



## wwPDB EM Validation Summary Report ⓘ

May 20, 2024 – 01:04 AM JST

PDB ID : 7CPV  
EMDB ID : EMD-30433  
Title : Cryo-EM structure of 80S ribosome from mouse testis  
Authors : Huo, Y.G.; He, X.; Jiang, T.; Qin, Y.; Guo, X.J.; Sha, J.H.  
Deposited on : 2020-08-08  
Resolution : 3.03 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](mailto: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>.

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

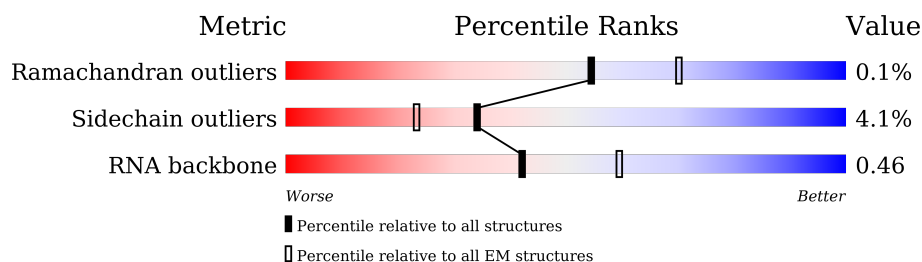
EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.03 Å.

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







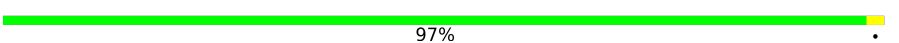
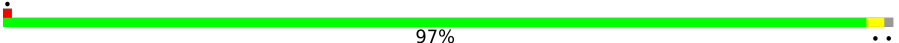

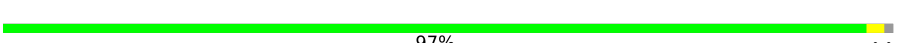

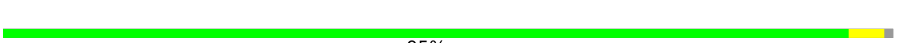
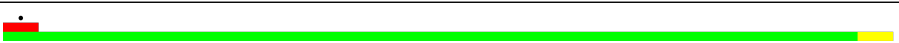



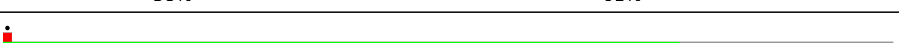
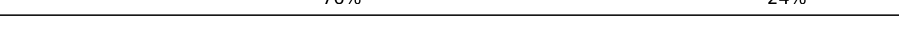
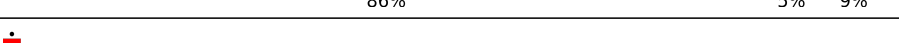
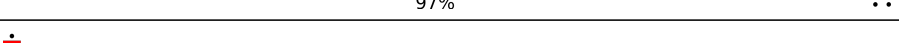
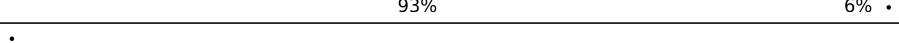




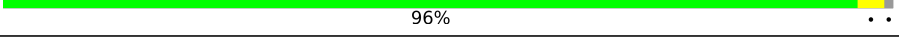
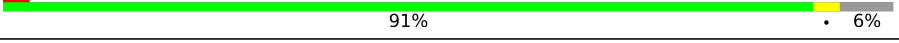
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	LA	257	
2	LB	403	
3	LC	419	
4	LD	297	
5	LE	296	
6	LF	270	
7	LG	266	
8	LH	192	

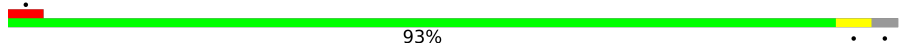

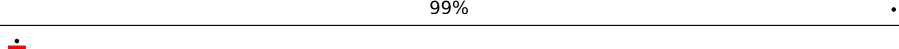
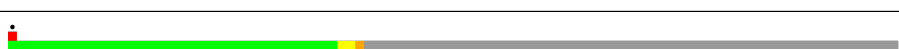

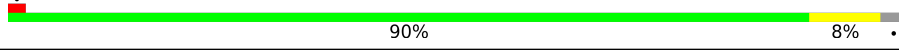
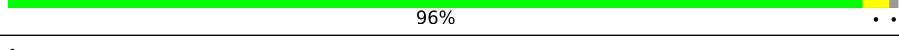
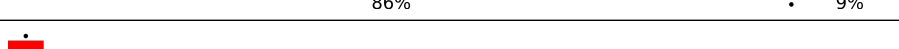



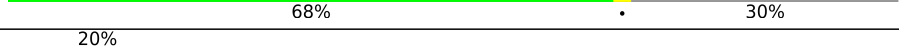

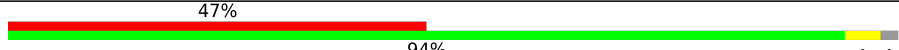


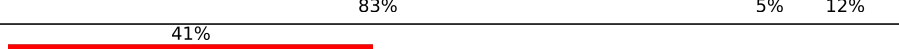


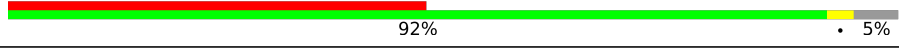
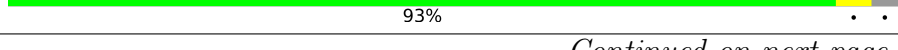



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Mol	Chain	Length	Quality of chain
9	LI	214	
10	LJ	178	
11	LL	211	
12	LM	217	
13	LN	204	
14	LO	203	
15	LP	184	
16	LQ	188	
17	LR	196	
18	LS	176	
19	LT	160	
20	LU	128	
21	LV	140	
22	LW	157	
23	LX	156	
24	LY	145	
25	LZ	136	
26	La	148	
27	Lb	160	
28	Lc	115	
29	Ld	125	
30	Le	135	
31	Lf	110	
32	Lg	117	
33	Lh	123	

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Mol	Chain	Length	Quality of chain
34	Li	105	
35	Lj	97	
36	Lk	70	
37	Ll	51	
38	Lm	128	
39	Ln	25	
40	Lo	106	
41	Lp	92	
42	Lr	137	
43	L5	4731	
44	L7	120	
45	L8	158	
46	S2	1870	
47	SA	295	
48	SB	264	
49	SD	243	
50	SE	263	
51	SF	204	
52	SH	194	
53	SI	208	
54	SK	165	
55	SL	158	
56	SP	145	
57	SQ	146	
58	SR	135	

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Mol	Chain	Length	Quality of chain
59	SS	152	
60	ST	145	
61	SU	119	
62	SV	83	
63	SX	143	
64	Sa	115	
65	Sc	69	
66	Sd	56	
67	Sg	317	
68	SC	293	
69	SG	249	
70	SJ	194	
71	SN	151	
72	SO	151	
73	SW	130	
74	SY	133	
75	SZ	125	
76	Sb	84	
77	Se	133	
78	S6	75	

## 2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 206030 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L8.

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

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	397	Total	C	N	O	S	0	0
			3202	2039	603	546	14		

- Molecule 3 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LC	362	Total	C	N	O	S	0	0
			2891	1819	577	480	15		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LD	293	Total	C	N	O	S	0	0
			2385	1506	440	425	14		

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LE	231	Total	C	N	O	S	0	0
			1874	1195	358	317	4		

- Molecule 6 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LF	214	Total	C	N	O	S	0	0
			1771	1139	337	287	8		

- Molecule 7 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LG	229	Total	C	N	O	S	0	0
			1848	1179	354	311	4		

- Molecule 8 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LH	190	Total	C	N	O	S	0	0
			1519	956	284	273	6		

- Molecule 9 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	201	Total	C	N	O	S	0	0
			1631	1037	316	267	11		

- Molecule 10 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	171	Total	C	N	O	S	0	0
			1371	866	255	244	6		

- Molecule 11 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LL	206	Total	C	N	O	S	0	0
			1667	1043	343	277	4		

- Molecule 12 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LM	136	Total	C	N	O	S	0	0
			1125	721	218	179	7		

- Molecule 13 is a protein called 60S ribosomal protein L15.

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

- Molecule 14 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LO	201	Total	C	N	O	S	0	0
			1640	1055	320	259	6		

- Molecule 15 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LP	154	Total	C	N	O	S	0	0
			1251	782	243	217	9		

- Molecule 16 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LQ	187	Total	C	N	O	S	0	0
			1515	948	314	249	4		

- Molecule 17 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LR	174	Total	C	N	O	S	0	0
			1457	901	316	231	9		

- Molecule 18 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LS	175	Total	C	N	O	S	0	0
			1451	924	283	234	10		

- Molecule 19 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LT	160	Total	C	N	O	S	0	0
			1307	829	253	218	7		

- Molecule 20 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LU	100	Total	C	N	O	S	0	0
			817	523	143	149	2		

- Molecule 21 is a protein called 60S ribosomal protein L23.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	LV	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 22 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 23 is a protein called 60S ribosomal protein L23a.

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

- Molecule 24 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LY	132	Total	C	N	O	S	0	0
			1102	692	223	184	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

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

- Molecule 26 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	La	147	Total	C	N	O	S	0	0
			1164	736	239	185	4		

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Lb	99	Total	C	N	O	S	0	0
			807	505	174	124	4		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lc	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 29 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ld	108	Total	C	N	O	S	0	0
			896	566	172	156	2		

- Molecule 30 is a protein called 60S ribosomal protein L32.

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

- Molecule 31 is a protein called 60S ribosomal protein L35a.

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

- Molecule 32 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lg	110	Total	C	N	O	S	0	0
			873	546	180	141	6		

- Molecule 33 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lh	122	Total	C	N	O	S	0	0
			1015	643	204	167	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

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

- Molecule 35 is a protein called 60S ribosomal protein L37.

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

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lk	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

- Molecule 37 is a protein called Ribosomal protein L39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ll	50	Total	C	N	O	S	0	0
			438	279	93	64	2		

- Molecule 38 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lm	51	Total	C	N	O	S	0	0
			419	260	88	65	6		

- Molecule 39 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ln	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lo	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lr	124	Total	C	N	O	S	0	0
			994	616	206	167	5		

- Molecule 43 is a RNA chain called Mus musculus 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L5	3541	Total	C	N	O	P	0	0
			75913	33809	13873	24691	3540		

- Molecule 44 is a RNA chain called Mus musculus 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 45 is a RNA chain called Mus musculus 5.8S ribosomal RNA.

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

- Molecule 46 is a RNA chain called Mus musculus 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S2	1637	Total	C	N	O	P	0	0
			34941	15601	6275	11429	1636		

- Molecule 47 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SA	207	Total	C	N	O	S	0	0
			1636	1042	288	298	8		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD	224	Total	C	N	O	S	0	0
			1744	1111	314	312	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SE	258	Total	C	N	O	S	0	0
			2050	1311	381	350	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SF	179	Total	C	N	O	S	0	0
			1416	888	262	259	7		

- Molecule 52 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SH	180	Total	C	N	O	S	0	0
			1449	924	266	258	1		

- Molecule 53 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SI	183	Total	C	N	O	S	0	0
			1499	943	293	258	5		

- Molecule 54 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SK	90	Total	C	N	O	S	0	0
			760	495	135	124	6		

- Molecule 55 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SL	135	Total	C	N	O	S	0	0
			1110	708	207	189	6		

- Molecule 56 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SP	118	Total	C	N	O	S	0	0
			981	625	183	166	7		

- Molecule 57 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SQ	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 58 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SR	131	Total	C	N	O	S	0	0
			1064	668	198	194	4		

- Molecule 59 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SS	140	Total	C	N	O	S	0	0
			1157	728	231	197	1		

- Molecule 60 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	ST	140	Total	C	N	O	S	0	0
			1090	681	212	195	2		

- Molecule 61 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SU	95	Total	C	N	O	S	0	0
			753	471	142	136	4		

- Molecule 62 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SV	81	Total	C	N	O	S	0	0
			619	379	116	119	5		

- Molecule 63 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SX	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 64 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Sa	99	Total	C	N	O	S	0	0
			792	492	165	130	5		

- Molecule 65 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Sc	54	Total	C	N	O	S	0	0
			416	257	80	77	2		

- Molecule 66 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sd	54	Total	C	N	O	S	0	0
			455	284	93	73	5		

- Molecule 67 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sg	276	Total	C	N	O	S	0	0
			2148	1357	378	401	12		

- Molecule 68 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SC	215	Total	C	N	O	S	1	0
			1673	1085	288	291	9		

- Molecule 69 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SG	204	Total	C	N	O	S	0	0
			1645	1029	330	280	6		

- Molecule 70 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SJ	138	Total	C	N	O	S	0	0
			1162	743	230	187	2		

- Molecule 71 is a protein called 40S ribosomal protein S13.

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

- Molecule 72 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SO	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 73 is a protein called 40S ribosomal protein S15a.

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

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SY	110	Total	C	N	O	S	0	0
			891	565	173	149	4		

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SZ	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 76 is a protein called 40S ribosomal protein S27.

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

- Molecule 77 is a protein called 40S ribosomal protein S30.



Mol	Chain	Residues	Atoms					AltConf	Trace
77	Se	48	Total	C	N	O	S	0	0
			384	234	86	63	1		

- Molecule 78 is a RNA chain called Met-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 79 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
79	LN	1	Total	Mg	0
			1	1	
79	LP	1	Total	Mg	0
			1	1	
79	LT	1	Total	Mg	0
			1	1	
79	LV	1	Total	Mg	0
			1	1	
79	Le	1	Total	Mg	0
			1	1	
79	Lf	1	Total	Mg	0
			1	1	
79	L5	173	Total	Mg	0
			173	173	
79	L7	3	Total	Mg	0
			3	3	
79	L8	5	Total	Mg	0
			5	5	
79	S2	59	Total	Mg	0
			59	59	
79	SF	1	Total	Mg	0
			1	1	

- Molecule 80 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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

- Molecule 81 is water.

Mol	Chain	Residues	Atoms		AltConf
81	LB	1	Total 1	O 1	0
81	LH	1	Total 1	O 1	0
81	LI	2	Total 2	O 2	0
81	LN	1	Total 1	O 1	0
81	La	1	Total 1	O 1	0
81	L5	7	Total 7	O 7	0
81	S2	2	Total 2	O 2	0

### 3 Residue-property plots

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

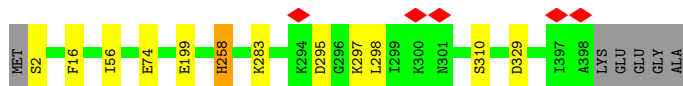
- Molecule 1: 60S ribosomal protein L8

Chain LA:  94%




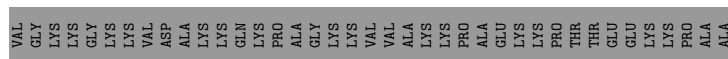
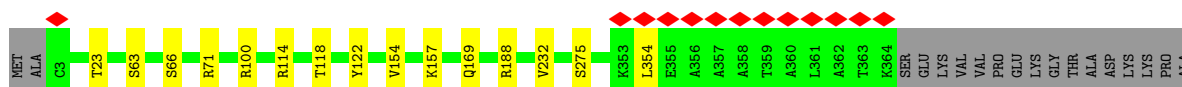
- Molecule 2: 60S ribosomal protein L3

Chain LB:  96%



- Molecule 3: 60S ribosomal protein L4

Chain LC:  83% 14%




- Molecule 4: 60S ribosomal protein L5

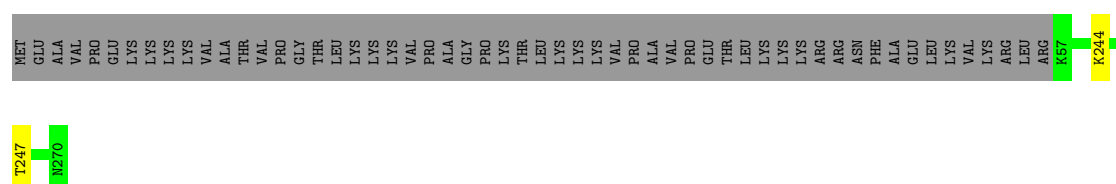
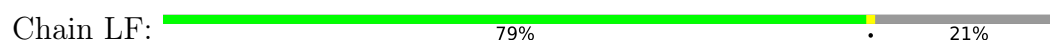
Chain LD:  94% 5%



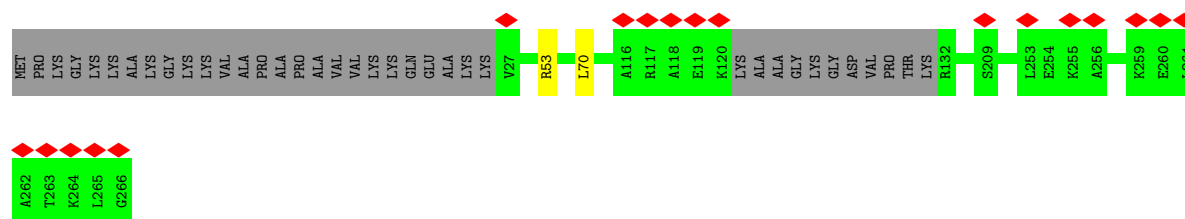
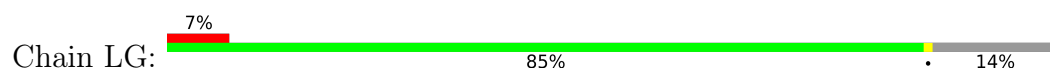
- Molecule 5: 60S ribosomal protein L6

Chain LE:  8% 73% 5% 22%

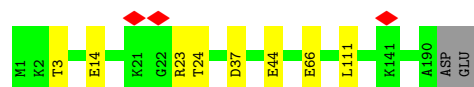
- Molecule 6: 60S ribosomal protein L7



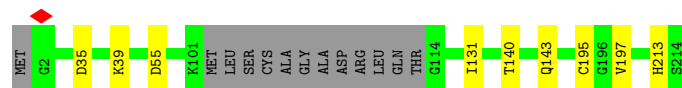
- Molecule 7: 60S ribosomal protein L7a



- Molecule 8: 60S ribosomal protein L9



- Molecule 9: 60S ribosomal protein L10-like

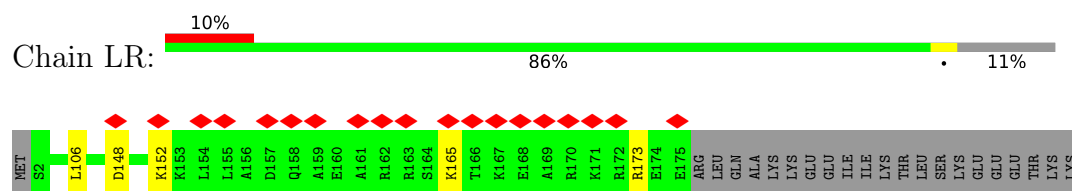


- Molecule 10: 60S ribosomal protein L11

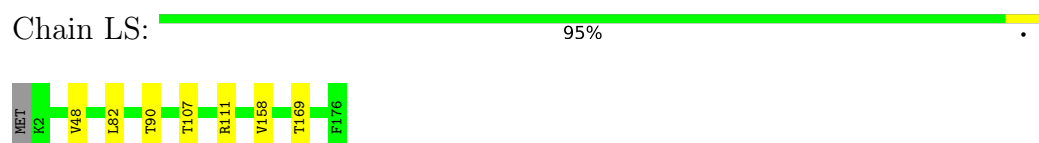




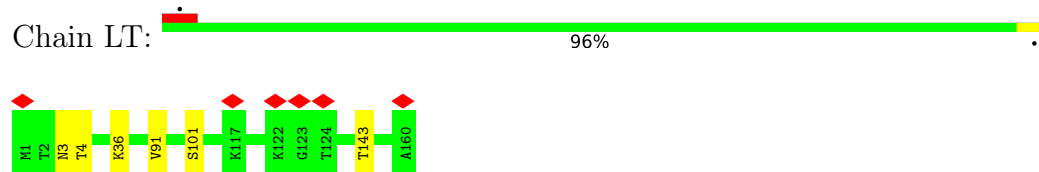
- Molecule 17: 60S ribosomal protein L19



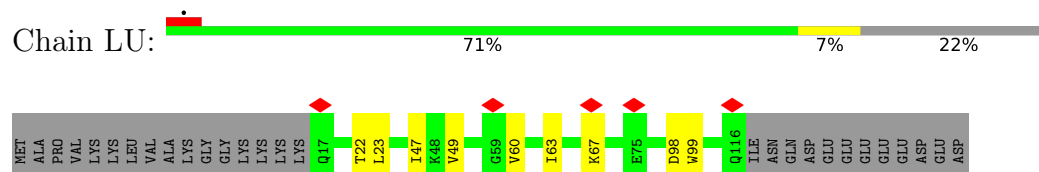
- Molecule 18: 60S ribosomal protein L18a



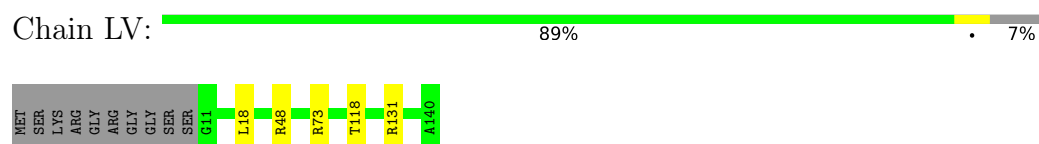
- Molecule 19: 60S ribosomal protein L21



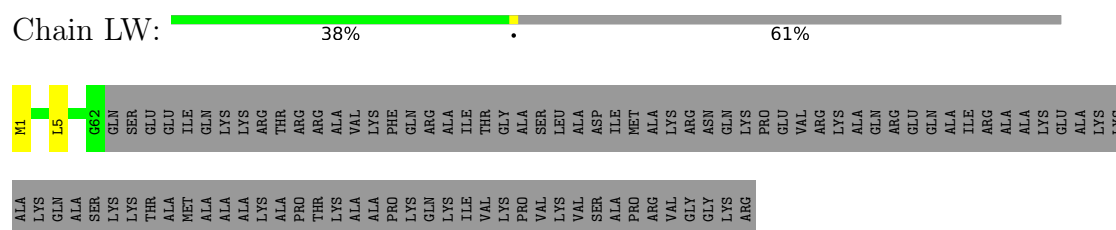
- Molecule 20: 60S ribosomal protein L22



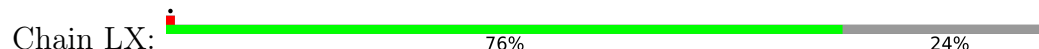
- Molecule 21: 60S ribosomal protein L23



- Molecule 22: 60S ribosomal protein L24




- Molecule 23: 60S ribosomal protein L23a





- Molecule 30: 60S ribosomal protein L32

Chain Le:  91% 5%



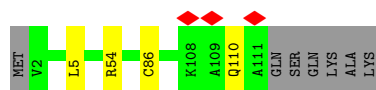
- Molecule 31: 60S ribosomal protein L35a

Chain Lf:  96%



- Molecule 32: 60S ribosomal protein L34

Chain Lg:  91% 6%



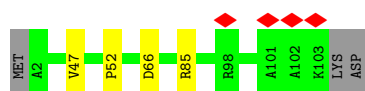
- Molecule 33: 60S ribosomal protein L35

Chain Lh:  98%




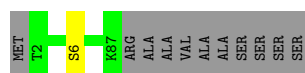
- Molecule 34: 60S ribosomal protein L36

Chain Li:  93%



- Molecule 35: 60S ribosomal protein L37

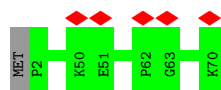
Chain Lj:  88% 11%



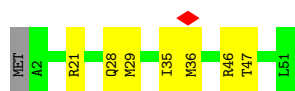
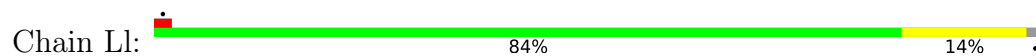
- Molecule 36: 60S ribosomal protein L38

Chain Lk:  7% 99%

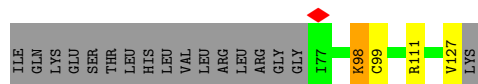
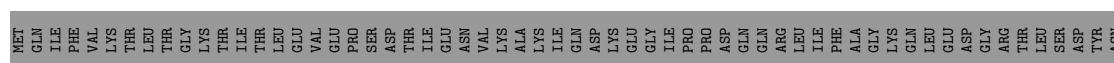




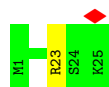
- Molecule 37: Ribosomal protein L39-like



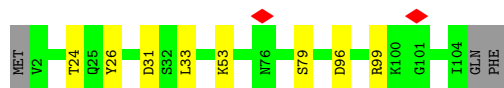
- Molecule 38: Ubiquitin-60S ribosomal protein L40



- Molecule 39: 60S ribosomal protein L41



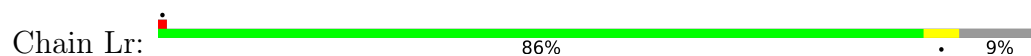
- Molecule 40: 60S ribosomal protein L36a

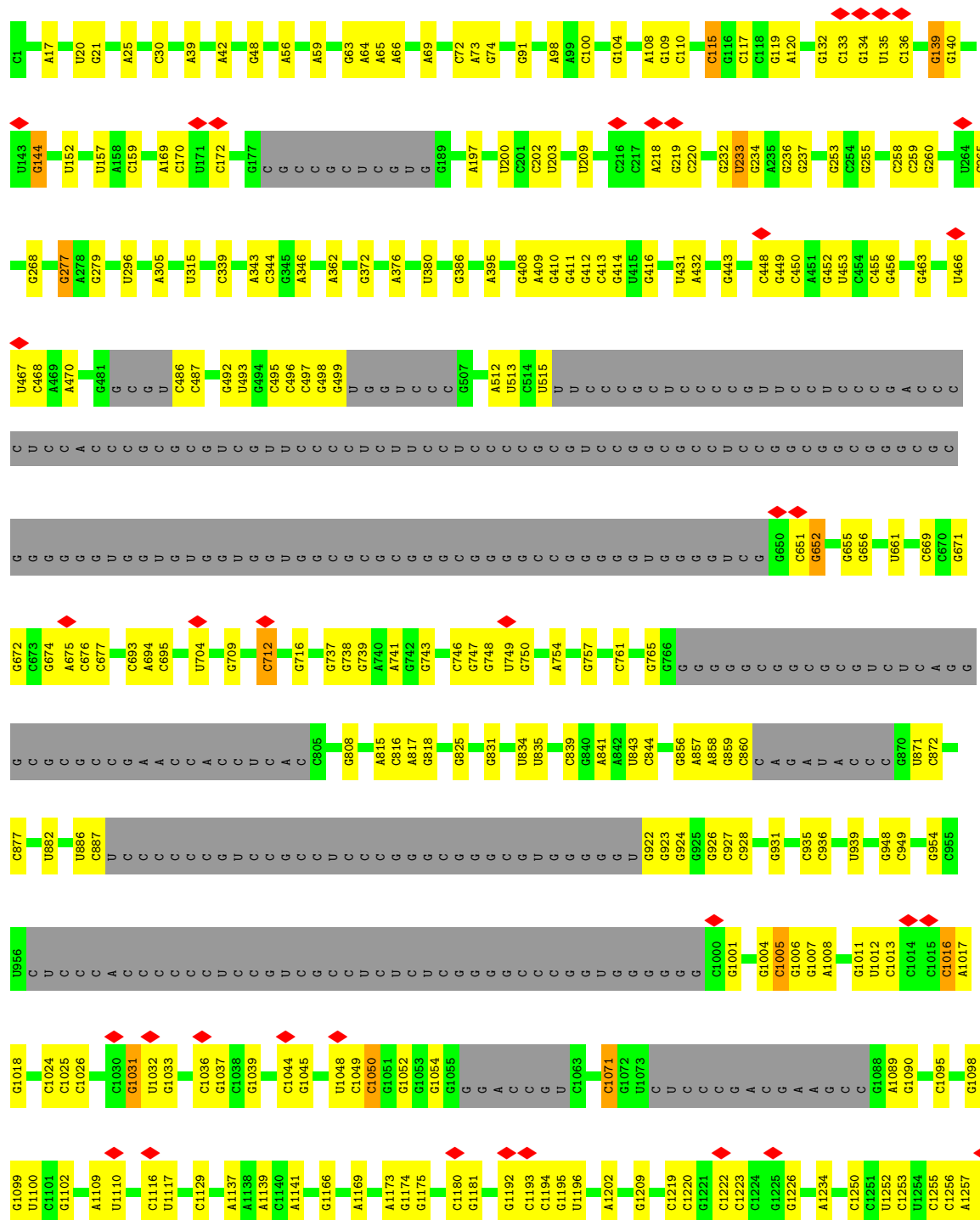


- Molecule 41: 60S ribosomal protein L37a



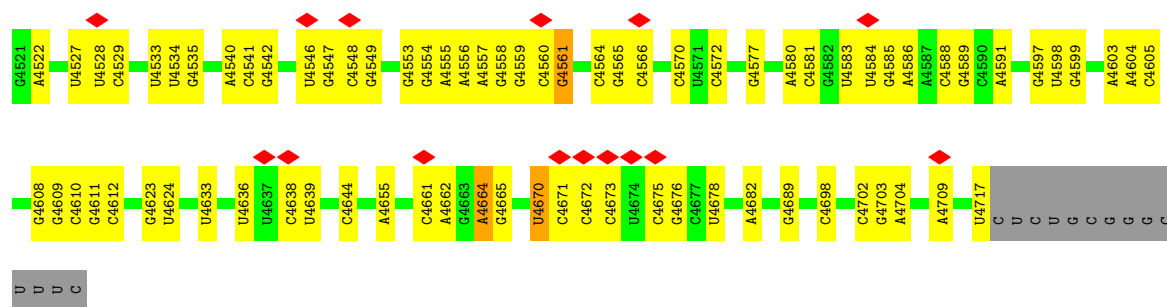
- Molecule 42: 60S ribosomal protein L28



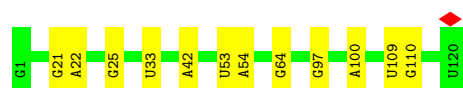
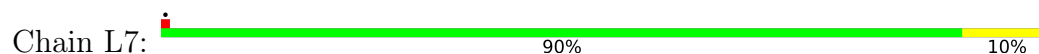




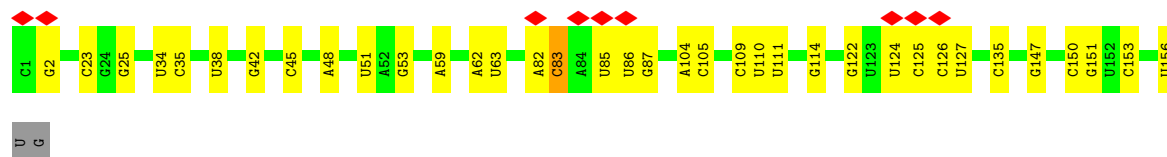
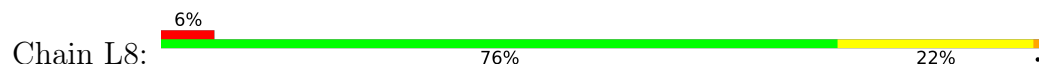




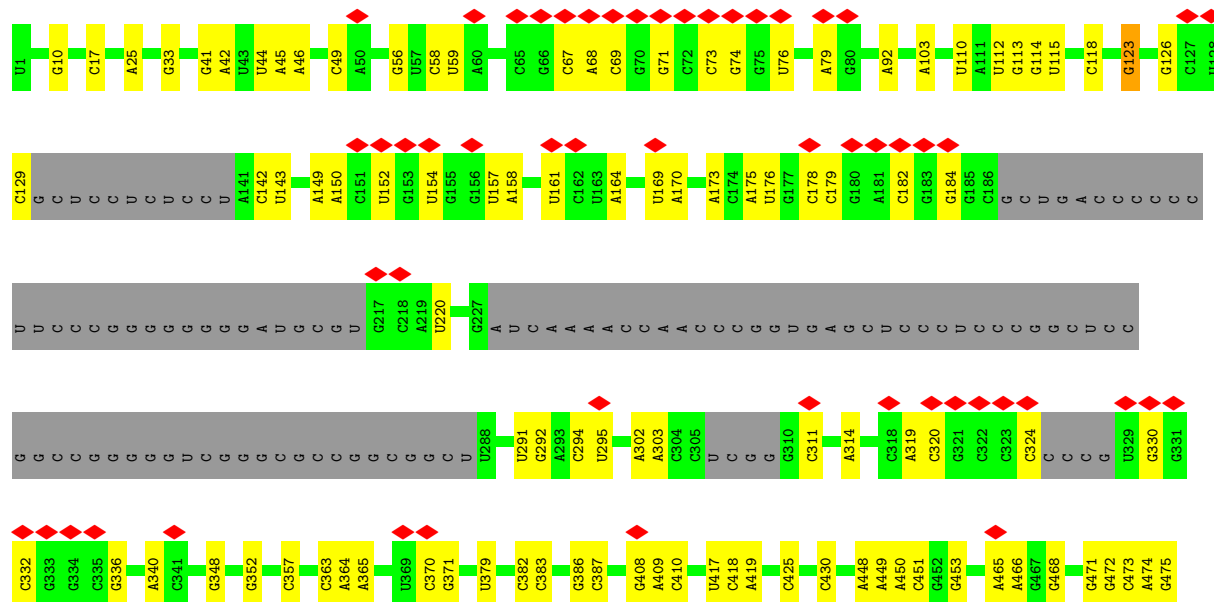
- Molecule 44: Mus musculus 5S ribosomal RNA



- Molecule 45: Mus musculus 5.8S ribosomal RNA



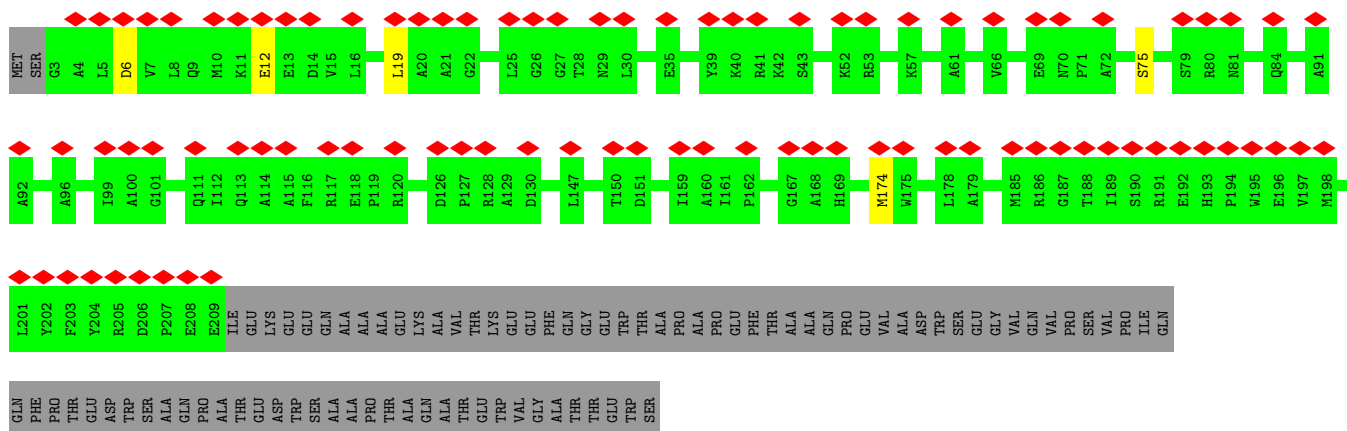
- Molecule 46: Mus musculus 18S ribosomal RNA



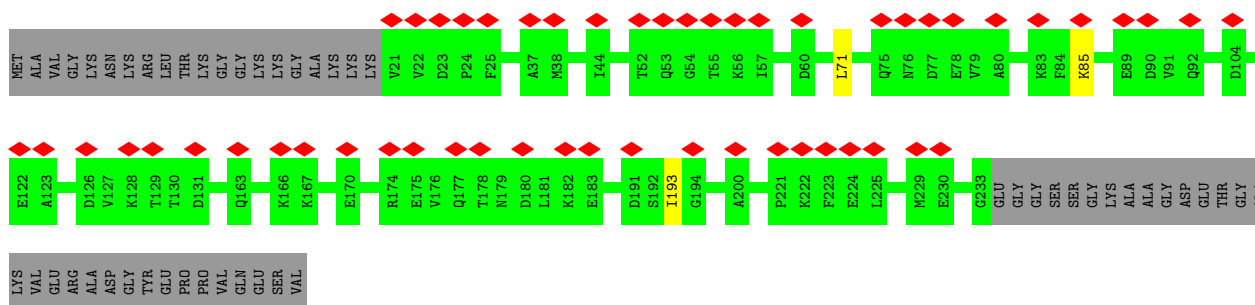
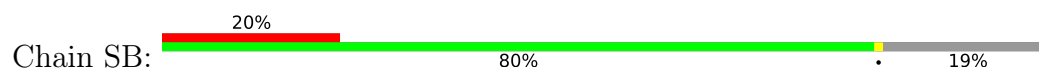


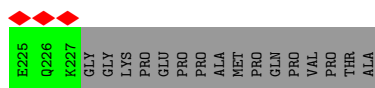


• Molecule 47: 40S ribosomal protein SA

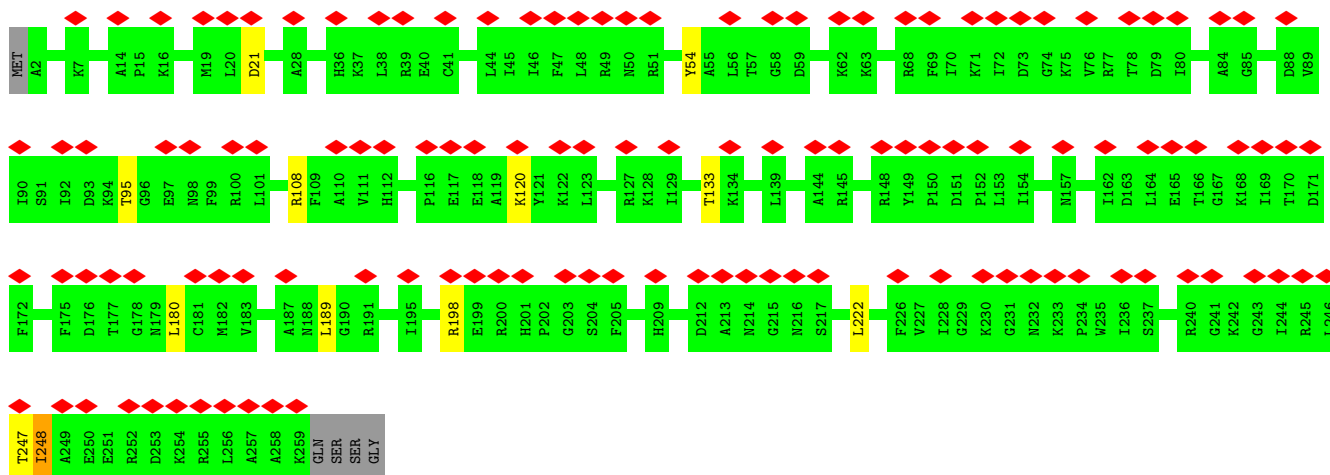


• Molecule 48: 40S ribosomal protein S3a

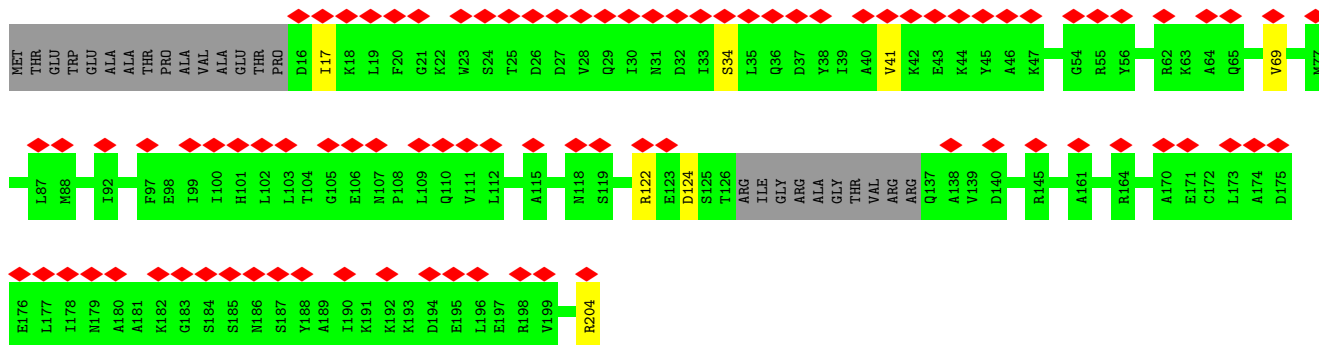
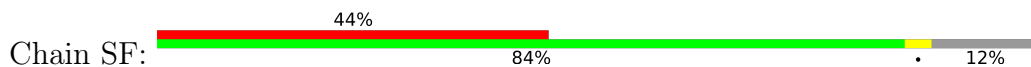




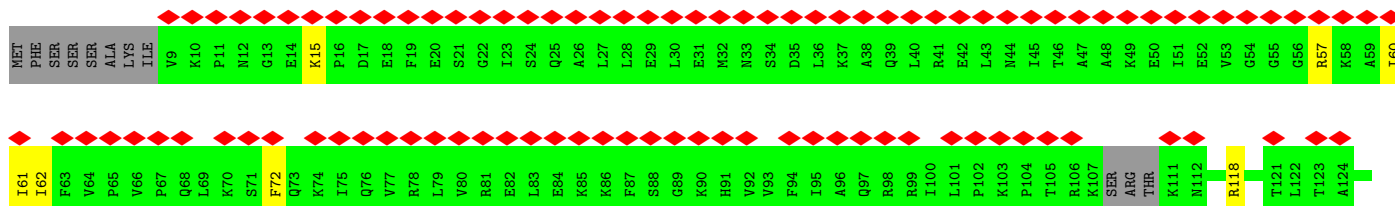
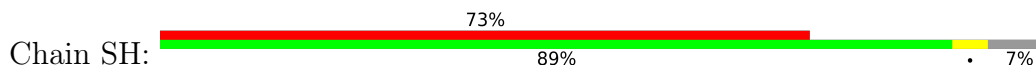
- Molecule 50: 40S ribosomal protein S4, X isoform



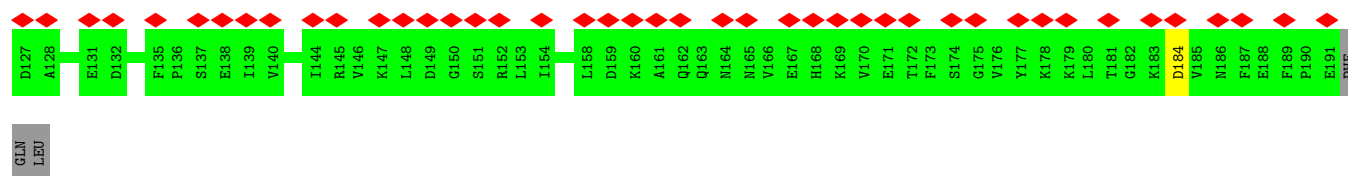
- Molecule 51: 40S ribosomal protein S5



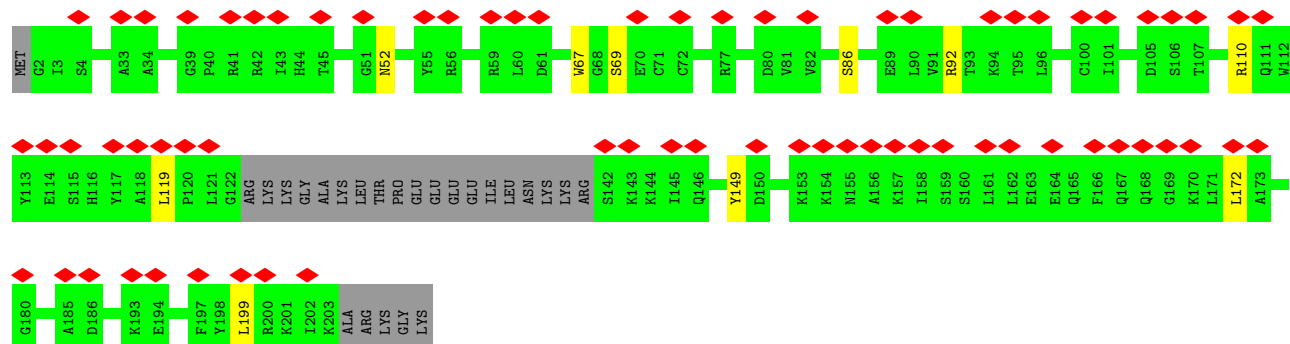
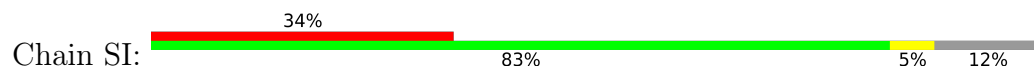
- Molecule 52: 40S ribosomal protein S7



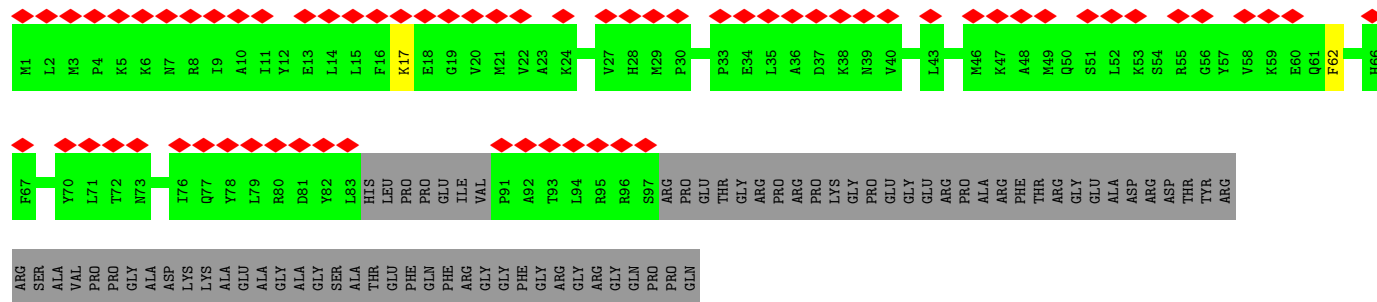
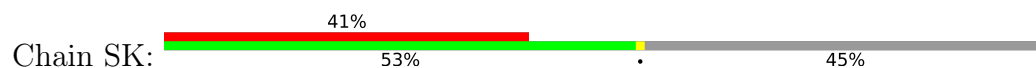




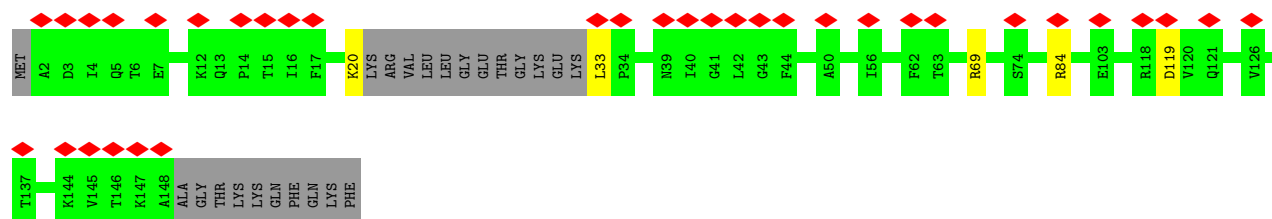
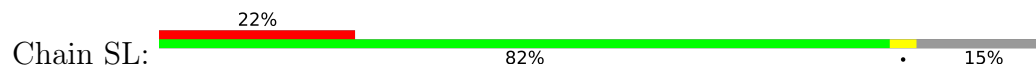
- Molecule 53: 40S ribosomal protein S8



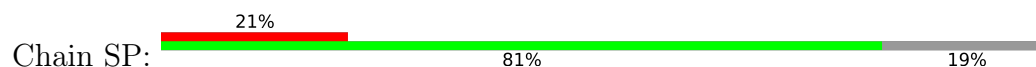
- Molecule 54: 40S ribosomal protein S10

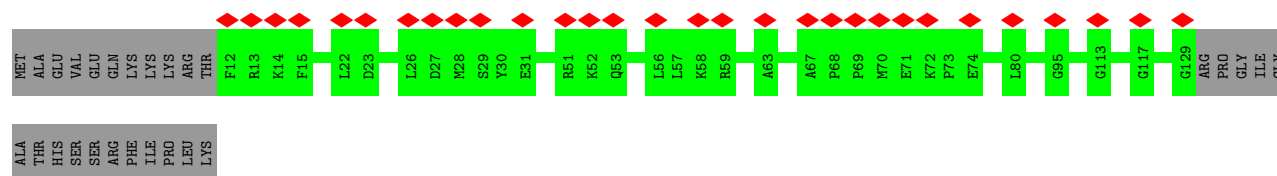


- Molecule 55: 40S ribosomal protein S11

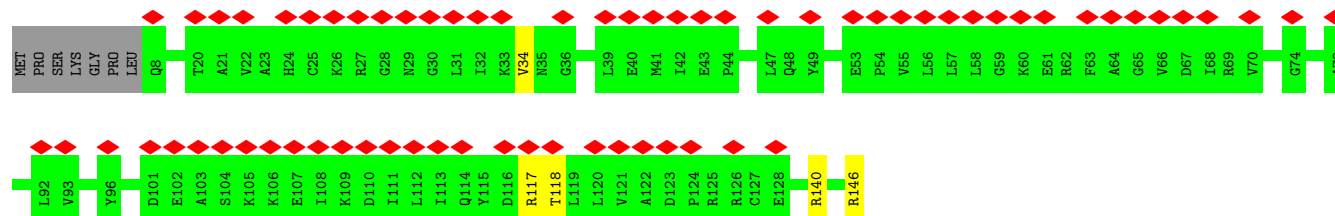


- Molecule 56: 40S ribosomal protein S15

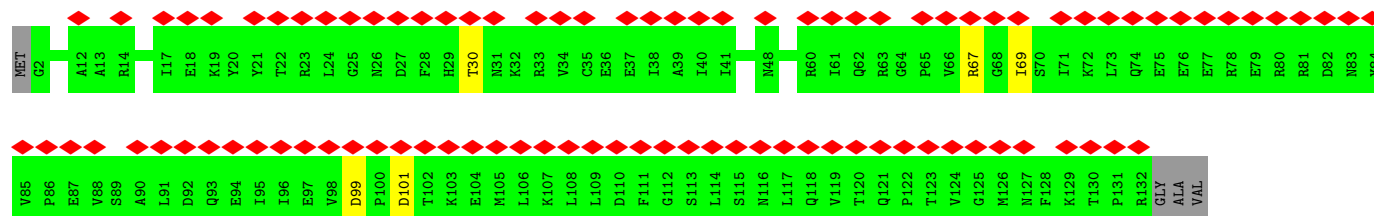
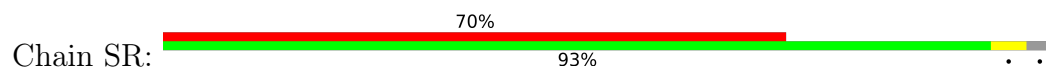




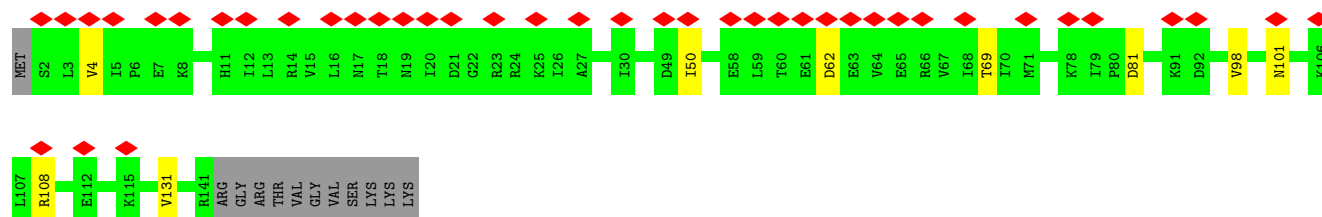
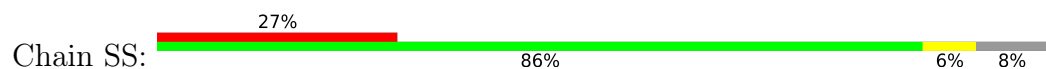
• Molecule 57: 40S ribosomal protein S16



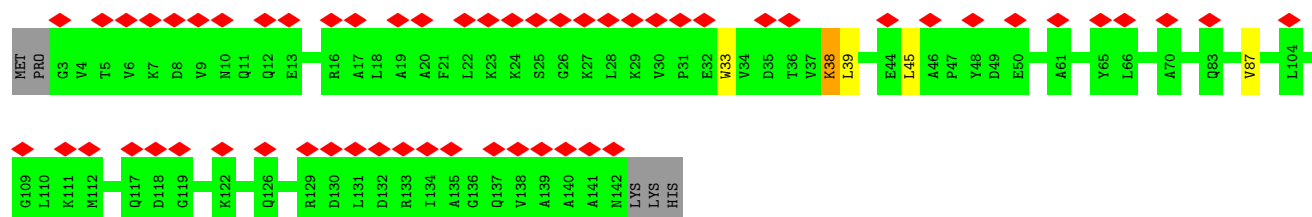
• Molecule 58: 40S ribosomal protein S17



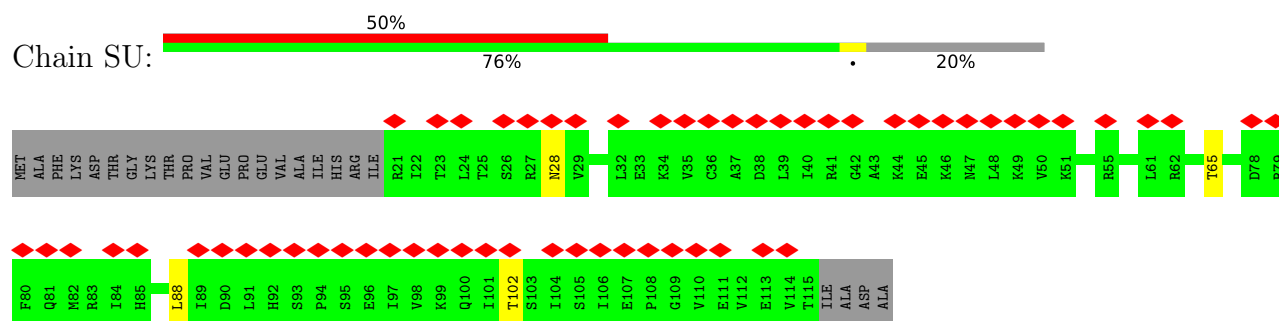
• Molecule 59: 40S ribosomal protein S18



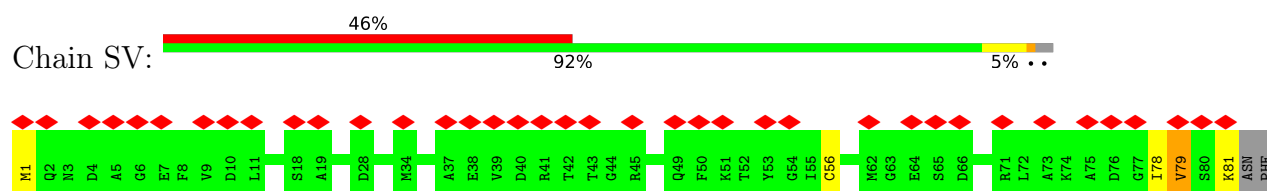
• Molecule 60: 40S ribosomal protein S19



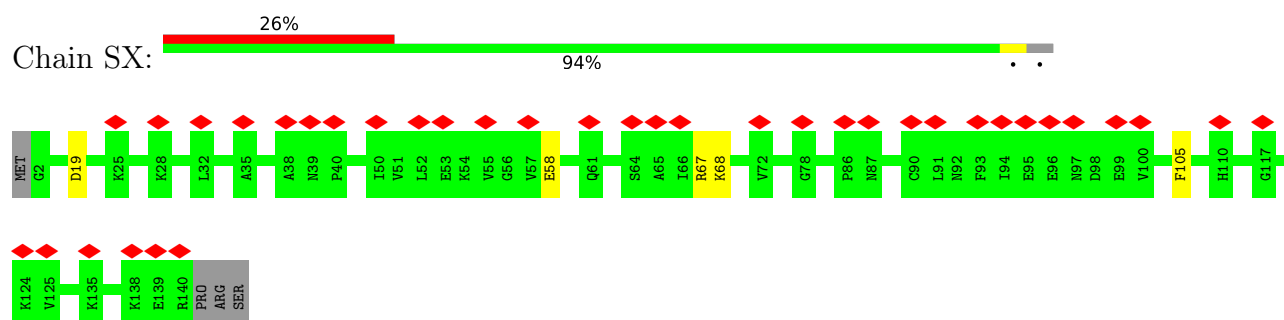
- Molecule 61: 40S ribosomal protein S20



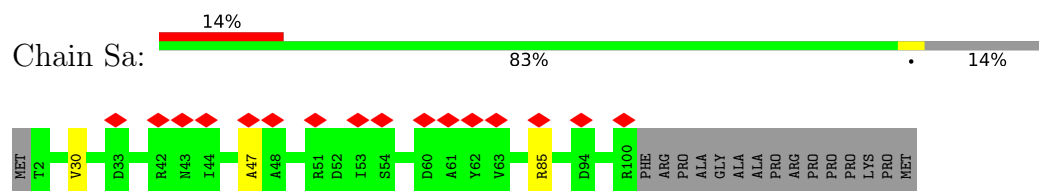
- Molecule 62: 40S ribosomal protein S21



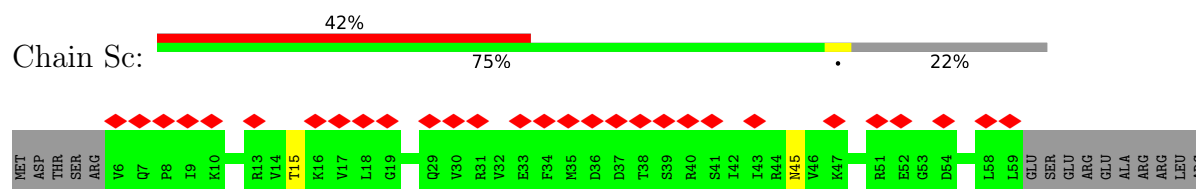
- Molecule 63: 40S ribosomal protein S23



- Molecule 64: 40S ribosomal protein S26

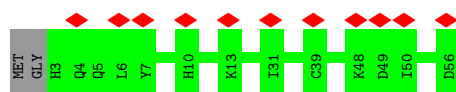


- Molecule 65: 40S ribosomal protein S28

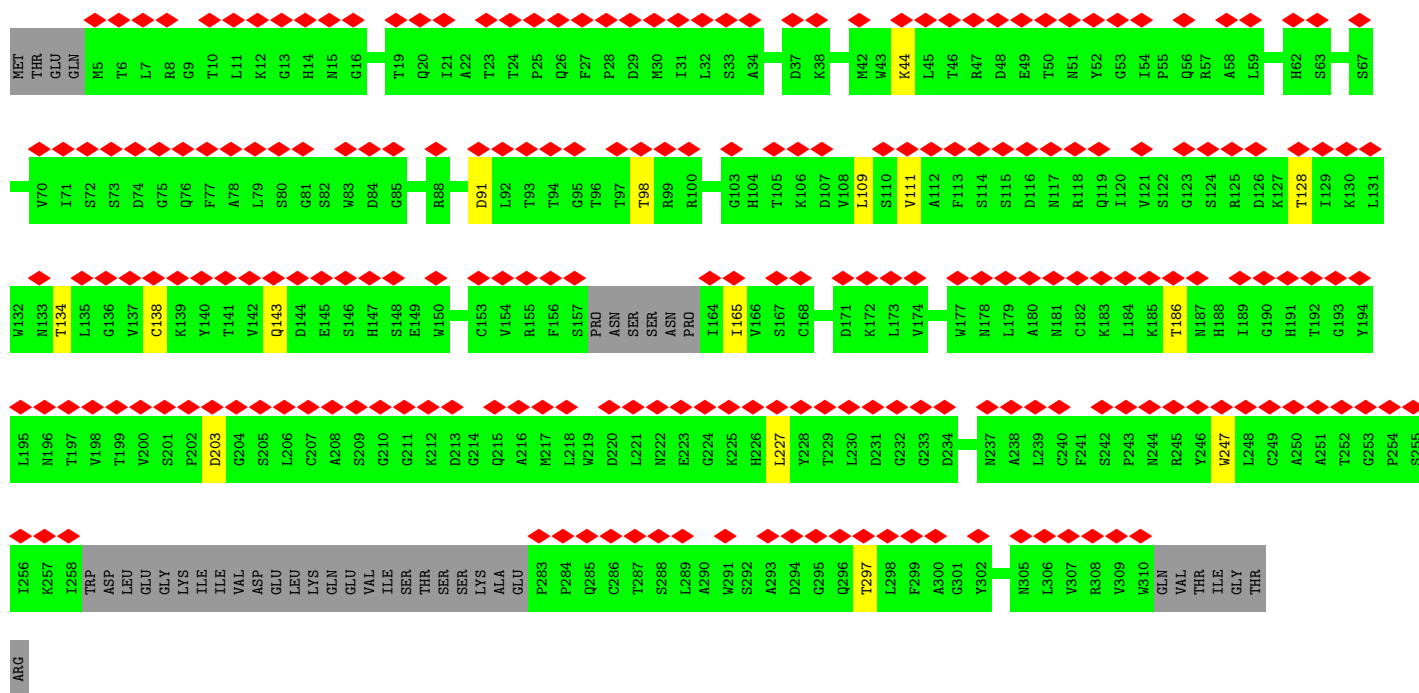
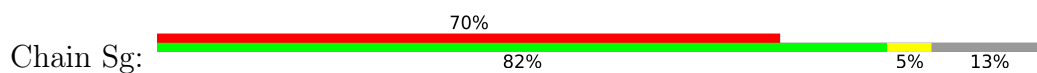


- Molecule 66: 40S ribosomal protein S29

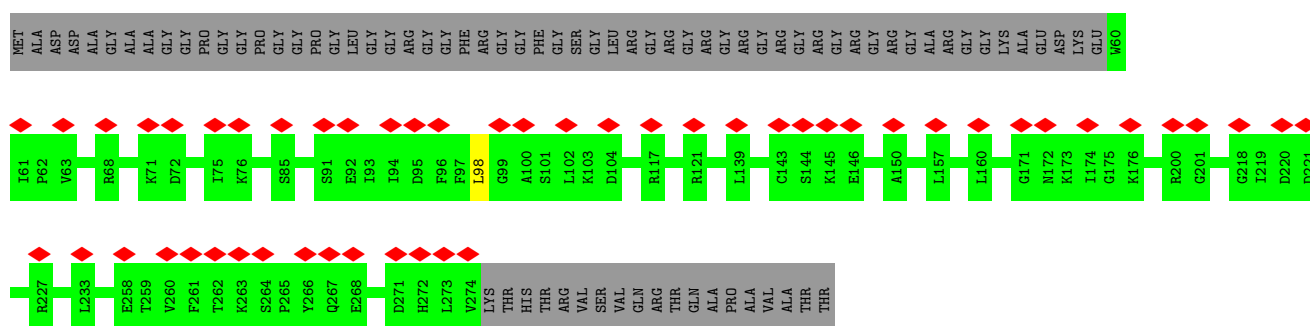
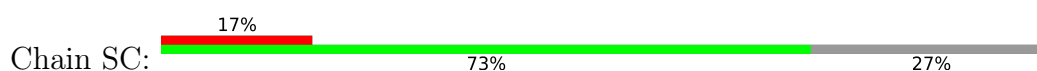




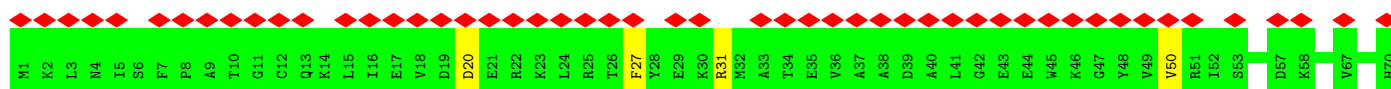
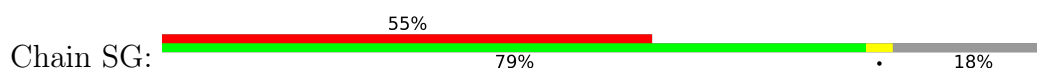
- Molecule 67: Receptor of activated protein C kinase 1

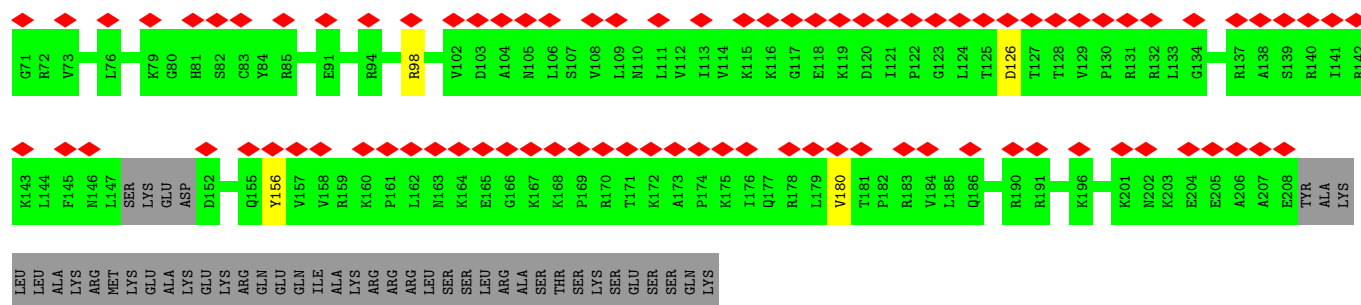


- Molecule 68: 40S ribosomal protein S2

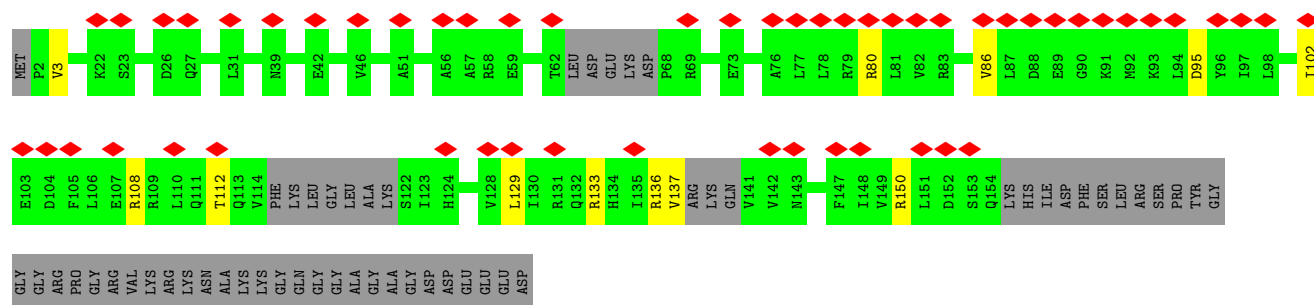


- Molecule 69: 40S ribosomal protein S6

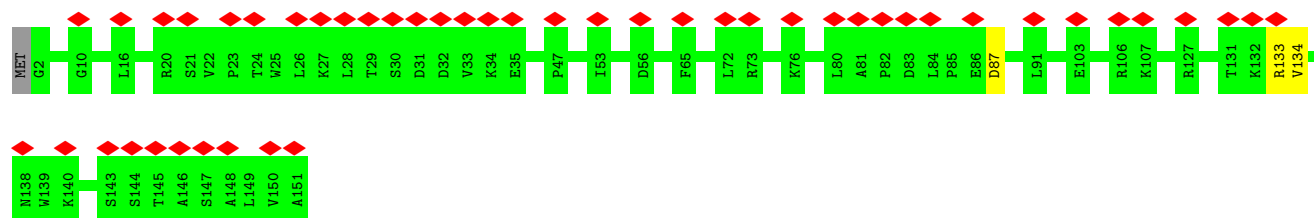




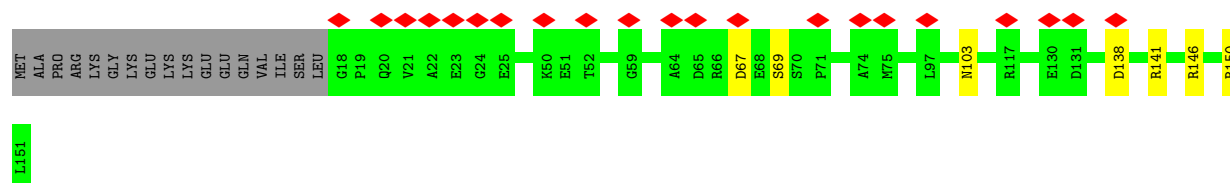
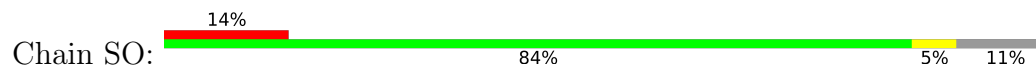
- Molecule 70: 40S ribosomal protein S9



- Molecule 71: 40S ribosomal protein S13

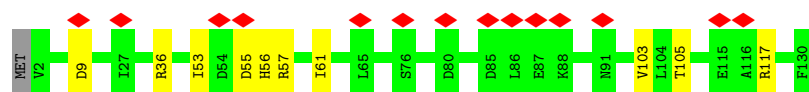


- Molecule 72: 40S ribosomal protein S14

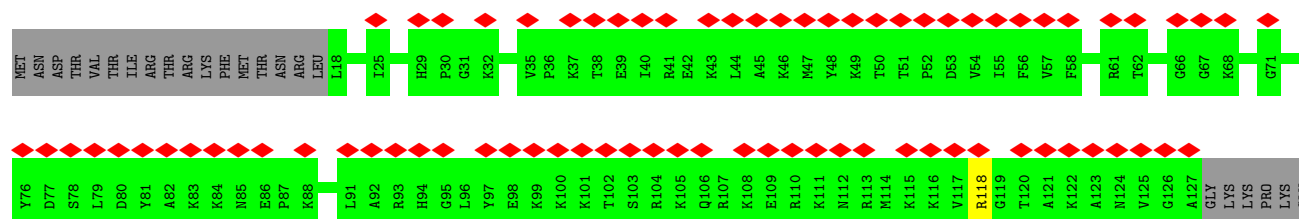
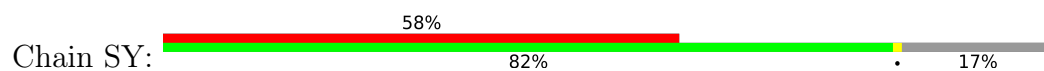


- Molecule 73: 40S ribosomal protein S15a

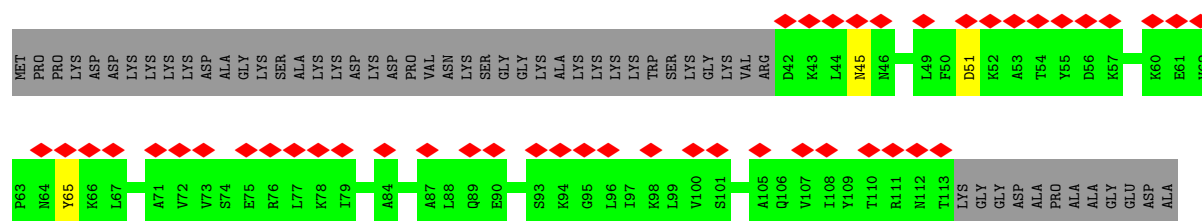
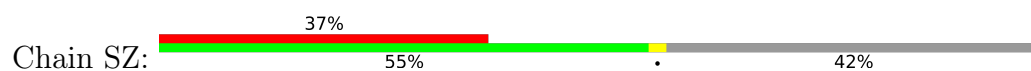




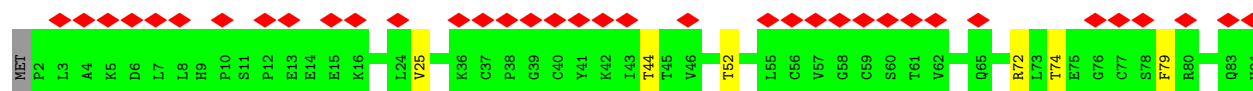
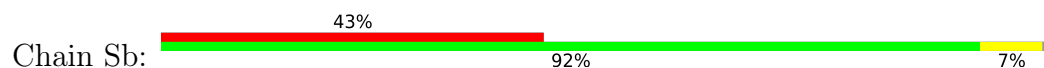
- Molecule 74: 40S ribosomal protein S24



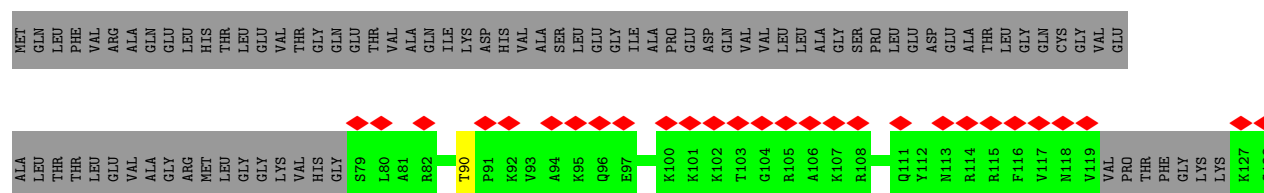
- Molecule 75: 40S ribosomal protein S25



- Molecule 76: 40S ribosomal protein S27

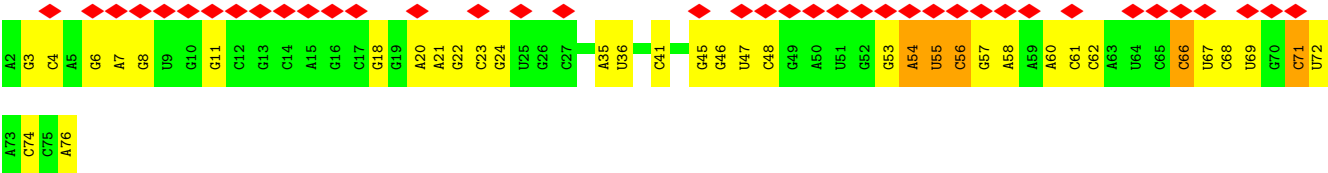


- Molecule 77: 40S ribosomal protein S30



- Molecule 78: Met-tRNA





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	100403	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.220	Depositor
Minimum map value	-0.102	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.026	Depositor
Map size ( $\text{\AA}$ )	416.0, 416.0, 416.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.04, 1.04, 1.04	Depositor



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	LA	0.63	1/1936 (0.1%)	0.58	0/2596
2	LB	0.61	0/3269	0.56	0/4375
3	LC	0.61	0/2945	0.58	0/3953
4	LD	0.56	0/2431	0.52	0/3256
5	LE	0.52	0/1910	0.56	0/2562
6	LF	0.64	0/1805	0.56	0/2408
7	LG	0.51	0/1880	0.54	0/2531
8	LH	0.52	0/1537	0.57	0/2065
9	LI	0.57	0/1669	0.50	0/2227
10	LJ	0.43	0/1394	0.55	0/1864
11	LL	0.56	0/1698	0.53	0/2274
12	LM	0.60	0/1146	0.54	0/1531
13	LN	0.71	0/1746	0.55	0/2338
14	LO	0.61	0/1670	0.53	0/2232
15	LP	0.63	0/1277	0.53	0/1712
16	LQ	0.66	0/1539	0.59	0/2053
17	LR	0.52	0/1473	0.52	0/1947
18	LS	0.65	0/1491	0.55	0/2000
19	LT	0.60	0/1335	0.50	0/1781
20	LU	0.47	0/831	0.52	0/1115
21	LV	0.59	0/987	0.58	0/1324
22	LW	0.62	0/532	0.52	0/708
23	LX	0.55	0/984	0.49	0/1323
24	LY	0.59	0/1119	0.53	0/1488
25	LZ	0.58	0/1130	0.53	0/1507
26	La	0.63	0/1193	0.55	0/1593
27	Lb	0.49	0/821	0.50	0/1082
28	Lc	0.54	0/742	0.56	0/996
29	Ld	0.58	0/911	0.54	0/1227
30	Le	0.66	0/1071	0.56	0/1429
31	Lf	0.68	0/895	0.61	0/1198
32	Lg	0.59	0/883	0.55	0/1178

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Lh	0.52	0/1023	0.53	0/1350
34	Li	0.48	0/843	0.53	0/1115
35	Lj	0.64	0/720	0.58	0/952
36	Lk	0.49	0/574	0.50	0/760
37	Ll	0.54	0/448	0.56	0/592
38	Lm	0.52	0/425	0.54	0/564
39	Ln	0.37	0/240	0.47	0/305
40	Lo	0.55	0/855	0.57	0/1128
41	Lp	0.59	0/718	0.55	0/953
42	Lr	0.61	0/1009	0.52	0/1353
43	L5	1.22	0/84917	0.97	116/132450 (0.1%)
44	L7	1.19	0/2858	0.89	0/4455
45	L8	1.26	0/3701	0.93	3/5766 (0.1%)
46	S2	0.65	0/39073	0.94	53/60890 (0.1%)
47	SA	0.35	0/1673	0.54	0/2275
48	SB	0.36	0/1756	0.53	0/2350
49	SD	0.35	0/1772	0.57	0/2385
50	SE	0.33	0/2092	0.55	0/2816
51	SF	0.33	0/1436	0.51	0/1930
52	SH	0.33	0/1470	0.53	0/1968
53	SI	0.38	0/1526	0.54	0/2038
54	SK	0.34	0/780	0.52	0/1046
55	SL	0.40	0/1130	0.54	0/1514
56	SP	0.37	0/1000	0.50	0/1335
57	SQ	0.36	0/1126	0.56	0/1506
58	SR	0.33	0/1078	0.52	0/1447
59	SS	0.36	0/1175	0.52	0/1575
60	ST	0.34	0/1108	0.49	0/1486
61	SU	0.30	0/762	0.54	0/1023
62	SV	0.38	0/625	0.52	0/836
63	SX	0.38	0/1097	0.56	0/1464
64	Sa	0.42	0/805	0.54	0/1079
65	Sc	0.31	0/418	0.57	0/562
66	Sd	0.38	0/466	0.49	0/618
67	Sg	0.32	0/2199	0.59	0/2989
68	SC	0.41	0/1712	0.55	0/2314
69	SG	0.32	0/1666	0.54	1/2222 (0.0%)
70	SJ	0.32	0/1178	0.55	0/1574
71	SN	0.39	1/1232 (0.1%)	0.51	0/1656
72	SO	0.38	0/1015	0.57	0/1361
73	SW	0.39	0/1051	0.53	0/1406
74	SY	0.31	0/907	0.53	0/1204
75	SZ	0.31	0/580	0.53	0/780

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Sb	0.34	0/665	0.54	0/891
77	Se	0.34	0/386	0.53	0/504
78	S6	0.55	0/1795	1.10	8/2798 (0.3%)
All	All	0.89	2/221335 (0.0%)	0.83	181/325458 (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
2	LB	0	2
3	LC	0	2
10	LJ	0	1
12	LM	0	1
31	Lf	0	1
50	SE	0	1
52	SH	0	1
60	ST	0	1
70	SJ	0	1
All	All	0	11

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	LA	220	GLY	C-N	-5.13	1.22	1.34
71	SN	134	VAL	C-N	-5.00	1.22	1.34

The worst 5 of 181 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	L5	923	G	N3-C4-N9	-10.16	119.90	126.00
43	L5	416	G	O4'-C1'-N9	9.74	115.99	108.20
43	L5	923	G	C5-C6-O6	9.31	134.19	128.60
78	S6	55	U	O5'-P-OP1	-8.86	97.73	105.70
43	L5	2464	C	C2-N1-C1'	8.61	128.27	118.80

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	LB	16	PHE	Peptide
2	LB	258	HIS	Peptide
3	LC	354	LEU	Peptide
3	LC	66	SER	Peptide
10	LJ	173	ILE	Peptide

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	246/257 (96%)	218 (89%)	28 (11%)	0	100	100
2	LB	395/403 (98%)	367 (93%)	28 (7%)	0	100	100
3	LC	360/419 (86%)	326 (91%)	33 (9%)	1 (0%)	41	74
4	LD	291/297 (98%)	270 (93%)	21 (7%)	0	100	100
5	LE	227/296 (77%)	207 (91%)	20 (9%)	0	100	100
6	LF	212/270 (78%)	200 (94%)	12 (6%)	0	100	100
7	LG	225/266 (85%)	209 (93%)	16 (7%)	0	100	100
8	LH	188/192 (98%)	169 (90%)	19 (10%)	0	100	100
9	LI	197/214 (92%)	187 (95%)	10 (5%)	0	100	100
10	LJ	169/178 (95%)	147 (87%)	22 (13%)	0	100	100
11	LL	204/211 (97%)	186 (91%)	17 (8%)	1 (0%)	29	65
12	LM	134/217 (62%)	121 (90%)	13 (10%)	0	100	100
13	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	15	49
14	LO	199/203 (98%)	190 (96%)	9 (4%)	0	100	100
15	LP	152/184 (83%)	140 (92%)	12 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	LQ	185/188 (98%)	173 (94%)	12 (6%)	0	100	100
17	LR	172/196 (88%)	166 (96%)	6 (4%)	0	100	100
18	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
19	LT	158/160 (99%)	150 (95%)	8 (5%)	0	100	100
20	LU	98/128 (77%)	85 (87%)	13 (13%)	0	100	100
21	LV	128/140 (91%)	118 (92%)	10 (8%)	0	100	100
22	LW	60/157 (38%)	55 (92%)	5 (8%)	0	100	100
23	LX	116/156 (74%)	112 (97%)	4 (3%)	0	100	100
24	LY	130/145 (90%)	124 (95%)	6 (5%)	0	100	100
25	LZ	133/136 (98%)	116 (87%)	17 (13%)	0	100	100
26	La	145/148 (98%)	131 (90%)	14 (10%)	0	100	100
27	Lb	95/160 (59%)	88 (93%)	7 (7%)	0	100	100
28	Lc	92/115 (80%)	85 (92%)	7 (8%)	0	100	100
29	Ld	106/125 (85%)	93 (88%)	13 (12%)	0	100	100
30	Le	126/135 (93%)	116 (92%)	9 (7%)	1 (1%)	19	54
31	Lf	107/110 (97%)	102 (95%)	5 (5%)	0	100	100
32	Lg	108/117 (92%)	104 (96%)	4 (4%)	0	100	100
33	Lh	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
34	Li	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
35	Lj	84/97 (87%)	78 (93%)	6 (7%)	0	100	100
36	Lk	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
38	Lm	49/128 (38%)	46 (94%)	1 (2%)	2 (4%)	3	14
39	Ln	23/25 (92%)	23 (100%)	0	0	100	100
40	Lo	101/106 (95%)	93 (92%)	8 (8%)	0	100	100
41	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
42	Lr	122/137 (89%)	115 (94%)	7 (6%)	0	100	100
47	SA	205/295 (70%)	179 (87%)	25 (12%)	1 (0%)	29	65
48	SB	211/264 (80%)	193 (92%)	18 (8%)	0	100	100
49	SD	222/243 (91%)	193 (87%)	29 (13%)	0	100	100
50	SE	256/263 (97%)	229 (90%)	26 (10%)	1 (0%)	34	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	SF	175/204 (86%)	156 (89%)	19 (11%)	0	100	100
52	SH	176/194 (91%)	155 (88%)	21 (12%)	0	100	100
53	SI	179/208 (86%)	168 (94%)	11 (6%)	0	100	100
54	SK	86/165 (52%)	73 (85%)	13 (15%)	0	100	100
55	SL	131/158 (83%)	124 (95%)	7 (5%)	0	100	100
56	SP	116/145 (80%)	110 (95%)	6 (5%)	0	100	100
57	SQ	137/146 (94%)	118 (86%)	18 (13%)	1 (1%)	22	57
58	SR	129/135 (96%)	116 (90%)	13 (10%)	0	100	100
59	SS	138/152 (91%)	125 (91%)	12 (9%)	1 (1%)	22	57
60	ST	138/145 (95%)	131 (95%)	7 (5%)	0	100	100
61	SU	93/119 (78%)	86 (92%)	7 (8%)	0	100	100
62	SV	79/83 (95%)	71 (90%)	7 (9%)	1 (1%)	12	42
63	SX	137/143 (96%)	123 (90%)	14 (10%)	0	100	100
64	Sa	97/115 (84%)	87 (90%)	9 (9%)	1 (1%)	15	49
65	Sc	52/69 (75%)	42 (81%)	10 (19%)	0	100	100
66	Sd	52/56 (93%)	47 (90%)	5 (10%)	0	100	100
67	Sg	270/317 (85%)	218 (81%)	52 (19%)	0	100	100
68	SC	214/293 (73%)	199 (93%)	15 (7%)	0	100	100
69	SG	200/249 (80%)	184 (92%)	16 (8%)	0	100	100
70	SJ	130/194 (67%)	118 (91%)	12 (9%)	0	100	100
71	SN	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
72	SO	132/151 (87%)	116 (88%)	15 (11%)	1 (1%)	19	54
73	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
74	SY	108/133 (81%)	93 (86%)	15 (14%)	0	100	100
75	SZ	70/125 (56%)	62 (89%)	8 (11%)	0	100	100
76	Sb	81/84 (96%)	73 (90%)	8 (10%)	0	100	100
77	Se	44/133 (33%)	38 (86%)	6 (14%)	0	100	100
All	All	10668/12499 (85%)	9753 (91%)	901 (8%)	14 (0%)	54	84

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
64	Sa	47	ALA

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Mol	Chain	Res	Type
30	Le	92	ASN
47	SA	12	GLU
11	LL	51	ALA
13	LN	84	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	190/199 (96%)	185 (97%)	5 (3%)	46	76
2	LB	344/348 (99%)	333 (97%)	11 (3%)	39	72
3	LC	304/348 (87%)	292 (96%)	12 (4%)	32	66
4	LD	245/249 (98%)	230 (94%)	15 (6%)	18	50
5	LE	208/256 (81%)	194 (93%)	14 (7%)	16	46
6	LF	185/234 (79%)	183 (99%)	2 (1%)	73	90
7	LG	197/223 (88%)	195 (99%)	2 (1%)	76	91
8	LH	169/171 (99%)	161 (95%)	8 (5%)	26	61
9	LI	170/180 (94%)	161 (95%)	9 (5%)	22	56
10	LJ	144/149 (97%)	136 (94%)	8 (6%)	21	54
11	LL	173/178 (97%)	165 (95%)	8 (5%)	27	61
12	LM	116/157 (74%)	112 (97%)	4 (3%)	37	70
13	LN	171/172 (99%)	168 (98%)	3 (2%)	59	83
14	LO	172/173 (99%)	168 (98%)	4 (2%)	50	78
15	LP	135/163 (83%)	131 (97%)	4 (3%)	41	73
16	LQ	164/165 (99%)	160 (98%)	4 (2%)	49	78
17	LR	154/175 (88%)	149 (97%)	5 (3%)	39	72
18	LS	155/156 (99%)	148 (96%)	7 (4%)	27	62
19	LT	140/140 (100%)	134 (96%)	6 (4%)	29	63
20	LU	90/114 (79%)	81 (90%)	9 (10%)	7	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	LV	100/107 (94%)	95 (95%)	5 (5%)	24	58
22	LW	54/126 (43%)	52 (96%)	2 (4%)	34	68
23	LX	106/133 (80%)	106 (100%)	0	100	100
24	LY	123/135 (91%)	116 (94%)	7 (6%)	20	53
25	LZ	117/118 (99%)	114 (97%)	3 (3%)	46	76
26	La	120/121 (99%)	111 (92%)	9 (8%)	13	41
27	Lb	83/124 (67%)	78 (94%)	5 (6%)	19	51
28	Lc	79/97 (81%)	75 (95%)	4 (5%)	24	57
29	Ld	99/110 (90%)	99 (100%)	0	100	100
30	Le	114/121 (94%)	110 (96%)	4 (4%)	36	69
31	Lf	88/89 (99%)	86 (98%)	2 (2%)	50	78
32	Lg	94/100 (94%)	90 (96%)	4 (4%)	29	63
33	Lh	109/110 (99%)	107 (98%)	2 (2%)	59	83
34	Li	86/89 (97%)	82 (95%)	4 (5%)	26	61
35	Lj	73/80 (91%)	72 (99%)	1 (1%)	67	86
36	Lk	64/65 (98%)	64 (100%)	0	100	100
37	Ll	46/47 (98%)	39 (85%)	7 (15%)	3	12
38	Lm	47/116 (40%)	44 (94%)	3 (6%)	17	48
39	Ln	24/24 (100%)	23 (96%)	1 (4%)	30	64
40	Lo	91/94 (97%)	83 (91%)	8 (9%)	10	34
41	Lp	74/75 (99%)	71 (96%)	3 (4%)	30	65
42	Lr	108/121 (89%)	102 (94%)	6 (6%)	21	54
47	SA	173/242 (72%)	169 (98%)	4 (2%)	50	78
48	SB	194/229 (85%)	191 (98%)	3 (2%)	65	86
49	SD	188/202 (93%)	182 (97%)	6 (3%)	39	72
50	SE	221/225 (98%)	210 (95%)	11 (5%)	24	58
51	SF	152/170 (89%)	145 (95%)	7 (5%)	27	61
52	SH	161/174 (92%)	154 (96%)	7 (4%)	29	63
53	SI	159/180 (88%)	149 (94%)	10 (6%)	18	49
54	SK	81/136 (60%)	79 (98%)	2 (2%)	47	77
55	SL	123/142 (87%)	118 (96%)	5 (4%)	30	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	SP	107/130 (82%)	107 (100%)	0	100	100
57	SQ	115/121 (95%)	111 (96%)	4 (4%)	36	69
58	SR	119/121 (98%)	114 (96%)	5 (4%)	30	64
59	SS	122/132 (92%)	114 (93%)	8 (7%)	16	47
60	ST	110/115 (96%)	105 (96%)	5 (4%)	27	62
61	SU	88/107 (82%)	84 (96%)	4 (4%)	27	62
62	SV	65/67 (97%)	60 (92%)	5 (8%)	13	40
63	SX	111/115 (96%)	106 (96%)	5 (4%)	27	62
64	Sa	86/98 (88%)	84 (98%)	2 (2%)	50	78
65	Sc	48/62 (77%)	46 (96%)	2 (4%)	30	64
66	Sd	48/49 (98%)	48 (100%)	0	100	100
67	Sg	237/275 (86%)	222 (94%)	15 (6%)	18	49
68	SC	182/224 (81%)	181 (100%)	1 (0%)	88	95
69	SG	178/218 (82%)	171 (96%)	7 (4%)	32	66
70	SJ	126/168 (75%)	115 (91%)	11 (9%)	10	34
71	SN	130/131 (99%)	128 (98%)	2 (2%)	65	86
72	SO	104/119 (87%)	98 (94%)	6 (6%)	20	52
73	SW	112/113 (99%)	102 (91%)	10 (9%)	9	33
74	SY	93/115 (81%)	92 (99%)	1 (1%)	73	90
75	SZ	64/103 (62%)	61 (95%)	3 (5%)	26	61
76	Sb	75/76 (99%)	69 (92%)	6 (8%)	12	38
77	Se	39/106 (37%)	37 (95%)	2 (5%)	24	57
All	All	9336/10617 (88%)	8957 (96%)	379 (4%)	34	65

5 of 379 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	SD	162	ASP
59	SS	62	ASP
50	SE	133	THR
53	SI	69	SER
61	SU	102	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 145 such sidechains are listed below:

Mol	Chain	Res	Type
63	SX	110	HIS
76	Sb	26	GLN
66	Sd	5	GLN
69	SG	186	GLN
20	LU	94	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
43	L5	3523/4731 (74%)	905 (25%)	22 (0%)
44	L7	119/120 (99%)	12 (10%)	0
45	L8	155/158 (98%)	35 (22%)	0
46	S2	1627/1870 (87%)	448 (27%)	7 (0%)
78	S6	74/75 (98%)	35 (47%)	2 (2%)
All	All	5498/6954 (79%)	1435 (26%)	31 (0%)

5 of 1435 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	L5	17	A
43	L5	20	U
43	L5	21	G
43	L5	25	A
43	L5	30	C

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
43	L5	2540	C
46	S2	1343	U
43	L5	3417	A
78	S6	53	G
46	S2	547	G

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

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

Of 254 ligands modelled in this entry, 254 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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

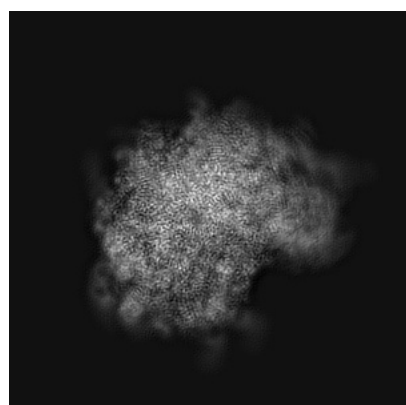
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30433. These allow visual inspection of the internal detail of the map and identification of artifacts.

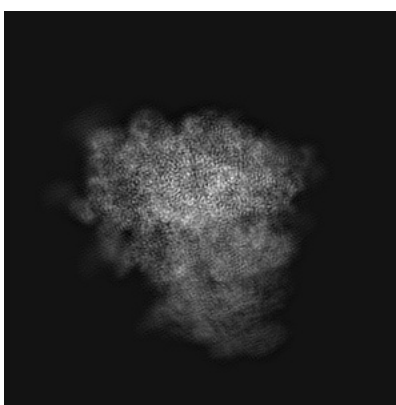
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

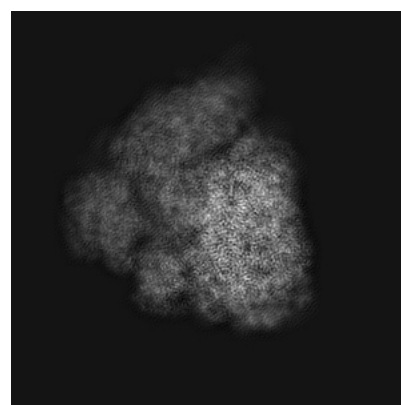
#### 6.1.1 Primary map



X



Y

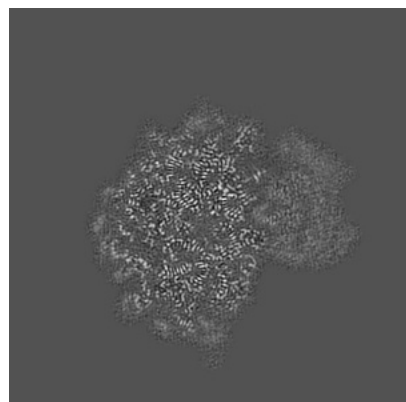


Z

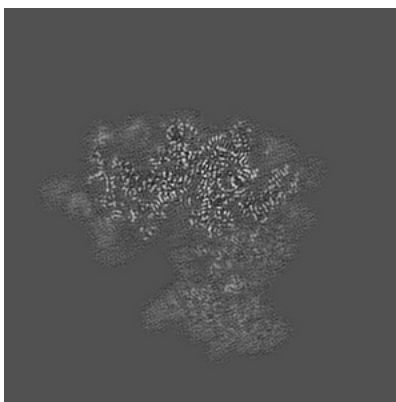
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

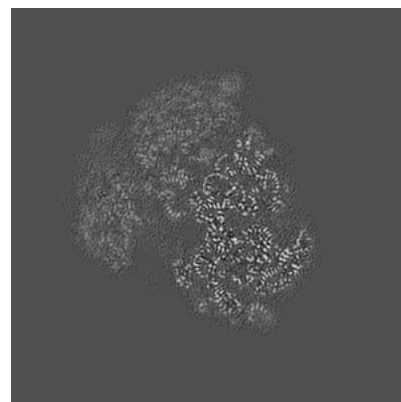
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

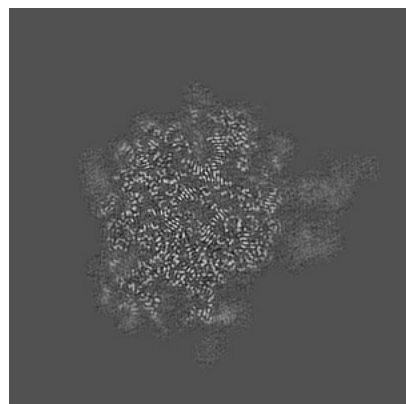


Z Index: 200

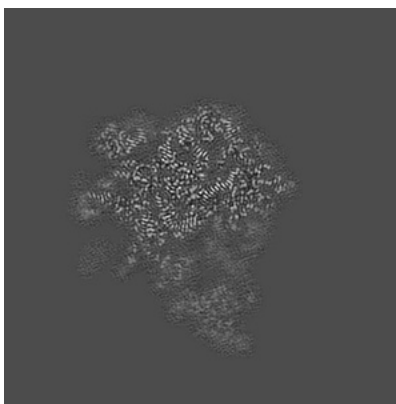
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

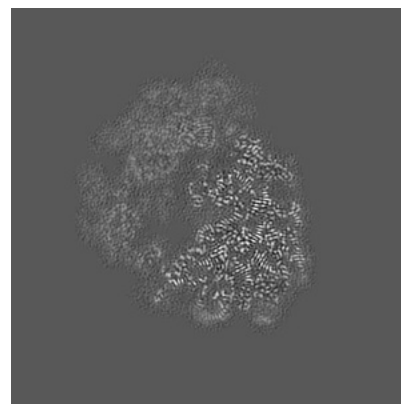
### 6.3.1 Primary map



X Index: 229



Y Index: 158

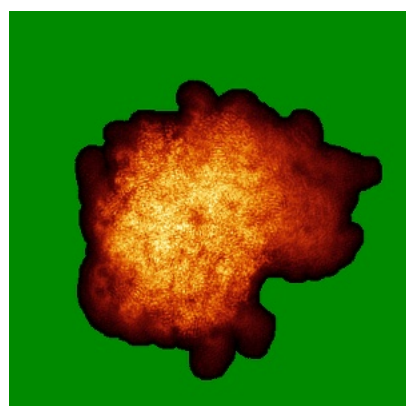


Z Index: 183

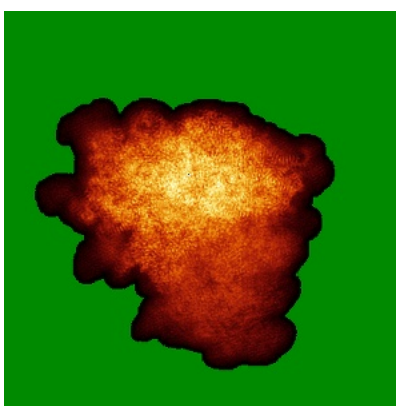
The images above show the largest variance slices of the map in three orthogonal directions.

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

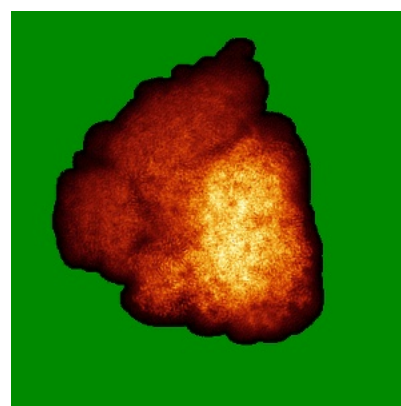
### 6.4.1 Primary map



X



Y

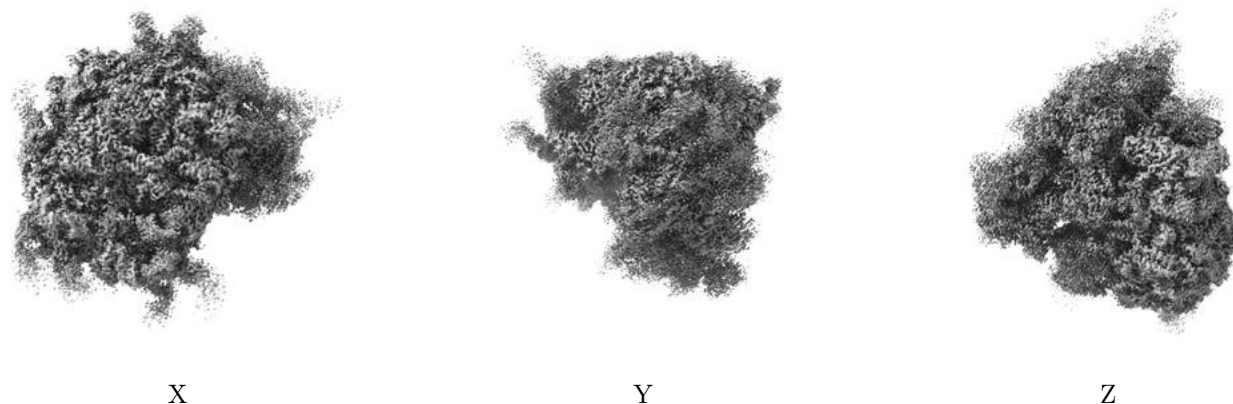


Z

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 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

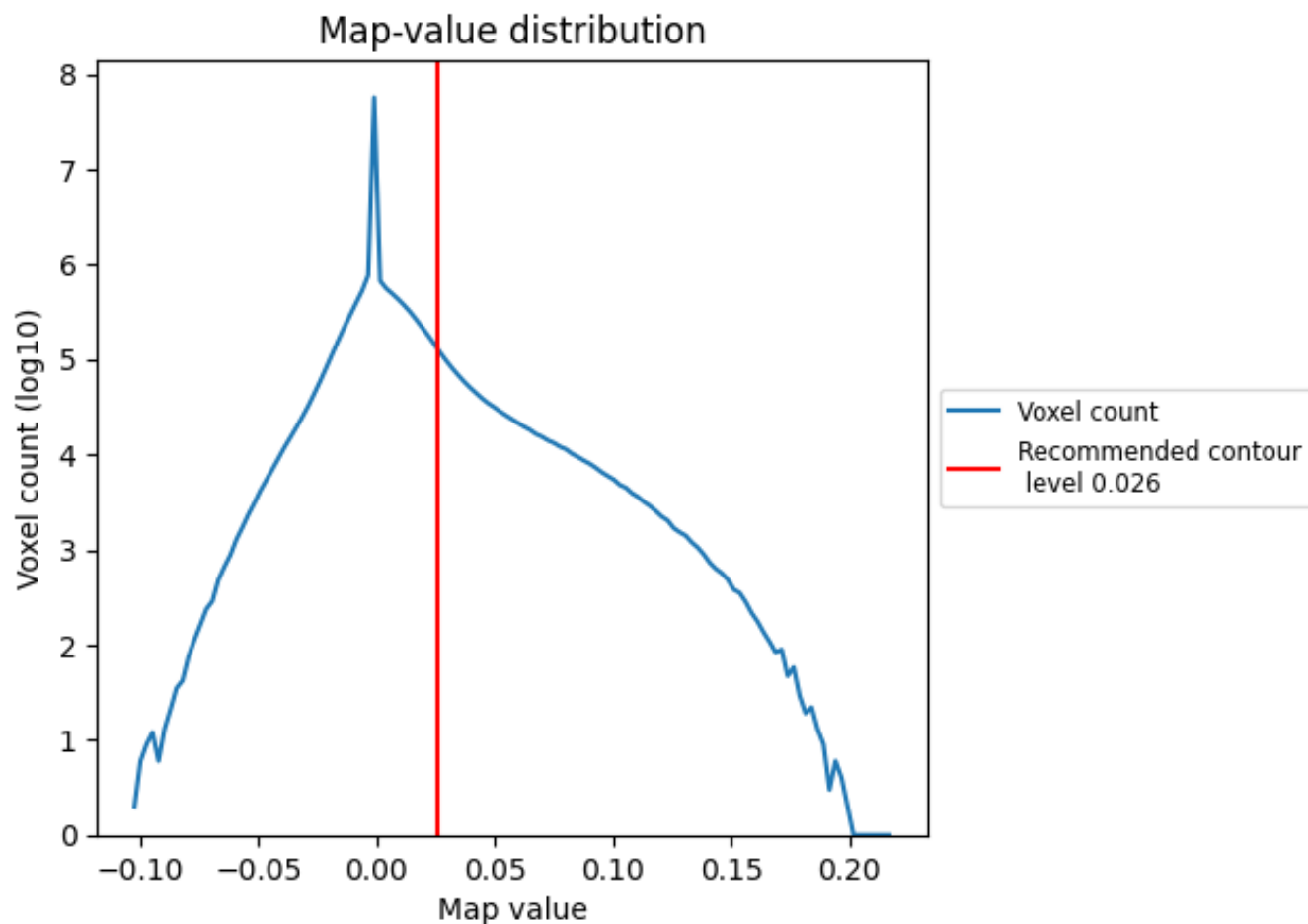
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

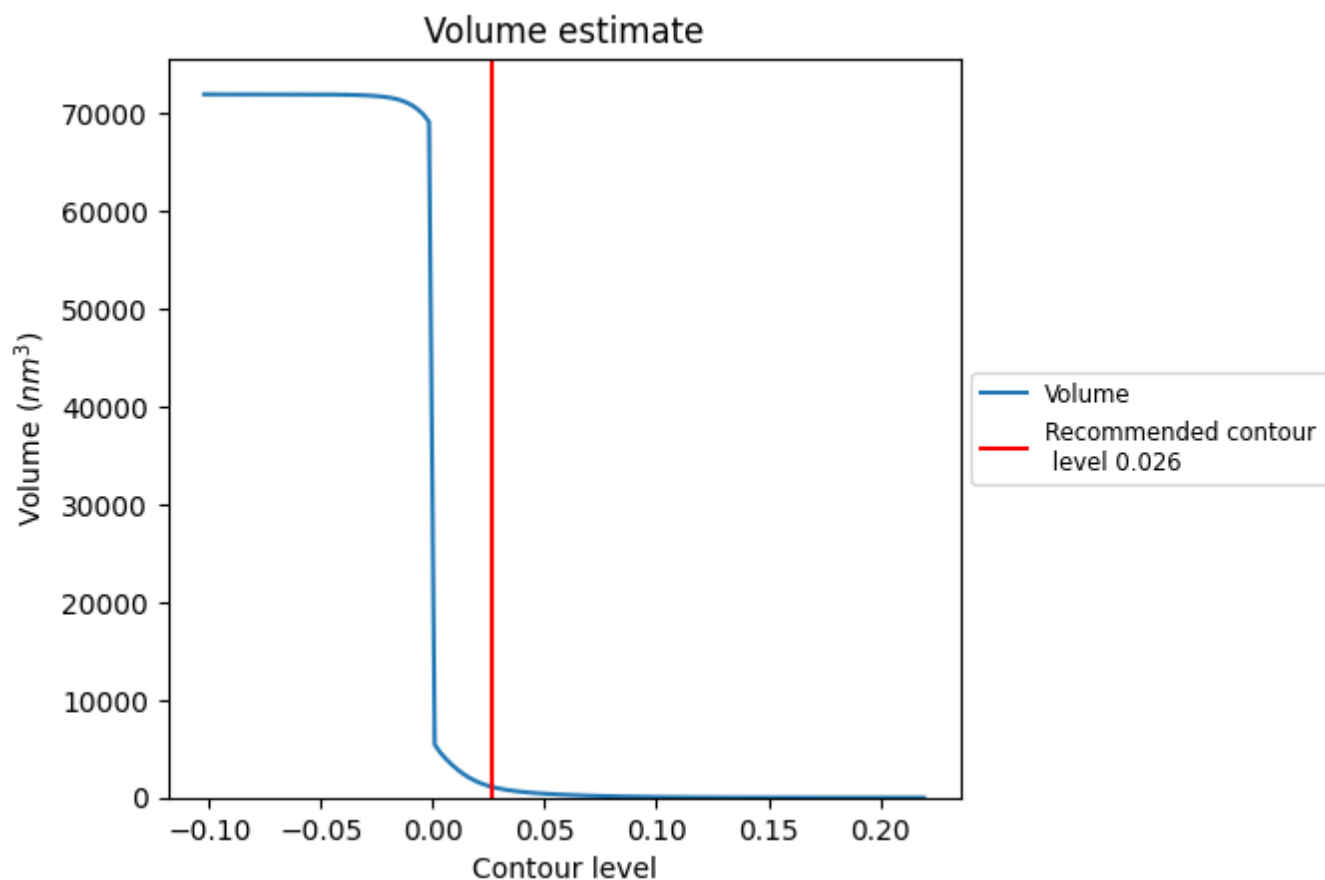
This section contains the results of statistical analysis of the map.

### 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](#)

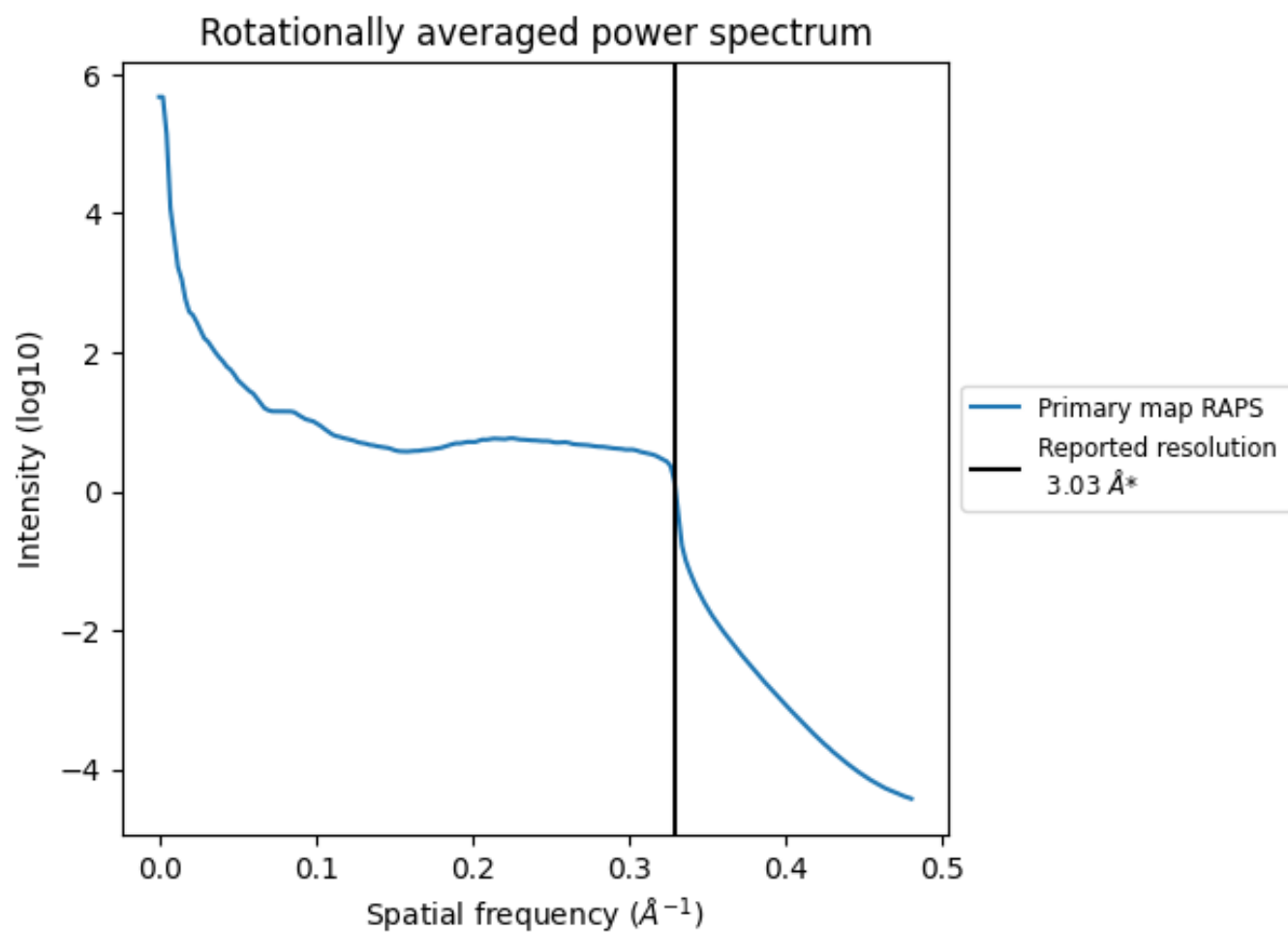


The volume at the recommended contour level is 1121 nm<sup>3</sup>; this corresponds to an approximate mass of 1013 kDa.

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 0.330 Å<sup>-1</sup>

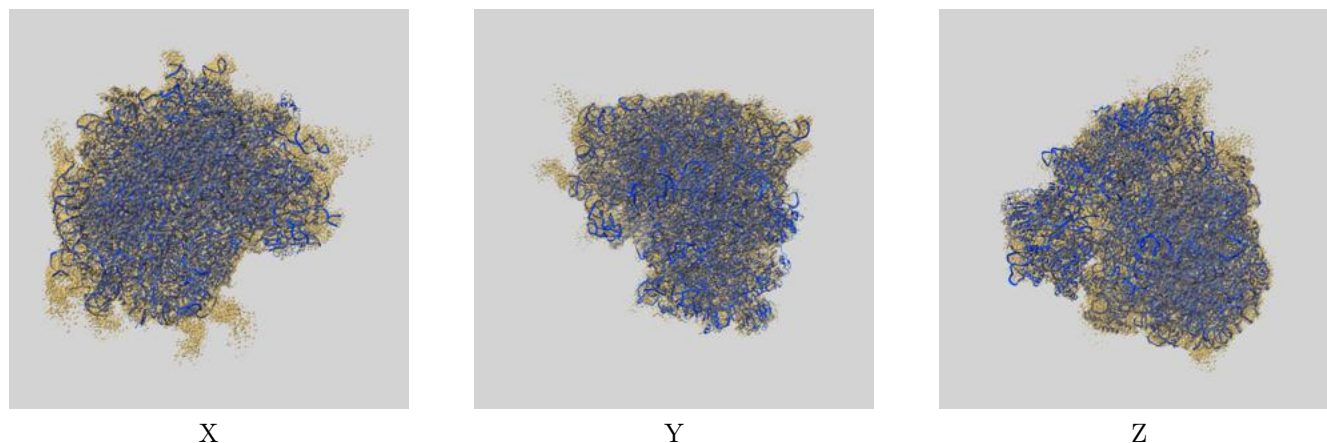
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

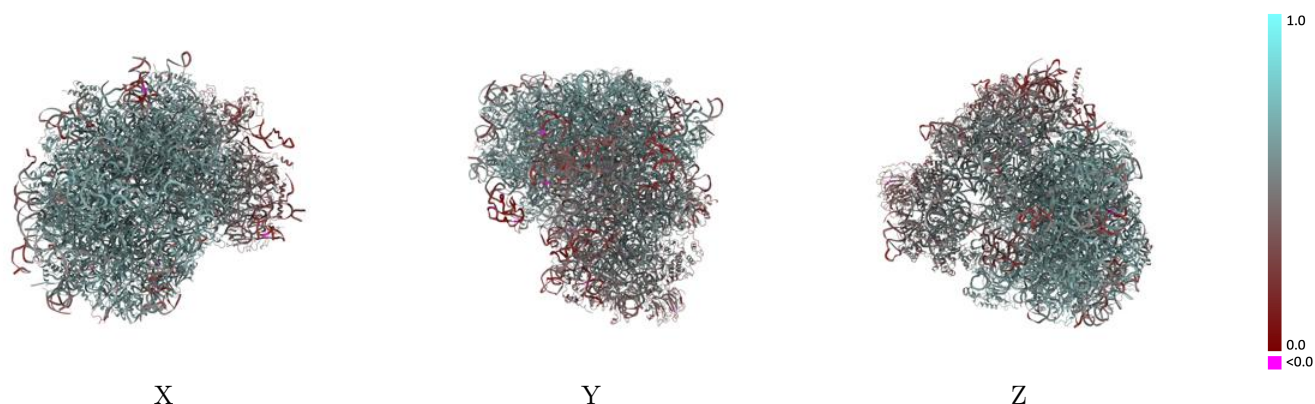
This section contains information regarding the fit between EMDB map EMD-30433 and PDB model 7CPV. Per-residue inclusion information can be found in section 3 on page 19.

### 9.1 Map-model overlay [i](#)



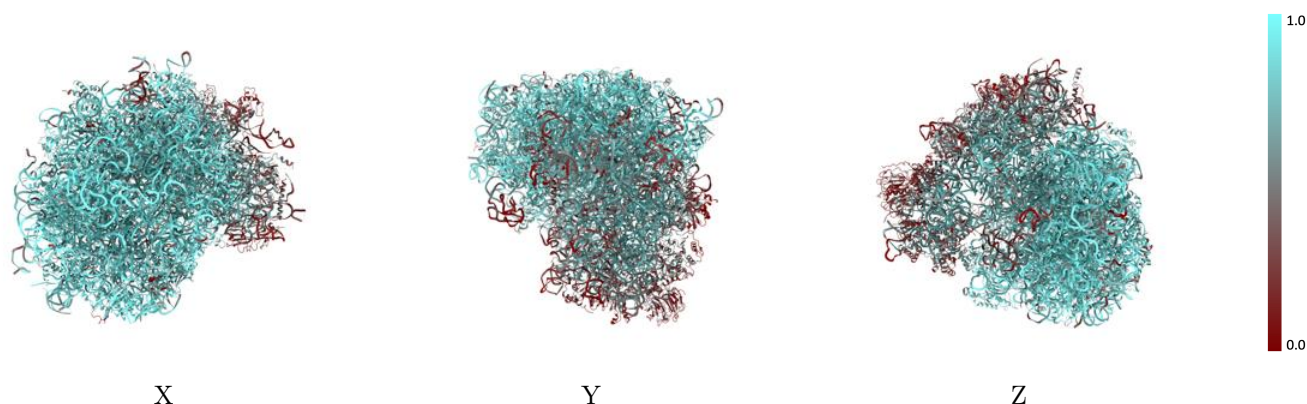
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



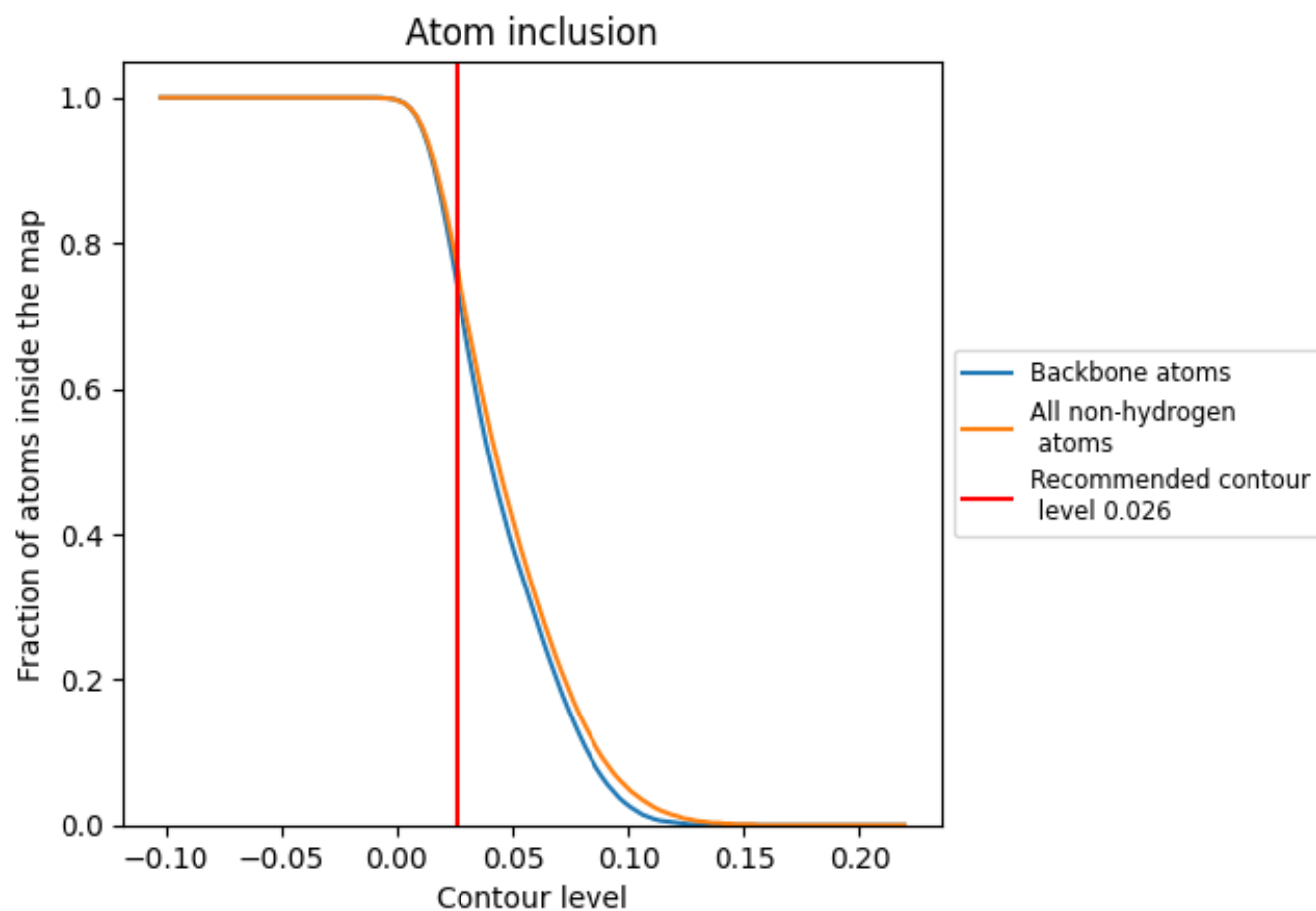
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7670	 0.5340
L5	 0.8900	 0.5640
L7	 0.9650	 0.6030
L8	 0.9130	 0.5840
LA	 0.8920	 0.6090
LB	 0.8740	 0.6030
LC	 0.8800	 0.5980
LD	 0.8430	 0.5780
LE	 0.7930	 0.5590
LF	 0.9000	 0.6140
LG	 0.7880	 0.5620
LH	 0.8490	 0.5800
LI	 0.8500	 0.5940
LJ	 0.7540	 0.5370
LL	 0.8490	 0.5880
LM	 0.8920	 0.5970
LN	 0.9330	 0.6220
LO	 0.8870	 0.6070
LP	 0.8860	 0.6100
LQ	 0.8970	 0.6160
LR	 0.7950	 0.5690
LS	 0.9110	 0.6180
LT	 0.8540	 0.5890
LU	 0.7580	 0.5440
LV	 0.8500	 0.5990
LW	 0.8660	 0.5990
LX	 0.8510	 0.5980
LY	 0.8700	 0.5980
LZ	 0.8350	 0.5760
La	 0.9150	 0.6210
Lb	 0.8260	 0.5870
Lc	 0.8290	 0.5700
Ld	 0.8250	 0.5880
Le	 0.8870	 0.6100
Lf	 0.9250	 0.6250







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Chain	Atom inclusion	Q-score
Lg	 0.8720	 0.5960
Lh	 0.8390	 0.5850
Li	 0.8250	 0.5760
Lj	 0.9200	 0.6130
Lk	 0.7270	 0.5590
Ll	 0.8690	 0.5980
Lm	 0.8920	 0.5950
Ln	 0.7290	 0.5580
Lo	 0.8400	 0.5970
Lp	 0.8230	 0.5980
Lr	 0.9030	 0.6060
S2	 0.6850	 0.4640
S6	 0.4330	 0.3540
SA	 0.4490	 0.4730
SB	 0.5820	 0.5100
SC	 0.5770	 0.4920
SD	 0.3150	 0.4170
SE	 0.4280	 0.4080
SF	 0.4180	 0.4670
SG	 0.3030	 0.4010
SH	 0.2560	 0.4030
SI	 0.5010	 0.4340
SJ	 0.4790	 0.3900
SK	 0.2770	 0.3950
SL	 0.6020	 0.4990
SN	 0.5330	 0.5020
SO	 0.6280	 0.5060
SP	 0.5700	 0.4750
SQ	 0.4200	 0.4580
SR	 0.2780	 0.4180
SS	 0.5480	 0.4830
ST	 0.4700	 0.4660
SU	 0.3200	 0.4240
SV	 0.4430	 0.4620
SW	 0.6370	 0.5280
SX	 0.5610	 0.4960
SY	 0.2950	 0.3490
SZ	 0.3480	 0.4350
Sa	 0.6500	 0.5190
Sb	 0.4570	 0.4450
Sc	 0.3690	 0.4500
Sd	 0.6390	 0.4780

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Chain	Atom inclusion	Q-score
Se	 0.3500	 0.4080
Sg	 0.2380	 0.3800