



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 10:46 AM UTC

PDB ID : 6Z6J / pdb_00006z6j
EMDB ID : EMD-11096
Title : Cryo-EM structure of yeast Lso2 bound to 80S ribosomes under native condition
Authors : Wells, J.N.; Buschauer, R.; Mackens-Kiani, T.; Best, K.; Kratzat, H.; Berninghausen, O.; Becker, T.; Cheng, J.; Beckmann, R.
Deposited on : 2020-05-28
Resolution : 3.40 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:

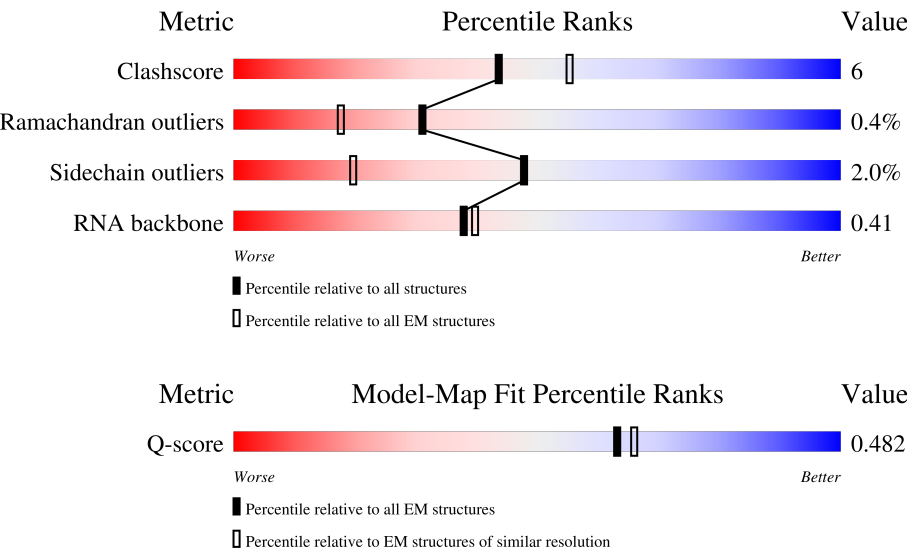
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 Å.

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



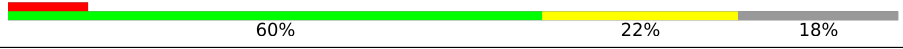
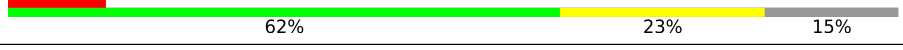
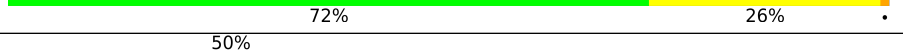
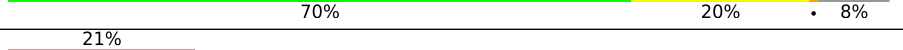
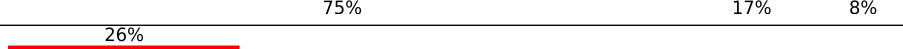
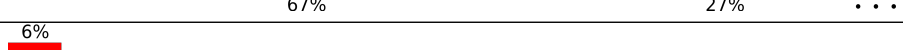
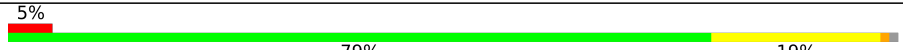
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	C2	1800	14% 51% 36% 7% 6%
2	C5	92	52% 72% 14% 14%
3	C1	3396	5% 58% 29% 5% 8%

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Mol	Chain	Length	Quality of chain
4	C4	121	
5	C3	158	
6	SA	252	
7	SB	255	
8	SC	254	
9	SD	240	
10	SE	261	
11	SF	225	
12	SG	236	
13	SH	190	
14	SI	200	
15	SJ	197	
16	SK	105	
17	SL	156	
18	SM	143	
19	SN	151	
20	SO	137	
21	SP	142	
22	SQ	143	
23	SR	136	
24	SS	146	
25	ST	144	
26	SU	121	
27	SV	87	
28	SW	130	

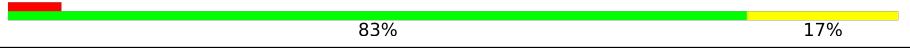
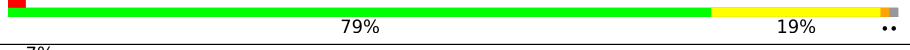
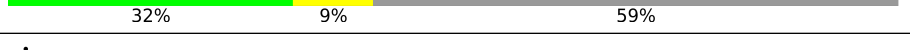
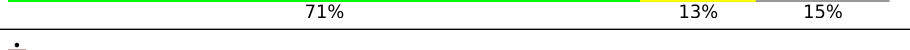
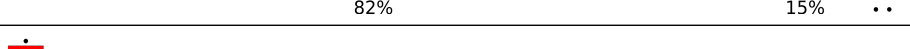
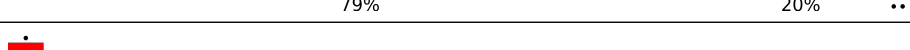
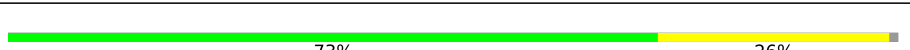
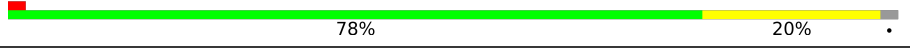
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Mol	Chain	Length	Quality of chain
29	SX	145	
30	SY	135	
31	SZ	108	
32	Sa	119	
33	Sb	82	
34	Sc	67	
35	Sd	56	
36	Se	63	
37	Sf	152	
38	Sg	319	
39	LA	254	
40	LB	387	
41	LC	362	
42	LD	297	
43	LE	176	
44	LF	244	
45	LG	256	
46	LH	191	
47	LI	221	
48	LJ	174	
49	LL	199	
50	LM	138	
51	LN	204	
52	LO	199	
53	LP	184	

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Mol	Chain	Length	Quality of chain
54	LQ	186	
55	LR	189	
56	LS	172	
57	LT	160	
58	LU	121	
59	LV	137	
60	LW	155	
61	LX	142	
62	LY	127	
63	LZ	136	
64	La	149	
65	Lb	59	
66	Lc	105	
67	Ld	113	
68	Le	130	
69	Lf	107	
70	Lg	121	
71	Lh	120	
72	Li	100	
73	Lj	88	
74	Lk	78	
75	Ll	51	
76	Lm	128	
77	Ln	25	
78	Lo	106	

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Mol	Chain	Length	Quality of chain
79	Lp	92	86% 12% ..

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 196350 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C2	1700	Total	C	N	O	P	0	0
			36234	16201	6426	11907	1700		

- Molecule 2 is a protein called Protein LSO2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C5	79	Total	C	N	O	S	0	0
			633	379	128	125	1		

- Molecule 3 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C1	3127	Total	C	N	O	P	0	0
			66891	29878	12066	21820	3127		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C3	157	Total	C	N	O	P	0	0
			3333	1491	584	1101	157		

- Molecule 6 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SA	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		

- Molecule 7 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SB	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		

- Molecule 8 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SC	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 9 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SD	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 10 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SE	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 11 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SF	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 12 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SG	218	Total	C	N	O	S	0	0
			1751	1100	337	311	3		

- Molecule 13 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	SH	185	Total	C	N	O	0	0
			1486	954	266	266		

- Molecule 14 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SI	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 15 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 16 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SK	92	Total	C	N	O	S	0	0
			741	478	121	140	2		

- Molecule 17 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SL	146	Total	C	N	O	S	0	0
			1168	747	221	197	3		

- Molecule 18 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SM	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 19 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 20 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SO	128	Total	C	N	O	S	0	0
			949	582	188	176	3		

- Molecule 21 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SP	119	Total	C	N	O	S	0	0
			939	595	176	161	7		

- Molecule 22 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SQ	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 23 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SR	115	Total	C	N	O	S	0	0
			896	557	172	165	2		

- Molecule 24 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 25 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	ST	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 26 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SU	101	Total	C	N	O	S	0	0
			805	512	145	147	1		

- Molecule 27 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 28 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 29 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 30 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SY	134	Total	C	N	O		0	0
			1073	676	208	189			

- Molecule 31 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SZ	69	Total	C	N	O		0	0
			558	357	103	98			

- Molecule 32 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Sb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 34 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 35 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Sd	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 36 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Se	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 37 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Sf	33	Total	C	N	O	S	0	0
			248	153	46	45	4		

- Molecule 38 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Sg	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LA	252	Total	C	N	O	S	0	0
			1912	1190	388	333	1		

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 41 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 42 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LD	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 43 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LE	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LF	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LG	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LH	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 47 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LI	209	Total	C	N	O	S	0	0
			1696	1077	321	293	5		

- Molecule 48 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LJ	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	LL	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LM	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LO	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	LP	175	Total	C	N	O	0	0
			1378	856	273	249		

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	LR	174	Total	C	N	O	0	0
			1359	840	283	236		

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LS	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LU	98	Total	C	N	O	S	0	0
			778	505	127	146			

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LV	134	Total	C	N	O	S	0	0
			993	623	187	176	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LW	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 61 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LX	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LY	124	Total	C	N	O	S	0	0
			976	614	190	172			

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	LZ	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 64 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	La	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 65 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	Lb	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 66 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Lc	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ld	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 68 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Le	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Lf	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Lg	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lh	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Li	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Lj	82	Total	C	N	O	S	0	0
			650	396	142	107	5		

- Molecule 74 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Lk	77	Total	C	N	O		0	0
			608	388	114	106			

- Molecule 75 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ll	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 76 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Lm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 77 is a protein called 60S ribosomal protein L41-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ln	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Lo	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

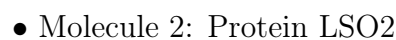
- Molecule 79 is a protein called 60S ribosomal protein L43-A.

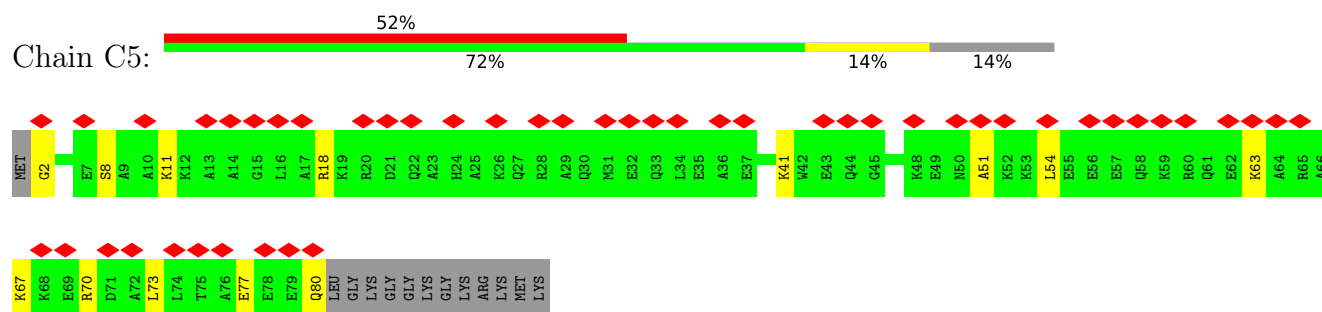
Mol	Chain	Residues	Atoms					AltConf	Trace
79	Lp	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 80 is ZINC ION (CCD ID: ZN) (formula: Zn).

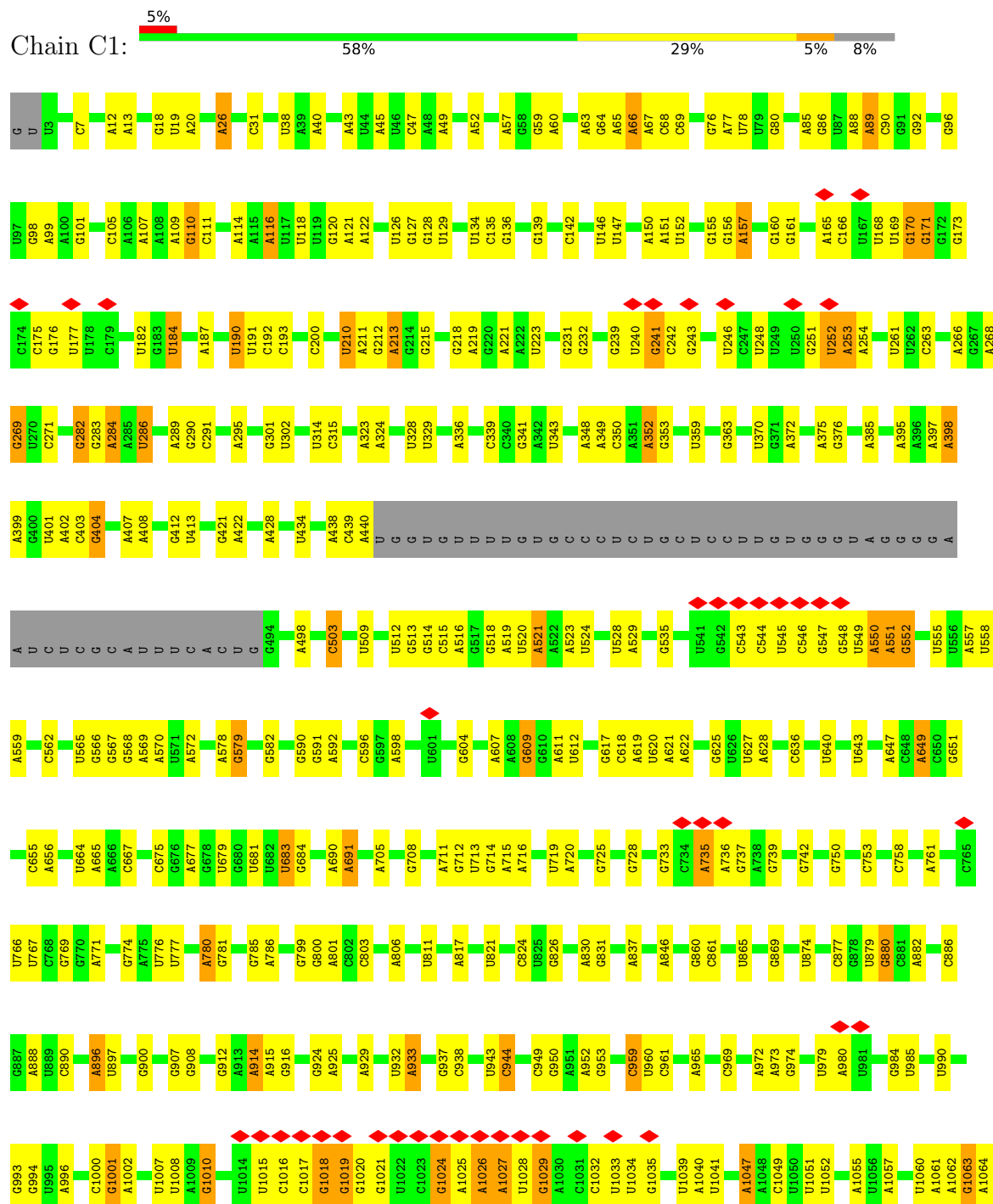
Mol	Chain	Residues	Atoms		AltConf
80	C2	1	Total	Zn	0
			1	1	
80	Sa	1	Total	Zn	0
			1	1	
80	Sb	1	Total	Zn	0
			1	1	
80	Sf	1	Total	Zn	0
			1	1	
80	Lg	1	Total	Zn	0
			1	1	
80	Lj	1	Total	Zn	0
			1	1	
80	Lm	1	Total	Zn	0
			1	1	
80	Lo	1	Total	Zn	0
			1	1	
80	Lp	1	Total	Zn	0
			1	1	

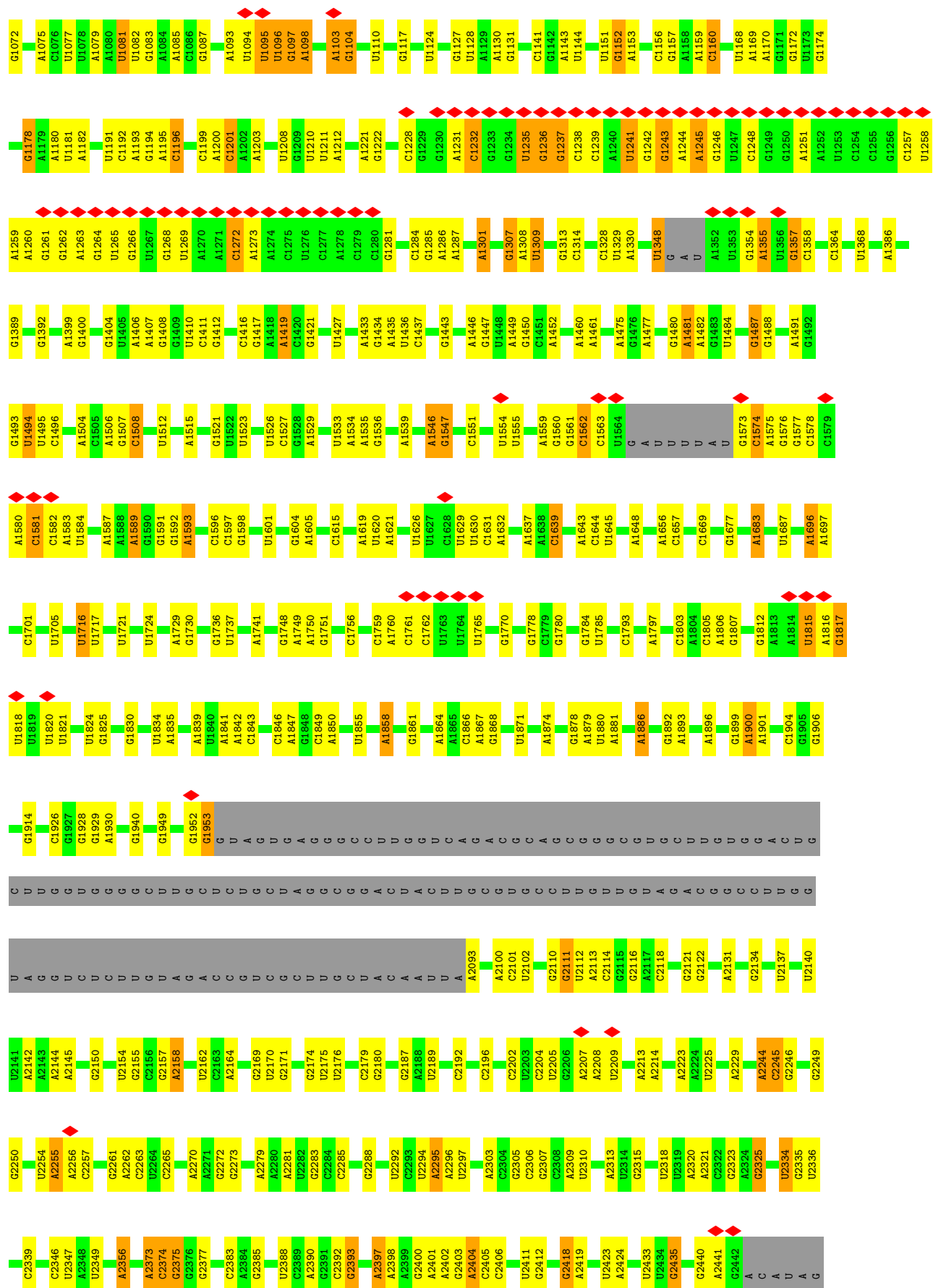


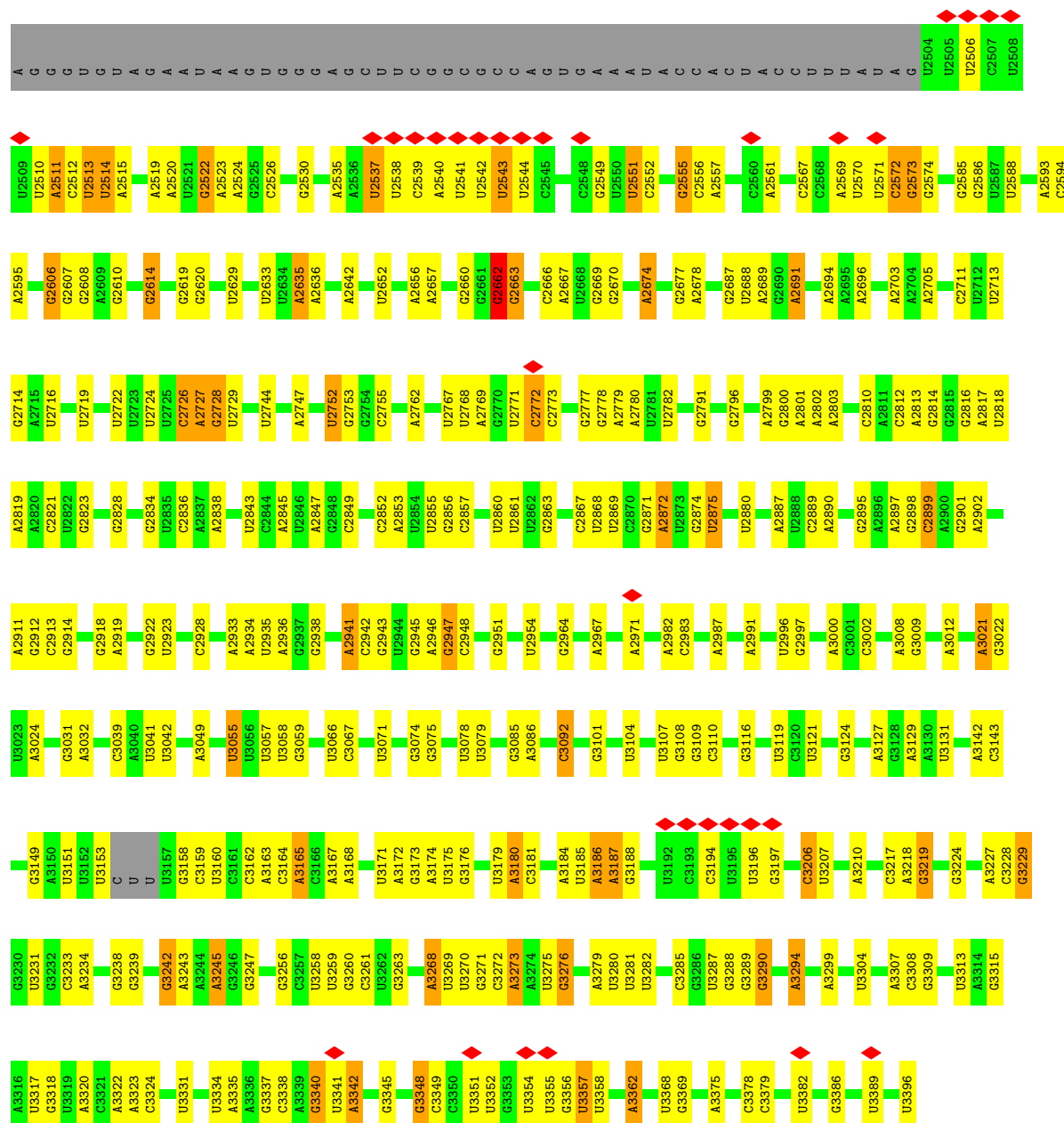




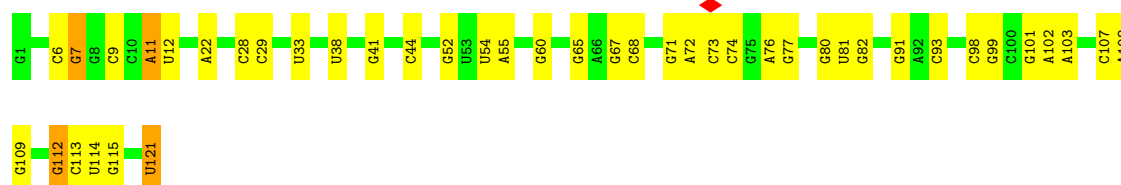
• Molecule 3: 25S rRNA





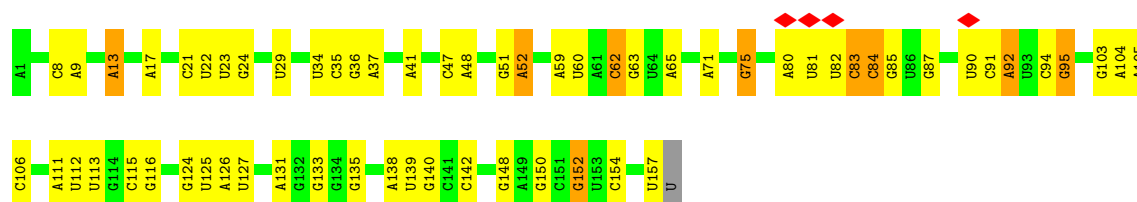


• Molecule 4: 5S rRNA



• Molecule 5: 5.8S rRNA

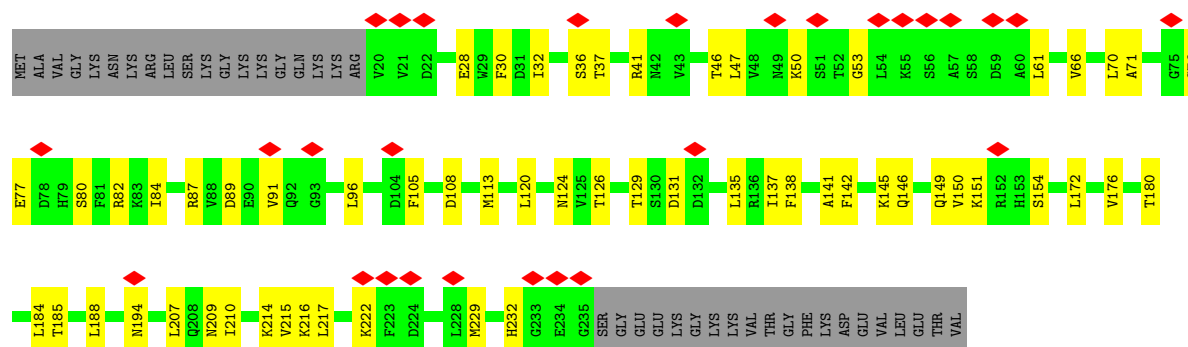




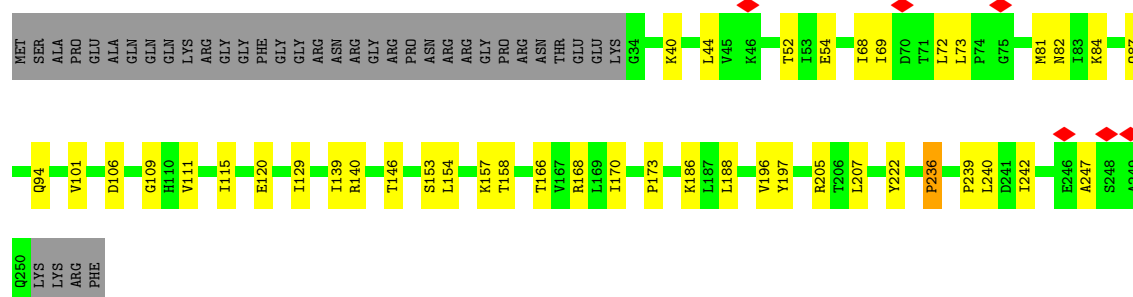
• Molecule 6: 40S ribosomal protein S0-A



• Molecule 7: 40S ribosomal protein S1-A

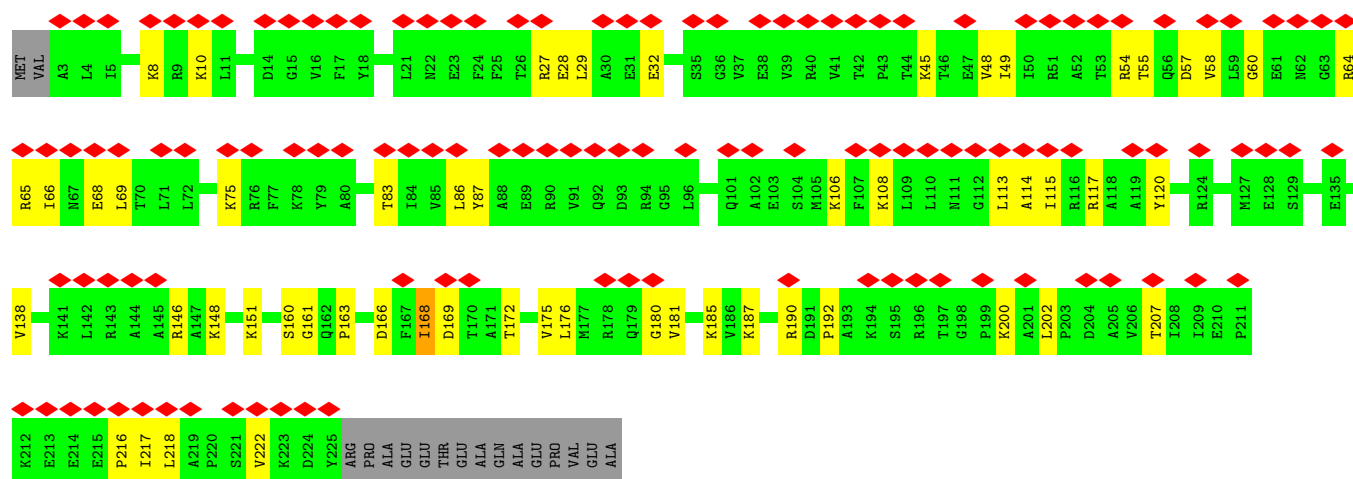


• Molecule 8: 40S ribosomal protein S2



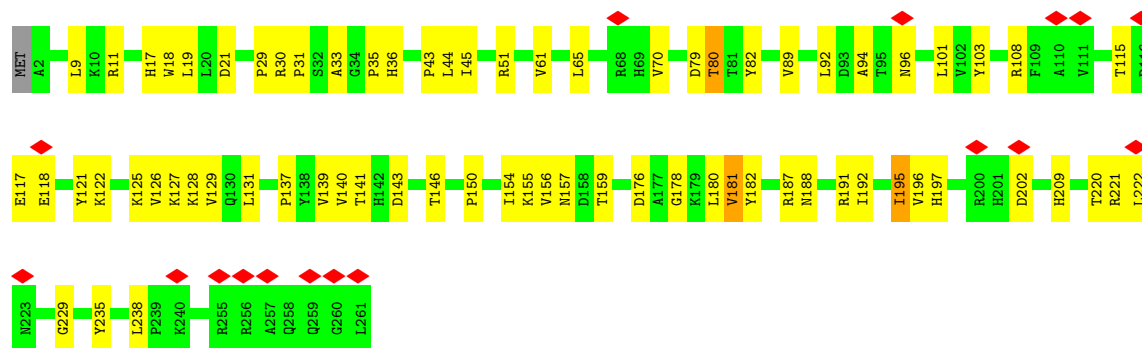
• Molecule 9: 40S ribosomal protein S3

Chain SD: 



• Molecule 10: 40S ribosomal protein S4-A

Chain SE: 

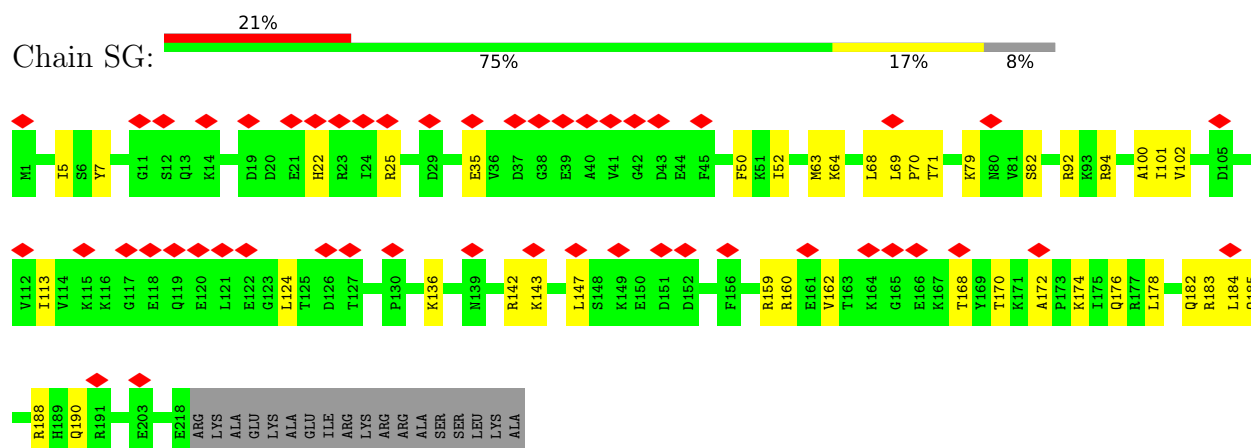


• Molecule 11: 40S ribosomal protein S5

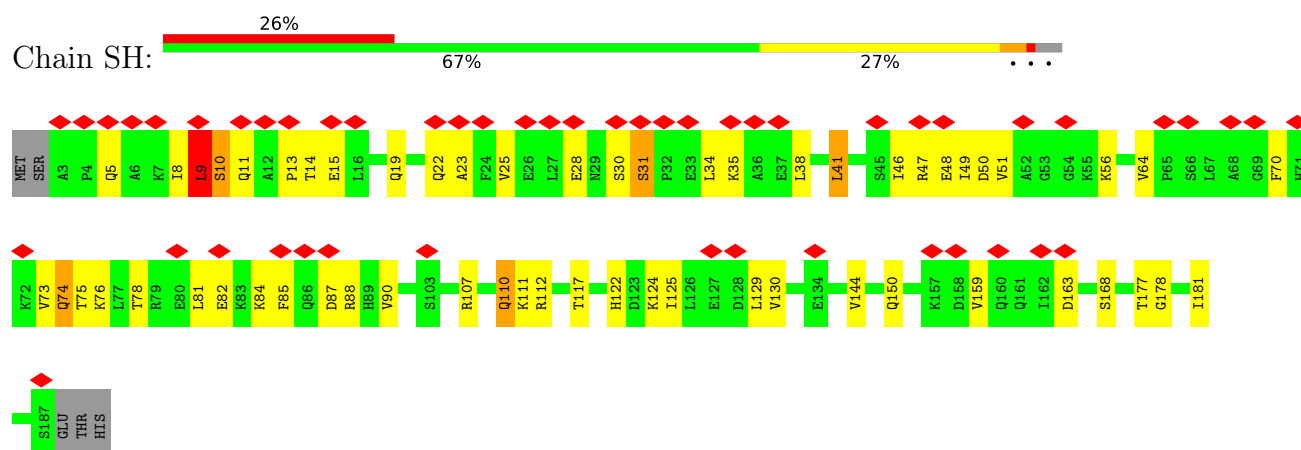
Chain SF: 



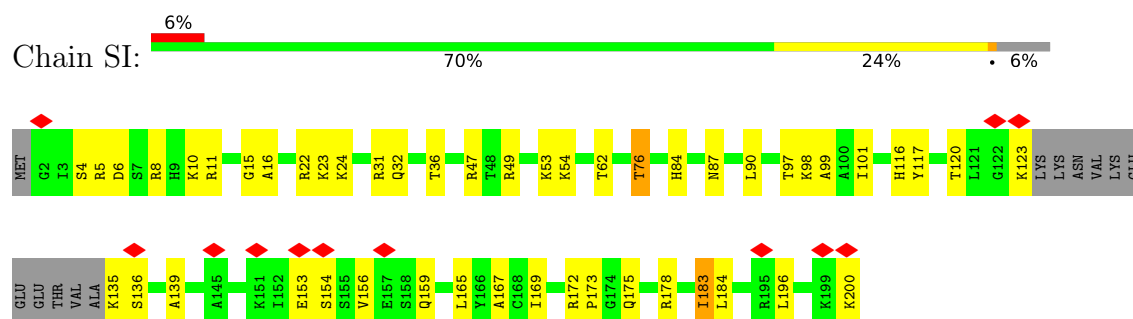
- Molecule 12: 40S ribosomal protein S6-A



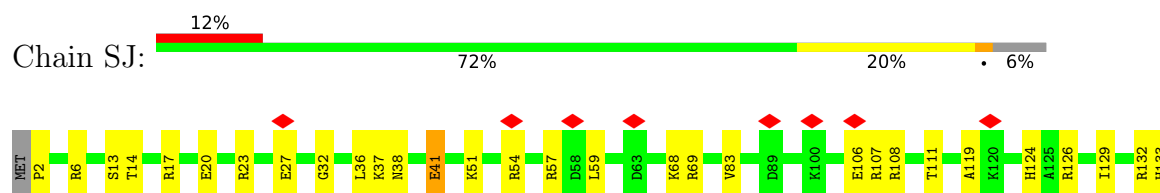
- Molecule 13: 40S ribosomal protein S7-A

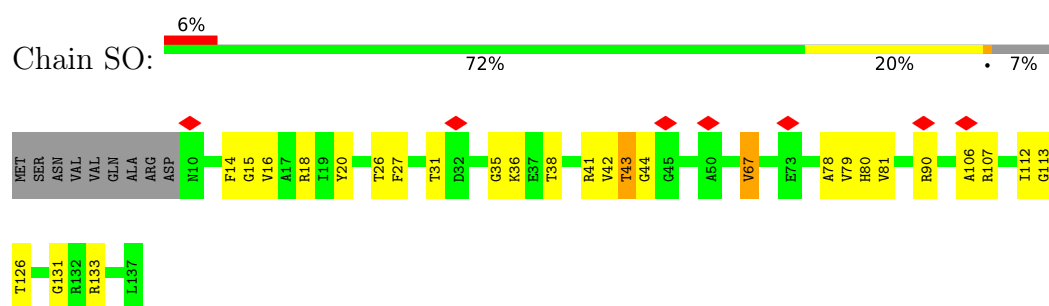


- Molecule 14: 40S ribosomal protein S8-A

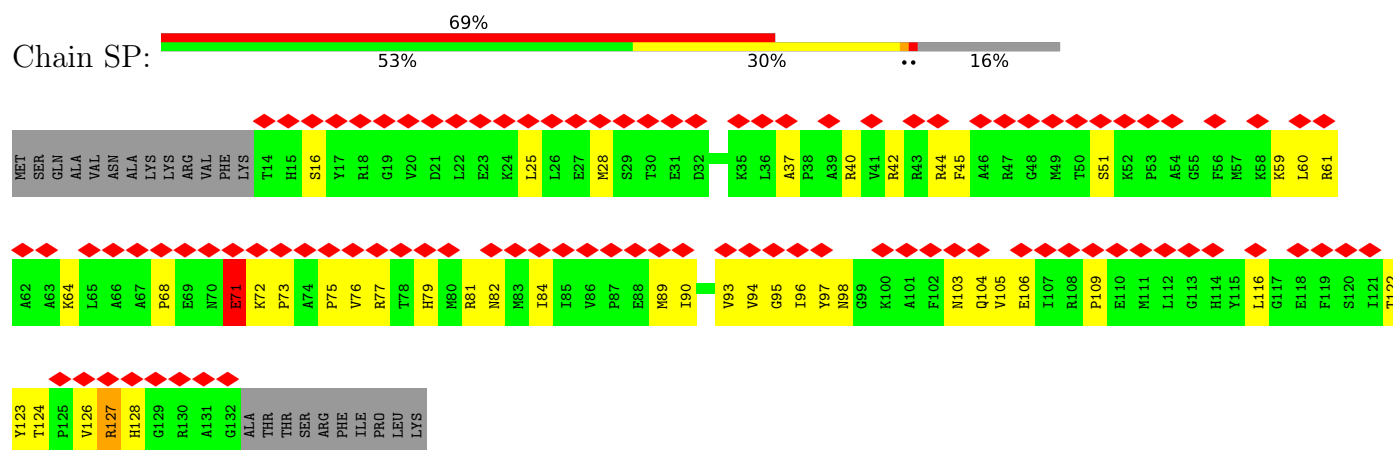


- Molecule 15: 40S ribosomal protein S9-A

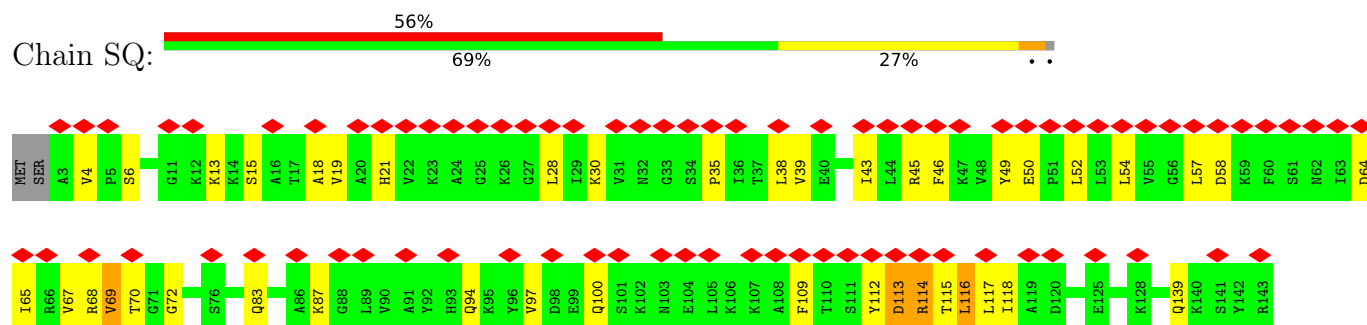




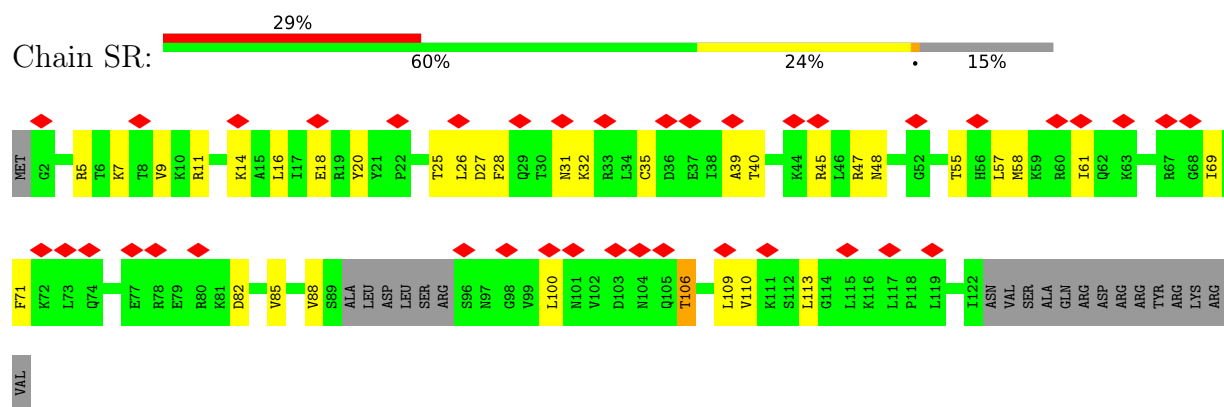
- Molecule 21: 40S ribosomal protein S15



- Molecule 22: 40S ribosomal protein S16-A

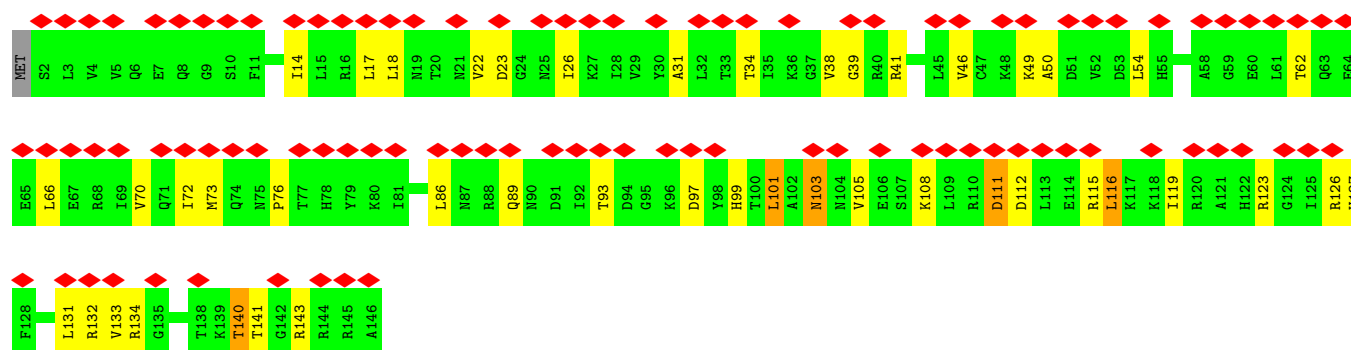


- Molecule 23: 40S ribosomal protein S17-A



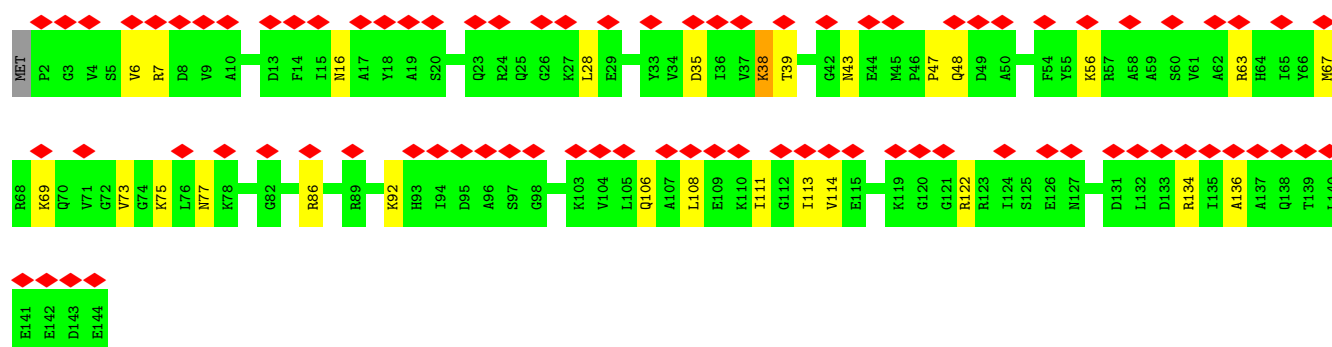
- Molecule 24: 40S ribosomal protein S18-A

Chain SS: 



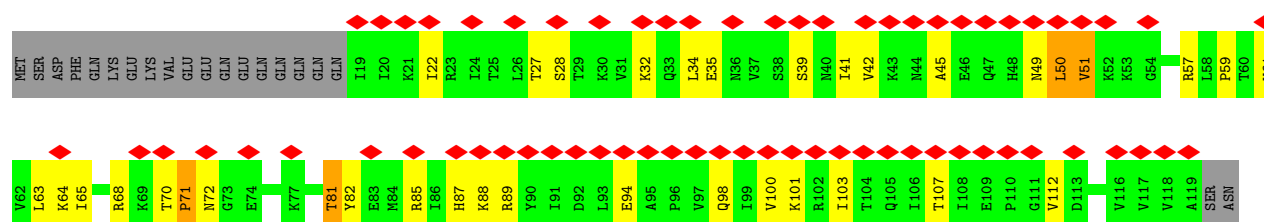
• Molecule 25: 40S ribosomal protein S19-A

Chain ST: 



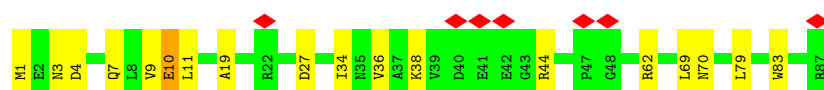
• Molecule 26: 40S ribosomal protein S20

Chain SU: 



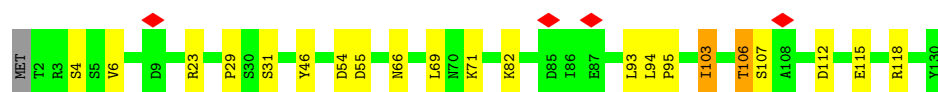
• Molecule 27: 40S ribosomal protein S21-A

Chain SV: 

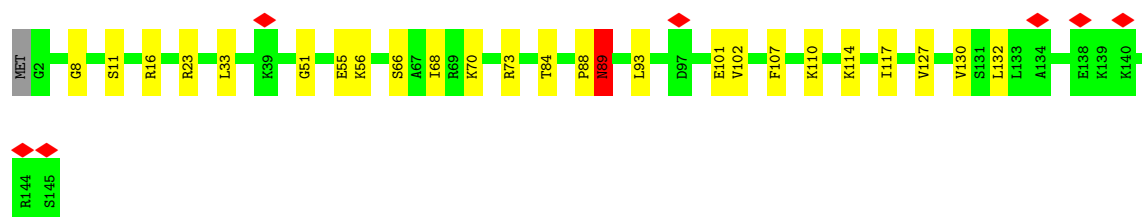
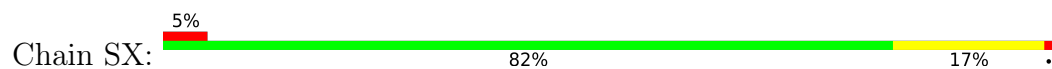


• Molecule 28: 40S ribosomal protein S22-A

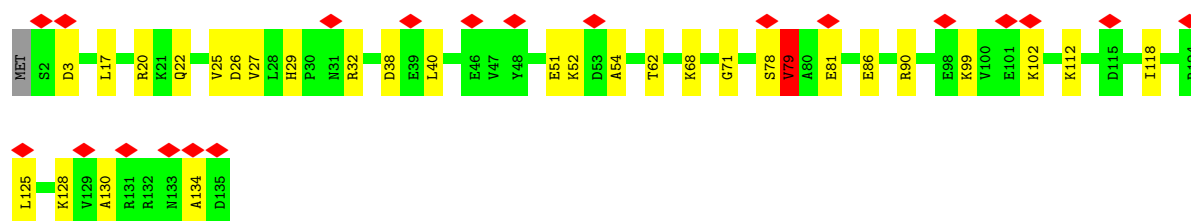
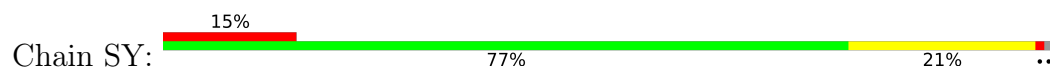
Chain SW: 



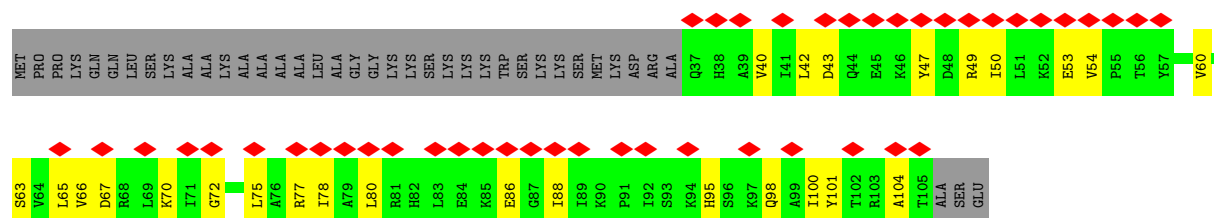
- Molecule 29: 40S ribosomal protein S23-A



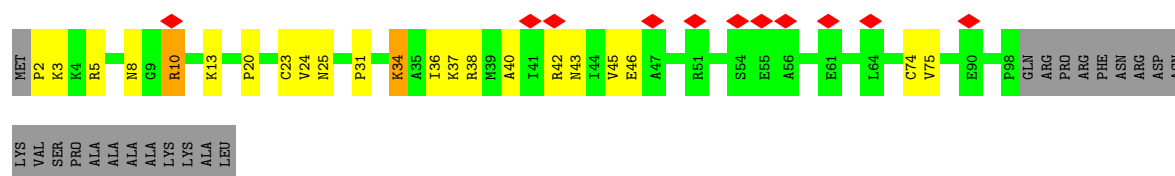
- Molecule 30: 40S ribosomal protein S24-A



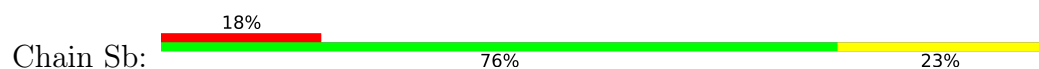
- Molecule 31: 40S ribosomal protein S25-A

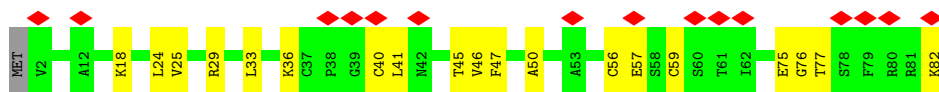


- Molecule 32: 40S ribosomal protein S26-B

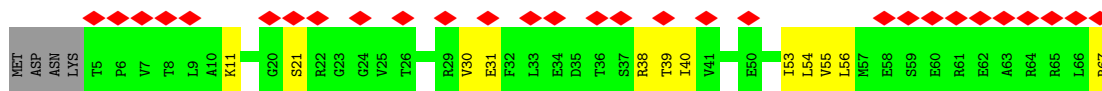
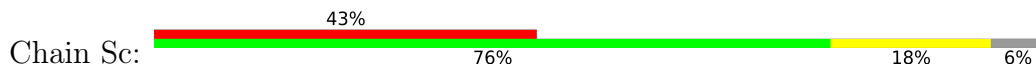


- Molecule 33: 40S ribosomal protein S27-A

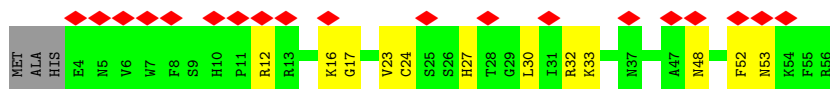
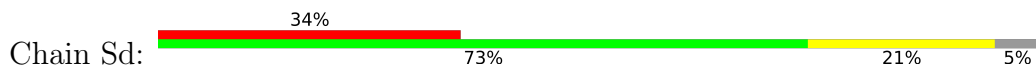




- Molecule 34: 40S ribosomal protein S28-A



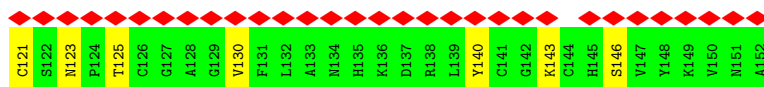
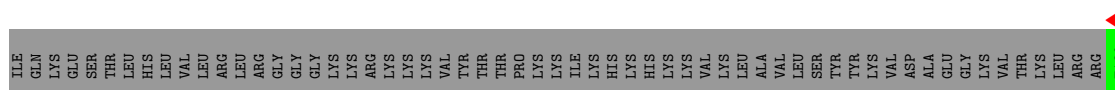
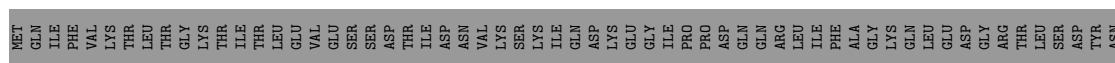
- Molecule 35: 40S ribosomal protein S29-A



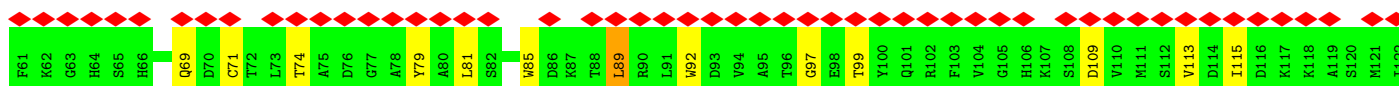
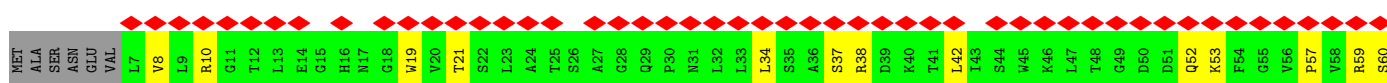
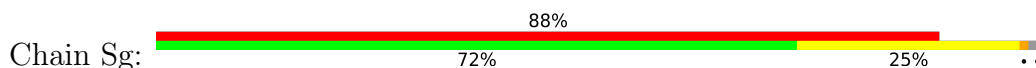
- Molecule 36: 40S ribosomal protein S30-A

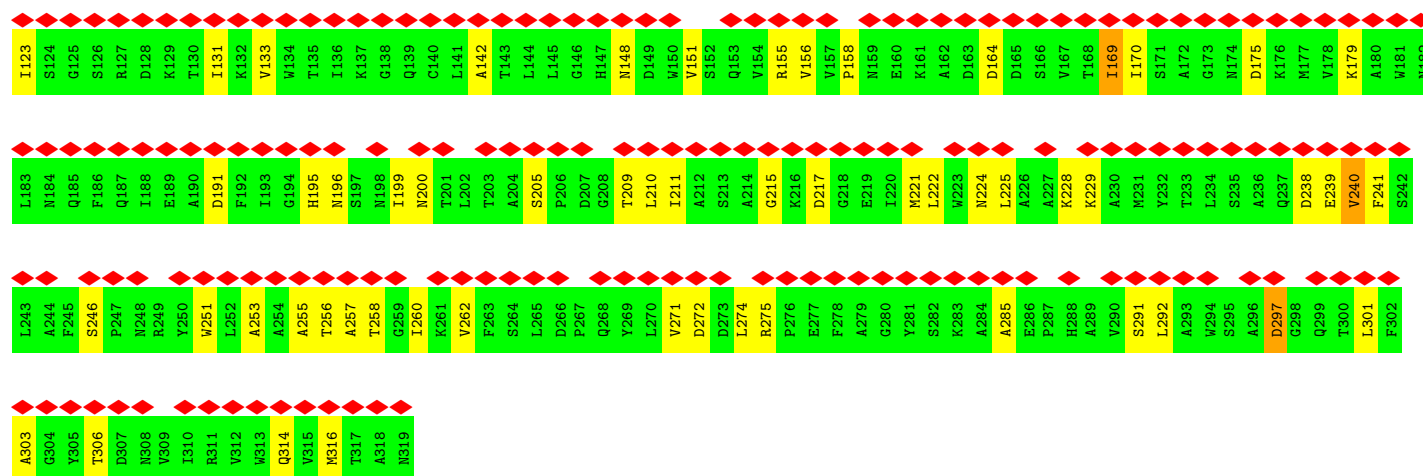


- Molecule 37: Ubiquitin-40S ribosomal protein S31



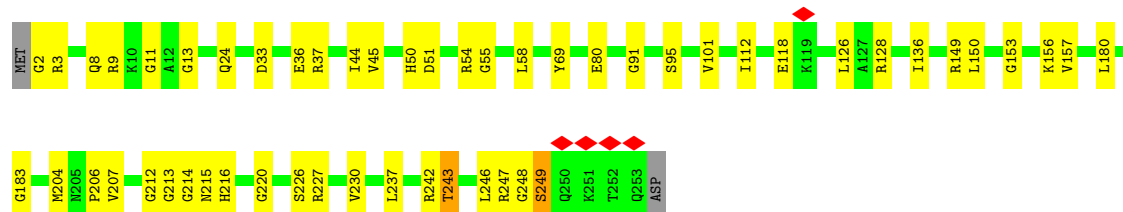
- Molecule 38: Guanine nucleotide-binding protein subunit beta-like protein





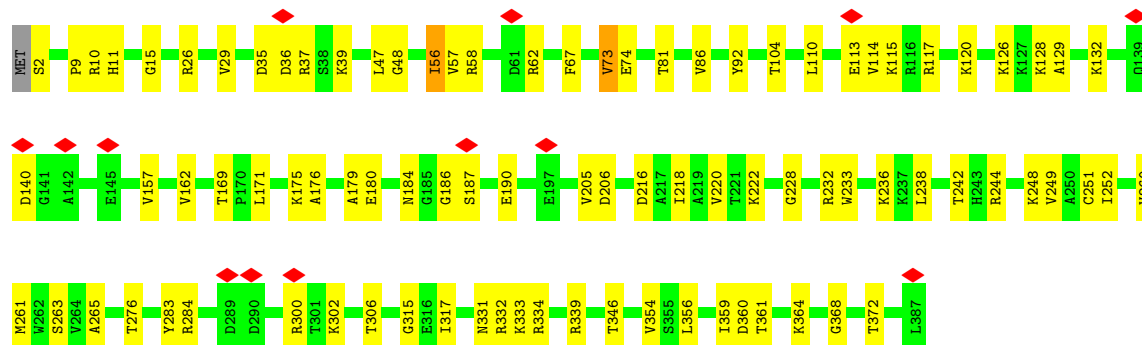
- Molecule 39: 60S ribosomal protein L2-A

Chain LA: 78% 20% ..



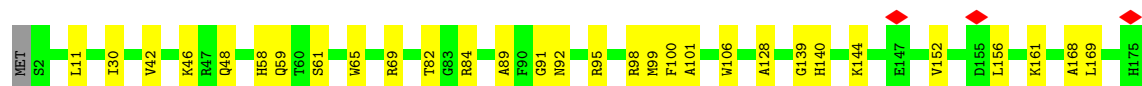
- Molecule 40: 60S ribosomal protein L3

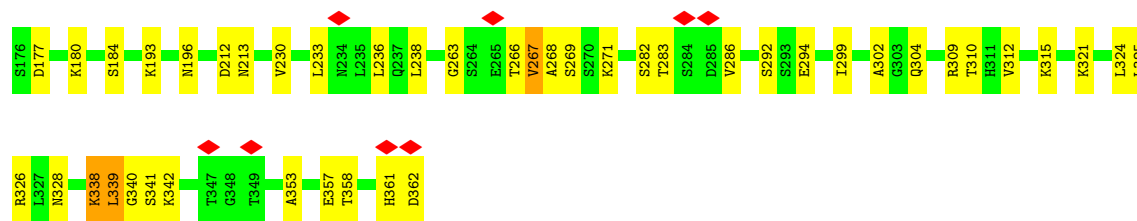
Chain LB: 76% 23% .



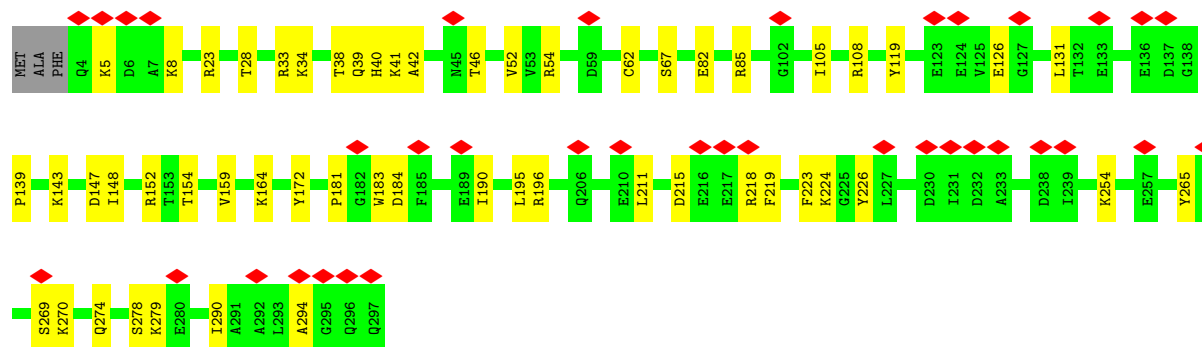
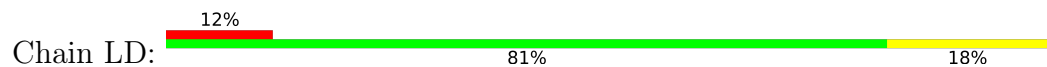
- Molecule 41: 60S ribosomal protein L4-A

Chain LC: 79% 20% .

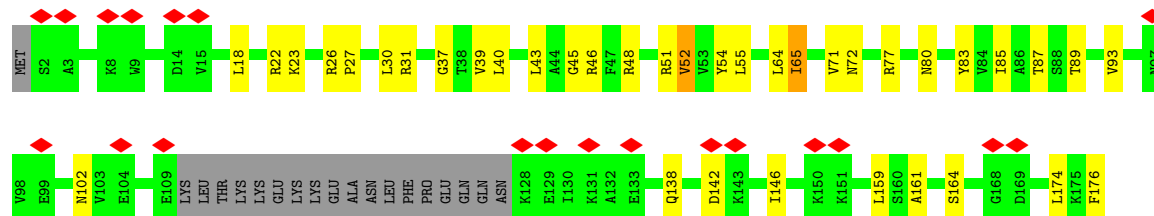




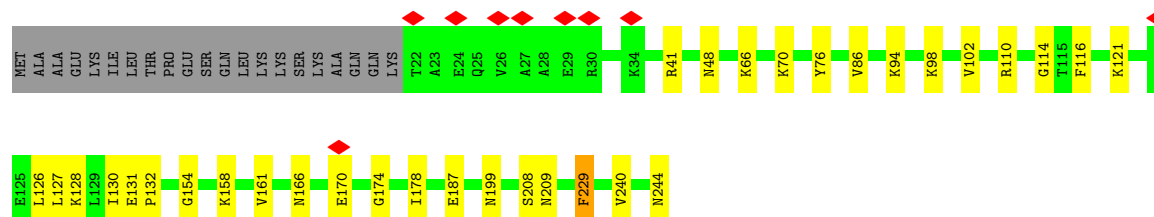
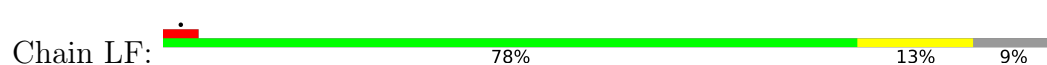
• Molecule 42: 60S ribosomal protein L5



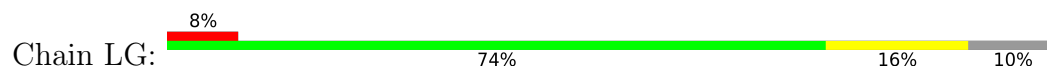
• Molecule 43: 60S ribosomal protein L6-A

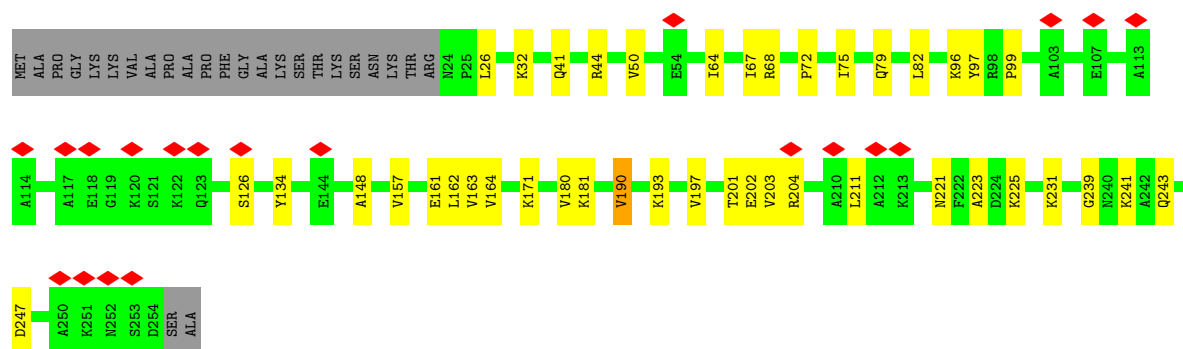


• Molecule 44: 60S ribosomal protein L7-A



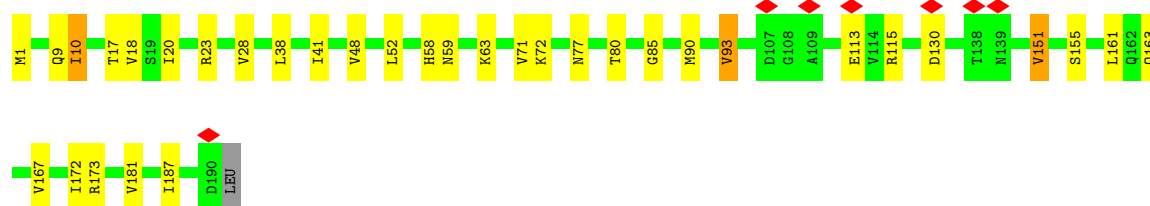
• Molecule 45: 60S ribosomal protein L8-A





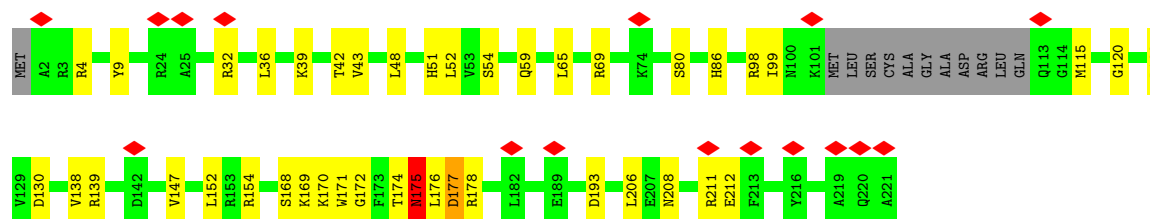
- Molecule 46: 60S ribosomal protein L9-A

Chain LH: 82% 16% ..



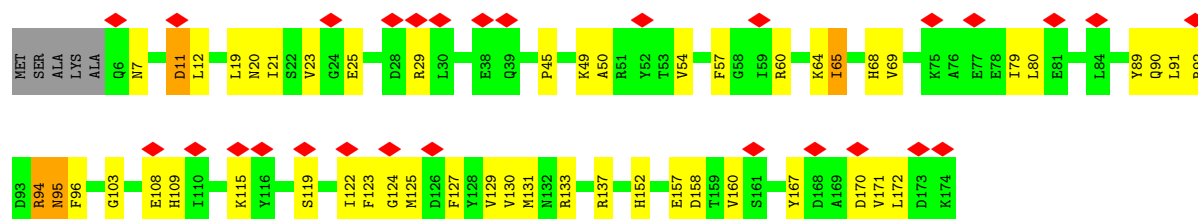
- Molecule 47: 60S ribosomal protein L10

Chain LI: 76% 18% 5%



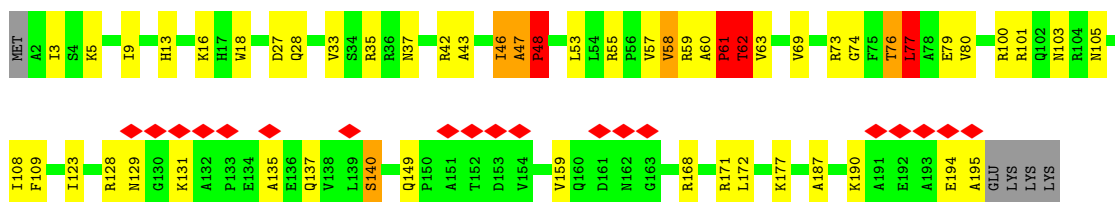
- Molecule 48: 60S ribosomal protein L11-A

Chain LJ: 68% 27% ..

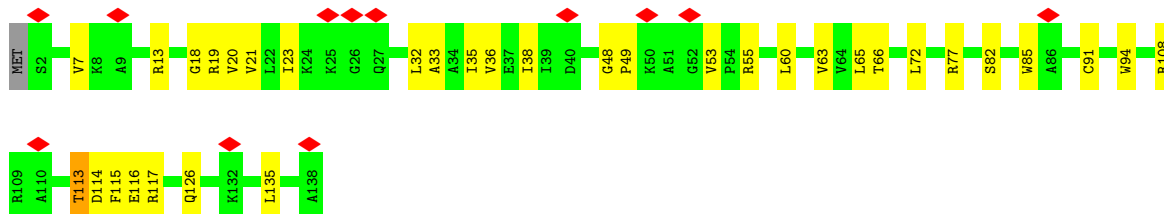
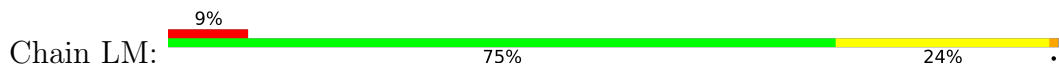


- Molecule 49: 60S ribosomal protein L13-A

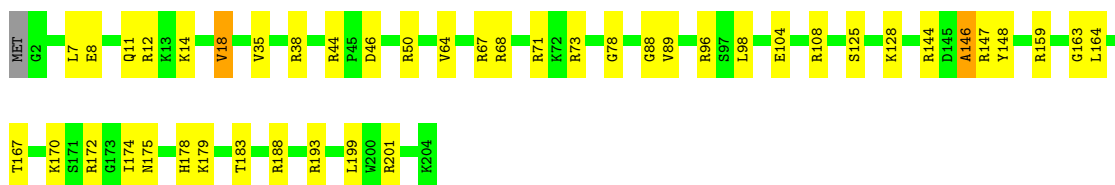
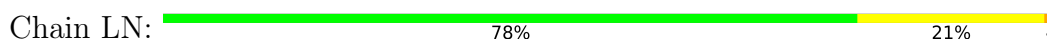
Chain LL: 70% 23% ..



• Molecule 50: 60S ribosomal protein L14-A



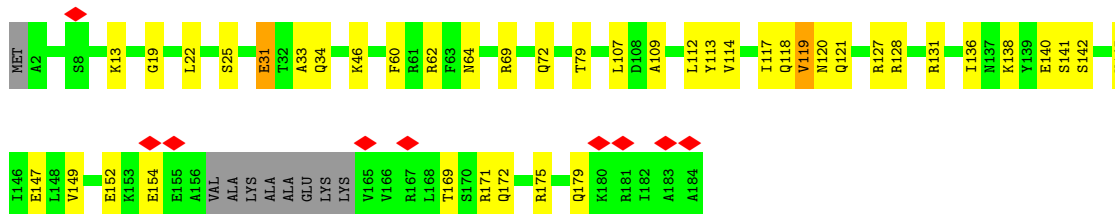
• Molecule 51: 60S ribosomal protein L15-A



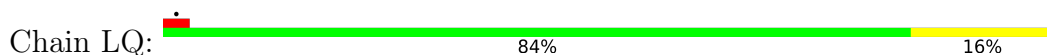
• Molecule 52: 60S ribosomal protein L16-A

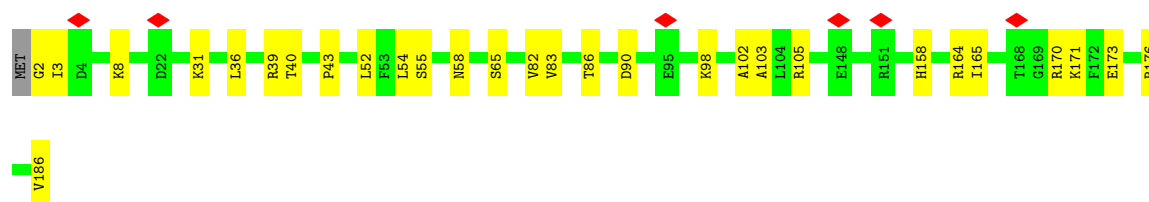


• Molecule 53: 60S ribosomal protein L17-A

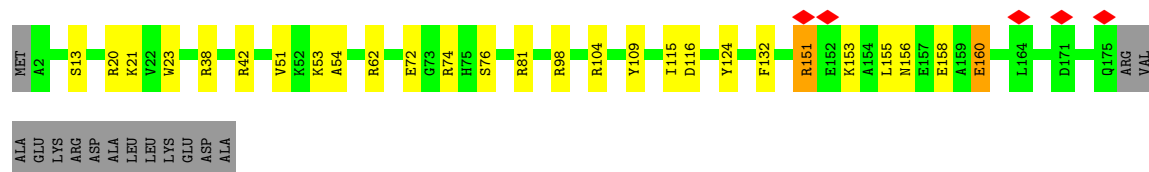
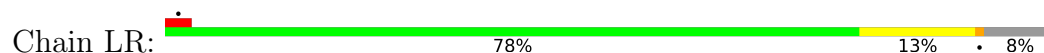


• Molecule 54: 60S ribosomal protein L18-A

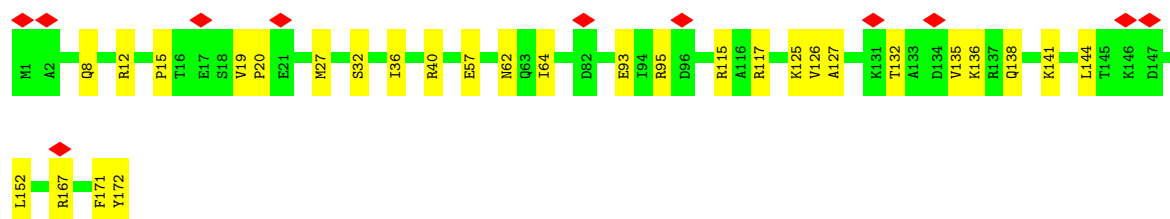
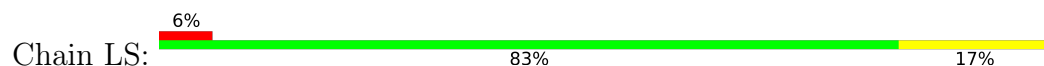




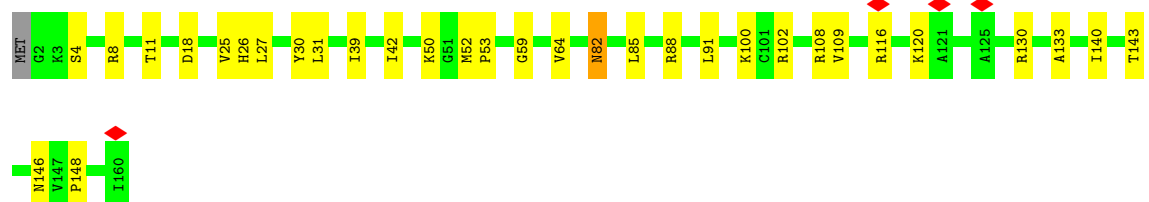
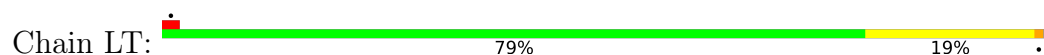
- Molecule 55: 60S ribosomal protein L19-A



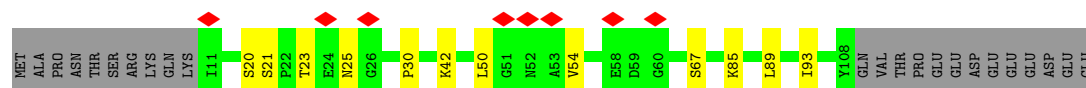
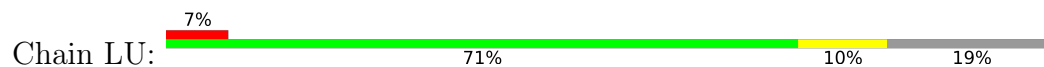
- Molecule 56: 60S ribosomal protein L20-A



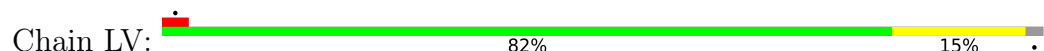
- Molecule 57: 60S ribosomal protein L21-A



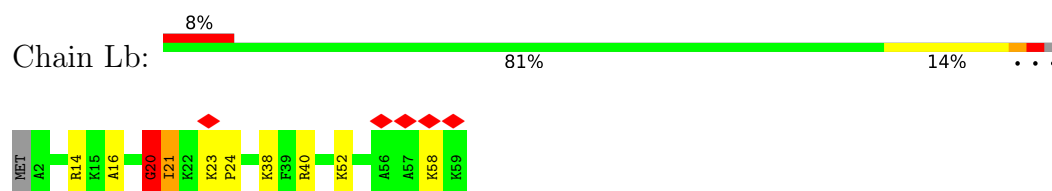
- Molecule 58: 60S ribosomal protein L22-A



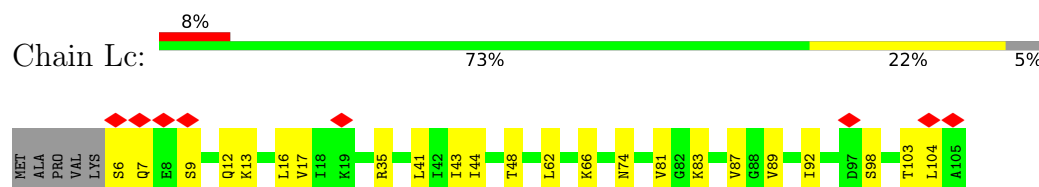
- Molecule 59: 60S ribosomal protein L23-A



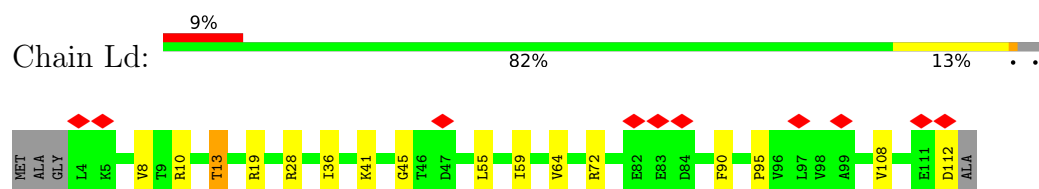
- Molecule 65: 60S ribosomal protein L29



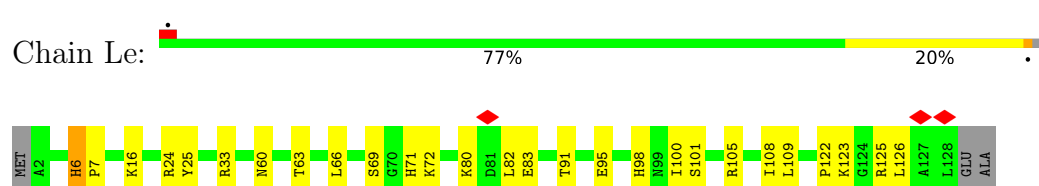
- Molecule 66: 60S ribosomal protein L30



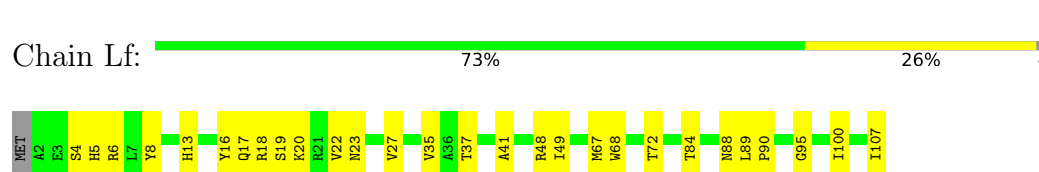
- Molecule 67: 60S ribosomal protein L31-A



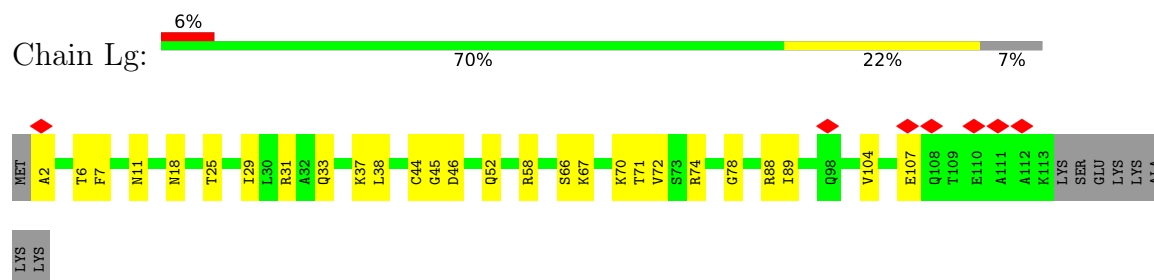
- Molecule 68: 60S ribosomal protein L32



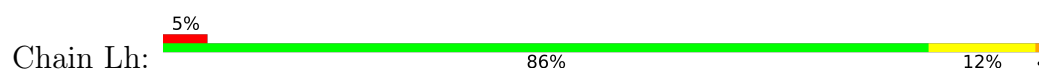
- Molecule 69: 60S ribosomal protein L33-A



- Molecule 70: 60S ribosomal protein L34-A

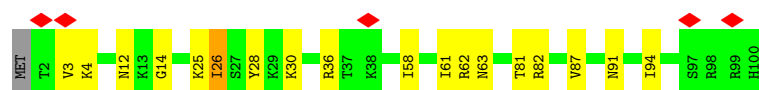
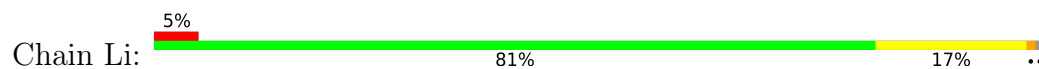


- Molecule 71: 60S ribosomal protein L35-A

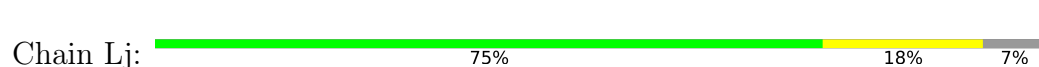




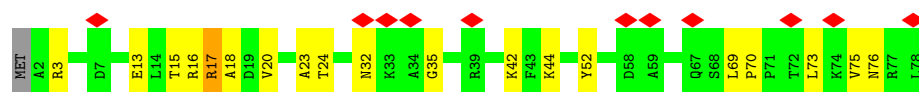
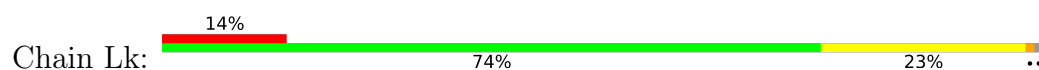
- Molecule 72: 60S ribosomal protein L36-A



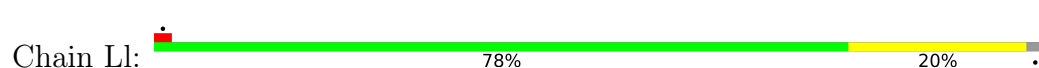
- Molecule 73: 60S ribosomal protein L37-A



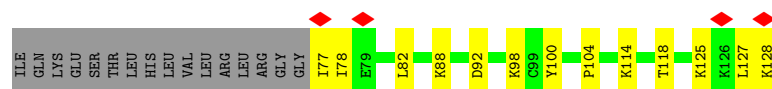
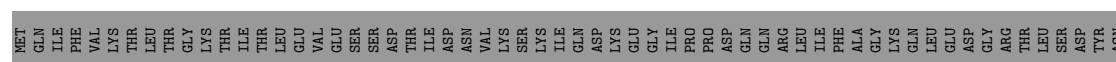
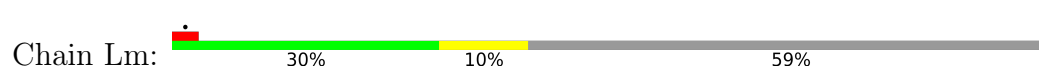
- Molecule 74: 60S ribosomal protein L38



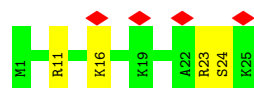
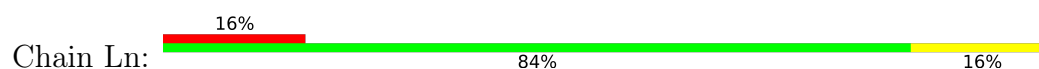
- Molecule 75: 60S ribosomal protein L39



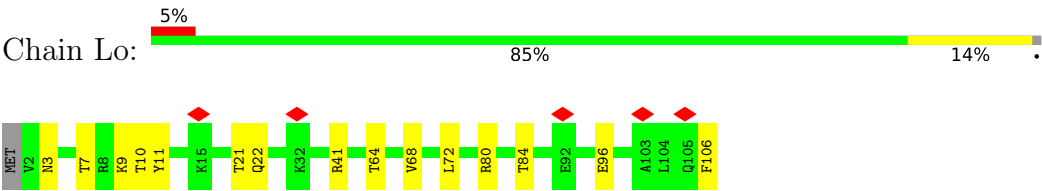
- Molecule 76: Ubiquitin-60S ribosomal protein L40



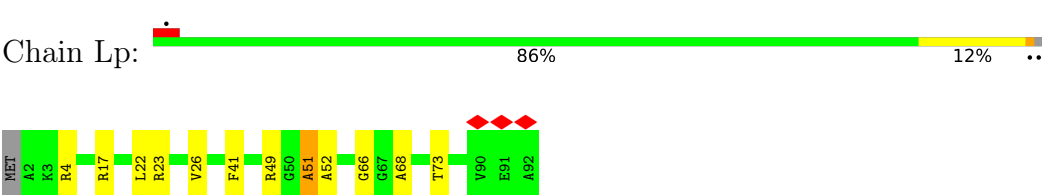
- Molecule 77: 60S ribosomal protein L41-B



● Molecule 78: 60S ribosomal protein L42-A



● Molecule 79: 60S ribosomal protein L43-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34951	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.865	Depositor
Minimum map value	-0.566	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	433.6, 433.6, 433.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	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

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	C2	0.52	0/40528	0.60	17/63141 (0.0%)
2	C5	0.32	0/636	0.56	0/837
3	C1	0.65	0/74873	0.58	9/116727 (0.0%)
4	C4	0.54	0/2883	0.49	0/4491
5	C3	0.64	0/3724	0.55	0/5798
6	SA	0.45	0/1623	0.77	2/2222 (0.1%)
7	SB	0.51	0/1748	0.75	0/2352
8	SC	0.52	0/1665	0.74	0/2263
9	SD	0.37	0/1759	0.72	0/2368
10	SE	0.48	0/2109	0.77	0/2839
11	SF	0.37	0/1629	0.75	0/2202
12	SG	0.42	0/1775	0.68	1/2374 (0.0%)
13	SH	0.50	0/1511	0.92	9/2036 (0.4%)
14	SI	0.58	0/1514	0.71	0/2021
15	SJ	0.45	0/1519	0.71	1/2035 (0.0%)
16	SK	0.35	0/757	0.79	0/1022
17	SL	0.55	0/1194	0.69	0/1610
18	SM	0.34	0/898	1.01	3/1220 (0.2%)
19	SN	0.51	0/1215	0.75	2/1638 (0.1%)
20	SO	0.53	0/960	0.78	0/1290
21	SP	0.40	0/959	0.83	2/1288 (0.2%)
22	SQ	0.36	0/1125	0.87	3/1510 (0.2%)
23	SR	0.38	0/904	0.71	0/1210
24	SS	0.36	0/1211	0.72	0/1628
25	ST	0.36	0/1130	0.73	2/1517 (0.1%)
26	SU	0.39	0/815	0.74	0/1102
27	SV	0.47	0/693	0.71	1/935 (0.1%)
28	SW	0.61	0/1038	0.70	0/1395
29	SX	0.53	0/1139	0.72	0/1518
30	SY	0.42	0/1087	0.78	0/1449
31	SZ	0.36	0/566	0.87	2/761 (0.3%)
32	Sa	0.54	0/782	0.80	0/1047

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Sb	0.47	0/620	0.73	0/838
34	Sc	0.37	0/499	0.77	0/670
35	Sd	0.36	0/452	0.74	0/600
36	Se	0.40	0/483	0.79	1/643 (0.2%)
37	Sf	0.36	0/253	0.78	0/340
38	Sg	0.34	0/2456	0.74	0/3343
39	LA	0.69	0/1946	0.81	2/2614 (0.1%)
40	LB	0.62	0/3146	0.72	0/4228
41	LC	0.62	0/2800	0.80	1/3790 (0.0%)
42	LD	0.46	0/2408	0.66	0/3248
43	LE	0.51	0/1269	0.67	0/1705
44	LF	0.60	0/1828	0.71	0/2461
45	LG	0.53	0/1795	0.77	0/2429
46	LH	0.48	0/1531	0.69	0/2062
47	LI	0.51	0/1732	0.66	1/2323 (0.0%)
48	LJ	0.48	0/1374	0.89	2/1842 (0.1%)
49	LL	0.58	0/1573	0.93	6/2113 (0.3%)
50	LM	0.51	0/1074	0.62	0/1446
51	LN	0.67	0/1757	0.76	1/2354 (0.0%)
52	LO	0.60	0/1585	0.69	1/2128 (0.0%)
53	LP	0.67	1/1400 (0.1%)	0.75	0/1882
54	LQ	0.58	0/1465	0.72	0/1965
55	LR	0.69	0/1376	0.72	1/1842 (0.1%)
56	LS	0.58	0/1481	0.66	0/1990
57	LT	0.60	0/1300	0.67	0/1743
58	LU	0.44	0/794	0.68	0/1076
59	LV	0.59	0/1008	0.70	0/1356
60	LW	0.59	0/533	0.68	0/707
61	LX	0.55	0/974	0.79	0/1314
62	LY	0.52	0/987	0.64	0/1318
63	LZ	0.54	0/1118	0.67	0/1497
64	La	0.63	0/1204	0.80	1/1612 (0.1%)
65	Lb	0.49	0/473	0.86	2/629 (0.3%)
66	Lc	0.55	0/775	0.67	0/1040
67	Ld	0.60	0/897	0.70	0/1205
68	Le	0.60	0/1041	0.77	0/1394
69	Lf	0.68	0/868	0.72	0/1168
70	Lg	0.61	0/890	0.70	0/1189
71	Lh	0.52	0/974	0.59	0/1297
72	Li	0.49	0/777	0.70	0/1033
73	Lj	0.72	0/665	0.75	0/882
74	Lk	0.49	0/614	0.74	0/822
75	Ll	0.64	0/443	0.71	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Lm	0.57	0/423	0.67	0/562
77	Ln	0.48	0/234	0.58	0/300
78	Lo	0.52	0/860	0.63	0/1136
79	Lp	0.60	0/701	0.75	0/934
All	All	0.58	1/210825 (0.0%)	0.65	73/309504 (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	SA	0	4
7	SB	0	1
8	SC	0	1
10	SE	0	3
12	SG	0	1
13	SH	0	5
15	SJ	0	1
16	SK	0	2
18	SM	0	3
19	SN	0	2
20	SO	0	2
21	SP	0	2
22	SQ	0	2
24	SS	0	1
26	SU	0	3
28	SW	0	1
30	SY	0	2
31	SZ	0	1
32	Sa	0	2
33	Sb	0	2
36	Se	0	3
39	LA	0	4
40	LB	0	2
41	LC	0	4
45	LG	0	1
48	LJ	0	1
49	LL	0	4
51	LN	0	1
54	LQ	0	1
56	LS	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
58	LU	0	1
63	LZ	0	2
64	La	0	1
65	Lb	0	2
67	Ld	0	1
71	Lh	0	2
72	Li	0	1
79	Lp	0	1
All	All	0	74

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	LP	72	GLN	CA-C	-5.45	1.44	1.52

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C2	853	G	O4'-C1'-N9	8.54	121.01	108.20
64	La	48	TYR	CB-CA-C	-8.38	101.53	109.83
49	LL	140	SER	CA-C-N	8.38	137.54	121.54
49	LL	140	SER	C-N-CA	8.38	137.54	121.54
1	C2	854	U	C5'-C4'-O4'	7.96	121.75	109.80

There are no chirality outliers.

5 of 74 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	SA	184	LEU	Peptide
6	SA	186	GLY	Peptide
6	SA	43	ASP	Peptide
6	SA	94	GLY	Peptide
7	SB	105	PHE	Peptide

5.2 Too-close contacts

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	C2	36234	0	18229	404	0
2	C5	633	0	637	12	0
3	C1	66891	0	33617	512	0
4	C4	2579	0	1304	22	0
5	C3	3333	0	1685	29	0
6	SA	1583	0	1578	34	0
7	SB	1722	0	1793	37	0
8	SC	1635	0	1723	28	0
9	SD	1734	0	1817	40	0
10	SE	2068	0	2154	49	0
11	SF	1609	0	1675	37	0
12	SG	1751	0	1842	28	0
13	SH	1486	0	1576	34	0
14	SI	1489	0	1525	34	0
15	SJ	1494	0	1573	30	0
16	SK	741	0	691	15	0
17	SL	1168	0	1233	16	0
18	SM	890	0	887	18	0
19	SN	1192	0	1255	22	0
20	SO	949	0	985	17	0
21	SP	939	0	968	29	0
22	SQ	1105	0	1166	28	0
23	SR	896	0	902	26	0
24	SS	1192	0	1222	35	0
25	ST	1112	0	1124	25	0
26	SU	805	0	874	25	0
27	SV	684	0	672	14	0
28	SW	1021	0	1060	15	0
29	SX	1121	0	1196	17	0
30	SY	1073	0	1132	17	0
31	SZ	558	0	598	15	0
32	Sa	769	0	815	14	0
33	Sb	610	0	632	10	0
34	Sc	497	0	535	9	0
35	Sd	442	0	431	10	0
36	Se	475	0	525	16	0
37	Sf	248	0	237	4	0
38	Sg	2403	0	2350	54	0
39	LA	1912	0	1976	34	0
40	LB	3075	0	3142	51	0
41	LC	2748	0	2859	52	0
42	LD	2359	0	2311	41	0
43	LE	1248	0	1339	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	LF	1791	0	1869	24	0
45	LG	1763	0	1819	30	0
46	LH	1510	0	1576	22	0
47	LI	1696	0	1731	31	0
48	LJ	1353	0	1383	30	0
49	LL	1548	0	1613	38	0
50	LM	1059	0	1154	25	0
51	LN	1720	0	1779	37	0
52	LO	1555	0	1659	18	0
53	LP	1378	0	1404	26	0
54	LQ	1441	0	1543	21	0
55	LR	1359	0	1403	24	0
56	LS	1445	0	1487	17	0
57	LT	1276	0	1323	25	0
58	LU	778	0	791	6	0
59	LV	993	0	1040	14	0
60	LW	521	0	551	10	0
61	LX	959	0	1023	14	0
62	LY	976	0	1064	16	0
63	LZ	1092	0	1155	22	0
64	La	1173	0	1215	29	0
65	Lb	462	0	491	6	0
66	Lc	767	0	816	13	0
67	Ld	883	0	918	9	0
68	Le	1020	0	1090	18	0
69	Lf	850	0	880	17	0
70	Lg	880	0	942	21	0
71	Lh	965	0	1067	13	0
72	Li	770	0	846	11	0
73	Lj	650	0	650	11	0
74	Lk	608	0	671	13	0
75	Ll	436	0	475	8	0
76	Lm	417	0	455	10	0
77	Ln	233	0	284	4	0
78	Lo	847	0	915	11	0
79	Lp	694	0	734	11	0
80	C2	1	0	0	0	0
80	Lg	1	0	0	0	0
80	Lj	1	0	0	0	0
80	Lm	1	0	0	0	0
80	Lo	1	0	0	0	0
80	Lp	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	Sa	1	0	0	0	0
80	Sb	1	0	0	0	0
80	Sf	1	0	0	0	0
All	All	196350	0	145661	2142	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 6.

The worst 5 of 2142 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)
1:C2:1681:A:C2	1:C2:1720:G:N2	1.80	1.49
1:C2:1681:A:H2	1:C2:1720:G:N2	1.31	1.06
1:C2:1677:C:H42	1:C2:1724:U:H3	1.01	1.01
55:LR:151:ARG:HG2	55:LR:151:ARG:HH11	1.24	1.00
3:C1:3121:U:C4	3:C1:3124:G:O6	2.16	0.99

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C5	77/92 (84%)	73 (95%)	4 (5%)	0	100	100
6	SA	204/252 (81%)	175 (86%)	29 (14%)	0	100	100
7	SB	214/255 (84%)	190 (89%)	24 (11%)	0	100	100
8	SC	215/254 (85%)	195 (91%)	19 (9%)	1 (0%)	24	54
9	SD	221/240 (92%)	196 (89%)	25 (11%)	0	100	100
10	SE	258/261 (99%)	233 (90%)	24 (9%)	1 (0%)	30	59
11	SF	204/225 (91%)	177 (87%)	26 (13%)	1 (0%)	24	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	SG	216/236 (92%)	201 (93%)	15 (7%)	0	100	100
13	SH	183/190 (96%)	156 (85%)	24 (13%)	3 (2%)	7	29
14	SI	184/200 (92%)	173 (94%)	11 (6%)	0	100	100
15	SJ	183/197 (93%)	166 (91%)	15 (8%)	2 (1%)	11	38
16	SK	90/105 (86%)	70 (78%)	20 (22%)	0	100	100
17	SL	144/156 (92%)	123 (85%)	21 (15%)	0	100	100
18	SM	122/143 (85%)	83 (68%)	36 (30%)	3 (2%)	4	21
19	SN	148/151 (98%)	135 (91%)	13 (9%)	0	100	100
20	SO	126/137 (92%)	109 (86%)	17 (14%)	0	100	100
21	SP	117/142 (82%)	95 (81%)	20 (17%)	2 (2%)	7	28
22	SQ	139/143 (97%)	126 (91%)	12 (9%)	1 (1%)	18	47
23	SR	111/136 (82%)	96 (86%)	15 (14%)	0	100	100
24	SS	143/146 (98%)	123 (86%)	20 (14%)	0	100	100
25	ST	141/144 (98%)	127 (90%)	14 (10%)	0	100	100
26	SU	99/121 (82%)	91 (92%)	7 (7%)	1 (1%)	12	40
27	SV	85/87 (98%)	72 (85%)	12 (14%)	1 (1%)	10	35
28	SW	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
29	SX	142/145 (98%)	128 (90%)	12 (8%)	2 (1%)	9	31
30	SY	132/135 (98%)	113 (86%)	17 (13%)	2 (2%)	8	30
31	SZ	67/108 (62%)	61 (91%)	6 (9%)	0	100	100
32	Sa	95/119 (80%)	80 (84%)	14 (15%)	1 (1%)	11	38
33	Sb	79/82 (96%)	64 (81%)	14 (18%)	1 (1%)	9	33
34	Sc	61/67 (91%)	53 (87%)	8 (13%)	0	100	100
35	Sd	51/56 (91%)	46 (90%)	5 (10%)	0	100	100
36	Se	58/63 (92%)	46 (79%)	12 (21%)	0	100	100
37	Sf	31/152 (20%)	23 (74%)	8 (26%)	0	100	100
38	Sg	311/319 (98%)	275 (88%)	36 (12%)	0	100	100
39	LA	250/254 (98%)	213 (85%)	37 (15%)	0	100	100
40	LB	384/387 (99%)	352 (92%)	32 (8%)	0	100	100
41	LC	359/362 (99%)	314 (88%)	44 (12%)	1 (0%)	36	65
42	LD	292/297 (98%)	273 (94%)	19 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	LE	153/176 (87%)	132 (86%)	21 (14%)	0	100	100
44	LF	221/244 (91%)	207 (94%)	14 (6%)	0	100	100
45	LG	229/256 (90%)	199 (87%)	30 (13%)	0	100	100
46	LH	188/191 (98%)	178 (95%)	10 (5%)	0	100	100
47	LI	205/221 (93%)	189 (92%)	15 (7%)	1 (0%)	24	54
48	LJ	167/174 (96%)	139 (83%)	25 (15%)	3 (2%)	6	26
49	LL	192/199 (96%)	164 (85%)	19 (10%)	9 (5%)	2	12
50	LM	135/138 (98%)	126 (93%)	9 (7%)	0	100	100
51	LN	201/204 (98%)	180 (90%)	20 (10%)	1 (0%)	24	54
52	LO	195/199 (98%)	188 (96%)	6 (3%)	1 (0%)	24	54
53	LP	171/184 (93%)	159 (93%)	12 (7%)	0	100	100
54	LQ	183/186 (98%)	172 (94%)	11 (6%)	0	100	100
55	LR	172/189 (91%)	161 (94%)	11 (6%)	0	100	100
56	LS	170/172 (99%)	157 (92%)	13 (8%)	0	100	100
57	LT	157/160 (98%)	145 (92%)	12 (8%)	0	100	100
58	LU	96/121 (79%)	91 (95%)	5 (5%)	0	100	100
59	LV	132/137 (96%)	122 (92%)	10 (8%)	0	100	100
60	LW	61/155 (39%)	58 (95%)	3 (5%)	0	100	100
61	LX	118/142 (83%)	109 (92%)	9 (8%)	0	100	100
62	LY	122/127 (96%)	114 (93%)	8 (7%)	0	100	100
63	LZ	133/136 (98%)	114 (86%)	18 (14%)	1 (1%)	16	44
64	La	146/149 (98%)	130 (89%)	14 (10%)	2 (1%)	9	31
65	Lb	56/59 (95%)	46 (82%)	9 (16%)	1 (2%)	6	26
66	Lc	98/105 (93%)	89 (91%)	9 (9%)	0	100	100
67	Ld	107/113 (95%)	99 (92%)	8 (8%)	0	100	100
68	Le	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	44
69	Lf	104/107 (97%)	91 (88%)	13 (12%)	0	100	100
70	Lg	110/121 (91%)	107 (97%)	3 (3%)	0	100	100
71	Lh	117/120 (98%)	109 (93%)	8 (7%)	0	100	100
72	Li	97/100 (97%)	89 (92%)	8 (8%)	0	100	100
73	Lj	80/88 (91%)	76 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	Lk	75/78 (96%)	69 (92%)	5 (7%)	1 (1%)	9	33
75	Ll	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
76	Lm	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
77	Ln	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
78	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
79	Lp	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
All	All	10892/11972 (91%)	9760 (90%)	1088 (10%)	44 (0%)	31	59

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	SQ	116	LEU
41	LC	339	LEU
48	LJ	95	ASN
49	LL	48	PRO
49	LL	62	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	
2	C5	60/70 (86%)	60 (100%)	0	100	100
6	SA	165/210 (79%)	162 (98%)	3 (2%)	51	67
7	SB	192/224 (86%)	190 (99%)	2 (1%)	68	75
8	SC	176/205 (86%)	171 (97%)	5 (3%)	38	60
9	SD	182/195 (93%)	178 (98%)	4 (2%)	45	63
10	SE	221/222 (100%)	217 (98%)	4 (2%)	51	67
11	SF	173/191 (91%)	170 (98%)	3 (2%)	53	67
12	SG	186/201 (92%)	185 (100%)	1 (0%)	81	81
13	SH	165/170 (97%)	161 (98%)	4 (2%)	43	62
14	SI	150/161 (93%)	147 (98%)	3 (2%)	48	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	SJ	158/166 (95%)	151 (96%)	7 (4%)	25	51
16	SK	73/98 (74%)	73 (100%)	0	100	100
17	SL	129/137 (94%)	128 (99%)	1 (1%)	73	77
18	SM	88/119 (74%)	86 (98%)	2 (2%)	44	63
19	SN	127/128 (99%)	124 (98%)	3 (2%)	43	62
20	SO	97/105 (92%)	92 (95%)	5 (5%)	21	48
21	SP	98/118 (83%)	97 (99%)	1 (1%)	68	75
22	SQ	117/119 (98%)	115 (98%)	2 (2%)	53	67
23	SR	92/124 (74%)	90 (98%)	2 (2%)	45	63
24	SS	128/129 (99%)	122 (95%)	6 (5%)	23	50
25	ST	115/116 (99%)	115 (100%)	0	100	100
26	SU	94/114 (82%)	92 (98%)	2 (2%)	47	64
27	SV	74/74 (100%)	73 (99%)	1 (1%)	59	70
28	SW	110/111 (99%)	107 (97%)	3 (3%)	39	60
29	SX	119/120 (99%)	116 (98%)	3 (2%)	42	62
30	SY	112/113 (99%)	108 (96%)	4 (4%)	31	56
31	SZ	61/89 (68%)	60 (98%)	1 (2%)	55	68
32	Sa	83/100 (83%)	83 (100%)	0	100	100
33	Sb	70/71 (99%)	70 (100%)	0	100	100
34	Sc	56/60 (93%)	55 (98%)	1 (2%)	51	67
35	Sd	47/49 (96%)	46 (98%)	1 (2%)	47	64
36	Se	51/54 (94%)	51 (100%)	0	100	100
37	Sf	27/135 (20%)	27 (100%)	0	100	100
38	Sg	255/262 (97%)	250 (98%)	5 (2%)	48	65
39	LA	192/196 (98%)	183 (95%)	9 (5%)	23	50
40	LB	318/323 (98%)	307 (96%)	11 (4%)	32	56
41	LC	288/289 (100%)	282 (98%)	6 (2%)	47	64
42	LD	243/245 (99%)	242 (100%)	1 (0%)	84	83
43	LE	135/153 (88%)	132 (98%)	3 (2%)	45	63
44	LF	187/205 (91%)	186 (100%)	1 (0%)	81	81
45	LG	177/208 (85%)	174 (98%)	3 (2%)	53	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	LH	170/171 (99%)	162 (95%)	8 (5%)	23	50
47	LI	177/187 (95%)	175 (99%)	2 (1%)	65	74
48	LJ	147/150 (98%)	143 (97%)	4 (3%)	39	60
49	LL	154/159 (97%)	151 (98%)	3 (2%)	50	66
50	LM	108/109 (99%)	106 (98%)	2 (2%)	50	66
51	LN	175/176 (99%)	173 (99%)	2 (1%)	65	74
52	LO	160/162 (99%)	159 (99%)	1 (1%)	78	80
53	LP	139/146 (95%)	132 (95%)	7 (5%)	22	49
54	LQ	150/151 (99%)	149 (99%)	1 (1%)	76	78
55	LR	132/154 (86%)	128 (97%)	4 (3%)	36	59
56	LS	156/156 (100%)	153 (98%)	3 (2%)	50	66
57	LT	136/137 (99%)	130 (96%)	6 (4%)	25	51
58	LU	85/107 (79%)	84 (99%)	1 (1%)	63	72
59	LV	103/105 (98%)	102 (99%)	1 (1%)	68	75
60	LW	55/129 (43%)	53 (96%)	2 (4%)	31	56
61	LX	104/118 (88%)	102 (98%)	2 (2%)	50	66
62	LY	107/110 (97%)	105 (98%)	2 (2%)	50	66
63	LZ	115/116 (99%)	115 (100%)	0	100	100
64	La	118/119 (99%)	118 (100%)	0	100	100
65	Lb	46/47 (98%)	45 (98%)	1 (2%)	45	63
66	Lc	84/88 (96%)	83 (99%)	1 (1%)	63	72
67	Ld	94/97 (97%)	91 (97%)	3 (3%)	34	58
68	Le	109/111 (98%)	108 (99%)	1 (1%)	70	76
69	Lf	90/91 (99%)	87 (97%)	3 (3%)	33	57
70	Lg	95/103 (92%)	95 (100%)	0	100	100
71	Lh	103/105 (98%)	102 (99%)	1 (1%)	68	75
72	Li	80/82 (98%)	78 (98%)	2 (2%)	42	62
73	Lj	67/71 (94%)	67 (100%)	0	100	100
74	Lk	67/69 (97%)	67 (100%)	0	100	100
75	Ll	45/46 (98%)	44 (98%)	1 (2%)	45	63
76	Lm	47/116 (40%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
77	Ln	23/23 (100%)	23 (100%)	0	100	100
78	Lo	90/91 (99%)	88 (98%)	2 (2%)	45	63
79	Lp	71/72 (99%)	70 (99%)	1 (1%)	59	70
All	All	9193/10053 (91%)	9013 (98%)	180 (2%)	48	65

5 of 180 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	LH	18	VAL
55	LR	151	ARG
46	LH	93	VAL
50	LM	66	THR
57	LT	18	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 168 such sidechains are listed below:

Mol	Chain	Res	Type
53	LP	50	GLN
65	Lb	10	HIS
53	LP	172	GLN
57	LT	122	GLN
69	Lf	42	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C2	1693/1800 (94%)	473 (27%)	31 (1%)
3	C1	3120/3396 (91%)	700 (22%)	39 (1%)
4	C4	120/121 (99%)	21 (17%)	0
5	C3	156/158 (98%)	37 (23%)	2 (1%)
All	All	5089/5475 (92%)	1231 (24%)	72 (1%)

5 of 1231 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C2	2	A
1	C2	4	C
1	C2	25	C
1	C2	26	A

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Mol	Chain	Res	Type
1	C2	27	U

5 of 72 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	C1	2522	G
5	C3	106	C
3	C1	2714	G
3	C1	3269	U
1	C2	1255	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 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.

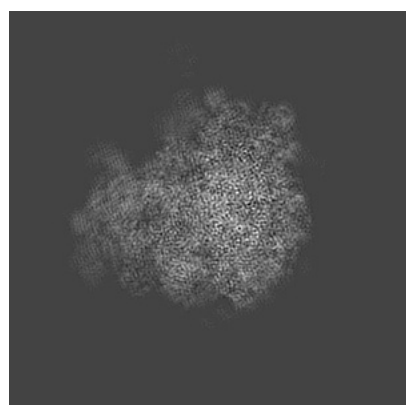
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11096. These allow visual inspection of the internal detail of the map and identification of artifacts.

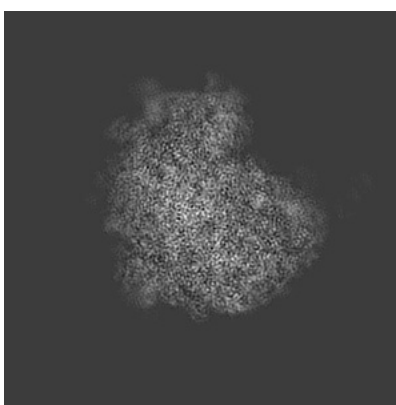
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

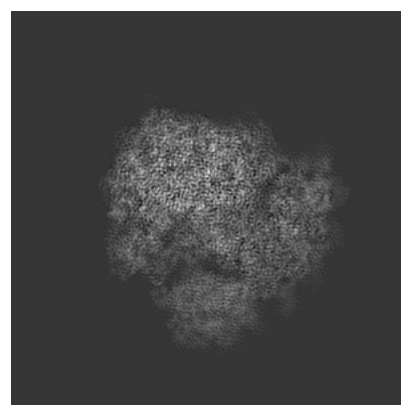
6.1.1 Primary map



X



Y

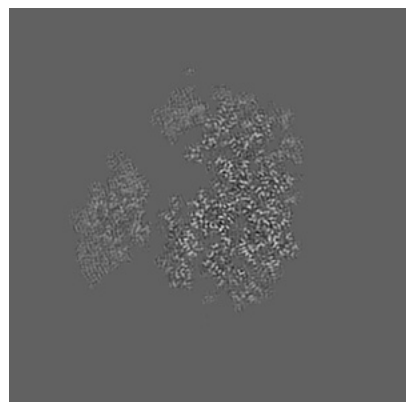


Z

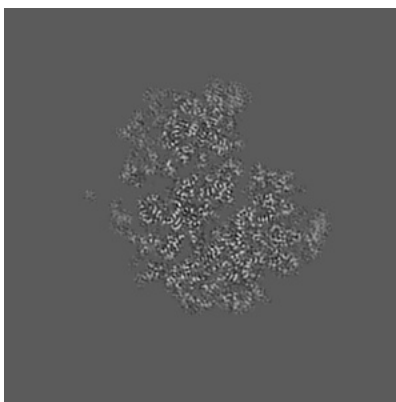
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

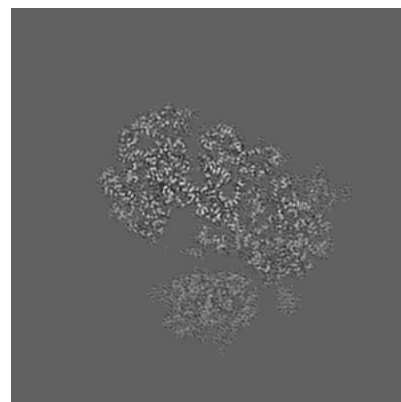
6.2.1 Primary map



X Index: 200



Y Index: 200

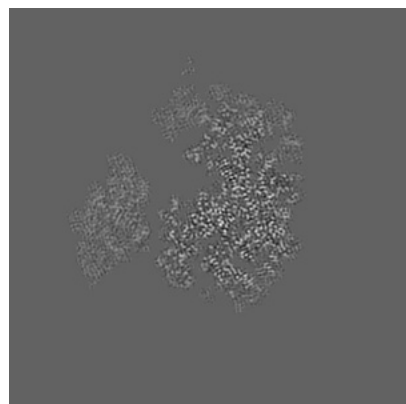


Z Index: 200

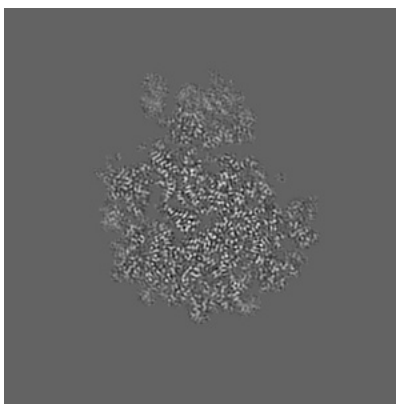
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

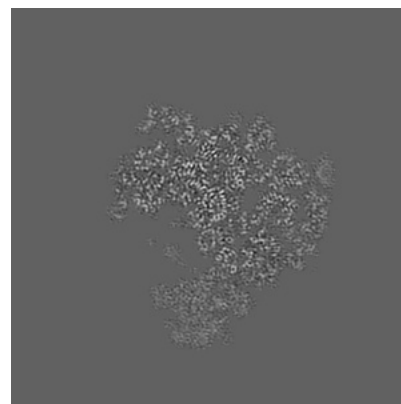
6.3.1 Primary map



X Index: 198



Y Index: 227

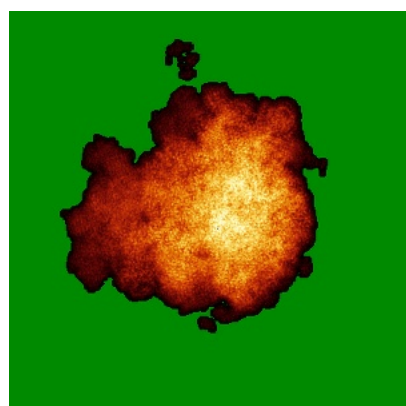


Z Index: 181

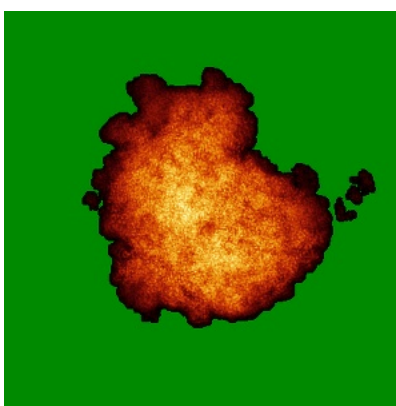
The images above show the largest variance slices of the map in three orthogonal directions.

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

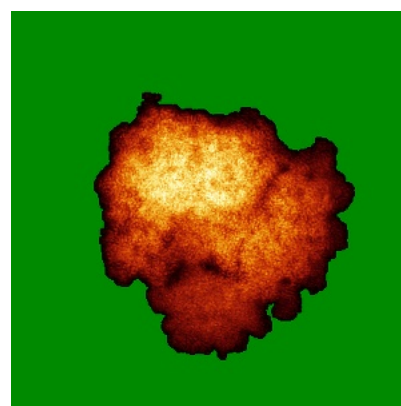
6.4.1 Primary map



X



Y

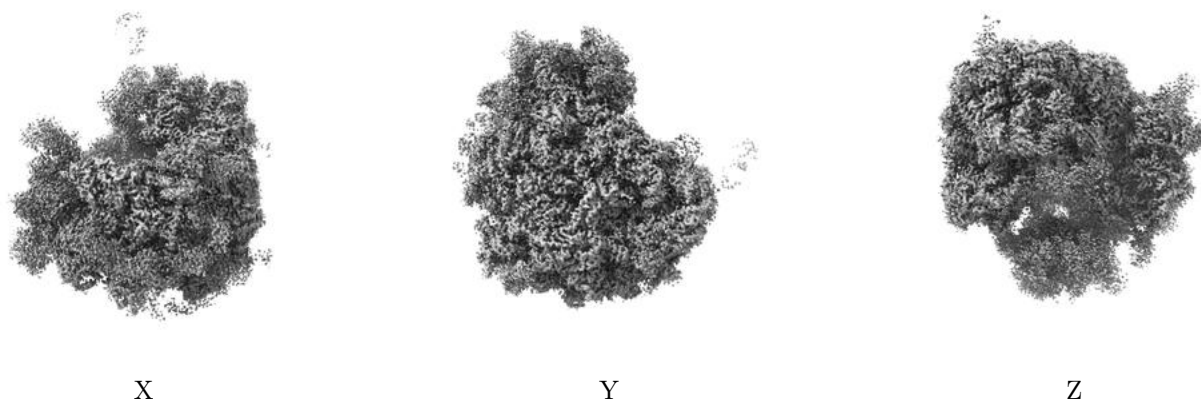


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

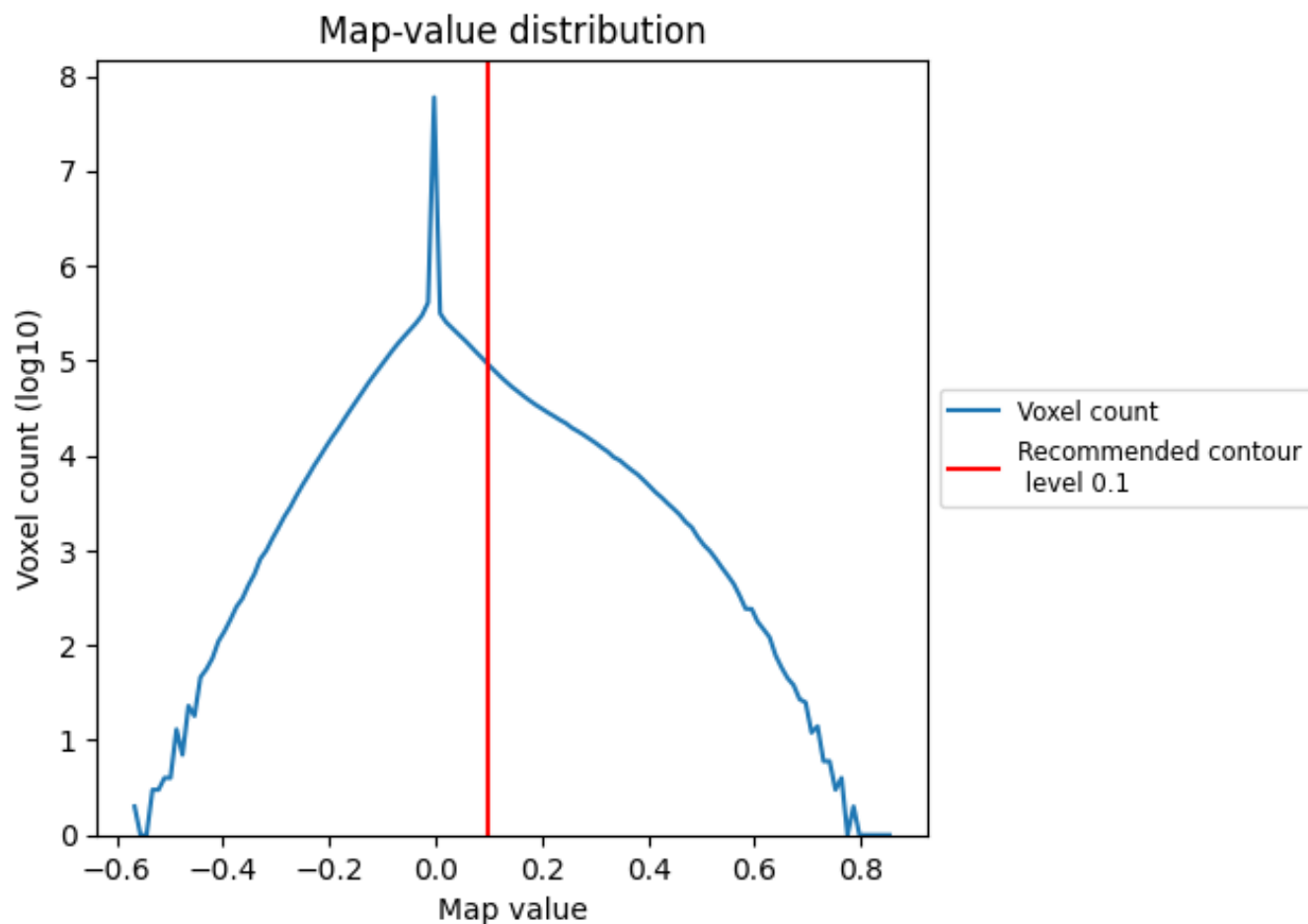
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

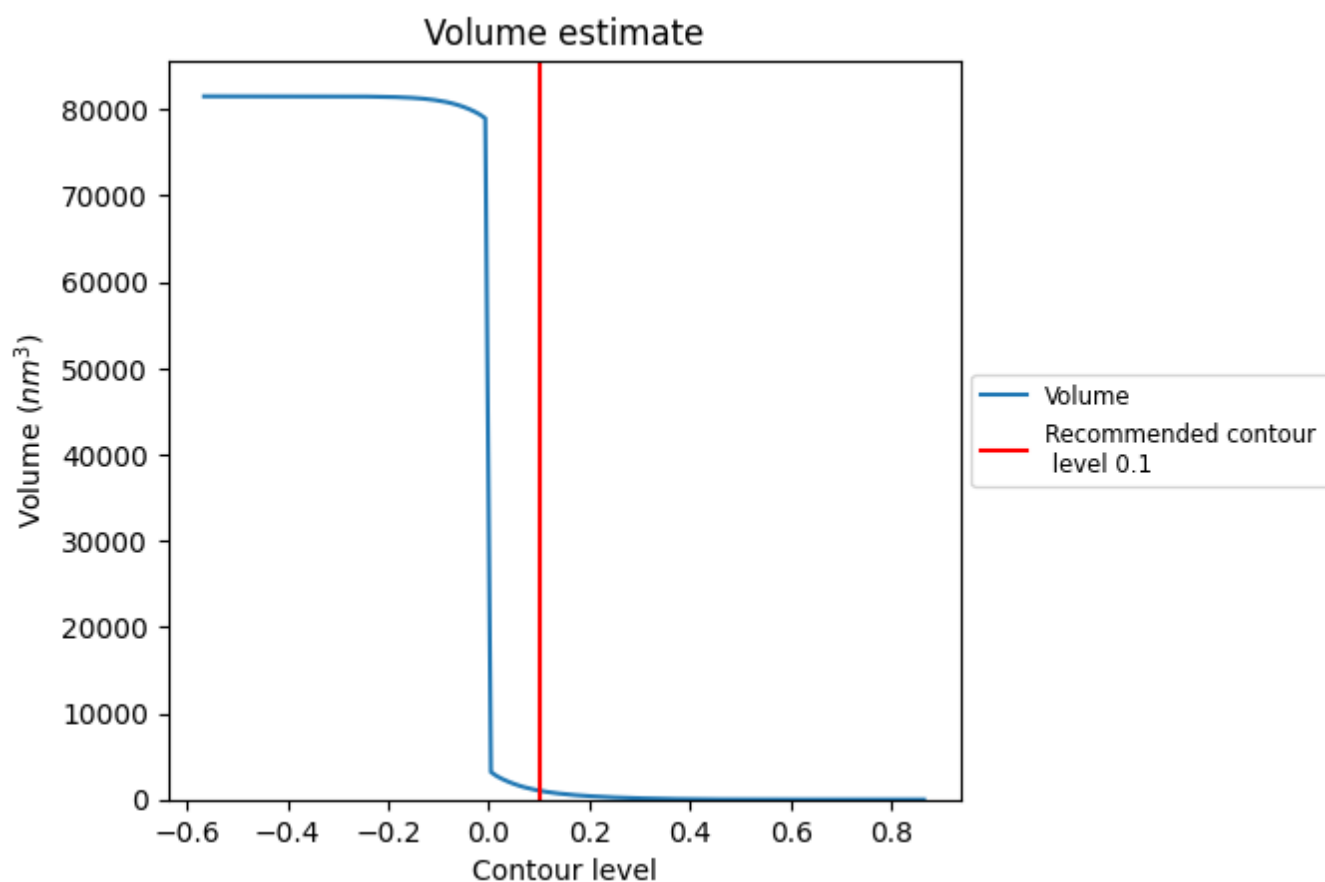
This section contains the results of statistical analysis of the map.

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.

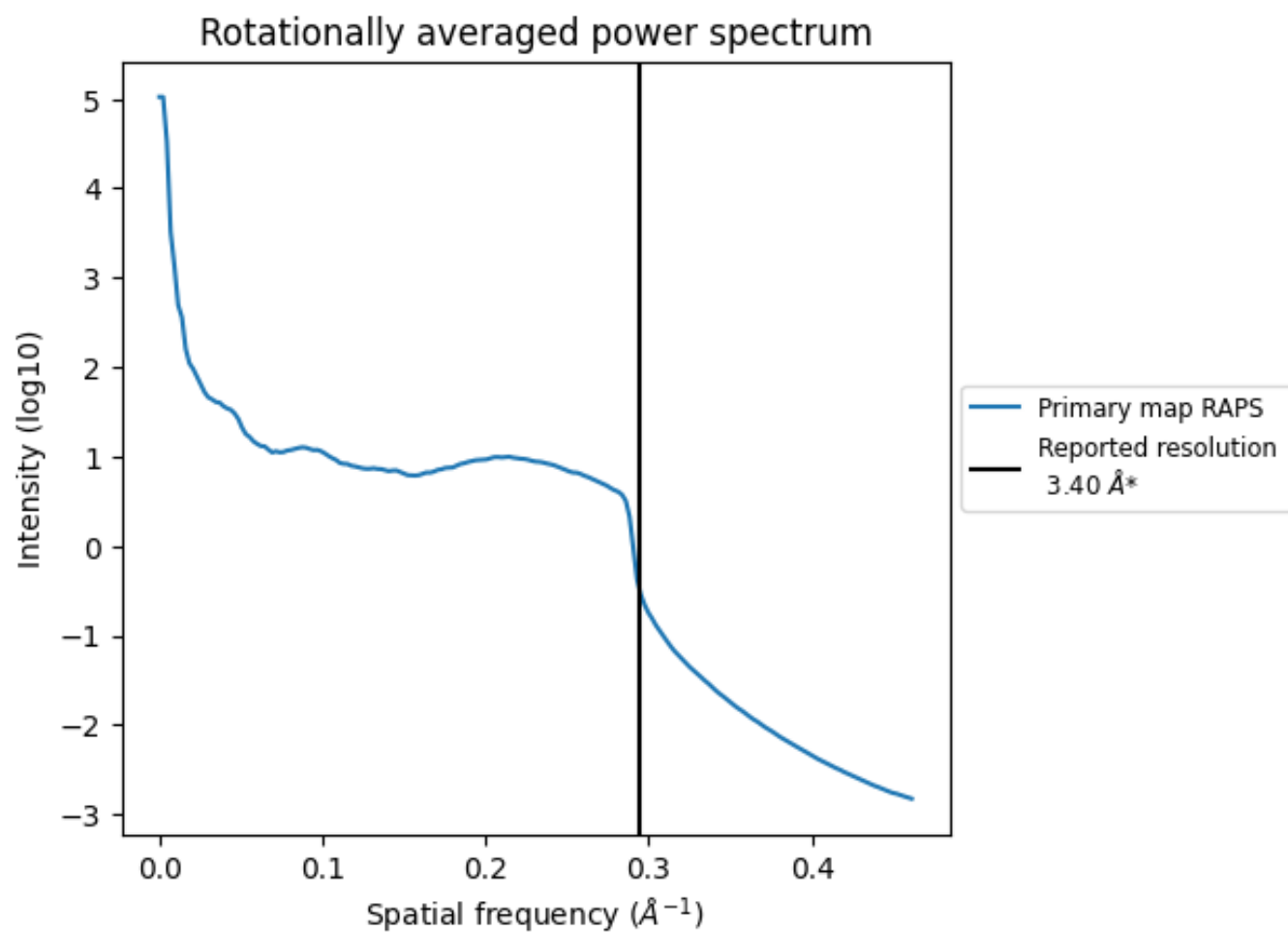
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1042 nm³; this corresponds to an approximate mass of 941 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 ⓘ

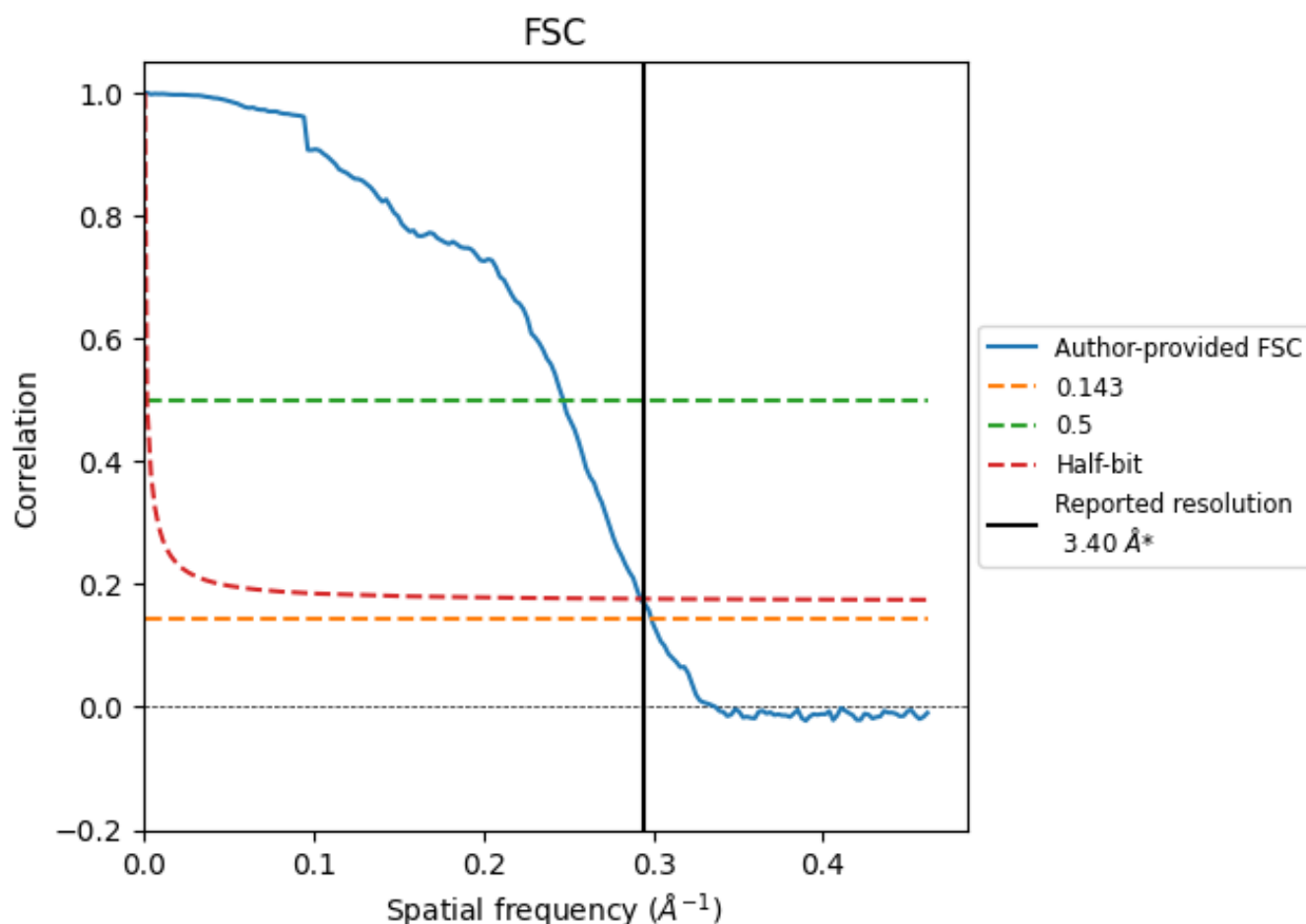


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

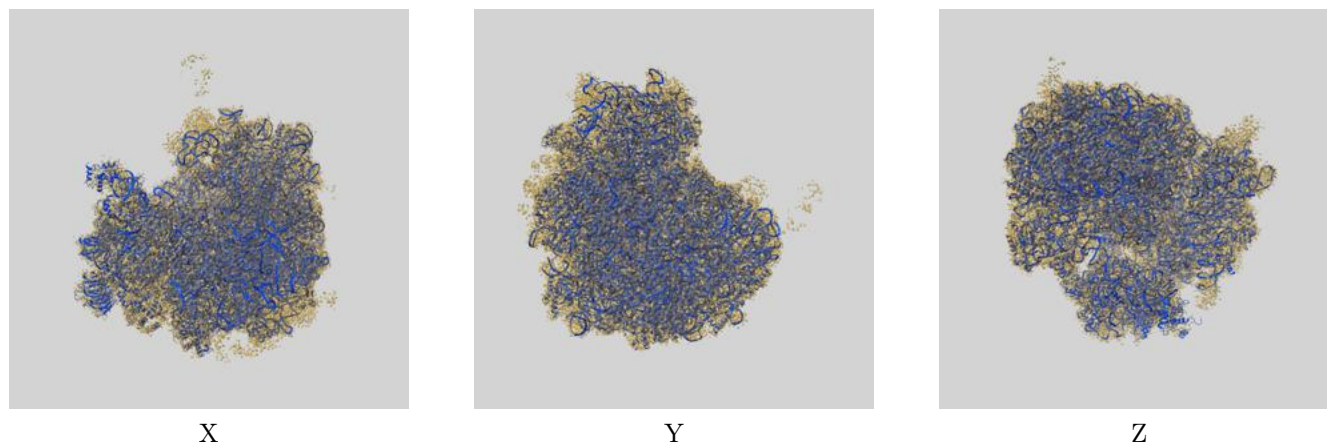
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.34	4.05	3.42
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

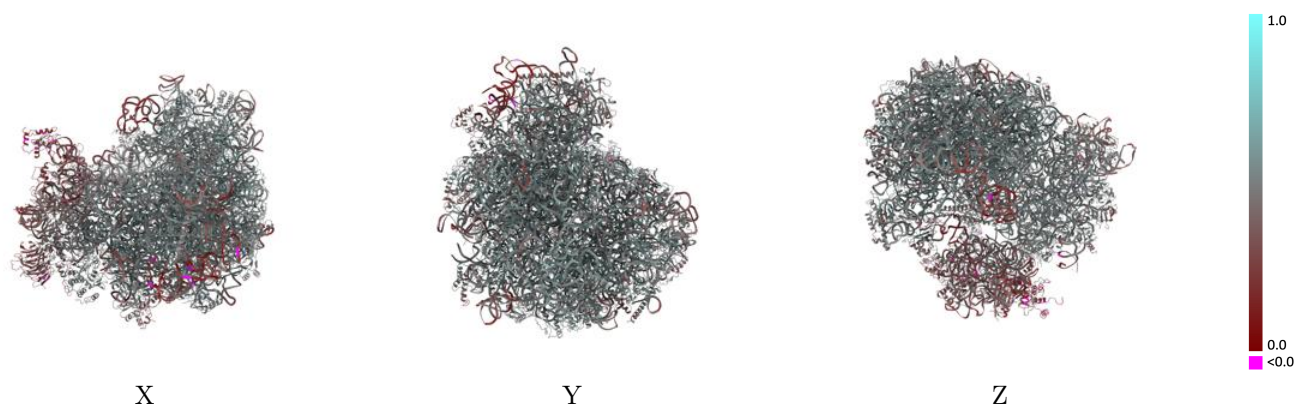
This section contains information regarding the fit between EMDB map EMD-11096 and PDB model 6Z6J. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



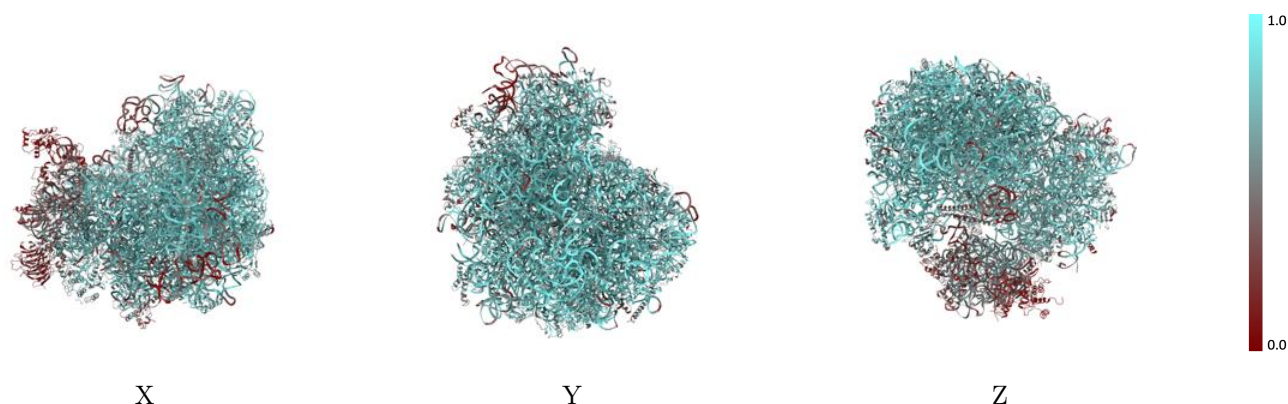
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



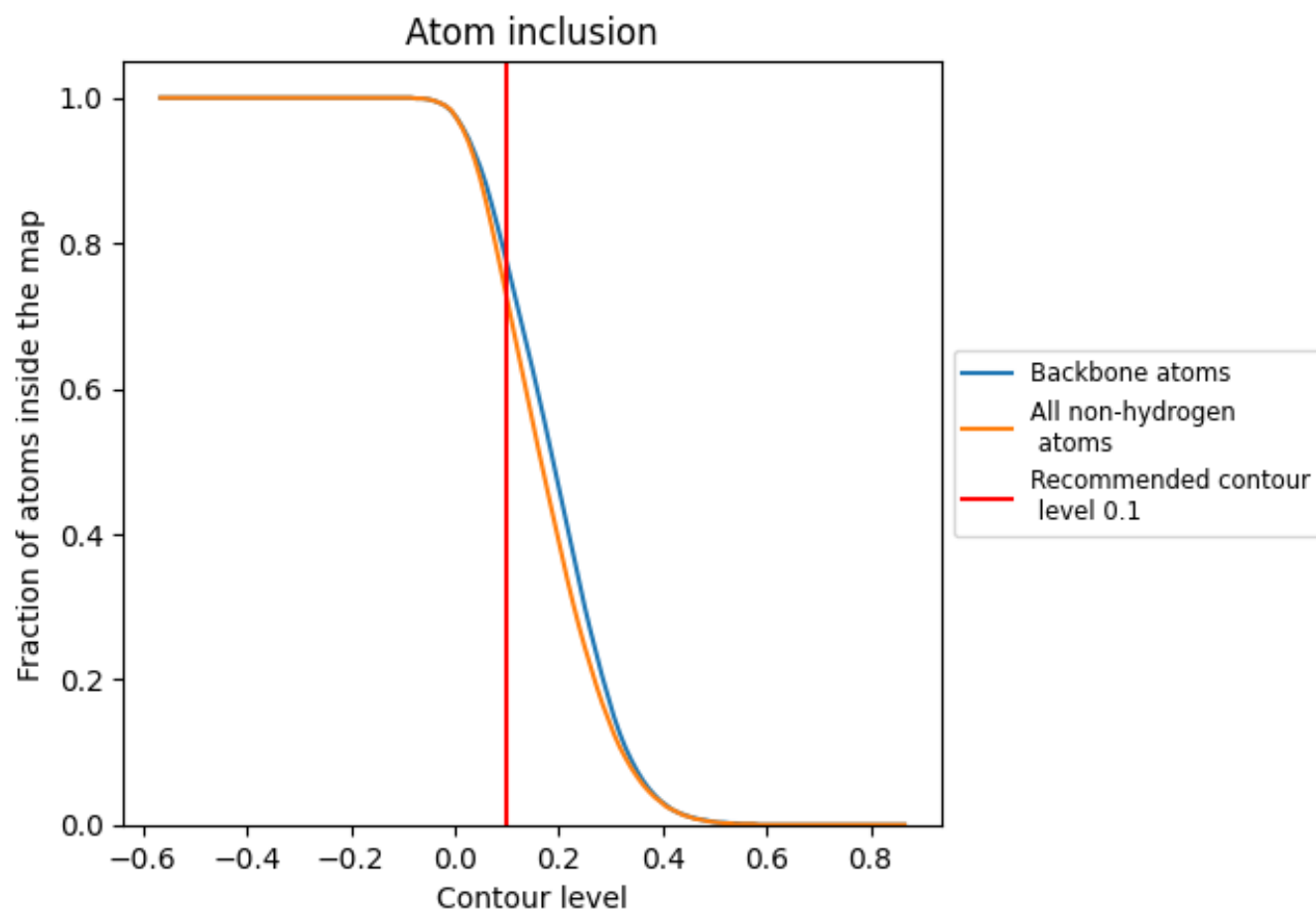
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 72% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7250	 0.4820
C1	 0.8260	 0.4970
C2	 0.7010	 0.4390
C3	 0.8490	 0.5050
C4	 0.8490	 0.4930
C5	 0.3880	 0.4340
LA	 0.7900	 0.5480
LB	 0.7780	 0.5390
LC	 0.7640	 0.5270
LD	 0.6610	 0.4830
LE	 0.6730	 0.4960
LF	 0.7440	 0.5260
LG	 0.7020	 0.4990
LH	 0.7090	 0.5130
LI	 0.7150	 0.5200
LJ	 0.6130	 0.4620
LL	 0.7250	 0.5060
LM	 0.7050	 0.5090
LN	 0.8080	 0.5530
LO	 0.7810	 0.5350
LP	 0.7820	 0.5400
LQ	 0.7660	 0.5310
LR	 0.7720	 0.5400
LS	 0.7610	 0.5390
LT	 0.7590	 0.5310
LU	 0.6920	 0.4920
LV	 0.7590	 0.5480
LW	 0.7540	 0.5370
LX	 0.7350	 0.5240
LY	 0.7470	 0.5260
LZ	 0.7330	 0.5200
La	 0.7940	 0.5450
Lb	 0.6990	 0.4940
Lc	 0.7230	 0.5170
Ld	 0.7350	 0.5260



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Chain	Atom inclusion	Q-score
Le	 0.7810	 0.5440
Lf	 0.8160	 0.5600
Lg	 0.7530	 0.5370
Lh	 0.7110	 0.5220
Li	 0.7060	 0.5040
Lj	 0.8500	 0.5630
Lk	 0.6200	 0.4840
Ll	 0.7930	 0.5470
Lm	 0.7380	 0.5310
Ln	 0.6410	 0.5120
Lo	 0.7530	 0.5380
Lp	 0.7210	 0.5370
SA	 0.6610	 0.4790
SB	 0.6320	 0.4930
SC	 0.7100	 0.5160
SD	 0.3830	 0.3800
SE	 0.6970	 0.5080
SF	 0.3740	 0.3930
SG	 0.5800	 0.4690
SH	 0.5580	 0.4420
SI	 0.7210	 0.5260
SJ	 0.6620	 0.4960
SK	 0.2850	 0.3240
SL	 0.7270	 0.5260
SM	 0.1060	 0.2230
SN	 0.7300	 0.5180
SO	 0.6830	 0.5080
SP	 0.2530	 0.2970
SQ	 0.3730	 0.3740
SR	 0.5100	 0.4320
SS	 0.3110	 0.3330
ST	 0.3860	 0.3700
SU	 0.3150	 0.3560
SV	 0.6930	 0.4930
SW	 0.7550	 0.5400
SX	 0.7200	 0.5290
SY	 0.6220	 0.4690
SZ	 0.3140	 0.3300
Sa	 0.7070	 0.5170
Sb	 0.6390	 0.4950
Sc	 0.4170	 0.4190
Sd	 0.4940	 0.4340

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Chain	Atom inclusion	Q-score
Se	 0.5470	 0.4430
Sf	 0.1390	 0.2310
Sg	 0.2000	 0.3160