93%)	16 (7%)	0	100	100
71	SJ	183/185 (99%)	168 (92%)	15 (8%)	0	100	100
72	SY	129/131 (98%)	120 (93%)	9 (7%)	0	100	100
73	Se	56/58 (97%)	51 (91%)	5 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	SA	219/221 (99%)	196 (90%)	23 (10%)	0	100	100
75	SB	212/214 (99%)	206 (97%)	6 (3%)	0	100	100
76	SH	182/189 (96%)	159 (87%)	23 (13%)	0	100	100
77	SV	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
78	Sa	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
79	SC	220/222 (99%)	206 (94%)	13 (6%)	1 (0%)	25	52
80	SN	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
81	SO	138/140 (99%)	123 (89%)	15 (11%)	0	100	100
82	SW	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
83	Sb	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
84	CB	842/856 (98%)	795 (94%)	43 (5%)	4 (0%)	25	52
All	All	12973/13206 (98%)	12018 (93%)	938 (7%)	17 (0%)	50	76

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
49	Lt	144	ASP
52	SK	96	ARG
56	ST	39	LEU
84	CB	407	LYS
84	CB	779	THR

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	LR	166/166 (100%)	147 (89%)	19 (11%)	4	14
6	LA	190/190 (100%)	175 (92%)	15 (8%)	10	28
7	LB	348/348 (100%)	323 (93%)	25 (7%)	12	31
8	LC	306/306 (100%)	288 (94%)	18 (6%)	16	41
9	LD	246/247 (100%)	229 (93%)	17 (7%)	13	34

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	LE	209/220 (95%)	198 (95%)	11 (5%)	19	46
11	LF	194/194 (100%)	180 (93%)	14 (7%)	12	31
12	LG	203/205 (99%)	184 (91%)	19 (9%)	7	20
13	LH	169/169 (100%)	151 (89%)	18 (11%)	5	15
14	LI	172/180 (96%)	164 (95%)	8 (5%)	22	51
15	LJ	148/148 (100%)	133 (90%)	15 (10%)	6	17
16	LL	176/176 (100%)	160 (91%)	16 (9%)	7	22
17	LM	118/118 (100%)	112 (95%)	6 (5%)	20	47
18	LN	171/171 (100%)	162 (95%)	9 (5%)	19	46
19	LO	173/173 (100%)	163 (94%)	10 (6%)	17	42
20	LP	134/134 (100%)	118 (88%)	16 (12%)	4	12
21	LQ	164/164 (100%)	155 (94%)	9 (6%)	18	44
22	LS	156/156 (100%)	147 (94%)	9 (6%)	17	42
23	LT	139/139 (100%)	129 (93%)	10 (7%)	12	31
24	LU	91/91 (100%)	79 (87%)	12 (13%)	3	9
25	LV	101/101 (100%)	95 (94%)	6 (6%)	16	41
26	LX	108/108 (100%)	98 (91%)	10 (9%)	7	21
27	LY	124/124 (100%)	116 (94%)	8 (6%)	14	37
28	LZ	117/117 (100%)	110 (94%)	7 (6%)	16	40
29	La	120/120 (100%)	113 (94%)	7 (6%)	17	42
30	Lb	88/101 (87%)	82 (93%)	6 (7%)	13	34
31	Lc	83/83 (100%)	73 (88%)	10 (12%)	4	12
32	Ld	98/98 (100%)	91 (93%)	7 (7%)	12	32
33	Le	114/114 (100%)	109 (96%)	5 (4%)	24	53
34	Lf	88/88 (100%)	85 (97%)	3 (3%)	32	63
35	Lg	98/98 (100%)	92 (94%)	6 (6%)	15	40
36	Lh	109/109 (100%)	106 (97%)	3 (3%)	38	69
37	Li	86/86 (100%)	82 (95%)	4 (5%)	22	51
38	Lj	73/73 (100%)	70 (96%)	3 (4%)	26	56
39	Lk	64/64 (100%)	58 (91%)	6 (9%)	7	20
40	Ll	47/47 (100%)	44 (94%)	3 (6%)	14	37

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	Lm	48/48 (100%)	46 (96%)	2 (4%)	25	55
42	Ln	23/23 (100%)	22 (96%)	1 (4%)	25	54
43	Lo	93/93 (100%)	85 (91%)	8 (9%)	8	24
44	Lp	74/74 (100%)	73 (99%)	1 (1%)	62	85
45	Lr	109/109 (100%)	93 (85%)	16 (15%)	2	7
46	Lz	195/196 (100%)	181 (93%)	14 (7%)	12	31
47	CA	303/305 (99%)	280 (92%)	23 (8%)	11	29
48	Ls	162/164 (99%)	142 (88%)	20 (12%)	4	11
49	Lt	112/115 (97%)	103 (92%)	9 (8%)	10	27
50	SD	190/190 (100%)	161 (85%)	29 (15%)	2	6
51	SF	159/159 (100%)	145 (91%)	14 (9%)	8	23
52	SK	89/89 (100%)	80 (90%)	9 (10%)	6	17
53	SP	107/107 (100%)	99 (92%)	8 (8%)	11	30
54	SQ	119/119 (100%)	103 (87%)	16 (13%)	3	9
55	SS	126/126 (100%)	107 (85%)	19 (15%)	2	6
56	ST	113/113 (100%)	101 (89%)	12 (11%)	5	16
57	SU	94/94 (100%)	87 (93%)	7 (7%)	11	30
58	Sc	57/57 (100%)	47 (82%)	10 (18%)	1	4
59	Sd	48/48 (100%)	44 (92%)	4 (8%)	9	26
60	Sg	272/272 (100%)	238 (88%)	34 (12%)	3	11
61	SM	102/104 (98%)	89 (87%)	13 (13%)	3	11
62	SZ	66/66 (100%)	61 (92%)	5 (8%)	11	29
63	Sf	60/60 (100%)	54 (90%)	6 (10%)	6	18
64	CD	46/46 (100%)	41 (89%)	5 (11%)	5	15
65	LW	97/103 (94%)	89 (92%)	8 (8%)	9	26
66	SE	224/224 (100%)	204 (91%)	20 (9%)	8	23
67	SI	178/178 (100%)	161 (90%)	17 (10%)	7	19
68	SL	137/137 (100%)	119 (87%)	18 (13%)	3	9
69	SX	113/113 (100%)	105 (93%)	8 (7%)	12	32
70	SG	207/207 (100%)	180 (87%)	27 (13%)	3	10
71	SJ	161/161 (100%)	141 (88%)	20 (12%)	4	11

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	SY	113/113 (100%)	94 (83%)	19 (17%)	1	5
73	Se	47/47 (100%)	41 (87%)	6 (13%)	3	10
74	SA	183/183 (100%)	168 (92%)	15 (8%)	9	26
75	SB	195/195 (100%)	167 (86%)	28 (14%)	2	7
76	SH	166/169 (98%)	151 (91%)	15 (9%)	8	22
77	SV	67/67 (100%)	56 (84%)	11 (16%)	2	5
78	Sa	89/89 (100%)	82 (92%)	7 (8%)	10	28
79	SC	188/188 (100%)	165 (88%)	23 (12%)	4	11
80	SN	130/130 (100%)	114 (88%)	16 (12%)	4	11
81	SO	110/110 (100%)	100 (91%)	10 (9%)	7	22
82	SW	112/112 (100%)	104 (93%)	8 (7%)	12	32
83	Sb	75/75 (100%)	64 (85%)	11 (15%)	2	7
84	CB	722/728 (99%)	646 (90%)	76 (10%)	5	16
All	All	11272/11332 (100%)	10254 (91%)	1018 (9%)	10	22

5 of 1018 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	Lt	146	ARG
79	SC	206	SER
57	SU	23	THR
79	SC	93	ILE
84	CB	20	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
54	SQ	11	GLN
81	SO	38	ASN
62	SZ	64	ASN
83	Sb	51	GLN
76	SH	91	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	S2	1717/1869 (91%)	467 (27%)	5 (0%)
3	L5	3705/5070 (73%)	877 (23%)	22 (0%)
4	L7	119/120 (99%)	14 (11%)	0
5	L8	155/156 (99%)	29 (18%)	0
85	Et	73/75 (97%)	55 (75%)	0
All	All	5769/7290 (79%)	1442 (24%)	27 (0%)

5 of 1442 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	S2	4	C
2	S2	13	C
2	S2	14	C
2	S2	17	C
2	S2	23	G

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	L5	2416	G
3	L5	2760	G
3	L5	4600	G
3	L5	2675	G
3	L5	2786	C

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 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
64	CD	1
49	Lt	1
85	Et	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	CD	225:LEU	C	282:THR	N	57.40
1	Lt	87:GLU	C	104:ILE	N	8.75
1	Et	16:C	O3'	18:U	P	5.31

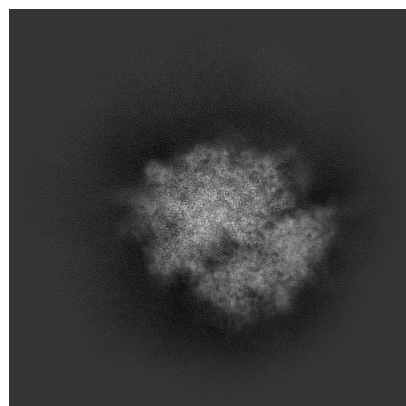
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44039. These allow visual inspection of the internal detail of the map and identification of artifacts.

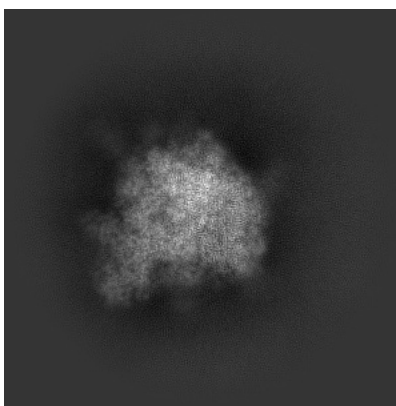
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

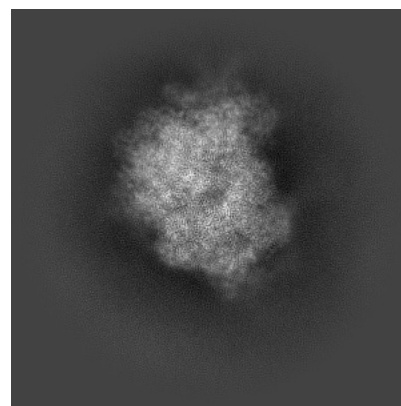
6.1.1 Primary map



X

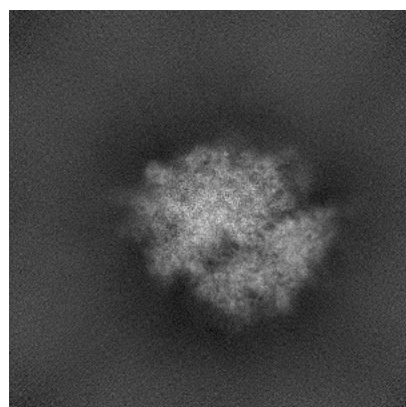


Y

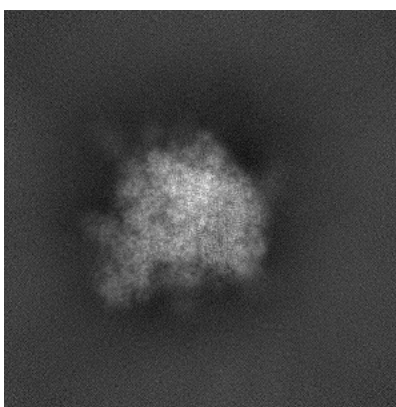


Z

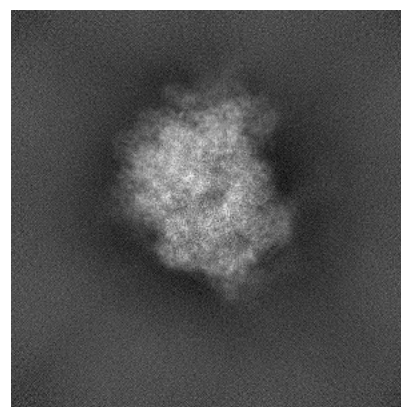
6.1.2 Raw map



X



Y

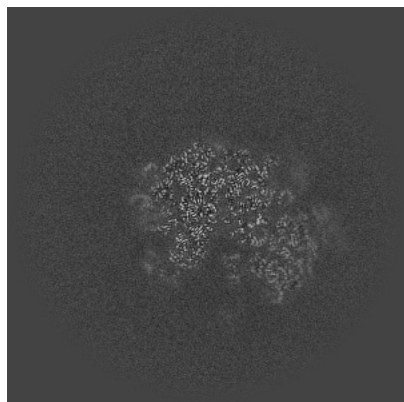


Z

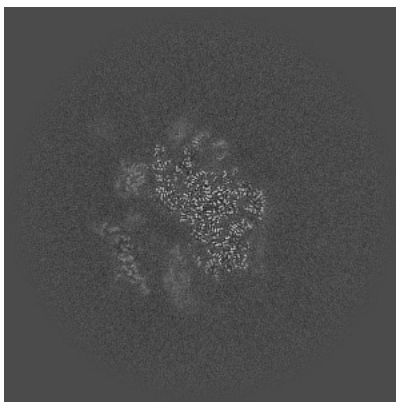
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

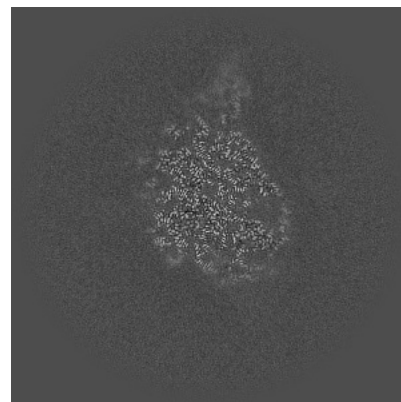
6.2.1 Primary map



X Index: 256

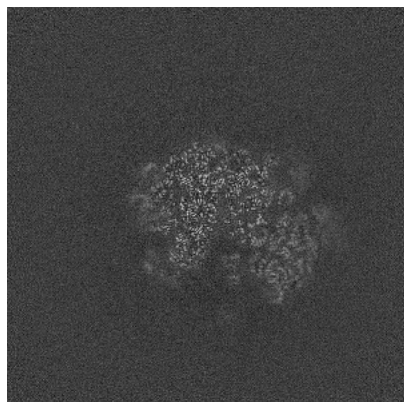


Y Index: 256

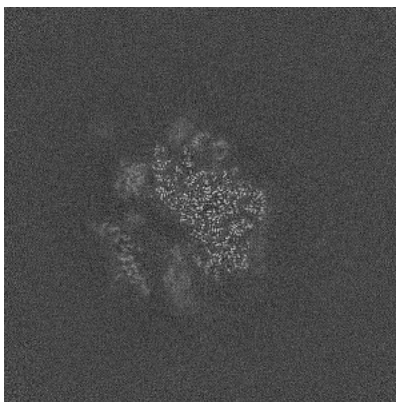


Z Index: 256

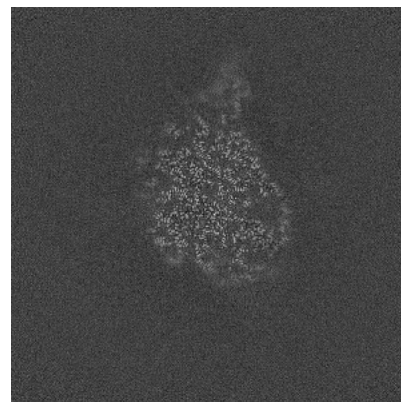
6.2.2 Raw map



X Index: 256



Y Index: 256

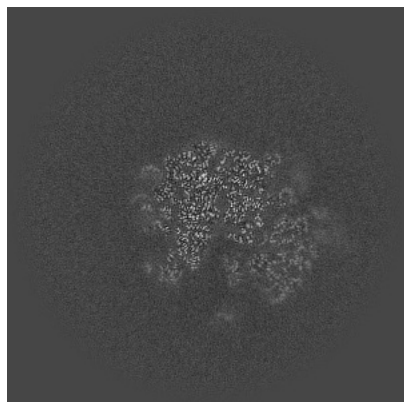


Z Index: 256

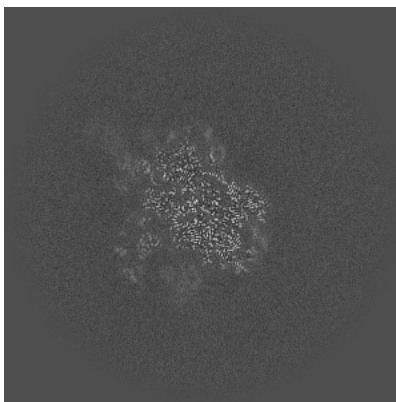
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

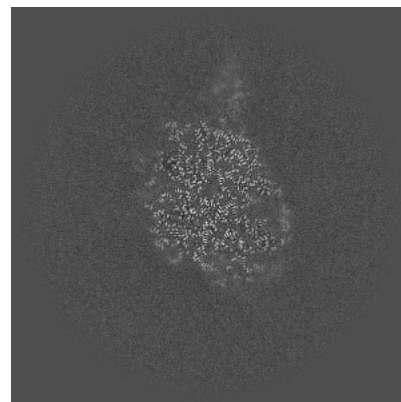
6.3.1 Primary map



X Index: 253

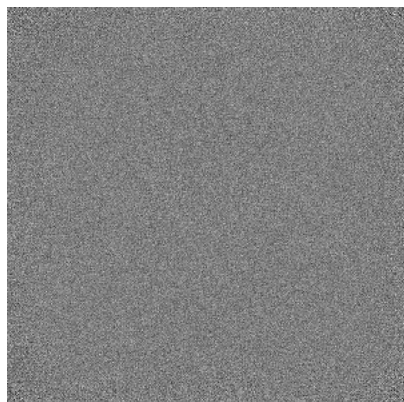


Y Index: 243

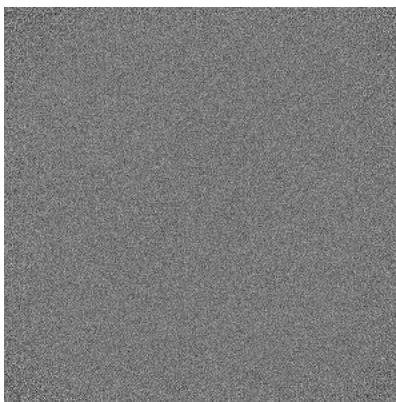


Z Index: 258

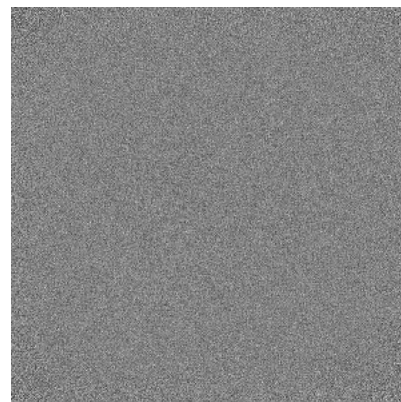
6.3.2 Raw map



X Index: 0



Y Index: 0

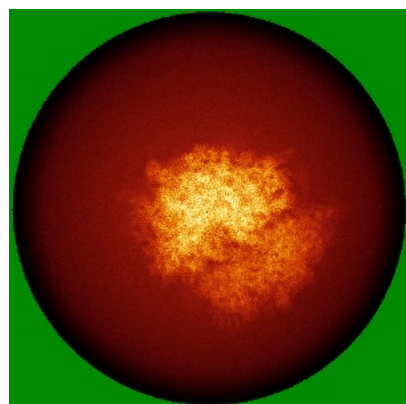


Z Index: 0

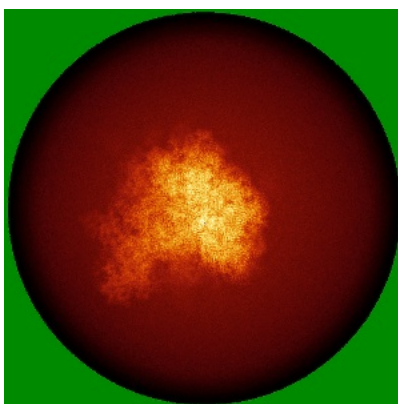
The images above show the largest variance slices of the map in three orthogonal directions.

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

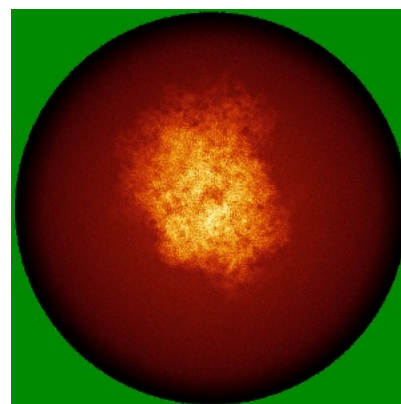
6.4.1 Primary map



X

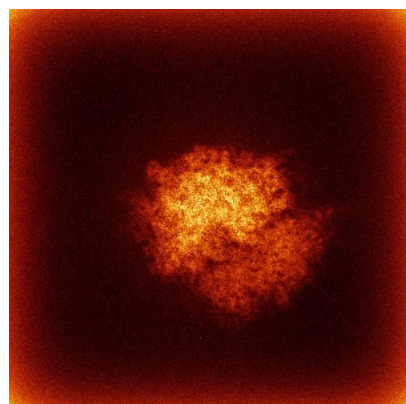


Y

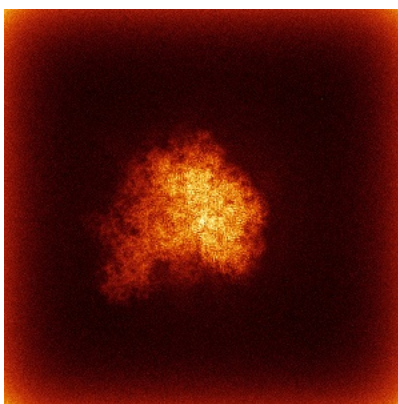


Z

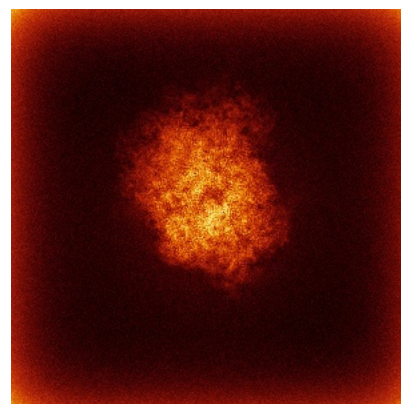
6.4.2 Raw map



X



Y

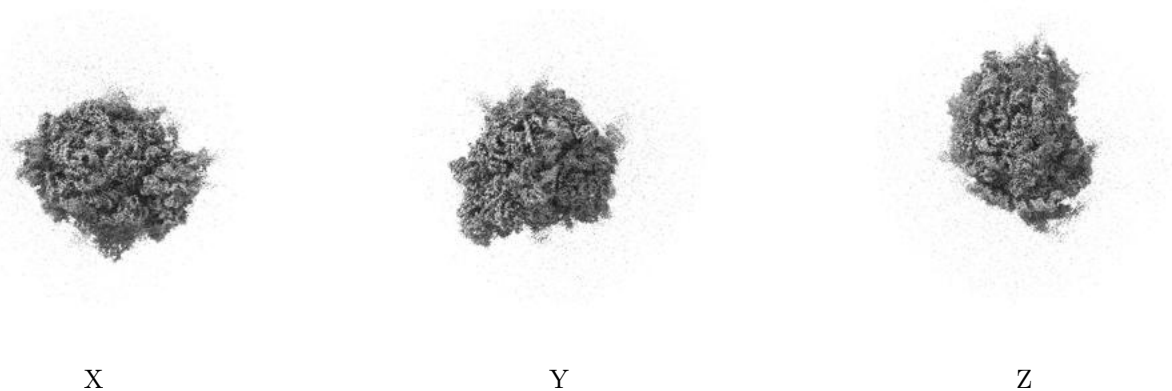


Z

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.

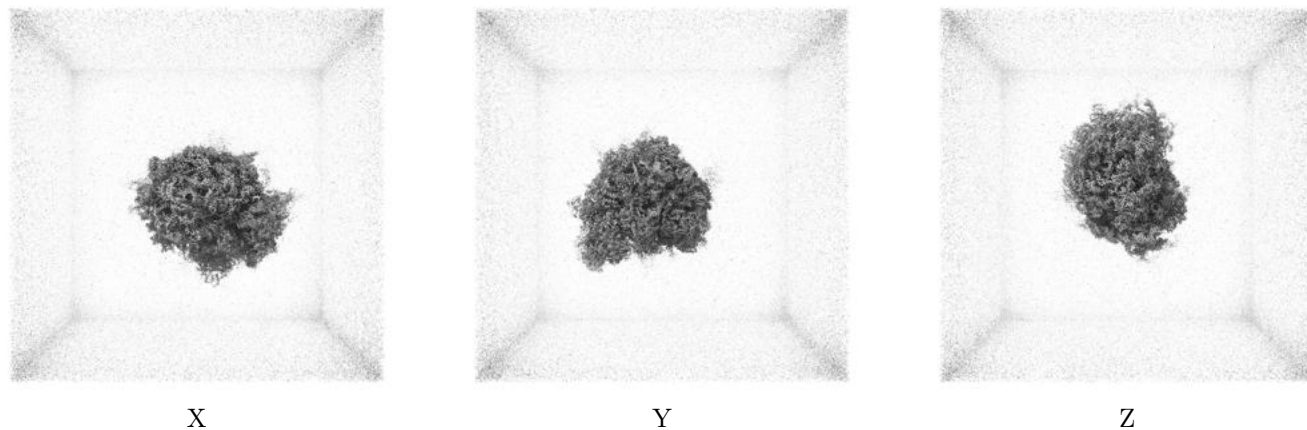
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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.

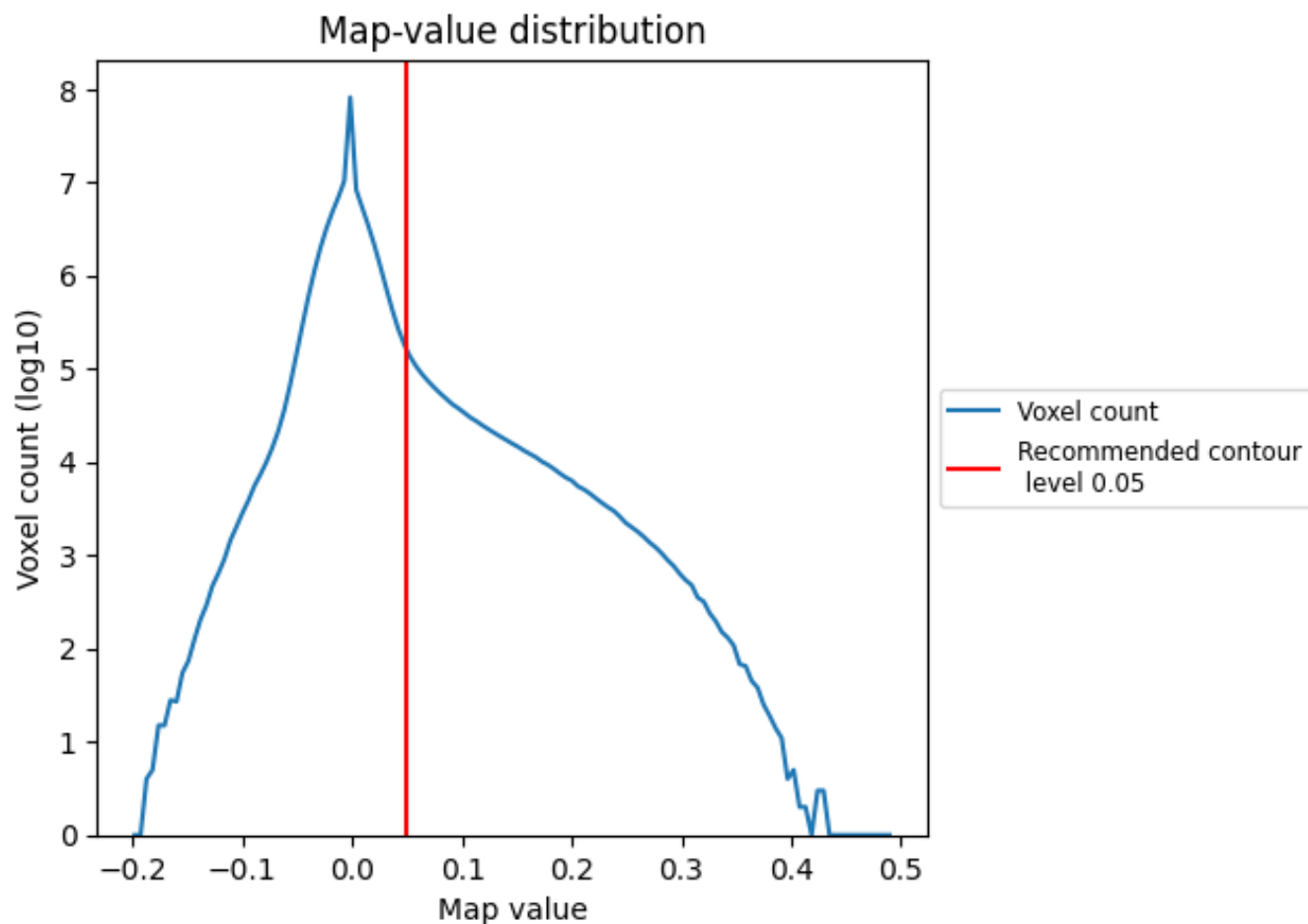
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

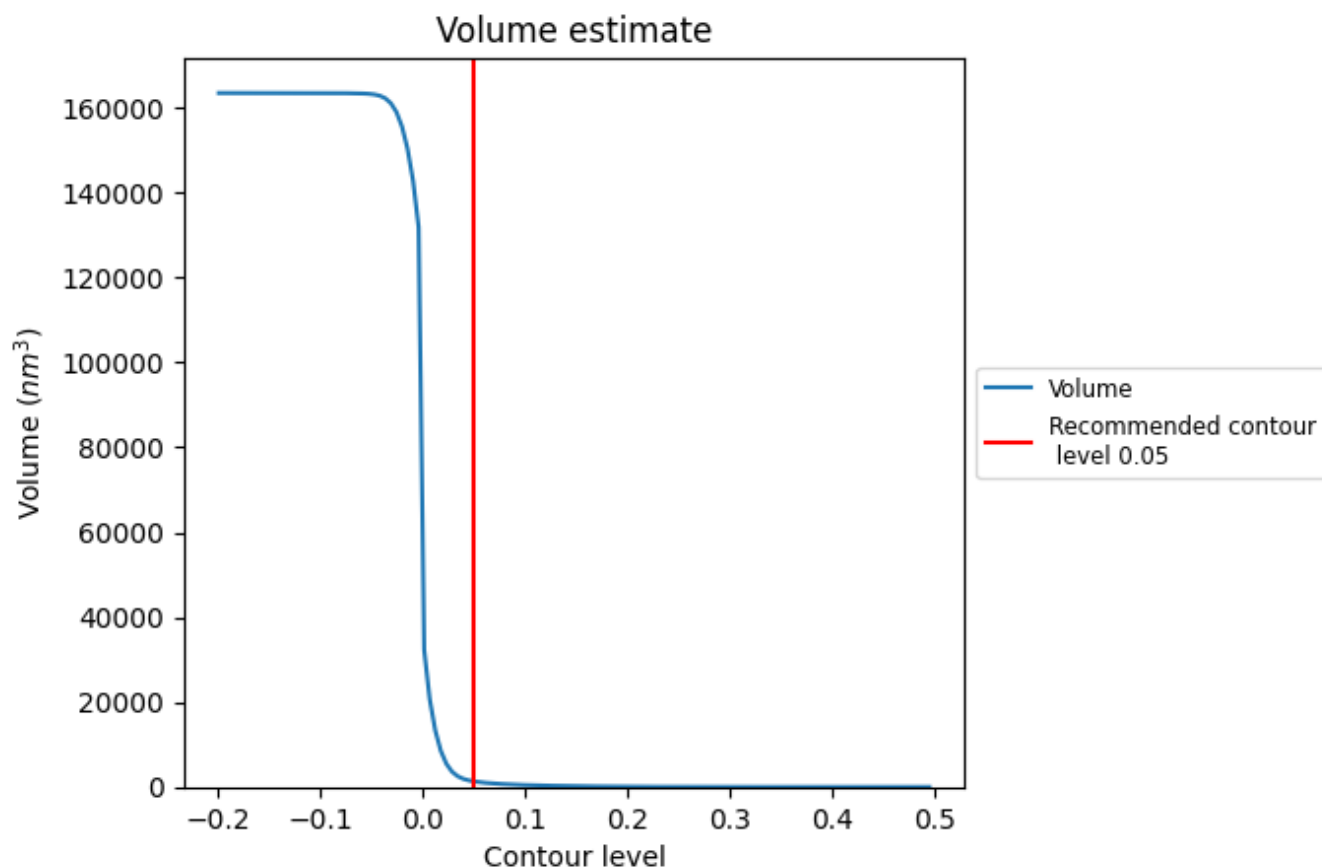
This section contains the results of statistical analysis of the map.

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.

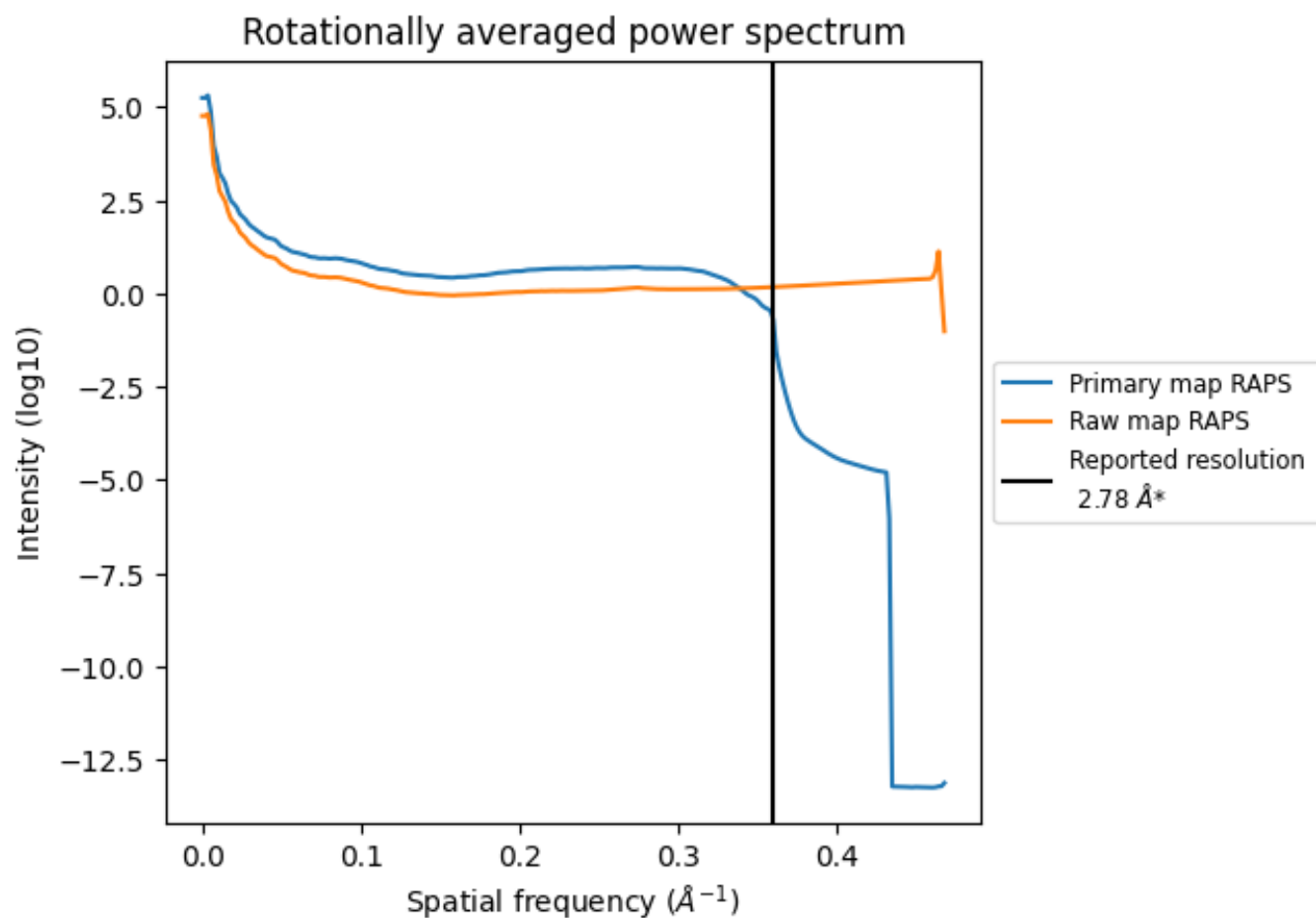
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1337 nm^3 ; this corresponds to an approximate mass of 1207 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 ⓘ

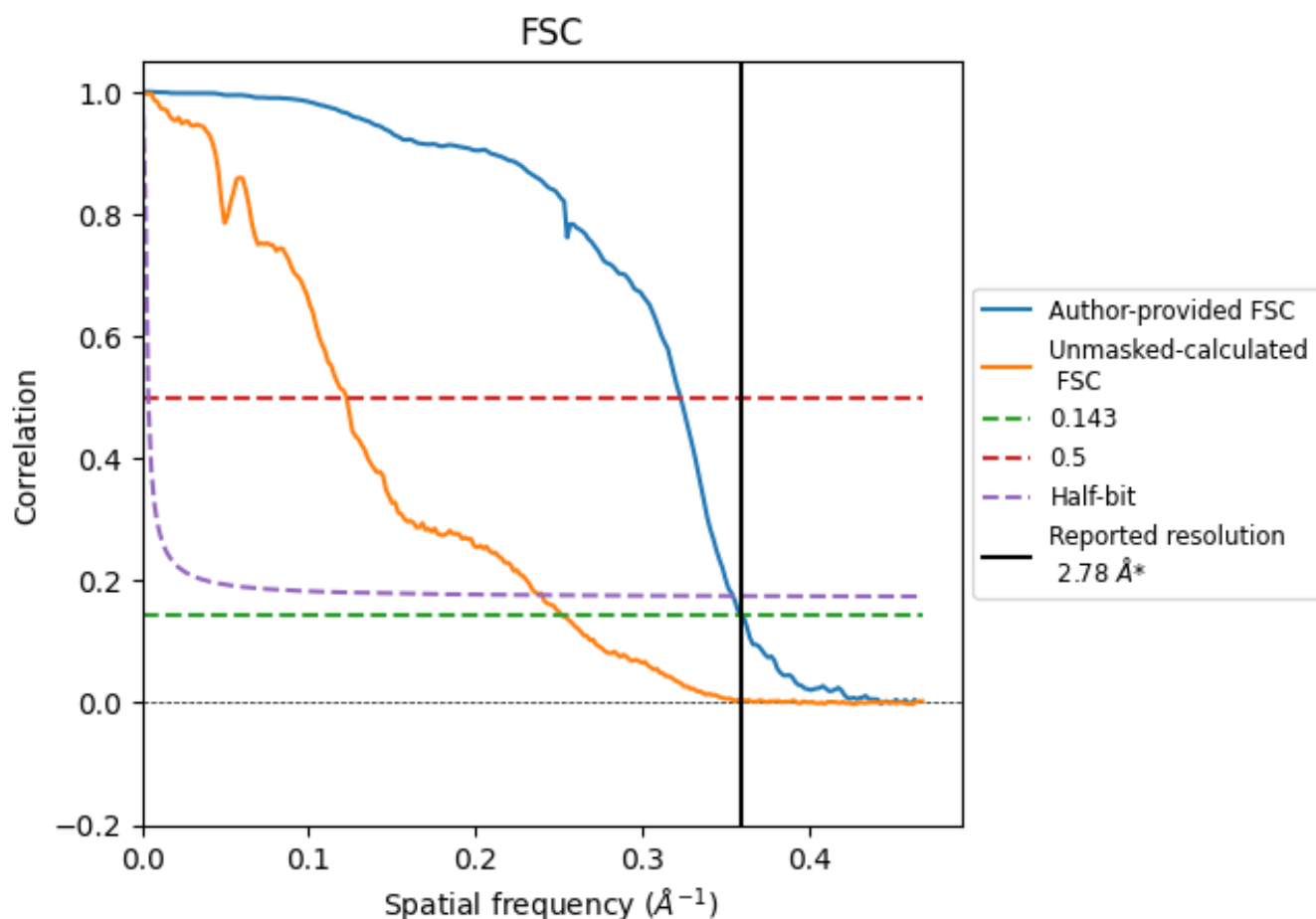


*Reported resolution corresponds to spatial frequency of 0.360 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.360 \AA^{-1}

8.2 Resolution estimates [i](#)

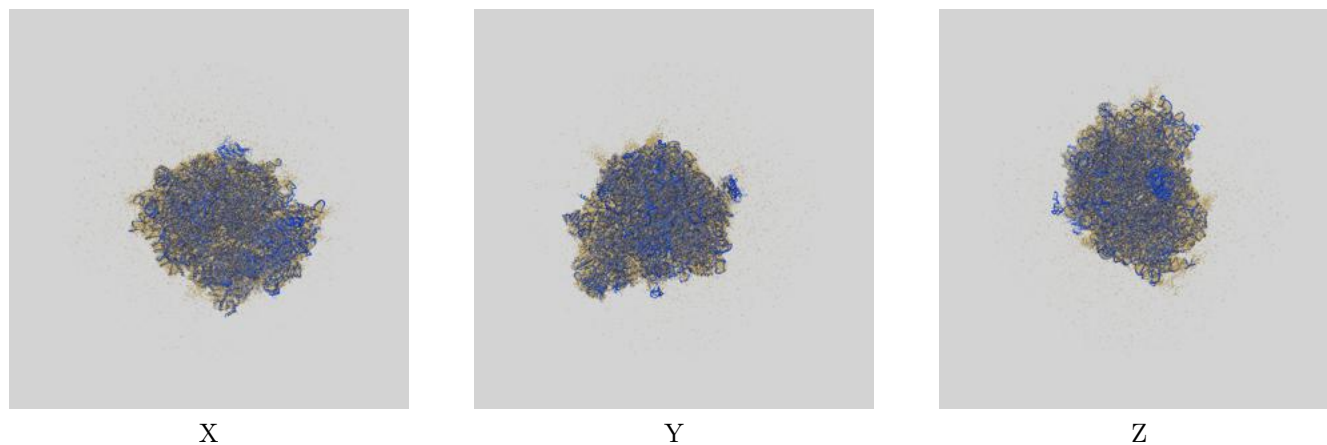
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.78	-	-
Author-provided FSC curve	2.78	3.10	2.82
Unmasked-calculated*	3.97	8.16	4.17

*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 3.97 differs from the reported value 2.78 by more than 10 %

9 Map-model fit [i](#)

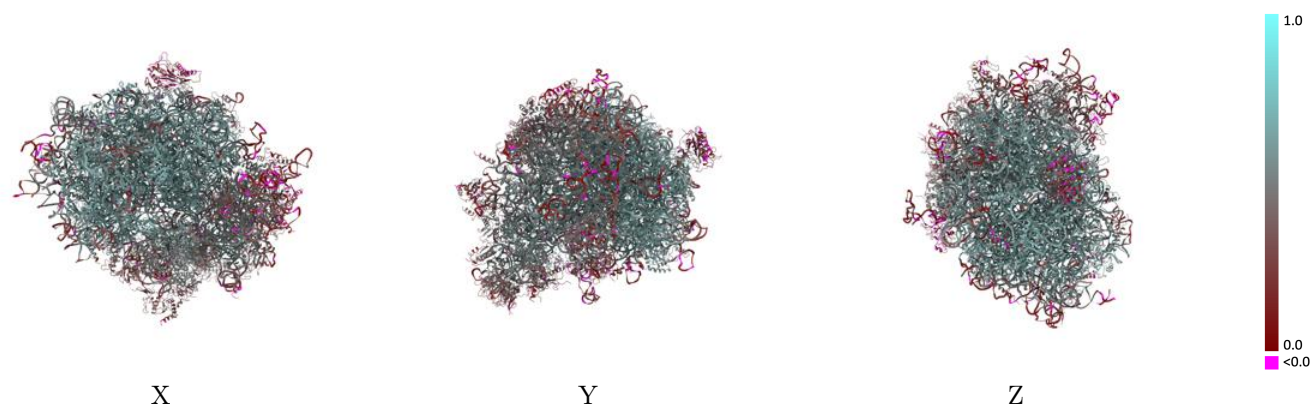
This section contains information regarding the fit between EMDB map EMD-44039 and PDB model 9B0F. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



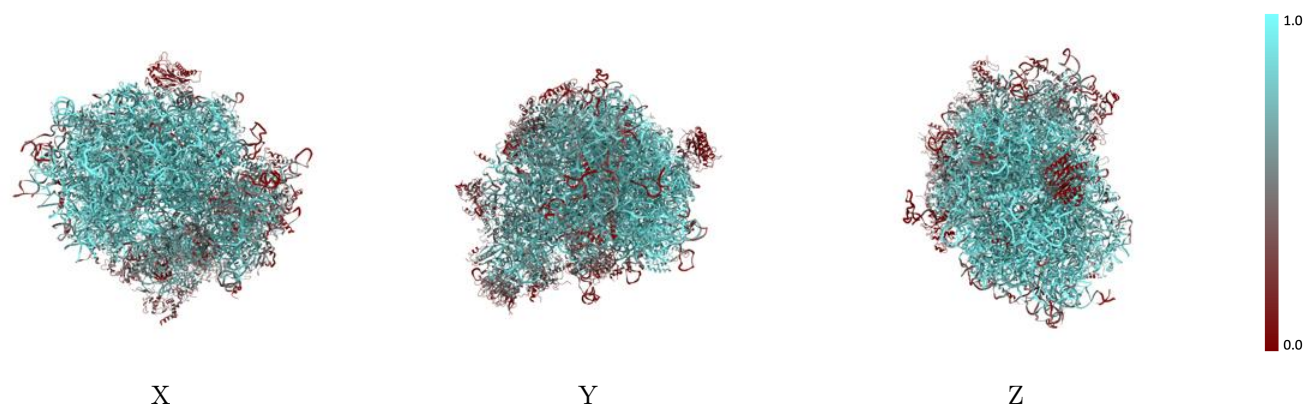
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



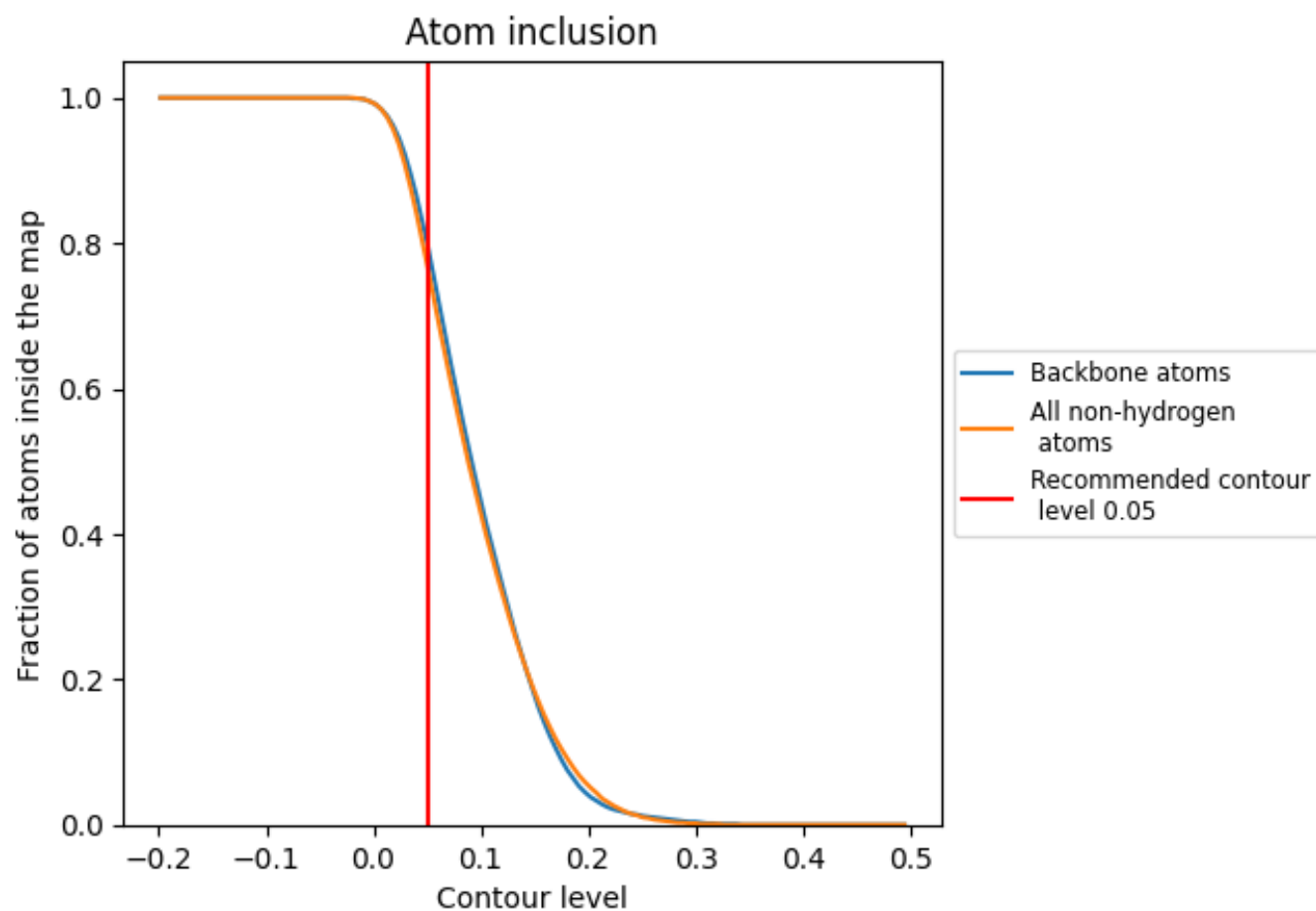
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 77% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7710	 0.5060
CA	 0.1210	 0.2390
CB	 0.5370	 0.4600
CD	 0.5560	 0.4260
Et	 0.2860	 0.1280
L5	 0.8640	 0.5390
L7	 0.9700	 0.6060
L8	 0.9130	 0.5780
LA	 0.9360	 0.6180
LB	 0.8900	 0.6000
LC	 0.8990	 0.6000
LD	 0.8280	 0.5640
LE	 0.7830	 0.5340
LF	 0.9190	 0.6090
LG	 0.7710	 0.5440
LH	 0.8620	 0.5860
LI	 0.8990	 0.6080
LJ	 0.7040	 0.4980
LL	 0.8420	 0.5730
LM	 0.8920	 0.5910
LN	 0.9730	 0.6330
LO	 0.9330	 0.6170
LP	 0.9100	 0.6190
LQ	 0.9410	 0.6280
LR	 0.7920	 0.5500
LS	 0.9340	 0.6170
LT	 0.8700	 0.5870
LU	 0.7010	 0.4780
LV	 0.9040	 0.6130
LW	 0.5590	 0.4080
LX	 0.8540	 0.5920
LY	 0.8900	 0.6010
LZ	 0.8540	 0.5850
La	 0.9260	 0.6240
Lb	 0.7540	 0.5320





















Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Lc	 0.8300	 0.5580
Ld	 0.8590	 0.5900
Le	 0.9410	 0.6240
Lf	 0.9480	 0.6230
Lg	 0.8750	 0.5930
Lh	 0.8650	 0.5930
Li	 0.8420	 0.5800
Lj	 0.9450	 0.6220
Lk	 0.7380	 0.5400
Ll	 0.9170	 0.6120
Lm	 0.8940	 0.6030
Ln	 0.8470	 0.6040
Lo	 0.8650	 0.5950
Lp	 0.8850	 0.6070
Lr	 0.9150	 0.6020
Ls	 0.4300	 0.3790
Lt	 0.1790	 0.2200
Lz	 0.0200	 0.1060
S2	 0.8040	 0.4660
SA	 0.5910	 0.4480
SB	 0.4710	 0.3730
SC	 0.7260	 0.5230
SD	 0.5950	 0.4620
SE	 0.6110	 0.4630
SF	 0.5260	 0.4080
SG	 0.3840	 0.2970
SH	 0.3910	 0.3360
SI	 0.6080	 0.4570
SJ	 0.6760	 0.4860
SK	 0.6000	 0.4470
SL	 0.6760	 0.4820
SM	 0.2480	 0.2830
SN	 0.6630	 0.4910
SO	 0.5580	 0.4210
SP	 0.5990	 0.4670
SQ	 0.5780	 0.4270
SS	 0.5510	 0.4310
ST	 0.5890	 0.4440
SU	 0.5570	 0.4070
SV	 0.6160	 0.4540
SW	 0.7560	 0.5260
SX	 0.7600	 0.5470

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SY	 0.4710	 0.3540
SZ	 0.3720	 0.3280
Sa	 0.6770	 0.4890
Sb	 0.5150	 0.4020
Sc	 0.3830	 0.3300
Sd	 0.7800	 0.5220
Se	 0.5610	 0.4360
Sf	 0.2550	 0.2660
Sg	 0.3670	 0.3560