



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:51 PM UTC

PDB ID : 8UKB / pdb_00008ukb
EMDB ID : EMD-42351
Title : In situ HHT and CHX treated human hibernating state without E-tRNA 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2023-10-12
Resolution : 3.05 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

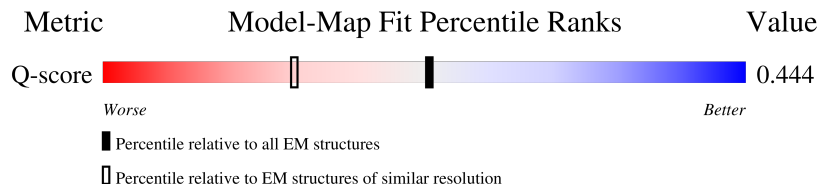
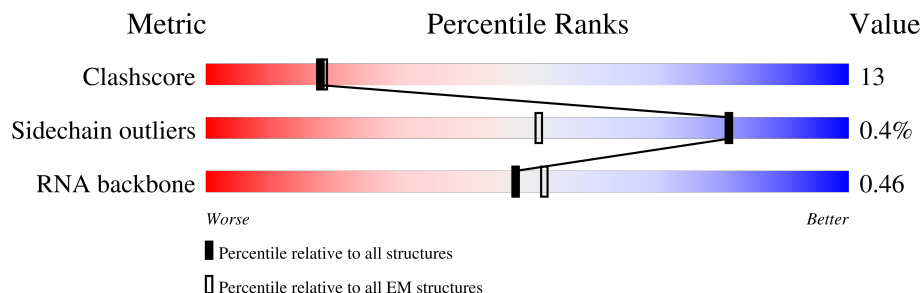
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.05 Å.

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



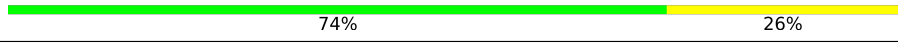
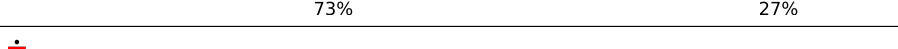
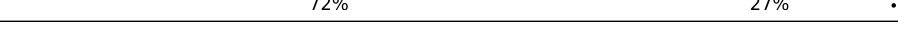
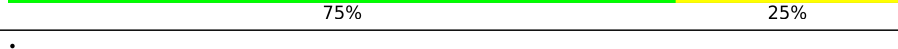
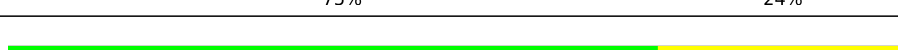
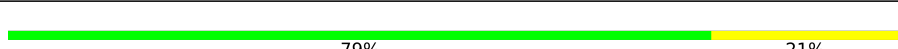
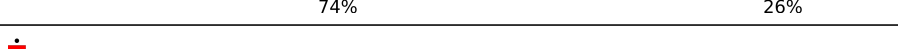
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13971 (2.55 - 3.55)

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

Mol	Chain	Length	Quality of chain
1	CB	856	
2	CD	55	
3	L5	3740	
4	L7	120	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	L8	156	
6	LA	248	
7	LB	402	
8	LC	368	
9	LD	293	
10	LE	247	
11	LF	225	
12	LG	241	
13	LH	190	
14	LI	213	
15	LJ	176	
16	LL	210	
17	LM	139	
18	LN	203	
19	LO	201	
20	LP	153	
21	LQ	187	
22	LR	187	
23	LS	175	
24	LT	159	
25	LU	101	
26	LV	131	
27	LW	124	
28	LX	120	
29	LY	134	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
30	LZ	135	
31	La	147	
32	Lb	121	
33	Lc	98	
34	Ld	107	
35	Le	128	
36	Lf	109	
37	Lg	114	
38	Lh	122	
39	Li	102	
40	Lj	86	
41	Lk	69	
42	Ll	50	
43	Lm	52	
44	Ln	24	
45	Lo	105	
46	Lp	91	
47	Lr	125	
48	Ls	196	
49	Lt	141	
50	Lz	217	
51	S2	1740	
52	SA	221	
53	SB	214	
54	SC	222	

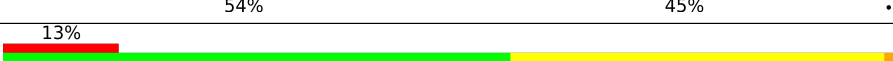
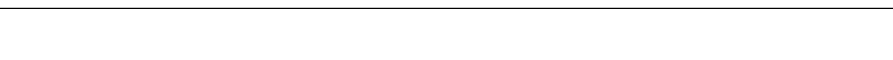
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
55	SD	227	
56	SE	262	
57	SF	189	
58	SG	237	
59	SH	189	
60	SI	206	
61	SJ	185	
62	SK	98	
63	SL	153	
64	SM	122	
65	SN	150	
66	SO	140	
67	SP	121	
68	SQ	144	
69	SR	135	
70	SS	145	
71	ST	143	
72	SU	104	
73	SV	83	
74	SW	129	
75	SX	141	
76	SY	131	
77	SZ	75	
78	Sa	102	
79	Sb	83	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
80	Sc	64	
81	Sd	55	
82	Se	58	
83	Sf	67	
84	Sg	313	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 226649 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 Elongation factor 2.

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

- Molecule 2 is a protein called Serbp1.

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

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

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

- Molecule 4 is a RNA chain called 5S rRNA [Homo sapiens].

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

- Molecule 5 is a RNA chain called 5.8S rRNA [Homo sapiens].

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 22 is a protein called 60S ribosomal protein L19.

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

- Molecule 23 is a protein called 60S ribosomal protein L18a.

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

- Molecule 24 is a protein called 60S ribosomal protein L21.

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

- Molecule 25 is a protein called Heparin-binding protein HBp15.

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

- Molecule 26 is a protein called 60S ribosomal protein L23.

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

- Molecule 27 is a protein called Ribosomal protein L24.

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

- Molecule 28 is a protein called 60S ribosomal protein L23a.

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

- Molecule 29 is a protein called 60S ribosomal protein L26.

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

- Molecule 30 is a protein called 60S ribosomal protein L27.

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

- Molecule 31 is a protein called 60S ribosomal protein L27a.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 33 is a protein called 60S ribosomal protein L30.

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

- Molecule 34 is a protein called 60S ribosomal protein L31.

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

- Molecule 35 is a protein called 60S ribosomal protein L32.

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

- Molecule 36 is a protein called 60S ribosomal protein L35a.

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

- Molecule 37 is a protein called 60S ribosomal protein L34.

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

- Molecule 38 is a protein called 60S ribosomal protein L35.

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

- Molecule 39 is a protein called 60S ribosomal protein L36.

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

- Molecule 40 is a protein called 60S ribosomal protein L37.

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

- Molecule 41 is a protein called 60S ribosomal protein L38.

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

- Molecule 42 is a protein called 60S ribosomal protein L39.

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

- Molecule 43 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 44 is a protein called 60S ribosomal protein L41.

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

- Molecule 45 is a protein called 60S ribosomal protein L36a.

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

- Molecule 46 is a protein called 60S ribosomal protein L37a.

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

- Molecule 47 is a protein called 60S ribosomal protein L28.

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

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

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

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

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

- Molecule 50 is a protein called 60S ribosomal protein L10a.

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

- Molecule 51 is a RNA chain called 18S rRNA.

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

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

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

- Molecule 53 is a protein called 40S ribosomal protein S3a.

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

- Molecule 54 is a protein called 40S ribosomal protein S2.

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

- Molecule 55 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 56 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 57 is a protein called 40S ribosomal protein S5.

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

- Molecule 58 is a protein called 40S ribosomal protein S6.

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

- Molecule 59 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 60 is a protein called 40S ribosomal protein S8.

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

- Molecule 61 is a protein called 40S ribosomal protein S9.

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

- Molecule 62 is a protein called 40S ribosomal protein S10.

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

- Molecule 63 is a protein called 40S ribosomal protein S11.

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

- Molecule 64 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 65 is a protein called 40S ribosomal protein S13.

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

- Molecule 66 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	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 S17.

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

- Molecule 70 is a protein called 40S ribosomal protein S18.

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

- Molecule 71 is a protein called 40S ribosomal protein S19.

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

- Molecule 72 is a protein called 40S ribosomal protein S20.

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

- Molecule 73 is a protein called 40S ribosomal protein S21.

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

- Molecule 74 is a protein called 40S ribosomal protein S15a.

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

- Molecule 75 is a protein called 40S ribosomal protein S23.

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

- Molecule 76 is a protein called 40S ribosomal protein S24.

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

- Molecule 77 is a protein called Small ribosomal subunit protein eS25.

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

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

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

- Molecule 79 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 80 is a protein called 40S ribosomal protein S28.

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

- Molecule 81 is a protein called 40S ribosomal protein S29.

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

- Molecule 82 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 83 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

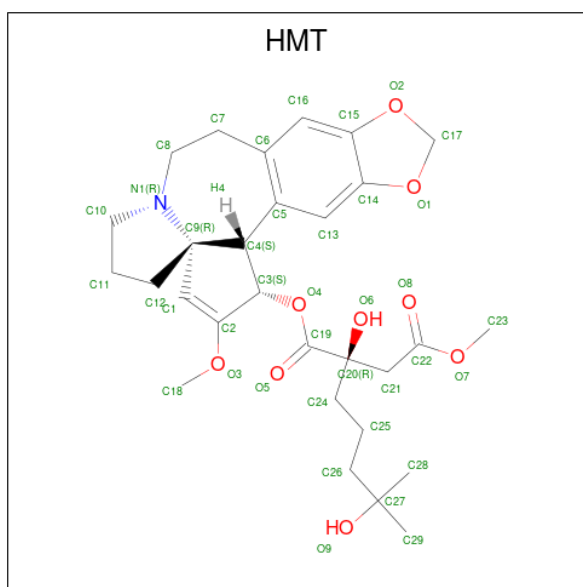
- Molecule 84 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

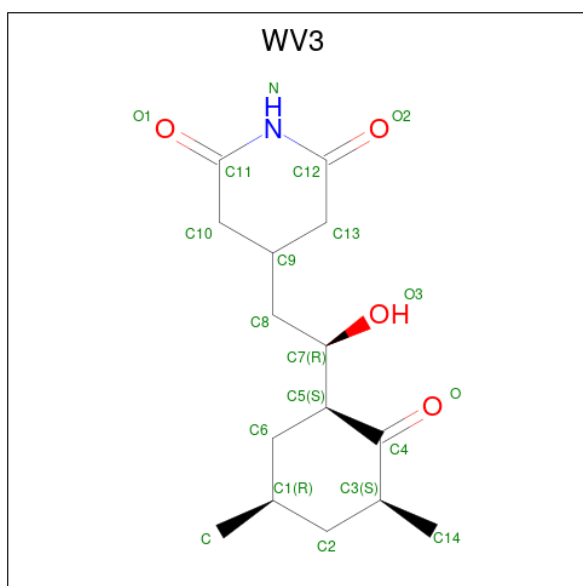
Mol	Chain	Residues	Atoms		AltConf
85	L5	212	Total	Mg	0
			212	212	
85	L7	3	Total	Mg	0
			3	3	
85	L8	4	Total	Mg	0
			4	4	
85	LA	1	Total	Mg	0
			1	1	
85	LI	1	Total	Mg	0
			1	1	
85	LP	1	Total	Mg	0
			1	1	
85	LV	1	Total	Mg	0
			1	1	
85	Le	1	Total	Mg	0
			1	1	
85	Lj	1	Total	Mg	0
			1	1	
85	S2	30	Total	Mg	0
			30	30	

- Molecule 86 is (3beta)-O 3 -[(2R)-2,6-dihydroxy-2-(2-methoxy-2-oxoethyl)-6-methylheptanoyl]cephalotaxine (CCD ID: HMT) (formula: C₂₉H₃₉NO₉) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
86	L5	1	Total	C	N	O	0
			39	29	1	9	

- Molecule 87 is 4-{(2R)-2-[(1R,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: WV3) (formula: $C_{15}H_{23}NO_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
87	L5	1	Total	C	N	O	0
			20	15	1	4	

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by

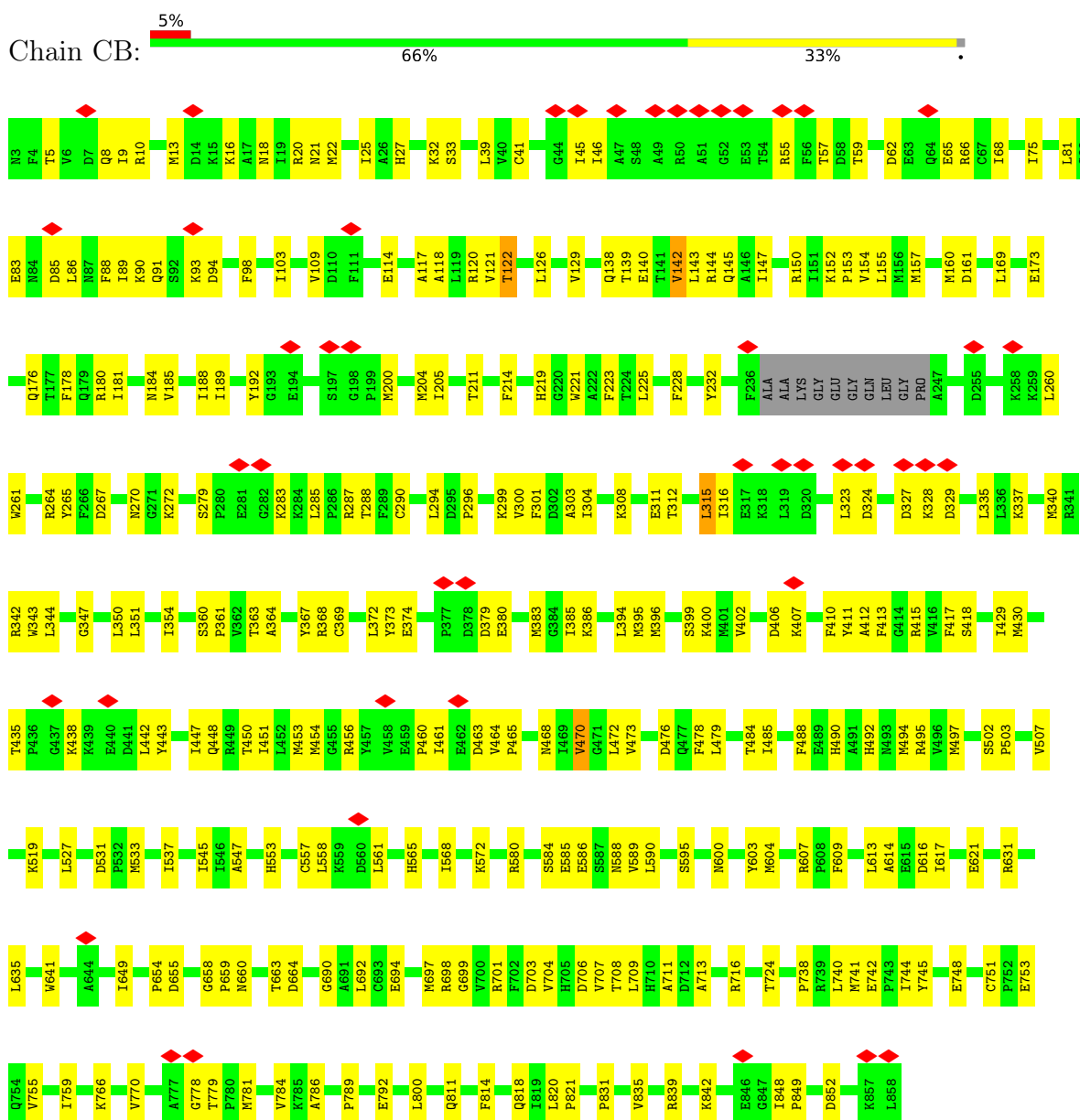
depositor).

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

3 Residue-property plots

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

• Molecule 1: Elongation factor 2



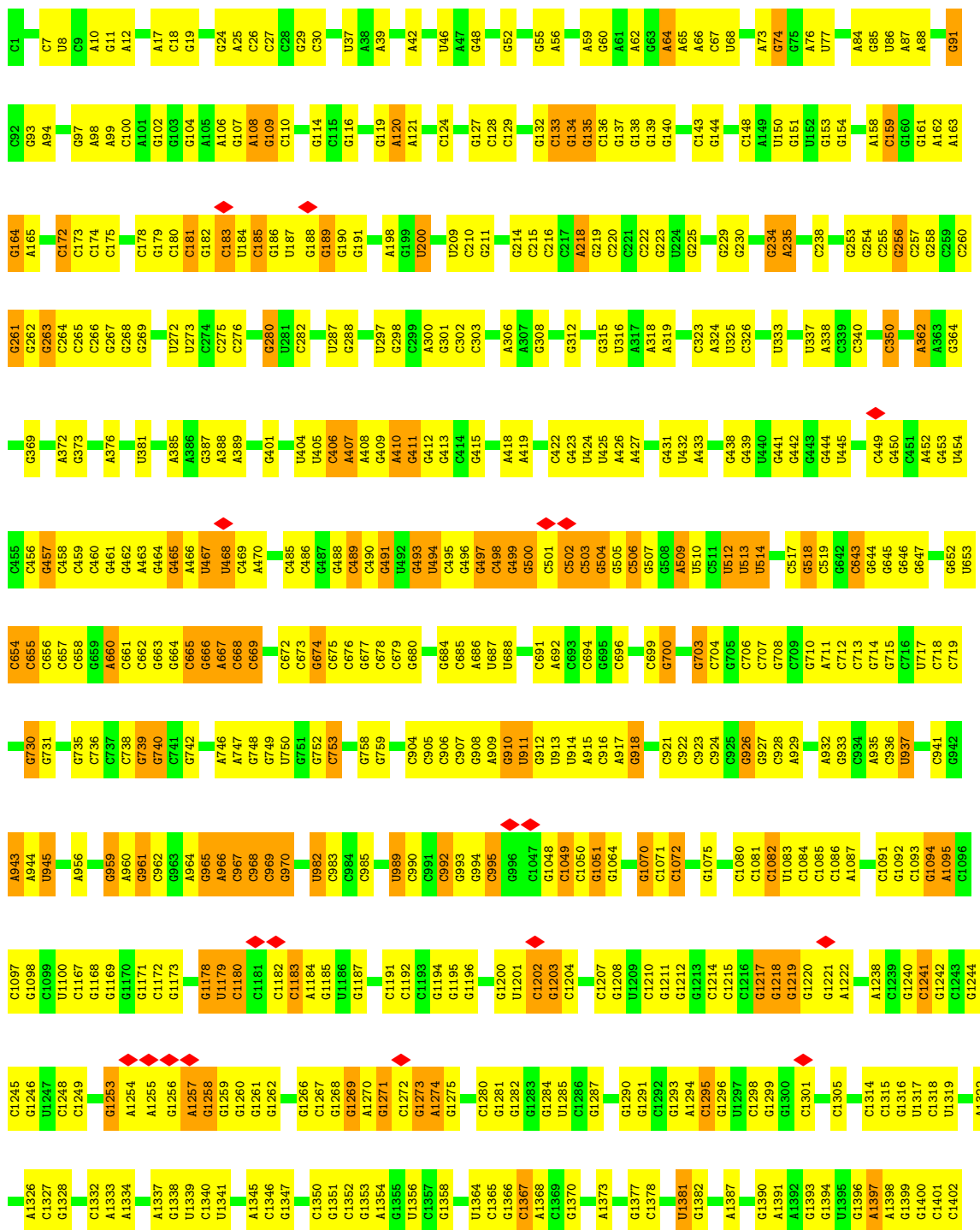
• Molecule 2: Serbp1

Chain CD:  55% 44%



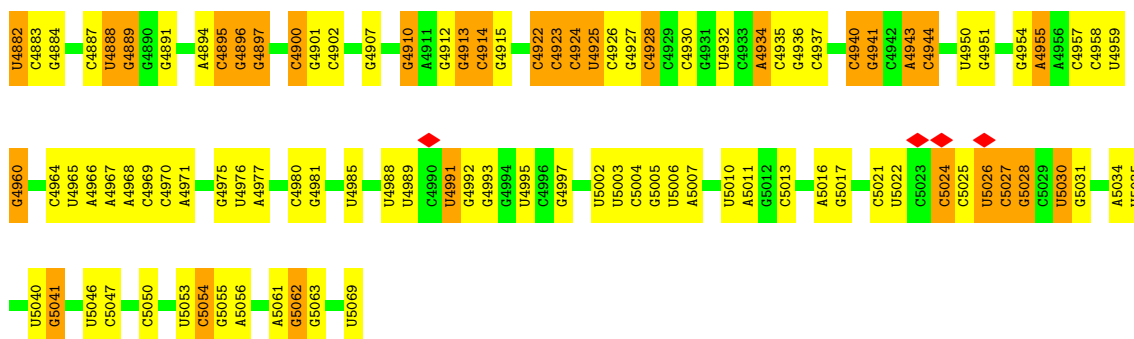
• Molecule 3: 28S rRNA

Chain L5:  51% 39% 10%



U2763	A2676	G2579	C2491	U2398	C2936	C2078	A1984	C1893	G1803	C1703	G1618	A1497	G1403
A2764	U2687	G2582	C2492	G2402	G2296	G2079	G1985	C1894	A1804	C1704	G1624	G1498	G1404
A2765	G2688	A2582	U2494	A2403	U2298	U2080	G1989	G1895	A1805	G1705	G1625	G1499	C1405
U2769	C2583	C2583	U2495	A2404	G2299	C2081	A1990	A1896	C1806	A1706	G1626	A1500	G1406
C2770	U2691	G2496	U2496	G2405	A2300	C2084	A1991	A1897	C1807	C1707	C1628	C1501	C1407
G2771	U2692	G2497	C2497	G2406	G2301	C2084	U1992	C1900	G1810	G1708	G1629	A1503	G1408
C2779	U2693	C2588	C2498	G2407	C2302	C2084	C1993	C1900	G1811	C1715	A1630	A1504	C1409
C2780	G2694	C2589	G2502	C2411	U2303	U2090	C1994	U1906	G1812	C1716	A1631	U1410	U1410
C2781	A2695	G2599	G2503	A2412	U2304	G2092	G1995	A1907	G1813	C1718	A1632	C1509	C1411
U2782	A2696	A2600	C2504	U2413	G2305	G2093	U1997	G1912	G1814	C1719	A1633	G1516	G1412
A2783	G2702	A2601	C2505	U2414	G2306	G2094	A1998	G1913	G1815	U1726	A1634	G1517	G1413
C2784	G2703	G2608	G2506	U2415	A2313	A2095	A1999	G1914	C1820	U1727	C1640	G1518	G1414
C2785	G2704	G2609	G2507	U2416	G2318	A2096	G2000	G1915	G1821	U1728	G1641	A1516	G1415
C2786	G2705	G2610	G2508	U2417	G2319	U2097	A2001	A1917	G1822	C1731	C1642	A1523	G1416
A2787	U2706	A2611	A2511	G2421	G2321	G2098	A2002	U1918	G1823	G1741	C1645	A1524	A1524
U2788	U2707	G2612	A2512	G2422	G2322	C2101	G2003	G1919	G1824	A1742	C1646	A1525	A1525
A2789	U2708	G2613	A2513	G2423	G2323	G2102	A2004	G1920	G1825	A1743	C1647	A1526	A1526
U2790	C2709	G2614	A2514	G2424	G2324	G2103	A2005	G1921	G1826	G1744	C1648	A1527	A1527
C2791	G2710	G2615	A2515	U2425	G2325	G2104	A2006	G1922	G1827	A1745	C1649	A1528	A1528
C2792	U2711	A2623	A2516	U2426	G2326	G2105	A2007	G1923	G1828	G1746	C1650	A1529	A1529
G2793	G2712	G2627	A2517	U2427	G2327	G2106	A2008	G1924	G1829	G1747	C1651	A1530	A1530
A2806	C2713	C2628	A2518	U2428	G2328	G2107	A2009	G1925	G1830	G1748	C1652	A1531	A1531
A2807	G2714	U2630	A2519	U2429	G2329	G2108	A2010	G1926	G1831	G1749	C1653	A1532	A1532
G2808	U2715	U2631	A2520	U2430	G2330	G2109	A2011	G1927	G1832	G1750	C1654	A1533	A1533
G2809	G2716	G2632	A2521	U2431	G2331	G2110	A2012	G1928	G1833	G1751	C1655	A1534	A1534
U2810	U2717	U2633	A2522	U2432	G2332	G2111	A2013	G1929	G1834	G1752	C1656	A1535	A1535
G2811	G2718	U2634	A2523	U2433	G2333	G2112	A2014	G1930	G1835	G1753	C1657	A1536	A1536
U2812	C2719	U2635	A2524	U2434	G2334	G2113	A2015	G1931	G1836	G1754	C1658	A1537	A1537
A2813	G2720	G2636	A2525	U2435	G2335	G2114	A2016	G1932	G1837	G1755	C1659	A1538	A1538
U2814	U2721	U2637	A2526	U2436	G2336	G2115	A2017	G1933	G1838	G1756	C1660	A1539	A1539
G2815	G2722	G2638	A2527	U2437	G2337	G2116	A2018	G1934	G1839	G1757	C1661	A1540	A1540
U2816	U2723	U2639	A2528	U2438	G2338	G2117	A2019	G1935	G1840	G1758	C1662	A1541	A1541
A2817	C2724	G2640	A2529	U2439	G2339	G2118	A2020	G1936	G1841	G1759	C1663	A1542	A1542
G2818	G2725	U2641	A2530	U2440	G2340	G2119	A2021	G1937	G1842	G1760	C1664	A1543	A1543
U2819	U2726	G2642	A2531	U2441	G2341	G2120	A2022	G1938	G1843	G1761	C1665	A1544	A1544
G2820	G2727	G2643	A2532	U2442	G2342	G2121	A2023	G1939	G1844	G1762	C1666	A1545	A1545
U2821	U2728	U2644	A2533	U2443	G2343	G2122	A2024	G1940	G1845	G1763	C1667	A1546	A1546
A2822	C2729	G2645	A2534	U2444	G2344	G2123	A2025	G1941	G1846	G1764	C1668	A1547	A1547
U2823	G2730	U2646	A2535	U2445	G2345	G2124	A2026	G1942	G1847	G1765	C1669	A1548	A1548
U2824	C2731	G2647	A2536	U2446	G2346	G2125	A2027	G1943	G1848	G1766	C1670	A1549	A1549
G2825	G2732	G2648	A2537	U2447	G2347	G2126	A2028	G1944	G1849	G1767	C1671	A1550	A1550
U2826	U2733	U2649	A2538	U2448	G2348	G2127	A2029	G1945	G1850	G1768	C1672	A1551	A1551
G2827	C2734	G2650	A2539	U2449	G2349	G2128	A2030	G1946	G1851	G1769	C1673	A1552	A1552
A2828	U2735	U2651	A2540	U2450	G2350	G2129	A2031	G1947	G1852	G1770	C1674	A1553	A1553
U2829	G2736	G2652	A2541	U2451	G2351	G2130	A2032	G1948	G1853	G1771	C1675	A1554	A1554
A2830	C2737	G2653	A2542	U2452	G2352	G2131	A2033	G1949	G1854	G1772	C1676	A1555	A1555
G2831	U2738	U2654	A2543	U2453	G2353	G2132	A2034	G1950	G1855	G1773	C1677	A1556	A1556
U2832	C2739	G2655	A2544	U2454	G2354	G2133	A2035	G1951	G1856	G1774	C1678	A1557	A1557
A2833	G2740	U2656	A2545	U2455	G2355	G2134	A2036	G1952	G1857	G1775	C1679	A1558	A1558
U2834	U2741	G2657	A2546	U2456	G2356	G2135	A2037	G1953	G1858	G1776	C1680	A1559	A1559
A2835	C2742	G2658	A2547	U2457	G2357	G2136	A2038	G1954	G1859	G1777	C1681	A1560	A1560
U2836	G2743	U2659	A2548	U2458	G2358	G2137	A2039	G1955	G1860	G1778	C1682	A1561	A1561
A2837	C2744	G2660	A2549	U2459	G2359	G2138	A2040	G1956	G1861	G1779	C1683	A1562	A1562
U2838	U2745	U2661	A2550	U2460	G2360	G2139	A2041	G1957	G1862	G1780	C1684	A1563	A1563
A2839	G2746	G2662	A2551	U2461	G2361	G2140	A2042	G1958	G1863	G1781	C1685	A1564	A1564
U2840	C2747	G2663	A2552	U2462	G2362	G2141	A2043	G1959	G1864	G1782	C1686	A1565	A1565
G2841	U2748	U2664	A2553	U2463	G2363	G2142	A2044	G1960	G1865	G1783	C1687	A1566	A1566
U2842	C2749	G2665	A2554	U2464	G2364	G2143	A2045	G1961	G1866	G1784	C1688	A1567	A1567
A2843	G2750	G2666	A2555	U2465	G2365	G2144	A2046	G1962	G1867	G1785	C1689	A1568	A1568
U2844	U2751	U2667	A2556	U2466	G2366	G2145	A2047	G1963	G1868	G1786	C1690	A1569	A1569
A2845	C2752	G2668	A2557	U2467	G2367	G2146	A2048	G1964	G1869	G1787	C1691	A1570	A1570
G2846	U2753	U2669	A2558	U2468	G2368	G2147	A2049	G1965	G1870	G1788	C1692	A1571	A1571
U2847	C2754	G2670	A2559	U2469	G2369	G2148	A2050	G1966	G1871	G1789	C1693	A1572	A1572
A2848	G2755	U2671	A2560	U2470	G2370	G2149	A2051	G1967	G1872	G1790	C1694	A1573	A1573
G2849	U2756	U2672	A2561	U2471	G2371	G2150	A2052	G1968	G1873	G1791	C1695	A1574	A1574
U2850	C2757	G2673	A2562	U2472	G2372	G2151	A2053	G1969	G1874	G1792	C1696	A1575	A1575
A2851	G2758	U2674	A2563	U2473	G2373	G2152	A2054	G1970	G1875	G1793	C1697	A1576	A1576
U2852	C2759	G2675	A2564	U2474	G2374	G2153	A2055	G1971	G1876	G1794	C1698	A1577	A1577
G2853	U2760	U2676	A2565	U2475	G2375	G2154	A2056	G1972	G1877	G1795	C1699	A1578	A1578
A2854	C2761	G2677	A2566	U2476	G2376	G2155	A2057	G1973	G1878	G1796	C1700	A1579	A1579
U2855	U2762	U2678	A2567	U2477	G2377	G2156	A2058	G1974	G1879	G1797	C1701	A1580	A1580
G2856	C2763	G2679	A2568	U2478	G2378	G2157	A2059	G1975	G1880	G1798	C1702	A1581	A1581
U2857	U2764	U2680	A2569	U2479	G2379	G2158	A2060	G1976	G1881	G1799	C1703	A1582	A1582
A2858	C2765	G2681	A2570	U2480	G2380	G2159	A2061	G1977	G1882	G1800	C1704	A1583	A1583
U2859	U2766	U2682	A2571	U2481	G2381	G2160	A2062	G1978	G1883	G1801	C1705	A1584	A1584
G2860	C2767	G2683	A2572	U2482	G2382	G2161	A2063	G1979	G1884	G1802	C1706	A1585	A1585
A2861	U2768	U2684	A2573	U2483	G2383	G2162	A2064	G1980	G1885	G1803	C1707	A1586	A1586
U2862	C2769	G2685	A2574	U2484	G2384	G2163	A2065	G1981	G1886	G1804	C1708	A1587	A1587
A2863	U2770	U2686	A2575	U2485	G2385	G2164	A2066	G1982	G1887	G1805	C1709	A1588	A1588
G2864	C2771	G2687	A2576	U2486	G2386	G2165	A2067	G1983	G1888	G1806	C1710	A1589	A1589
U2865	U2772	U2688	A2577	U2487	G2387	G2166	A2068	G1984	G1889	G1807	C1711	A1590	A1590
A2866	C2773	G2689	A2578	U2488	G2388	G2167	A2069	G1985	G1890	G1808	C1712	A1591	A1591
U2867	U2774	U2690	A2579	U2489	G2389	G2168	A2070	G1986	G1891	G1809	C1713	A1592	A1592
G2868	C2775	G2691	A2580	U2490	G2390	G2169	A2071	G1987	G1892	G1810	C1714	A1593	A1593
A2869	U2776	U2692	A2581	U2491	G2391	G2170	A2072	G1988	G1893	G1811	C1715	A1594	A1594
U2870	C2777	G2693	A2582	U2492	G2392	G2171	A2073	G1989	G1894	G1812	C1716	A1595	A1595
A2871	U2778	U2694	A2583	U2493	G2393	G2172	A2074	G1990	G1895	G1813	C1717	A1596	A1596
G2872	C2779	G2695	A2584	U2494	G2394	G2173	A2075	G1991	G1896	G1814	C1718	A1597	A1597
U2873	U2780	U2696	A2585	U2495	G2395	G2174	A2076	G1992	G1897	G1815	C1719	A1598	A1598
A2874	C2781	G2697	A2586	U2496	G2396	G2175	A2077	G1993	G1898	G1816	C1720	A1599	A1599
U2875	U2782	U2698	A2587	U2497	G2397	G2176	A2078	G1994	G1899	G1817	C1721	A1600	A1600
G2876	C2783	G2699	A2588	U2498	G2398	G2177	A2079	G1995	G1900	G1818	C1722	A1601	A1601
A2877	U2784	U2700	A2589	U2499	G2399	G2178	A2080	G1996					

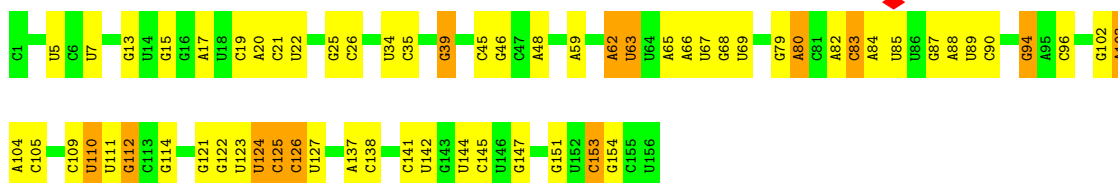
C4710	C4711	C4716	C4717	C4718	C4719	A4724	A4727	A4728	A4729	C4730	C4731	A4734	A4735	C4736	C4737	C4741	C4742	C4743	A4744	C4745	C4754	C4757	C4758	C4759	C4760	A4761	A4762	C4763	A4764	C4765	C4769	C4770	C4771	C4772	C4773	C4774	C4775	C4776	C4860	C4861	C4870	C4871	C4875	C4876	C4877	C4880	C4881	
G4600	U4601	A4605	A4610	A4611	G4612	G4617	U4620	U4728	C4621	A4622	A4623	G4627	A4630	A4631	G4632	A4635	U4636	G4637	U4638	A4644	G4645	G4646	G4647	A4648	G4652	A4656	A4657	C4670	C4671	A4672	G4680	A4681	U4682	C4685	G4686	C4687	C4688	C4689	C4694	C4695	U4689	A4700	C4704	A4707	A4708	U4709		
A4513	G4516	A4517	A4518	A4519	A4520	U4521	A4522	A4523	A4524	A4525	U4526	U4531	U4532	C4537	G4538	G4541	A4544	G4545	A4548	G4549	G4550	G4554	U4555	C4560	U4563	C4565	U4566	G4567	C4570	A4571	G4572	G4573	U4574	G4575	G4578	U4579	C4582	C4583	A4584	U4585	A4586	G4589	A4590	U4591	C4592			
U4406	G4407	C4413	C4421	U4422	U4423	G4424	U4431	U4432	C4433	C4434	U4438	U4442	U4446	C4447	U4448	U4449	U4450	C4451	U4452	C4453	G4454	U4457	C4458	U4459	U4460	U4464	U4465	C4466	A4467	G4472	A4473	A4474	A4475	C4476	A4477	G4478	A4488	U4492	U4500	C4506	A4507	C4508	U4512					
G4225	G4228	U4229	U4232	A4233	U4234	U4235	G4236	C4237	G4238	A4239	G4240	C4243	A4244	G4245	G4246	G4247	A4248	G4249	A4251	G4254	A4255	A4256	A4257	C4258	U4260	C4261	U4262	G4263	G4264	U4265	A4268	A4273	A4274	G4275	A4281	U4290	G4291	A4292	U4293	U4294	U4295	U4296	G4297	U4298	U4299	U4300	U4301	U4302
A4304	G4305	C4314	A4315	C4319	U4320	U4321	G4322	A4325	A4326	C4327	G4330	C4331	C4332	A4336	C4337	C4342	U4343	U4344	C4345	U4346	C4349	U4354	A4363	G4364	C4365	G4373	G4377	A4378	A4379	A4380	A4385	C4386	C4387	A4388	A4389	C4391	G4392	U4393	U4394	U4395	U4399	G4400	G4401	G4405				
U4406	G4407	C4413	C4421	U4422	U4423	G4424	U4431	U4432	C4433	C4434	U4438	U4442	U4446	C4447	U4448	U4449	U4450	C4451	U4452	C4453	G4454	U4457	C4458	U4459	U4460	U4464	U4465	C4466	A4467	G4472	A4473	A4474	A4475	C4476	A4477	G4478	A4488	U4492	U4500	C4506	A4507	C4508	U4512					
A4513	G4516	A4517	A4518	A4519	A4520	U4521	A4522	A4523	A4524	A4525	U4526	U4531	U4532	C4537	G4538	G4541	A4544	G4545	A4548	G4549	G4550	G4554	U4555	C4560	U4563	C4565	U4566	G4567	C4570	A4571	G4572	G4573	U4574	G4575	G4578	U4579	C4582	C4583	A4584	U4585	A4586	G4589	A4590	U4591	C4592			
G4600	U4601	A4605	A4610	A4611	G4612	G4617	U4620	U4728	C4621	A4622	A4623	G4627	A4630	A4631	G4632	A4635	U4636	G4637	U4638	A4644	G4645	G4646	G4647	A4648	G4652	A4656	A4657	C4670	C4671	A4672	G4680	A4681	U4682	C4685	G4686	C4687	C4688	C4689	C4694	C4695	U4689	A4700	C4704	A4707	A4708	U4709		
C4710	C4711	C4716	C4717	C4718	C4719	A4724	A4727	A4728	A4729	C4730	C4731	A4734	A4735	C4736	C4737	C4741	C4742	C4743	A4744	C4745	C4754	C4757	C4758	C4759	C4760	A4761	A4762	C4763	A4764	C4765	C4769	C4770	C4771	C4772	C4773	C4774	C4775	C4776	C4860	C4861	C4870	C4871	C4875	C4876	C4877	C4880	C4881	



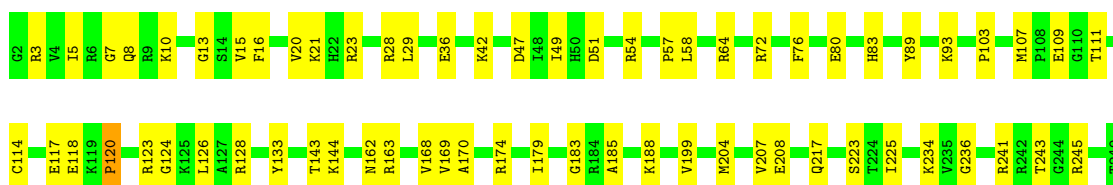
• Molecule 4: 5S rRNA [Homo sapiens]



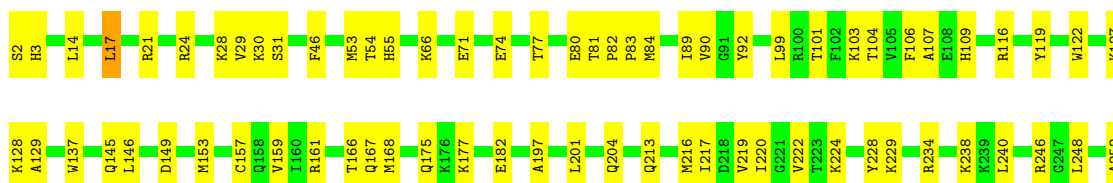
• Molecule 5: 5.8S rRNA [Homo sapiens]

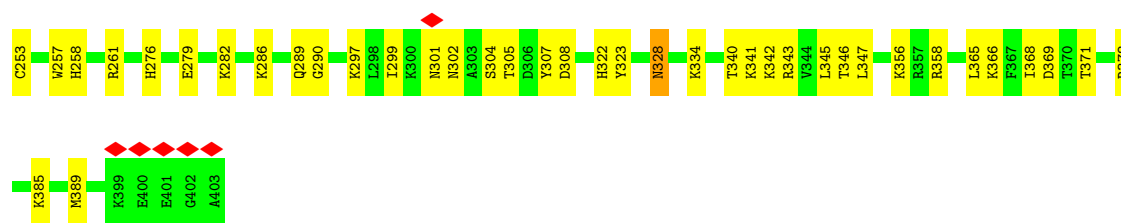


• Molecule 6: 60S ribosomal protein L8

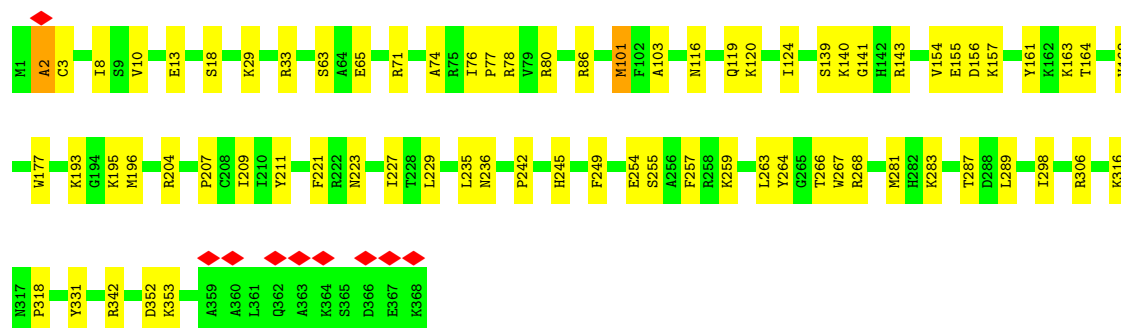
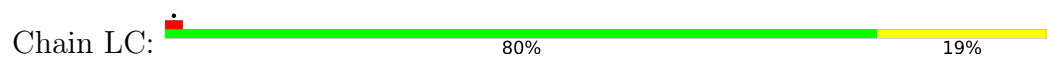


• Molecule 7: Large ribosomal subunit protein uL3

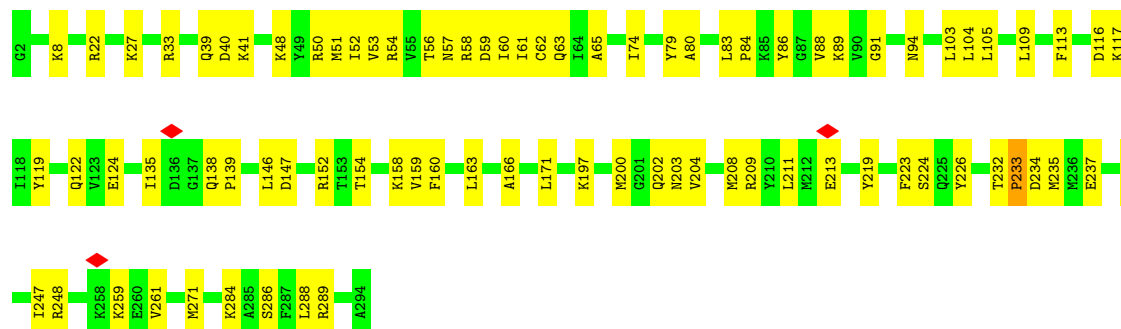
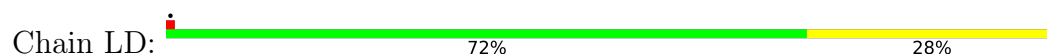




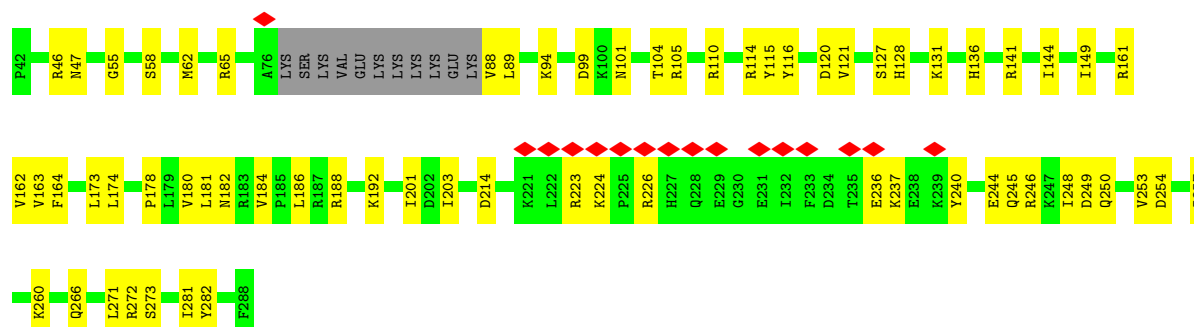
• Molecule 8: 60S ribosomal protein L4



• Molecule 9: Large ribosomal subunit protein uL18

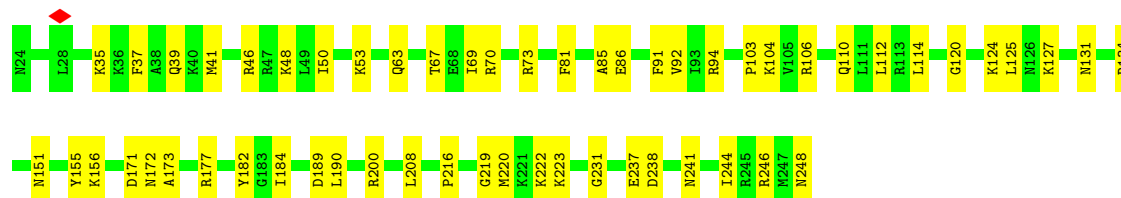


• Molecule 10: Large ribosomal subunit protein eL6



- Molecule 11: 60S ribosomal protein L7

Chain LF:  75% 25%



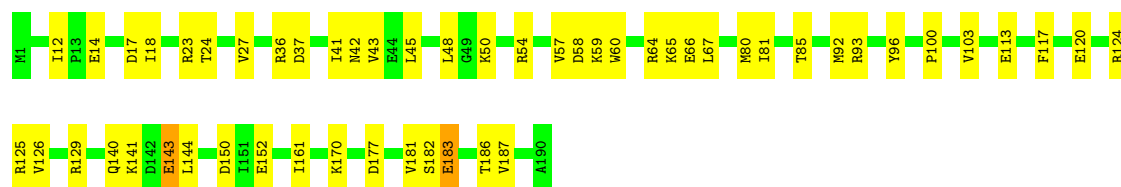
- Molecule 12: 60S ribosomal protein L7a

Chain LG:  7% 79% 21%



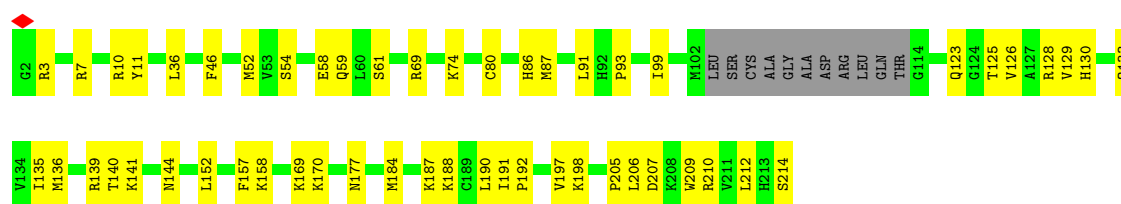
- Molecule 13: 60S ribosomal protein L9

Chain LH:  72% 27%



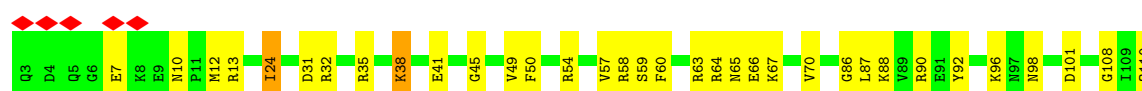
- Molecule 14: Ribosomal protein uL16-like

Chain LI:  70% 25% 5%



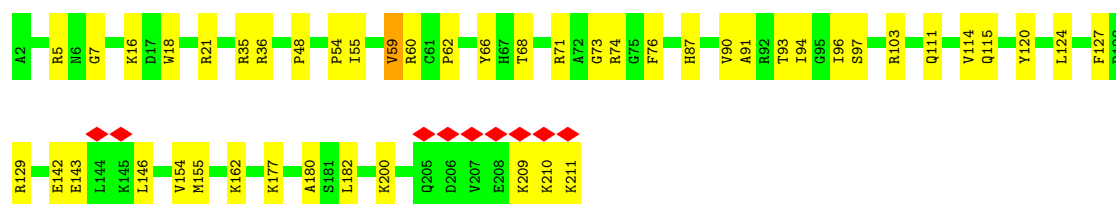
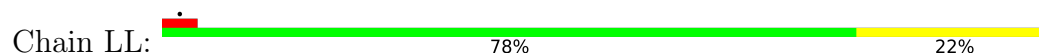
- Molecule 15: 60S ribosomal protein L11

Chain LJ:  5% 68% 31%

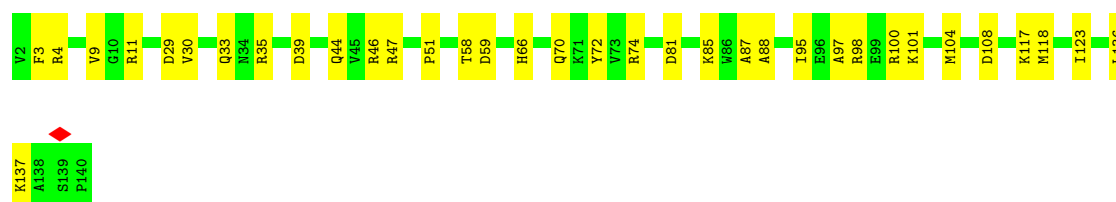
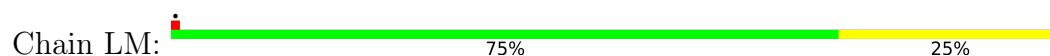




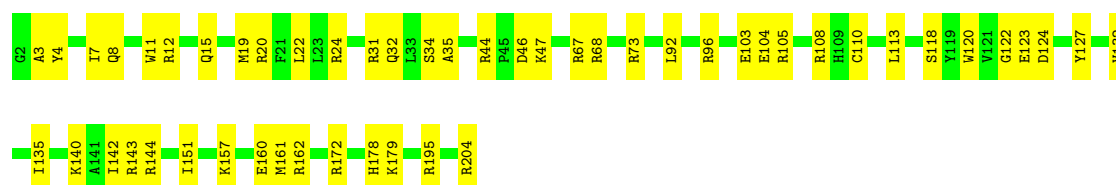
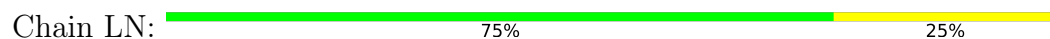
- Molecule 16: Large ribosomal subunit protein eL13



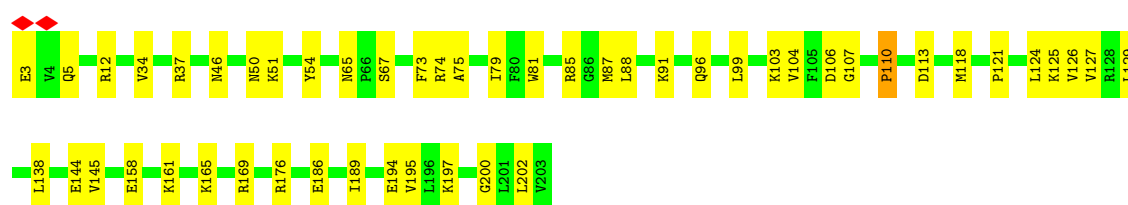
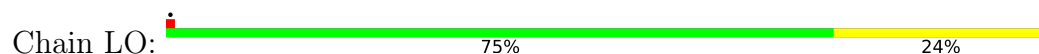
- Molecule 17: 60S ribosomal protein L14



- Molecule 18: 60S ribosomal protein L15



- Molecule 19: 60S ribosomal protein L13a



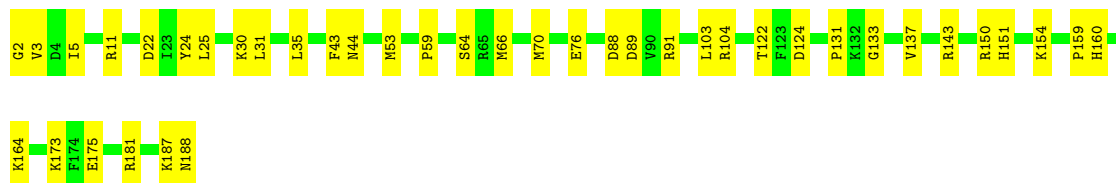
- Molecule 20: 60S ribosomal protein L17





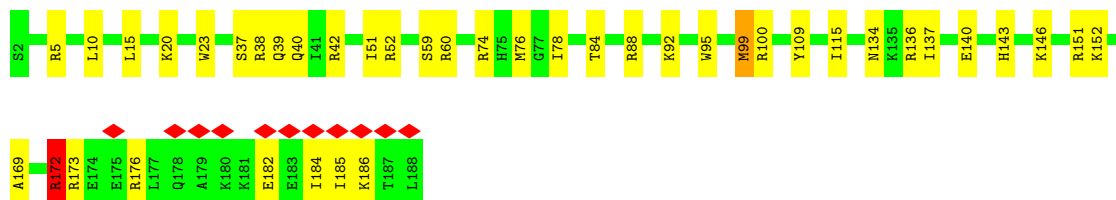
- Molecule 21: 60S ribosomal protein L18

Chain LQ: 79% 21%



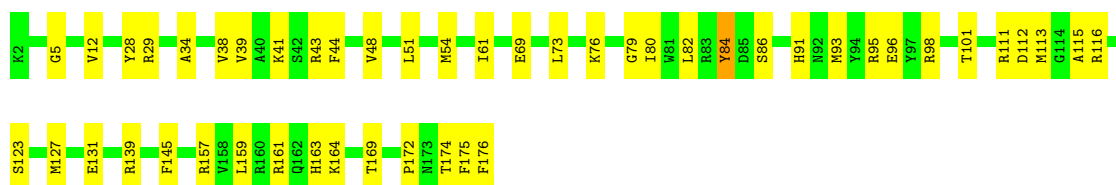
- Molecule 22: 60S ribosomal protein L19

Chain LR: 6% 78% 21% ..



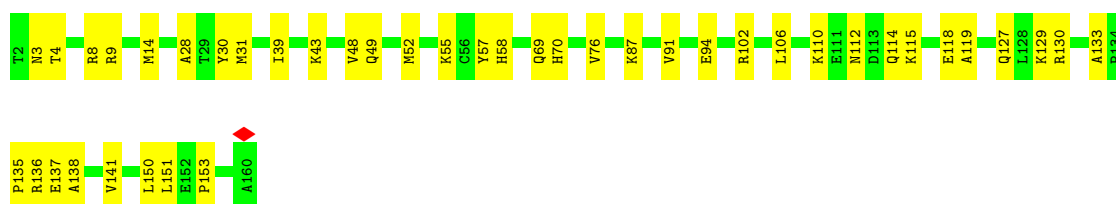
- Molecule 23: 60S ribosomal protein L18a

Chain LS: 73% 27% .

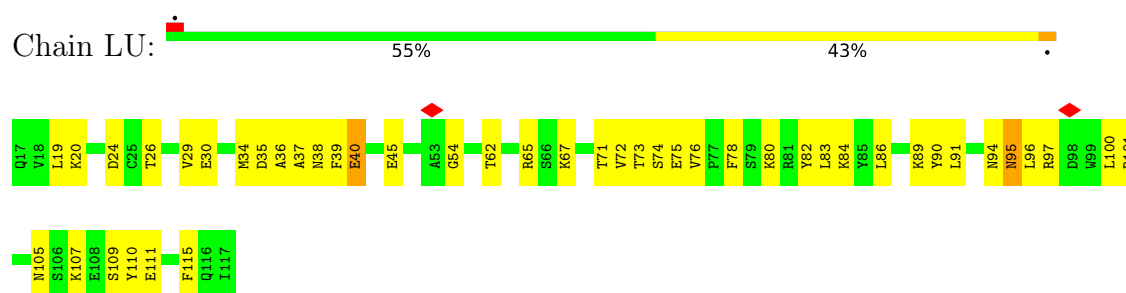


- Molecule 24: 60S ribosomal protein L21

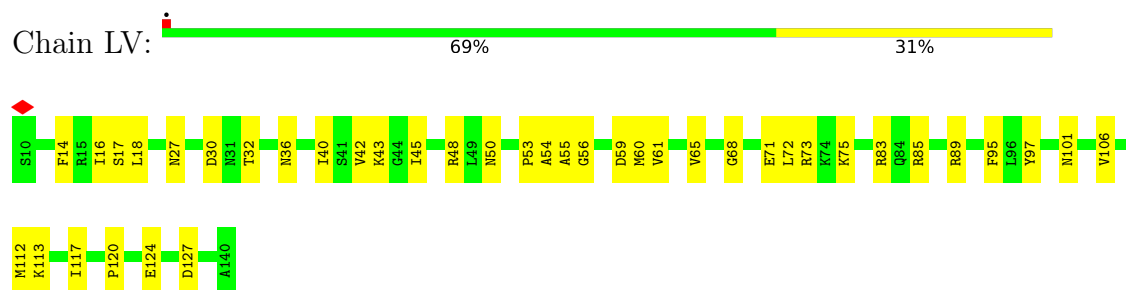
Chain LT: 74% 26%



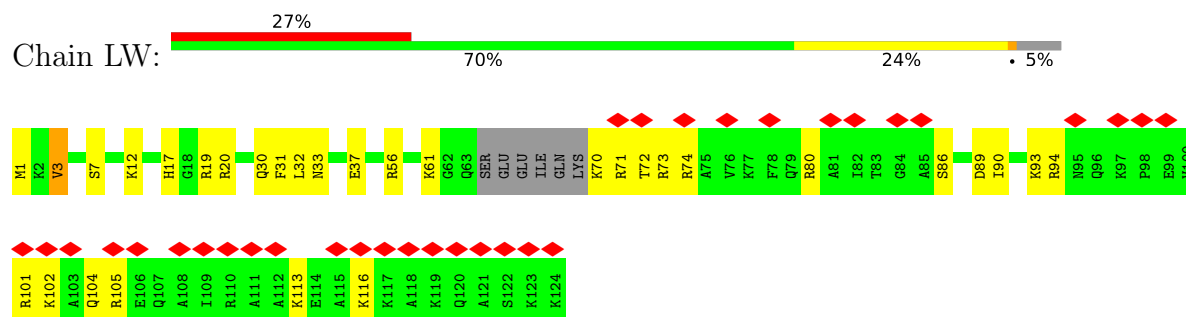
- Molecule 25: Heparin-binding protein HBp15



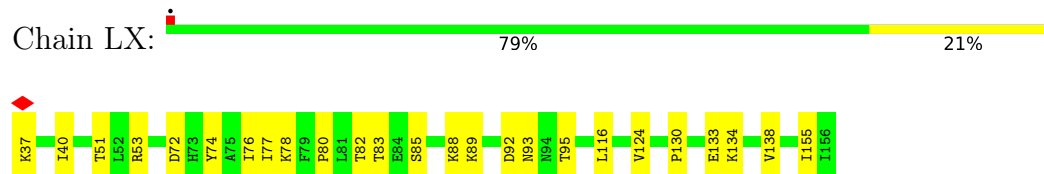
- Molecule 26: 60S ribosomal protein L23



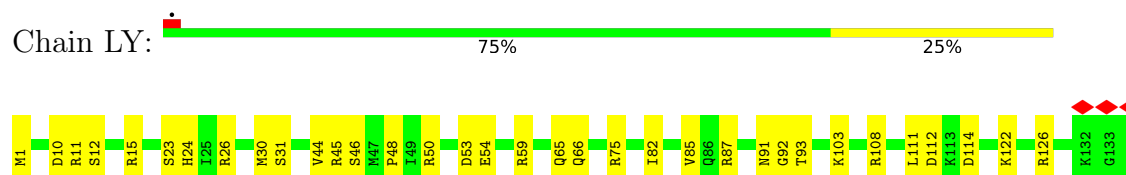
- Molecule 27: Ribosomal protein L24



- Molecule 28: 60S ribosomal protein L23a

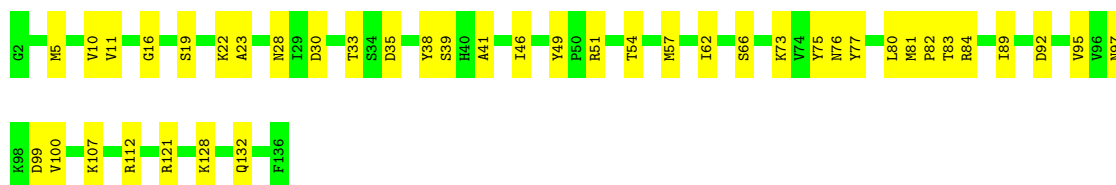


- Molecule 29: 60S ribosomal protein L26



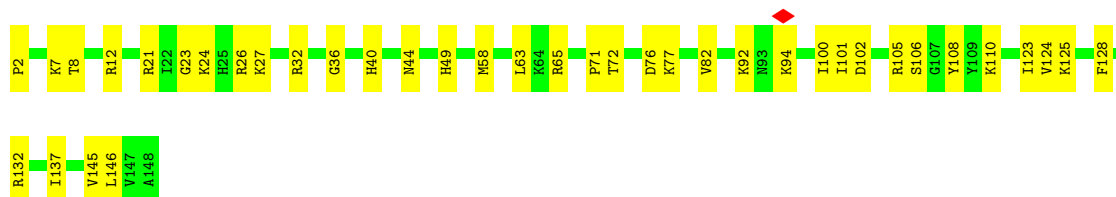
- Molecule 30: 60S ribosomal protein L27





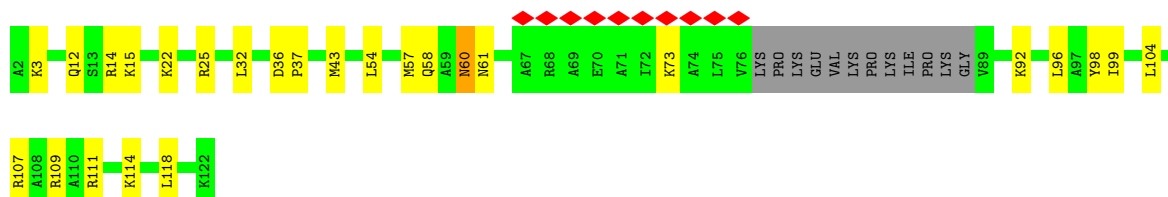
- Molecule 31: 60S ribosomal protein L27a

Chain La: 73% 27%



- Molecule 32: Large ribosomal subunit protein eL29

Chain Lb: 8% 69% 21% 10%



- Molecule 33: 60S ribosomal protein L30

Chain Lc: 67% 33%



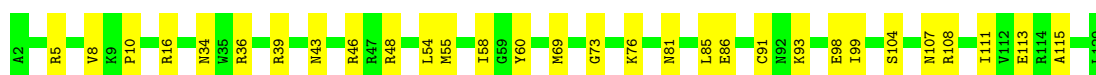
- Molecule 34: 60S ribosomal protein L31

Chain Ld: 81% 19%



- Molecule 35: 60S ribosomal protein L32

Chain Le: 77% 23%



- Molecule 36: 60S ribosomal protein L35a

Chain Lf:  75% 23%



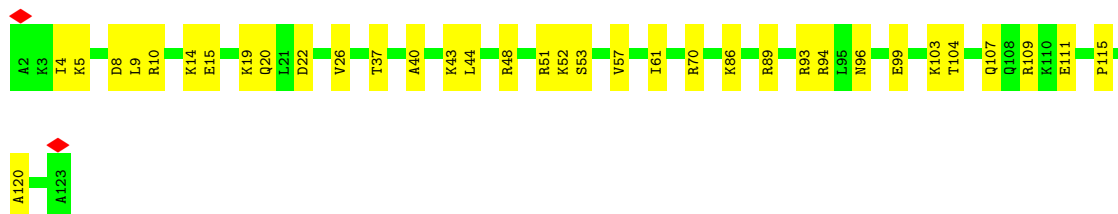
- Molecule 37: 60S ribosomal protein L34

Chain Lg:  83% 17%



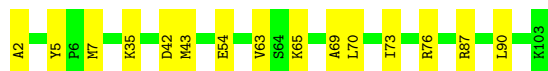
- Molecule 38: 60S ribosomal protein L35

Chain Lh:  71% 29%



- Molecule 39: 60S ribosomal protein L36

Chain Li:  85% 15%



- Molecule 40: 60S ribosomal protein L37

Chain Lj:  66% 33%



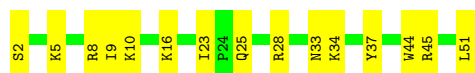
- Molecule 41: 60S ribosomal protein L38

Chain Lk:  68% 32%



- Molecule 42: 60S ribosomal protein L39

Chain Ll:  70% 30%



- Molecule 43: Large ribosomal subunit protein eL40

Chain Lm:  75% 25%



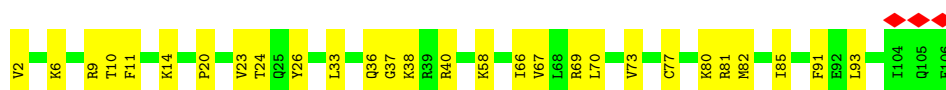
- Molecule 44: 60S ribosomal protein L41

Chain Ln:  79% 21%



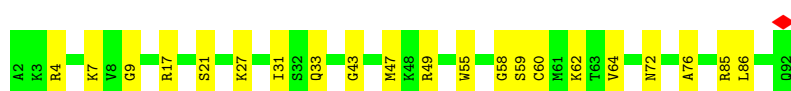
- Molecule 45: 60S ribosomal protein L36a

Chain Lo:  73% 27%



- Molecule 46: 60S ribosomal protein L37a

Chain Lp:  77% 23%



- Molecule 47: 60S ribosomal protein L28

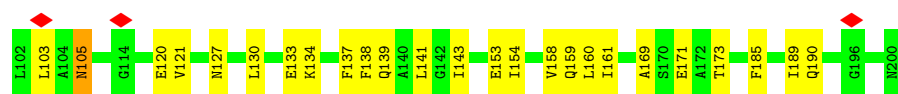
Chain Lr:  78% 22%



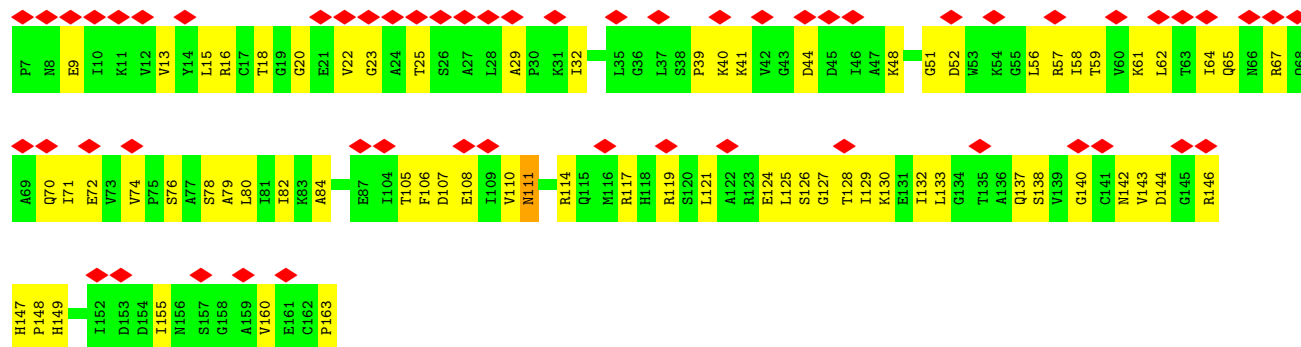
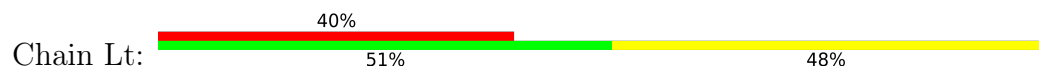
- Molecule 48: 60S acidic ribosomal protein P0

Chain Ls:  68% 31%

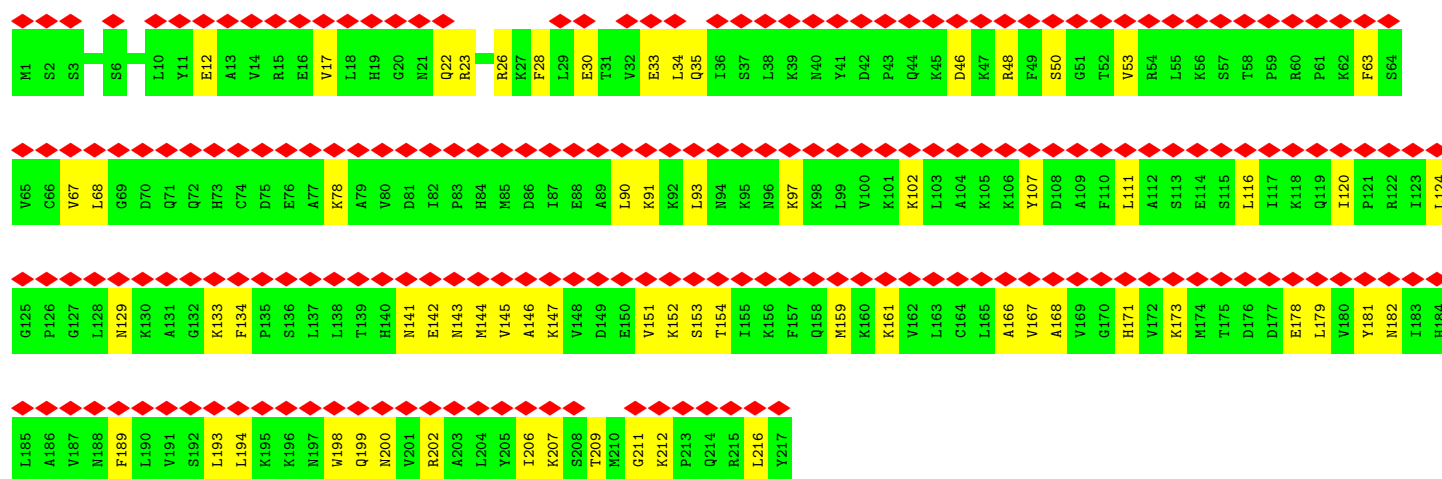
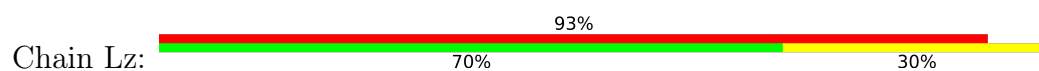




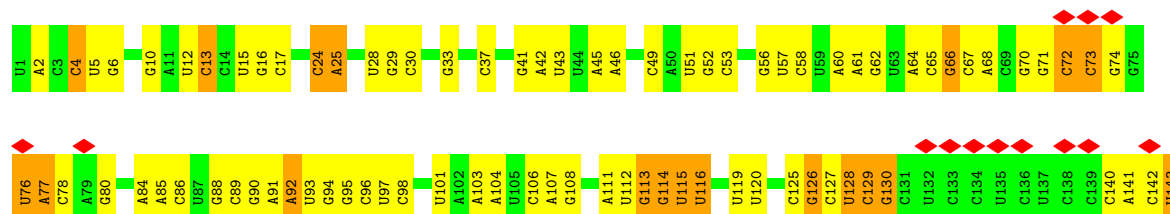
- Molecule 49: 60S ribosomal protein L12 [Homo sapiens]



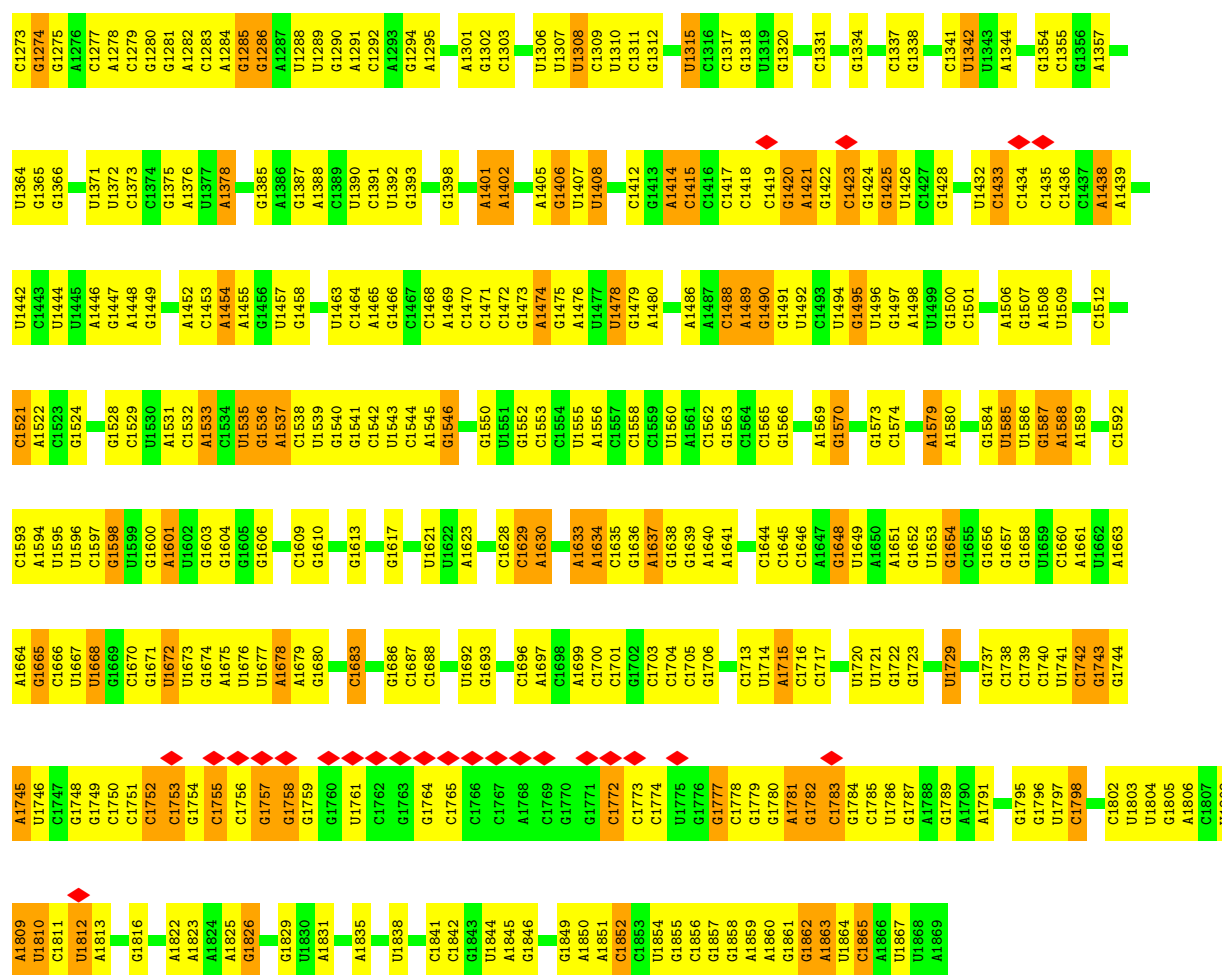
- Molecule 50: 60S ribosomal protein L10a

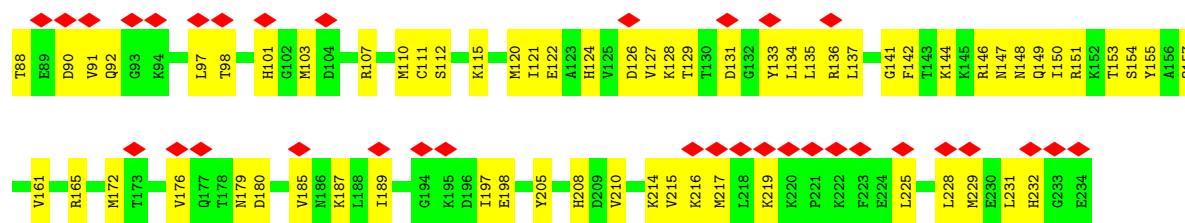


- Molecule 51: 18S rRNA

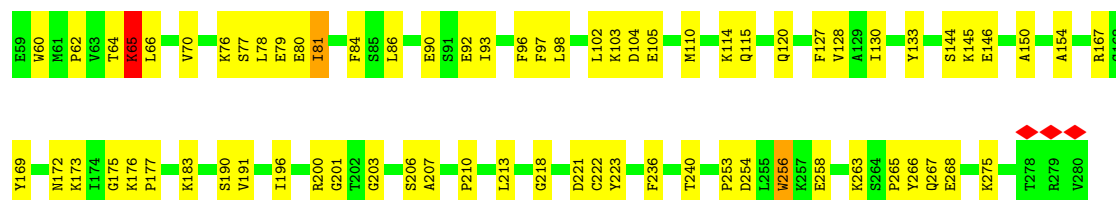


A1204	A1122	U1046	G975	U906	G932	G998	G623	C548	A485	A414	G338	G213	U144
G1207	C1123	C1047	G978	G907	C833	C730	G626	C849	A486	A415	A339	U214	G145
A1208	C1124	G1048	C979	A908	C834	G731	U627	U551	U488	G419	A350	U215	G146
A1209	C1125	G1051	A909	G909	C835	U732	A628	U553	C491	G421	C341	U216	A147
G1210	C1126	A1052	A981	G913	G836	C733	A629	A554	G492	A426	U345	U217	U148
G1211	C1127	A1052	A982	U914	A837	C734	U630	A555	C493	A427	C346	U218	A149
G1212	C1128	A1055	A983	U915	G838	C737	U631	A556	C494	A428	U347	U219	A150
G1213	C1129	A1060	C984	G916	C839	C738	G635	U557	C495	U428	C348	U220	C151
C1214	G1130	A1061	G985	U917	G840	C738	A634	U558	C496	U429	A348	U222	G153
C1215	C1131	U917	G841	U918	G842	U747	C638	A560	C497	G431	C350	U224	U154
A1216	C1132	U918	C842	U919	C843	U748	C639	A561	C498	G432	U352	G288	U157
A1217	C1133	A919	G846	A920	A847	U749	C640	U562	C499	A433	C353	G289	A158
C1218	C1134	C1063	G847	A921	G847	C750	A641	G563	C501	A434	C356	G290	A159
C1219	C1135	U1066	C851	G921	C851	C751	U642	A564	C502	A435	C356	G291	U160
A1220	C1138	U1066	G852	A922	G852	C752	A643	C567	C503	G436	C356	A292	U161
G1221	G1142	G1071	G855	G923	G855	C753	G644	C568	G504	G437	A360	C293	C162
G1222	C1143	G925	C856	G924	C856	C785	U647	C569	G505	C441	U361	U294	U163
A1223	A1143	A926	U857	G925	U857	C786	A648	C570	G506	C442	C362	C295	A164
G1224	A1144	U1074	A858	A926	A858	G787	U648	U571	G507	C443	A363	U296	G165
U1225	A1145	C1074	A859	G927	A859	U571	U648	U572	G508	C444	A364	A297	A166
G1226	C1146	A1080	A861	G928	A861	G788	U651	U573	G509	G445	C365	G298	G167
G1227	C1147	U1002	A862	G929	A862	G789	U652	U574	G510	G446	U366	A299	C168
A1228	A1148	U1081	U863	C931	U863	C790	U653	A575	U511	A447	U367	U300	U169
A1082	C1082	C931	U864	G932	U864	C791	A862	A576	A512	A448	U368	A301	A170
C1230	A1083	G932	A865	G933	A865	C792	G656	C576	A513	A449	C369	A302	A171
C1231	C1085	G934	A866	G934	A866	C793	G657	U580	A514	G450	C370	C303	U172
U1232	A1086	A866	A867	G935	A867	G793	G658	U581	A515	C451	A371	C304	A173
G1233	U1087	G936	C968	G936	C968	C797	G659	U582	A516	G452	U372	U305	C179
C1237	U1088	U939	A870	U940	A870	C798	G660	U583	A517	G453	G373	C306	G180
A1240	G1092	U940	U871	C941	U871	U799	U661	U584	A518	C454	G374	G307	U189
A1241	A1093	G941	U872	C942	A872	U800	G662	U585	A519	C455	U375	G308	A181
U1242	C1094	G942	A873	G943	A873	U801	A664	G586	A520	C456	A376	G309	C182
U1243	C1095	U943	G874	U944	G874	U802	A665	U587	A521	C457	U377	C310	
U1244	U1015	U944	C974	A944	C974	U803	A666	U588	A522	A460	U378	C311	C186
G1245	U1016	U945	C975	U945	C975	U804	A667	U589	A523	C458	C379	G312	G187
U1248	C1098	U946	C976	U946	C976	U805	A668	G590	A524	A461	G380	A313	C188
C1249	G1099	G947	C977	U947	C977	U806	A669	U591	A525	A462	C381	G316	U197
A1251	U1101	C948	C978	U948	C978	U807	A670	U592	A526	A463	C382	C317	G189
C1252	C1102	C949	C979	C949	C979	U808	A671	U593	A527	A464	C383	C318	G190
A1253	C1103	G949	G880	G949	G880	A809	A672	U594	A528	A465	U384	C319	A191
C1253	U1022	G952	G881	G952	G881	A810	G673	U595	A529	A466	C385	G320	C196
A1253	A1023	C953	U882	C953	U882	A811	G677	U596	A530	A467	C386	C321	U198
G1256	A1027	U954	U883	U954	U883	U814	U681	G601	A531	A468	C387	C322	C199
G1257	A1028	A955	U884	U955	U884	U815	U682	G602	A532	A469	C388	C323	G200
A1258	G1029	G956	U885	G956	U885	U816	U683	G603	A533	A470	U389	C324	C201
A1259	A1030	A957	G891	G957	G891	G817	G684	C803	A534	A471	A389	C325	G202
A1260	A1031	G958	U892	G958	U892	G818	U685	A536	A535	A472	C390	G326	U199
C1261	C1032	G959	U893	G959	U893	G819	U686	U609	A536	A473	C391	C327	G203
C1262	U1113	A962	G894	G962	G894	U820	U688	G610	C537	A474	C392	C328	G204
U1263	A1036	A963	G895	A963	G895	U821	U689	G611	C538	A475	U393	G329	G205
C1264	G1037	U963	U896	U963	U896	U822	G690	G612	U540	A476	U394	G330	G206
G1268	U1038	G970	U897	G970	U897	U823	G691	G613	U541	A477	G395	C331	G207
U1201	C1039	G971	U898	G971	U898	C824	G692	G614	U542	A478	U396	G332	G208
C1271	C1118	A1119	A925	A925	A925	A826	G693	G615	U543	A479	G407	G333	A209
U1202	G1040	A972	C900	A972	C900	A827	G694	A616	C543	G480	A408	G334	U210
G1203	U1045	C974	G902	A972	G902	G828	G695	G617	C544	G481	C409	C335	G211
			A903	G902	A903	G829	G696	G620	C545	G482	C409	C335	G212
			G831	G831	G831	G831	G697	G621	C546	A484	C409	C335	G212

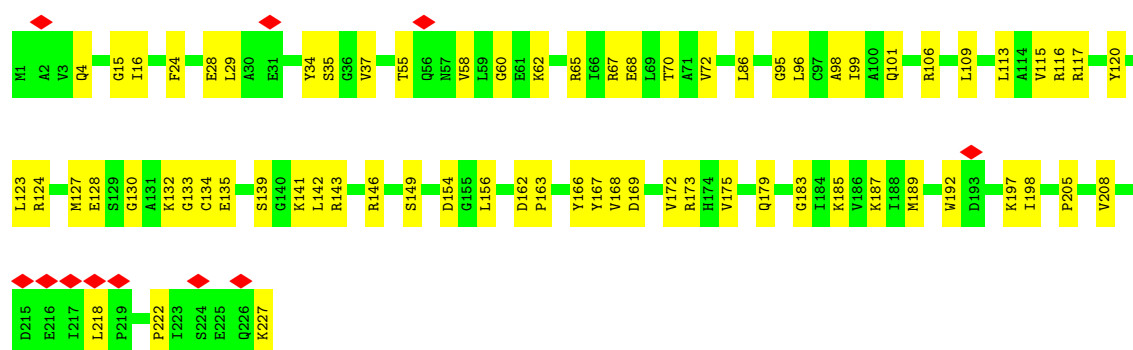




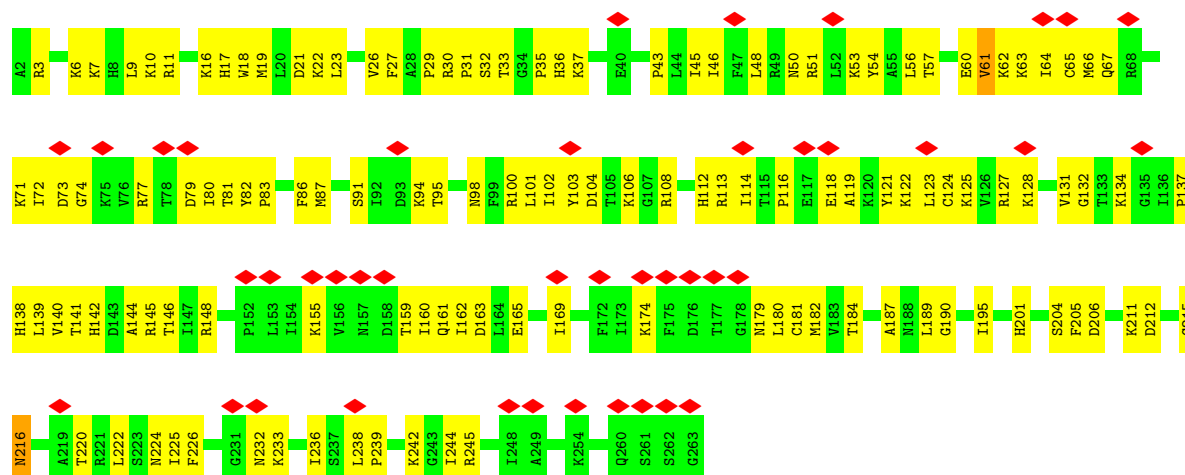
• Molecule 54: 40S ribosomal protein S2



• Molecule 55: Small ribosomal subunit protein uS3

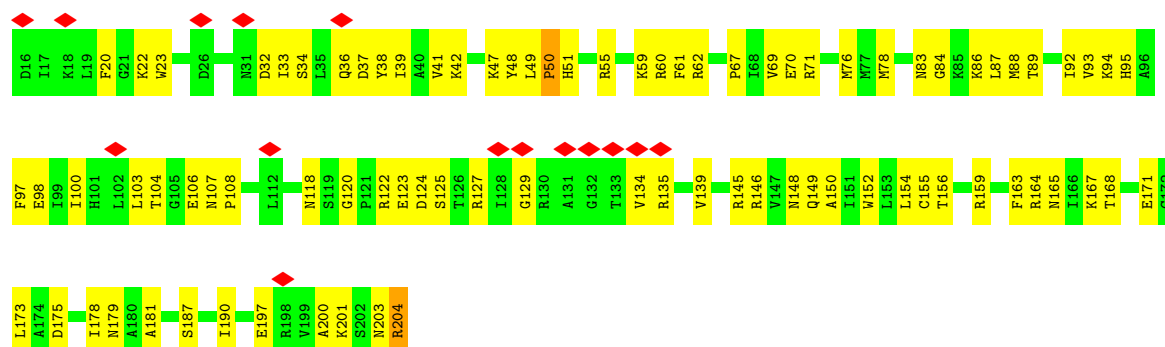


• Molecule 56: Small ribosomal subunit protein eS4, X isoform



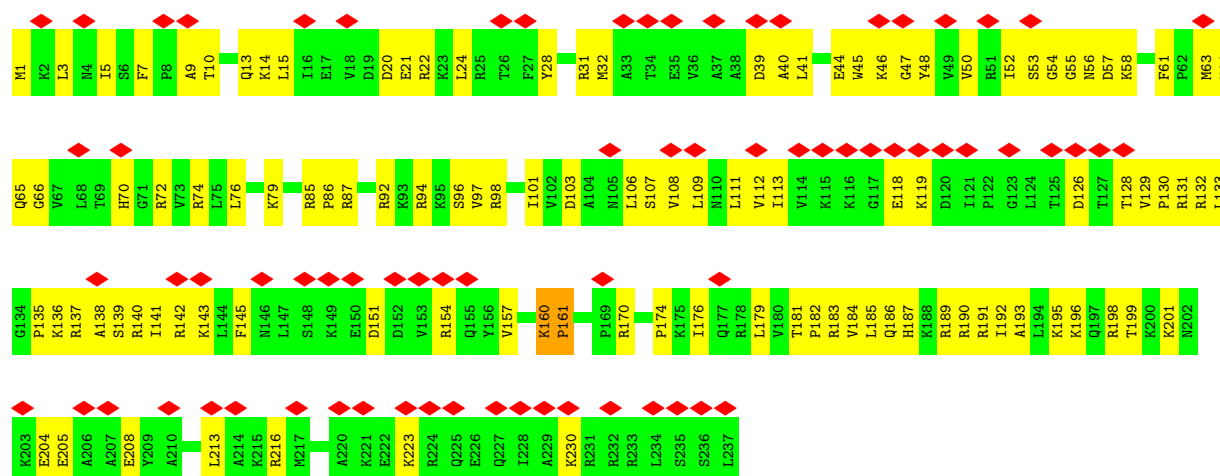
- Molecule 57: 40S ribosomal protein S5

Chain SF: 



- Molecule 58: 40S ribosomal protein S6

Chain SG: 

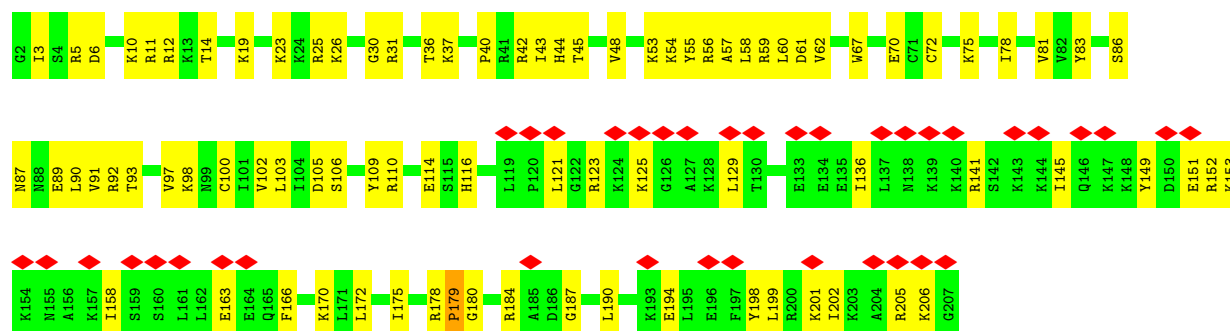


- Molecule 59: Small ribosomal subunit protein eS7

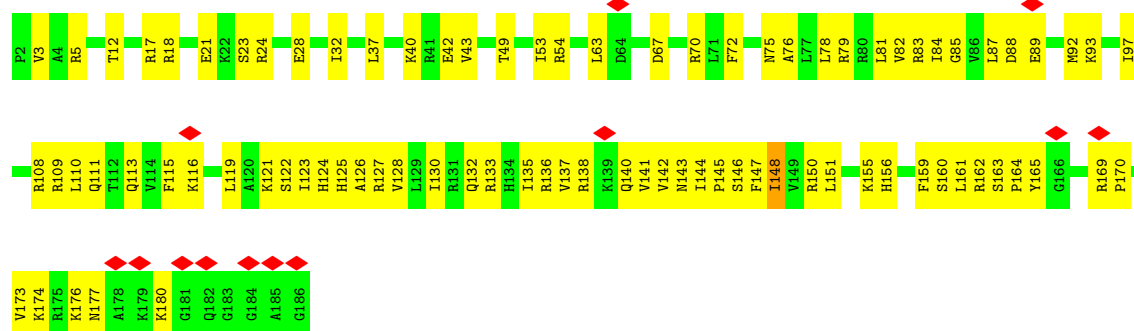
Chain SH: 



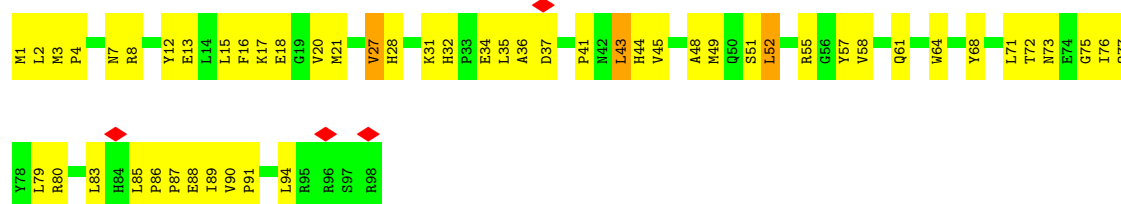
- Molecule 60: 40S ribosomal protein S8



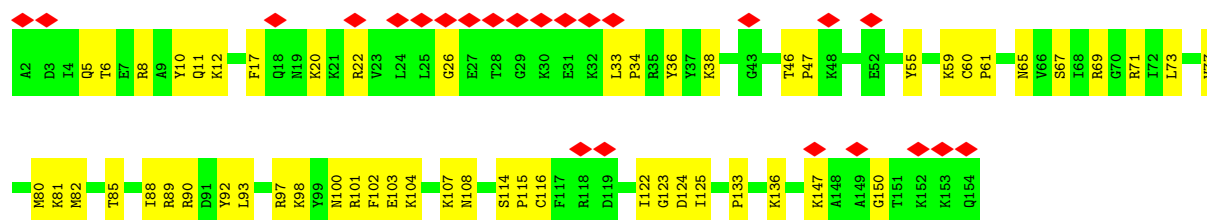
• Molecule 61: 40S ribosomal protein S9



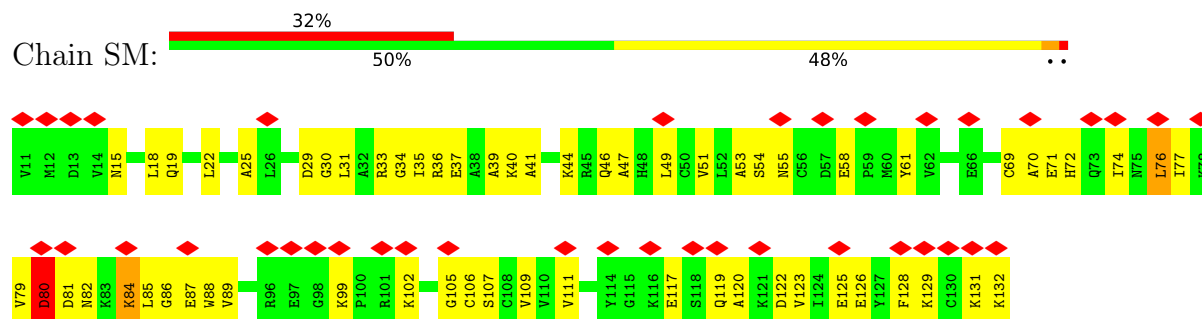
• Molecule 62: 40S ribosomal protein S10



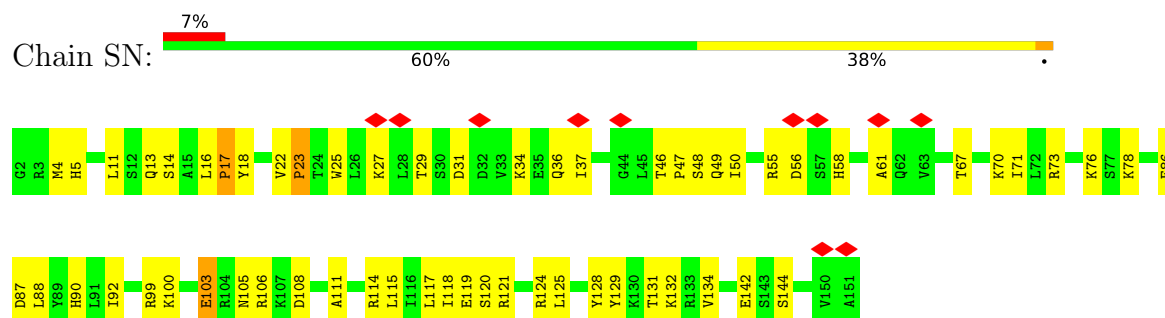
• Molecule 63: 40S ribosomal protein S11



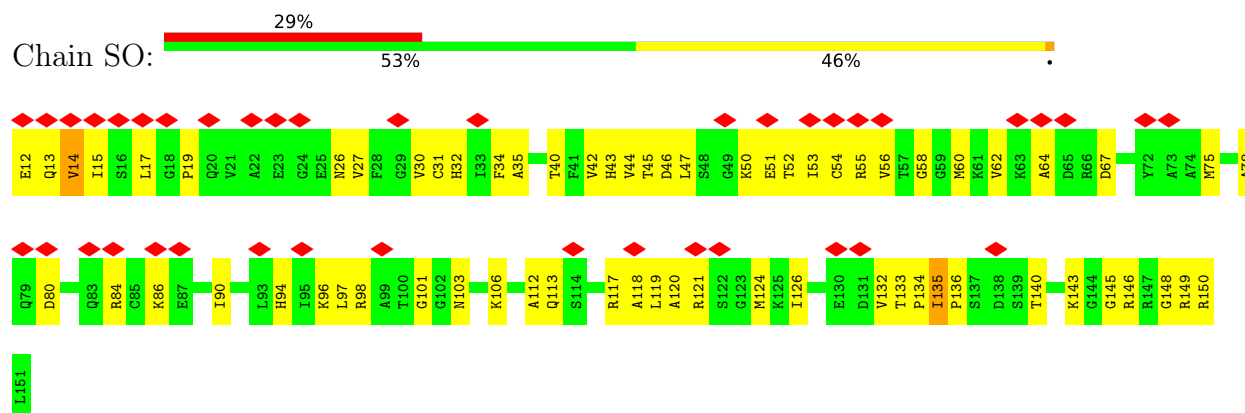
- Molecule 64: Small ribosomal subunit protein eS12



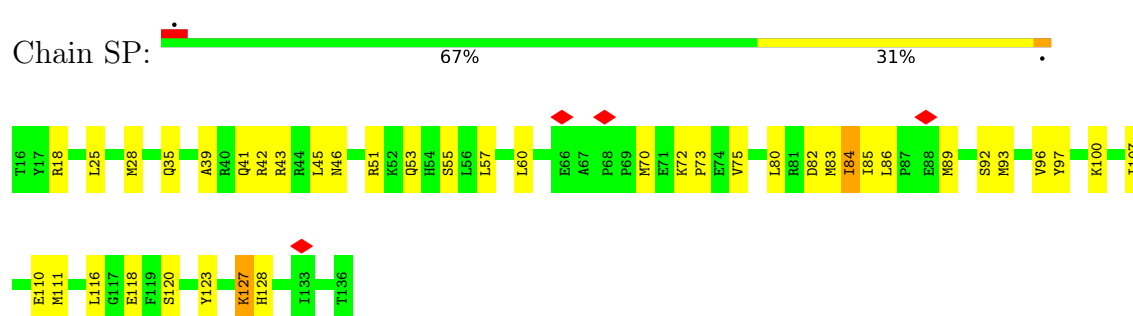
- Molecule 65: 40S ribosomal protein S13



- Molecule 66: Small ribosomal subunit protein uS11

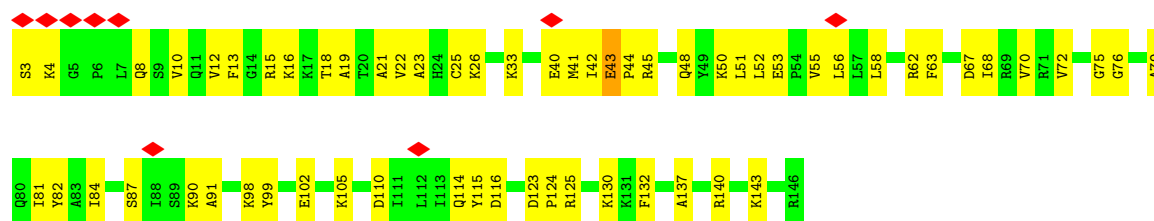


- Molecule 67: Small ribosomal subunit protein uS19

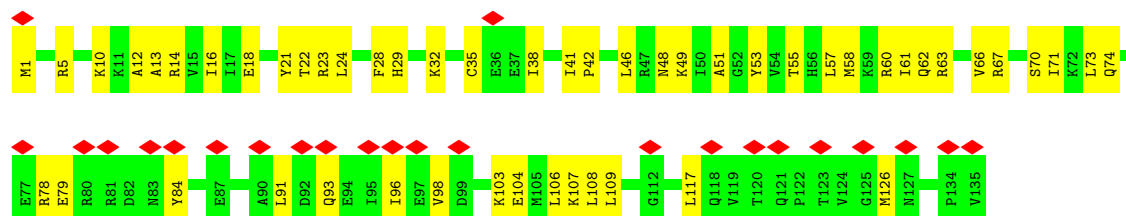


- Molecule 68: Small ribosomal subunit protein uS9

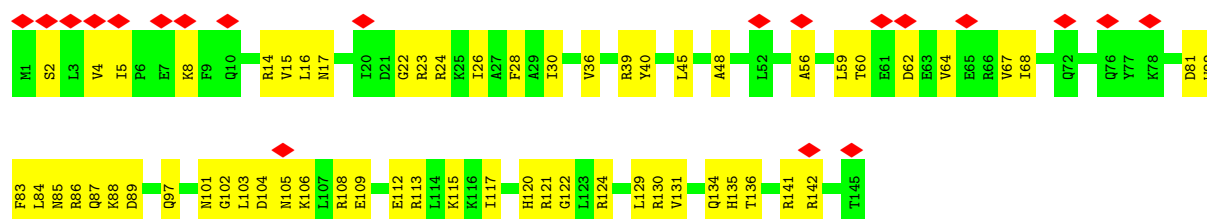




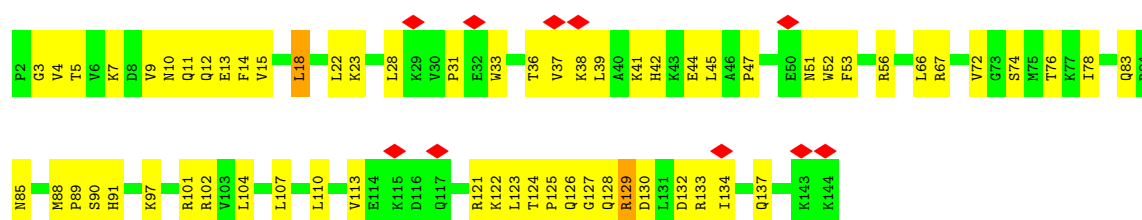
• Molecule 69: 40S ribosomal protein S17



• Molecule 70: 40S ribosomal protein S18

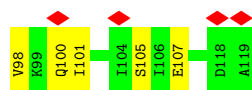


• Molecule 71: 40S ribosomal protein S19



• Molecule 72: 40S ribosomal protein S20

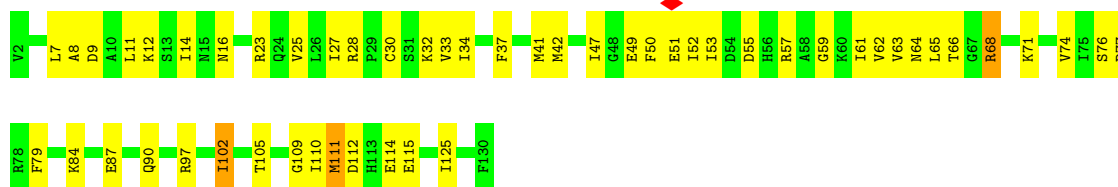




- Molecule 73: 40S ribosomal protein S21



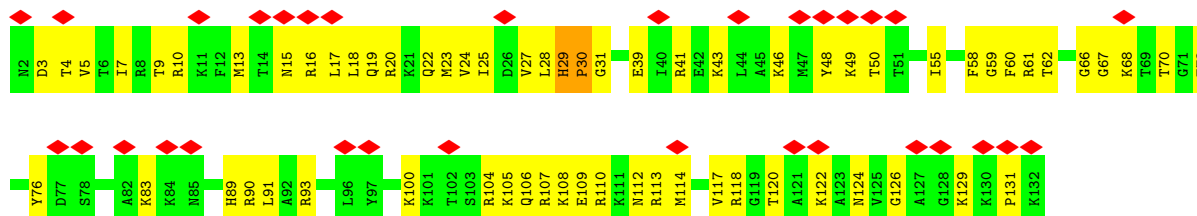
- Molecule 74: 40S ribosomal protein S15a



- Molecule 75: 40S ribosomal protein S23

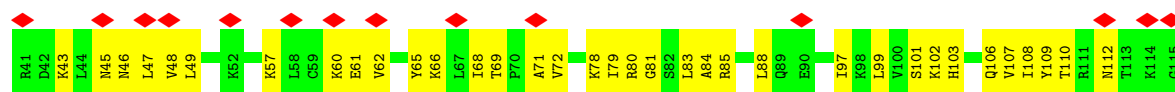


- Molecule 76: 40S ribosomal protein S24

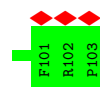


- Molecule 77: Small ribosomal subunit protein eS25

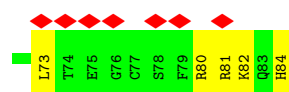
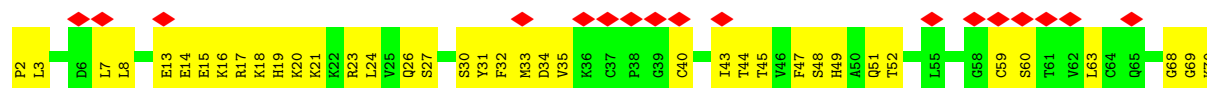




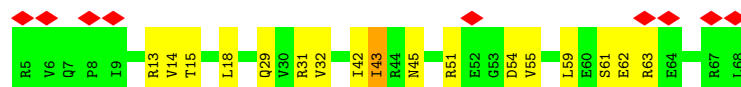
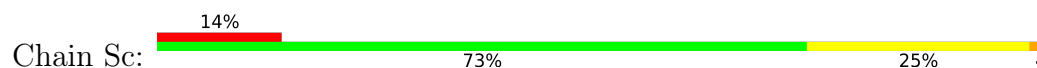
- Molecule 78: 40S ribosomal protein S26



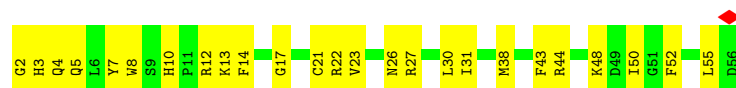
- Molecule 79: Small ribosomal subunit protein eS27



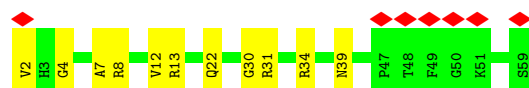
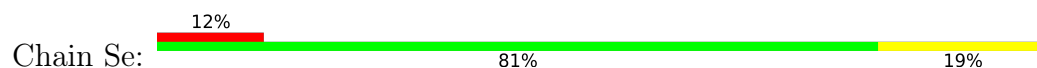
- Molecule 80: 40S ribosomal protein S28



- Molecule 81: 40S ribosomal protein S29



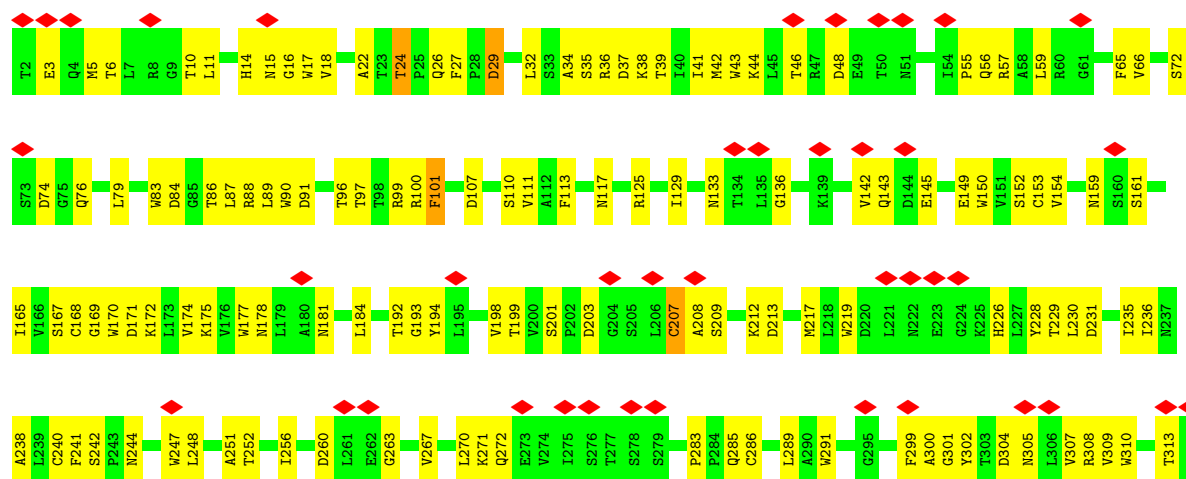
- Molecule 82: Small ribosomal subunit protein eS30



- Molecule 83: Ubiquitin-40S ribosomal protein S27a



• Molecule 84: Receptor of activated protein C kinase 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52735	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.024	Depositor
Minimum map value	-0.475	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.134	Depositor
Map size ($\text{\AA}$)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.068, 1.068, 1.068	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: HMT, ZN, WV3, 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	CB	0.28	2/6734 (0.0%)	0.45	1/9094 (0.0%)
2	CD	0.30	0/447	0.44	0/592
3	L5	0.24	0/89313	0.32	0/139291
4	L7	0.22	0/2861	0.27	0/4459
5	L8	0.23	0/3701	0.29	0/5766
6	LA	0.29	0/1936	0.46	1/2596 (0.0%)
7	LB	0.28	0/3306	0.44	0/4424
8	LC	0.29	1/2981 (0.0%)	0.47	2/4002 (0.0%)
9	LD	0.26	0/2428	0.45	1/3252 (0.0%)
10	LE	0.28	0/1942	0.49	0/2606
11	LF	0.26	0/1905	0.38	0/2539
12	LG	0.25	0/1960	0.41	0/2637
13	LH	0.34	1/1537 (0.1%)	0.51	0/2066
14	LI	0.25	0/1673	0.41	0/2233
15	LJ	0.31	1/1433 (0.1%)	0.53	0/1915
16	LL	0.30	1/1732 (0.1%)	0.41	0/2315
17	LM	0.26	0/1161	0.45	0/1554
18	LN	0.25	0/1746	0.38	0/2338
19	LO	0.25	0/1682	0.38	0/2250
20	LP	0.29	0/1268	0.43	0/1701
21	LQ	0.25	0/1537	0.38	0/2052
22	LR	0.55	2/1582 (0.1%)	0.51	3/2091 (0.1%)
23	LS	0.32	0/1493	0.44	0/2003
24	LT	0.29	0/1326	0.45	0/1770
25	LU	0.45	1/839 (0.1%)	0.65	0/1126
26	LV	0.30	0/993	0.39	0/1332
27	LW	0.32	1/979 (0.1%)	0.41	0/1295
28	LX	0.25	0/1002	0.40	0/1345
29	LY	0.23	0/1132	0.35	0/1504
30	LZ	0.25	0/1130	0.42	0/1507
31	La	0.27	0/1191	0.39	0/1591
32	Lb	0.23	0/889	0.39	0/1175

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lc	0.27	0/774	0.44	0/1038
34	Ld	0.30	0/903	0.44	0/1216
35	Le	0.31	0/1071	0.43	0/1429
36	Lf	0.33	1/895 (0.1%)	0.46	0/1198
37	Lg	0.27	0/916	0.41	0/1220
38	Lh	0.19	0/1023	0.36	0/1351
39	Li	0.26	0/843	0.39	0/1115
40	Lj	0.26	0/720	0.40	0/952
41	Lk	0.27	0/575	0.46	0/761
42	Ll	0.25	0/454	0.36	0/599
43	Lm	0.24	0/435	0.48	0/575
44	Ln	0.18	0/231	0.29	0/294
45	Lo	0.27	0/876	0.44	0/1156
46	Lp	0.26	0/718	0.36	0/953
47	Lr	0.25	0/1017	0.40	0/1364
48	Ls	0.41	2/1519 (0.1%)	0.59	4/2052 (0.2%)
49	Lt	0.51	1/1058 (0.1%)	0.68	0/1430
50	Lz	0.19	0/1769	0.42	0/2371
51	S2	0.18	0/41243	0.31	1/64259 (0.0%)
52	SA	0.34	1/1778 (0.1%)	0.54	3/2416 (0.1%)
53	SB	0.20	0/1765	0.45	0/2362
54	SC	0.61	5/1762 (0.3%)	0.57	3/2381 (0.1%)
55	SD	0.21	0/1793	0.45	0/2414
56	SE	0.25	0/2118	0.49	0/2849
57	SF	0.53	2/1516 (0.1%)	0.60	1/2037 (0.0%)
58	SG	0.69	4/1946 (0.2%)	0.83	10/2590 (0.4%)
59	SH	0.37	1/1519 (0.1%)	0.59	0/2033
60	SI	0.69	4/1715 (0.2%)	0.94	5/2287 (0.2%)
61	SJ	0.27	0/1550	0.52	0/2069
62	SK	0.51	2/851 (0.2%)	0.61	2/1147 (0.2%)
63	SL	0.21	0/1268	0.43	0/1696
64	SM	0.62	3/950 (0.3%)	0.59	2/1275 (0.2%)
65	SN	1.24	9/1232 (0.7%)	1.36	11/1656 (0.7%)
66	SO	0.48	3/1062 (0.3%)	0.83	6/1425 (0.4%)
67	SP	0.23	0/1003	0.56	0/1342
68	SQ	0.33	0/1160	0.56	0/1553
69	SR	0.31	0/1105	0.52	0/1484
70	SS	0.23	0/1216	0.44	0/1628
71	ST	0.38	1/1131 (0.1%)	0.55	0/1515
72	SU	0.80	1/831 (0.1%)	0.53	0/1115
73	SV	0.28	0/643	0.57	0/860
74	SW	0.59	3/1051 (0.3%)	0.67	5/1406 (0.4%)
75	SX	0.28	0/1116	0.47	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SY	0.37	0/1083	0.71	3/1438 (0.2%)
77	SZ	0.32	0/604	0.59	0/810
78	Sa	0.27	0/836	0.42	0/1121
79	Sb	0.32	0/665	0.48	0/891
80	Sc	0.31	0/508	0.53	0/680
81	Sd	0.40	0/470	0.54	0/623
82	Se	0.19	0/465	0.42	0/612
83	Sf	0.47	1/560 (0.2%)	0.84	6/745 (0.8%)
84	Sg	0.34	2/2493 (0.1%)	0.52	1/3394 (0.0%)
All	All	0.30	56/242644 (0.0%)	0.41	71/355098 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
6	LA	0	1
7	LB	0	2
17	LM	0	2
19	LO	0	1
22	LR	0	1
24	LT	0	1
36	Lf	0	1
38	Lh	0	1
40	Lj	0	1
57	SF	0	1
59	SH	0	2
67	SP	0	2
68	SQ	0	1
75	SX	0	1
All	All	0	18

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	SG	160	LYS	C-N	23.21	1.88	1.33
72	SU	82	MET	SD-CE	-21.42	1.26	1.79
65	SN	23	PRO	CG-CD	-19.12	0.85	1.50
65	SN	23	PRO	CA-CB	-17.79	1.34	1.54
60	SI	179	PRO	N-CD	-17.04	1.24	1.47

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	SN	23	PRO	CB-CG-CD	-33.14	0.04	106.10
60	SI	179	PRO	CA-N-CD	-27.22	73.89	112.00
65	SN	23	PRO	CA-N-CD	-22.09	81.07	112.00
60	SI	179	PRO	CB-CG-CD	-21.49	37.34	106.10
66	SO	136	PRO	CA-N-CD	-17.05	88.14	112.00

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	LA	13	GLY	Peptide
7	LB	17	LEU	Peptide
7	LB	258	HIS	Peptide
17	LM	87	ALA	Peptide
17	LM	88	ALA	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CB	6605	0	6679	245	0
2	CD	440	0	402	42	0
3	L5	79860	0	40297	1172	0
4	L7	2561	0	1295	28	0
5	L8	3314	0	1683	50	0
6	LA	1898	0	1993	57	0
7	LB	3238	0	3376	94	0
8	LC	2927	0	3104	66	0
9	LD	2382	0	2410	73	0
10	LE	1904	0	2055	52	0
11	LF	1870	0	1996	45	0
12	LG	1927	0	2074	43	0
13	LH	1518	0	1601	45	0
14	LI	1634	0	1671	42	0
15	LJ	1410	0	1441	44	0
16	LL	1701	0	1818	49	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	LM	1138	0	1204	29	0
18	LN	1701	0	1749	45	0
19	LO	1650	0	1794	45	0
20	LP	1242	0	1269	35	0
21	LQ	1513	0	1628	35	0
22	LR	1566	0	1729	59	0
23	LS	1453	0	1490	44	0
24	LT	1298	0	1366	38	0
25	LU	825	0	850	41	0
26	LV	979	0	1039	31	0
27	LW	965	0	1029	31	0
28	LX	985	0	1066	22	0
29	LY	1115	0	1205	29	0
30	LZ	1107	0	1182	30	0
31	La	1162	0	1213	35	0
32	Lb	876	0	948	27	0
33	Lc	764	0	804	25	0
34	Ld	888	0	930	17	0
35	Le	1053	0	1147	28	0
36	Lf	876	0	912	28	0
37	Lg	906	0	998	19	0
38	Lh	1015	0	1148	31	0
39	Li	832	0	917	17	0
40	Lj	705	0	737	26	0
41	Lk	569	0	637	15	0
42	Ll	444	0	483	17	0
43	Lm	429	0	465	11	0
44	Ln	230	0	276	4	0
45	Lo	862	0	929	23	0
46	Lp	708	0	756	17	0
47	Lr	1002	0	1068	21	0
48	Ls	1496	0	1540	56	0
49	Lt	1046	0	1076	65	0
50	Lz	1741	0	1854	49	0
51	S2	36898	0	18603	848	0
52	SA	1741	0	1746	93	0
53	SB	1738	0	1809	81	0
54	SC	1725	0	1813	70	0
55	SD	1765	0	1865	63	0
56	SE	2076	0	2177	120	0
57	SF	1495	0	1549	96	0
58	SG	1923	0	2089	114	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	SH	1497	0	1590	93	0
60	SI	1686	0	1772	82	0
61	SJ	1525	0	1640	84	0
62	SK	827	0	854	69	0
63	SL	1247	0	1323	47	0
64	SM	940	0	965	60	0
65	SN	1208	0	1294	69	0
66	SO	1049	0	1073	82	0
67	SP	985	0	1031	39	0
68	SQ	1142	0	1213	56	0
69	SR	1090	0	1149	64	0
70	SS	1198	0	1261	66	0
71	ST	1112	0	1146	85	0
72	SU	821	0	883	53	0
73	SV	636	0	637	31	0
74	SW	1034	0	1080	77	0
75	SX	1098	0	1167	42	0
76	SY	1065	0	1142	88	0
77	SZ	598	0	656	45	0
78	Sa	821	0	870	39	0
79	Sb	651	0	672	54	0
80	Sc	506	0	536	30	0
81	Sd	459	0	452	35	0
82	Se	459	0	503	13	0
83	Sf	548	0	555	28	0
84	Sg	2436	0	2393	119	0
85	L5	212	0	0	0	0
85	L7	3	0	0	0	0
85	L8	4	0	0	0	0
85	LA	1	0	0	0	0
85	LI	1	0	0	0	0
85	LP	1	0	0	0	0
85	LV	1	0	0	0	0
85	Le	1	0	0	0	0
85	Lj	1	0	0	0	0
85	S2	30	0	0	0	0
86	L5	39	0	37	2	0
87	L5	20	0	0	1	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
All	All	226649	0	170878	5253	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

The worst 5 of 5253 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:SW:68:ARG:CG	74:SW:68:ARG:CD	1.81	1.53
64:SM:84:LYS:NZ	64:SM:84:LYS:CE	1.70	1.52
22:LR:169:ALA:HA	22:LR:172:ARG:NH1	1.34	1.39
58:SG:160:LYS:C	58:SG:161:PRO:N	1.88	1.31
65:SN:23:PRO:CG	65:SN:23:PRO:N	1.95	1.27

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	CB	722/728 (99%)	720 (100%)	2 (0%)	86	85
2	CD	46/46 (100%)	45 (98%)	1 (2%)	45	67
6	LA	190/190 (100%)	190 (100%)	0	100	100
7	LB	348/348 (100%)	347 (100%)	1 (0%)	86	85

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	LC	306/306 (100%)	306 (100%)	0	100	100
9	LD	246/247 (100%)	246 (100%)	0	100	100
10	LE	209/220 (95%)	208 (100%)	1 (0%)	81	82
11	LF	194/194 (100%)	194 (100%)	0	100	100
12	LG	203/205 (99%)	203 (100%)	0	100	100
13	LH	169/169 (100%)	168 (99%)	1 (1%)	78	81
14	LI	172/180 (96%)	171 (99%)	1 (1%)	78	81
15	LJ	148/148 (100%)	145 (98%)	3 (2%)	48	69
16	LL	176/176 (100%)	176 (100%)	0	100	100
17	LM	118/118 (100%)	118 (100%)	0	100	100
18	LN	171/171 (100%)	171 (100%)	0	100	100
19	LO	173/173 (100%)	173 (100%)	0	100	100
20	LP	134/134 (100%)	134 (100%)	0	100	100
21	LQ	164/164 (100%)	164 (100%)	0	100	100
22	LR	166/166 (100%)	165 (99%)	1 (1%)	78	81
23	LS	156/156 (100%)	155 (99%)	1 (1%)	78	81
24	LT	139/139 (100%)	138 (99%)	1 (1%)	76	80
25	LU	91/91 (100%)	90 (99%)	1 (1%)	65	76
26	LV	101/101 (100%)	101 (100%)	0	100	100
27	LW	97/103 (94%)	97 (100%)	0	100	100
28	LX	108/108 (100%)	108 (100%)	0	100	100
29	LY	124/124 (100%)	123 (99%)	1 (1%)	73	79
30	LZ	117/117 (100%)	117 (100%)	0	100	100
31	La	120/120 (100%)	120 (100%)	0	100	100
32	Lb	88/101 (87%)	87 (99%)	1 (1%)	65	76
33	Lc	83/83 (100%)	82 (99%)	1 (1%)	63	75
34	Ld	98/98 (100%)	98 (100%)	0	100	100
35	Le	114/114 (100%)	113 (99%)	1 (1%)	70	78
36	Lf	88/88 (100%)	87 (99%)	1 (1%)	65	76
37	Lg	98/98 (100%)	98 (100%)	0	100	100
38	Lh	109/109 (100%)	109 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Li	86/86 (100%)	86 (100%)	0	100	100
40	Lj	73/73 (100%)	73 (100%)	0	100	100
41	Lk	64/64 (100%)	63 (98%)	1 (2%)	55	72
42	Ll	47/47 (100%)	47 (100%)	0	100	100
43	Lm	48/48 (100%)	48 (100%)	0	100	100
44	Ln	23/23 (100%)	23 (100%)	0	100	100
45	Lo	93/93 (100%)	93 (100%)	0	100	100
46	Lp	74/74 (100%)	73 (99%)	1 (1%)	59	73
47	Lr	109/109 (100%)	109 (100%)	0	100	100
48	Ls	162/164 (99%)	162 (100%)	0	100	100
49	Lt	112/115 (97%)	112 (100%)	0	100	100
50	Lz	195/196 (100%)	195 (100%)	0	100	100
52	SA	183/183 (100%)	181 (99%)	2 (1%)	65	76
53	SB	195/195 (100%)	195 (100%)	0	100	100
54	SC	188/188 (100%)	185 (98%)	3 (2%)	55	72
55	SD	190/190 (100%)	190 (100%)	0	100	100
56	SE	224/224 (100%)	221 (99%)	3 (1%)	61	74
57	SF	159/159 (100%)	159 (100%)	0	100	100
58	SG	207/207 (100%)	207 (100%)	0	100	100
59	SH	166/169 (98%)	166 (100%)	0	100	100
60	SI	178/178 (100%)	178 (100%)	0	100	100
61	SJ	161/161 (100%)	160 (99%)	1 (1%)	78	81
62	SK	89/89 (100%)	88 (99%)	1 (1%)	65	76
63	SL	137/137 (100%)	136 (99%)	1 (1%)	76	80
64	SM	102/104 (98%)	100 (98%)	2 (2%)	48	69
65	SN	130/130 (100%)	128 (98%)	2 (2%)	57	73
66	SO	110/110 (100%)	110 (100%)	0	100	100
67	SP	107/107 (100%)	106 (99%)	1 (1%)	70	78
68	SQ	119/119 (100%)	119 (100%)	0	100	100
69	SR	122/122 (100%)	122 (100%)	0	100	100
70	SS	126/126 (100%)	126 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	ST	113/113 (100%)	112 (99%)	1 (1%)	70	78
72	SU	94/94 (100%)	93 (99%)	1 (1%)	65	76
73	SV	67/67 (100%)	67 (100%)	0	100	100
74	SW	112/112 (100%)	111 (99%)	1 (1%)	70	78
75	SX	113/113 (100%)	112 (99%)	1 (1%)	70	78
76	SY	113/113 (100%)	113 (100%)	0	100	100
77	SZ	66/66 (100%)	66 (100%)	0	100	100
78	Sa	89/89 (100%)	89 (100%)	0	100	100
79	Sb	75/75 (100%)	75 (100%)	0	100	100
80	Sc	57/57 (100%)	56 (98%)	1 (2%)	51	70
81	Sd	48/48 (100%)	48 (100%)	0	100	100
82	Se	47/47 (100%)	47 (100%)	0	100	100
83	Sf	60/60 (100%)	60 (100%)	0	100	100
84	Sg	272/272 (100%)	271 (100%)	1 (0%)	84	84
All	All	11091/11149 (100%)	11048 (100%)	43 (0%)	81	84

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	SE	216	ASN
65	SN	103	GLU
61	SJ	148	ILE
64	SM	76	LEU
71	ST	129	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 121 such sidechains are listed below:

Mol	Chain	Res	Type
48	Ls	105	ASN
75	SX	97	ASN
53	SB	159	GLN
74	SW	113	HIS
84	Sg	26	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	L5	3704/3740 (99%)	850 (22%)	21 (0%)
4	L7	119/120 (99%)	13 (10%)	1 (0%)
5	L8	155/156 (99%)	27 (17%)	0
51	S2	1715/1740 (98%)	490 (28%)	7 (0%)
All	All	5693/5756 (98%)	1380 (24%)	29 (0%)

5 of 1380 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	L5	17	A
3	L5	25	A
3	L5	30	C
3	L5	39	A
3	L5	42	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	L5	3614	G
51	S2	1434	C
3	L5	4061	G
51	S2	531	A
3	L5	3948	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 263 ligands modelled in this entry, 261 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
87	WV3	L5	5314	3	21,21,21	1.78	7 (33%)	23,30,30	2.13	10 (43%)
86	HMT	L5	5313	3	41,43,43	2.24	12 (29%)	43,66,66	1.77	9 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	WV3	L5	5314	3	-	3/8/36/36	0/2/2/2
86	HMT	L5	5313	3	-	7/27/74/74	0/5/5/5

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	L5	5313	HMT	O4-C19	6.74	1.47	1.34
86	L5	5313	HMT	C1-C2	5.26	1.40	1.32
86	L5	5313	HMT	C12-C9	-4.51	1.47	1.54
87	L5	5314	WV3	C5-C4	4.13	1.56	1.51
86	L5	5313	HMT	O4-C3	-3.94	1.37	1.44

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	L5	5313	HMT	O7-C22-C21	5.15	120.19	111.16
86	L5	5313	HMT	O4-C19-C20	4.66	119.79	111.24
87	L5	5314	WV3	C6-C5-C4	4.19	115.22	108.29
87	L5	5314	WV3	C2-C3-C4	4.05	117.72	109.66
87	L5	5314	WV3	C11-N-C12	-3.53	121.62	125.87

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	L5	5313	HMT	C1-C2-O3-C18
86	L5	5313	HMT	C3-C2-O3-C18
86	L5	5313	HMT	C25-C26-C27-C28
86	L5	5313	HMT	C25-C26-C27-C29

Continued on next page...

Continued from previous page...

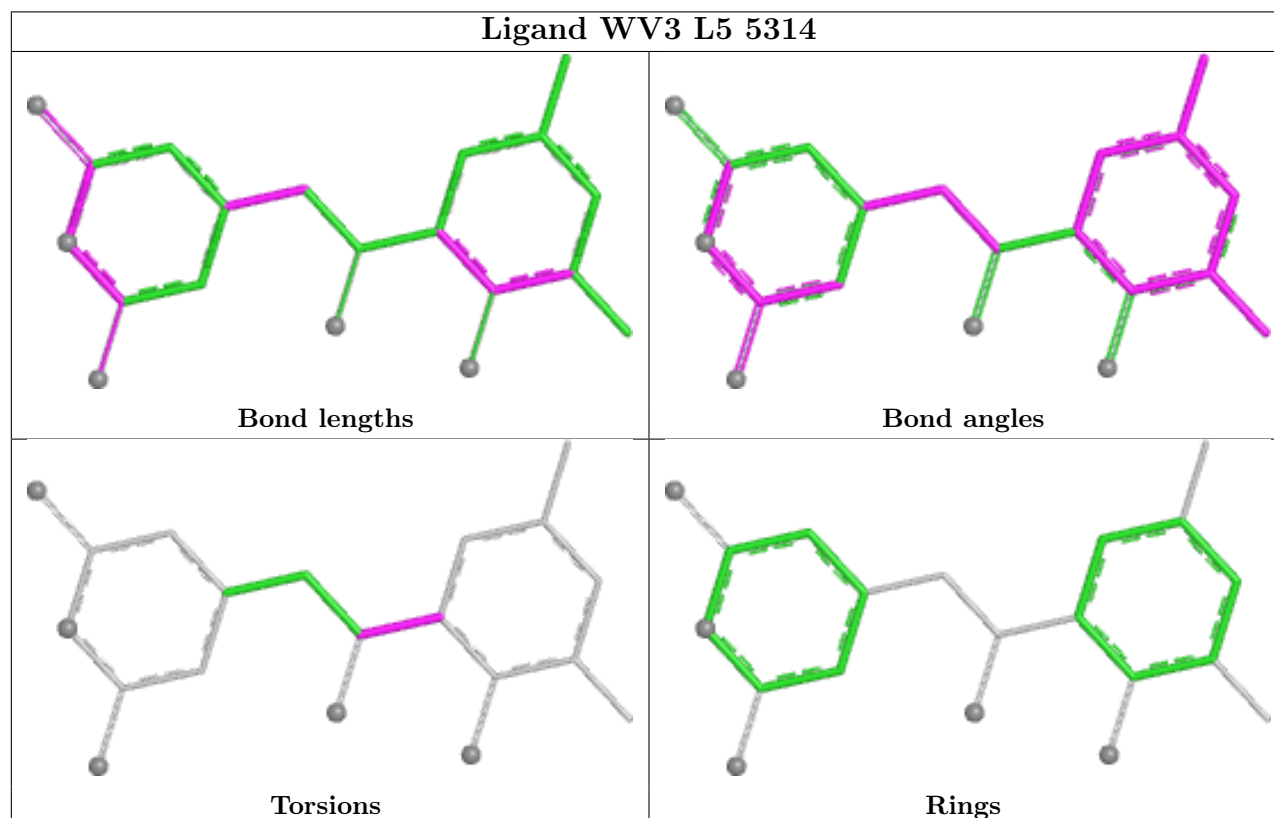
Mol	Chain	Res	Type	Atoms
86	L5	5313	HMT	C25-C26-C27-O9

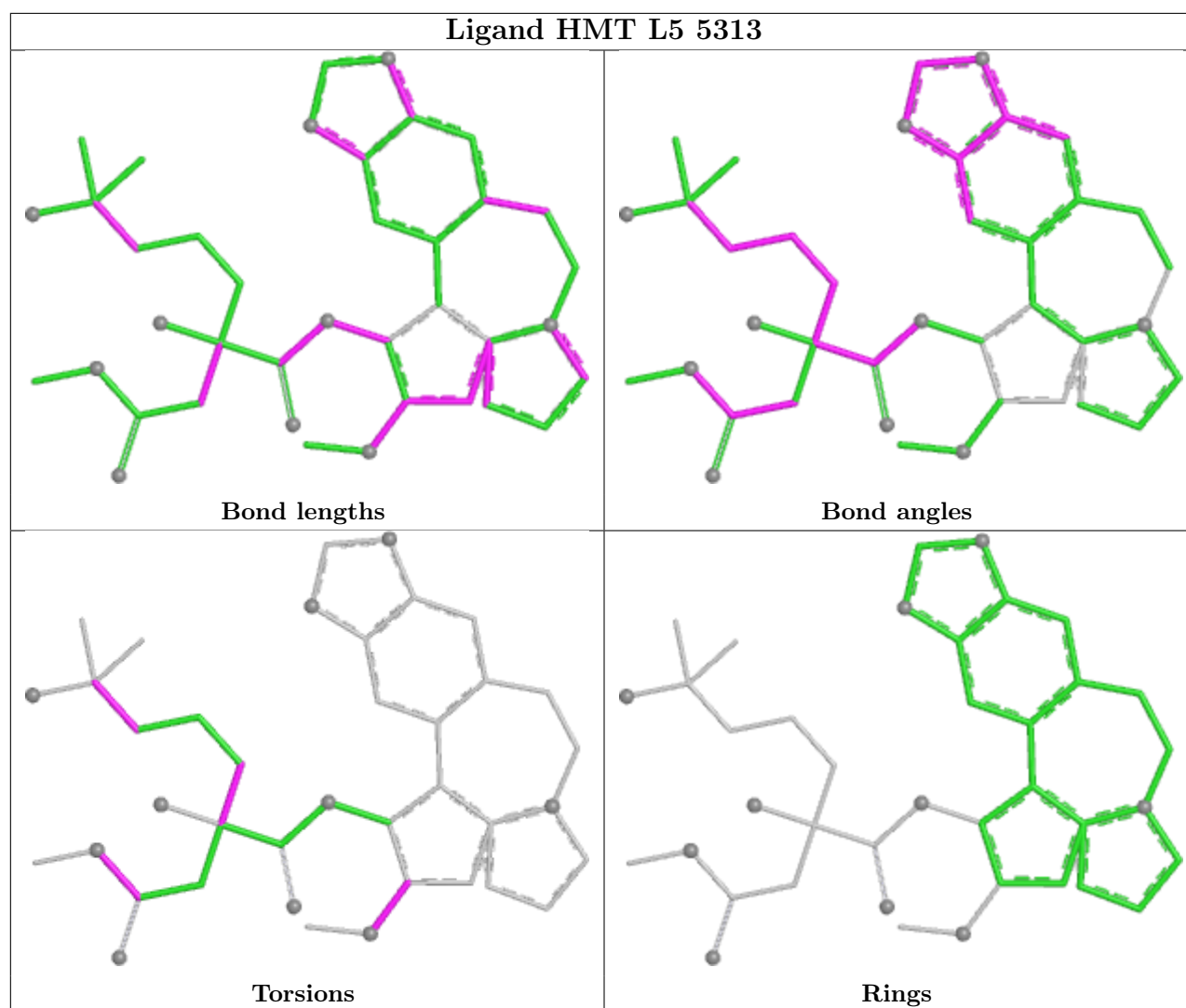
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	L5	5314	WV3	1	0
86	L5	5313	HMT	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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
3	L5	11
51	S2	5
2	CD	1
49	Lt	1
58	SG	1

The worst 5 of 19 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	CD	225:LEU	C	282:THR	N	57.52
1	S2	753:C	O3'	785:C	P	27.35
1	L5	2910:G	O3'	3584:C	P	20.24
1	S2	698:G	O3'	730:C	P	16.90
1	L5	760:G	O3'	903:C	P	16.83

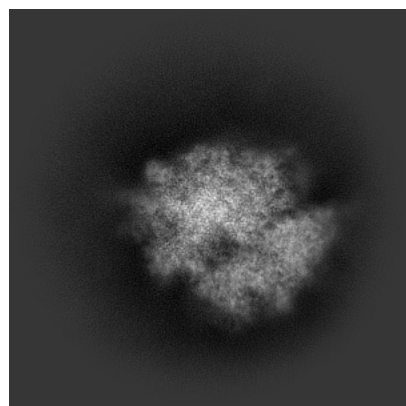
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42351. These allow visual inspection of the internal detail of the map and identification of artifacts.

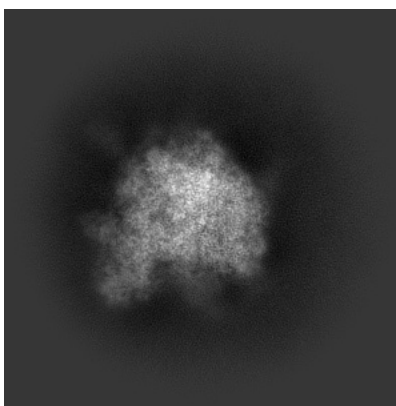
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

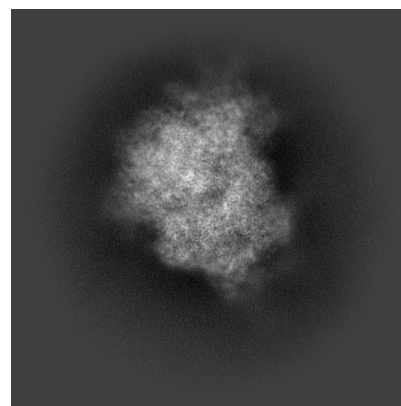
6.1.1 Primary map



X

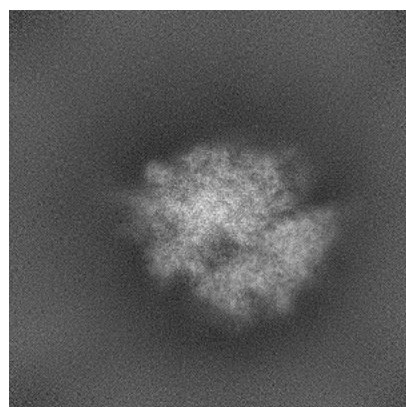


Y

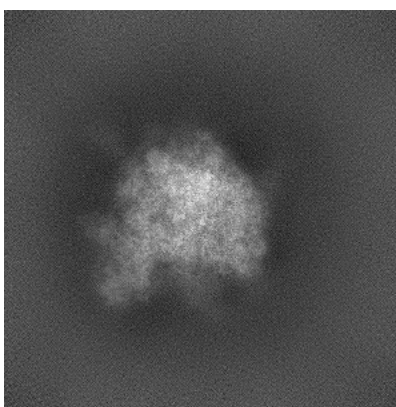


Z

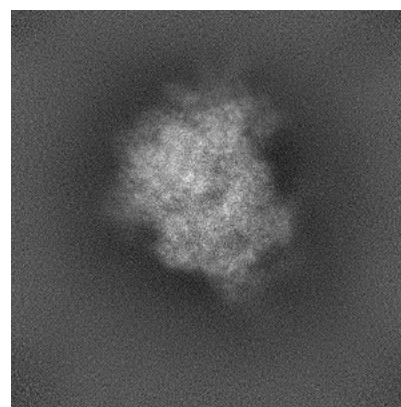
6.1.2 Raw map



X



Y

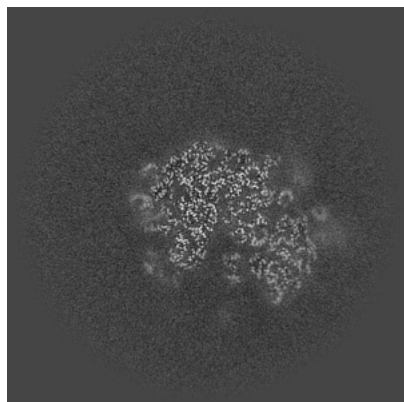


Z

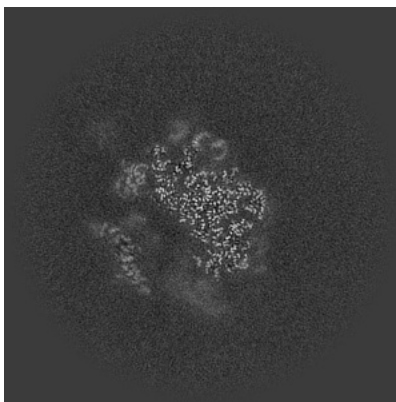
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

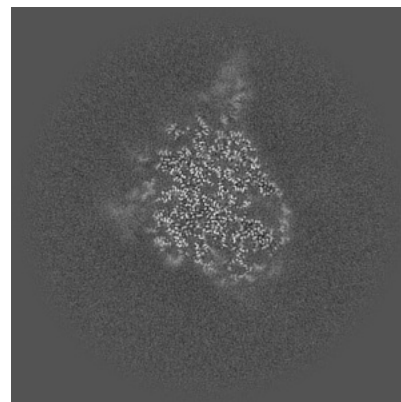
6.2.1 Primary map



X Index: 256

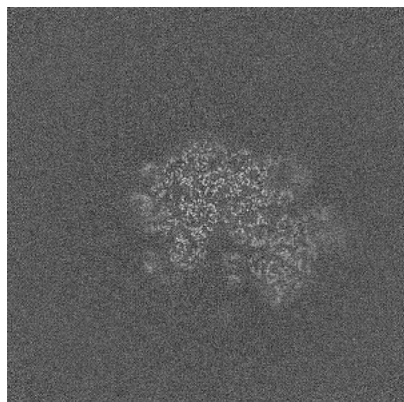


Y Index: 256

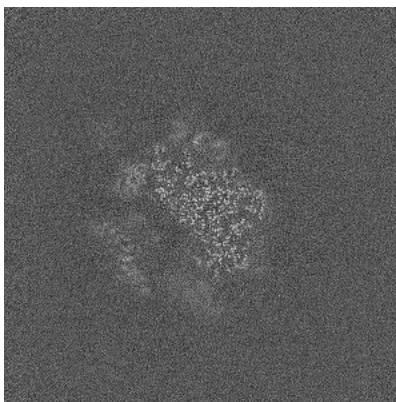


Z Index: 256

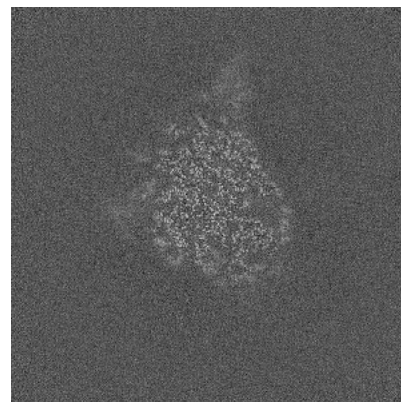
6.2.2 Raw map



X Index: 256



Y Index: 256

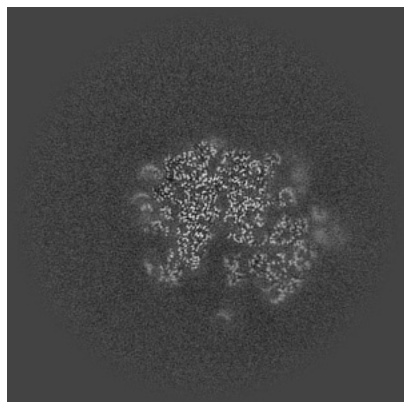


Z Index: 256

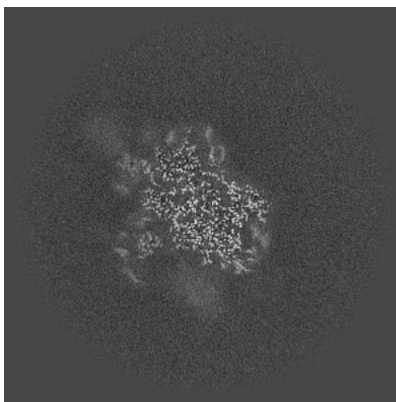
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

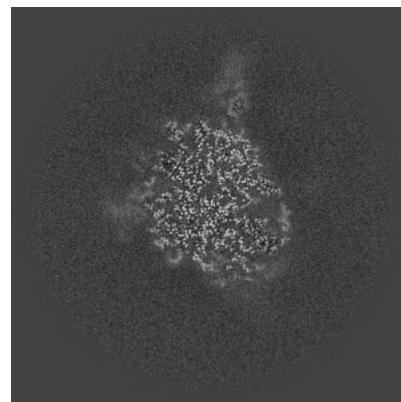
6.3.1 Primary map



X Index: 253

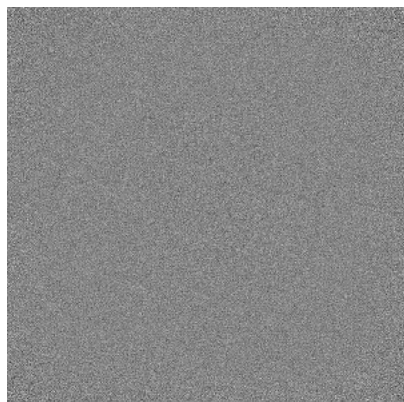


Y Index: 243

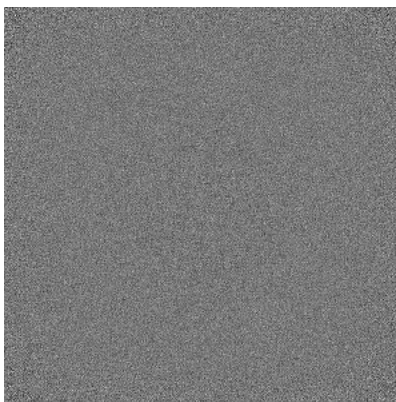


Z Index: 258

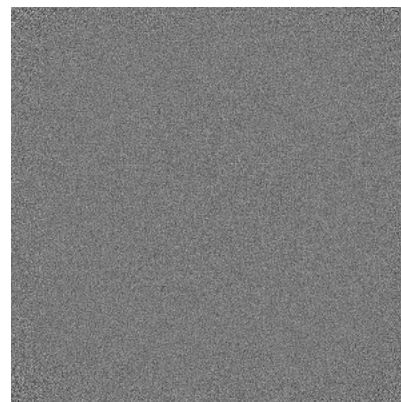
6.3.2 Raw map



X Index: 0



Y Index: 0

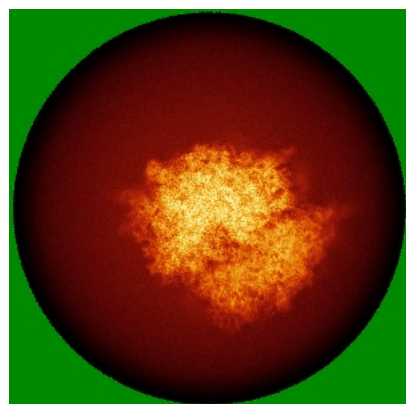


Z Index: 0

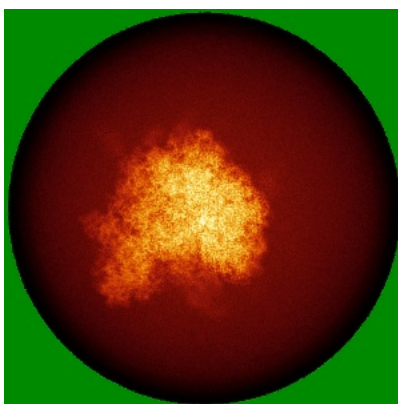
The images above show the largest variance slices of the map in three orthogonal directions.

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

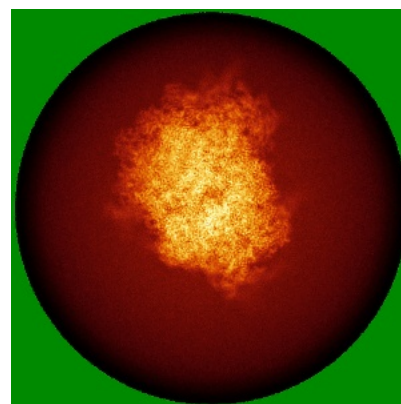
6.4.1 Primary map



X

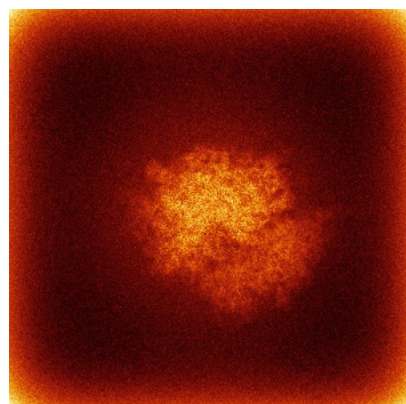


Y

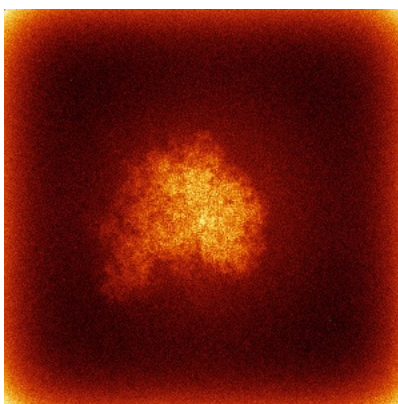


Z

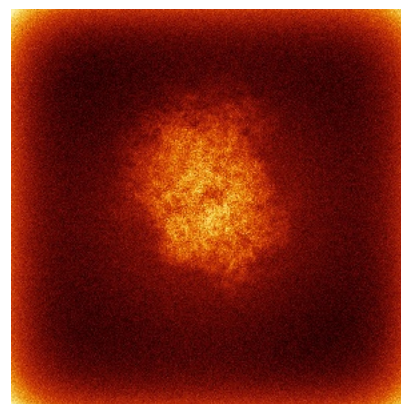
6.4.2 Raw map



X



Y

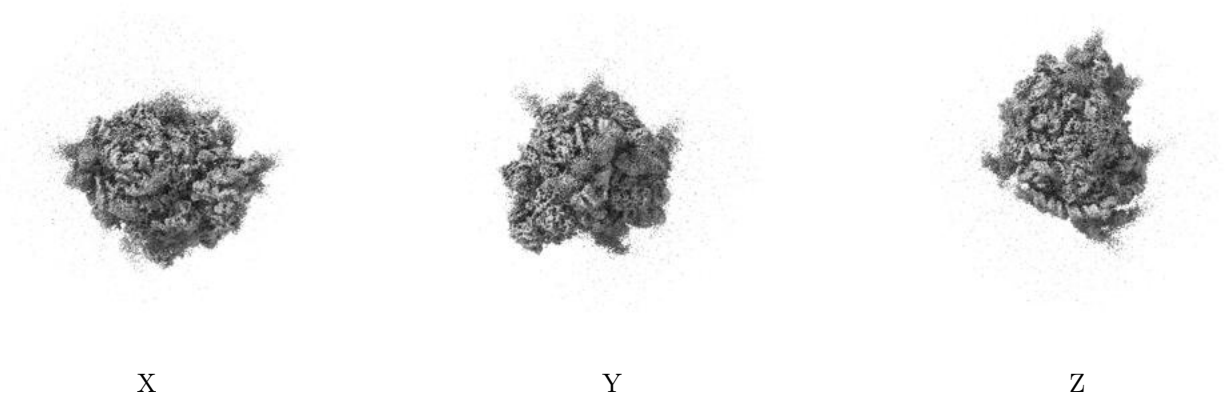


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.134. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

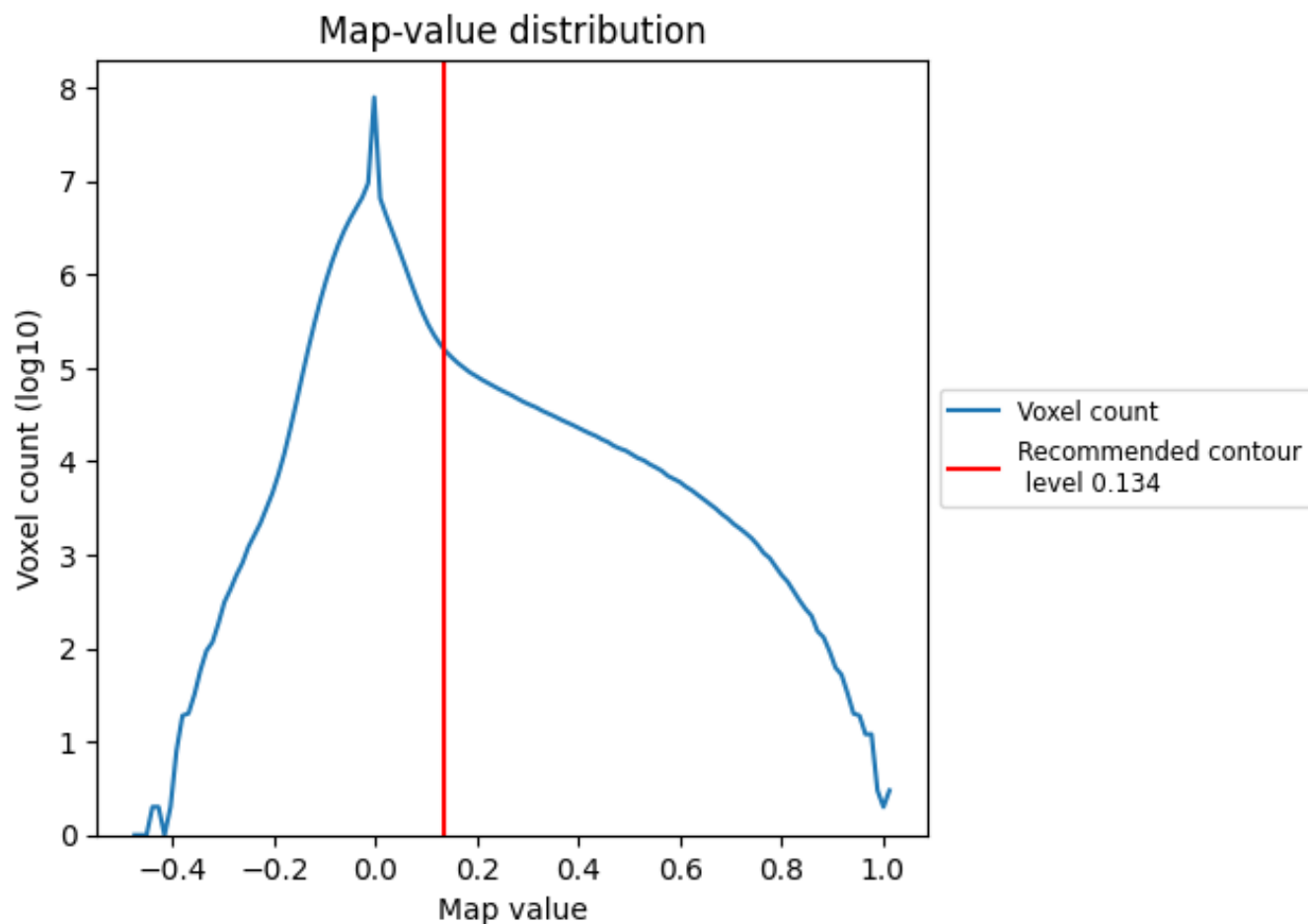
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

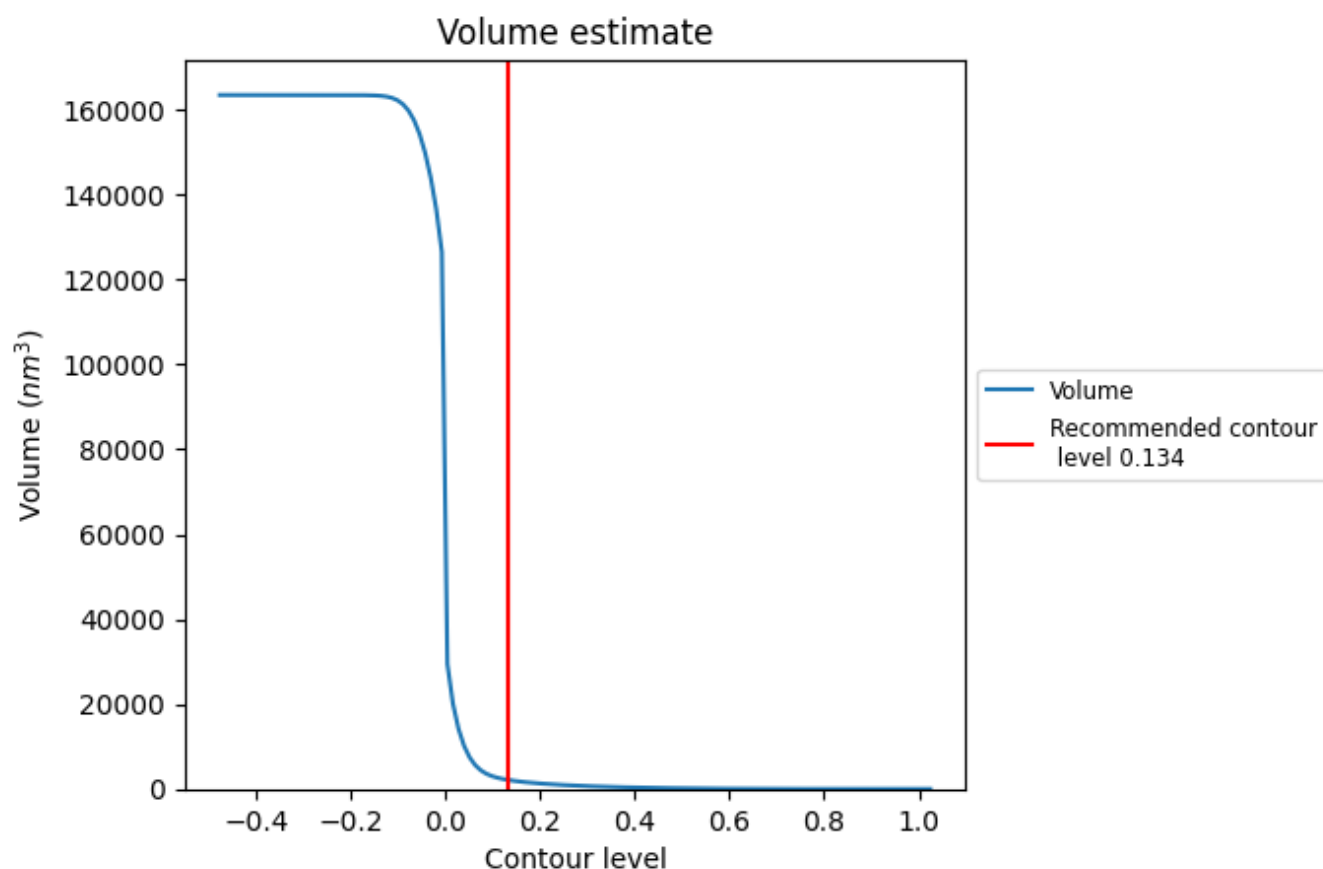
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

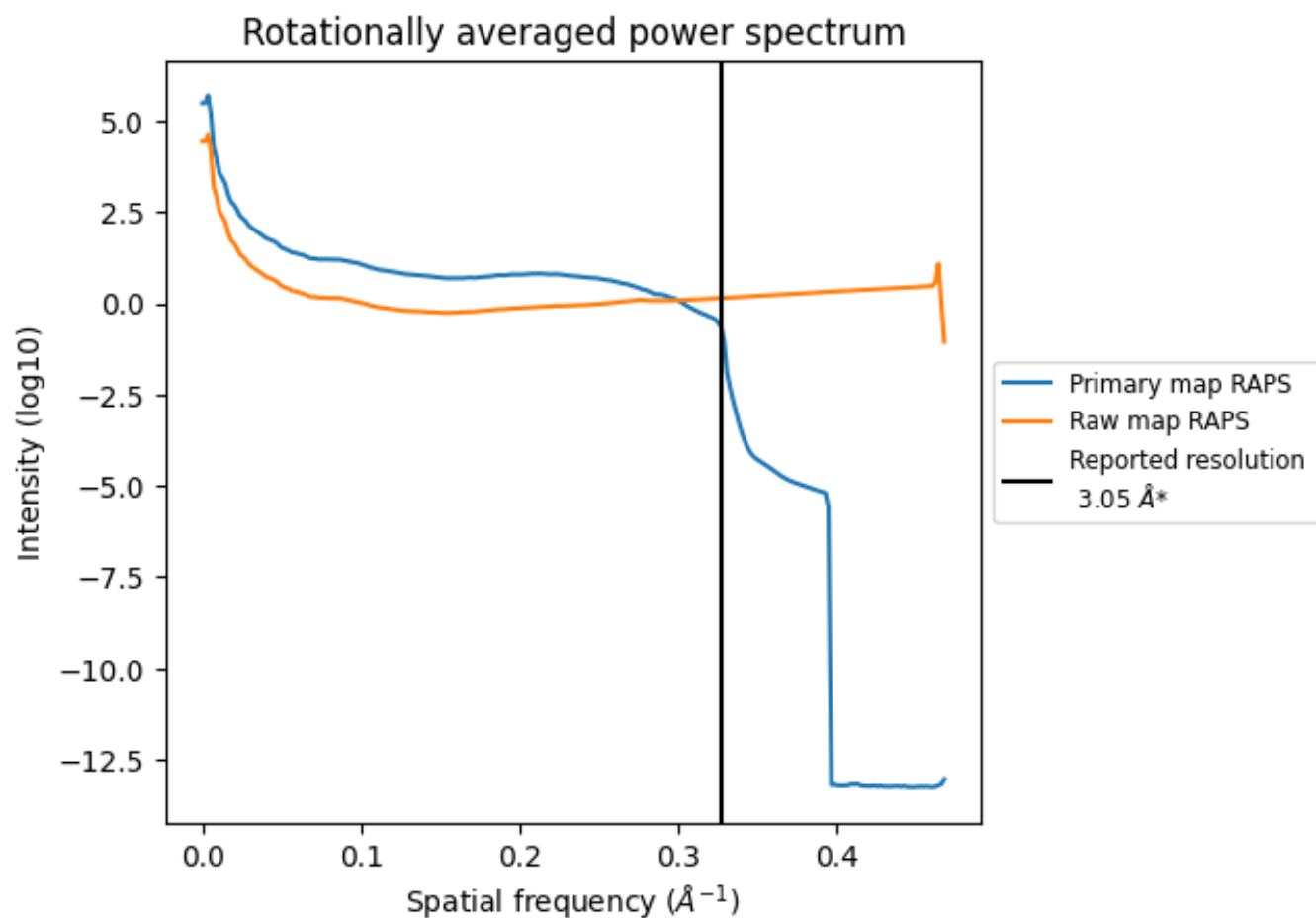
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2106 nm³; this corresponds to an approximate mass of 1903 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

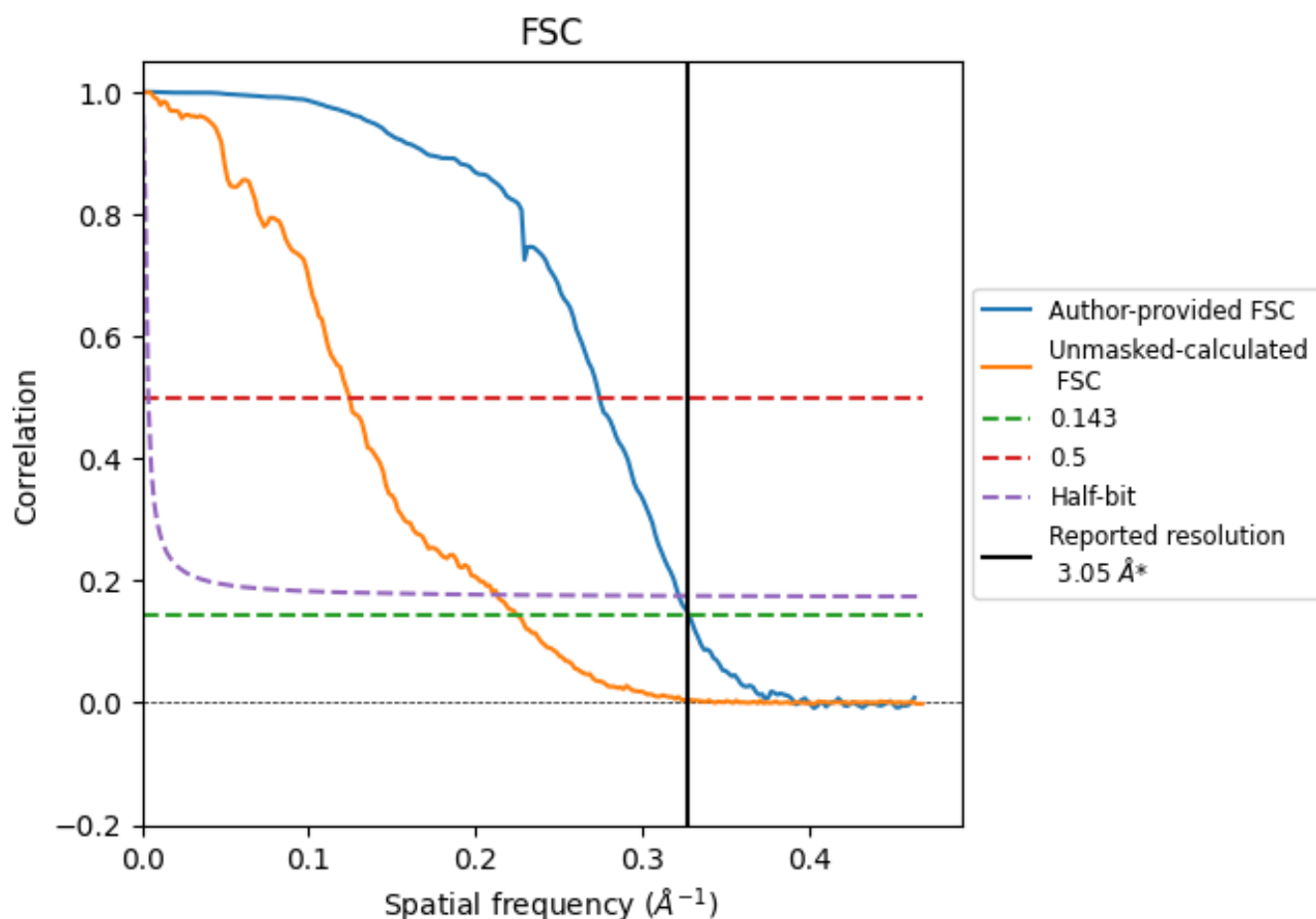


*Reported resolution corresponds to spatial frequency of 0.328 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.328 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

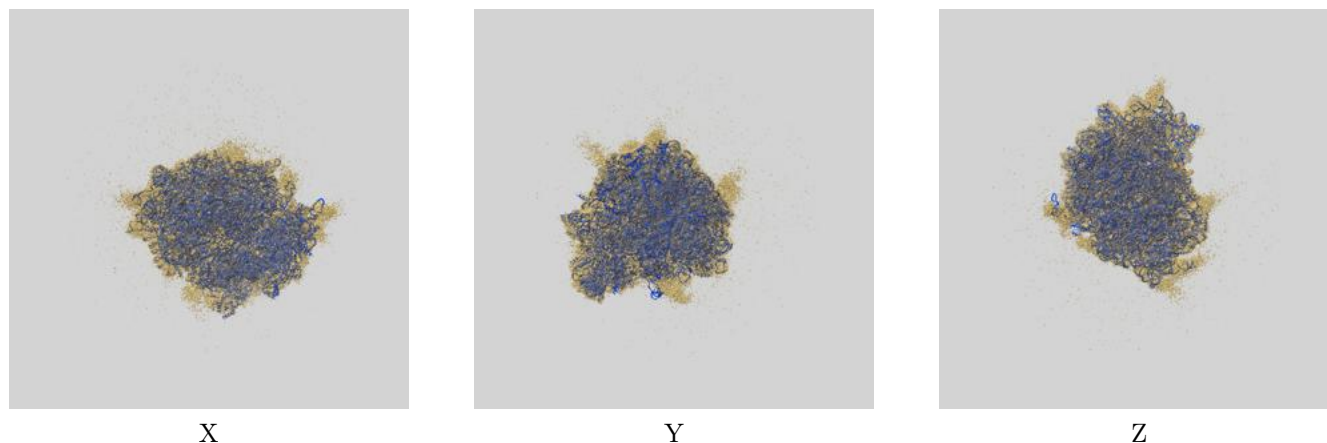
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.05	-	-
Author-provided FSC curve	3.05	3.64	3.10
Unmasked-calculated*	4.44	8.05	4.69

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.44 differs from the reported value 3.05 by more than 10 %

9 Map-model fit [i](#)

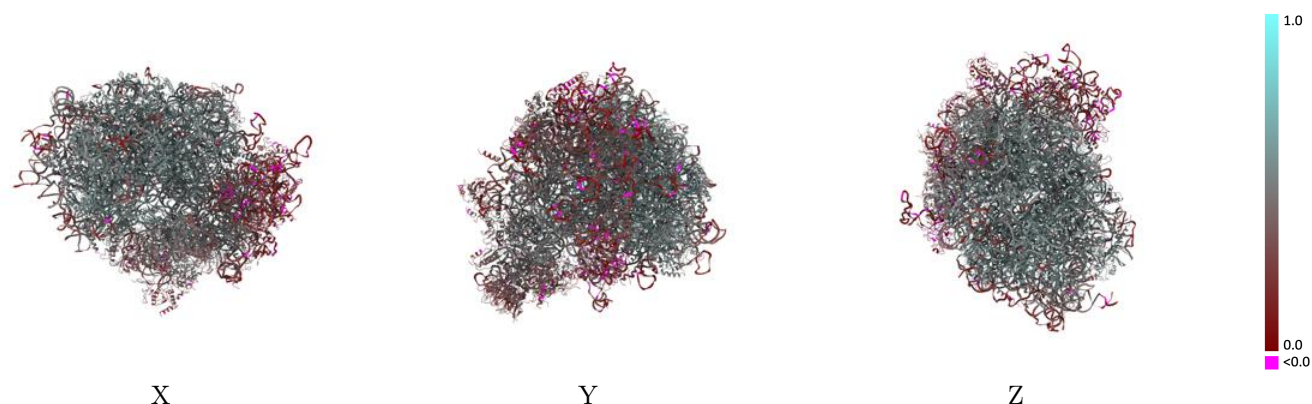
This section contains information regarding the fit between EMDB map EMD-42351 and PDB model 8UKB. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.134 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

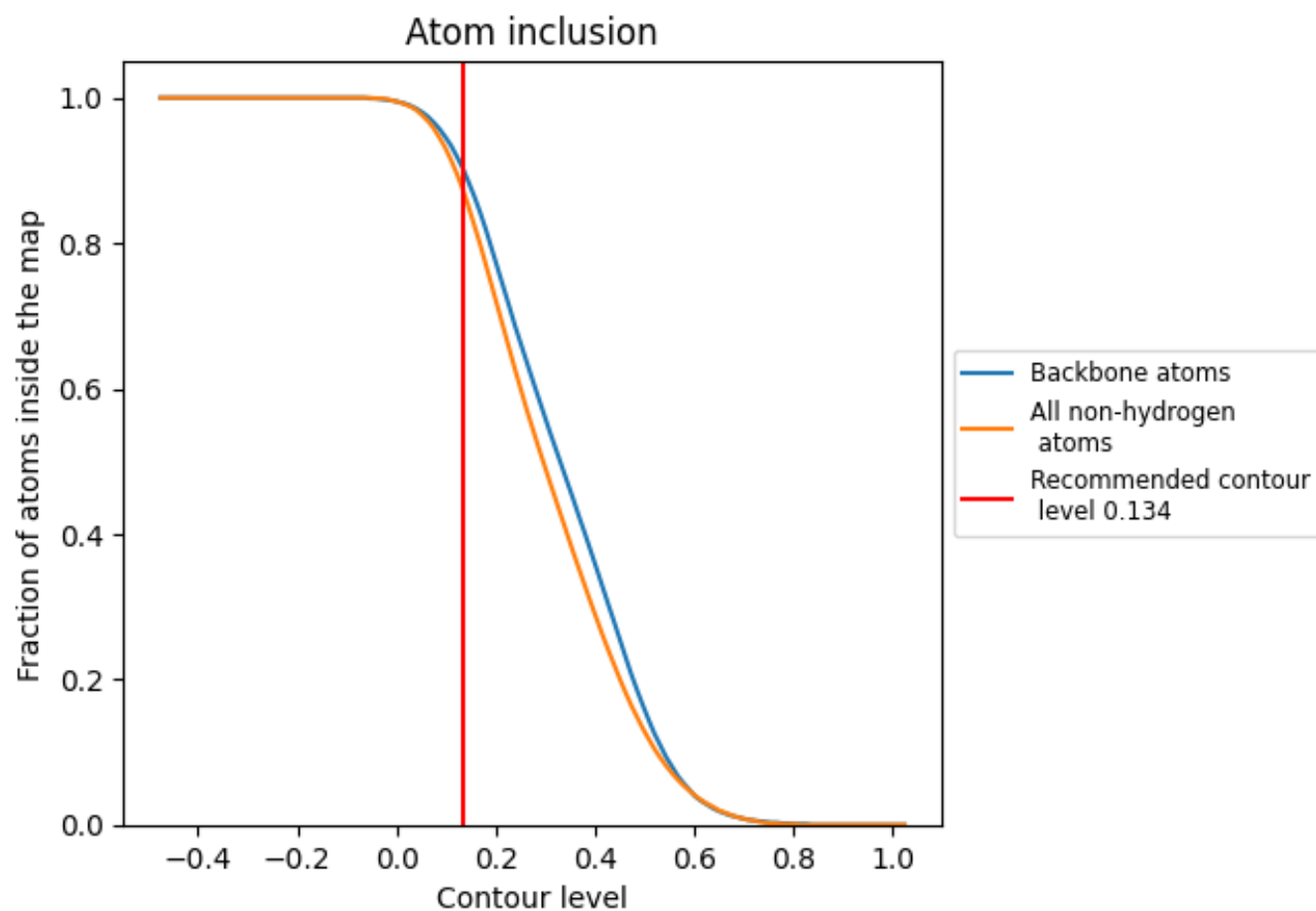


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 87% 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 (0.134) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.4440
CB	 0.7680	 0.4310
CD	 0.8250	 0.4340
L5	 0.9340	 0.4700
L7	 0.9880	 0.5150
L8	 0.9640	 0.4960
LA	 0.9490	 0.5570
LB	 0.9130	 0.5410
LC	 0.9200	 0.5410
LD	 0.8900	 0.5060
LE	 0.8660	 0.4940
LF	 0.9320	 0.5440
LG	 0.8560	 0.4880
LH	 0.9110	 0.5280
LI	 0.9100	 0.5400
LJ	 0.8260	 0.4620
LL	 0.8890	 0.5140
LM	 0.9350	 0.5300
LN	 0.9690	 0.5690
LO	 0.9390	 0.5470
LP	 0.9440	 0.5560
LQ	 0.9480	 0.5610
LR	 0.8810	 0.5060
LS	 0.9550	 0.5620
LT	 0.9180	 0.5330
LU	 0.8650	 0.4620
LV	 0.9210	 0.5510
LW	 0.6700	 0.3570
LX	 0.9090	 0.5270
LY	 0.9190	 0.5350
LZ	 0.9260	 0.5240
La	 0.9560	 0.5620
Lb	 0.8480	 0.4780
Lc	 0.8880	 0.4960
Ld	 0.9040	 0.5240



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Le	 0.9560	 0.5600
Lf	 0.9470	 0.5600
Lg	 0.9330	 0.5450
Lh	 0.9220	 0.5380
Li	 0.9220	 0.5180
Lj	 0.9670	 0.5580
Lk	 0.8550	 0.4800
Ll	 0.9620	 0.5580
Lm	 0.9250	 0.5480
Ln	 0.9380	 0.5460
Lo	 0.9080	 0.5320
Lp	 0.9320	 0.5410
Lr	 0.9290	 0.5450
Ls	 0.7400	 0.3930
Lt	 0.4870	 0.2210
Lz	 0.0810	 0.1110
S2	 0.9030	 0.3840
SA	 0.7510	 0.3810
SB	 0.5890	 0.2450
SC	 0.8710	 0.4860
SD	 0.7960	 0.4290
SE	 0.6830	 0.2840
SF	 0.7580	 0.3660
SG	 0.5730	 0.2010
SH	 0.5380	 0.2180
SI	 0.7190	 0.3420
SJ	 0.7870	 0.4000
SK	 0.8160	 0.4080
SL	 0.7520	 0.4020
SM	 0.5130	 0.2420
SN	 0.7950	 0.3970
SO	 0.6020	 0.2480
SP	 0.8100	 0.4190
SQ	 0.7870	 0.3870
SR	 0.6800	 0.3350
SS	 0.7340	 0.3700
ST	 0.7880	 0.3760
SU	 0.7590	 0.3770
SV	 0.8260	 0.4270
SW	 0.8970	 0.4860
SX	 0.8710	 0.5050
SY	 0.6310	 0.2400

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SZ	 0.6480	 0.3060
Sa	 0.8300	 0.4230
Sb	 0.6230	 0.2550
Sc	 0.6870	 0.3710
Sd	 0.8960	 0.4620
Se	 0.7480	 0.4350
Sf	 0.6400	 0.2430
Sg	 0.6790	 0.3080