wwPDB EM Validation Summary Report (i)

Dec 6, 2023 – 06:30 pm GMT

PDB ID	:	7QCA
EMDB ID	:	EMD-13892
Title	:	Spraguea lophii ribosome
Authors	:	Gil Diez, P.; McLaren, M.; Isupov, M.N.; Daum, B.; Conners, R.; Williams, B.
Deposited on	:	2021-11-22
Resolution	:	2.79 Å(reported)
Based on initial model	:	6RM3

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 (i) 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 (i)) were used in the production of this report:

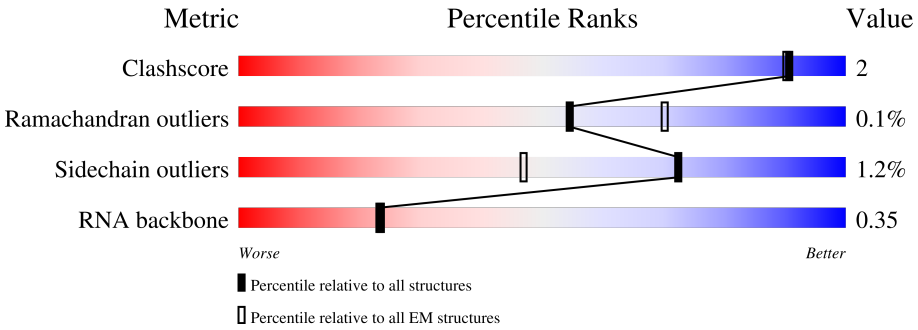
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.79 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.



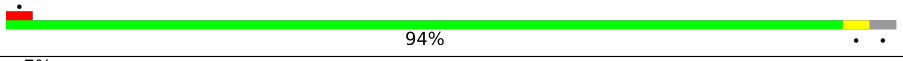
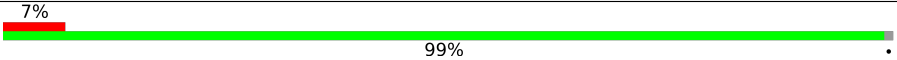
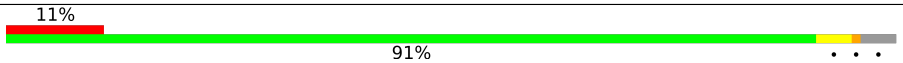
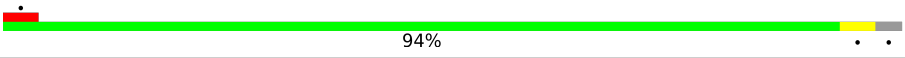
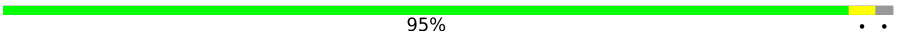
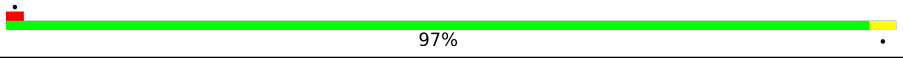
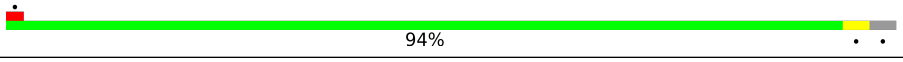
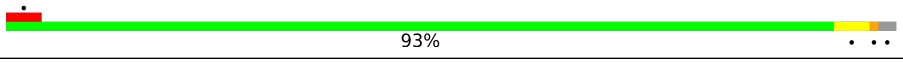
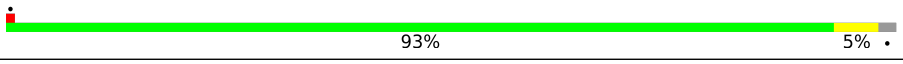
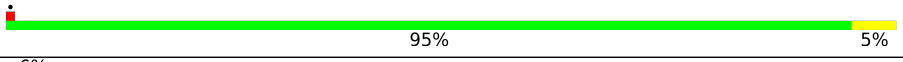
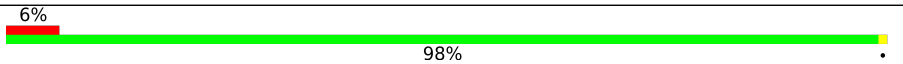
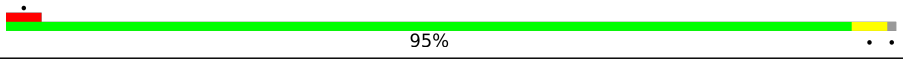
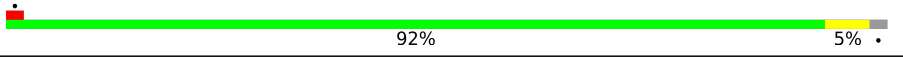
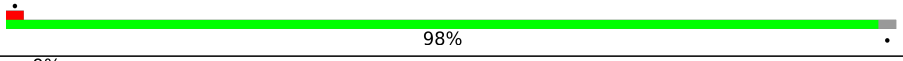
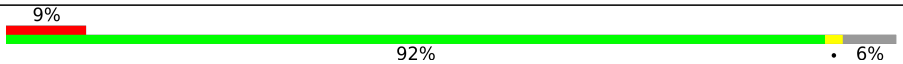
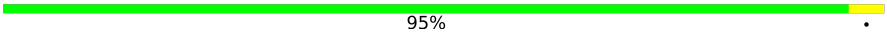
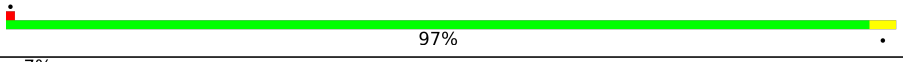
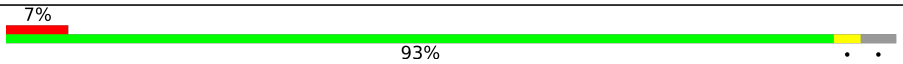
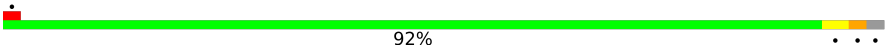
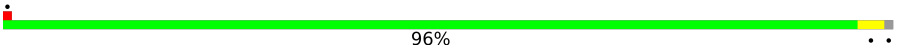
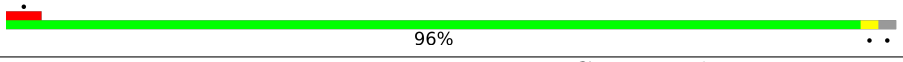
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	L50	2618	62% 29% • 5%
2	L70	119	60% 35% 5%
3	LA0	246	97% •
4	LAA	147	93% 7%
5	LB0	392	94% • •
6	LC0	328	95% • •
7	LCC	110	88% •• 10%

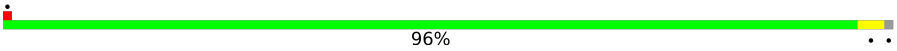
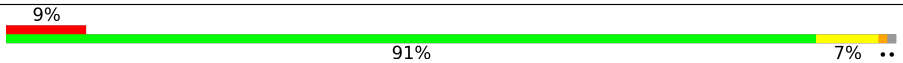
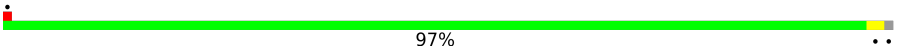
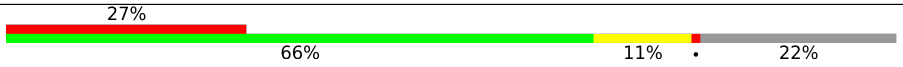
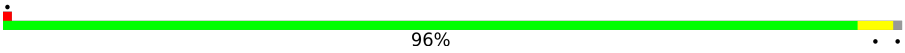
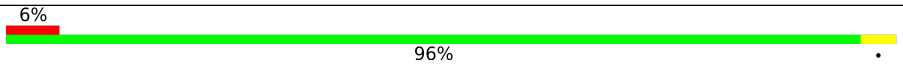
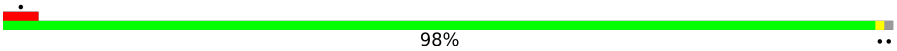
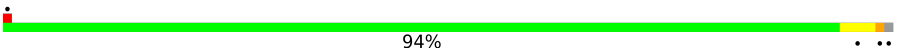
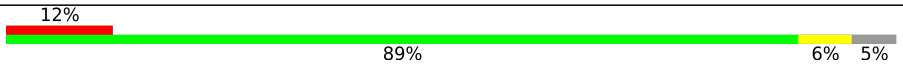
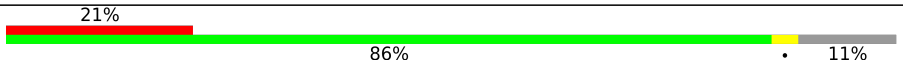
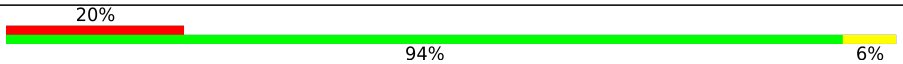
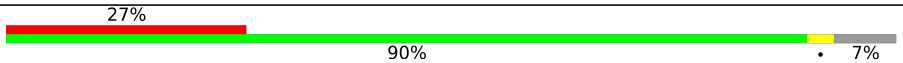
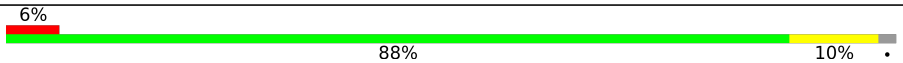
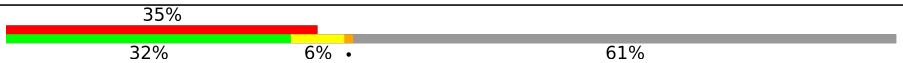
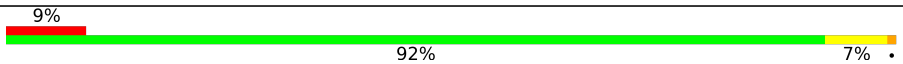
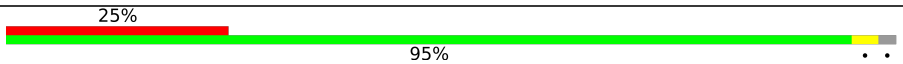
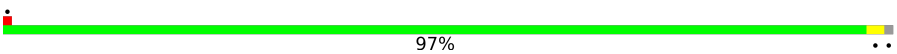
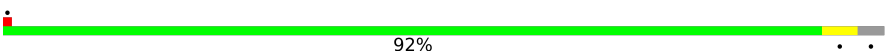
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	LD0	291	
9	LDD	110	
10	LE0	171	
11	LEE	139	
12	LF0	235	
13	LFF	111	
14	LG0	206	
15	LGG	106	
16	LH0	187	
17	LHH	119	
18	LI0	218	
19	LII	98	
20	LJ0	171	
21	LJJ	92	
22	LL0	165	
23	LLL	52	
24	LM0	122	
25	LMM	127	
26	LN0	204	
27	LO0	198	
28	LOO	104	
29	LP0	167	
30	LPP	89	
31	LQ0	183	
32	LR0	168	

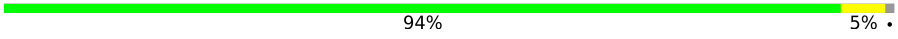
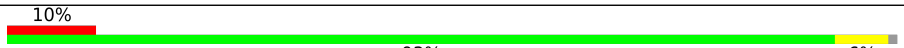
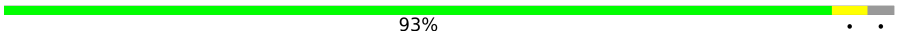
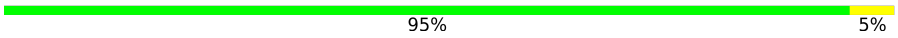
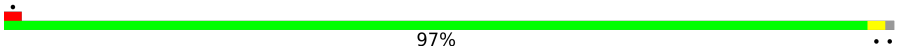
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	LS0	171	
34	LT0	158	
35	LU0	113	
36	LV0	142	
37	LW0	131	
38	LX0	113	
39	LY0	131	
40	LZ0	153	
41	S60	1368	
42	SA0	233	
43	SAA	102	
44	SB0	230	
45	SBB	82	
46	SC0	248	
47	SCC	65	
48	SD0	242	
49	SDD	65	
50	SE0	280	
51	SEE	60	
52	SF0	195	
53	SFF	150	
54	SG0	230	
55	SGG	326	
56	SH0	164	
57	SI0	173	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
58	SJ0	184	
59	SK0	107	
60	SL0	155	
61	SM0	130	
62	SN0	143	
63	SO0	135	
64	SP0	163	
65	SQ0	143	
66	SR0	120	
67	SS0	160	
68	ST0	143	
69	SU0	119	
70	SV0	67	
71	SW0	128	
72	SX0	141	
73	SY0	146	
74	SZ0	128	

2 Entry composition (i)

There are 77 unique types of molecules in this entry. The entry contains 171001 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 RNA 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	L50	2499	53655	23950	9876	17330	2499	0	0

- Molecule 2 is a RNA chain called RNA 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	L70	119	2542	1136	459	828	119	0	0

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	LA0	245	1889	1189	361	334	5	0	0

- Molecule 4 is a protein called uL15 LAA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	LAA	147	1167	738	229	194	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LB0	383	3039	1926	559	543	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	LC0	327	2604	1629	478	485	12	0	0

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		

- Molecule 9 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

- Molecule 11 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		

- Molecule 12 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		

- Molecule 13 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		

- Molecule 14 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG0	199	Total	C	N	O	S	0	0
			1590	1015	275	290	10		

- Molecule 15 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LGG	104	Total	C	N	O	S	0	0
			819	504	169	139	7		

- Molecule 16 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		

- Molecule 17 is a protein called Ribosomal L29 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LHH	119	Total	C	N	O	S	0	0
			992	626	188	175	3		

- Molecule 18 is a protein called S60 ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		

- Molecule 19 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		

- Molecule 20 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		

- Molecule 21 is a protein called eL37 LJJ.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		

- Molecule 22 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		

- Molecule 23 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		

- Molecule 24 is a protein called eL14 LM0.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		

- Molecule 25 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		

- Molecule 26 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

- Molecule 27 is a protein called Ribosomal protein L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		

- Molecule 28 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		

- Molecule 29 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		

- Molecule 30 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		

- Molecule 31 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		

- Molecule 32 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		

- Molecule 33 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		

- Molecule 34 is a protein called 60s ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		

- Molecule 35 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		

- Molecule 36 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		

- Molecule 37 is a protein called Ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		

- Molecule 38 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		

- Molecule 39 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		

- Molecule 40 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		

- Molecule 41 is a RNA chain called RNA SSU.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S60	1354	Total	C	N	O	P	0	0
			29181	13024	5463	9340	1354		

- Molecule 42 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	SA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		

- Molecule 43 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		

- Molecule 44 is a protein called eS1 SB0.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SB0	204	Total	C	N	O	S	0	0
			1609	1018	286	298	7		

- Molecule 45 is a protein called eS27 SBB.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		

- Molecule 46 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SC0	226	Total	C	N	O	S	0	0
			1727	1099	300	321	7		

- Molecule 47 is a protein called eS28 SCC.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		

- Molecule 48 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		

- Molecule 49 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		

- Molecule 50 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		

- Molecule 51 is a protein called eS30 SEE.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	SEE	56	Total	C	N	O	0	0
			447	284	89	74		

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		

- Molecule 53 is a protein called Ubiquitin/40s ribosomal protein S27a fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SFF	58	Total	C	N	O	S	0	0
			447	278	81	83	5		

- Molecule 54 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SG0	229	Total	C	N	O	S	0	0
			1835	1178	325	328	4		

- Molecule 55 is a protein called Guanine nucleotide binding protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		

- Molecule 56 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		

- Molecule 57 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		

- Molecule 58 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SJ0	168	Total	C	N	O	S	0	0
			1379	880	252	243	4		

- Molecule 59 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SK0	91	Total	C	N	O	S	0	0
			764	490	130	140	4		

- Molecule 60 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SL0	150	Total	C	N	O	S	0	0
			1229	790	217	216	6		

- Molecule 61 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		

- Molecule 62 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		

- Molecule 63 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SO0	129	Total 983	C 606	N 191	O 183	S 3	0	0

- Molecule 64 is a protein called Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SP0	117	Total 950	C 598	N 172	O 173	S 7	0	0

- Molecule 65 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SQ0	142	Total 1143	C 726	N 204	O 207	S 6	0	0

- Molecule 66 is a protein called eS17 SR0.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR0	119	Total 977	C 616	N 172	O 186	S 3	0	0

- Molecule 67 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS0	144	Total 1150	C 720	N 220	O 207	S 3	0	0

- Molecule 68 is a protein called 40S Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ST0	142	Total 1161	C 741	N 208	O 211	S 1	0	0

- Molecule 69 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SU0	100	Total 809	C 515	N 144	O 143	S 7	0	0

- Molecule 70 is a protein called Ribosomal protein S21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		

- Molecule 71 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		

- Molecule 72 is a protein called uS12 SX0.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		

- Molecule 73 is a protein called 40s ribosomal protein s24.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		

- Molecule 74 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

- Molecule 75 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
75	L50	145	Total	K	0
			145	145	
75	LA0	2	Total	K	0
			2	2	
75	LEE	1	Total	K	0
			1	1	
75	LLL	1	Total	K	0
			1	1	
75	LN0	1	Total	K	0
			1	1	
75	S60	44	Total	K	0
			44	44	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf
75	SN0	3	Total K 3 3	0
75	SO0	2	Total K 2 2	0

- Molecule 76 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
76	L50	104	Total Mg 104 104	0
76	L70	4	Total Mg 4 4	0
76	LB0	1	Total Mg 1 1	0
76	LF0	1	Total Mg 1 1	0
76	LII	1	Total Mg 1 1	0
76	LJJ	1	Total Mg 1 1	0
76	LV0	1	Total Mg 1 1	0
76	S60	46	Total Mg 46 46	0
76	SI0	1	Total Mg 1 1	0

- Molecule 77 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
77	LGG	1	Total Zn 1 1	0
77	LJJ	1	Total Zn 1 1	0
77	LMM	1	Total Zn 1 1	0
77	LOO	1	Total Zn 1 1	0
77	LPP	1	Total Zn 1 1	0
77	SAA	1	Total Zn 1 1	0

Continued on next page...

Continued from previous page...

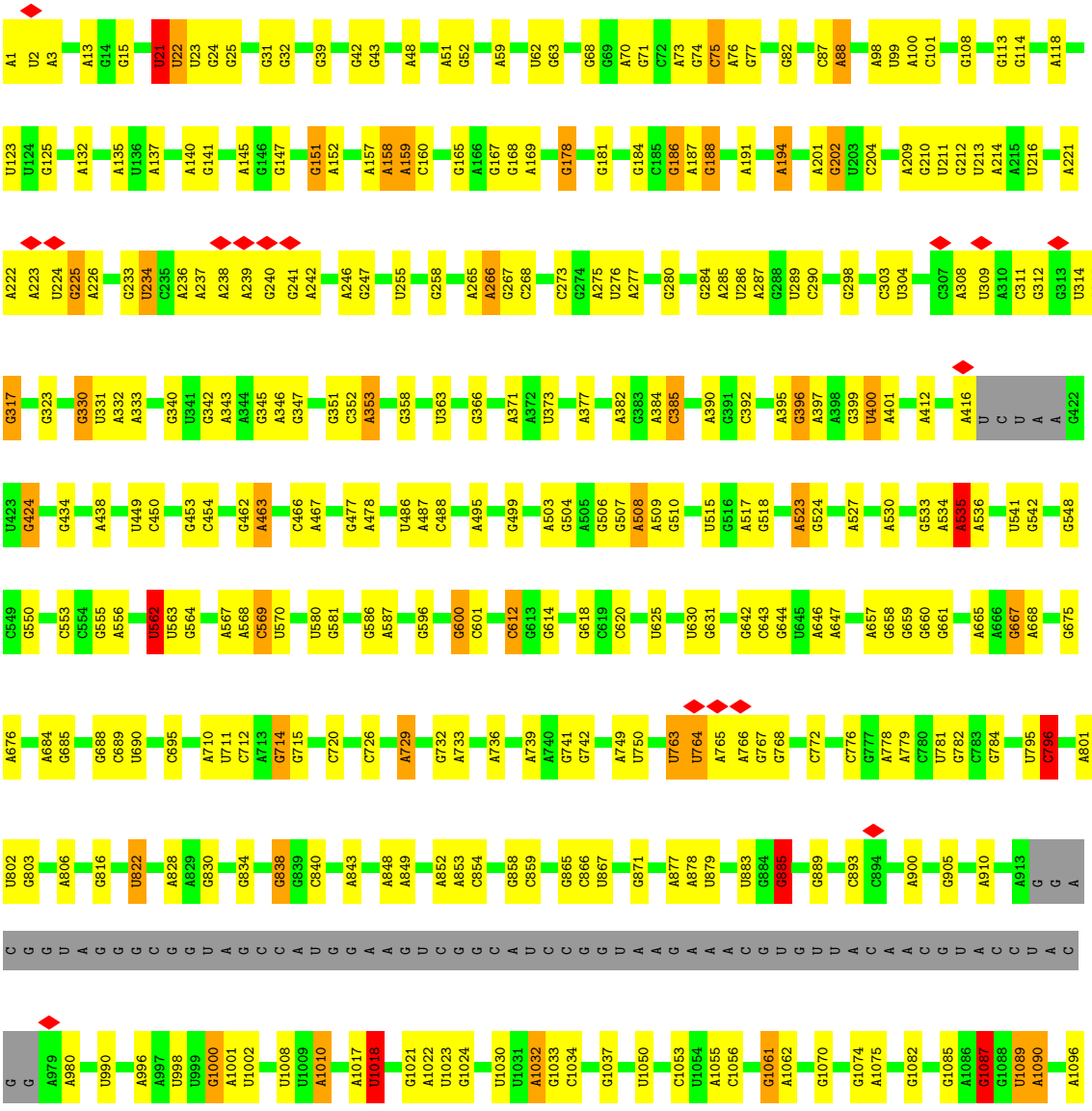
Mol	Chain	Residues	Atoms	AltConf
77	SBB	1	Total Zn 1 1	0
77	SDD	1	Total Zn 1 1	0
77	SFF	1	Total Zn 1 1	0

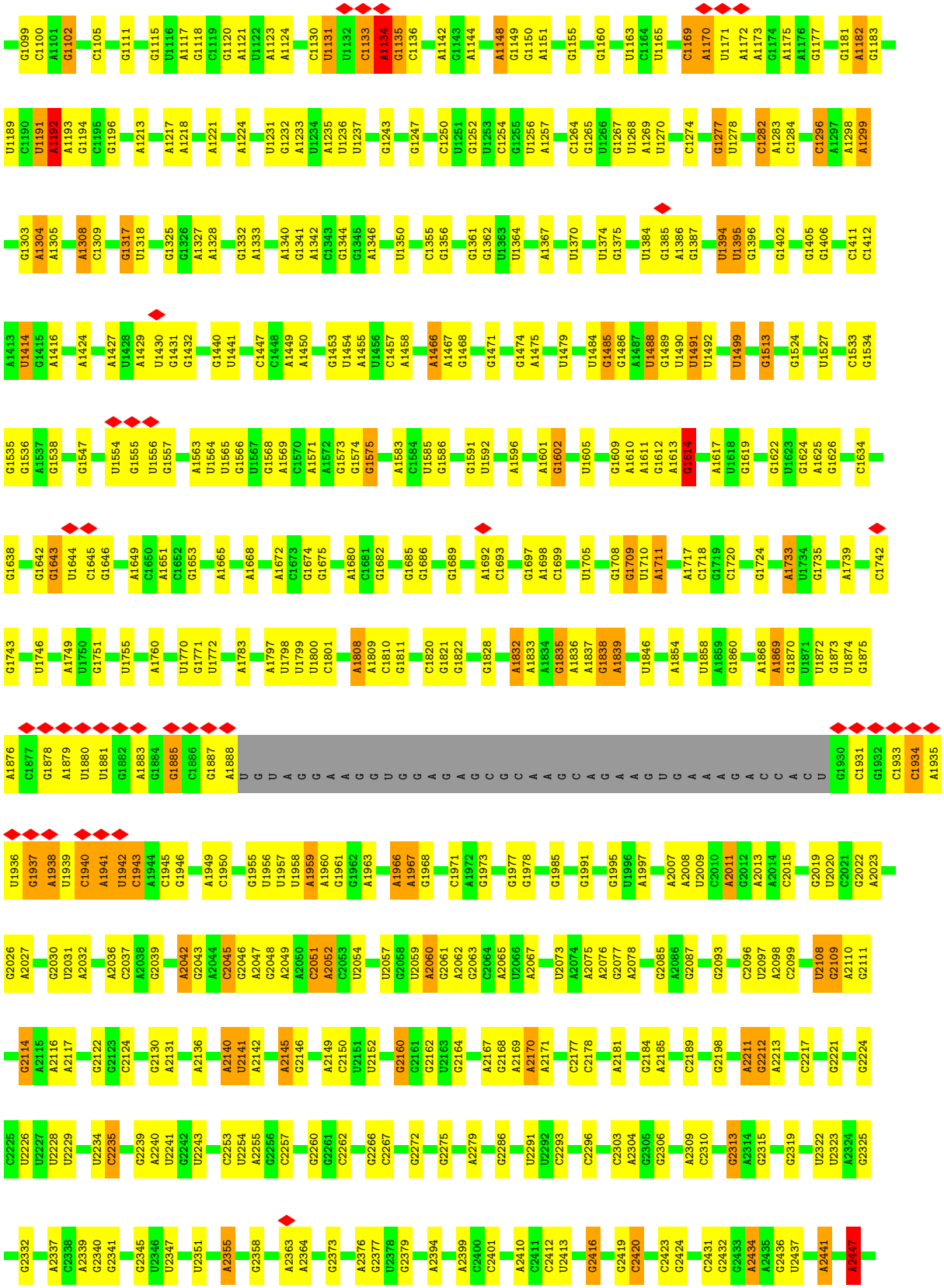
3 Residue-property plots (i)

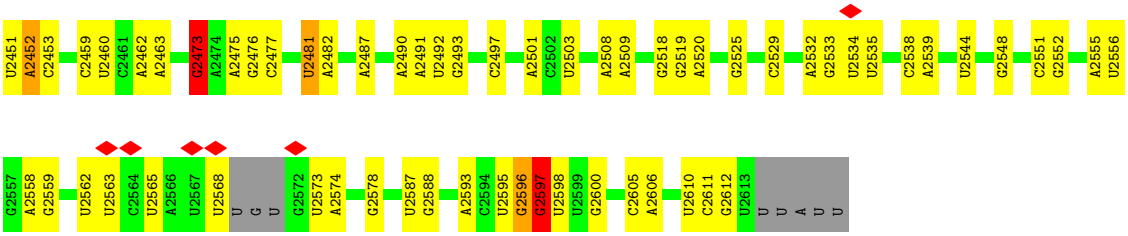
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: RNA 23S

Chain L50:

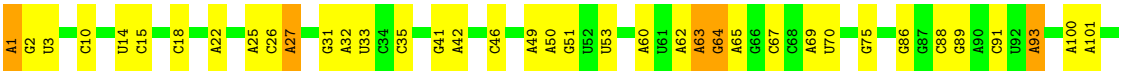


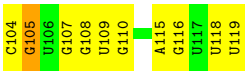

G1099 C1100 A1101 G1102 C1105 G1111 G1115 U1116 A1117 G1118 C1119 G1120 A1121 U1122 A1123 A1124 C1130 U1131 U1132 C1133 A1134 G1135 C1136 A1142 G1143 A1144 A1148 G1149 G1150 A1151 G1155 G1160 U1163 C1164 U1165 C1169 A1170 U1171 A1172 A1173 G1174 A1175 A1176 G1177 G1181 A1182 G1183
U1189 C1190 U1191 A1192 A1193 G1194 C1195 G1196 A1213 A1217 A1218 A1221 A1224 U1231 G1232 A1233 U1234 A1235 U1236 U1237 G1243 G1247 C1250 U1251 G1252 U1253 C1254 G1255 U1256 A1257 C1264 G1265 U1266 G1267 U1268 A1269 U1270 C1274 G1277 U1278 C1282 A1283 C1284 C1296 A1297 A1298 A1299
G1303 A1304 A1305 A1308 C1309 G1317 U1318 G1325 G1326 A1327 A1328 G1332 A1333 A1340 G1341 A1342 C1343 G1344 G1345 A1346 U1350 C1355 G1356 G1361 G1362 U1363 U1364 A1367 U1370 U1374 G1375 U1384 G1385 A1386 G1387 U1394 U1395 G1396 G1402 G1405 G1406 C1411 C1412
A1413 U1414 G1415 A1416 A1424 A1427 U1428 A1429 U1430 G1431 G1432 G1440 U1441 C1447 C1448 A1449 A1450 G1453 U1454 A1455 U1456 C1457 A1458 A1466 A1467 G1468 G1471 G1474 A1475 U1479 U1484 G1485 G1486 A1487 U1488 G1489 U1490 U1491 U1492 U1499 G1513 G1524 U1527 C1533 G1534
G1535 G1536 A1537 G1538 G1547 U1554 G1555 U1556 G1557 A1563 U1564 U1565 G1566 U1567 G1568 A1569 C1570 A1571 A1572 G1573 G1574 G1575 A1583 C1584 U1585 G1586 G1591 U1592 A1596 A1601 G1602 U1605 G1609 A1610 A1611 G1612 A1613 G1614 A1617 U1618 G1619 G1622 U1623 G1624 A1625 G1626 C1634
G1638 G1642 G1643 U1644 C1645 G1646 A1649 C1650 A1651 C1652 G1653 A1665 A1668 A1672 C1673 G1674 G1675 A1680 C1681 G1682 G1685 G1686 G1689 A1692 C1693 G1697 A1698 C1699 U1705 G1708 G1709 U1710 A1711 A1717 C1718 G1719 C1720 G1724 A1733 U1734 G1735 A1739 C1742
G1743 U1746 A1749 U1750 G1751 U1755 A1760 U1770 G1771 U1772 A1783 A1797 U1798 U1799 U1800 C1801 A1808 A1809 C1810 G1811 C1820 G1821 G1822 G1828 A1832 A1833 A1834 G1835 A1836 A1837 G1838 A1839 U1846 A1854 U1858 A1859 G1860 A1868 A1869 G1870 U1871 U1872 G1873 U1874 G1875
A1876 C1877 G1878 A1879 U1880 U1881 G1882 A1883 G1884 G1885 C1886 G1887 A1888 U G C U A G G A A G G U G G A G A G C G C A A G C A G A A G U G A A A A G C A C C G1930 C1931 G1932 C1933 C1934 A1935
U1936 G1937 A1938 U1939 C1940 A1941 U1942 C1943 A1944 C1945 G1946 A1949 C1950 G1955 U1956 U1957 U1958 A1959 A1960 G1961 G1962 A1963 A1966 A1967 G1968 C1971 A1972 G1973 G1977 G1978 G1985 G1991 G1995 U1996 A1997 A2007 A2008 U2009 C2010 A2011 G2012 A2013 A2014 C2015 G2019 U2020 C2021 G2022 A2023
G2026 A2027 G2030 U2031 A2032 A2036 C2037 A2038 G2039 A2042 G2043 A2044 C2045 G2046 A2047 G2048 A2049 A2050 C2051 A2052 C2053 U2054 U2057 G2058 U2059 A2060 G2061 A2062 G2063 C2064 A2065 U2066 A2067 U2073 A2074 A2075 A2076 G2077 A2078 G2085 A2086 G2087 G2093 C2096 U2097 A2098 C2099 U2108 G2109 A2110 G2111
G2114 A2115 A2116 A2117 G2122 G2123 C2124 G2130 A2131 A2136 A2140 U2141 A2142 A2145 G2146 A2149 C2150 U2151 U2152 G2160 G2161 G2162 U2163 G2164 A2167 G2168 A2169 A2170 A2171 C2177 C2178 A2181 G2184 A2185 C2189 G2198 A2211 G2212 A2213 C2217 G2221 G2224
C2225 U2226 U2227 U2228 U2229 U2234 C2235 G2239 A2240 U2241 G2242 U2243 C2253 U2254 A2255 G2256 C2257 G2260 G2261 C2262 G2266 C2267 G2272 G2275 A2279 G2286 U2291 U2292 C2293 C2296 C2303 A2304 G2305 G2306 A2309 C2310 G2313 A2314 G2315 G2319 U2322 U2323 A2324 G2325
G2332 A2337 C2338 A2339 G2340 G2341 G2345 U2346 U2347 U2351 A2355 G2358 A2363 A2364 G2373 A2376 G2377 U2378 G2379 A2394 A2399 C2400 C2401 A2410 C2411 C2412 U2413 G2416 G2419 C2420 C2423 G2424 C2431 G2432 G2433 A2434 A2435 G2436 U2437 A2441 A2447



• Molecule 2: RNA 5S

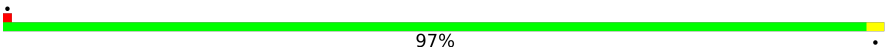
Chain L70:

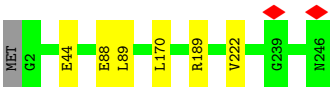




• Molecule 3: 60S ribosomal protein L8

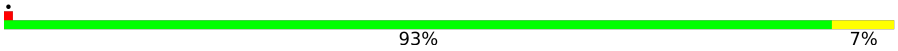
Chain LA0:

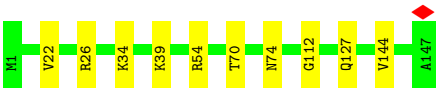




• Molecule 4: uL15 LAA

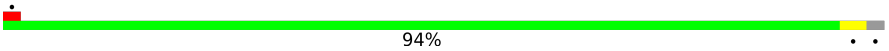
Chain LAA:

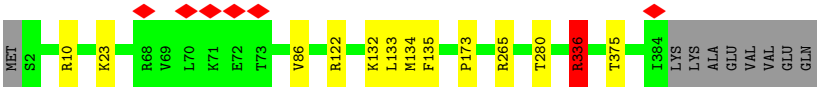




• Molecule 5: 60S ribosomal protein L3

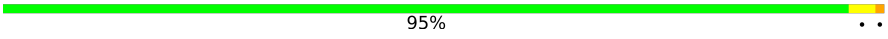
Chain LB0:





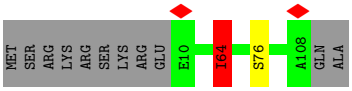
• Molecule 6: 60S ribosomal protein L4

Chain LC0:



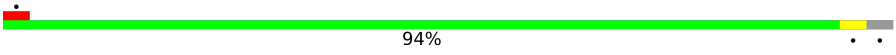
• Molecule 7: 60S ribosomal protein L3

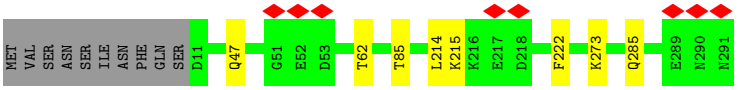
Chain LCC:



• Molecule 8: 60S ribosomal protein L5

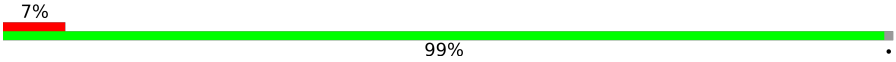
Chain LD0:

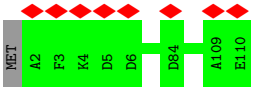




• Molecule 9: 60S ribosomal protein L31

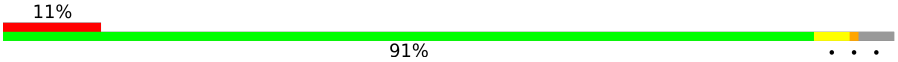
Chain LDD:

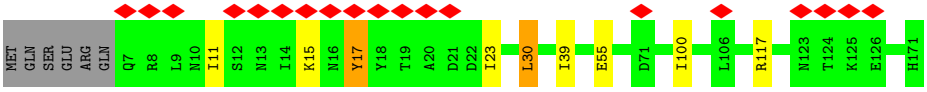




• Molecule 10: 60S ribosomal protein L6

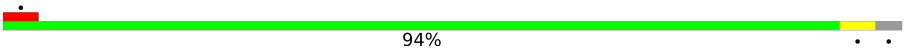
Chain LE0:

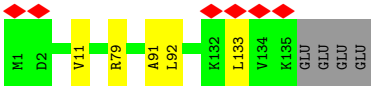




• Molecule 11: 60S ribosomal protein L32

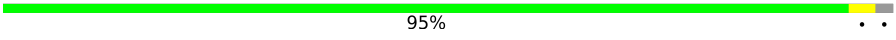
Chain LEE:





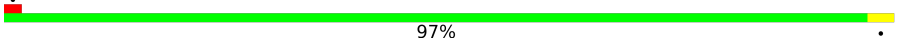
• Molecule 12: 60S ribosomal protein L7

Chain LF0:



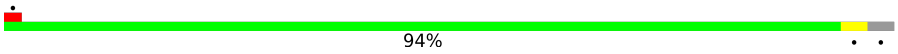
• Molecule 13: 60S ribosomal protein L35a

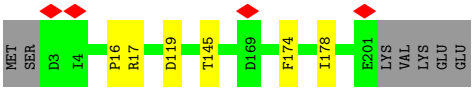
Chain LFF:



• Molecule 14: 60S ribosomal protein L8

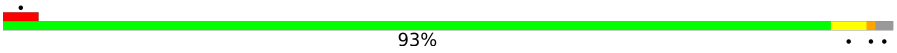
Chain LG0:

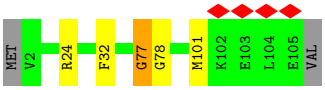




• Molecule 15: Ribosomal protein L34

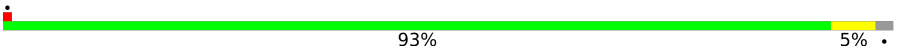
Chain LGG:

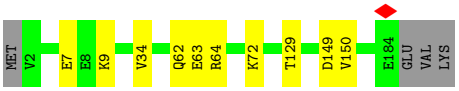




• Molecule 16: 60S ribosomal protein L9

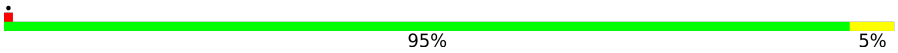
Chain LH0:

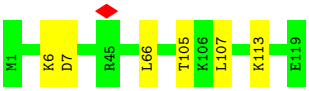




• Molecule 17: Ribosomal L29 protein

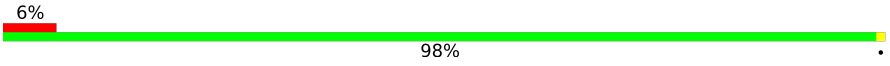
Chain LHH:

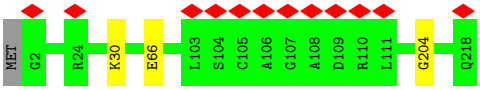




• Molecule 18: S60 ribosomal protein L10

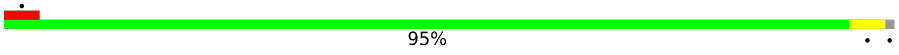
Chain LI0:

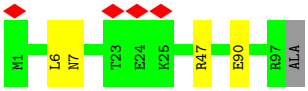




• Molecule 19: 60S ribosomal protein L36

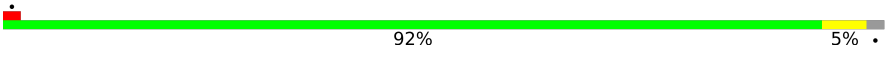
Chain LII:

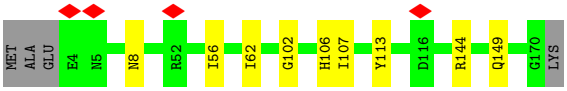




• Molecule 20: 60S ribosomal protein L11

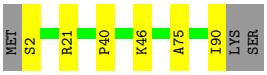
Chain LJ0:





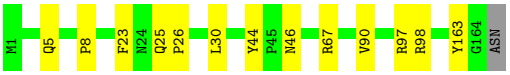
• Molecule 21: eL37 LJJ

Chain LJJ:



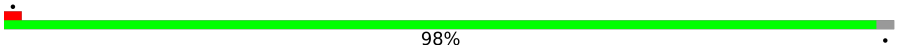
• Molecule 22: 60S ribosomal protein L13

Chain LL0:



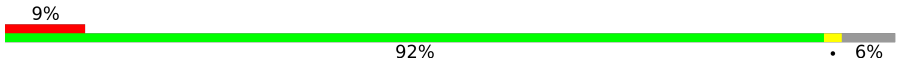
• Molecule 23: 60S ribosomal protein L39

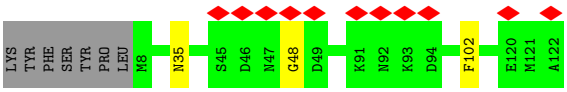
Chain LLL:



• Molecule 24: eL14 LM0

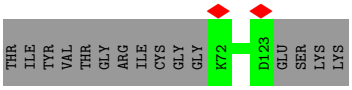
Chain LM0:





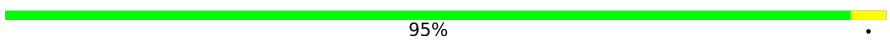
• Molecule 25: Ubiquitin

Chain LMM:



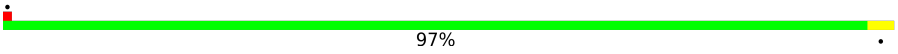
• Molecule 26: Ribosomal protein L15

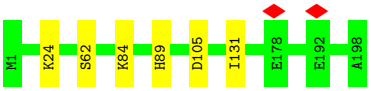
Chain LN0:



• Molecule 27: Ribosomal protein L13A

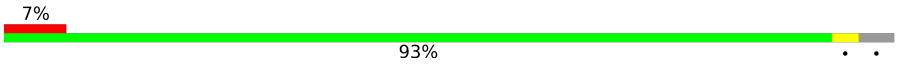
Chain LO0:

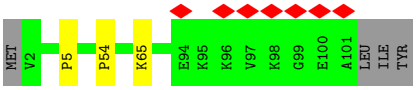




• Molecule 28: 60S ribosomal protein L44

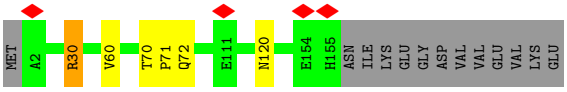
Chain LOO:





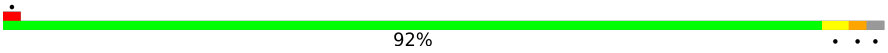
• Molecule 29: 60S ribosomal protein L17

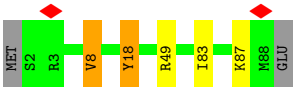
Chain LP0:



• Molecule 30: 60S ribosomal protein L37a

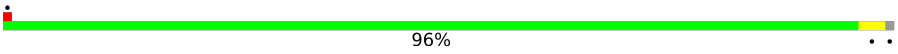
Chain LPP:





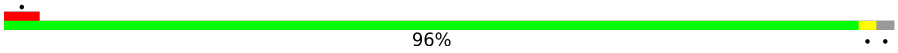
• Molecule 31: 60S ribosomal protein L18

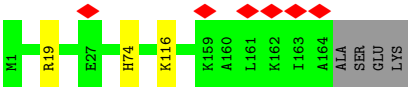
Chain LQ0:



• Molecule 32: 60S ribosomal protein L19

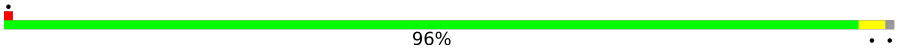
Chain LR0:

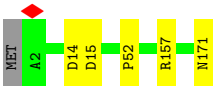




• Molecule 33: 60S ribosomal protein L20

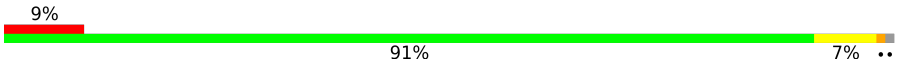
Chain LS0:

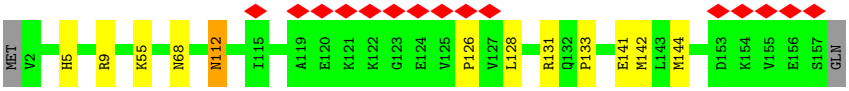




• Molecule 34: 60s ribosomal protein L21

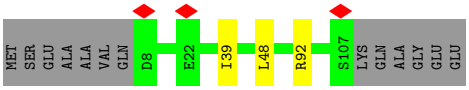
Chain LT0:





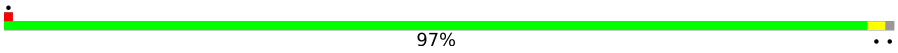
• Molecule 35: 60S ribosomal protein L22

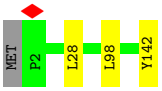
Chain LU0:



• Molecule 36: Ribosomal protein L23

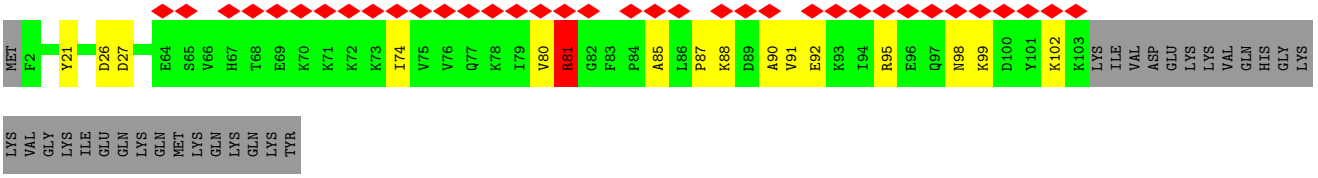
Chain LV0:





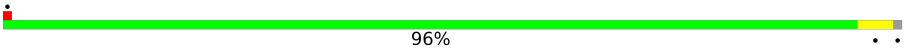
• Molecule 37: Ribosomal protein L24E

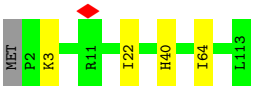
Chain LW0:



• Molecule 38: 60S ribosomal protein L23a

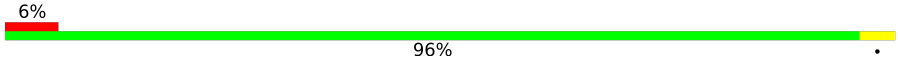
Chain LX0:

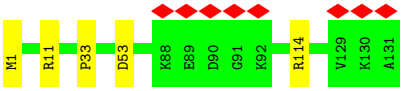




• Molecule 39: 60S ribosomal protein L26

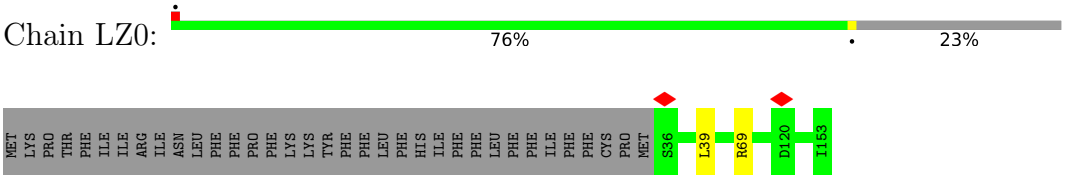
Chain LY0:





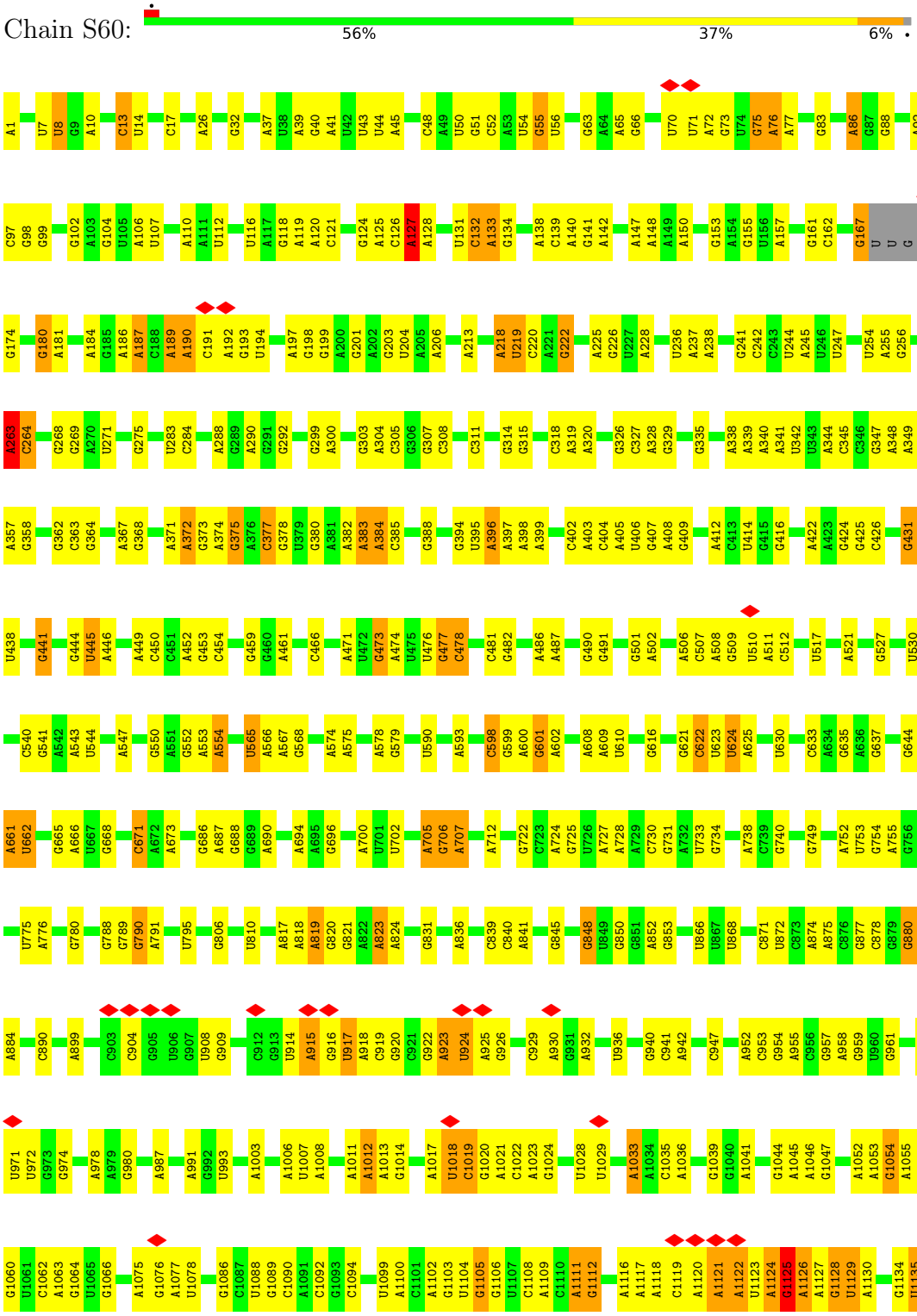
• Molecule 40: 60S ribosomal protein L27

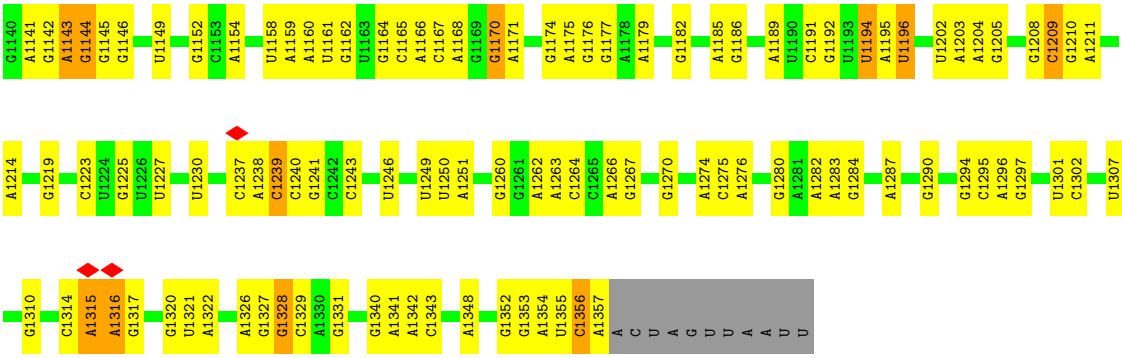
Chain LZ0:



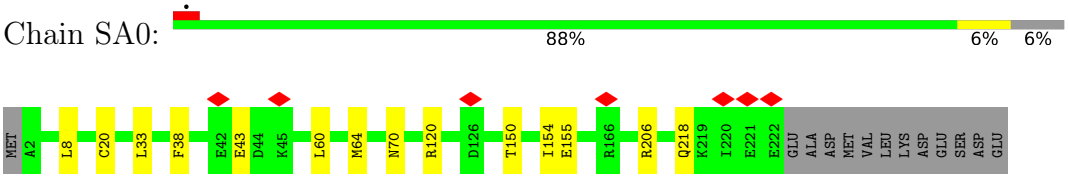
• Molecule 41: RNA SSU

Chain S60:

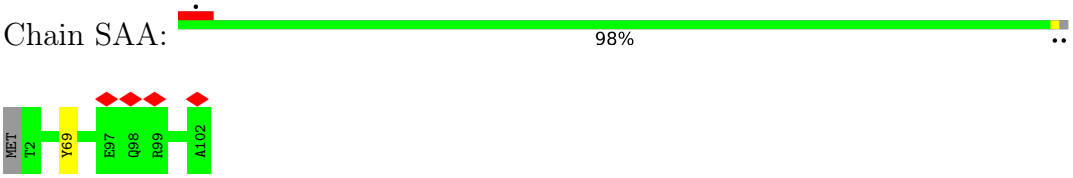




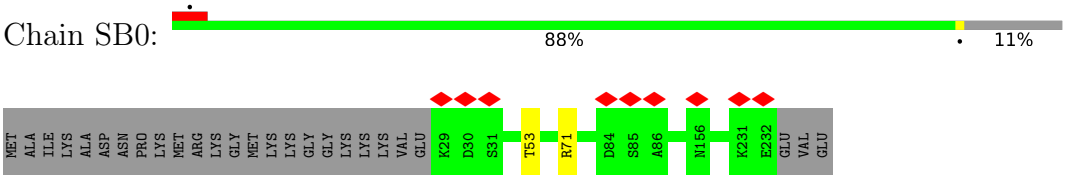
• Molecule 42: 40S ribosomal protein S0



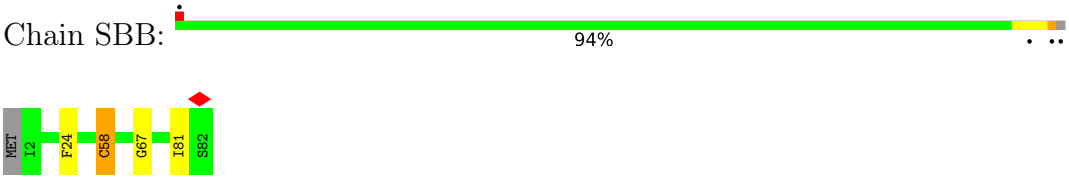
• Molecule 43: 40S ribosomal protein S26



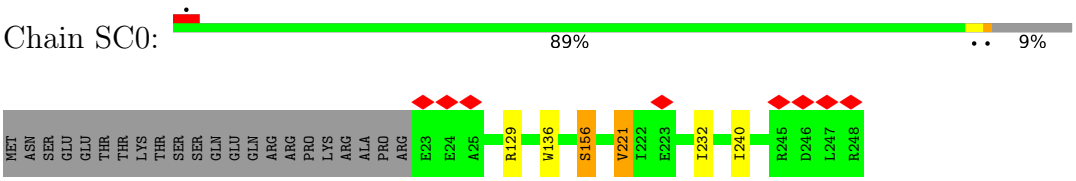
• Molecule 44: eS1 SB0



• Molecule 45: eS27 SBB

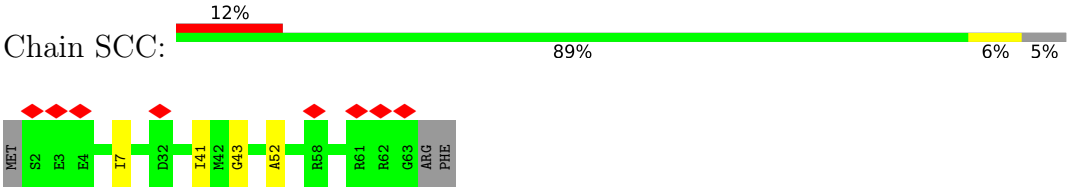


• Molecule 46: 40S ribosomal protein S2



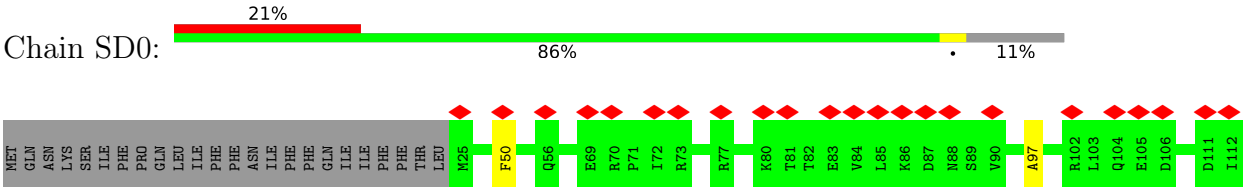
• Molecule 47: eS28 SCC

Chain SCC:



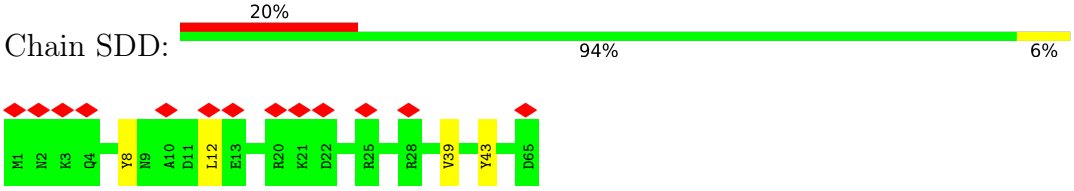
• Molecule 48: 40S ribosomal protein S3

Chain SD0:



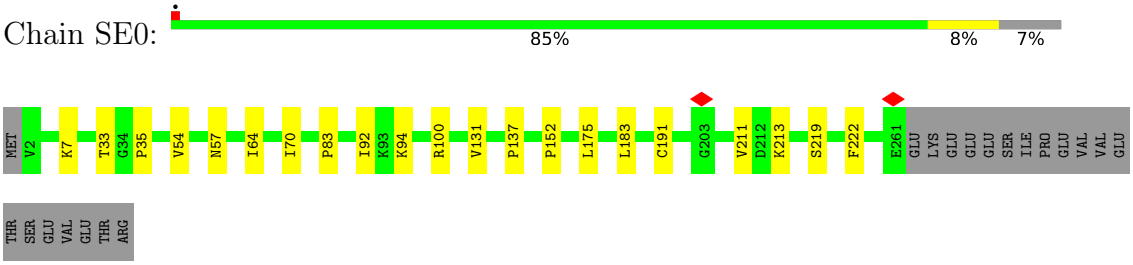
• Molecule 49: 40S ribosomal protein S29

Chain SDD:



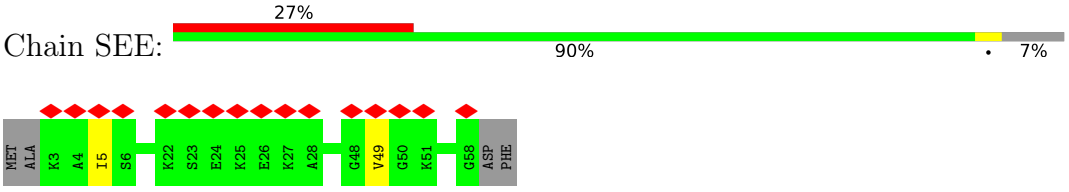
• Molecule 50: 40S ribosomal protein S4

Chain SE0:



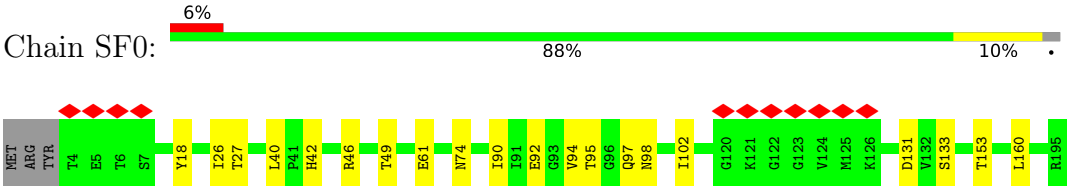
• Molecule 51: eS30 SEE

Chain SEE:



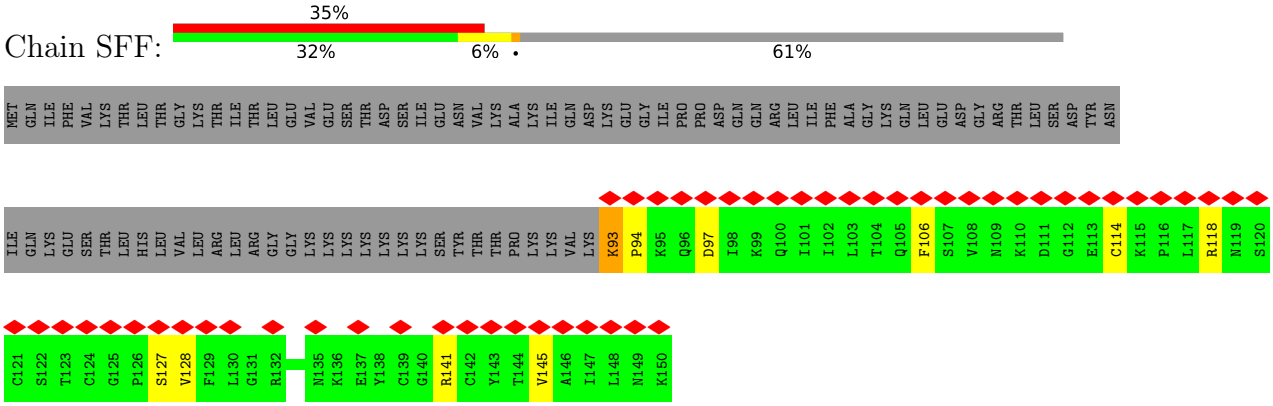
• Molecule 52: 40S ribosomal protein S5

Chain SF0:



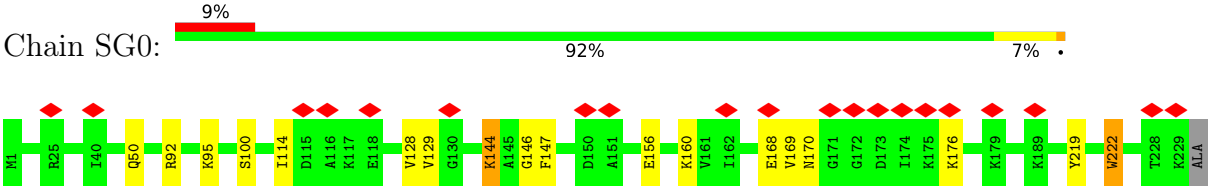
• Molecule 53: Ubiquitin/40s ribosomal protein S27a fusion

Chain SFF:



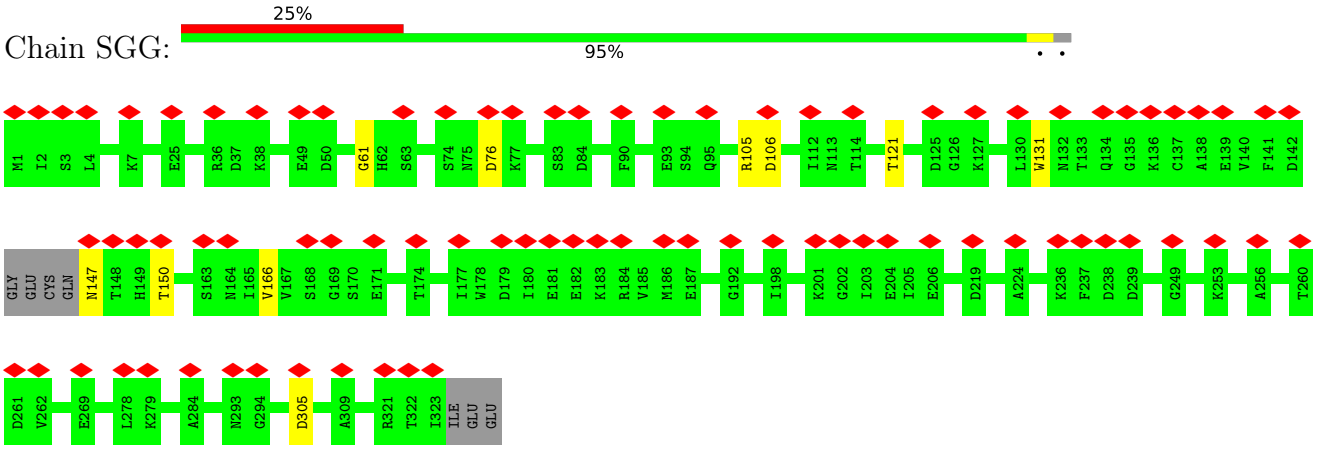
• Molecule 54: 40S ribosomal protein S6

Chain SG0:



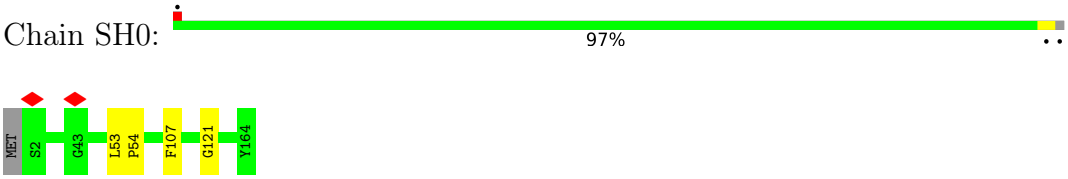
• Molecule 55: Guanine nucleotide binding protein beta subunit

Chain SGG:



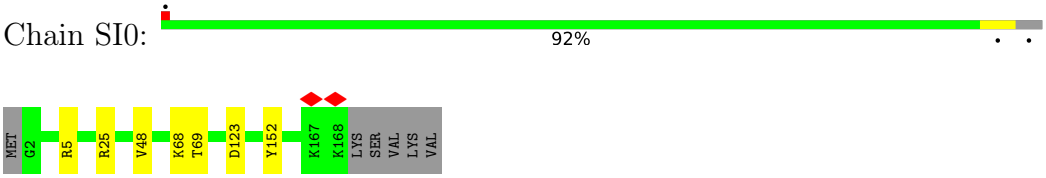
• Molecule 56: 40S ribosomal protein S7

Chain SH0:



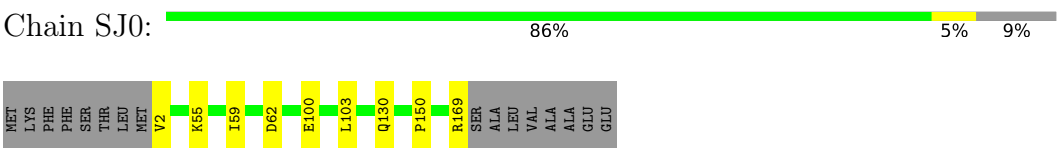
• Molecule 57: 40S ribosomal protein S8

Chain SI0:



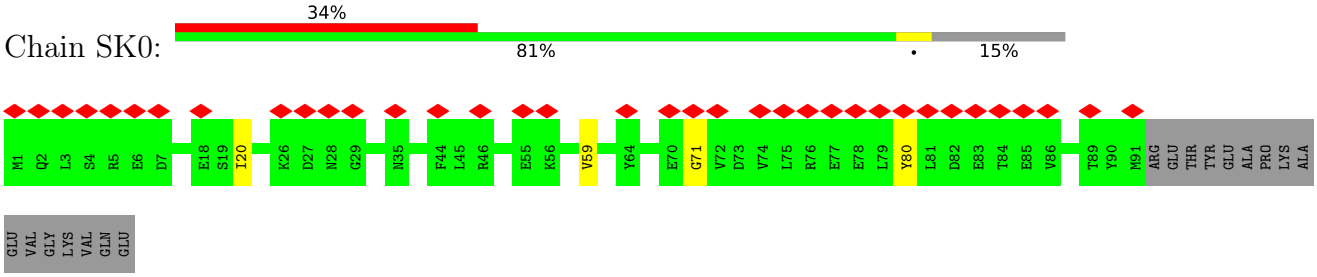
• Molecule 58: 40S ribosomal protein S9

Chain SJ0:



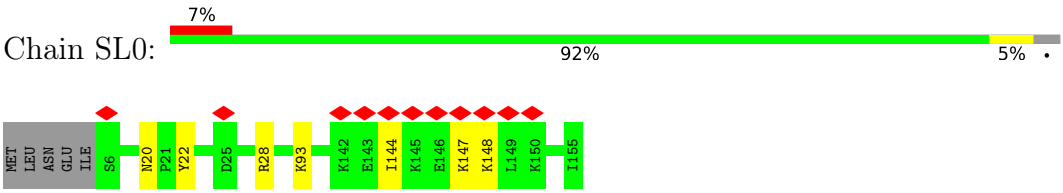
• Molecule 59: 40S ribosomal protein S10

Chain SK0:



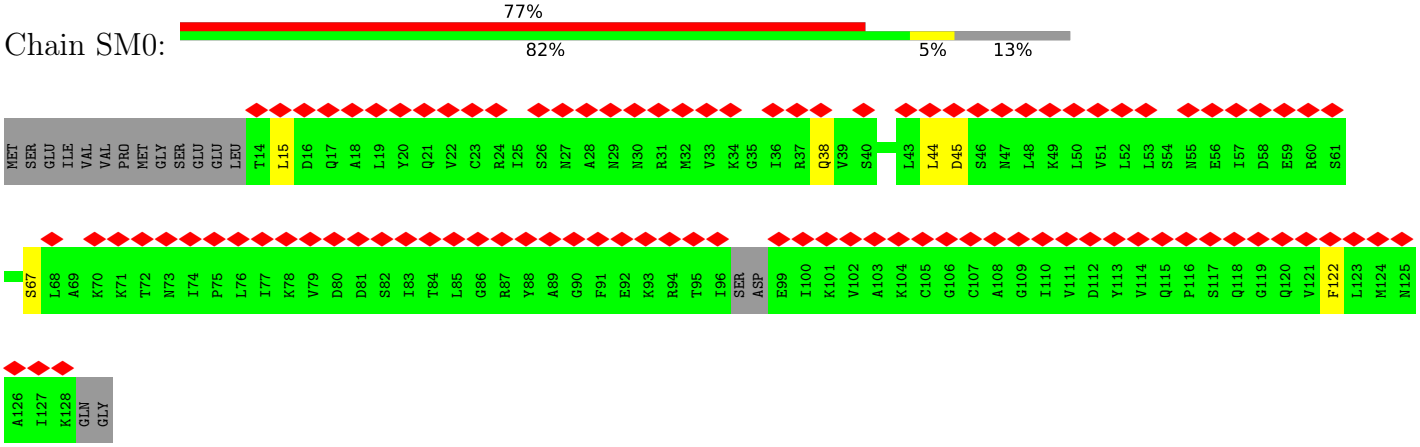
• Molecule 60: 40S ribosomal protein S11

Chain SL0:



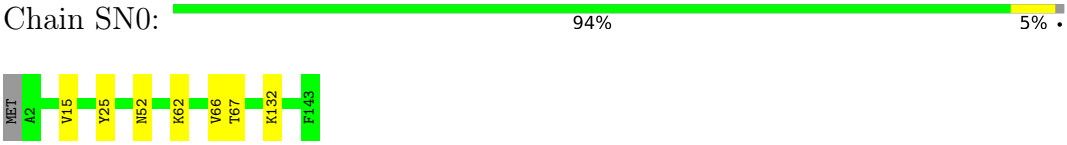
• Molecule 61: 40S ribosomal protein S12

Chain SM0:



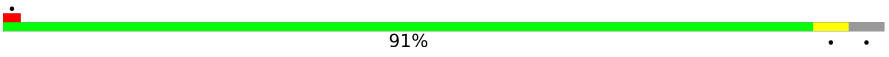
• Molecule 62: 40S ribosomal protein S13

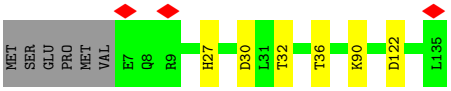
Chain SN0:



• Molecule 63: 40S ribosomal protein S14

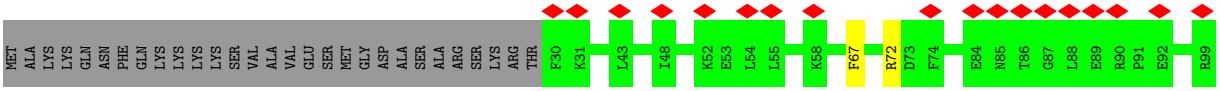
Chain SO0:

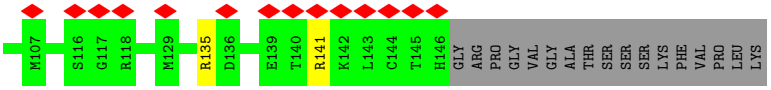




• Molecule 64: Ribosomal protein S19

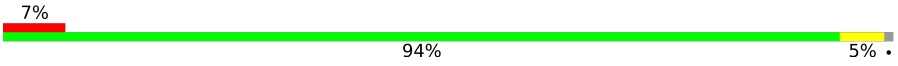
Chain SP0:

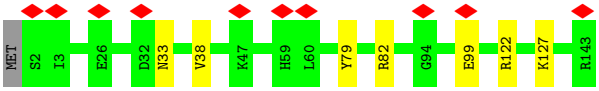




• Molecule 65: 40S ribosomal protein S16

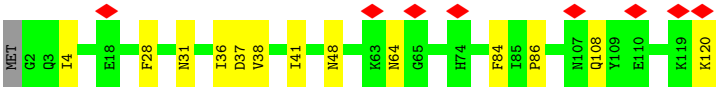
Chain SQ0:





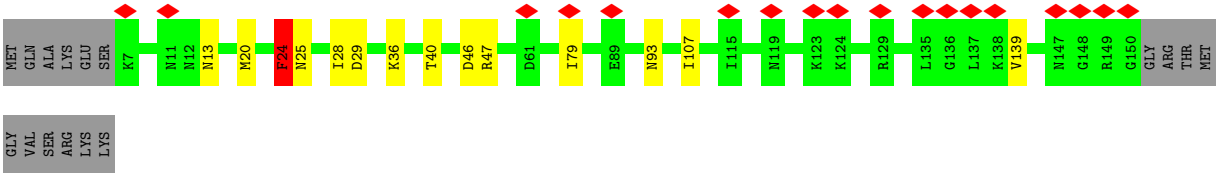
• Molecule 66: eS17 SR0

Chain SR0:



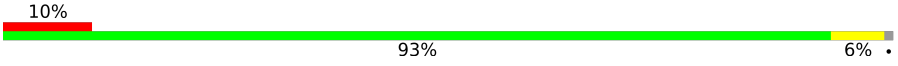
• Molecule 67: 40S ribosomal protein S18

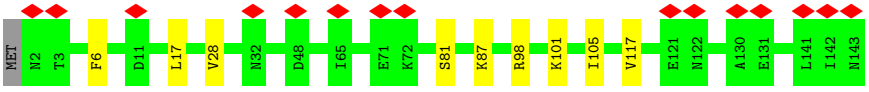
Chain SS0:



• Molecule 68: 40S Ribosomal protein S19

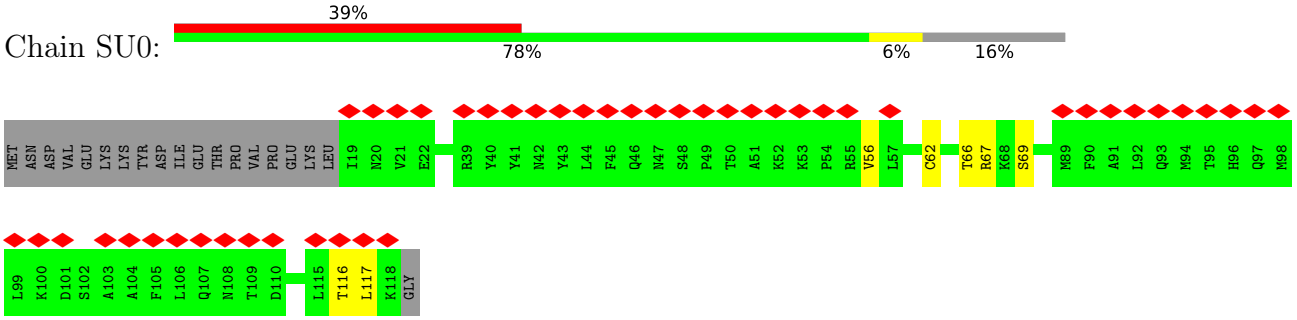
Chain ST0:





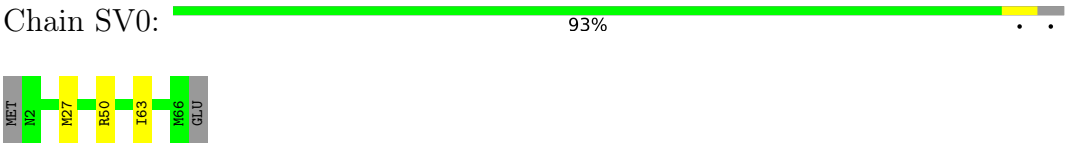
• Molecule 69: 40S ribosomal protein S20

Chain SU0:



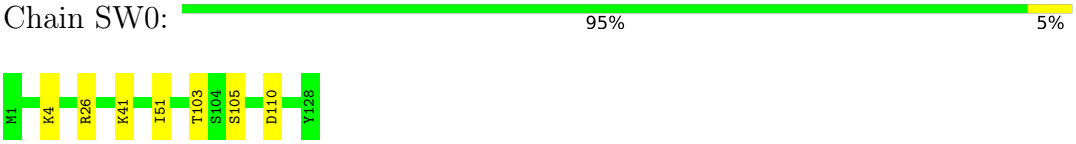
- Molecule 70: Ribosomal protein S21E

Chain SV0:



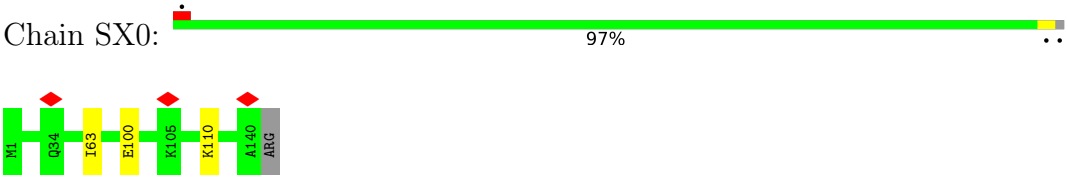
- Molecule 71: 40S ribosomal protein S15A

Chain SW0:



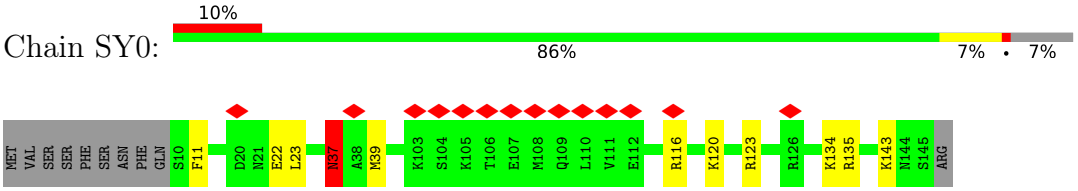
- Molecule 72: uS12 SX0

Chain SX0:



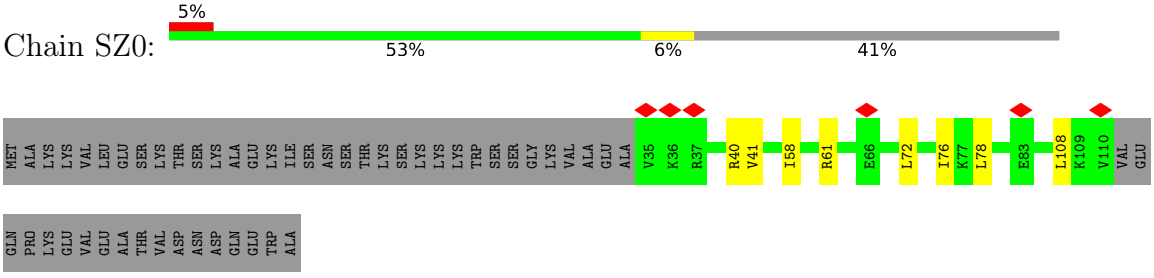
- Molecule 73: 40s ribosomal protein s24

Chain SY0:



- Molecule 74: 40S ribosomal protein S25

Chain SZ0:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	285940	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS, TFS TALOS	Depositor
Voltage (kV)	300, 200	Depositor
Electron dose ($e^-/Å^2$)	41.5, 41.34	Depositor
Minimum defocus (nm)	1200, 1200	Depositor
Maximum defocus (nm)	2500, 2500	Depositor
Magnification	Not provided, Not provided	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k), GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.403	Depositor
Minimum map value	-0.069	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.061	Depositor
Recommended contour level	0.05356	Depositor
Map size (Å)	337.28, 337.28, 337.28	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.054, 1.054, 1.054	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: K, 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	L50	0.75	1/60107 (0.0%)	1.19	158/93753 (0.2%)
2	L70	0.75	1/2844 (0.0%)	1.10	6/4429 (0.1%)
3	LA0	0.32	0/1926	0.74	0/2590
4	LAA	0.34	0/1191	0.66	0/1586
5	LB0	0.32	0/3092	0.70	1/4144 (0.0%)
6	LC0	0.32	0/2646	0.75	1/3555 (0.0%)
7	LCC	0.32	0/794	0.62	0/1067
8	LD0	0.28	0/2328	0.67	0/3098
9	LDD	0.29	0/913	0.66	0/1223
10	LE0	0.27	0/1394	0.65	0/1875
11	LEE	0.32	0/1108	0.69	0/1477
12	LF0	0.30	0/1963	0.68	0/2618
13	LFF	0.33	0/906	0.70	0/1207
14	LG0	0.28	0/1612	0.63	0/2163
15	LGG	0.34	0/825	0.77	1/1090 (0.1%)
16	LH0	0.30	0/1503	0.65	0/2018
17	LHH	0.28	0/999	0.66	0/1324
18	LI0	0.31	0/1781	0.69	0/2382
19	LII	0.29	0/790	0.59	0/1041
20	LJ0	0.30	0/1350	0.66	0/1797
21	LJJ	0.40	0/710	0.82	2/932 (0.2%)
22	LL0	0.30	0/1374	0.76	1/1827 (0.1%)
23	LLL	0.34	0/435	0.72	0/576
24	LM0	0.31	0/935	0.66	0/1251
25	LMM	0.41	0/431	0.68	0/568
26	LN0	0.35	0/1722	0.74	1/2297 (0.0%)
27	LO0	0.30	0/1626	0.65	0/2168
28	LOO	0.34	0/811	0.69	0/1071
29	LP0	0.31	0/1262	0.77	0/1689
30	LPP	0.40	0/693	0.78	2/918 (0.2%)
31	LQ0	0.30	0/1512	0.64	0/2014
32	LR0	0.31	0/1352	0.65	1/1790 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	LS0	0.30	0/1422	0.66	0/1898
34	LT0	0.31	0/1294	0.68	0/1736
35	LU0	0.30	0/826	0.67	0/1104
36	LV0	0.31	0/1068	0.70	0/1429
37	LW0	0.30	0/849	0.69	0/1129
38	LX0	0.28	0/883	0.67	0/1175
39	LY0	0.29	0/1058	0.68	1/1399 (0.1%)
40	LZ0	0.29	0/976	0.73	1/1302 (0.1%)
41	S60	0.71	1/32725 (0.0%)	1.07	53/51066 (0.1%)
42	SA0	0.35	1/1751 (0.1%)	0.64	0/2358
43	SAA	0.38	0/839	0.72	0/1120
44	SB0	0.29	0/1623	0.67	0/2169
45	SBB	0.47	1/634 (0.2%)	0.65	0/844
46	SC0	0.31	0/1751	0.69	2/2359 (0.1%)
47	SCC	0.33	0/480	0.73	0/644
48	SD0	0.30	0/1721	0.66	0/2304
49	SDD	0.39	0/559	0.75	1/742 (0.1%)
50	SE0	0.32	0/2080	0.72	3/2804 (0.1%)
51	SEE	0.35	0/453	0.74	1/596 (0.2%)
52	SF0	0.31	0/1527	0.68	0/2045
53	SFF	0.42	0/453	0.68	0/606
54	SG0	0.29	0/1863	0.68	0/2483
55	SGG	0.34	0/2517	0.71	1/3397 (0.0%)
56	SH0	0.31	0/1356	0.66	0/1820
57	SI0	0.33	0/1369	0.67	0/1825
58	SJ0	0.32	0/1403	0.68	0/1880
59	SK0	0.30	0/778	0.70	0/1047
60	SL0	0.32	0/1252	0.72	2/1672 (0.1%)
61	SM0	0.32	0/881	0.71	0/1182
62	SN0	0.37	0/1154	0.78	0/1557
63	SO0	0.32	0/993	0.72	0/1326
64	SP0	0.33	0/964	0.71	0/1289
65	SQ0	0.32	0/1163	0.74	3/1556 (0.2%)
66	SR0	0.33	0/988	0.75	1/1319 (0.1%)
67	SS0	0.34	0/1165	0.74	0/1566
68	ST0	0.34	0/1181	0.75	1/1585 (0.1%)
69	SU0	0.32	0/824	0.74	2/1110 (0.2%)
70	SV0	0.33	0/525	0.65	0/700
71	SW0	0.32	0/1037	0.71	0/1389
72	SX0	0.31	0/1113	0.70	0/1486
73	SY0	0.30	0/1131	0.72	1/1503 (0.1%)
74	SZ0	0.33	0/640	0.75	0/855
All	All	0.58	5/182204 (0.0%)	0.98	247/264914 (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
6	LC0	0	1
13	LFF	0	1
15	LGG	0	1
66	SR0	0	1
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	SA0	20	CYS	C-N	8.40	1.53	1.34
1	L50	1	A	OP3-P	-8.34	1.51	1.61
41	S60	1	A	OP3-P	-7.55	1.52	1.61
2	L70	1	A	OP3-P	-7.35	1.52	1.61
45	SBB	58	CYS	CB-SG	-5.21	1.73	1.81

The worst 5 of 247 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
41	S60	1356	C	O5'-P-OP1	-18.04	89.06	110.70
1	L50	330	G	C2'-C3'-O3'	10.41	132.39	109.50
1	L50	1265	G	OP1-P-OP2	-9.86	104.81	119.60
1	L50	535	A	P-O3'-C3'	9.42	131.00	119.70
1	L50	1395	U	C2'-C3'-O3'	9.04	129.39	109.50

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	LC0	87	ALA	Peptide
13	LFF	101	ILE	Peptide
15	LGG	77	GLY	Peptide
66	SR0	64	ASN	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L50	53655	0	26937	97	0
2	L70	2542	0	1282	8	0
3	LA0	1889	0	1985	3	0
4	LAA	1167	0	1214	5	0
5	LB0	3039	0	3183	5	0
6	LC0	2604	0	2638	10	0
7	LCC	781	0	803	2	0
8	LD0	2298	0	2384	7	0
9	LDD	895	0	948	0	0
10	LE0	1371	0	1389	13	0
11	LEE	1090	0	1173	10	0
12	LF0	1933	0	2011	10	0
13	LFF	893	0	945	2	0
14	LG0	1590	0	1709	4	0
15	LGG	819	0	882	1	0
16	LH0	1477	0	1528	4	0
17	LHH	992	0	1097	5	0
18	LI0	1750	0	1797	2	0
19	LII	784	0	873	2	0
20	LJ0	1332	0	1411	6	0
21	LJJ	701	0	753	4	0
22	LL0	1353	0	1433	4	0
23	LLL	427	0	468	0	0
24	LM0	927	0	961	3	0
25	LMM	427	0	461	0	0
26	LN0	1688	0	1752	5	0
27	LO0	1598	0	1681	4	0
28	LOO	801	0	886	3	0
29	LP0	1238	0	1304	3	0
30	LPP	684	0	720	2	0
31	LQ0	1491	0	1587	7	0
32	LR0	1336	0	1430	1	0
33	LS0	1400	0	1450	1	0
34	LT0	1270	0	1321	16	0
35	LU0	810	0	834	1	0
36	LV0	1057	0	1139	2	0
37	LW0	832	0	873	31	0
38	LX0	874	0	956	5	0
39	LY0	1048	0	1135	2	0
40	LZ0	963	0	1022	2	0
41	S60	29181	0	14618	125	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	SA0	1725	0	1750	15	0
43	SAA	827	0	859	1	0
44	SB0	1609	0	1728	6	0
45	SBB	627	0	651	3	0
46	SC0	1727	0	1802	4	0
47	SCC	476	0	488	4	0
48	SD0	1700	0	1815	7	0
49	SDD	550	0	542	4	0
50	SE0	2044	0	2116	26	0
51	SEE	447	0	483	1	0
52	SF0	1509	0	1604	22	0
53	SFF	447	0	456	14	0
54	SG0	1835	0	1968	27	0
55	SGG	2478	0	2458	4	0
56	SH0	1335	0	1356	2	0
57	SI0	1347	0	1379	9	0
58	SJ0	1379	0	1436	6	0
59	SK0	764	0	771	2	0
60	SL0	1229	0	1302	5	0
61	SM0	876	0	937	10	0
62	SN0	1130	0	1188	7	0
63	SO0	983	0	1028	9	0
64	SP0	950	0	984	4	0
65	SQ0	1143	0	1171	6	0
66	SR0	977	0	1012	12	0
67	SS0	1150	0	1207	17	0
68	ST0	1161	0	1219	10	0
69	SU0	809	0	838	5	0
70	SV0	521	0	525	6	0
71	SW0	1022	0	1052	7	0
72	SX0	1098	0	1183	3	0
73	SY0	1118	0	1166	13	0
74	SZ0	633	0	678	16	0
75	L50	145	0	0	0	0
75	LA0	2	0	0	0	0
75	LEE	1	0	0	0	0
75	LLL	1	0	0	0	0
75	LN0	1	0	0	0	0
75	S60	44	0	0	0	0
75	SN0	3	0	0	0	0
75	SO0	2	0	0	0	0
76	L50	104	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
76	L70	4	0	0	0	0
76	LB0	1	0	0	0	0
76	LF0	1	0	0	0	0
76	LII	1	0	0	0	0
76	LJJ	1	0	0	0	0
76	LV0	1	0	0	0	0
76	S60	46	0	0	0	0
76	SI0	1	0	0	0	0
77	LGG	1	0	0	0	0
77	LJJ	1	0	0	0	0
77	LMM	1	0	0	0	0
77	LOO	1	0	0	0	0
77	LPP	1	0	0	0	0
77	SAA	1	0	0	0	0
77	SBB	1	0	0	0	0
77	SDD	1	0	0	0	0
77	SFF	1	0	0	0	0
All	All	171001	0	132125	475	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 475 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SF0:90:ILE:HG23	74:SZ0:58:ILE:CD1	1.58	1.33
37:LW0:99:LYS:HA	37:LW0:102:LYS:HE2	1.32	1.09
73:SY0:22:GLU:O	73:SY0:23:LEU:HG	1.54	1.08
74:SZ0:61:ARG:HD3	74:SZ0:76:ILE:HD11	1.36	1.07
34:LT0:126:PRO:HB2	34:LT0:128:LEU:HG	1.34	1.07

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	LA0	243/246 (99%)	236 (97%)	7 (3%)	0	100	100
4	LAA	145/147 (99%)	142 (98%)	3 (2%)	0	100	100
5	LB0	381/392 (97%)	372 (98%)	9 (2%)	0	100	100
6	LC0	325/328 (99%)	313 (96%)	11 (3%)	1 (0%)	41	72
7	LCC	97/110 (88%)	94 (97%)	2 (2%)	1 (1%)	15	44
8	LD0	279/291 (96%)	274 (98%)	5 (2%)	0	100	100
9	LDD	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
10	LE0	163/171 (95%)	154 (94%)	9 (6%)	0	100	100
11	LEE	133/139 (96%)	127 (96%)	6 (4%)	0	100	100
12	LF0	229/235 (97%)	224 (98%)	5 (2%)	0	100	100
13	LFF	109/111 (98%)	106 (97%)	3 (3%)	0	100	100
14	LG0	197/206 (96%)	194 (98%)	3 (2%)	0	100	100
15	LGG	102/106 (96%)	96 (94%)	5 (5%)	1 (1%)	15	44
16	LH0	181/187 (97%)	177 (98%)	4 (2%)	0	100	100
17	LHH	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
18	LI0	215/218 (99%)	214 (100%)	1 (0%)	0	100	100
19	LII	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
20	LJ0	165/171 (96%)	156 (94%)	9 (6%)	0	100	100
21	LJJ	87/92 (95%)	86 (99%)	1 (1%)	0	100	100
22	LL0	162/165 (98%)	155 (96%)	6 (4%)	1 (1%)	25	56
23	LLL	49/52 (94%)	48 (98%)	1 (2%)	0	100	100
24	LM0	113/122 (93%)	106 (94%)	6 (5%)	1 (1%)	17	46
25	LMM	50/127 (39%)	50 (100%)	0	0	100	100
26	LN0	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
27	LO0	196/198 (99%)	193 (98%)	3 (2%)	0	100	100
28	LOO	98/104 (94%)	96 (98%)	2 (2%)	0	100	100
29	LP0	152/167 (91%)	145 (95%)	7 (5%)	0	100	100
30	LPP	85/89 (96%)	80 (94%)	4 (5%)	1 (1%)	13	39
31	LQ0	180/183 (98%)	175 (97%)	5 (3%)	0	100	100
32	LR0	162/168 (96%)	160 (99%)	2 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	LS0	168/171 (98%)	159 (95%)	9 (5%)	0	100	100
34	LT0	154/158 (98%)	145 (94%)	9 (6%)	0	100	100
35	LU0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
36	LV0	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
37	LW0	100/131 (76%)	94 (94%)	5 (5%)	1 (1%)	15	44
38	LX0	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
39	LY0	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
40	LZ0	116/153 (76%)	116 (100%)	0	0	100	100
42	SA0	218/233 (94%)	206 (94%)	12 (6%)	0	100	100
43	SAA	99/102 (97%)	98 (99%)	1 (1%)	0	100	100
44	SB0	202/230 (88%)	197 (98%)	5 (2%)	0	100	100
45	SBB	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
46	SC0	224/248 (90%)	220 (98%)	4 (2%)	0	100	100
47	SCC	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
48	SD0	214/242 (88%)	212 (99%)	2 (1%)	0	100	100
49	SDD	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
50	SE0	258/280 (92%)	247 (96%)	11 (4%)	0	100	100
51	SEE	54/60 (90%)	53 (98%)	1 (2%)	0	100	100
52	SF0	190/195 (97%)	180 (95%)	10 (5%)	0	100	100
53	SFF	56/150 (37%)	52 (93%)	4 (7%)	0	100	100
54	SG0	227/230 (99%)	213 (94%)	14 (6%)	0	100	100
55	SGG	315/326 (97%)	295 (94%)	19 (6%)	1 (0%)	41	72
56	SH0	161/164 (98%)	156 (97%)	4 (2%)	1 (1%)	25	56
57	SI0	165/173 (95%)	161 (98%)	4 (2%)	0	100	100
58	SJ0	166/184 (90%)	165 (99%)	1 (1%)	0	100	100
59	SK0	89/107 (83%)	84 (94%)	4 (4%)	1 (1%)	14	41
60	SL0	148/155 (96%)	141 (95%)	7 (5%)	0	100	100
61	SM0	109/130 (84%)	106 (97%)	3 (3%)	0	100	100
62	SN0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
63	SO0	127/135 (94%)	120 (94%)	7 (6%)	0	100	100
64	SP0	115/163 (71%)	113 (98%)	2 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
65	SQ0	140/143 (98%)	134 (96%)	6 (4%)	0	100 100
66	SR0	117/120 (98%)	112 (96%)	5 (4%)	0	100 100
67	SS0	142/160 (89%)	137 (96%)	4 (3%)	1 (1%)	22 53
68	ST0	140/143 (98%)	140 (100%)	0	0	100 100
69	SU0	98/119 (82%)	94 (96%)	4 (4%)	0	100 100
70	SV0	63/67 (94%)	62 (98%)	1 (2%)	0	100 100
71	SW0	126/128 (98%)	124 (98%)	2 (2%)	0	100 100
72	SX0	138/141 (98%)	136 (99%)	2 (1%)	0	100 100
73	SY0	134/146 (92%)	122 (91%)	10 (8%)	2 (2%)	10 33
74	SZ0	74/128 (58%)	69 (93%)	5 (7%)	0	100 100
All	All	10483/11325 (93%)	10120 (96%)	350 (3%)	13 (0%)	54 81

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	LGG	78	GLY
73	SY0	134	LYS
30	LPP	18	TYR
37	LW0	81	ARG
67	SS0	24	PHE

5.3.2 Protein sidechains (i)

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
3	LA0	202/203 (100%)	199 (98%)	3 (2%)	65 89
4	LAA	123/123 (100%)	119 (97%)	4 (3%)	38 72
5	LB0	328/336 (98%)	319 (97%)	9 (3%)	44 78
6	LC0	277/278 (100%)	274 (99%)	3 (1%)	73 92
7	LCC	87/97 (90%)	85 (98%)	2 (2%)	50 82
8	LD0	251/261 (96%)	249 (99%)	2 (1%)	81 94

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	LDD	99/100 (99%)	99 (100%)	0	100	100
10	LE0	153/159 (96%)	150 (98%)	3 (2%)	55	84
11	LEE	118/122 (97%)	118 (100%)	0	100	100
12	LF0	212/216 (98%)	211 (100%)	1 (0%)	88	96
13	LFF	98/98 (100%)	98 (100%)	0	100	100
14	LG0	183/190 (96%)	183 (100%)	0	100	100
15	LGG	88/90 (98%)	86 (98%)	2 (2%)	50	82
16	LH0	165/169 (98%)	161 (98%)	4 (2%)	49	81
17	LHH	110/110 (100%)	109 (99%)	1 (1%)	78	94
18	LI0	188/189 (100%)	188 (100%)	0	100	100
19	LII	84/84 (100%)	82 (98%)	2 (2%)	49	81
20	LJ0	146/149 (98%)	144 (99%)	2 (1%)	67	90
21	LJJ	78/81 (96%)	77 (99%)	1 (1%)	69	91
22	LL0	148/149 (99%)	142 (96%)	6 (4%)	30	64
23	LLL	46/47 (98%)	46 (100%)	0	100	100
24	LM0	110/117 (94%)	110 (100%)	0	100	100
25	LMM	46/112 (41%)	46 (100%)	0	100	100
26	LN0	175/176 (99%)	171 (98%)	4 (2%)	50	82
27	LO0	178/178 (100%)	177 (99%)	1 (1%)	86	96
28	LOO	85/89 (96%)	85 (100%)	0	100	100
29	LP0	135/147 (92%)	132 (98%)	3 (2%)	52	83
30	LPP	75/77 (97%)	73 (97%)	2 (3%)	44	78
31	LQ0	165/166 (99%)	165 (100%)	0	100	100
32	LR0	142/145 (98%)	141 (99%)	1 (1%)	84	95
33	LS0	155/156 (99%)	152 (98%)	3 (2%)	57	85
34	LT0	140/142 (99%)	138 (99%)	2 (1%)	67	90
35	LU0	89/98 (91%)	88 (99%)	1 (1%)	73	92
36	LV0	113/114 (99%)	112 (99%)	1 (1%)	78	94
37	LW0	93/120 (78%)	89 (96%)	4 (4%)	29	62
38	LX0	92/93 (99%)	91 (99%)	1 (1%)	73	92
39	LY0	116/116 (100%)	114 (98%)	2 (2%)	60	87

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	LZ0	106/141 (75%)	106 (100%)	0	100	100
42	SA0	194/206 (94%)	192 (99%)	2 (1%)	76	93
43	SAA	92/93 (99%)	92 (100%)	0	100	100
44	SB0	182/203 (90%)	182 (100%)	0	100	100
45	SBB	72/73 (99%)	71 (99%)	1 (1%)	67	90
46	SC0	187/209 (90%)	185 (99%)	2 (1%)	73	92
47	SCC	51/54 (94%)	51 (100%)	0	100	100
48	SD0	189/215 (88%)	189 (100%)	0	100	100
49	SDD	57/57 (100%)	57 (100%)	0	100	100
50	SE0	231/251 (92%)	229 (99%)	2 (1%)	78	94
51	SEE	44/47 (94%)	44 (100%)	0	100	100
52	SF0	167/170 (98%)	163 (98%)	4 (2%)	49	81
53	SFF	52/136 (38%)	51 (98%)	1 (2%)	57	85
54	SG0	199/200 (100%)	194 (98%)	5 (2%)	47	80
55	SGG	282/288 (98%)	278 (99%)	4 (1%)	67	90
56	SH0	153/154 (99%)	153 (100%)	0	100	100
57	SI0	147/153 (96%)	147 (100%)	0	100	100
58	SJ0	152/165 (92%)	150 (99%)	2 (1%)	69	91
59	SK0	86/99 (87%)	85 (99%)	1 (1%)	71	92
60	SL0	140/145 (97%)	139 (99%)	1 (1%)	84	95
61	SM0	99/114 (87%)	99 (100%)	0	100	100
62	SN0	126/127 (99%)	126 (100%)	0	100	100
63	SO0	102/108 (94%)	101 (99%)	1 (1%)	76	93
64	SP0	107/144 (74%)	106 (99%)	1 (1%)	78	94
65	SQ0	120/121 (99%)	119 (99%)	1 (1%)	81	94
66	SR0	110/111 (99%)	109 (99%)	1 (1%)	78	94
67	SS0	125/138 (91%)	124 (99%)	1 (1%)	81	94
68	ST0	129/130 (99%)	127 (98%)	2 (2%)	62	88
69	SU0	92/110 (84%)	92 (100%)	0	100	100
70	SV0	61/63 (97%)	61 (100%)	0	100	100
71	SW0	111/111 (100%)	110 (99%)	1 (1%)	78	94

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
72	SX0	115/116 (99%)	115 (100%)	0	100 100
73	SY0	126/136 (93%)	121 (96%)	5 (4%)	31 65
74	SZ0	73/118 (62%)	73 (100%)	0	100 100
All	All	9372/10003 (94%)	9264 (99%)	108 (1%)	72 92

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	LS0	157	ARG
42	SA0	154	ILE
67	SS0	24	PHE
34	LT0	55	LYS
37	LW0	91	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L50	2494/2618 (95%)	738 (29%)	102 (4%)
2	L70	118/119 (99%)	36 (30%)	4 (3%)
41	S60	1352/1368 (98%)	507 (37%)	65 (4%)
All	All	3964/4105 (96%)	1281 (32%)	171 (4%)

5 of 1281 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L50	2	U
1	L50	3	A
1	L50	13	A
1	L50	15	G
1	L50	21	U

5 of 171 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
41	S60	225	A
41	S60	877	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
41	S60	283	U
41	S60	445	U
41	S60	980	G

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 368 ligands modelled in this entry, 368 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)

There are no chain breaks in this entry.

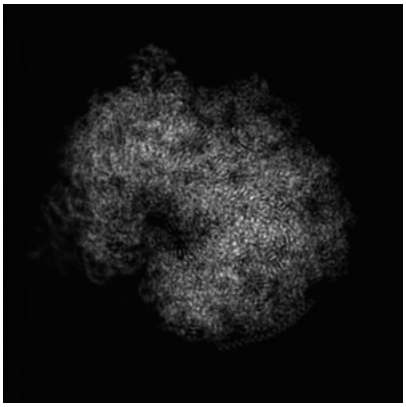
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13892. These allow visual inspection of the internal detail of the map and identification of artifacts.

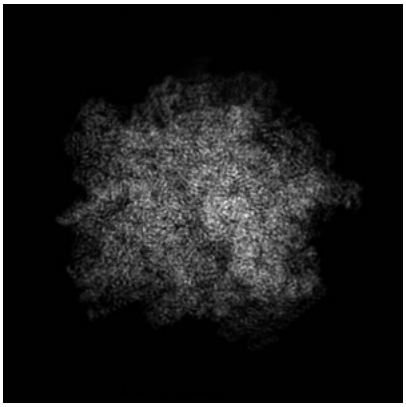
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

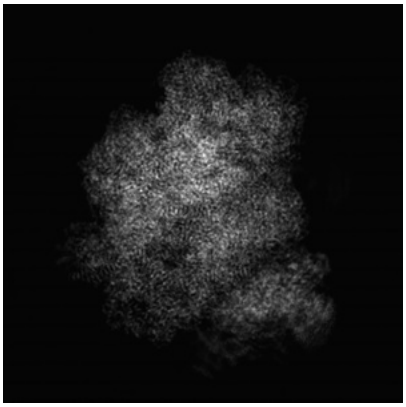
6.1.1 Primary map



X



Y

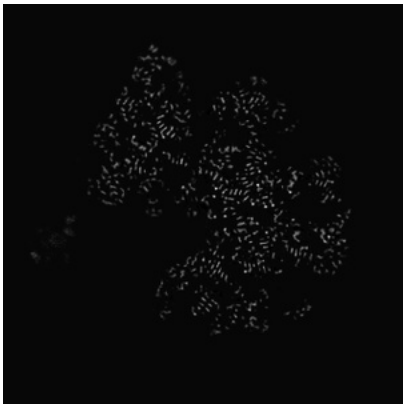


Z

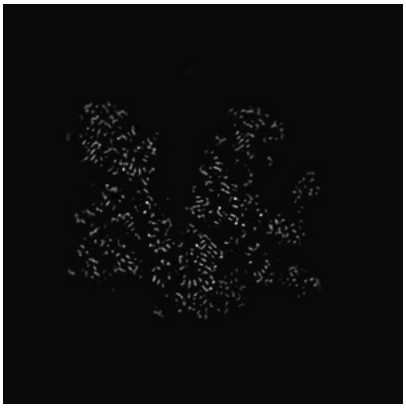
The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map



X Index: 160



Y Index: 160

Z Index: 160

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: 164

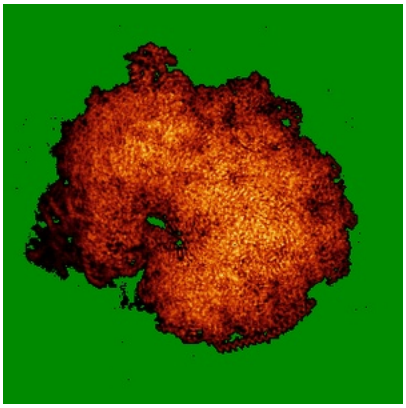
Y Index: 170

Z Index: 185

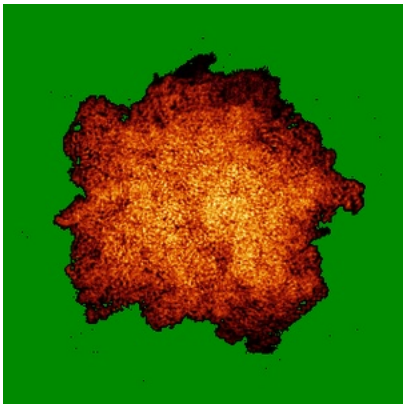
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

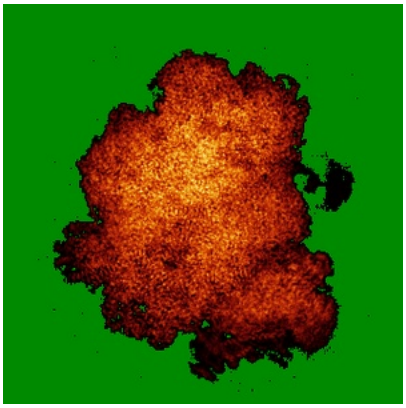
6.4.1 Primary map



X



Y

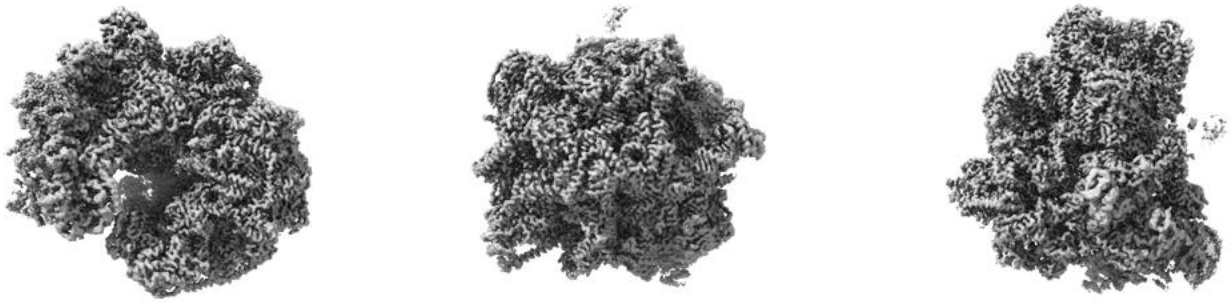


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05356. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

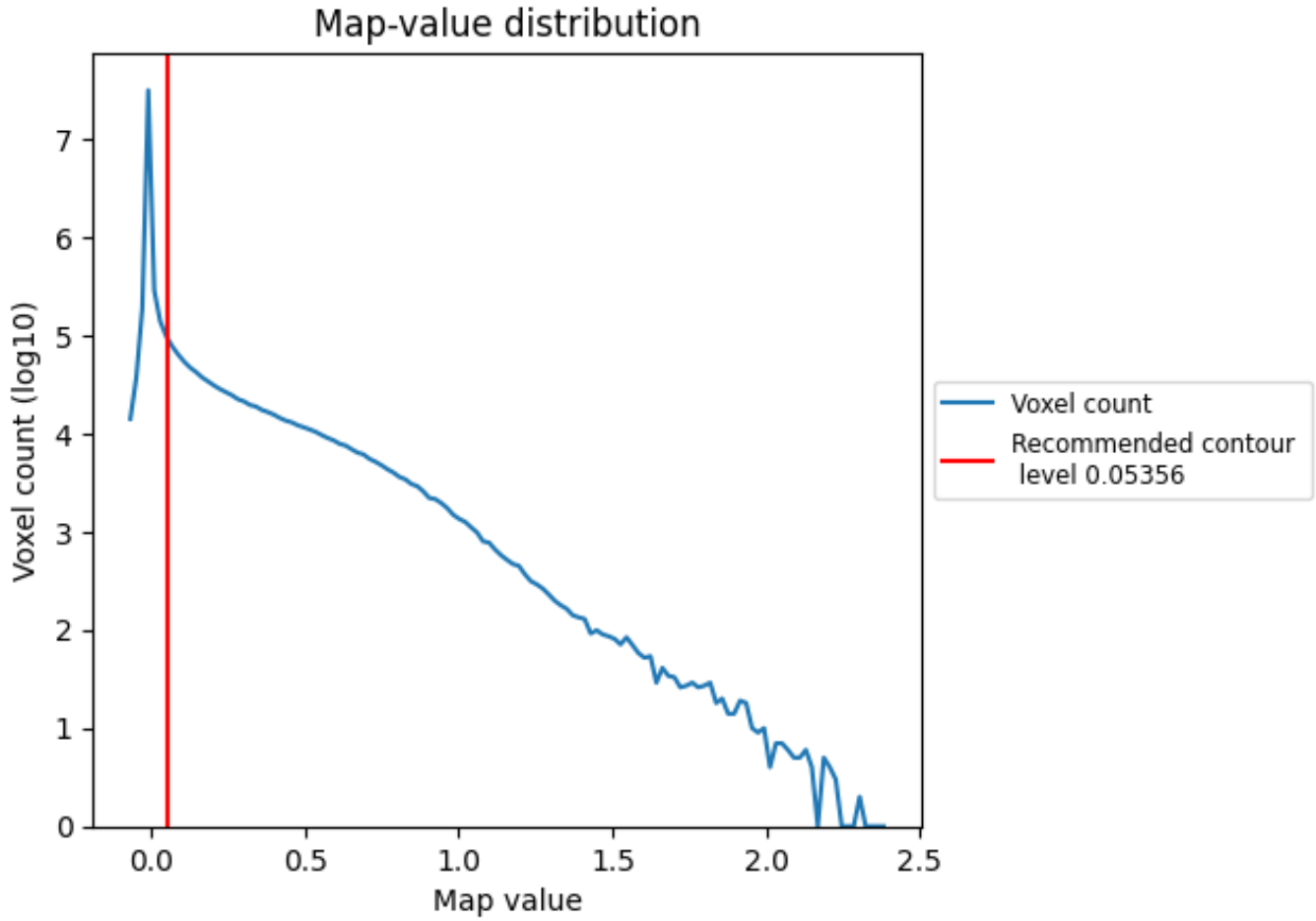
6.6 Mask visualisation (i)

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

7 Map analysis

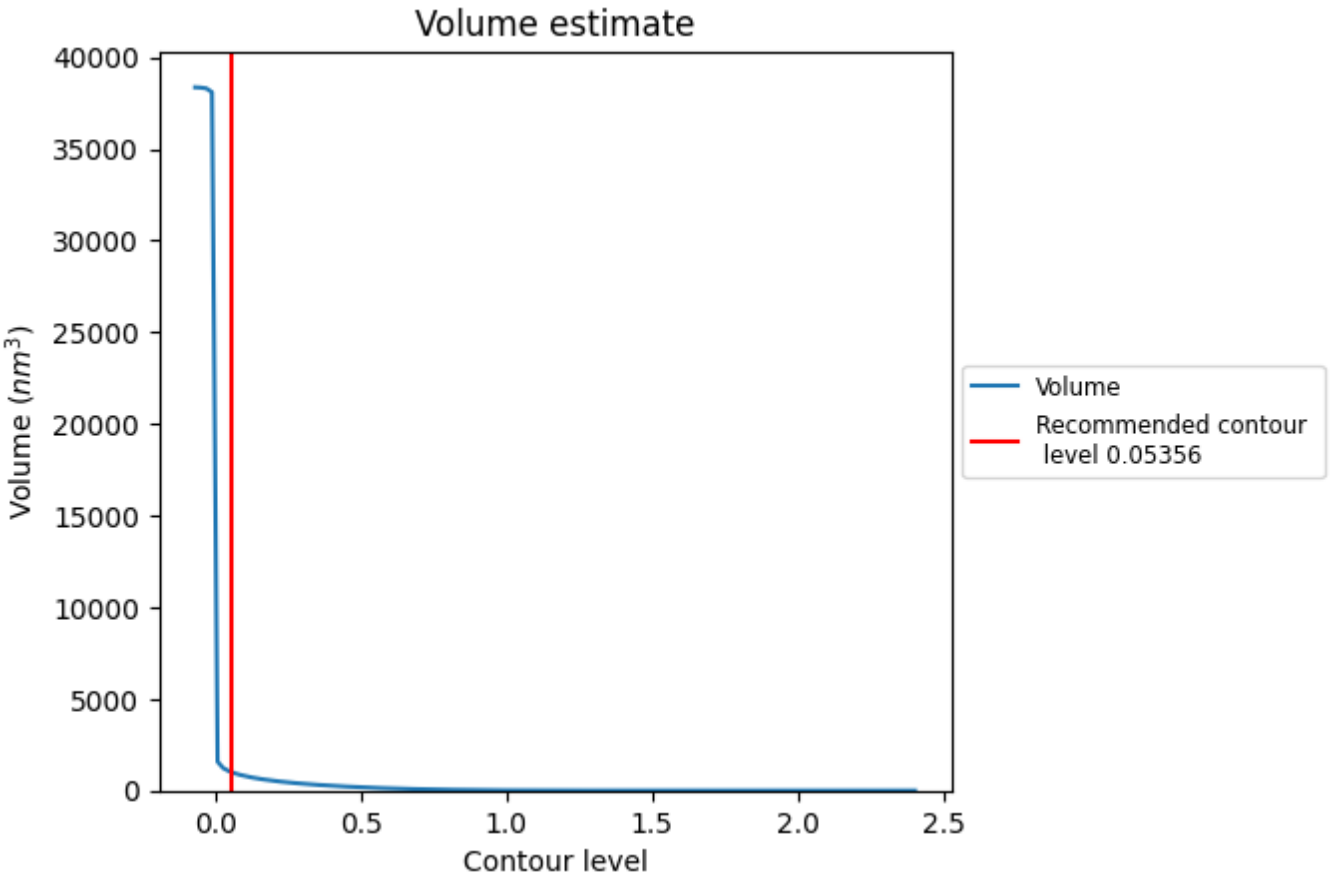
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

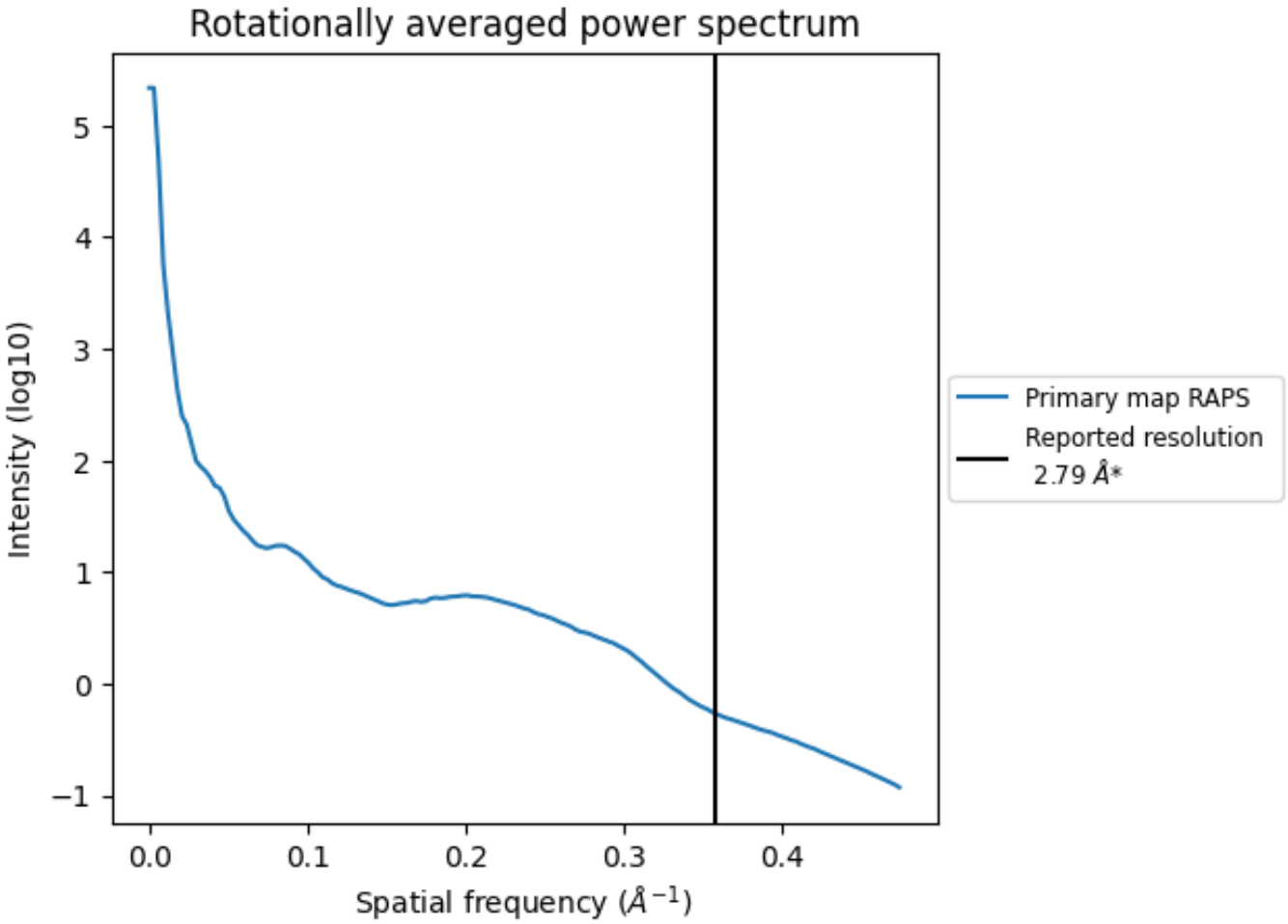
7.2 Volume estimate (i)



The volume at the recommended contour level is 1025 nm^3; this corresponds to an approximate mass of 926 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 (i)

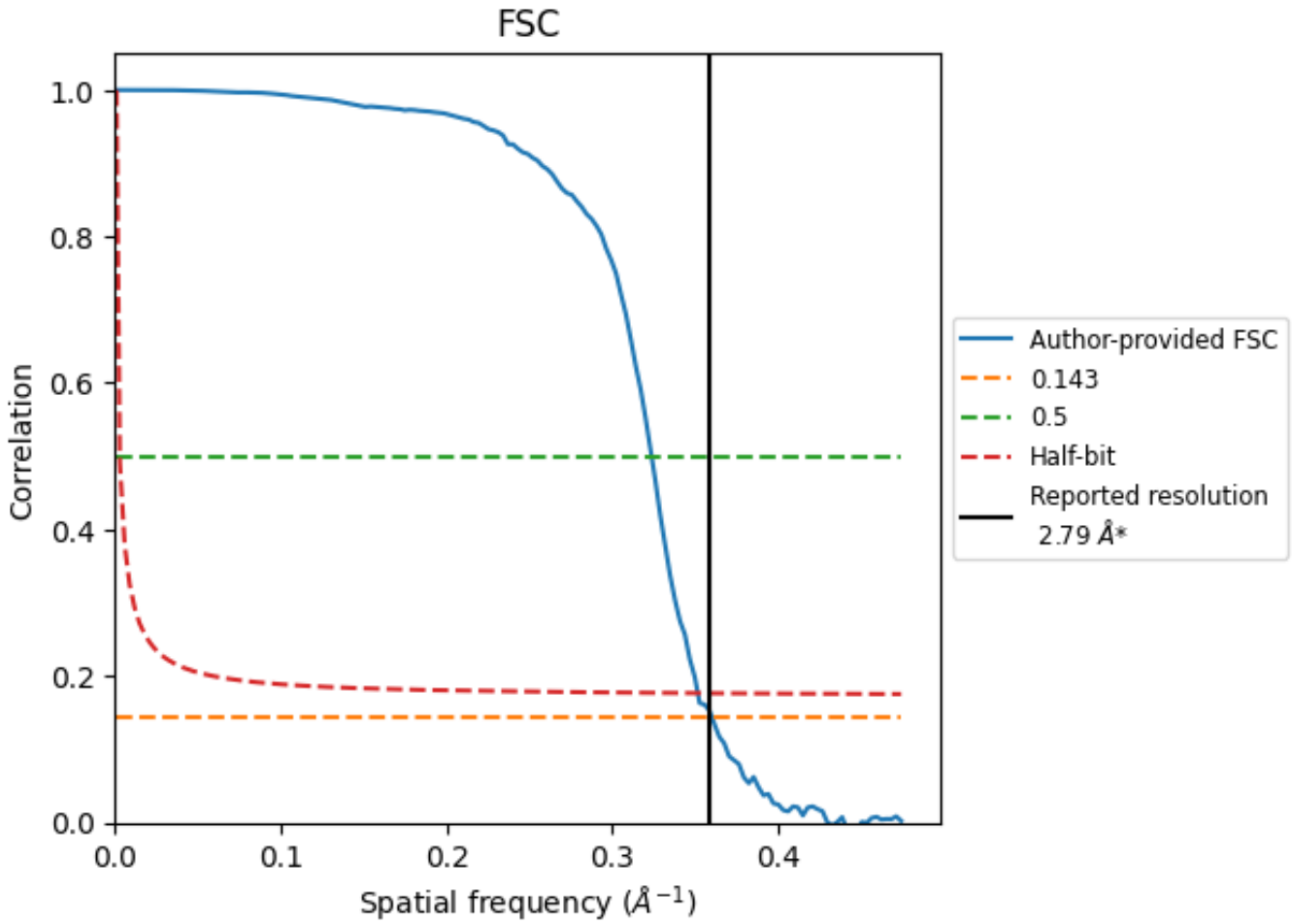


*Reported resolution corresponds to spatial frequency of 0.358 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.358 Å^{-1}

8.2 Resolution estimates (i)

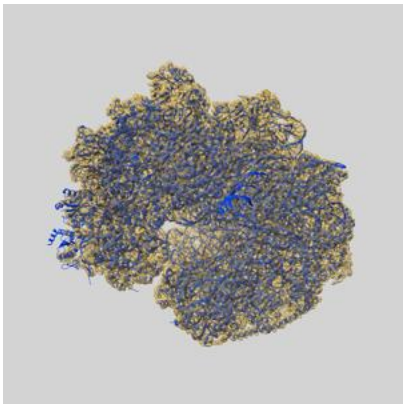
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.79	-	-
Author-provided FSC curve	2.78	3.09	2.84
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

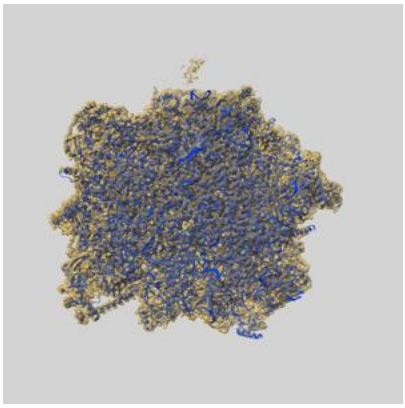
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-13892 and PDB model 7QCA. Per-residue inclusion information can be found in section 3 on page 19.

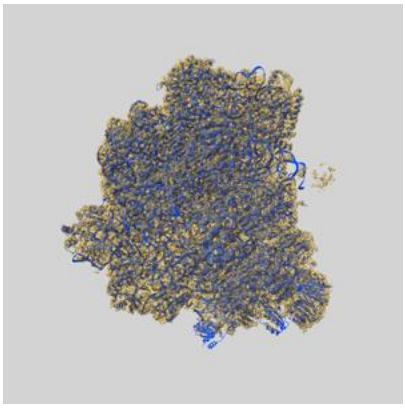
9.1 Map-model overlay



X



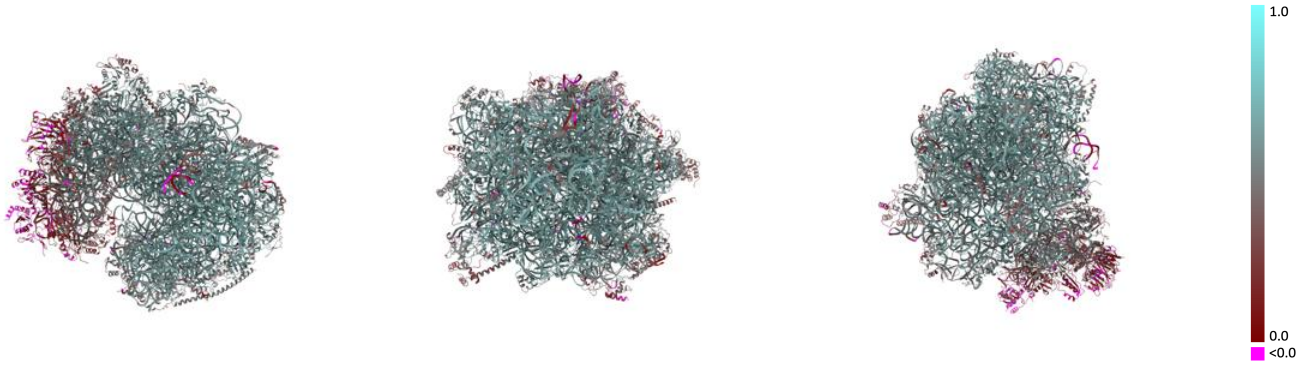
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05356 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.

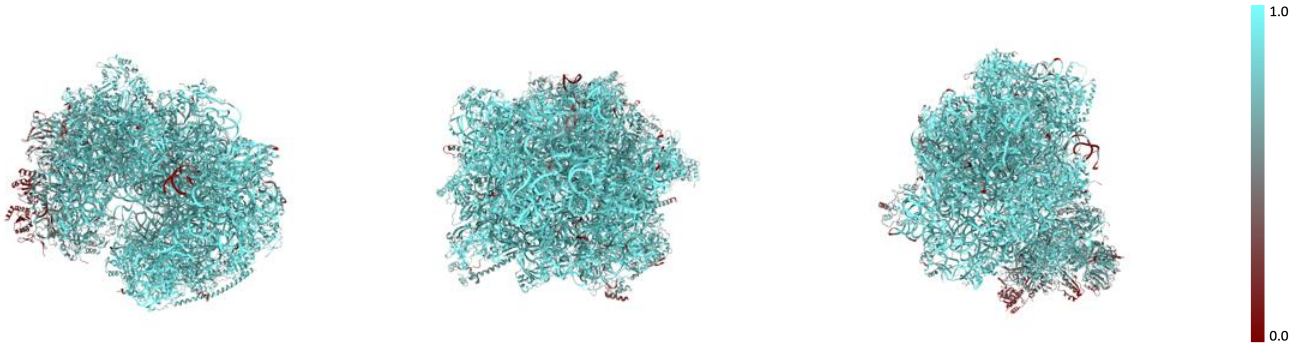
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

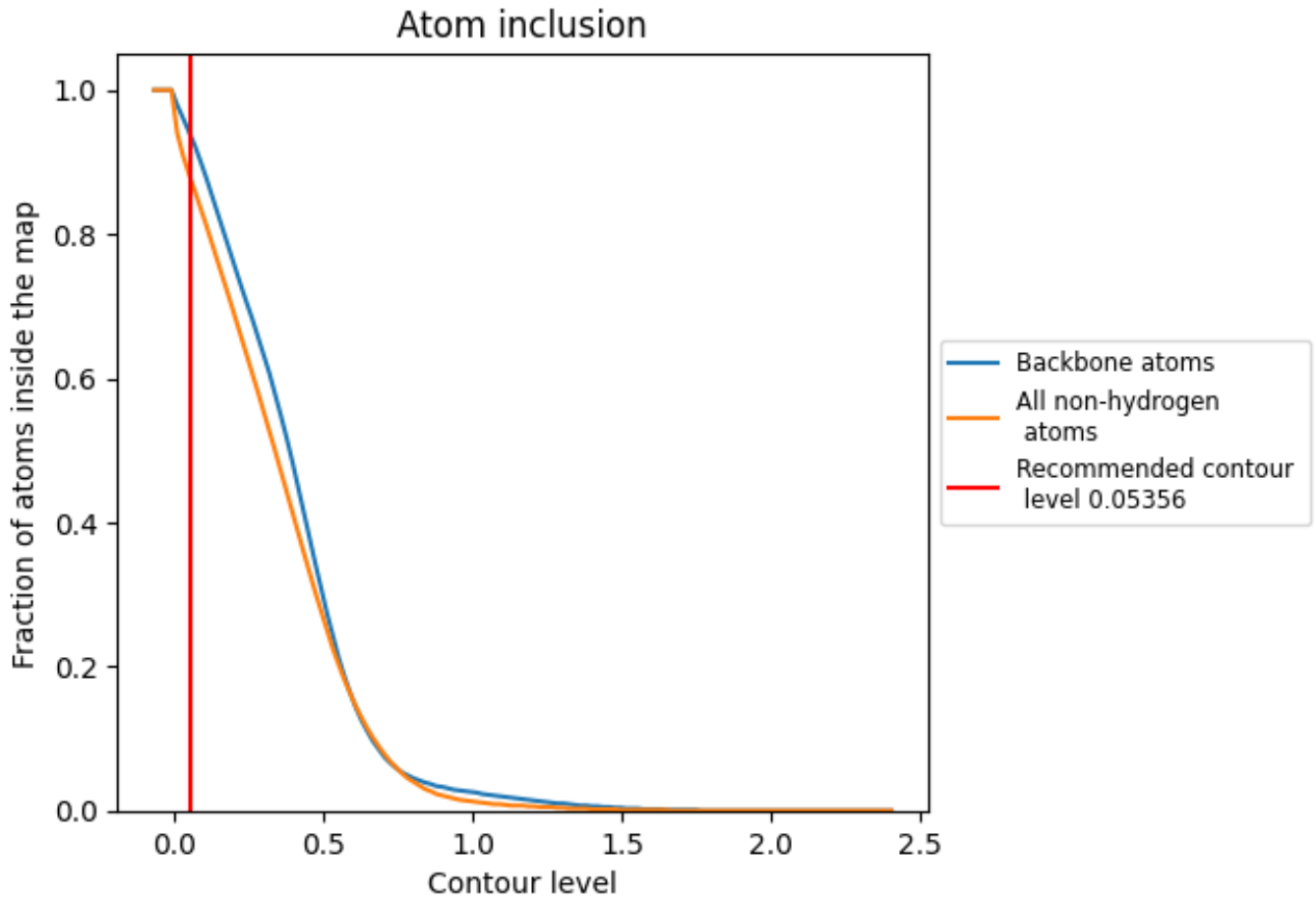
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.05356).

9.4 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 88% 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 (0.05356) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8760	0.5380
L50	0.9570	0.6180
L70	0.9820	0.6100
LA0	0.9150	0.6140
LAA	0.9390	0.6260
LB0	0.9020	0.5950
LC0	0.8950	0.5850
LCC	0.8850	0.5500
LD0	0.8320	0.5000
LDD	0.8410	0.5610
LE0	0.6950	0.4160
LEE	0.8720	0.5690
LF0	0.8880	0.5650
LFF	0.8920	0.5860
LG0	0.8530	0.5190
LGG	0.8770	0.5700
LH0	0.8930	0.5730
LHH	0.8600	0.5520
LI0	0.8710	0.5640
LII	0.8250	0.5130
LJ0	0.8050	0.4680
LJJ	0.9200	0.6250
LL0	0.8890	0.5740
LLL	0.9220	0.6080
LM0	0.7640	0.4460
LMM	0.8680	0.5660
LN0	0.9730	0.6600
LO0	0.8700	0.5570
LOO	0.8520	0.5540
LP0	0.8920	0.5830
LPP	0.9140	0.6080
LQ0	0.8870	0.5790
LR0	0.8420	0.5420
LS0	0.8810	0.5620
LT0	0.8270	0.5340

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
LU0	0.8100	0.4960
LV0	0.9070	0.6030
LW0	0.5830	0.4010
LX0	0.8620	0.5650
LY0	0.8200	0.5360
LZ0	0.8150	0.4790
S60	0.9330	0.5490
SA0	0.7810	0.4370
SAA	0.8700	0.5430
SB0	0.8290	0.5060
SBB	0.8770	0.5250
SC0	0.8400	0.5030
SCC	0.6750	0.4050
SD0	0.5730	0.2460
SDD	0.6060	0.2920
SE0	0.8340	0.5000
SEE	0.6120	0.4200
SF0	0.7490	0.4160
SFF	0.1090	0.0310
SG0	0.7030	0.4000
SGG	0.5550	0.1570
SH0	0.8180	0.4420
SI0	0.8880	0.5450
SJ0	0.8680	0.5180
SK0	0.4450	0.1240
SL0	0.8350	0.5200
SM0	0.1140	0.0140
SN0	0.9130	0.5590
SO0	0.8820	0.5480
SP0	0.5180	0.1740
SQ0	0.7360	0.3400
SR0	0.6850	0.2960
SS0	0.6410	0.2850
ST0	0.6950	0.2540
SU0	0.4050	0.1760
SV0	0.8430	0.4920
SW0	0.9330	0.5830
SX0	0.8450	0.5300
SY0	0.6700	0.3780
SZ0	0.6590	0.2470