wwPDB EM Validation Summary Report (i)

Mar 31, 2025 – 01:22 PM EDT

PDB ID	:	8UIZ / pdb_00008uiz
EMDB ID	:	EMD-42306
Title	:	In situ human P-E state 80S ribosome
Authors	:	Wei, Z.; Yong, X.
Deposited on	:	2023-10-10
Resolution	:	3.43 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

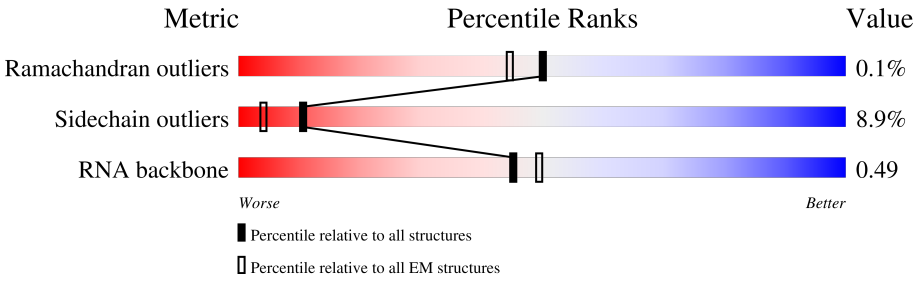
EMDB validation analysis	:	0.0.1.dev117
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

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 3.43 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	LR	187	11% 88% 12%
2	SE	262	91% 9%
3	SI	206	7% 91% 9%
4	SL	153	10% 84% 16%
5	SX	141	93% 7%
6	SG	237	17% 87% 13%
7	SJ	185	5% 96%
8	SY	131	15% 90% 10%

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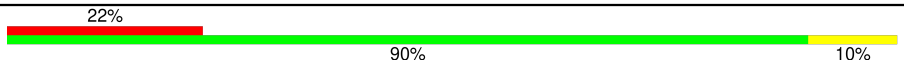
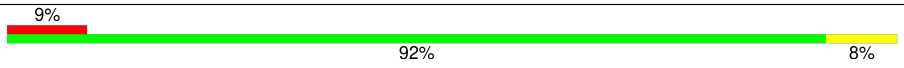
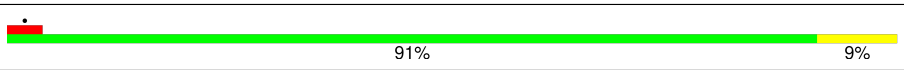
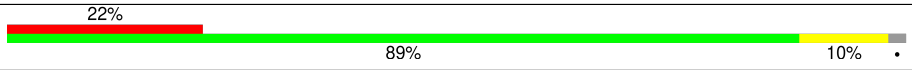
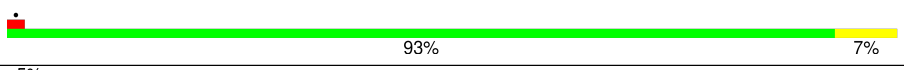
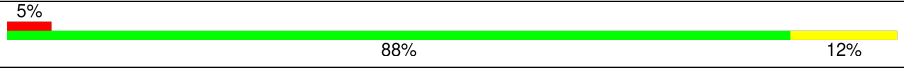
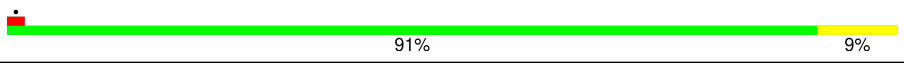
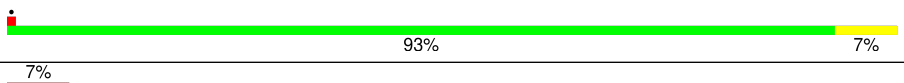
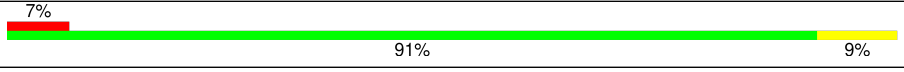
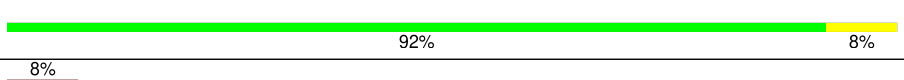
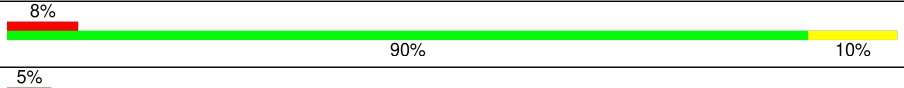
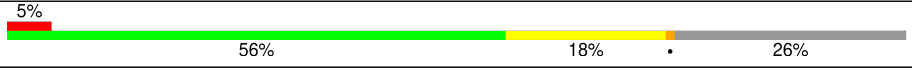
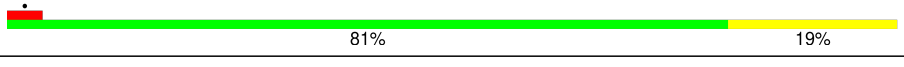
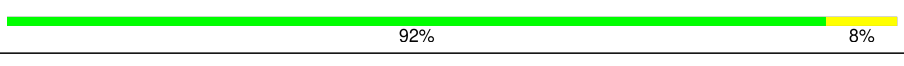
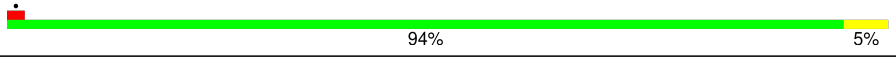
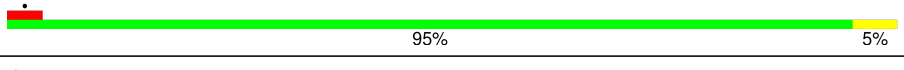
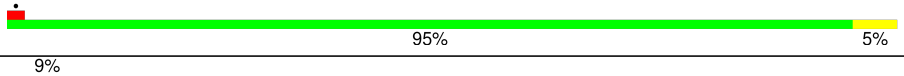
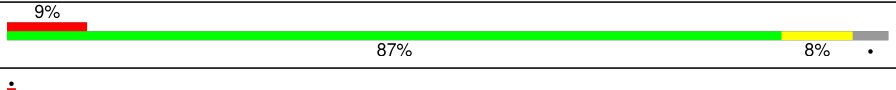
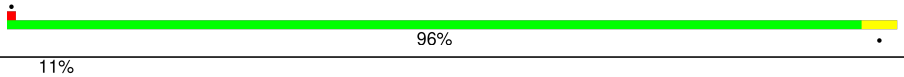
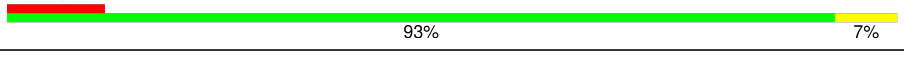
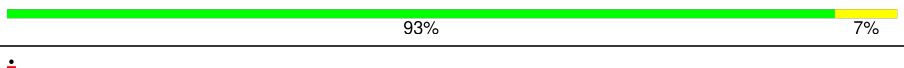
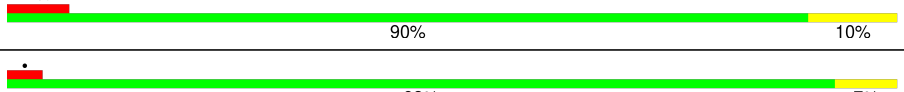
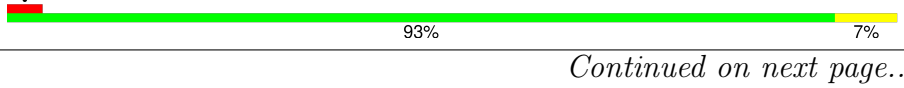
Mol	Chain	Length	Quality of chain
9	Se	58	
10	SA	221	
11	SB	214	
12	SH	189	
13	SV	83	
14	Sa	102	
15	SC	222	
16	SN	150	
17	SO	140	
18	SW	129	
19	Sb	83	
20	L5	5070	
21	L7	120	
22	L8	156	
23	LA	248	
24	LB	402	
25	LC	368	
26	LD	293	
27	LE	247	
28	LF	225	
29	LG	241	
30	LH	190	
31	LI	213	
32	LJ	176	
33	LL	210	

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Mol	Chain	Length	Quality of chain
34	LM	139	94% 6%
35	LN	203	97%
36	LO	201	95% 5%
37	LP	153	91% 9%
38	LQ	187	96%
39	LS	175	95% 5%
40	LT	159	93% 7%
41	LU	101	86% 14%
42	LV	131	93% 7%
43	LX	120	95% 5%
44	LY	134	96%
45	LZ	135	90% 10%
46	La	147	97%
47	Lb	121	12% 78% 12% 10%
48	Lc	98	92% 8%
49	Ld	107	89% 11%
50	Le	128	94% 6%
51	Lf	109	94% 6%
52	Lg	114	95% 5%
53	Lh	122	89% 11%
54	Li	102	97%
55	Lj	86	88% 12%
56	Lk	69	93% 7%
57	Ll	50	90% 10%
58	Lm	52	96%

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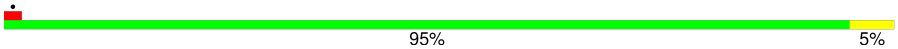
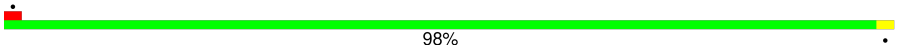
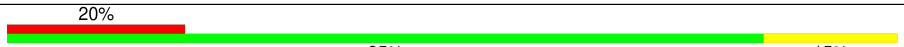
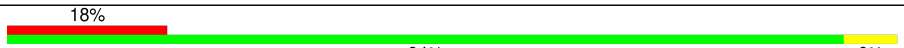
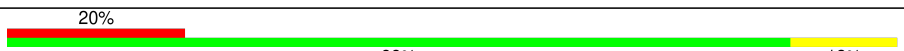
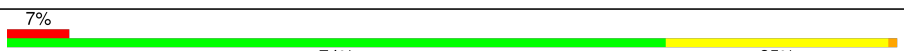
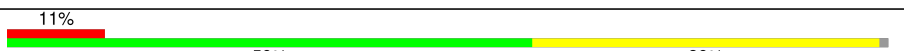
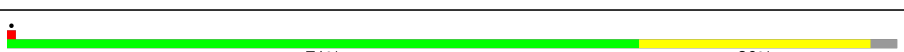
Mol	Chain	Length	Quality of chain
59	Ln	24	
60	Lo	105	
61	Lp	91	
62	Lr	125	
63	SR	135	
64	SD	227	
65	SF	189	
66	SK	98	
67	SP	121	
68	SQ	144	
69	SS	145	
70	ST	143	
71	SU	104	
72	Sc	64	
73	Sd	55	
74	Sg	313	
75	SM	122	
76	SZ	75	
77	Sf	67	
78	S2	1740	
79	Et	76	
80	Pt	76	
81	Lt	157	
82	Lz	217	
83	Ls	196	

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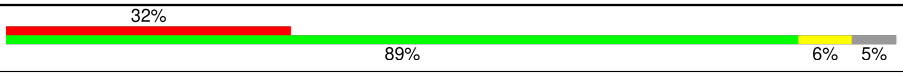
Mol	Chain	Length	Quality of chain
84	LW	124	

2 Entry composition (i)

There are 86 unique types of molecules in this entry. The entry contains 222714 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L19.

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

- Molecule 2 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 3 is a protein called 40S ribosomal protein S8.

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

- Molecule 4 is a protein called 40S ribosomal protein S11.

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

- Molecule 5 is a protein called 40S ribosomal protein S23.

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

- Molecule 6 is a protein called 40S ribosomal protein S6.

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

- Molecule 7 is a protein called 40S ribosomal protein S9.

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

- Molecule 8 is a protein called 40S ribosomal protein S24.

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

- Molecule 9 is a protein called Small ribosomal subunit protein eS30.

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

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

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

- Molecule 11 is a protein called 40S ribosomal protein S3a.

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

- Molecule 12 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 13 is a protein called 40S ribosomal protein S21.

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

- Molecule 14 is a protein called 40S ribosomal protein S26.

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

- Molecule 15 is a protein called 40S ribosomal protein S2.

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

- Molecule 16 is a protein called 40S ribosomal protein S13.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 18 is a protein called 40S ribosomal protein S15a.

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

- Molecule 19 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 20 is a RNA chain called 28S rRNA.

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

- Molecule 21 is a RNA chain called 5S rRNA [Homo sapiens].

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

- Molecule 22 is a RNA chain called 5.8S rRNA [Homo sapiens].

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

- Molecule 23 is a protein called 60S ribosomal protein L8.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 25 is a protein called 60S ribosomal protein L4.

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

- Molecule 26 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 27 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 28 is a protein called 60S ribosomal protein L7.

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

- Molecule 29 is a protein called 60S ribosomal protein L7a.

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

- Molecule 30 is a protein called 60S ribosomal protein L9.

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

- Molecule 31 is a protein called Ribosomal protein uL16-like.

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

- Molecule 32 is a protein called 60S ribosomal protein L11.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 34 is a protein called 60S ribosomal protein L14.

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

- Molecule 35 is a protein called 60S ribosomal protein L15.

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

- Molecule 36 is a protein called 60S ribosomal protein L13a.

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

- Molecule 37 is a protein called 60S ribosomal protein L17.

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

- Molecule 38 is a protein called 60S ribosomal protein L18.

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

- Molecule 39 is a protein called 60S ribosomal protein L18a.

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

- Molecule 40 is a protein called 60S ribosomal protein L21.

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

- Molecule 41 is a protein called Heparin-binding protein HBp15.

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

- Molecule 42 is a protein called 60S ribosomal protein L23.

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

- Molecule 43 is a protein called 60S ribosomal protein L23a.

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

- Molecule 44 is a protein called 60S ribosomal protein L26.

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

- Molecule 45 is a protein called 60S ribosomal protein L27.

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

- Molecule 46 is a protein called 60S ribosomal protein L27a.

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

- Molecule 47 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 48 is a protein called 60S ribosomal protein L30.

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

- Molecule 49 is a protein called 60S ribosomal protein L31.

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

- Molecule 50 is a protein called 60S ribosomal protein L32.

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

- Molecule 51 is a protein called 60S ribosomal protein L35a.

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

- Molecule 52 is a protein called 60S ribosomal protein L34.

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

- Molecule 53 is a protein called 60S ribosomal protein L35.

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

- Molecule 54 is a protein called 60S ribosomal protein L36.

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

- Molecule 55 is a protein called 60S ribosomal protein L37.

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

- Molecule 56 is a protein called 60S ribosomal protein L38.

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

- Molecule 57 is a protein called 60S ribosomal protein L39.

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

- Molecule 58 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 59 is a protein called 60S ribosomal protein L41.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L37a.

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

- Molecule 62 is a protein called 60S ribosomal protein L28.

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

- Molecule 63 is a protein called 40S ribosomal protein S17.

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

- Molecule 64 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 65 is a protein called 40S ribosomal protein S5.

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

- Molecule 66 is a protein called 40S ribosomal protein S10.

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

- Molecule 67 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 68 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 69 is a protein called 40S ribosomal protein S18.

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

- Molecule 70 is a protein called 40S ribosomal protein S19.

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

- Molecule 71 is a protein called 40S ribosomal protein S20.

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

- Molecule 72 is a protein called 40S ribosomal protein S28.

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

- Molecule 73 is a protein called 40S ribosomal protein S29.

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

- Molecule 74 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 75 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 76 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 77 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 78 is a RNA chain called 18S rRNA [Homo sapiens].

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

- Molecule 79 is a RNA chain called E site tRNA.

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

- Molecule 80 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Pt	74	Total	C	N	O	P	0	0
			1576	705	286	512	73		

- Molecule 81 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 82 is a protein called 60S ribosomal protein L10a.

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

- Molecule 83 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 84 is a protein called Ribosomal protein L24.

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

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

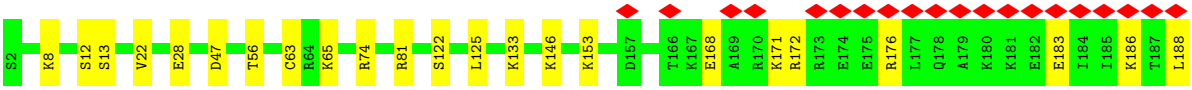
Mol	Chain	Residues	Atoms		AltConf
86	L5	212	Total	Mg	0
			212	212	
86	L7	3	Total	Mg	0
			3	3	
86	L8	5	Total	Mg	0
			5	5	
86	LA	1	Total	Mg	0
			1	1	
86	LB	1	Total	Mg	0
			1	1	
86	LP	1	Total	Mg	0
			1	1	
86	LV	1	Total	Mg	0
			1	1	
86	Le	1	Total	Mg	0
			1	1	
86	Lg	1	Total	Mg	0
			1	1	
86	S2	29	Total	Mg	0
			29	29	

3 Residue-property plots (i)

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

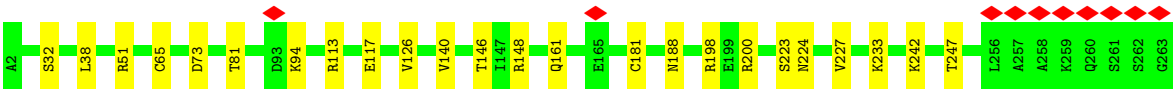
• Molecule 1: 60S ribosomal protein L19

Chain LR:



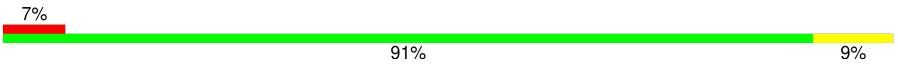
• Molecule 2: Small ribosomal subunit protein eS4, X isoform

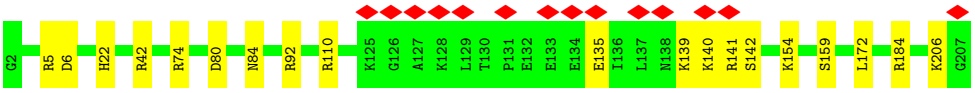
Chain SE:



• Molecule 3: 40S ribosomal protein S8

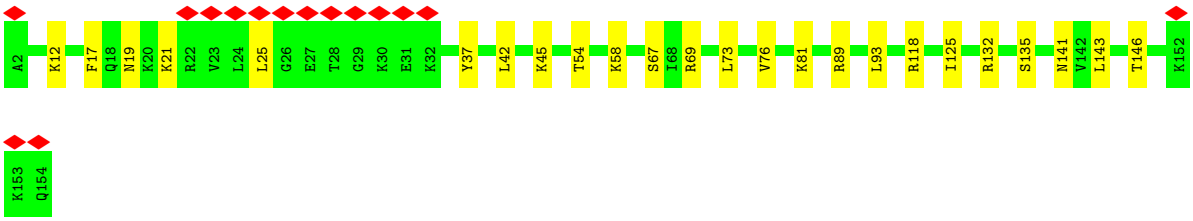
Chain SI:





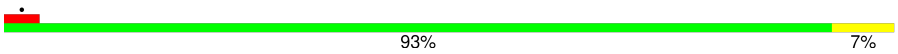
• Molecule 4: 40S ribosomal protein S11

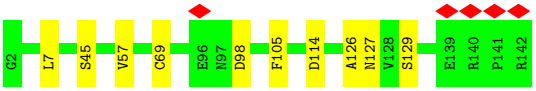
Chain SL:



• Molecule 5: 40S ribosomal protein S23

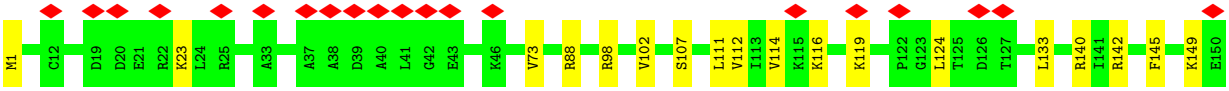
Chain SX:

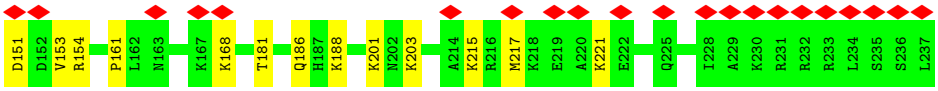




• Molecule 6: 40S ribosomal protein S6

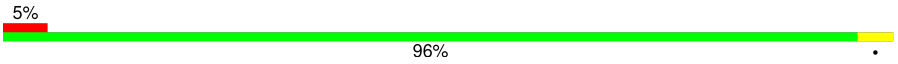
Chain SG:

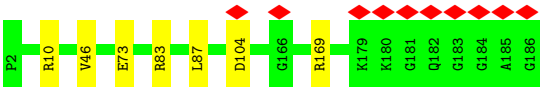




• Molecule 7: 40S ribosomal protein S9

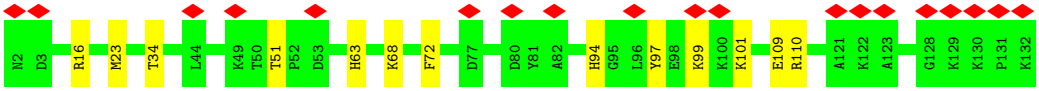
Chain SJ:





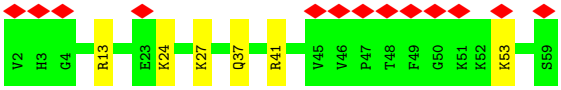
• Molecule 8: 40S ribosomal protein S24

Chain SY:



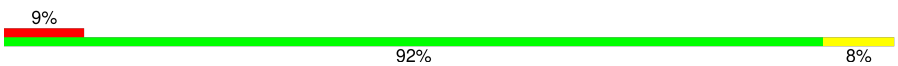
• Molecule 9: Small ribosomal subunit protein eS30

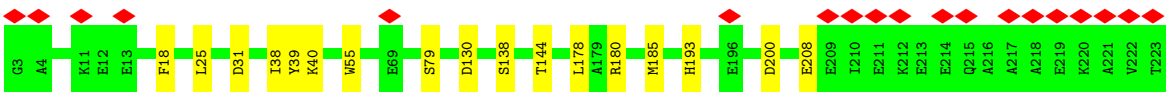
Chain Se:



• Molecule 10: 40S ribosomal protein SA

Chain SA:



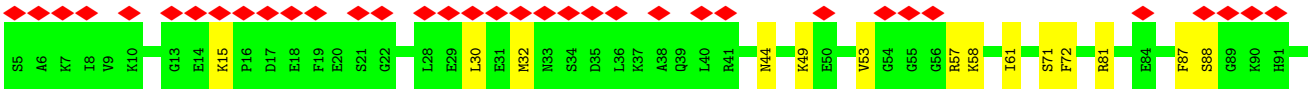


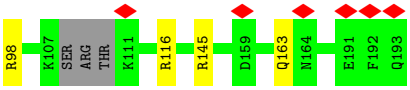
• Molecule 11: 40S ribosomal protein S3a

Chain SB:

• Molecule 12: Small ribosomal subunit protein eS7

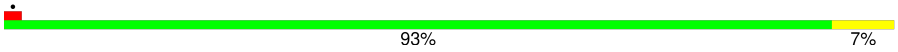
Chain SH:

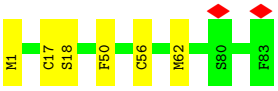




• Molecule 13: 40S ribosomal protein S21

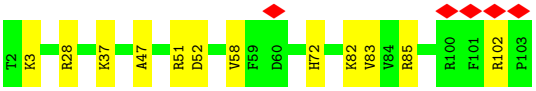
Chain SV:





• Molecule 14: 40S ribosomal protein S26

Chain Sa:

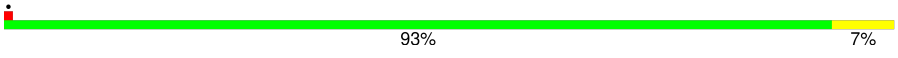


• Molecule 15: 40S ribosomal protein S2

Chain SC:

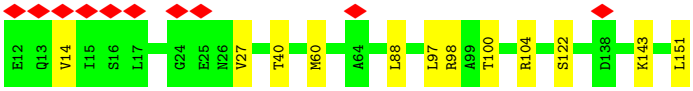
• Molecule 16: 40S ribosomal protein S13

Chain SN:



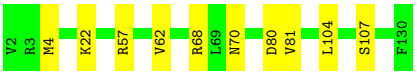
• Molecule 17: Small ribosomal subunit protein uS11

Chain SO:



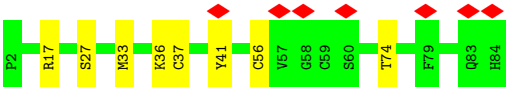
• Molecule 18: 40S ribosomal protein S15a

Chain SW:



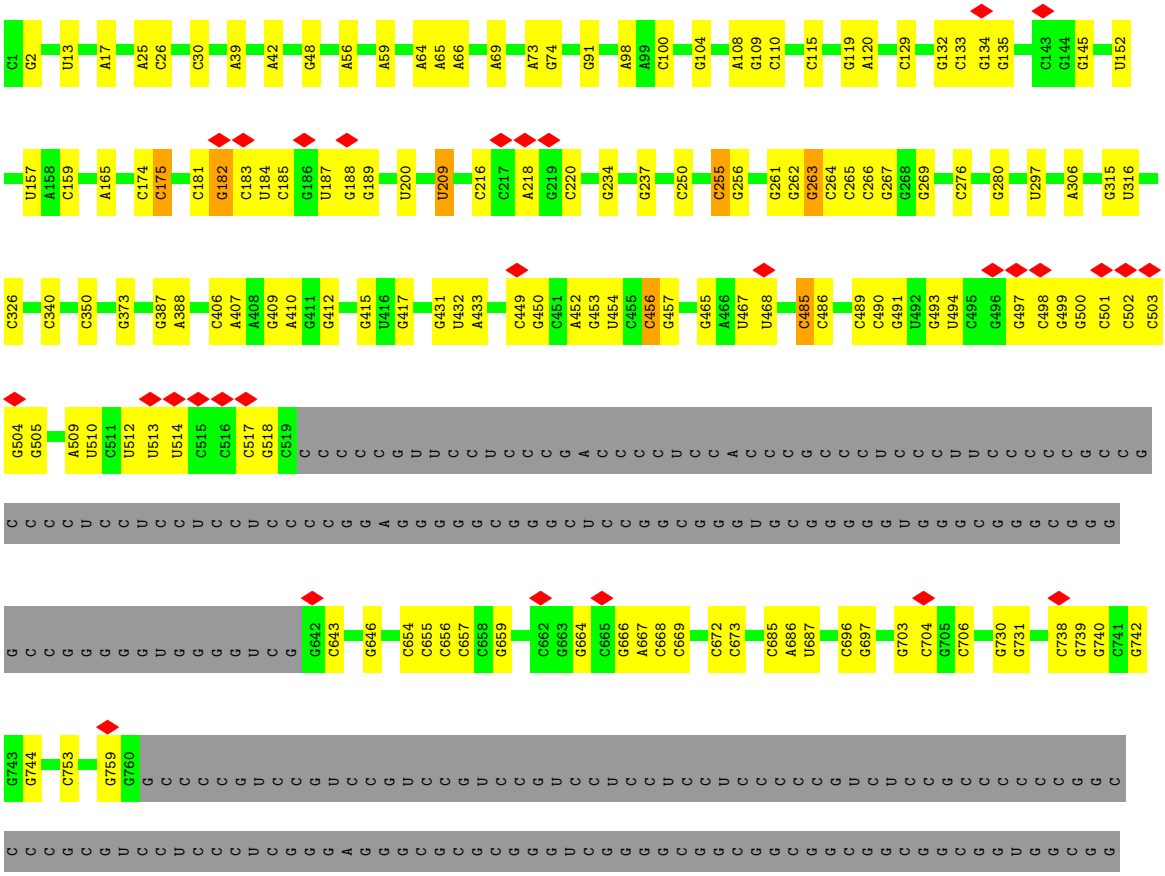
• Molecule 19: Small ribosomal subunit protein eS27

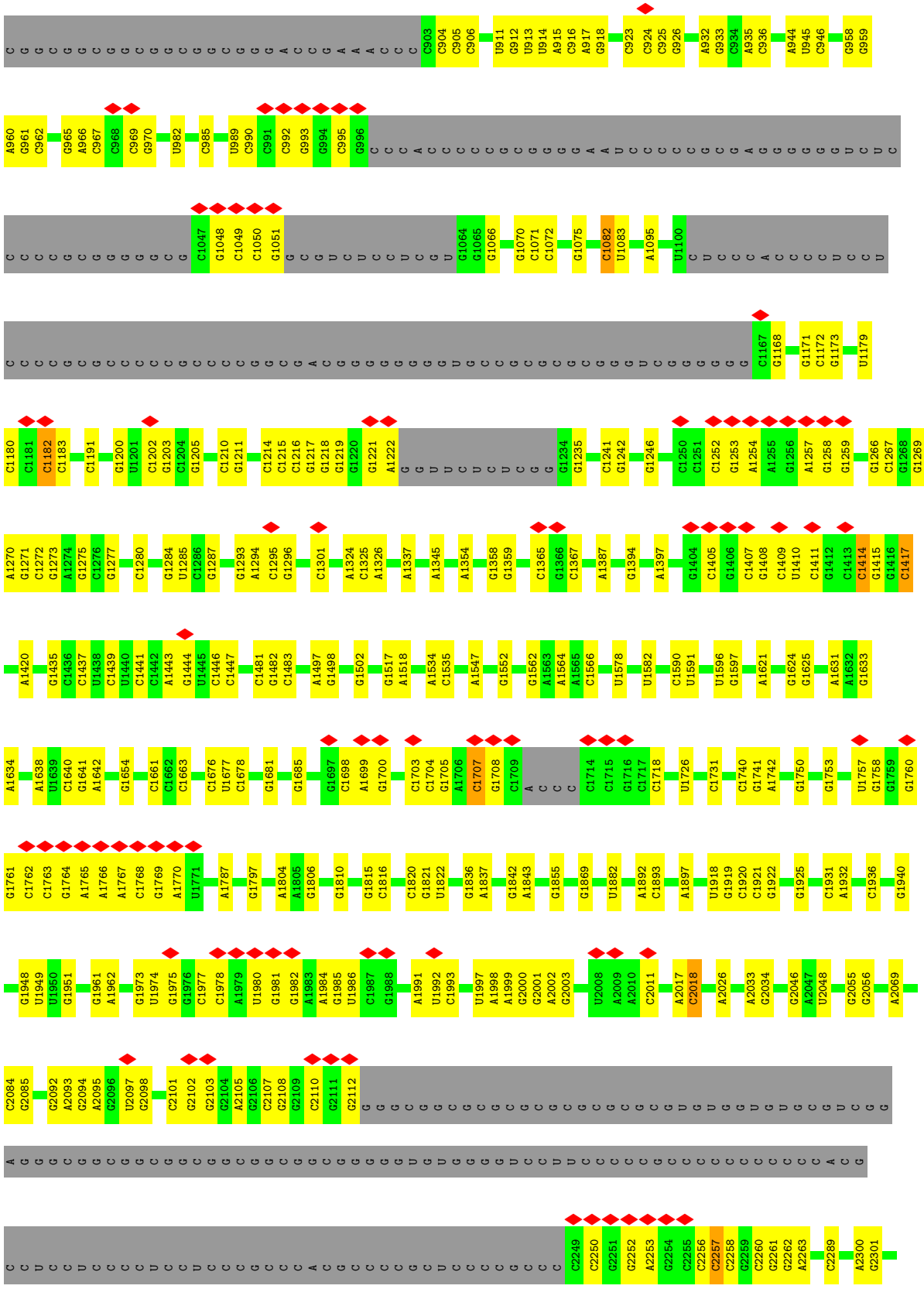
Chain Sb:

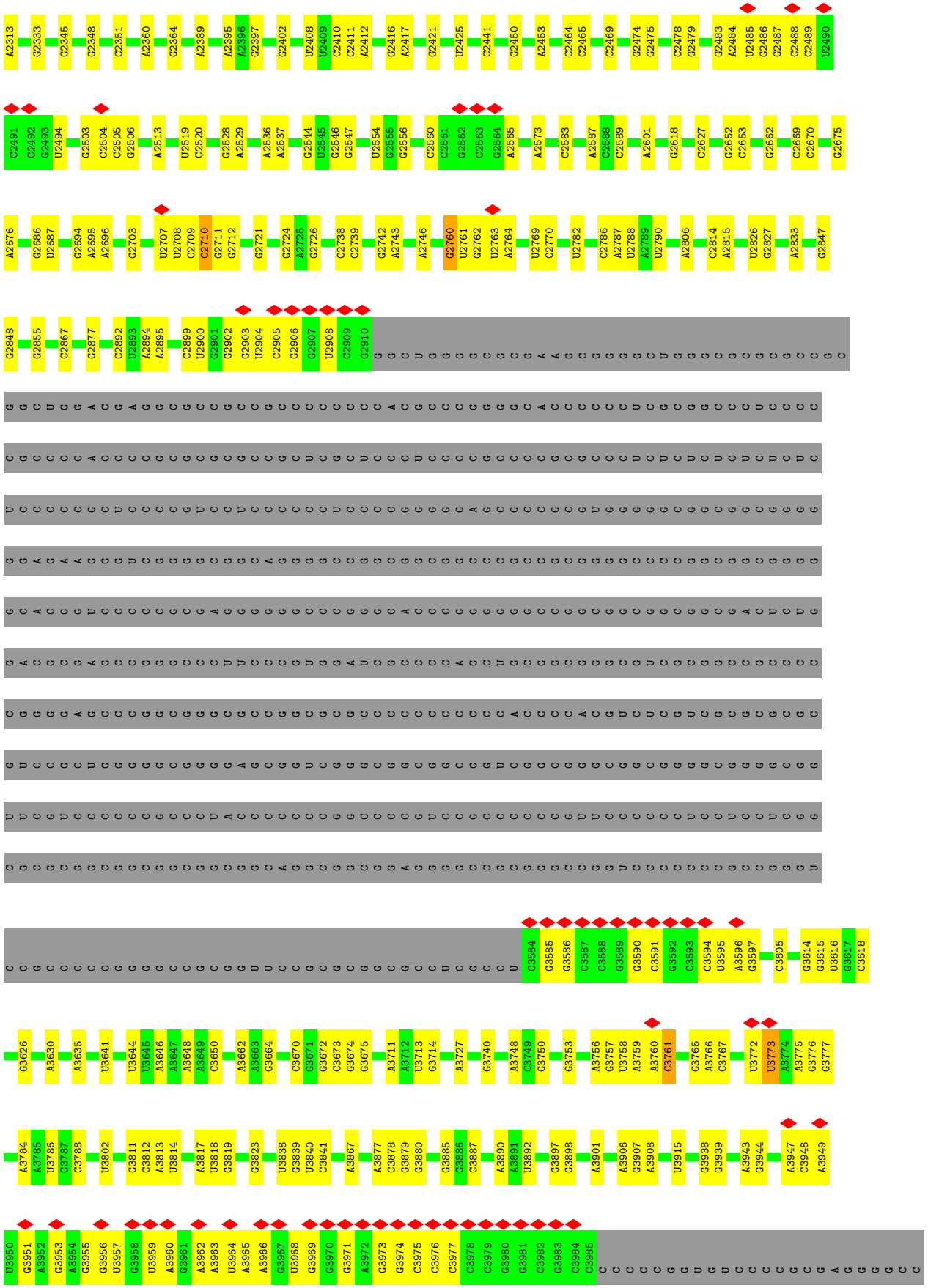


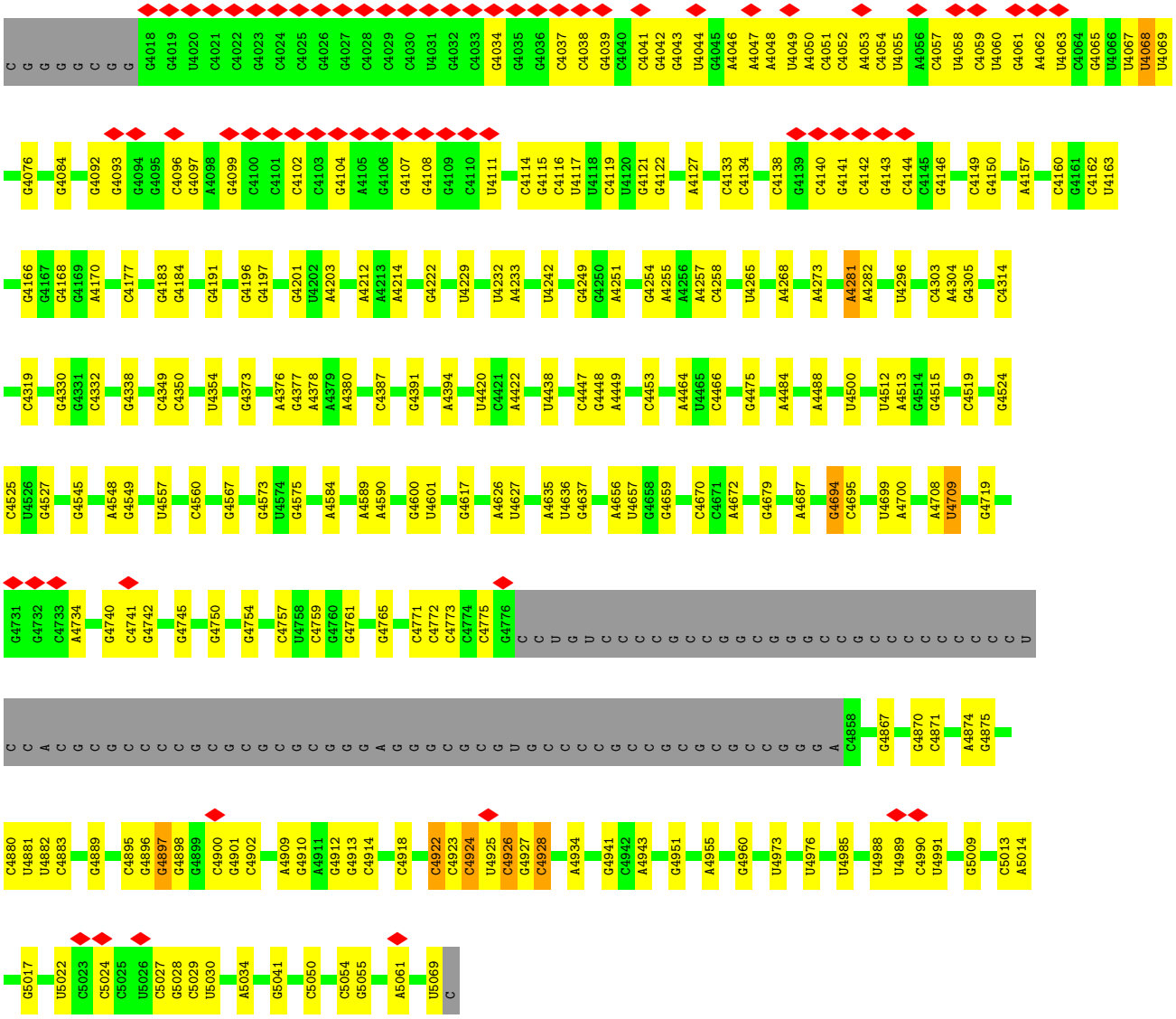
• Molecule 20: 28S rRNA

Chain L5:



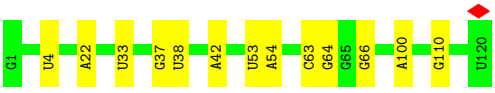






• Molecule 21: 5S rRNA [Homo sapiens]

Chain L7:

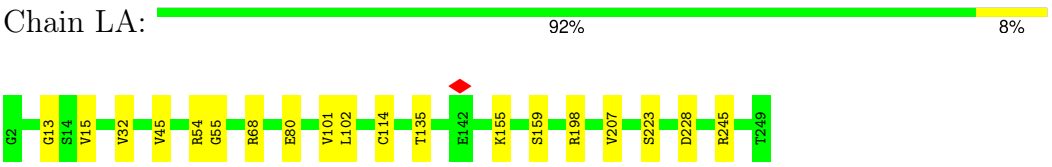


• Molecule 22: 5.8S rRNA [Homo sapiens]

Chain L8:

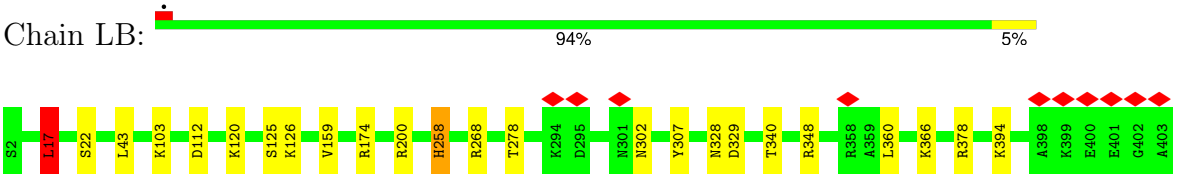
• Molecule 23: 60S ribosomal protein L8

Chain LA:



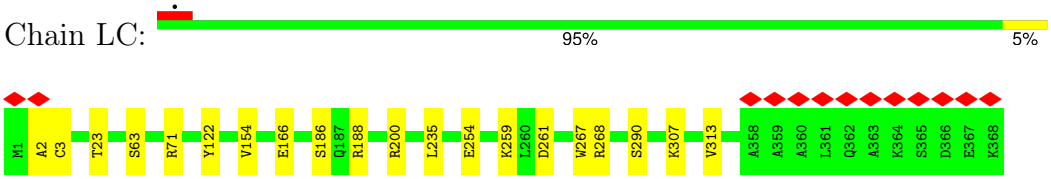
• Molecule 24: Large ribosomal subunit protein uL3

Chain LB:



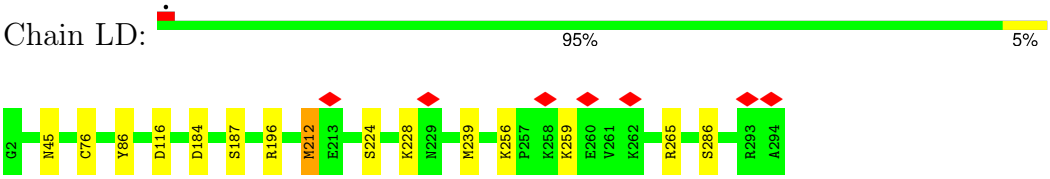
• Molecule 25: 60S ribosomal protein L4

Chain LC:



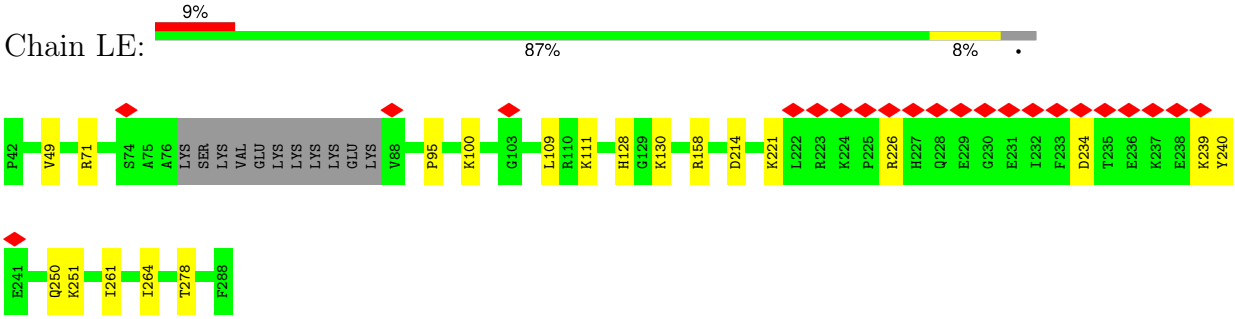
• Molecule 26: Large ribosomal subunit protein uL18

Chain LD:



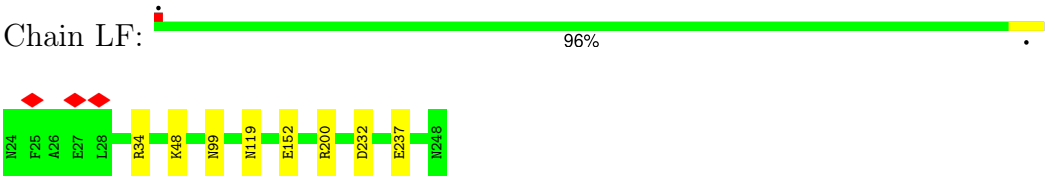
• Molecule 27: Large ribosomal subunit protein eL6

Chain LE:



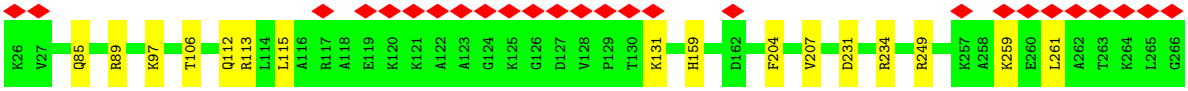
• Molecule 28: 60S ribosomal protein L7

Chain LF:

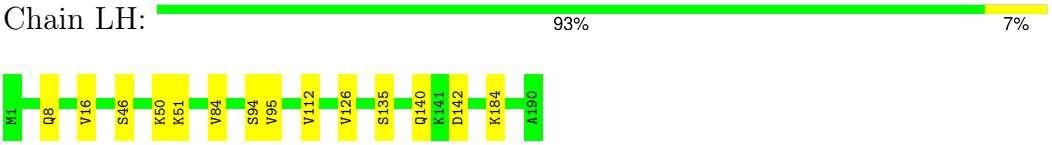


• Molecule 29: 60S ribosomal protein L7a

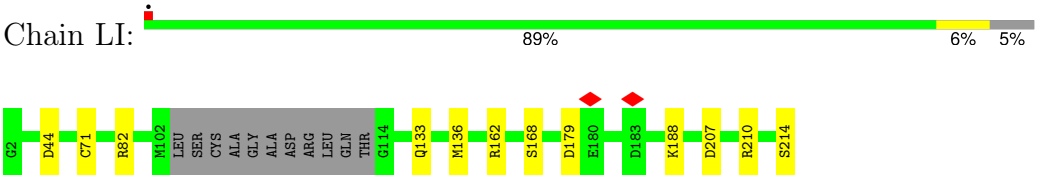
Chain LG:



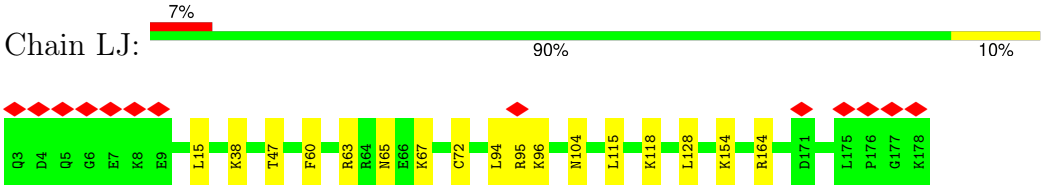
• Molecule 30: 60S ribosomal protein L9



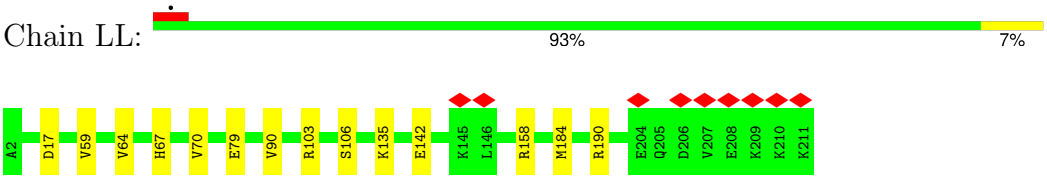
• Molecule 31: Ribosomal protein uL16-like



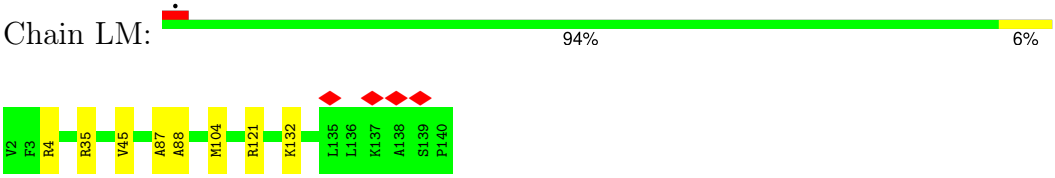
• Molecule 32: 60S ribosomal protein L11



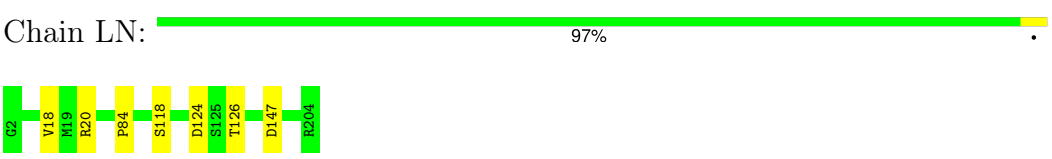
• Molecule 33: Large ribosomal subunit protein eL13



• Molecule 34: 60S ribosomal protein L14

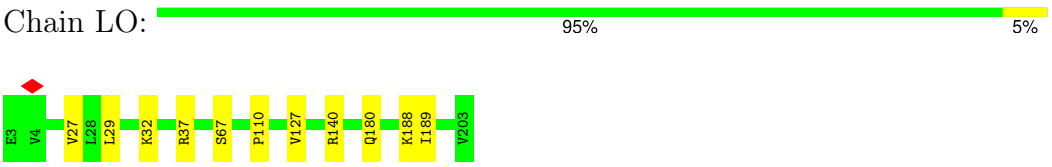


• Molecule 35: 60S ribosomal protein L15



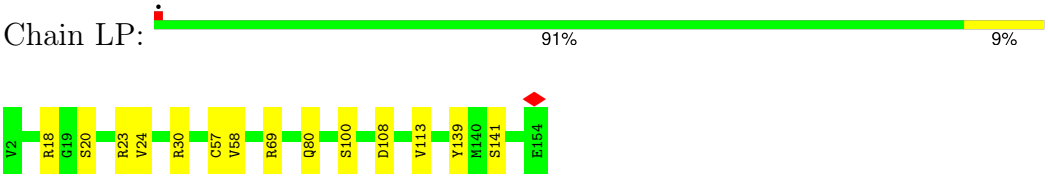
• Molecule 36: 60S ribosomal protein L13a

Chain LO:



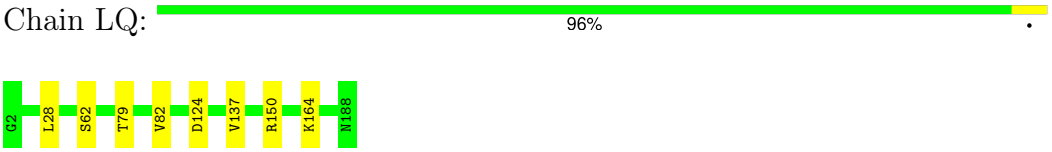
• Molecule 37: 60S ribosomal protein L17

Chain LP:



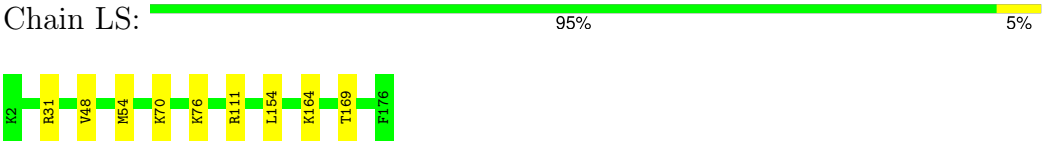
• Molecule 38: 60S ribosomal protein L18

Chain LQ:



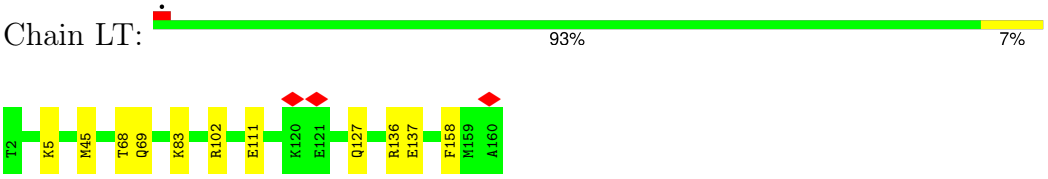
• Molecule 39: 60S ribosomal protein L18a

Chain LS:



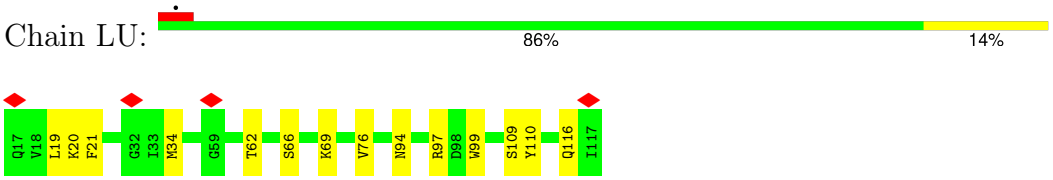
• Molecule 40: 60S ribosomal protein L21

Chain LT:



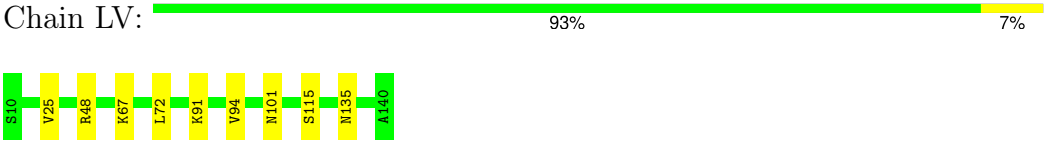
• Molecule 41: Heparin-binding protein HBp15

Chain LU:



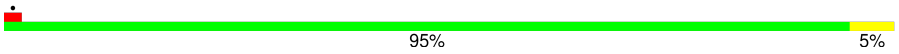
• Molecule 42: 60S ribosomal protein L23

Chain LV:



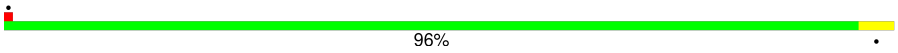
• Molecule 43: 60S ribosomal protein L23a

Chain LX:



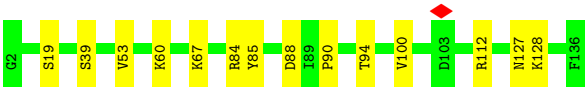
• Molecule 44: 60S ribosomal protein L26

Chain LY:



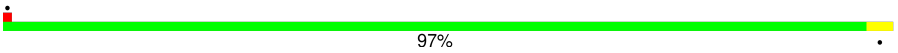
• Molecule 45: 60S ribosomal protein L27

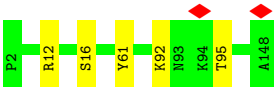
Chain LZ:



• Molecule 46: 60S ribosomal protein L27a

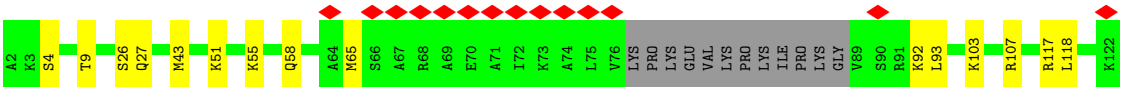
Chain La:





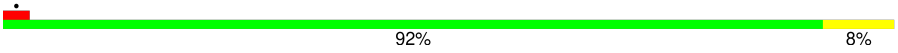
• Molecule 47: Large ribosomal subunit protein eL29

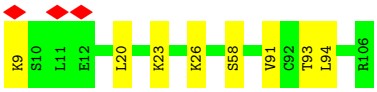
Chain Lb:



• Molecule 48: 60S ribosomal protein L30

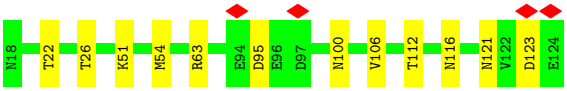
Chain Lc:





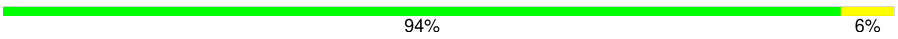
• Molecule 49: 60S ribosomal protein L31

Chain Ld:



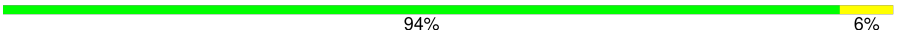
• Molecule 50: 60S ribosomal protein L32

Chain Le:



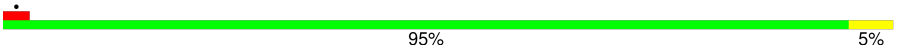
• Molecule 51: 60S ribosomal protein L35a

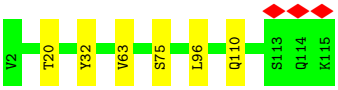
Chain Lf:



• Molecule 52: 60S ribosomal protein L34

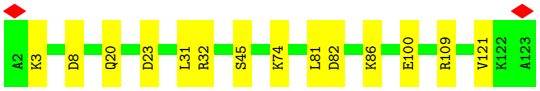
Chain Lg:





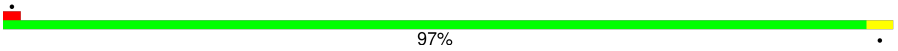
• Molecule 53: 60S ribosomal protein L35

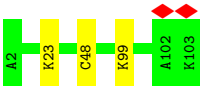
Chain Lh:



• Molecule 54: 60S ribosomal protein L36

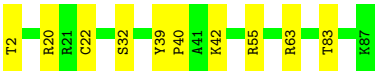
Chain Li:





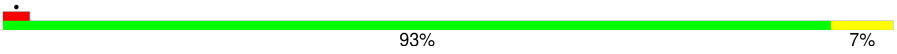
• Molecule 55: 60S ribosomal protein L37

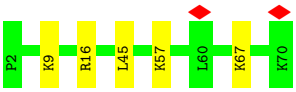
Chain Lj:



• Molecule 56: 60S ribosomal protein L38

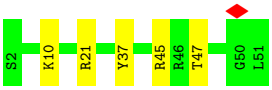
Chain Lk:





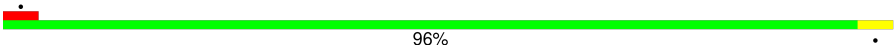
• Molecule 57: 60S ribosomal protein L39

Chain Ll:



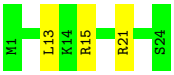
• Molecule 58: Large ribosomal subunit protein eL40

Chain Lm:



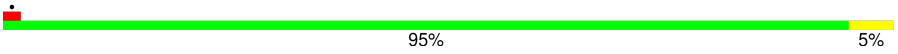
• Molecule 59: 60S ribosomal protein L41

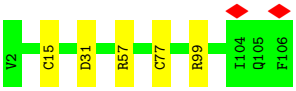
Chain Ln:



• Molecule 60: 60S ribosomal protein L36a

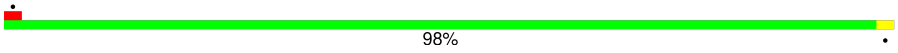
Chain Lo:

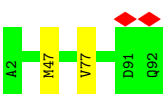




• Molecule 61: 60S ribosomal protein L37a

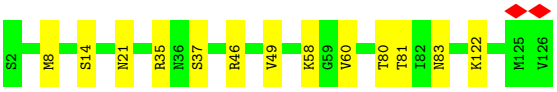
Chain Lp:





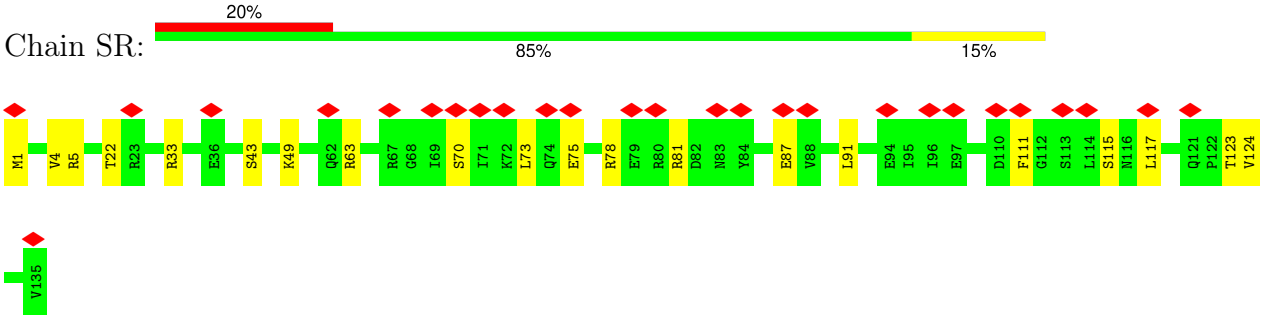
• Molecule 62: 60S ribosomal protein L28

Chain Lr:



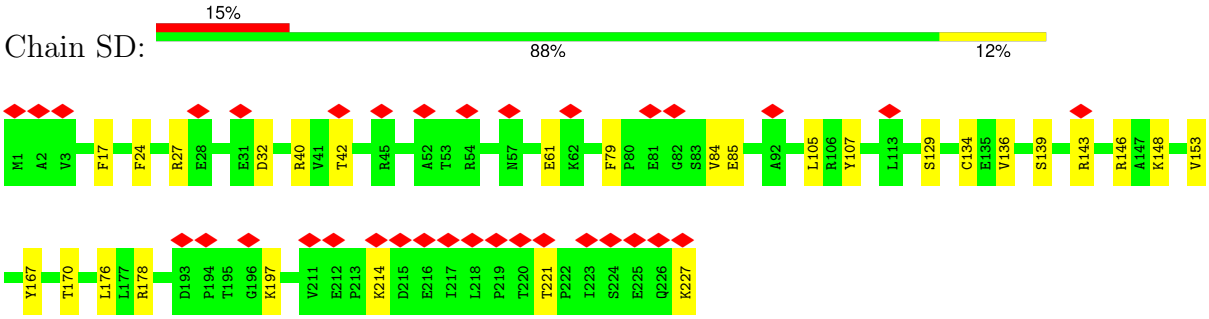
• Molecule 63: 40S ribosomal protein S17

Chain SR:



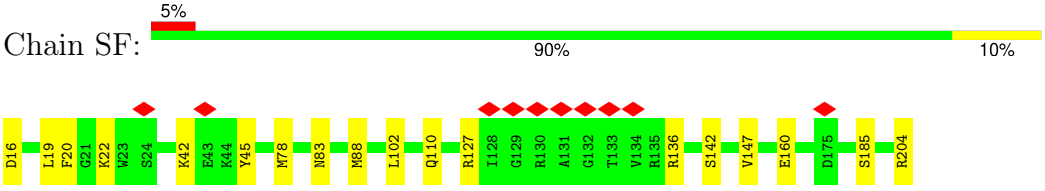
• Molecule 64: Small ribosomal subunit protein uS3

Chain SD:



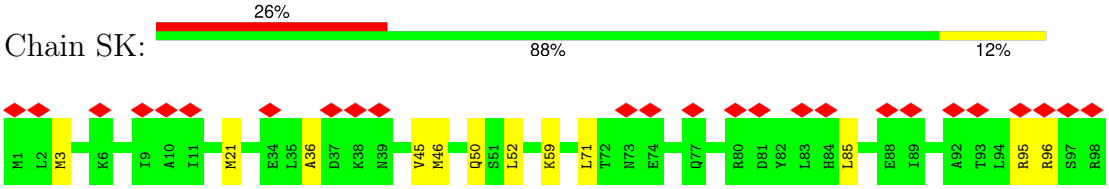
• Molecule 65: 40S ribosomal protein S5

Chain SF:



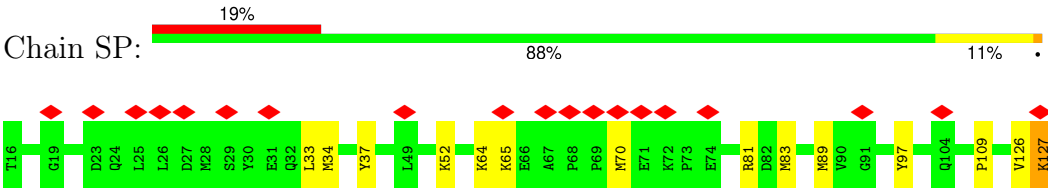
• Molecule 66: 40S ribosomal protein S10

Chain SK:



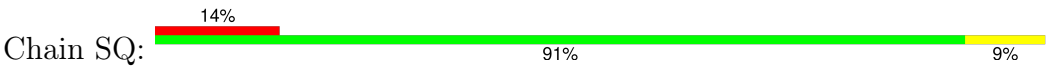
• Molecule 67: Small ribosomal subunit protein uS19

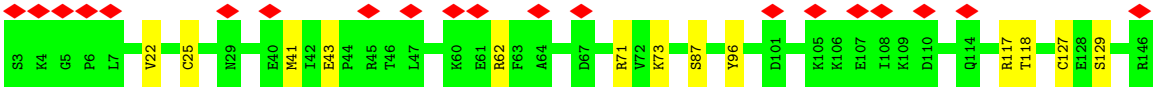
Chain SP:



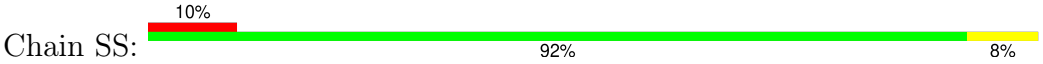
• Molecule 68: Small ribosomal subunit protein uS9

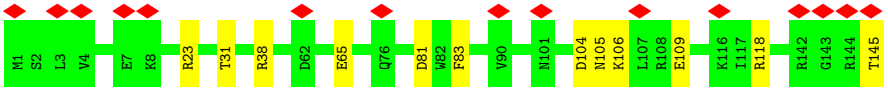
Chain SQ:



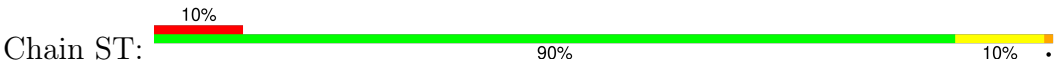


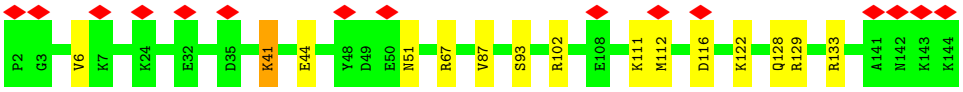
• Molecule 69: 40S ribosomal protein S18



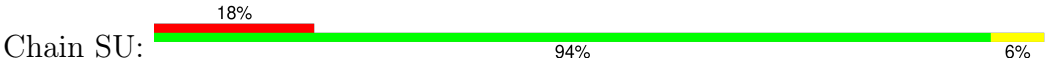


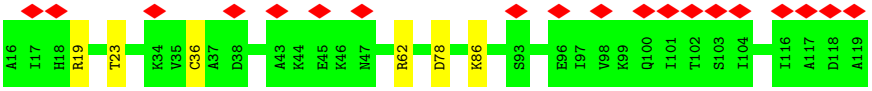
• Molecule 70: 40S ribosomal protein S19



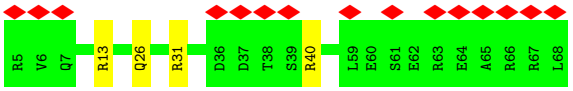


• Molecule 71: 40S ribosomal protein S20

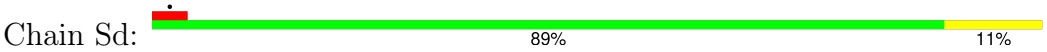




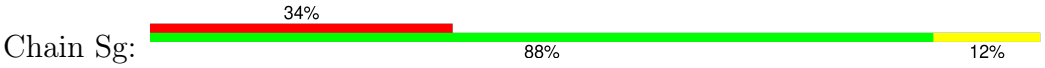
• Molecule 72: 40S ribosomal protein S28

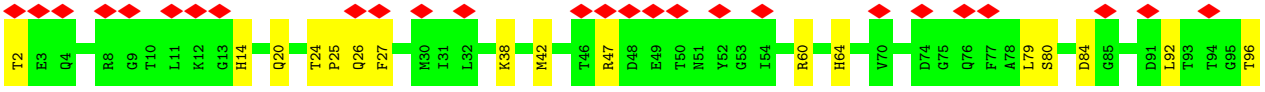


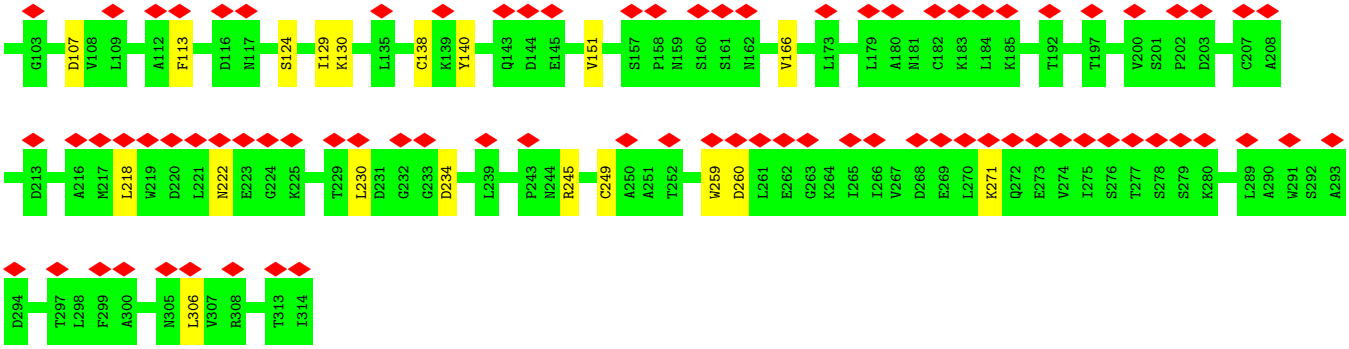
• Molecule 73: 40S ribosomal protein S29



• Molecule 74: Receptor of activated protein C kinase 1

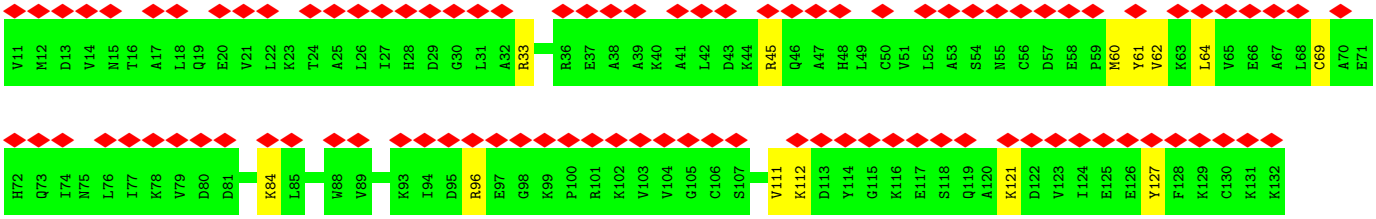






• Molecule 75: Small ribosomal subunit protein eS12

Chain SM:

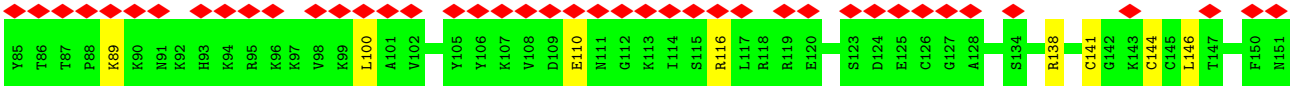


• Molecule 76: Small ribosomal subunit protein eS25

Chain SZ:

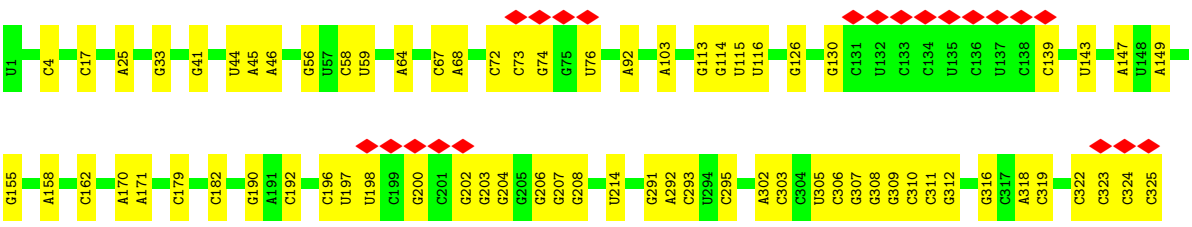
• Molecule 77: Ubiquitin-40S ribosomal protein S27a

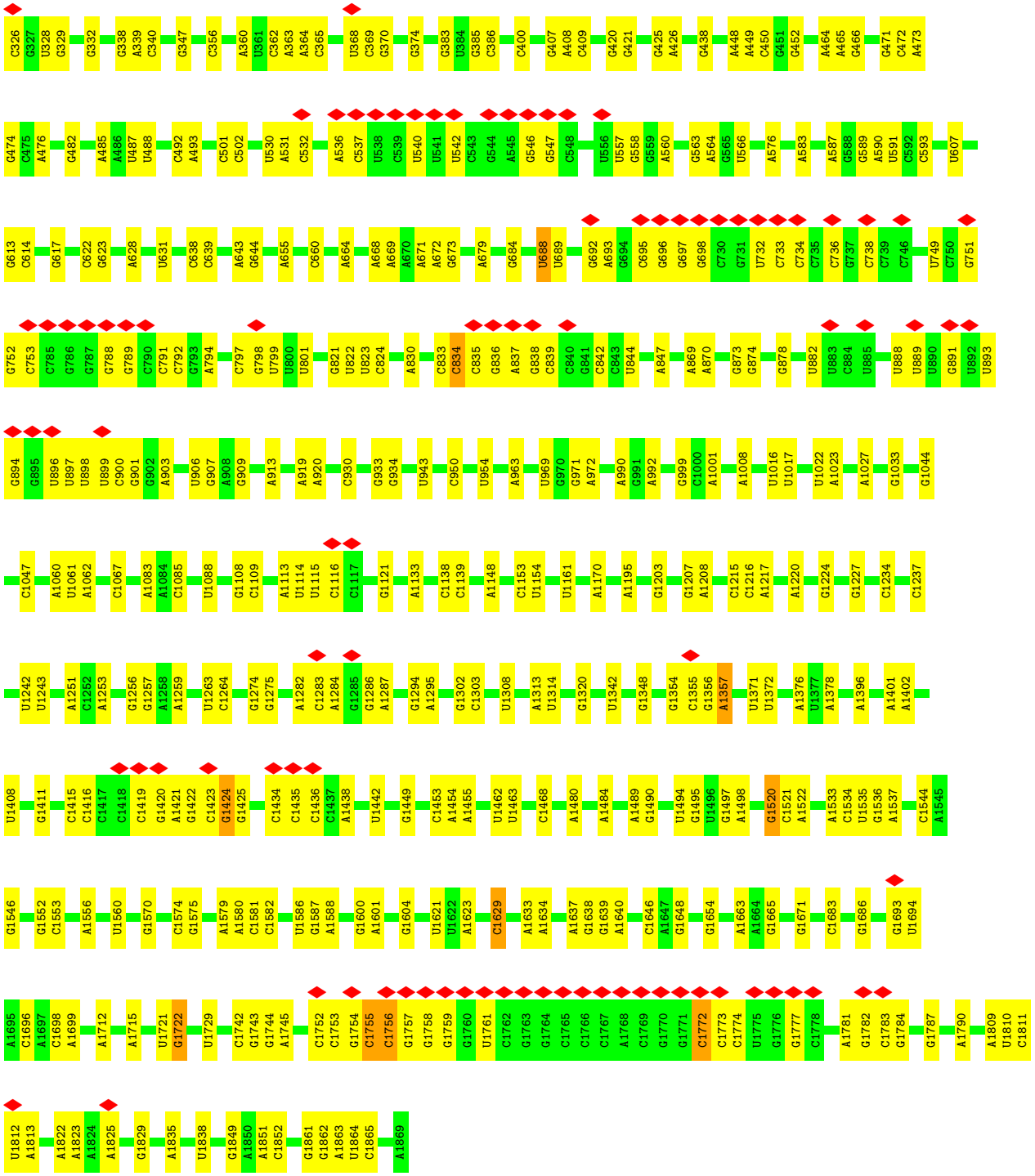
Chain Sf:



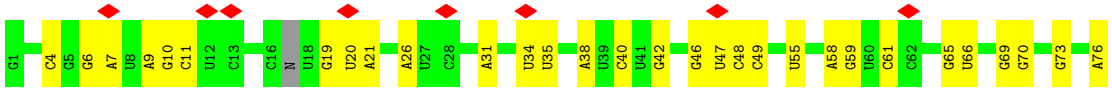
• Molecule 78: 18S rRNA [Homo sapiens]

Chain S2:



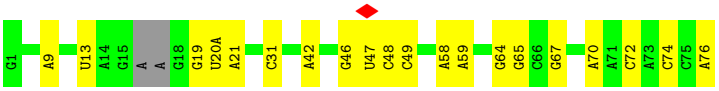


- Molecule 79: E site tRNA



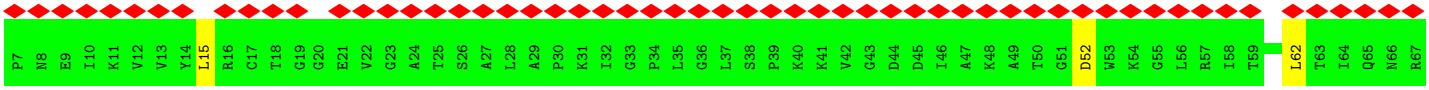
- Molecule 80: P site tRNA

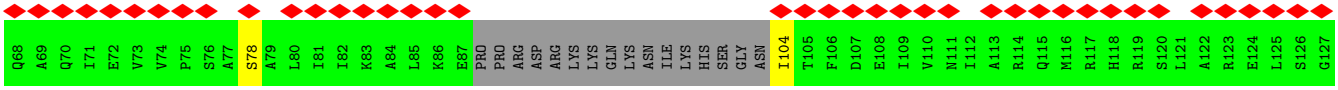
Chain Pt:

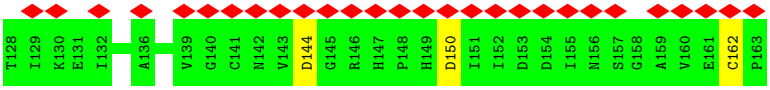


• Molecule 81: Large ribosomal subunit protein uL11

Chain Lt:

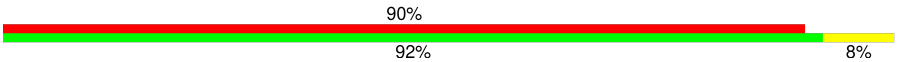


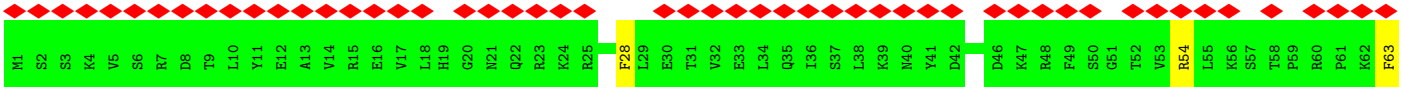


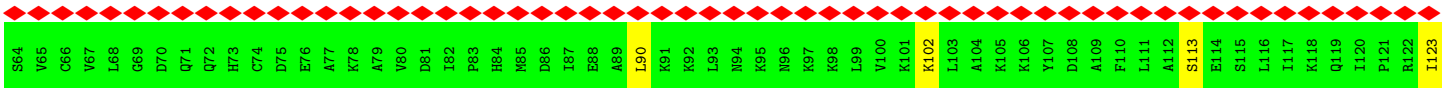


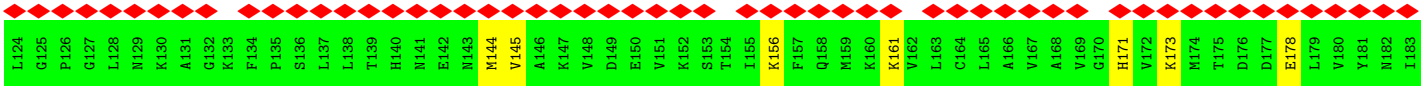
• Molecule 82: 60S ribosomal protein L10a

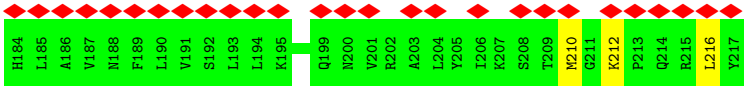
Chain Lz:





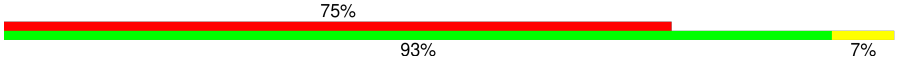


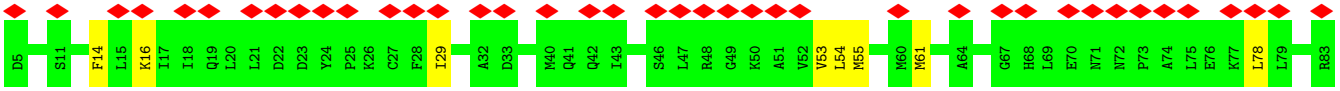


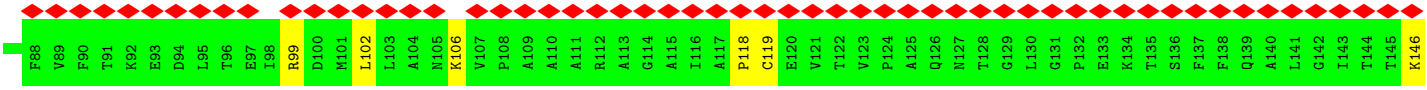


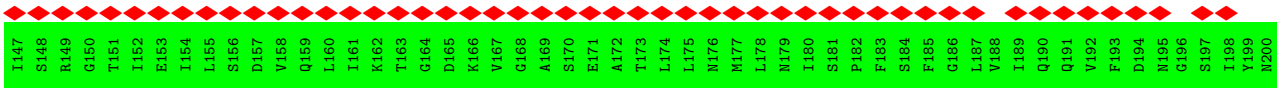
• Molecule 83: 60S acidic ribosomal protein P0

Chain Ls:



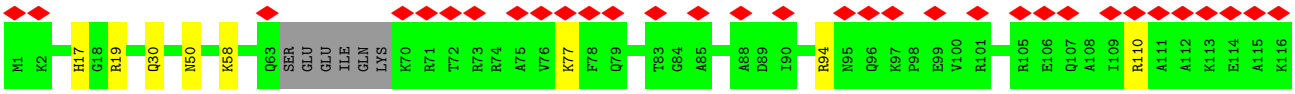


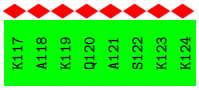




• Molecule 84: Ribosomal protein L24

Chain LW:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12376	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.286	Depositor
Minimum map value	-0.129	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0264	Depositor
Map size (Å)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	LR	0.40	0/1582	0.63	0/2091
2	SE	0.34	0/2118	0.58	0/2849
3	SI	0.36	0/1715	0.62	1/2287 (0.0%)
4	SL	0.40	0/1268	0.62	0/1696
5	SX	0.36	0/1116	0.56	0/1490
6	SG	0.33	0/1946	0.66	1/2590 (0.0%)
7	SJ	0.33	0/1550	0.60	0/2069
8	SY	0.31	0/1083	0.60	0/1438
9	Se	0.29	0/465	0.60	0/612
10	SA	0.35	0/1778	0.60	0/2416
11	SB	0.35	0/1765	0.57	0/2362
12	SH	0.33	0/1519	0.61	1/2033 (0.0%)
13	SV	0.32	0/643	0.63	0/860
14	Sa	0.39	0/836	0.64	0/1121
15	SC	0.36	0/1762	0.59	0/2381
16	SN	0.38	0/1232	0.56	0/1656
17	SO	0.35	0/1062	0.64	1/1425 (0.1%)
18	SW	0.37	0/1051	0.59	0/1406
19	Sb	0.34	0/665	0.56	0/891
20	L5	0.90	0/89312	0.91	93/139287 (0.1%)
21	L7	0.88	0/2861	0.84	0/4459
22	L8	0.92	0/3701	0.83	1/5766 (0.0%)
23	LA	0.50	0/1936	0.65	0/2596
24	LB	0.46	0/3306	0.61	1/4424 (0.0%)
25	LC	0.45	0/2981	0.62	1/4002 (0.0%)
26	LD	0.45	0/2428	0.61	2/3252 (0.1%)
27	LE	0.51	2/1942 (0.1%)	0.73	4/2606 (0.2%)
28	LF	0.48	0/1905	0.59	0/2539
29	LG	0.42	0/1960	0.60	1/2637 (0.0%)
30	LH	0.42	0/1537	0.65	1/2066 (0.0%)
31	LI	0.45	0/1673	0.59	0/2233
32	LJ	0.38	0/1433	0.61	0/1915

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	LL	0.42	0/1732	0.63	1/2315 (0.0%)
34	LM	0.43	0/1161	0.59	0/1554
35	LN	0.49	0/1746	0.62	0/2338
36	LO	0.46	0/1682	0.60	0/2250
37	LP	0.47	0/1268	0.60	0/1701
38	LQ	0.47	0/1537	0.65	0/2052
39	LS	0.49	0/1493	0.63	0/2003
40	LT	0.46	0/1326	0.61	0/1770
41	LU	0.45	0/839	0.65	0/1126
42	LV	0.47	0/993	0.61	0/1332
43	LX	0.42	0/1002	0.61	0/1345
44	LY	0.44	0/1132	0.60	0/1504
45	LZ	0.46	0/1130	0.57	0/1507
46	La	0.48	0/1191	0.58	0/1591
47	Lb	0.38	0/889	0.71	1/1175 (0.1%)
48	Lc	0.44	0/774	0.59	1/1038 (0.1%)
49	Ld	0.44	0/903	0.61	0/1216
50	Le	0.48	0/1071	0.63	0/1429
51	Lf	0.50	0/895	0.66	0/1198
52	Lg	0.46	0/916	0.66	1/1220 (0.1%)
53	Lh	0.41	0/1023	0.58	0/1351
54	Li	0.38	0/843	0.60	0/1115
55	Lj	0.51	0/720	0.66	0/952
56	Lk	0.39	0/575	0.59	0/761
57	Ll	0.43	0/454	0.62	0/599
58	Lm	0.42	0/435	0.57	0/575
59	Ln	0.40	0/231	0.81	1/294 (0.3%)
60	Lo	0.46	0/876	0.62	0/1156
61	Lp	0.47	0/718	0.55	0/953
62	Lr	0.45	0/1017	0.62	0/1364
63	SR	0.33	0/1105	0.68	0/1484
64	SD	0.36	0/1793	0.59	0/2414
65	SF	0.33	0/1516	0.62	1/2037 (0.0%)
66	SK	0.31	0/851	0.63	0/1147
67	SP	0.35	0/1003	0.68	0/1342
68	SQ	0.32	0/1160	0.60	0/1553
69	SS	0.32	0/1216	0.66	0/1628
70	ST	0.31	0/1131	0.58	0/1515
71	SU	0.29	0/831	0.59	0/1115
72	Sc	0.32	0/508	0.67	0/680
73	Sd	0.34	0/470	0.62	0/623
74	Sg	0.28	0/2493	0.58	0/3394
75	SM	0.33	0/950	0.64	1/1275 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	SZ	0.30	0/604	0.72	1/810 (0.1%)
77	Sf	0.28	0/560	0.57	0/745
78	S2	0.63	0/41242	0.85	52/64255 (0.1%)
79	Et	0.38	0/1778	0.90	0/2767
80	Pt	0.48	0/1761	0.82	1/2741 (0.0%)
81	Lt	0.27	0/1058	0.57	0/1430
82	Lz	0.27	0/1769	0.59	0/2371
83	Ls	0.29	0/1519	0.61	0/2052
84	LW	0.43	0/979	0.62	0/1295
All	All	0.68	2/239000 (0.0%)	0.80	169/350912 (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
5	SX	0	1
12	SH	0	1
23	LA	0	1
24	LB	0	3
32	LJ	0	1
34	LM	0	1
36	LO	0	1
40	LT	0	1
51	Lf	0	3
53	Lh	0	1
55	Lj	0	2
65	SF	0	1
67	SP	0	1
68	SQ	0	1
76	SZ	0	1
All	All	0	20

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	LE	95	PRO	CG-CD	-10.47	1.16	1.50
27	LE	95	PRO	N-CD	5.43	1.55	1.47

The worst 5 of 169 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
27	LE	95	PRO	CA-N-CD	-12.04	94.64	111.50
27	LE	95	PRO	N-CD-CG	-10.71	87.14	103.20
20	L5	3773	U	N3-C2-O2	-9.81	115.33	122.20
20	L5	174	C	N3-C2-O2	-9.73	115.09	121.90
20	L5	485	C	C2-N1-C1'	9.16	128.88	118.80

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	LA	13	GLY	Peptide
24	LB	17	LEU	Peptide
24	LB	258	HIS	Peptide
12	SH	15	LYS	Peptide
5	SX	126	ALA	Peptide

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	LR	185/187 (99%)	177 (96%)	8 (4%)	0	100 100
2	SE	260/262 (99%)	243 (94%)	17 (6%)	0	100 100
3	SI	204/206 (99%)	193 (95%)	11 (5%)	0	100 100
4	SL	151/153 (99%)	137 (91%)	14 (9%)	0	100 100
5	SX	139/141 (99%)	128 (92%)	10 (7%)	1 (1%)	19 52
6	SG	235/237 (99%)	221 (94%)	14 (6%)	0	100 100
7	SJ	183/185 (99%)	167 (91%)	16 (9%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	SY	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
9	Se	56/58 (97%)	48 (86%)	8 (14%)	0	100	100
10	SA	219/221 (99%)	194 (89%)	25 (11%)	0	100	100
11	SB	212/214 (99%)	203 (96%)	9 (4%)	0	100	100
12	SH	182/189 (96%)	160 (88%)	22 (12%)	0	100	100
13	SV	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
14	Sa	100/102 (98%)	90 (90%)	9 (9%)	1 (1%)	13	44
15	SC	220/222 (99%)	205 (93%)	15 (7%)	0	100	100
16	SN	148/150 (99%)	144 (97%)	4 (3%)	0	100	100
17	SO	138/140 (99%)	125 (91%)	13 (9%)	0	100	100
18	SW	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
19	Sb	81/83 (98%)	72 (89%)	9 (11%)	0	100	100
23	LA	246/248 (99%)	223 (91%)	22 (9%)	1 (0%)	30	63
24	LB	400/402 (100%)	375 (94%)	25 (6%)	0	100	100
25	LC	366/368 (100%)	341 (93%)	25 (7%)	0	100	100
26	LD	291/293 (99%)	272 (94%)	19 (6%)	0	100	100
27	LE	232/247 (94%)	211 (91%)	21 (9%)	0	100	100
28	LF	223/225 (99%)	212 (95%)	11 (5%)	0	100	100
29	LG	239/241 (99%)	220 (92%)	19 (8%)	0	100	100
30	LH	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
31	LI	198/213 (93%)	188 (95%)	10 (5%)	0	100	100
32	LJ	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
33	LL	208/210 (99%)	190 (91%)	18 (9%)	0	100	100
34	LM	137/139 (99%)	128 (93%)	8 (6%)	1 (1%)	19	52
35	LN	201/203 (99%)	189 (94%)	10 (5%)	2 (1%)	13	44
36	LO	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
37	LP	151/153 (99%)	142 (94%)	9 (6%)	0	100	100
38	LQ	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
39	LS	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
40	LT	157/159 (99%)	146 (93%)	11 (7%)	0	100	100
41	LU	99/101 (98%)	82 (83%)	17 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	LV	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
43	LX	118/120 (98%)	115 (98%)	3 (2%)	0	100	100
44	LY	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
45	LZ	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
46	La	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
47	Lb	105/121 (87%)	96 (91%)	9 (9%)	0	100	100
48	Lc	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
49	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
50	Le	126/128 (98%)	115 (91%)	10 (8%)	1 (1%)	16	49
51	Lf	107/109 (98%)	98 (92%)	8 (8%)	1 (1%)	14	46
52	Lg	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
53	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
54	Li	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
55	Lj	84/86 (98%)	79 (94%)	5 (6%)	0	100	100
56	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
57	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
58	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
59	Ln	22/24 (92%)	22 (100%)	0	0	100	100
60	Lo	103/105 (98%)	95 (92%)	8 (8%)	0	100	100
61	Lp	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
62	Lr	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
63	SR	133/135 (98%)	120 (90%)	12 (9%)	1 (1%)	16	49
64	SD	225/227 (99%)	209 (93%)	16 (7%)	0	100	100
65	SF	187/189 (99%)	168 (90%)	19 (10%)	0	100	100
66	SK	96/98 (98%)	81 (84%)	13 (14%)	2 (2%)	5	29
67	SP	119/121 (98%)	109 (92%)	10 (8%)	0	100	100
68	SQ	142/144 (99%)	123 (87%)	19 (13%)	0	100	100
69	SS	143/145 (99%)	135 (94%)	8 (6%)	0	100	100
70	ST	141/143 (99%)	128 (91%)	12 (8%)	1 (1%)	19	52
71	SU	102/104 (98%)	94 (92%)	8 (8%)	0	100	100
72	Sc	62/64 (97%)	54 (87%)	8 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
73	Sd	53/55 (96%)	48 (91%)	5 (9%)	0	100 100
74	Sg	311/313 (99%)	275 (88%)	36 (12%)	0	100 100
75	SM	120/122 (98%)	108 (90%)	11 (9%)	1 (1%)	16 49
76	SZ	73/75 (97%)	58 (80%)	15 (20%)	0	100 100
77	Sf	65/67 (97%)	54 (83%)	11 (17%)	0	100 100
81	Lt	137/157 (87%)	103 (75%)	33 (24%)	1 (1%)	19 52
82	Lz	215/217 (99%)	169 (79%)	46 (21%)	0	100 100
83	Ls	194/196 (99%)	183 (94%)	11 (6%)	0	100 100
84	LW	114/124 (92%)	108 (95%)	6 (5%)	0	100 100
All	All	11863/12090 (98%)	10927 (92%)	922 (8%)	14 (0%)	50 79

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	SX	127	ASN
34	LM	88	ALA
35	LN	124	ASP
63	SR	124	VAL
66	SK	36	ALA

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	LR	166/166 (100%)	143 (86%)	23 (14%)	3 15
2	SE	224/224 (100%)	200 (89%)	24 (11%)	5 23
3	SI	178/178 (100%)	160 (90%)	18 (10%)	6 25
4	SL	137/137 (100%)	113 (82%)	24 (18%)	1 8
5	SX	113/113 (100%)	105 (93%)	8 (7%)	12 38
6	SG	207/207 (100%)	177 (86%)	30 (14%)	2 13
7	SJ	161/161 (100%)	154 (96%)	7 (4%)	25 53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
8	SY	113/113 (100%)	100 (88%)	13 (12%)	4 20
9	Se	47/47 (100%)	41 (87%)	6 (13%)	3 17
10	SA	183/183 (100%)	166 (91%)	17 (9%)	7 28
11	SB	195/195 (100%)	176 (90%)	19 (10%)	6 26
12	SH	166/169 (98%)	150 (90%)	16 (10%)	7 27
13	SV	67/67 (100%)	61 (91%)	6 (9%)	8 29
14	Sa	89/89 (100%)	78 (88%)	11 (12%)	4 18
15	SC	188/188 (100%)	169 (90%)	19 (10%)	6 25
16	SN	130/130 (100%)	119 (92%)	11 (8%)	8 31
17	SO	110/110 (100%)	99 (90%)	11 (10%)	6 26
18	SW	112/112 (100%)	102 (91%)	10 (9%)	8 30
19	Sb	75/75 (100%)	67 (89%)	8 (11%)	5 23
23	LA	190/190 (100%)	173 (91%)	17 (9%)	8 30
24	LB	348/348 (100%)	325 (93%)	23 (7%)	14 41
25	LC	306/306 (100%)	287 (94%)	19 (6%)	15 42
26	LD	246/247 (100%)	231 (94%)	15 (6%)	15 43
27	LE	209/220 (95%)	190 (91%)	19 (9%)	7 29
28	LF	194/194 (100%)	186 (96%)	8 (4%)	26 54
29	LG	203/205 (99%)	188 (93%)	15 (7%)	11 36
30	LH	169/169 (100%)	156 (92%)	13 (8%)	10 35
31	LI	172/180 (96%)	160 (93%)	12 (7%)	12 39
32	LJ	148/148 (100%)	132 (89%)	16 (11%)	5 23
33	LL	176/176 (100%)	163 (93%)	13 (7%)	11 36
34	LM	118/118 (100%)	112 (95%)	6 (5%)	20 48
35	LN	171/171 (100%)	166 (97%)	5 (3%)	37 64
36	LO	173/173 (100%)	163 (94%)	10 (6%)	17 44
37	LP	134/134 (100%)	120 (90%)	14 (10%)	5 24
38	LQ	164/164 (100%)	156 (95%)	8 (5%)	21 49
39	LS	156/156 (100%)	147 (94%)	9 (6%)	17 44
40	LT	139/139 (100%)	129 (93%)	10 (7%)	12 38
41	LU	91/91 (100%)	77 (85%)	14 (15%)	2 11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
42	LV	101/101 (100%)	92 (91%)	9 (9%)	8 30
43	LX	108/108 (100%)	102 (94%)	6 (6%)	17 45
44	LY	124/124 (100%)	118 (95%)	6 (5%)	21 50
45	LZ	117/117 (100%)	103 (88%)	14 (12%)	4 19
46	La	120/120 (100%)	115 (96%)	5 (4%)	25 53
47	Lb	88/101 (87%)	74 (84%)	14 (16%)	2 11
48	Lc	83/83 (100%)	76 (92%)	7 (8%)	9 31
49	Ld	98/98 (100%)	86 (88%)	12 (12%)	4 18
50	Le	114/114 (100%)	107 (94%)	7 (6%)	15 43
51	Lf	88/88 (100%)	85 (97%)	3 (3%)	32 60
52	Lg	98/98 (100%)	93 (95%)	5 (5%)	20 48
53	Lh	109/109 (100%)	96 (88%)	13 (12%)	4 19
54	Li	86/86 (100%)	83 (96%)	3 (4%)	31 59
55	Lj	73/73 (100%)	65 (89%)	8 (11%)	5 22
56	Lk	64/64 (100%)	59 (92%)	5 (8%)	10 34
57	Ll	47/47 (100%)	42 (89%)	5 (11%)	5 23
58	Lm	48/48 (100%)	46 (96%)	2 (4%)	25 53
59	Ln	23/23 (100%)	21 (91%)	2 (9%)	8 30
60	Lo	93/93 (100%)	88 (95%)	5 (5%)	18 46
61	Lp	74/74 (100%)	72 (97%)	2 (3%)	40 66
62	Lr	109/109 (100%)	96 (88%)	13 (12%)	4 19
63	SR	122/122 (100%)	103 (84%)	19 (16%)	2 11
64	SD	190/190 (100%)	162 (85%)	28 (15%)	2 13
65	SF	159/159 (100%)	143 (90%)	16 (10%)	6 25
66	SK	89/89 (100%)	79 (89%)	10 (11%)	5 21
67	SP	107/107 (100%)	93 (87%)	14 (13%)	3 16
68	SQ	119/119 (100%)	107 (90%)	12 (10%)	6 25
69	SS	126/126 (100%)	114 (90%)	12 (10%)	7 27
70	ST	113/113 (100%)	98 (87%)	15 (13%)	3 16
71	SU	94/94 (100%)	88 (94%)	6 (6%)	14 41
72	Sc	57/57 (100%)	53 (93%)	4 (7%)	12 39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
73	Sd	48/48 (100%)	42 (88%)	6 (12%)	3 18
74	Sg	272/272 (100%)	236 (87%)	36 (13%)	3 16
75	SM	102/104 (98%)	91 (89%)	11 (11%)	5 23
76	SZ	66/66 (100%)	59 (89%)	7 (11%)	5 23
77	Sf	60/60 (100%)	52 (87%)	8 (13%)	3 16
81	Lt	112/130 (86%)	105 (94%)	7 (6%)	15 42
82	Lz	195/196 (100%)	178 (91%)	17 (9%)	8 30
83	Ls	162/164 (99%)	148 (91%)	14 (9%)	8 31
84	LW	97/103 (94%)	89 (92%)	8 (8%)	9 33
All	All	10323/10390 (99%)	9400 (91%)	923 (9%)	10 30

5 of 923 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	LO	29	LEU
82	Lz	63	PHE
47	Lb	55	LYS
81	Lt	15	LEU
71	SU	19	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
47	Lb	58	GLN
66	SK	44	HIS
63	SR	31	ASN
68	SQ	80	GLN
18	SW	98	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	L5	3704/5070 (73%)	883 (23%)	20 (0%)
21	L7	119/120 (99%)	13 (10%)	0
22	L8	155/156 (99%)	29 (18%)	0
78	S2	1715/1740 (98%)	437 (25%)	7 (0%)
79	Et	73/76 (96%)	30 (41%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
80	Pt	72/76 (94%)	19 (26%)	0
All	All	5838/7238 (80%)	1411 (24%)	27 (0%)

5 of 1411 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	L5	2	G
20	L5	13	U
20	L5	17	A
20	L5	25	A
20	L5	26	C

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	L5	2786	C
20	L5	4600	G
78	S2	1355	C
20	L5	3673	C
20	L5	4699	U

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
78	S2	6
20	L5	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	753:C	O3'	785:C	P	26.73
1	S2	698:G	O3'	730:C	P	16.85
1	S2	739:C	O3'	746:C	P	12.91
1	S2	225:G	O3'	287:U	P	7.44
1	S2	1693:G	O3'	1694:U	P	5.77

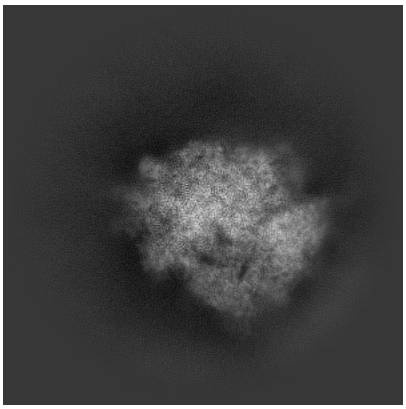
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-42306. These allow visual inspection of the internal detail of the map and identification of artifacts.

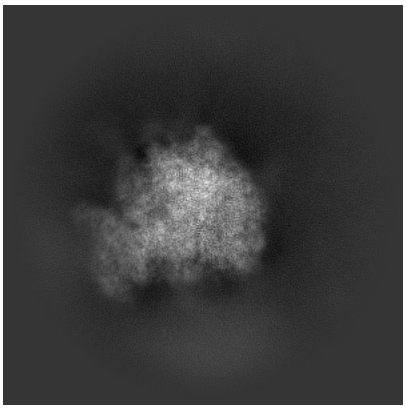
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

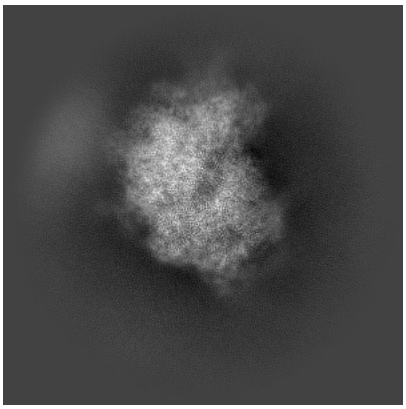
6.1.1 Primary map



X

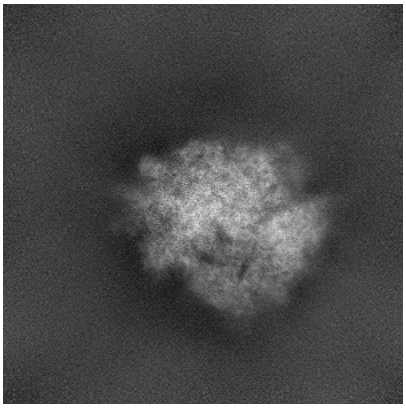


Y

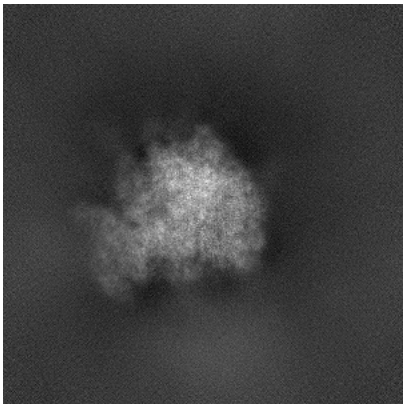


Z

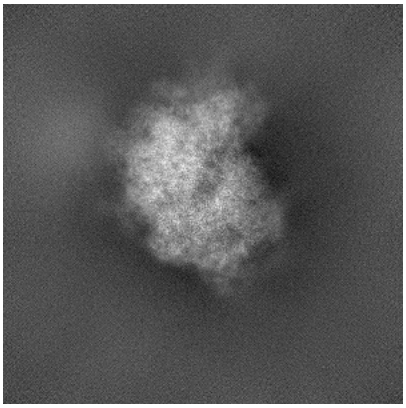
6.1.2 Raw map



X



Y

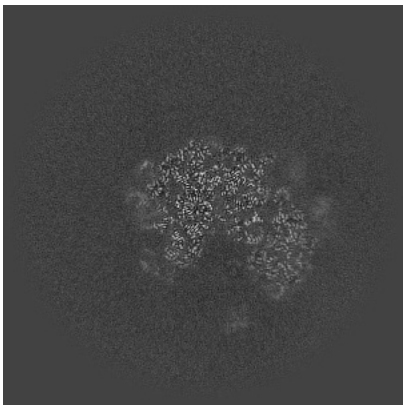


Z

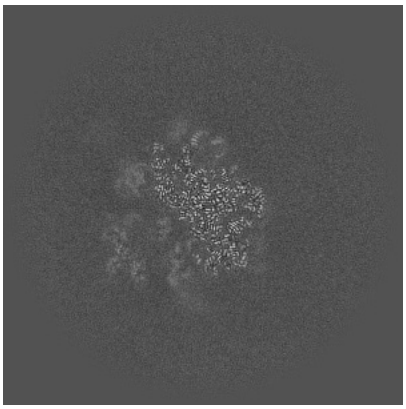
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

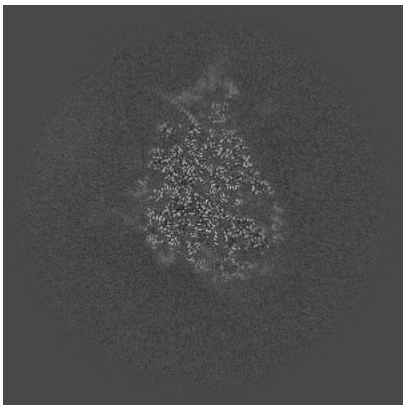
6.2.1 Primary map



X Index: 256

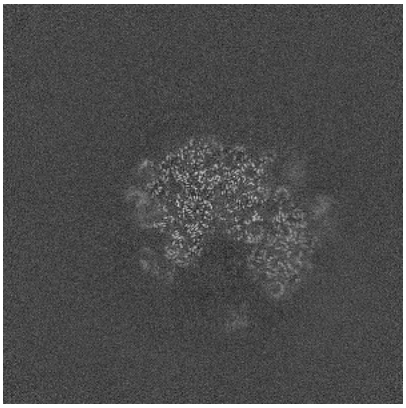


Y Index: 256

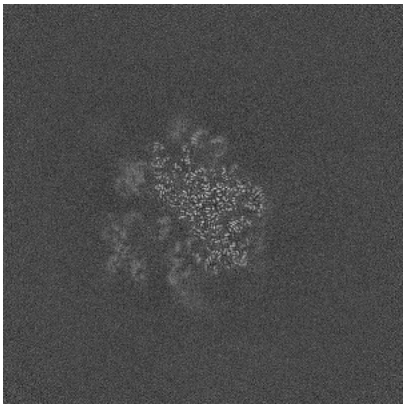


Z Index: 256

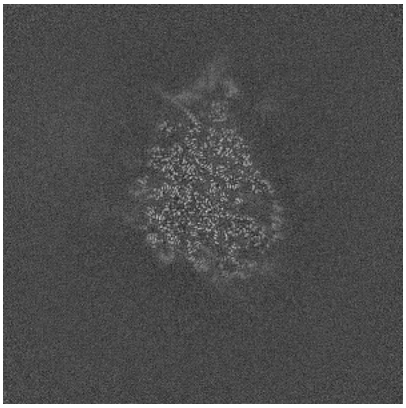
6.2.2 Raw map



X Index: 256



Y Index: 256

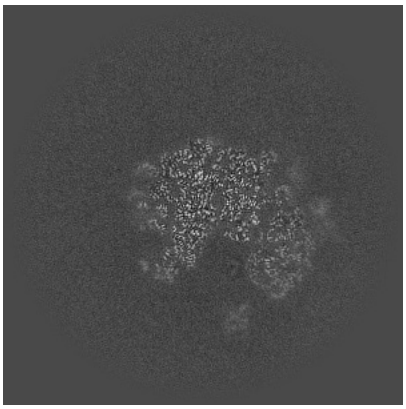


Z Index: 256

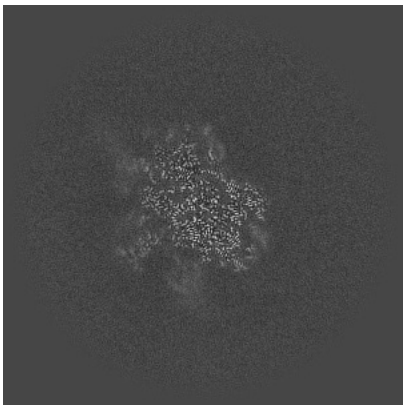
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

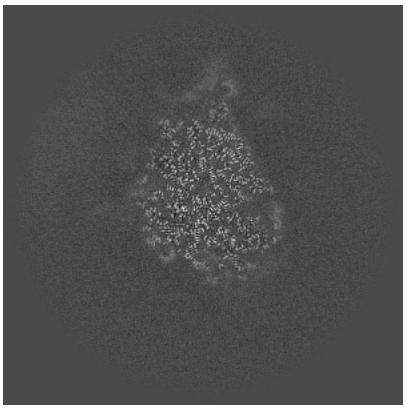
6.3.1 Primary map



X Index: 253

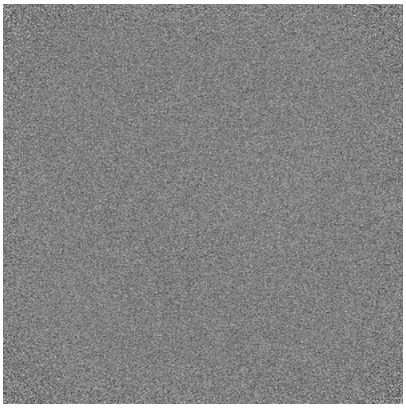


Y Index: 243

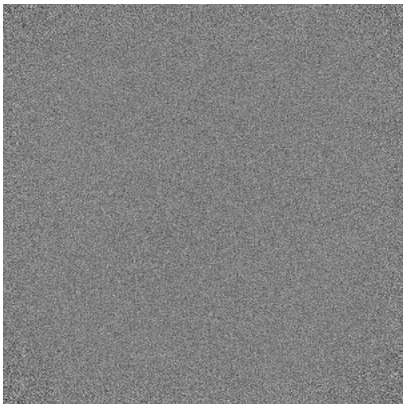


Z Index: 258

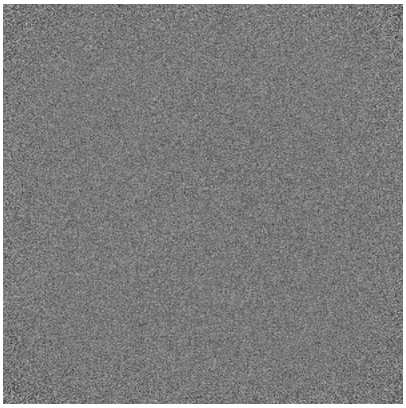
6.3.2 Raw map



X Index: 0



Y Index: 0

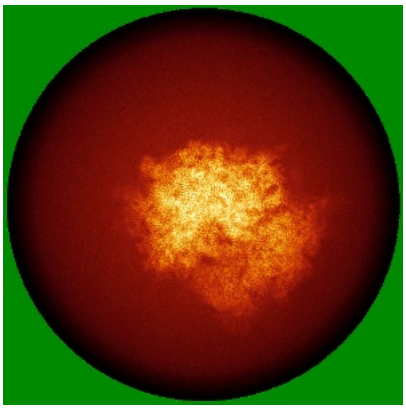


Z Index: 0

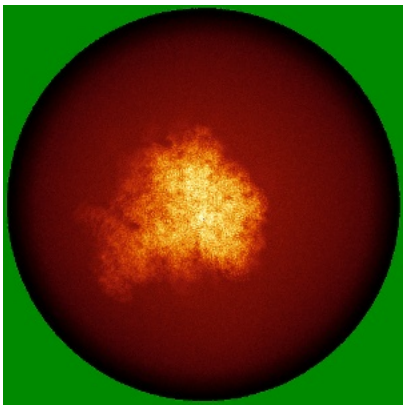
The images above show the largest variance slices of the map in three orthogonal directions.

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

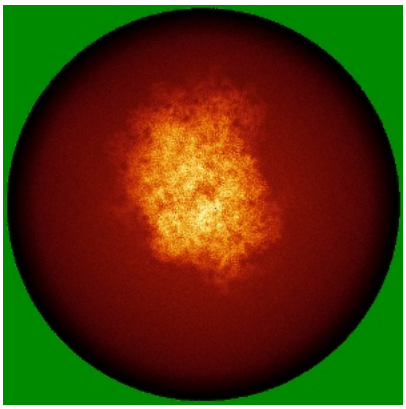
6.4.1 Primary map



X

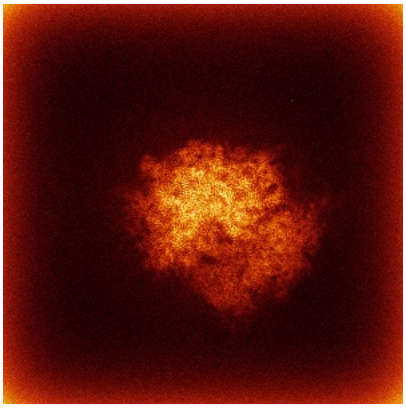


Y

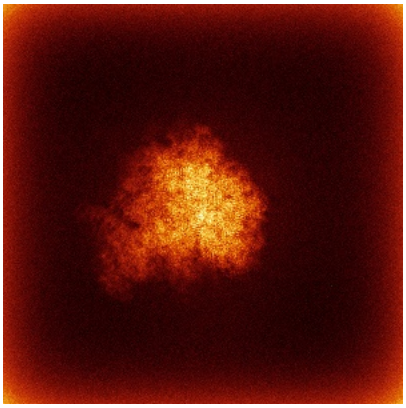


Z

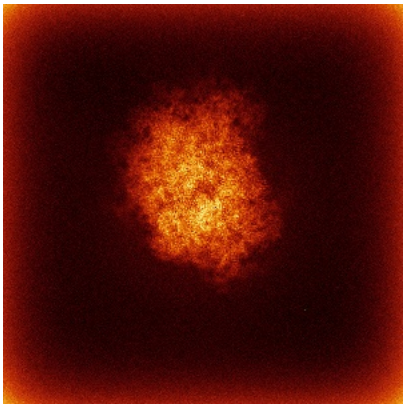
6.4.2 Raw map



X



Y

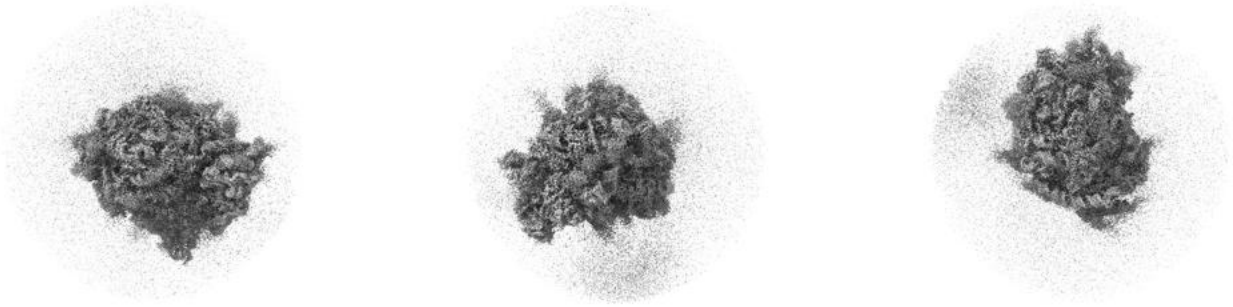


Z

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

6.5 Orthogonal surface views (i)

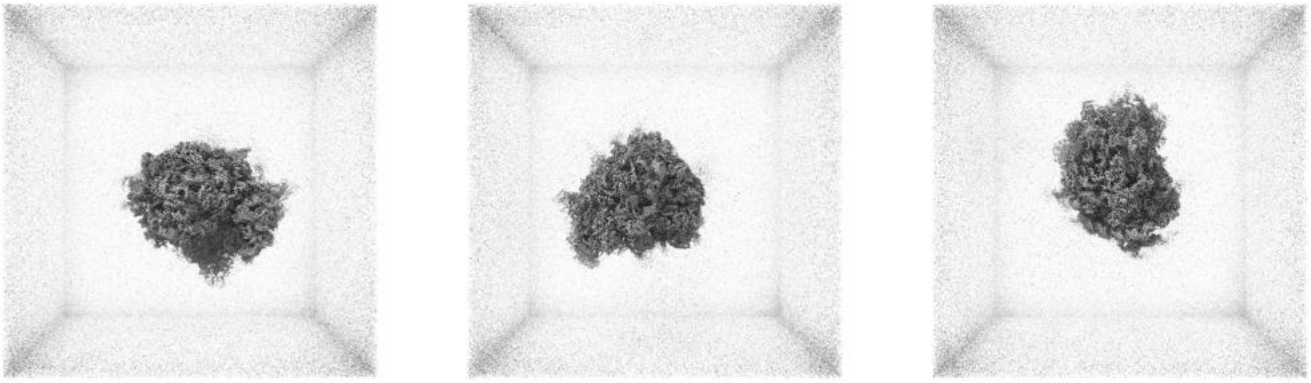
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0264. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

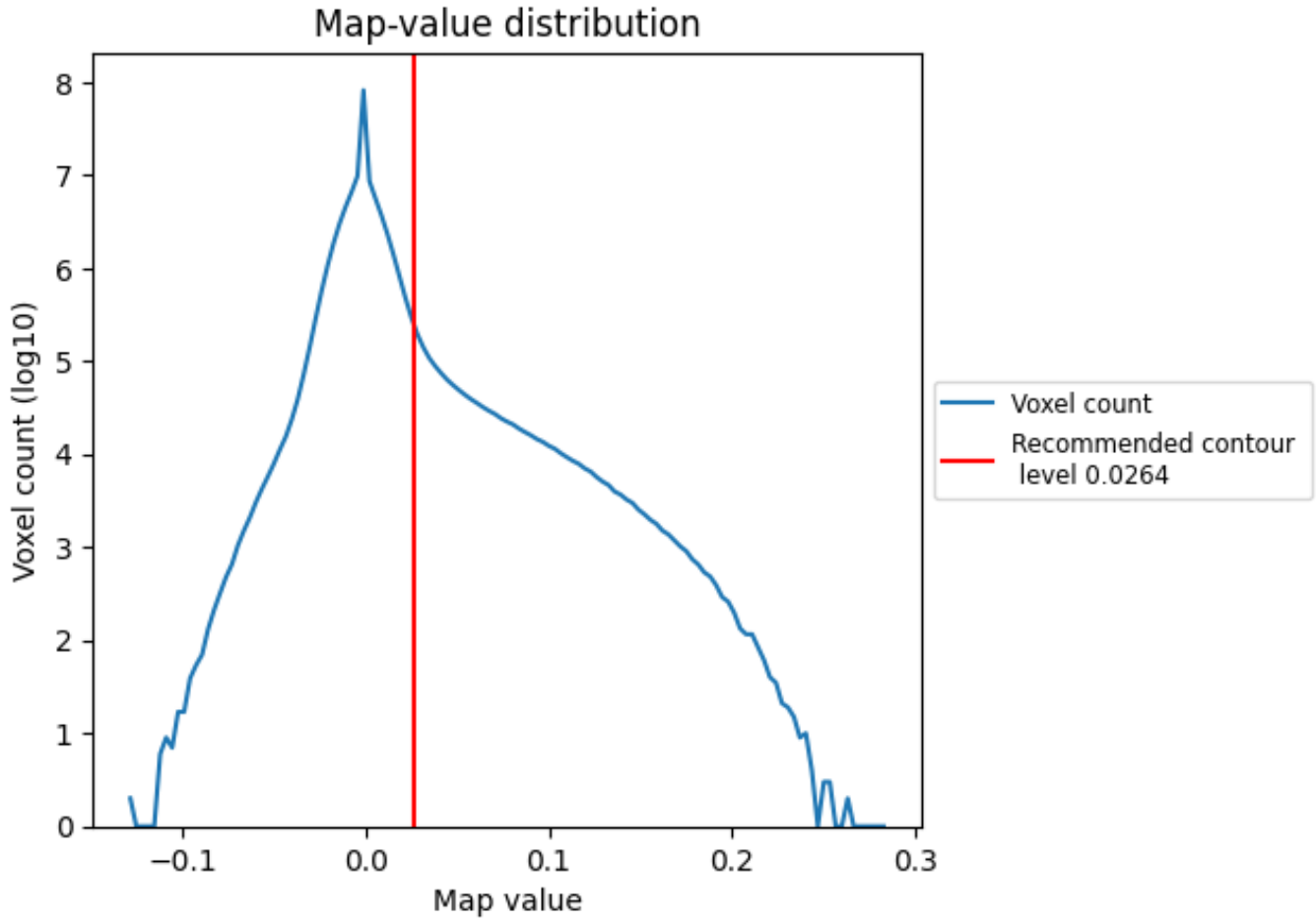
6.6 Mask visualisation (i)

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

7 Map analysis

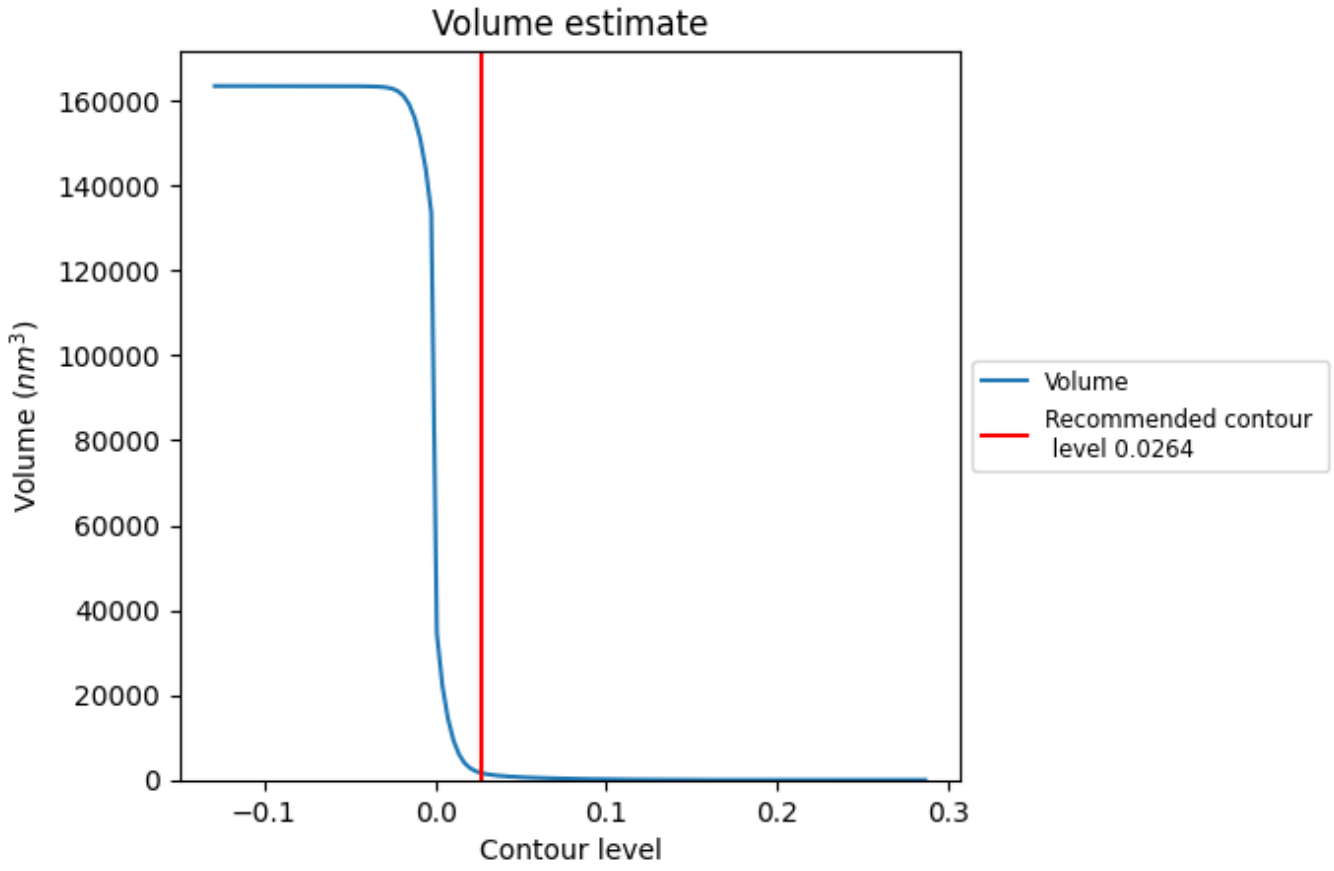
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

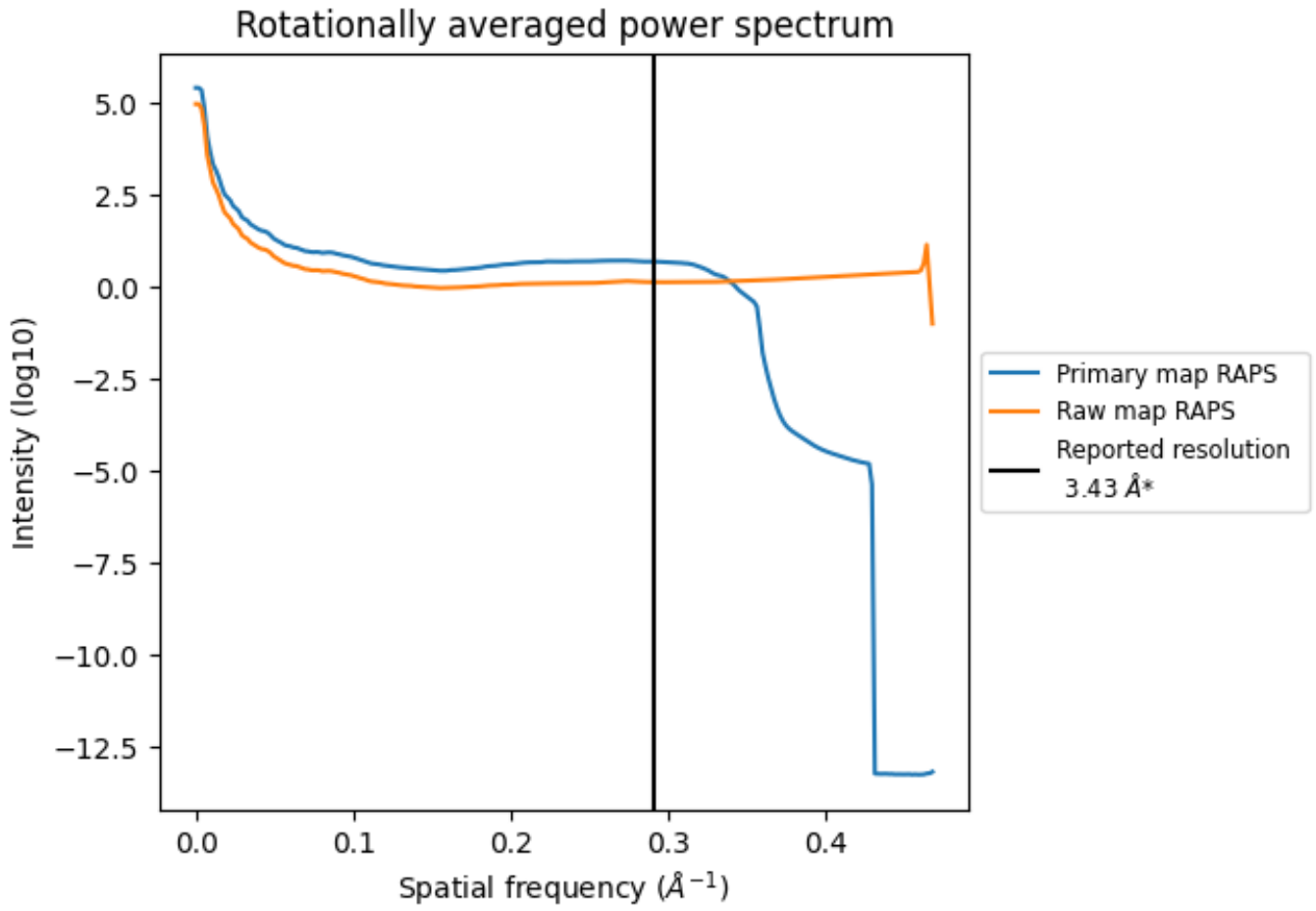
7.2 Volume estimate (i)



The volume at the recommended contour level is 1700 nm^3; this corresponds to an approximate mass of 1535 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

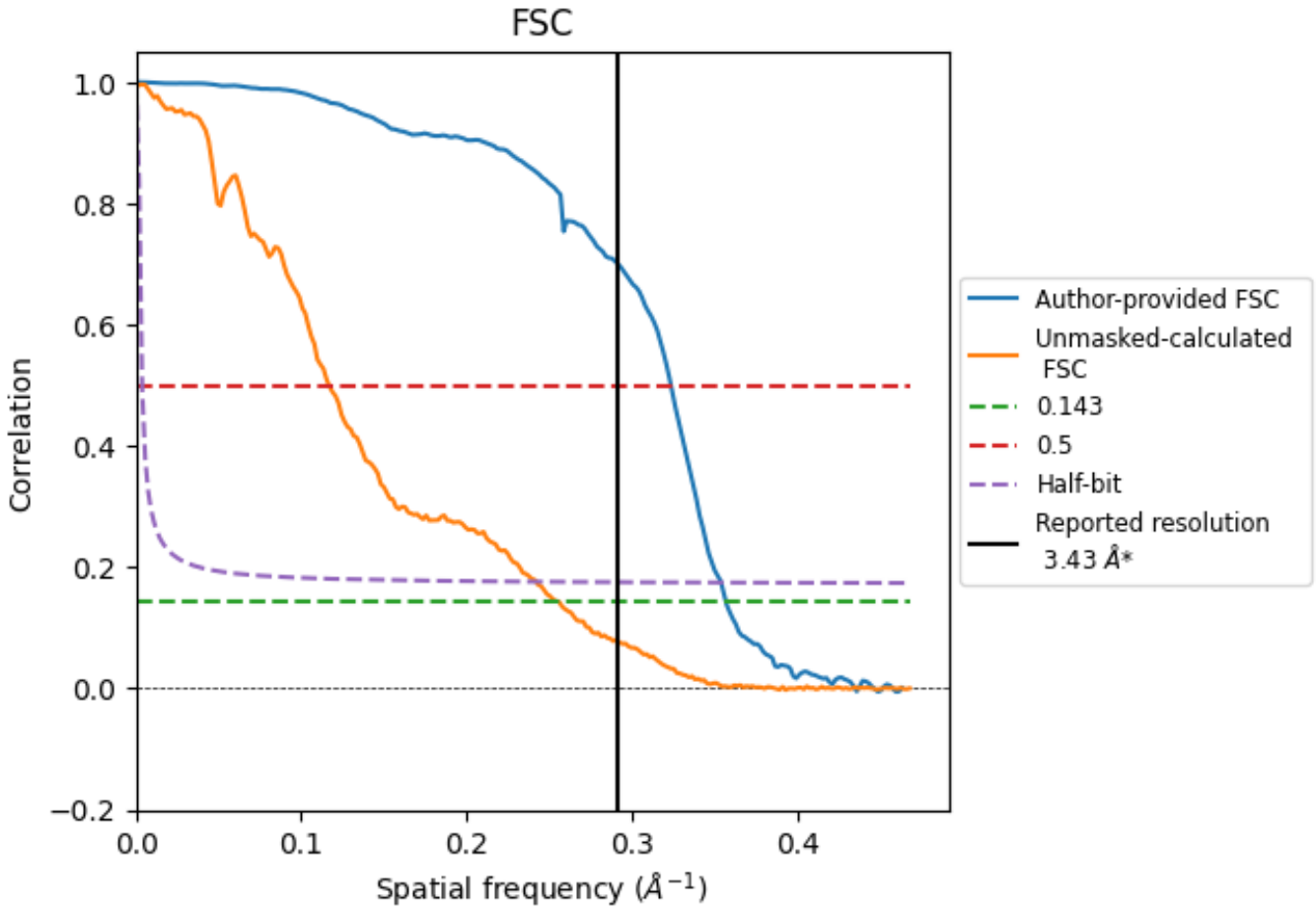


*Reported resolution corresponds to spatial frequency of 0.292 $Å^{-1}$

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.292 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.43	-	-
Author-provided FSC curve	2.80	3.09	2.82
Unmasked-calculated*	3.91	8.56	4.13

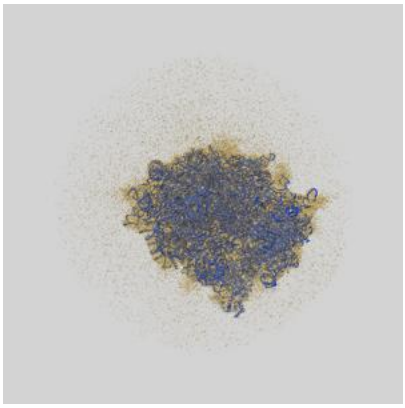
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.80 differs from the reported value 3.43 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.91 differs from the reported value 3.43 by more than 10 %

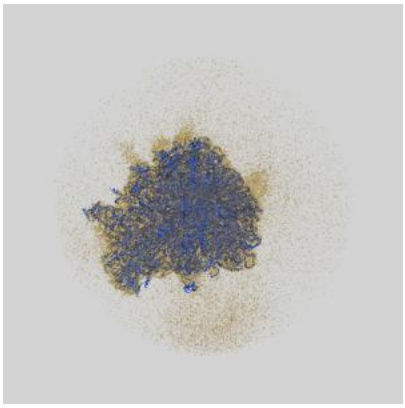
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-42306 and PDB model 8UIZ. Per-residue inclusion information can be found in section 3 on page 20.

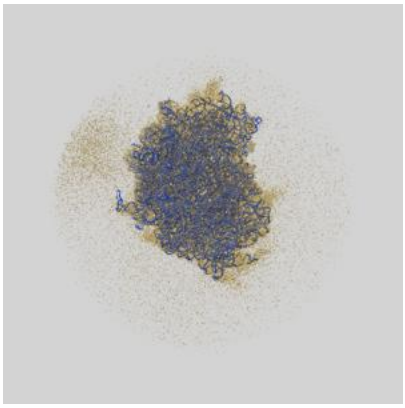
9.1 Map-model overlay



X



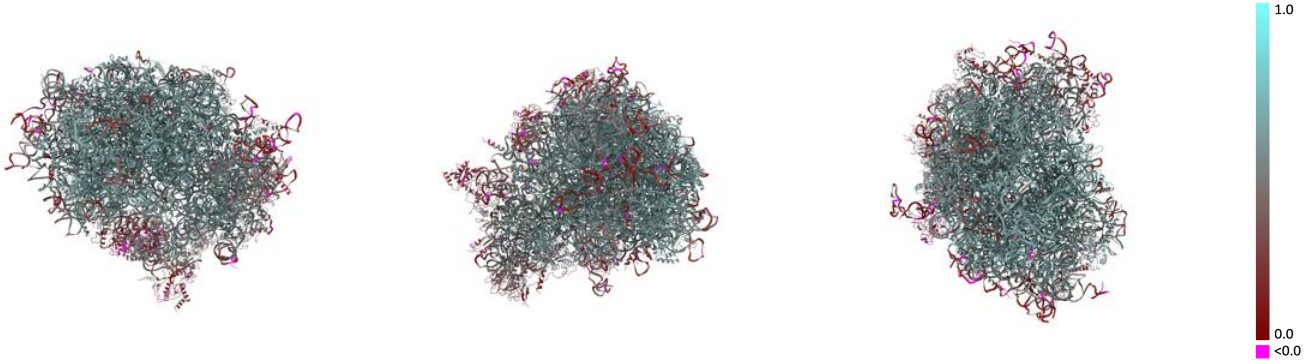
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0264 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.

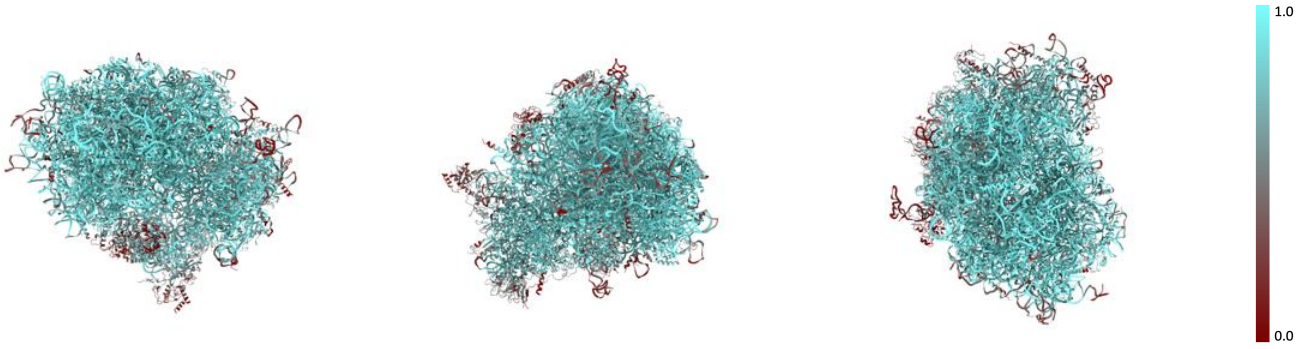
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

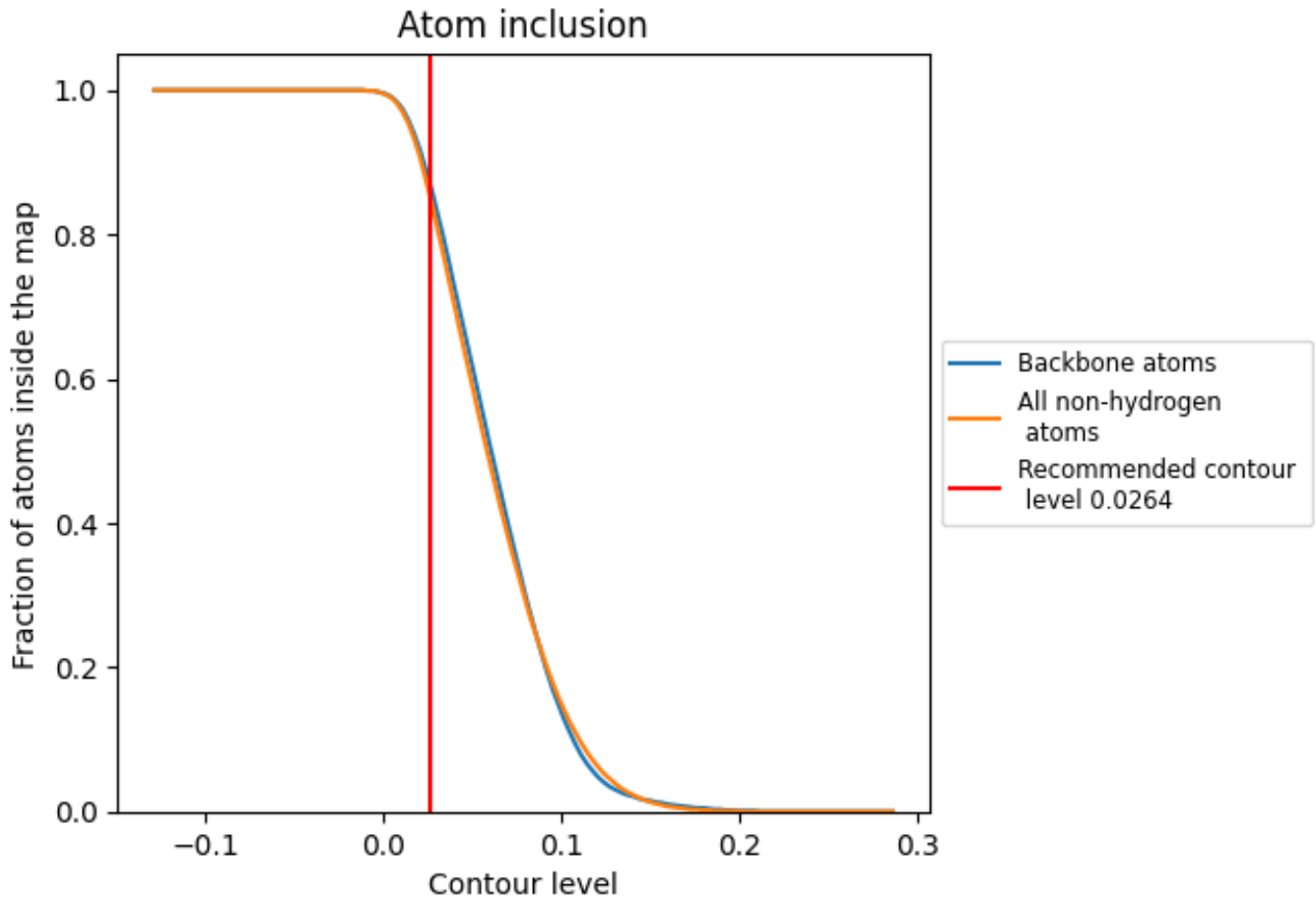
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0264).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0264) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8510	0.5270
Et	0.6410	0.2420
L5	0.8970	0.5440
L7	0.9810	0.6070
L8	0.9390	0.5810
LA	0.9650	0.6240
LB	0.9180	0.6030
LC	0.9200	0.6020
LD	0.8710	0.5690
LE	0.8260	0.5360
LF	0.9310	0.6090
LG	0.8140	0.5460
LH	0.9090	0.5940
LI	0.9200	0.6050
LJ	0.7910	0.5230
LL	0.8860	0.5780
LM	0.9140	0.5810
LN	0.9830	0.6330
LO	0.9410	0.6110
LP	0.9420	0.6160
LQ	0.9570	0.6260
LR	0.8390	0.5460
LS	0.9550	0.6240
LT	0.9040	0.5930
LU	0.7990	0.5020
LV	0.9310	0.6150
LW	0.6340	0.4200
LX	0.8970	0.5890
LY	0.9120	0.6000
LZ	0.9050	0.5850
La	0.9560	0.6290
Lb	0.8190	0.5290
Lc	0.9160	0.5790
Ld	0.9000	0.5880
Le	0.9660	0.6300

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Chain	Atom inclusion	Q-score
Lf	0.9640	0.6200
Lg	0.9230	0.5960
Lh	0.9180	0.6010
Li	0.8900	0.5890
Lj	0.9730	0.6190
Lk	0.8100	0.5460
Ll	0.9480	0.6090
Lm	0.9210	0.6090
Ln	0.9620	0.6140
Lo	0.9290	0.6060
Lp	0.9260	0.6100
Lr	0.9350	0.6060
Ls	0.2720	0.2200
Lt	0.1610	0.1590
Lz	0.1200	0.1390
Pt	0.8500	0.4960
S2	0.8850	0.5060
SA	0.7710	0.5100
SB	0.8230	0.5500
SC	0.8600	0.5490
SD	0.6710	0.4490
SE	0.8110	0.5170
SF	0.7500	0.4750
SG	0.6590	0.4250
SH	0.6310	0.4300
SI	0.8000	0.5300
SJ	0.7950	0.5070
SK	0.5880	0.3660
SL	0.8200	0.5370
SM	0.2360	0.2110
SN	0.8870	0.5750
SO	0.8170	0.5440
SP	0.6430	0.4180
SQ	0.7090	0.4700
SR	0.6380	0.4200
SS	0.7030	0.4550
ST	0.7130	0.4590
SU	0.6110	0.3910
SV	0.8090	0.5310
SW	0.9180	0.5780
SX	0.8510	0.5590
SY	0.7050	0.4400

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Chain	Atom inclusion	Q-score
SZ	0.6000	0.3990
Sa	0.8620	0.5560
Sb	0.7610	0.4980
Sc	0.6540	0.4240
Sd	0.8120	0.4970
Se	0.6350	0.4210
Sf	0.3420	0.2230
Sg	0.5040	0.3610