



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 05:11 AM UTC

PDB ID : 9G6K / pdb_00009g6k
EMDB ID : EMD-51104
Title : LSU structure derived from the LSU sample of the mitoribosome from *T. gondii*.
Authors : Rocha, R.E.O.; Barua, S.; Boissier, F.; Nguyen, T.T.; Hashem, Y.
Deposited on : 2024-07-18
Resolution : 2.89 Å(reported)
Based on initial model : .

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

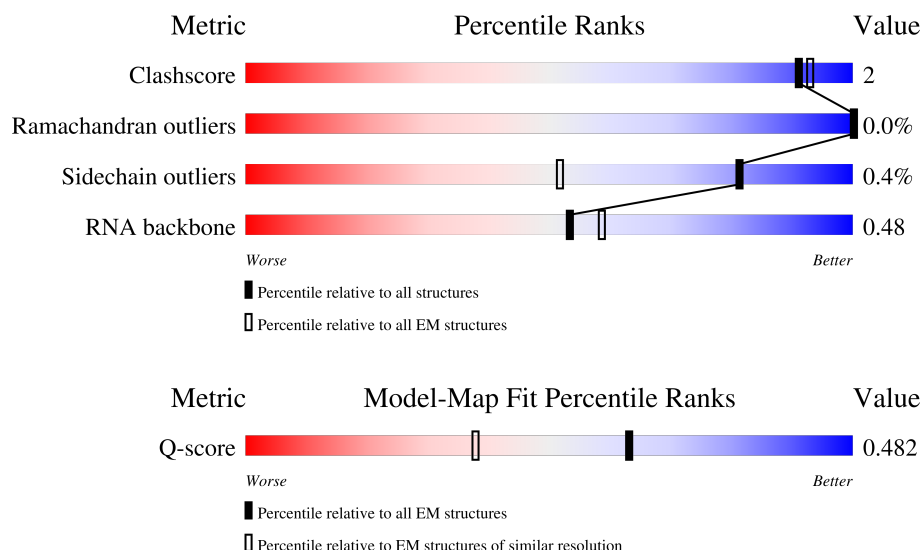
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.89 Å.

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



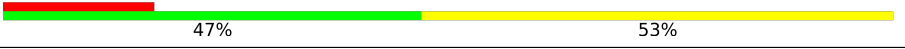
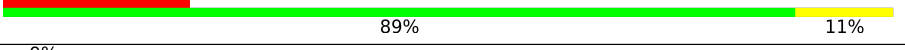
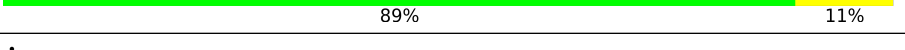
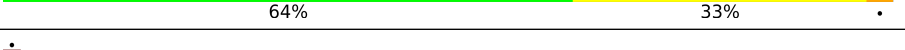
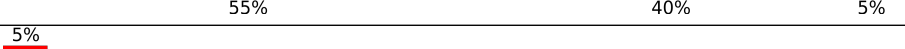
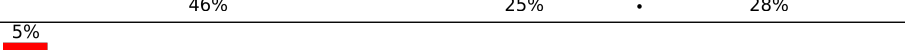
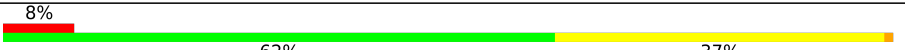
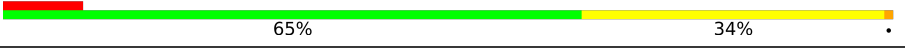
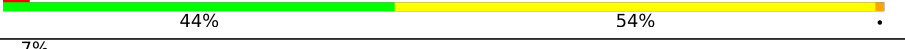
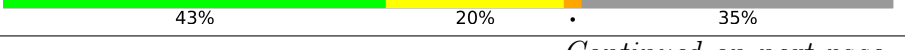
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12148 (2.39 - 3.39)

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	L0	405	5% 52% 35% 13%
2	L1	92	11% 67% 30% .
3	L2	270	9% 76% 23% .

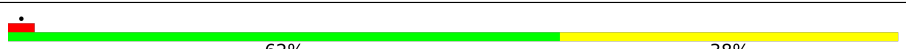
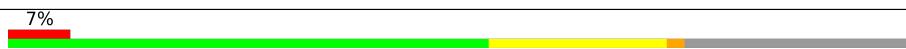
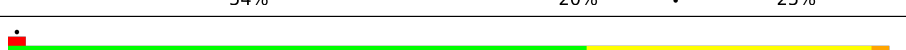
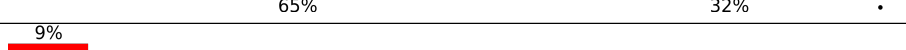
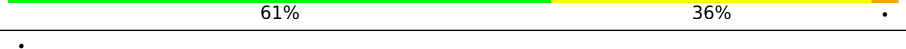
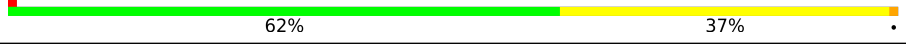
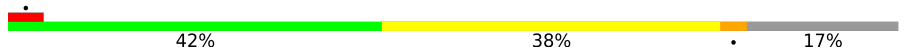
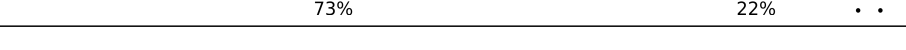
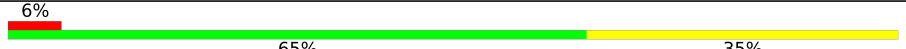
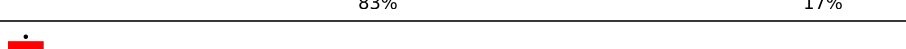
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Mol	Chain	Length	Quality of chain
4	L3	331	
5	L4	430	
6	L5	30	
7	L6	57	
8	L7	114	
9	L8	246	
10	L9	475	
11	LA	217	
12	LB	121	
13	LC	527	
14	LD	282	
15	LE	338	
16	LF	88	
17	LG	148	
18	LH	87	
19	LI	79	
20	LJ	443	
21	LK	219	
22	LL	855	
23	LM	177	
24	LN	113	
25	LO	344	
26	LP	230	
27	LQ	70	
28	LR	132	

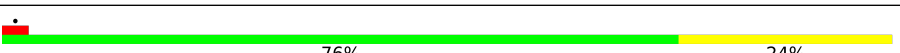
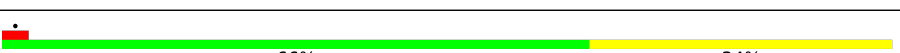
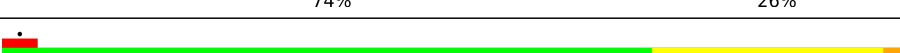
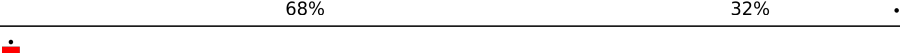
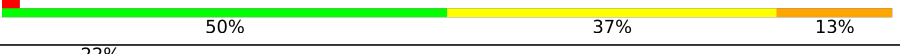
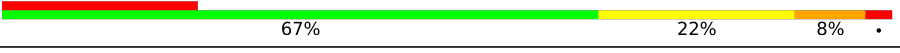
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Mol	Chain	Length	Quality of chain
29	LS	228	
30	LT	117	
31	LU	79	
32	LV	880	
33	LW	306	
34	LX	92	
35	LY	346	
36	LZ	197	
37	La	214	
38	Lb	733	
39	Lc	512	
40	Ld	437	
41	Le	376	
42	Lf	226	
43	Lg	214	
44	Lh	464	
45	Li	602	
46	Lj	122	
47	Lk	184	
48	Ll	190	
49	Lm	189	
50	Ln	60	
51	Lo	283	
52	Lp	368	
53	Lq	787	

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Mol	Chain	Length	Quality of chain
54	Lr	281	
55	Ls	311	
56	Lt	240	
57	Lu	232	
58	Lv	112	
59	Lw	179	
60	Lx	98	
61	Ly	404	
62	Lz	120	
63	UA	85	
64	UB	174	
65	UC	105	
66	UD	35	
67	UE	113	
68	UF	78	
69	UG	158	
70	UH	47	
71	UI	35	
72	10	44	
73	11	50	
74	12	31	
75	13	59	
76	14	94	
77	15	36	
78	16	50	

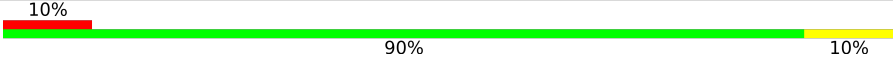
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Mol	Chain	Length	Quality of chain
79	I7	69	
80	I8	33	
81	I9	91	
82	IA	65	
83	IB	45	
84	IC	27	
85	ID	16	
86	IE	29	
87	IF	88	
88	IG	26	
89	IH	27	
90	II	48	
91	IJ	279	
92	IK	38	
93	IL	91	
94	IM	194	
95	IN	62	
96	IO	180	
97	IP	29	
98	IQ	37	
99	IR	28	
100	IS	7	
101	IT	14	
101	IW	14	
102	IU	15	

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Mol	Chain	Length	Quality of chain
103	IV	10	
103	IY	10	
104	IX	58	

2 Entry composition

There are 104 unique types of molecules in this entry. The entry contains 175729 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 RRM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L0	353	Total	C	N	O	S	0	0
			2984	1911	557	503	13		

- Molecule 2 is a protein called Large ribosomal subunit protein mL54.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	92	Total	C	N	O	S	0	0
			768	502	130	134	2		

- Molecule 3 is a protein called mL162.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	270	Total	C	N	O	S	0	0
			2111	1329	384	392	6		

- Molecule 4 is a protein called Ribosomal l25 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L3	272	Total	C	N	O	S	0	0
			2196	1411	389	383	13		

- Molecule 5 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L4	424	Total	C	N	O	S	0	0
			3430	2184	620	609	17		

- Molecule 6 is a protein called mL183.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	30	Total	C	N	O	S	0	0
			264	164	62	36	2		

- Molecule 7 is a protein called uL1m.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L6	57	Total	C	N	O	S	0	0
			476	312	92	71	1		

- Molecule 8 is a protein called uL14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	114	Total	C	N	O	S	0	0
			906	571	181	149	5		

- Molecule 9 is a protein called Putative 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L8	239	Total	C	N	O	S	0	0
			2008	1276	384	341	7		

- Molecule 10 is a protein called DUF6832 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L9	475	Total	C	N	O	S	0	0
			3888	2511	683	679	15		

- Molecule 11 is a protein called Putative 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LA	217	Total	C	N	O	S	0	0
			1708	1094	322	284	8		

- Molecule 12 is a protein called Putative ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LB	121	Total	C	N	O	S	0	0
			1033	663	200	165	5		

- Molecule 13 is a protein called Macro domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LC	380	Total	C	N	O	S	0	0
			2909	1822	549	528	10		

- Molecule 14 is a protein called Ribosomal protein L46.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LD	225	Total	C	N	O	S	0	0
			1847	1197	319	328	3		

- Molecule 15 is a protein called FAS1 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LE	267	Total	C	N	O	S	0	0
			2118	1345	398	367	8		

- Molecule 16 is a protein called bL36m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LF	88	Total	C	N	O	S	0	0
			731	466	152	109	4		

- Molecule 17 is a protein called Ribosomal protein RPL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LG	148	Total	C	N	O	S	0	0
			1253	804	235	211	3		

- Molecule 18 is a protein called Ribosomal protein L9, N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	LH	87	Total	C	N	O	0	0
			693	442	135	116		

- Molecule 19 is a protein called Putative 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LI	79	Total	C	N	O	S	0	0
			613	402	109	98	4		

- Molecule 20 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LJ	443	Total	C	N	O	S	0	0
			3640	2316	690	616	18		

- Molecule 21 is a protein called BIR protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LK	219	Total	C	N	O	S	0	0
			1905	1211	364	324	6		

- Molecule 22 is a protein called AMP-dependent synthetase/ligase domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LL	633	Total	C	N	O	S	0	0
			4847	3061	882	883	21		

- Molecule 23 is a protein called Large ribosomal subunit protein uL11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LM	177	Total	C	N	O	S	0	0
			1376	867	258	240	11		

- Molecule 24 is a protein called bL35m.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LN	113	Total	C	N	O	S	0	0
			986	626	205	153	2		

- Molecule 25 is a protein called LSU ribosomal protein L2P, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LO	344	Total	C	N	O	S	0	0
			2647	1662	530	448	7		

- Molecule 26 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LP	202	Total	C	N	O	S	0	0
			1636	1041	297	288	10		

- Molecule 27 is a protein called mL175.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	LQ	70	Total	C	N	O	0	0
			600	383	120	97		

- Molecule 28 is a protein called mL172.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LR	86	Total	C	N	O	S	0	0
			738	461	146	127	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL24c.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LS	228	Total	C	N	O	S	0	0
			1812	1154	333	314	11		

- Molecule 30 is a protein called Putative 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LT	113	Total	C	N	O	S	0	0
			965	622	184	156	3		

- Molecule 31 is a protein called Large ribosomal subunit protein mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LU	79	Total	C	N	O	S	0	0
			623	398	118	105	2		

- Molecule 32 is a protein called mL148.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LV	662	Total	C	N	O	S	0	0
			5149	3256	961	913	19		

- Molecule 33 is a protein called Putative 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LW	306	Total	C	N	O	S	0	0
			2433	1553	441	425	14		

- Molecule 34 is a protein called mL176.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LX	92	Total	C	N	O	S	0	0
			779	496	132	146	5		

- Molecule 35 is a protein called Ribosomal L22p/L17e protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LY	346	Total	C	N	O	S	0	0
			2909	1858	561	483	7		

- Molecule 36 is a protein called mL174.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LZ	197	Total	C	N	O	S	0	0
			1591	1012	304	267	8		

- Molecule 37 is a protein called Large ribosomal subunit protein uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	La	214	Total	C	N	O	S	0	0
			1769	1146	320	297	6		

- Molecule 38 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lb	609	Total	C	N	O	S	0	0
			4929	3140	925	849	15		

- Molecule 39 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lc	473	Total	C	N	O	S	0	0
			3797	2416	681	686	14		

- Molecule 40 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ld	437	Total	C	N	O	S	0	0
			3507	2233	626	633	15		

- Molecule 41 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Le	376	Total	C	N	O	S	0	0
			3057	1925	573	549	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Le	?	-	LEU	deletion	UNP S8GIP4

- Molecule 42 is a protein called HECT-domain (Ubiquitin-transferase) domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lf	216	Total	C	N	O	S	0	0
			1709	1093	315	294	7		

- Molecule 43 is a protein called Large ribosomal subunit protein uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lg	214	Total	C	N	O	S	0	0
			1824	1156	345	314	9		

- Molecule 44 is a protein called Large ribosomal subunit protein uL4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lh	443	Total	C	N	O	S	0	0
			3675	2351	682	628	14		

- Molecule 45 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Li	473	Total	C	N	O	S	0	0
			3833	2459	702	656	16		

- Molecule 46 is a protein called mL177.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lj	122	Total	C	N	O	S	0	0
			977	610	200	164	3		

- Molecule 47 is a protein called AP2 domain transcription factor AP2VIIb-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lk	184	Total	C	N	O	S	0	0
			1502	969	267	260	6		

- Molecule 48 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ll	190	Total	C	N	O	S	0	0
			1573	996	307	267	3		

- Molecule 49 is a protein called Large ribosomal subunit protein uL24c.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lm	184	Total	C	N	O	S	0	0
			1501	944	285	265	7		

- Molecule 50 is a protein called mL185.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ln	60	Total	C	N	O	S	0	0
			442	280	80	79	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ln	?	-	SER	deletion	UNP S8G210
Ln	?	-	ALA	deletion	UNP S8G210

- Molecule 51 is a protein called Transmembrane protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Lo	283	Total	C	N	O	S	0	0
			2219	1405	421	384	9		

- Molecule 52 is a protein called bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Lp	368	Total	C	N	O	S	0	0
			3074	1954	595	514	11		

- Molecule 53 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Lq	687	Total	C	N	O	S	0	0
			5268	3323	958	966	21		

- Molecule 54 is a protein called Putative ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Lr	281	Total	C	N	O	S	0	0
			2342	1475	461	398	8		

- Molecule 55 is a protein called Ribosomal protein L15, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Ls	311	Total	C	N	O	S	0	0
			2565	1615	507	438	5		

- Molecule 56 is a protein called mL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Lt	188	Total	C	N	O	S	0	0
			1556	999	276	274	7		

- Molecule 57 is a protein called mL164.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Lu	232	Total	C	N	O	S	0	0
			1834	1158	328	339	9		

- Molecule 58 is a protein called mL180.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Lv	112	Total	C	N	O	S	0	0
			928	599	165	159	5		

- Molecule 59 is a protein called Putative 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Lw	179	Total	C	N	O	S	0	0
			1440	916	282	240	2		

- Molecule 60 is a protein called mL173.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Lx	98	Total	C	N	O	S	0	0
			796	504	149	138	5		

- Molecule 61 is a protein called Large ribosomal subunit protein bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Ly	340	Total	C	N	O	S	0	0
			2821	1777	551	482	11		

- Molecule 62 is a protein called mL182.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Lz	120	Total	C	N	O	S	0	0
			994	620	188	184	2		

- Molecule 63 is a protein called mL178.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	UA	85	Total	C	N	O	S	0	0
			709	464	133	111	1		

- Molecule 64 is a protein called bL27m.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	UB	174	Total	C	N	O	S	0	0
			1451	921	281	245	4		

- Molecule 65 is a protein called mL179.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	UC	105	Total	C	N	O	S	0	0
			864	567	150	141	6		

- Molecule 66 is a protein called Transmembrane protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	UD	35	Total	C	N	O	S	0	0
			308	192	72	43	1		

- Molecule 67 is a protein called mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	UE	113	Total	C	N	O	S	0	0
			935	598	165	166	6		

- Molecule 68 is a protein called bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	UF	78	Total	C	N	O	S	0	0
			672	443	122	105	2		

- Molecule 69 is a protein called AP2 domain transcription factor AP2IV-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	UG	158	Total	C	N	O	S	0	0
			1343	846	266	227	4		

- Molecule 70 is a protein called mL181.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	UH	47	Total	C	N	O	S	0	0
			401	254	80	64	3		

- Molecule 71 is a protein called mL184.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	UI	35	Total	C	N	O	S	0	0
			293	178	71	41	3		

- Molecule 72 is a RNA chain called RNA23t.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	10	44	Total	C	N	O	P	0	0
			936	419	170	303	44		

- Molecule 73 is a RNA chain called RNA29.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	11	50	Total	C	N	O	P	0	0
			1070	480	197	343	50		

- Molecule 74 is a RNA chain called LSUB.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	12	31	Total	C	N	O	P	0	0
			660	296	116	217	31		

- Molecule 75 is a RNA chain called RNA6.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	13	59	Total	C	N	O	P	0	0
			1254	563	227	405	59		

- Molecule 76 is a RNA chain called RNA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	14	94	Total	C	N	O	P	0	0
			1991	893	346	658	94		

- Molecule 77 is a RNA chain called RNA31.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	15	36	Total	C	N	O	P	0	0
			761	341	129	255	36		

- Molecule 78 is a RNA chain called RNA14.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	16	50	Total	C	N	O	P	0	0
			1072	483	209	330	50		

- Molecule 79 is a RNA chain called RNA11.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	17	69	Total	C	N	O	P	0	0
			1481	666	279	467	69		

- Molecule 80 is a RNA chain called RNA36.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	18	33	Total	C	N	O	P	0	0
			707	318	136	220	33		

- Molecule 81 is a RNA chain called RNA3.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	19	91	Total	C	N	O	P	0	0
			1926	864	336	635	91		

- Molecule 82 is a RNA chain called RNA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	1A	65	Total	C	N	O	P	0	0
			1387	622	253	447	65		

- Molecule 83 is a RNA chain called RNA38.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	1B	45	Total	C	N	O	P	0	0
			985	439	197	304	45		

- Molecule 84 is a RNA chain called RNA35.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	1C	27	Total	C	N	O	P	0	0
			583	261	112	183	27		

- Molecule 85 is a RNA chain called RNA32.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	1D	16	Total	C	N	O	P	0	0
			338	153	62	107	16		

- Molecule 86 is a RNA chain called RNA15.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	1E	29	Total	C	N	O	P	0	0
			630	282	124	195	29		

- Molecule 87 is a RNA chain called RNA10.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	1F	88	Total	C	N	O	P	0	0
			1880	842	339	611	88		

- Molecule 88 is a RNA chain called LSUC.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	1G	26	Total	C	N	O	P	0	0
			561	252	110	173	26		

- Molecule 89 is a RNA chain called RNA16.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	lH	27	Total	C	N	O	P	0	0
			572	256	96	193	27		

- Molecule 90 is a RNA chain called RNA13.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	lI	48	Total	C	N	O	P	0	0
			1039	467	206	318	48		

- Molecule 91 is a RNA chain called LSUD/E.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	lJ	279	Total	C	N	O	P	0	0
			5929	2654	1045	1951	279		

- Molecule 92 is a RNA chain called SSUF.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	lK	38	Total	C	N	O	P	0	0
			821	367	157	259	38		

- Molecule 93 is a RNA chain called RNA7.

Mol	Chain	Residues	Atoms					AltConf	Trace
93	lL	91	Total	C	N	O	P	0	0
			1948	875	361	621	91		

- Molecule 94 is a RNA chain called LSUF/G.

Mol	Chain	Residues	Atoms					AltConf	Trace
94	lM	194	Total	C	N	O	P	0	0
			4121	1843	719	1365	194		

- Molecule 95 is a RNA chain called RNA37.

Mol	Chain	Residues	Atoms					AltConf	Trace
95	lN	62	Total	C	N	O	P	0	0
			1316	592	234	428	62		

- Molecule 96 is a RNA chain called LSUA.

Mol	Chain	Residues	Atoms					AltConf	Trace
96	lO	180	Total	C	N	O	P	0	0
			3841	1722	691	1248	180		

- Molecule 97 is a RNA chain called ulr1.

Mol	Chain	Residues	Atoms					AltConf	Trace
97	lP	29	Total	C	N	O	P	0	0
			580	261	58	232	29		

- Molecule 98 is a RNA chain called ulr2.

Mol	Chain	Residues	Atoms					AltConf	Trace
98	lQ	37	Total	C	N	O	P	0	0
			740	333	74	296	37		

- Molecule 99 is a RNA chain called ulr3.

Mol	Chain	Residues	Atoms					AltConf	Trace
99	lR	28	Total	C	N	O	P	0	0
			560	252	56	224	28		

- Molecule 100 is a RNA chain called ulr4.

Mol	Chain	Residues	Atoms					AltConf	Trace
100	lS	7	Total	C	N	O	P	0	0
			140	63	14	56	7		

- Molecule 101 is a RNA chain called ulr5.

Mol	Chain	Residues	Atoms					AltConf	Trace
101	lT	14	Total	C	N	O	P	0	0
			280	126	28	112	14		
101	lW	14	Total	C	N	O	P	0	0
			280	126	28	112	14		

- Molecule 102 is a RNA chain called ulr6.

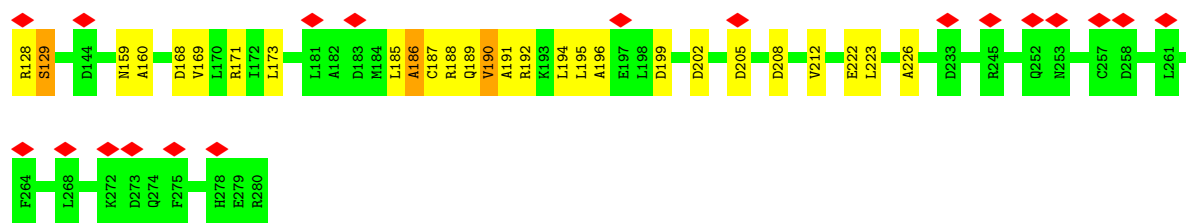
Mol	Chain	Residues	Atoms					AltConf	Trace
102	lU	15	Total	C	N	O	P	0	0
			300	135	30	120	15		

- Molecule 103 is a RNA chain called ulr7,ulr8.

Mol	Chain	Residues	Atoms					AltConf	Trace
103	IV	10	Total	C	N	O	P	0	0
			200	90	20	80	10		
103	IY	10	Total	C	N	O	P	0	0
			200	90	20	80	10		

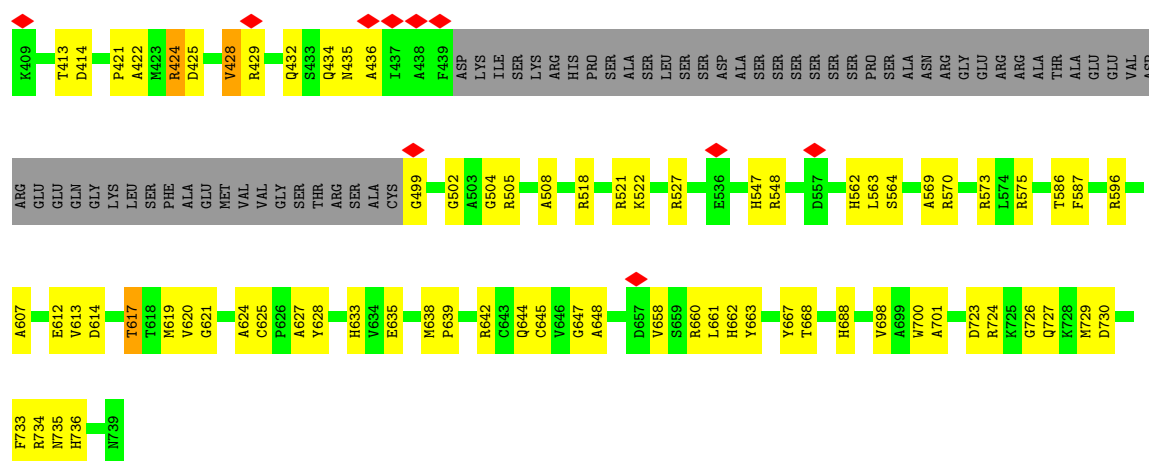
- Molecule 104 is a RNA chain called ulr9.

Mol	Chain	Residues	Atoms					AltConf	Trace
104	IX	58	Total	C	N	O	P	0	0
			1160	522	116	464	58		



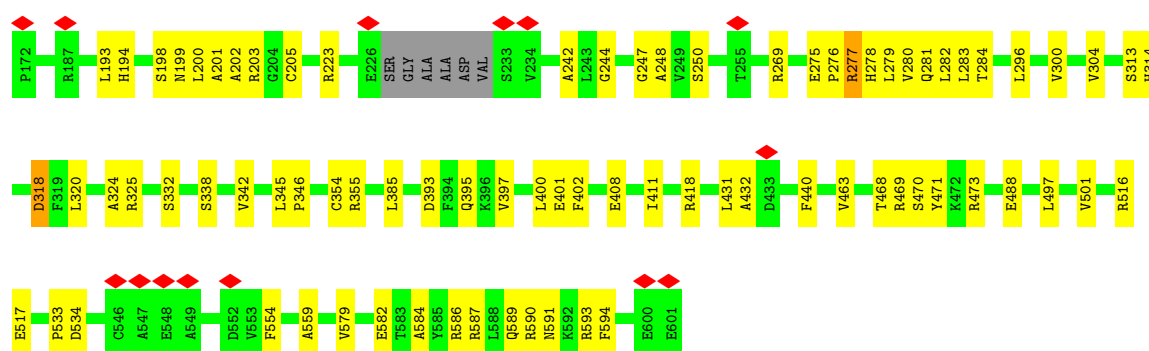
• Molecule 4: Ribosomal l25 family protein

Chain L3: 60% 22% 18%



• Molecule 5: RAP domain-containing protein

Chain L4: 80% 18%



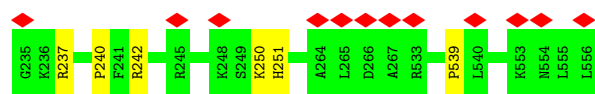
• Molecule 6: mL183

Chain L5: 17% 47% 53%

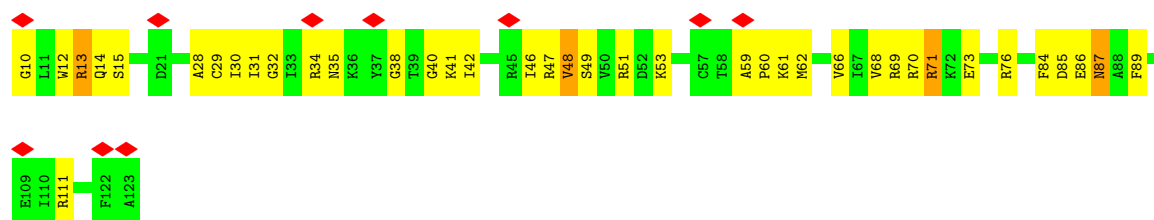


• Molecule 7: uL1m

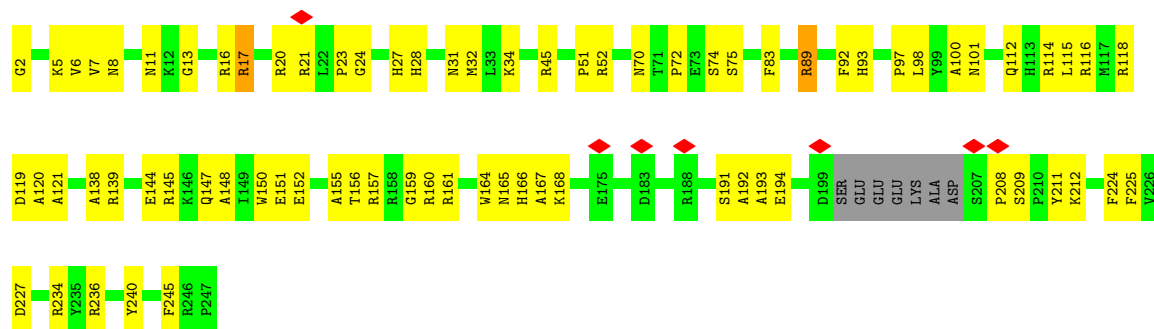
Chain L6: 21% 89% 11%



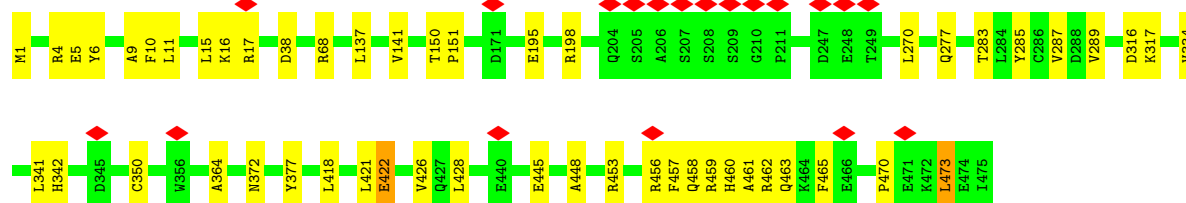
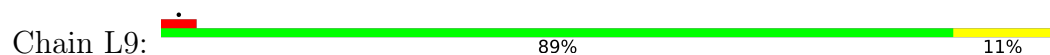
• Molecule 8: uL14m



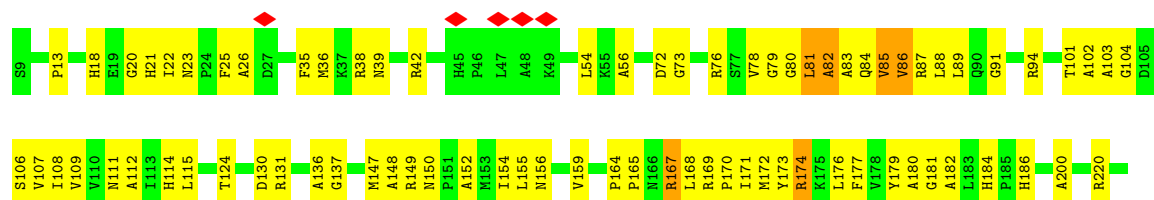
• Molecule 9: Putative 50S ribosomal protein L17



• Molecule 10: DUF6832 domain-containing protein



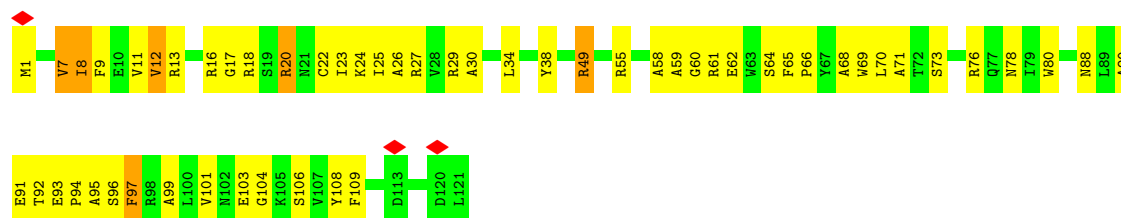
• Molecule 11: Putative 50S ribosomal protein L13



G225

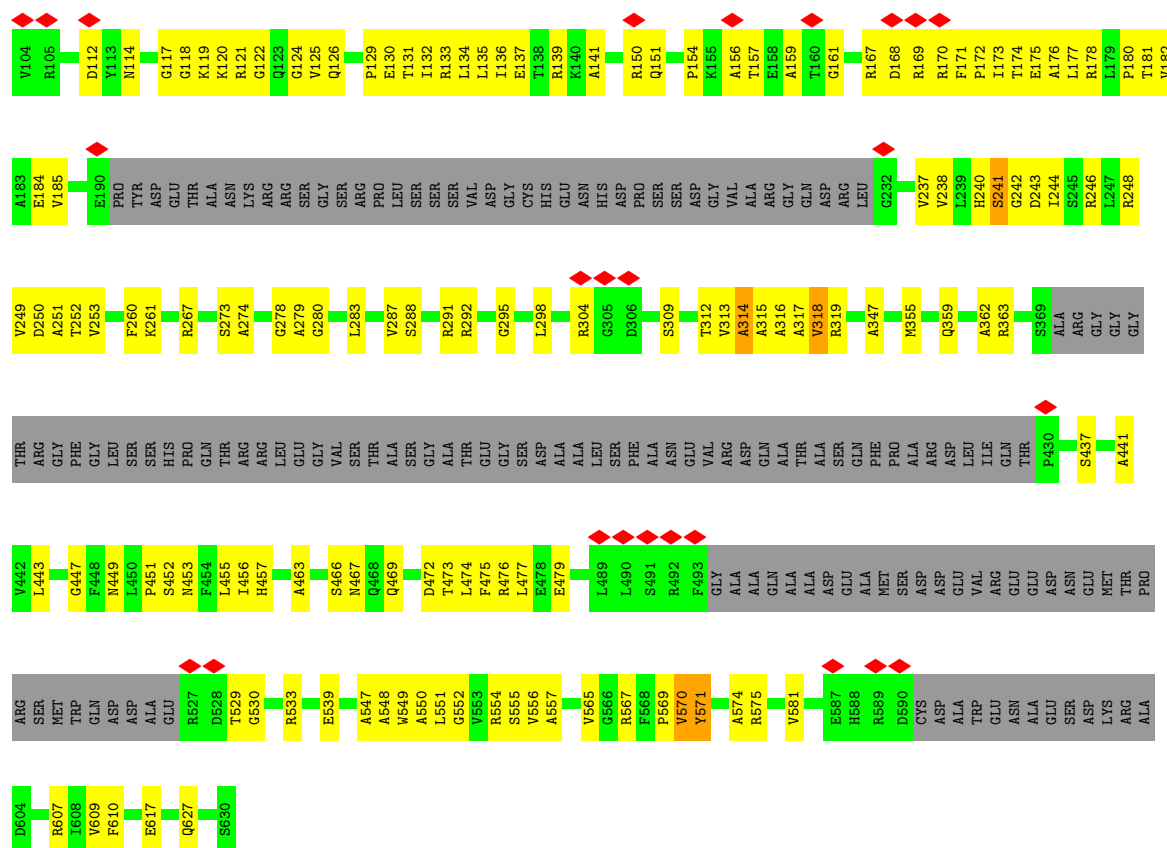
- Molecule 12: Putative ribosomal protein L20

Chain LB: 



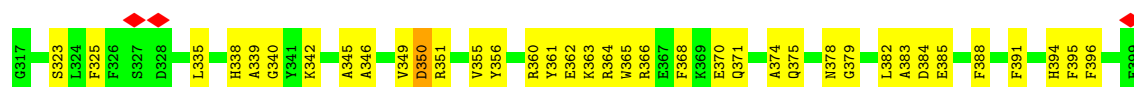
- Molecule 13: Macro domain-containing protein

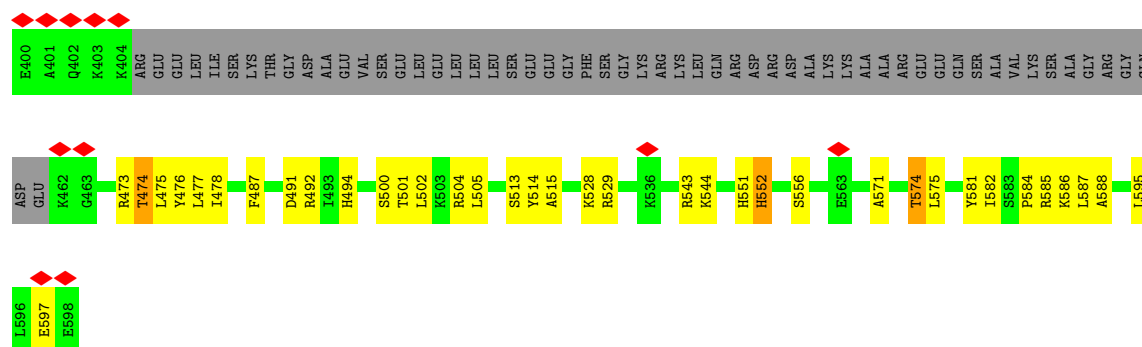
Chain LC: 



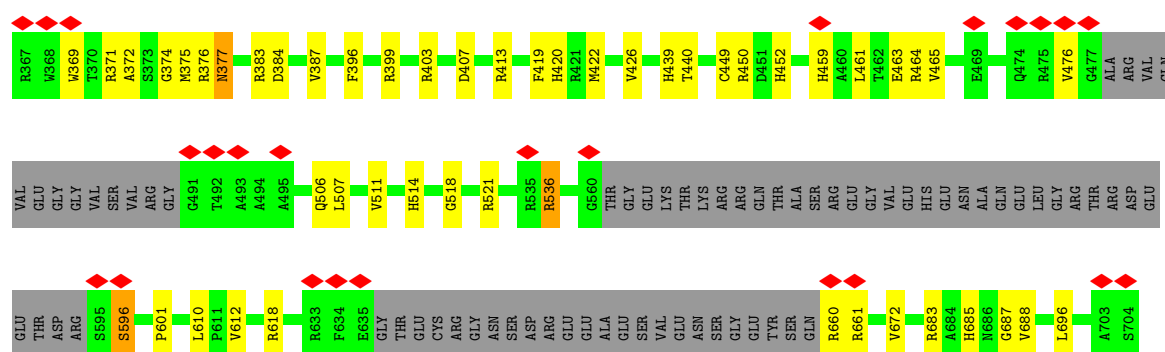
- Molecule 14: Ribosomal protein L46

Chain LD: 

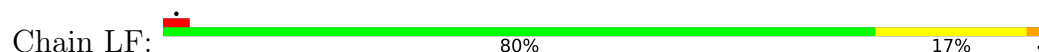




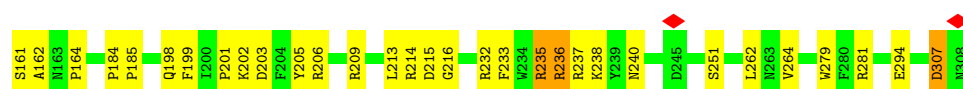
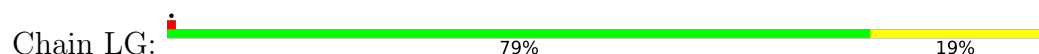
- Molecule 15: FAS1 domain-containing protein



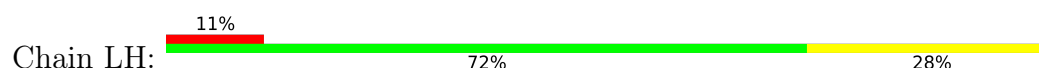
- Molecule 16: bL36m



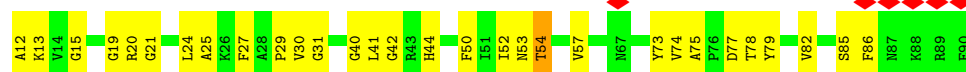
- Molecule 17: Ribosomal protein RPL22



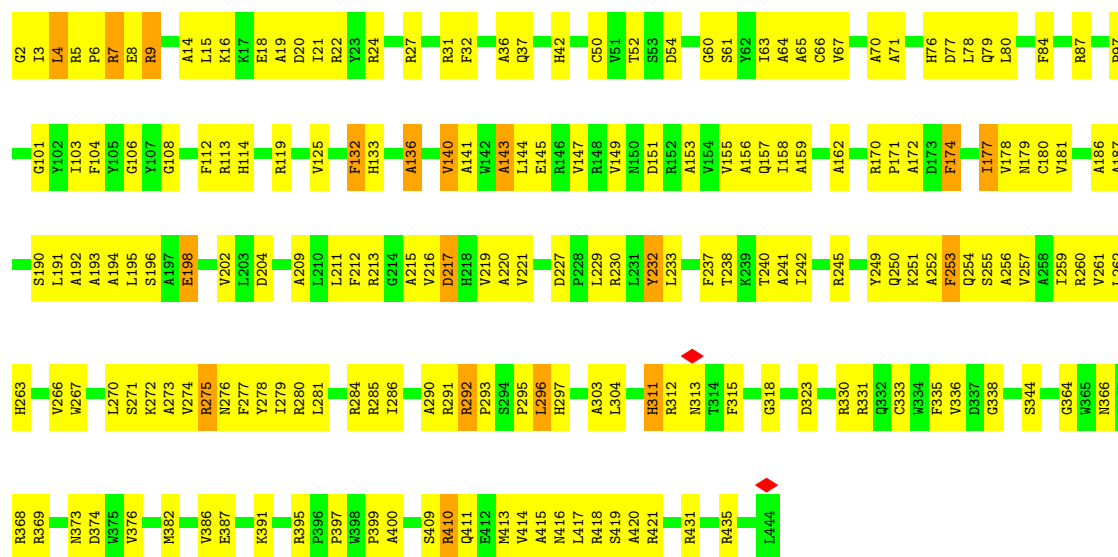
- Molecule 18: Ribosomal protein L9, N-terminal domain-containing protein



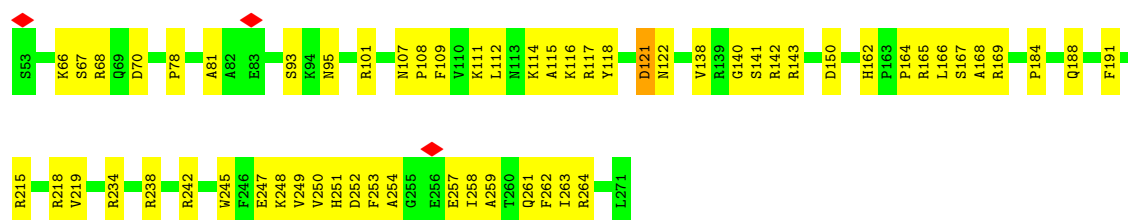
- Molecule 19: Putative 60S ribosomal protein L27



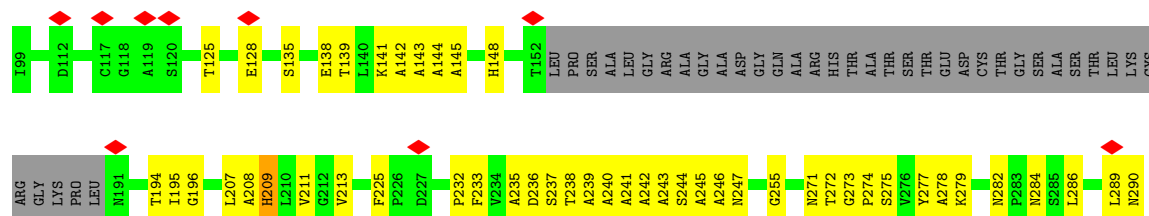
• Molecule 20: RAP domain-containing protein

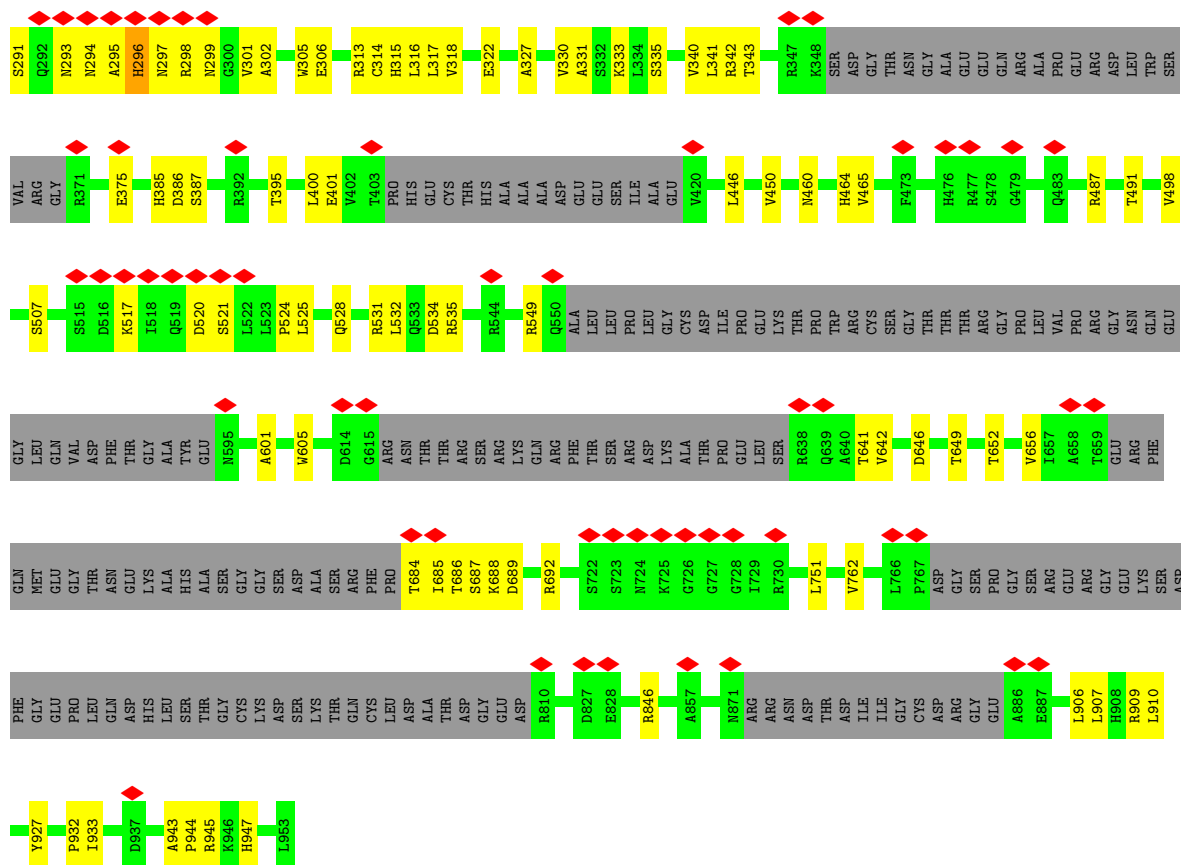


• Molecule 21: BIR protein

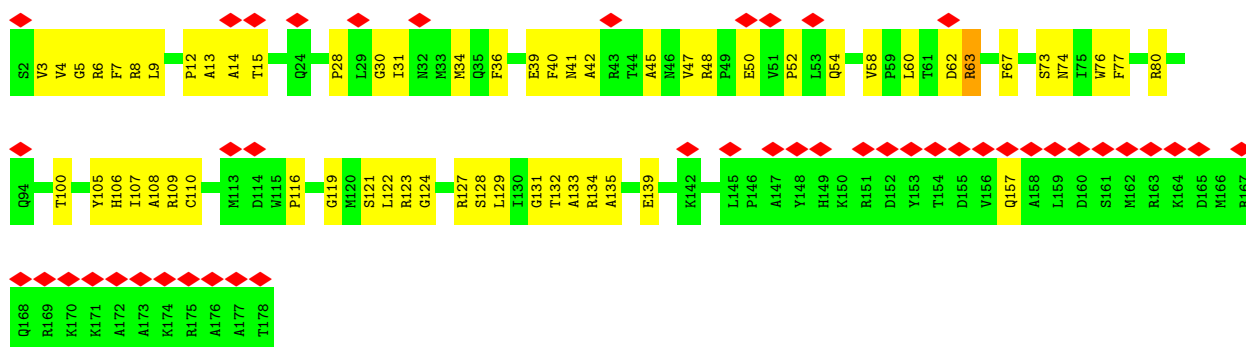


• Molecule 22: AMP-dependent synthetase/ligase domain-containing protein

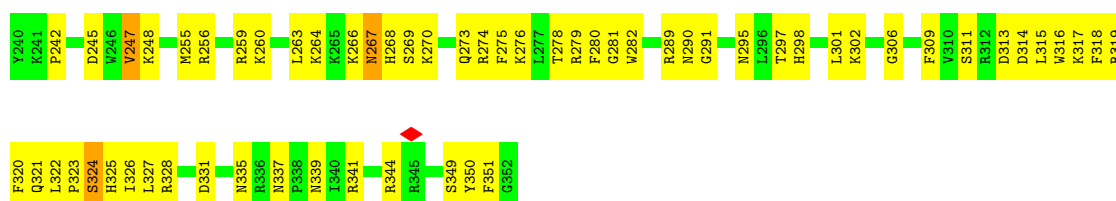




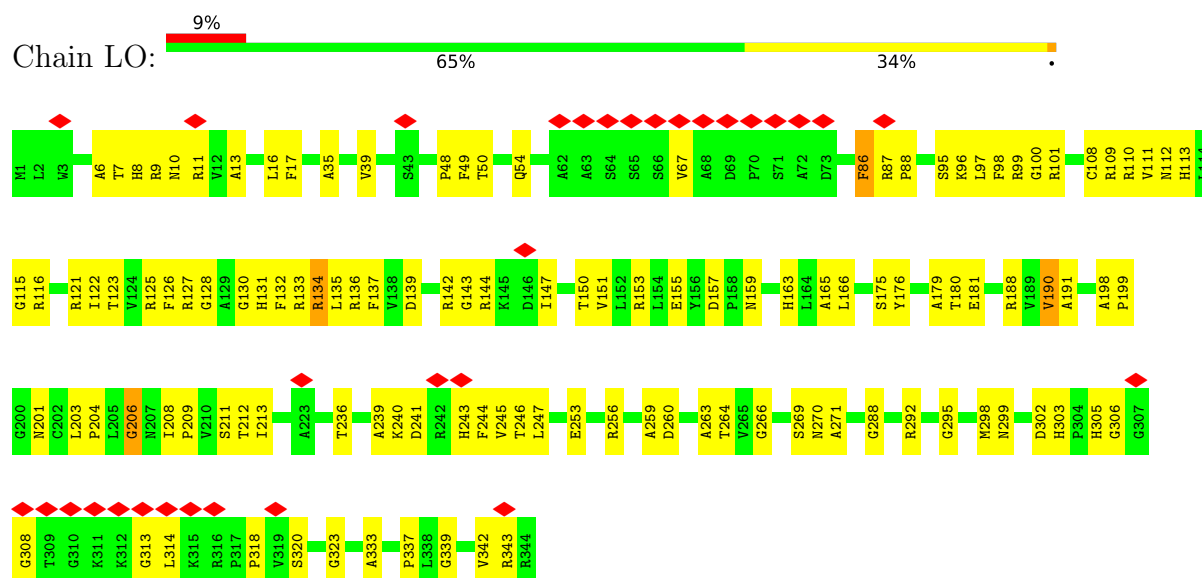
• Molecule 23: Large ribosomal subunit protein uL11m



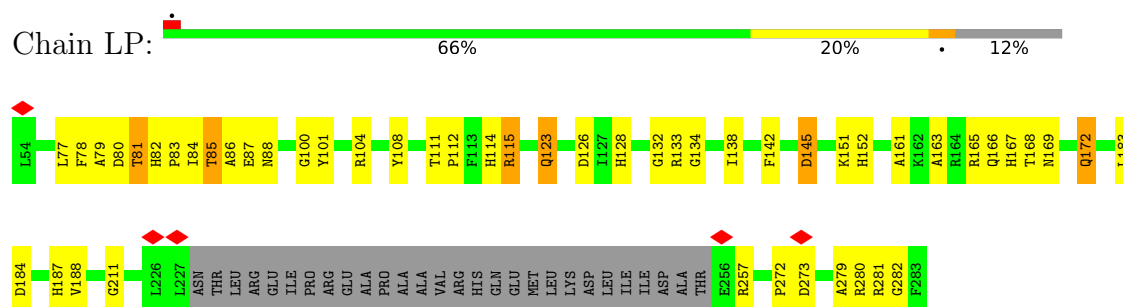
• Molecule 24: bL35m



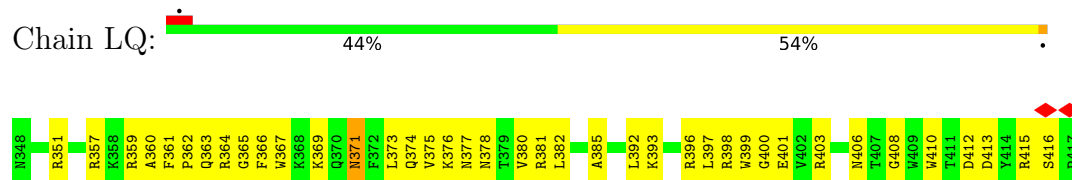
- Molecule 25: LSU ribosomal protein L2P, putative



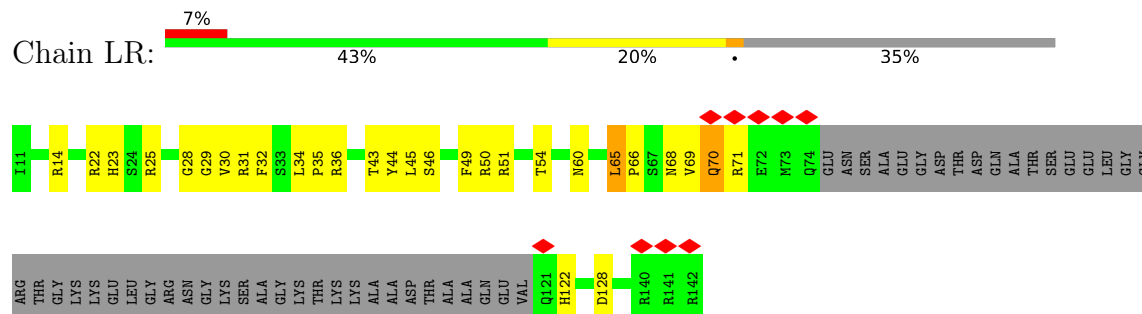
- Molecule 26: Peptidyl-prolyl cis-trans isomerase



- Molecule 27: mL175

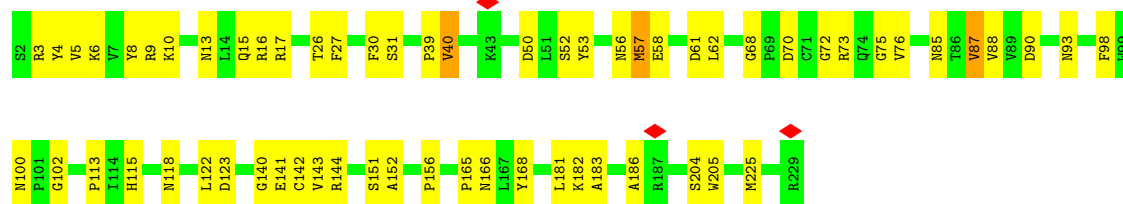


- Molecule 28: mL172



- Molecule 29: Large ribosomal subunit protein uL24c

Chain LS: 



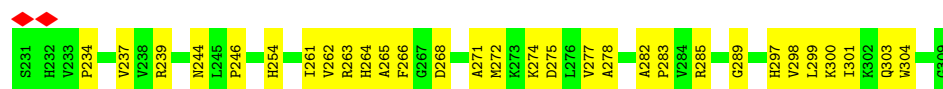
- Molecule 30: Putative 50S ribosomal protein L33

Chain LT: 



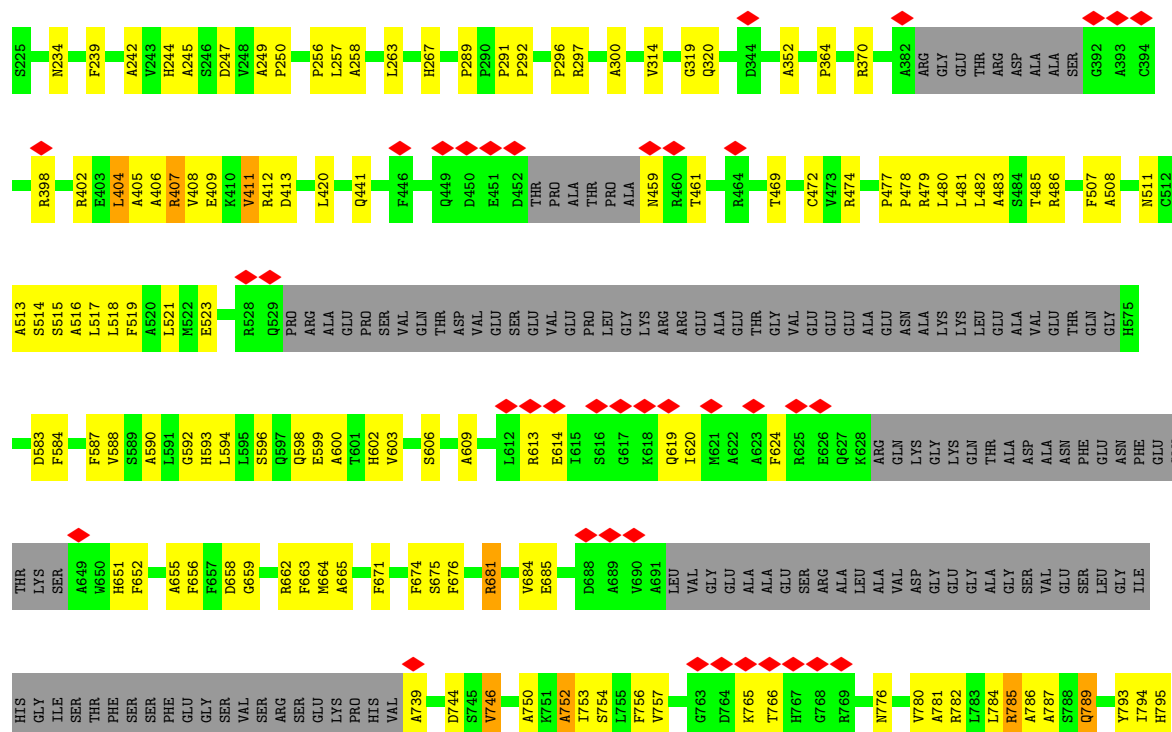
- Molecule 31: Large ribosomal subunit protein mL49

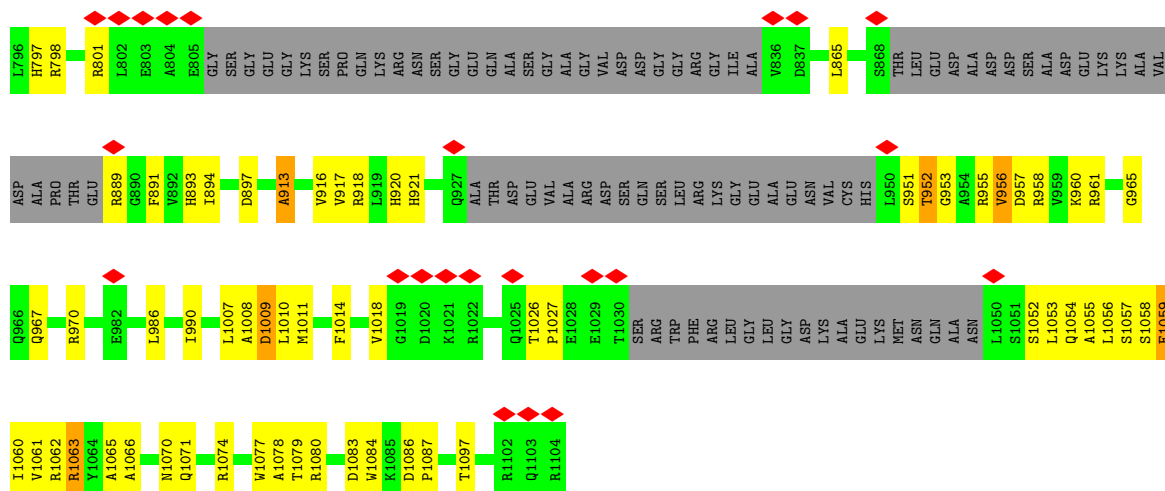
Chain LU: 



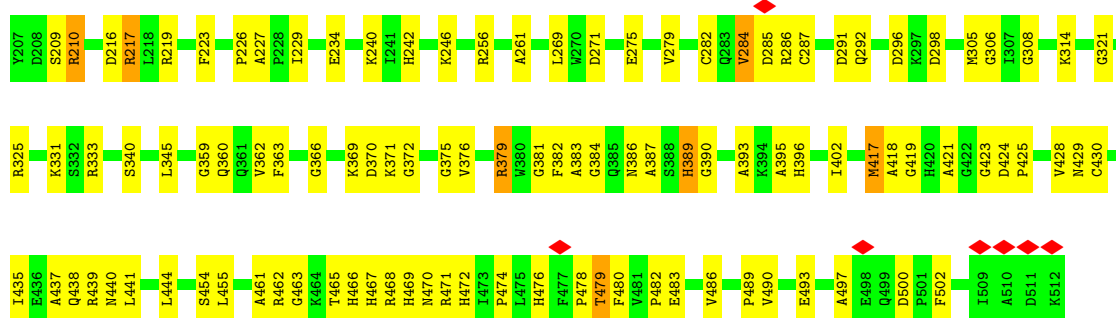
- Molecule 32: mL148

Chain LV: 

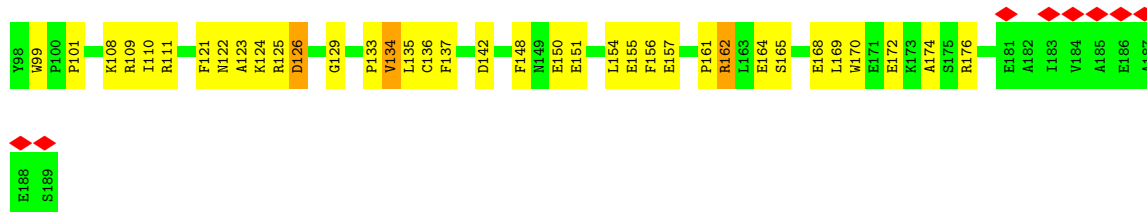




• Molecule 33: Putative 50S ribosomal protein L3

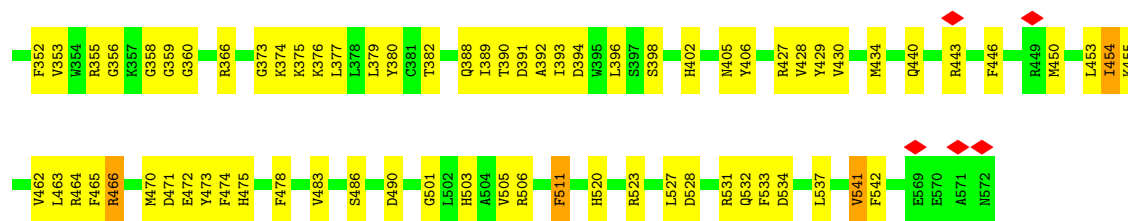


• Molecule 34: mL176



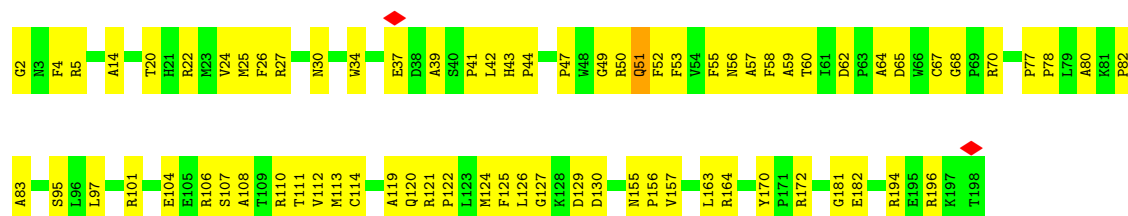
• Molecule 35: Ribosomal L22p/L17e protein





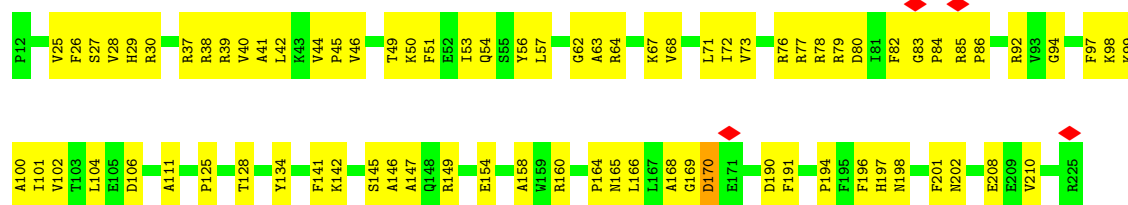
• Molecule 36: mL174

Chain LZ: 62% 37%



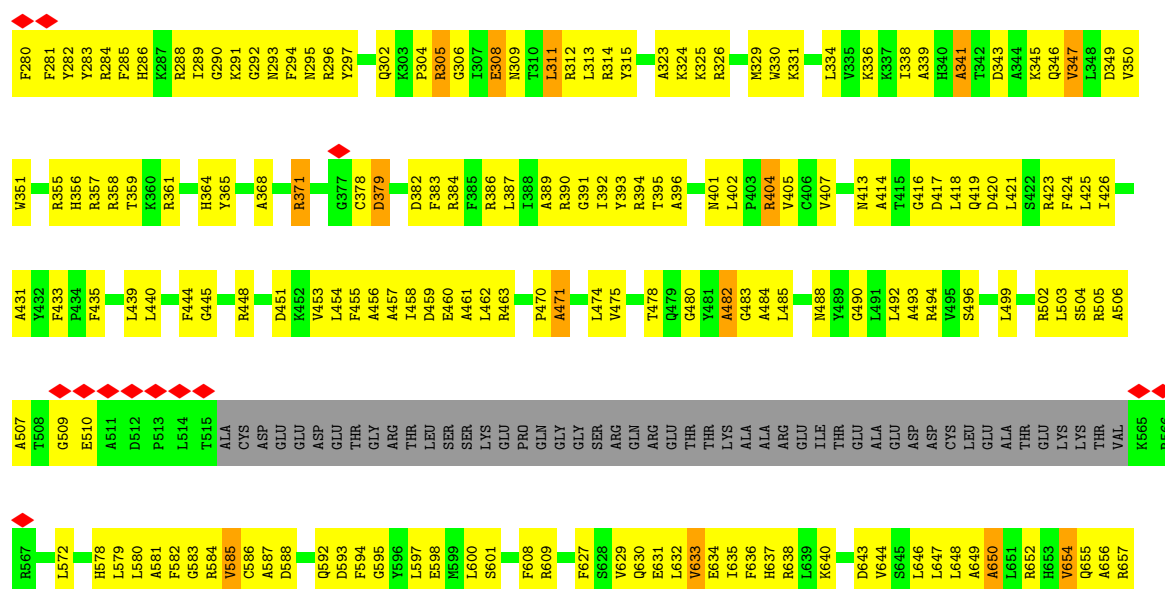
• Molecule 37: Large ribosomal subunit protein uL23m

Chain La: 63% 36%



• Molecule 38: RAP domain-containing protein

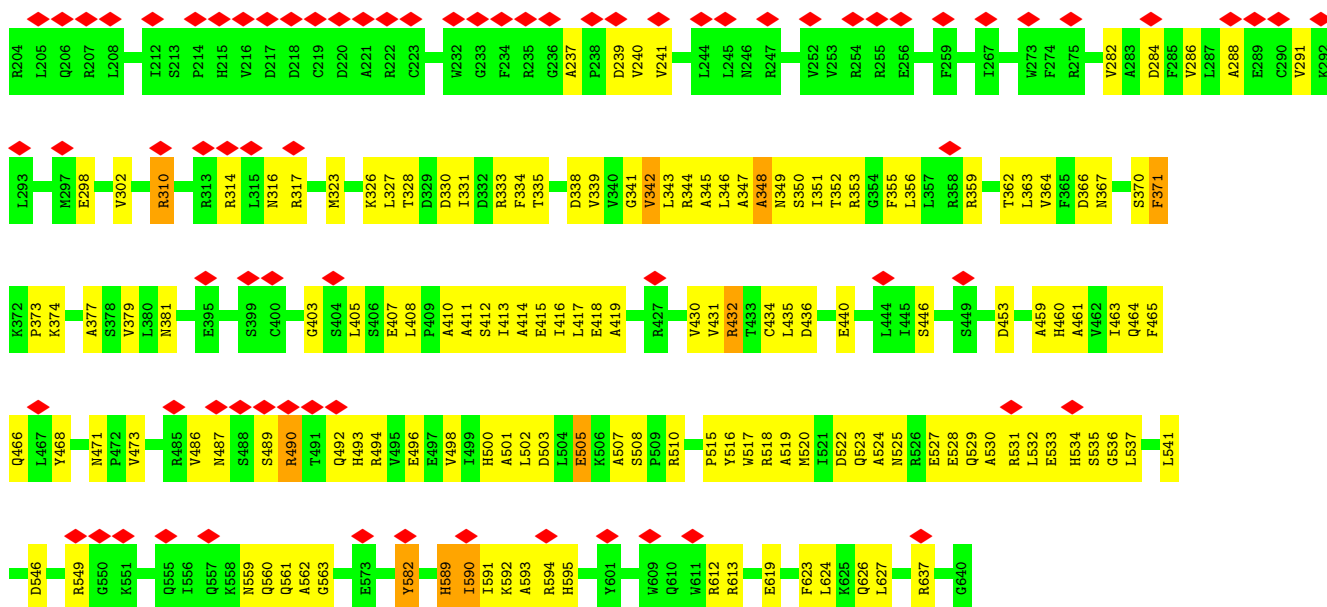
Chain Lb: 42% 38% 17%



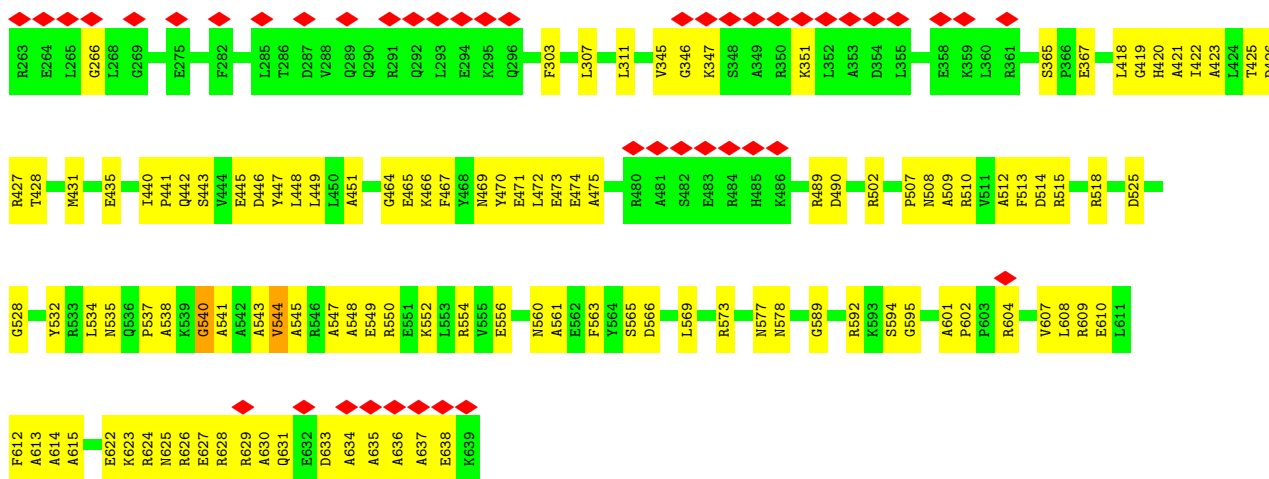


• Molecule 39: RAP domain-containing protein

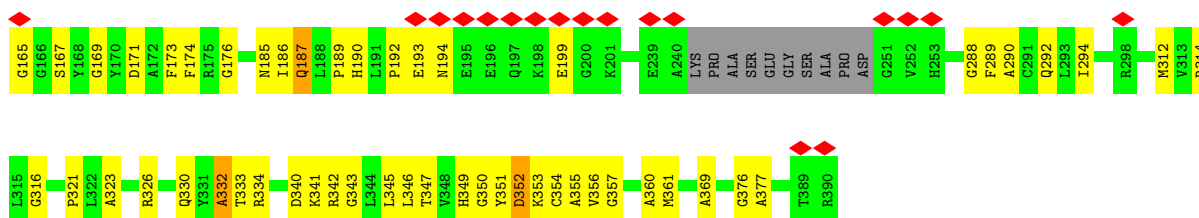
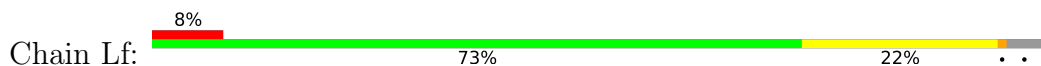
• Molecule 40: RAP domain-containing protein



• Molecule 41: RAP domain-containing protein

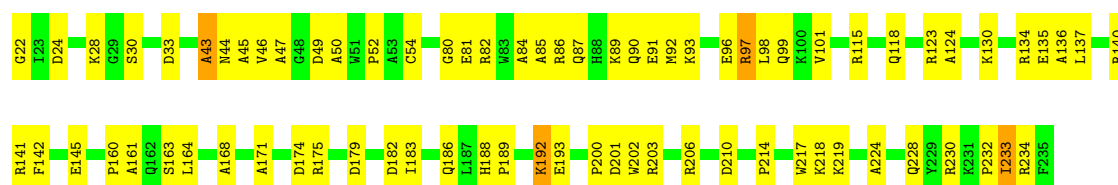


• Molecule 42: HECT-domain (Ubiquitin-transferase) domain-containing protein



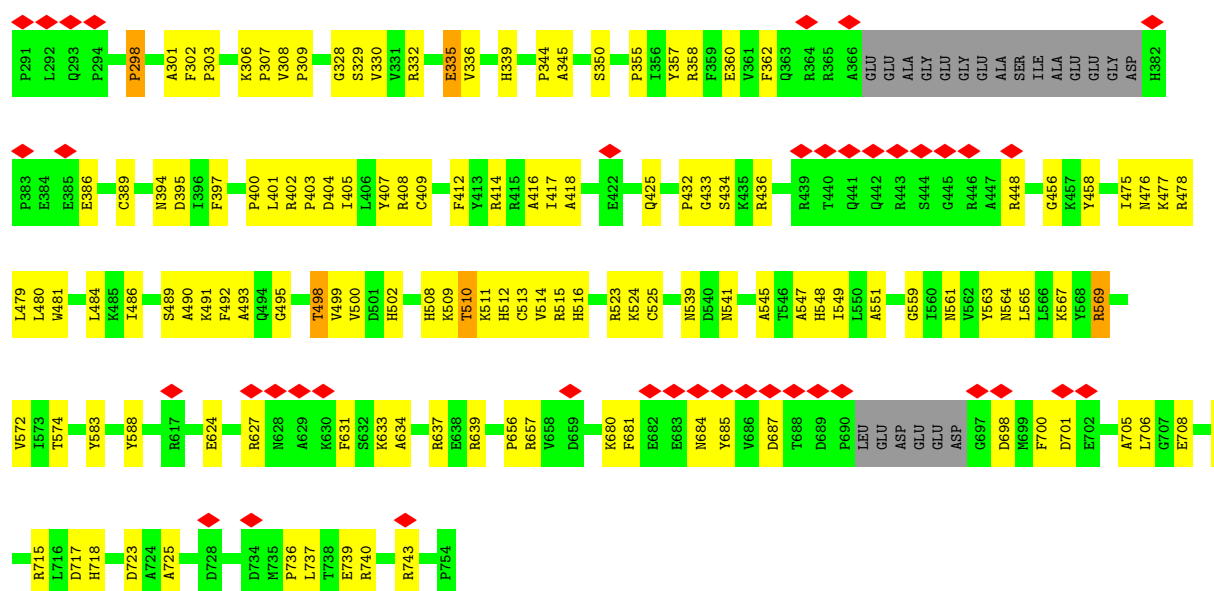
• Molecule 43: Large ribosomal subunit protein uL29m

Chain Lg:  64% 34%



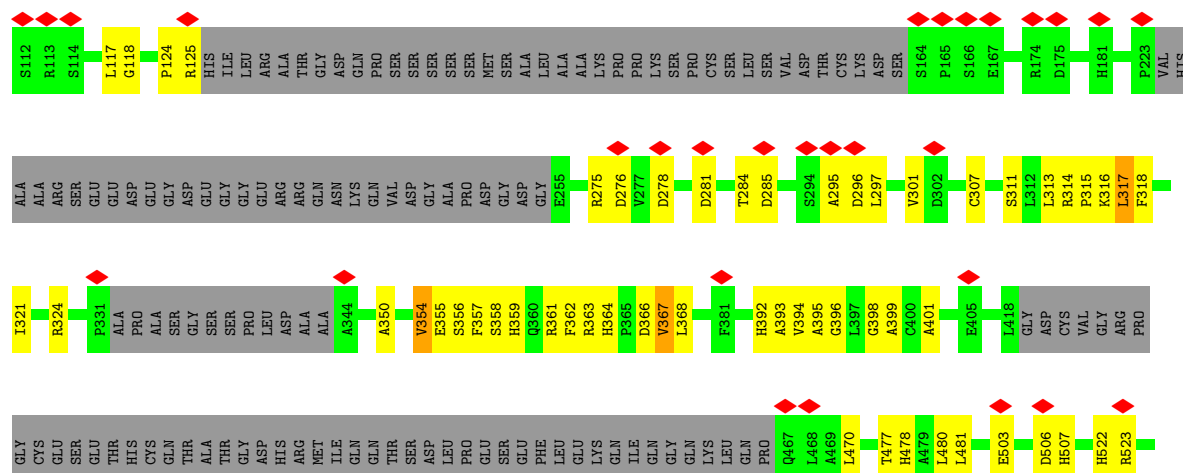
• Molecule 44: Large ribosomal subunit protein uL4m

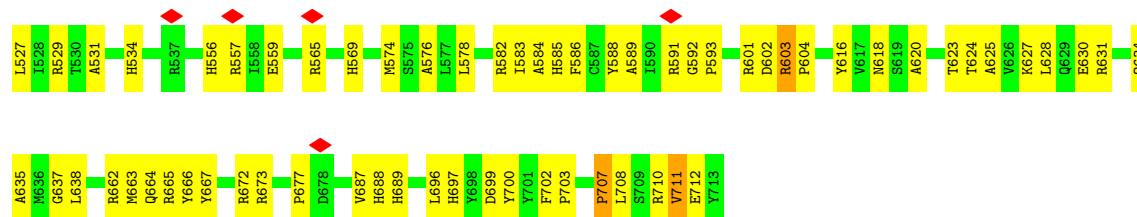
Chain Lh:  9% 67% 27% 5%



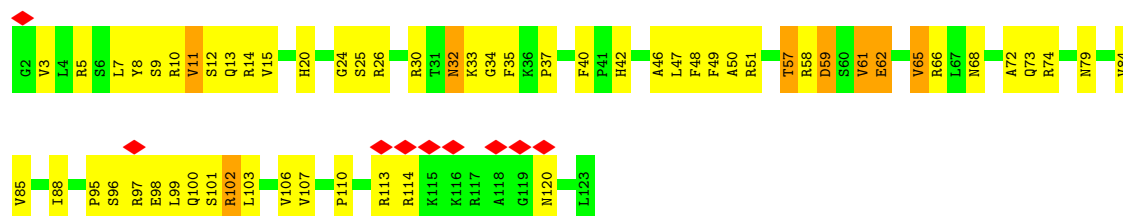
• Molecule 45: RAP domain-containing protein

Chain Li:  6% 59% 19% 21%

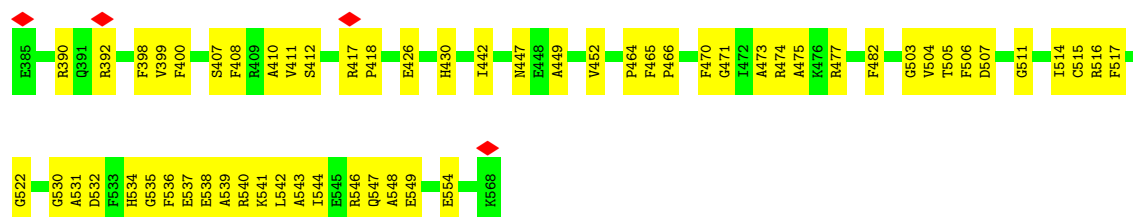




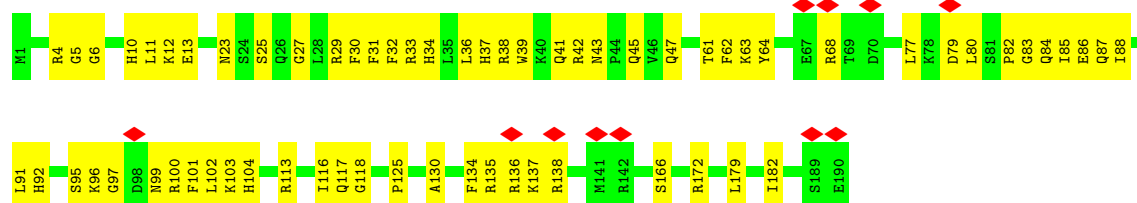
• Molecule 46: mL177



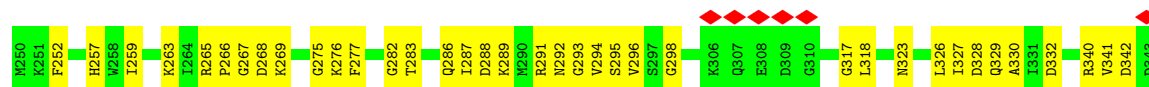
• Molecule 47: AP2 domain transcription factor AP2VIIb-2

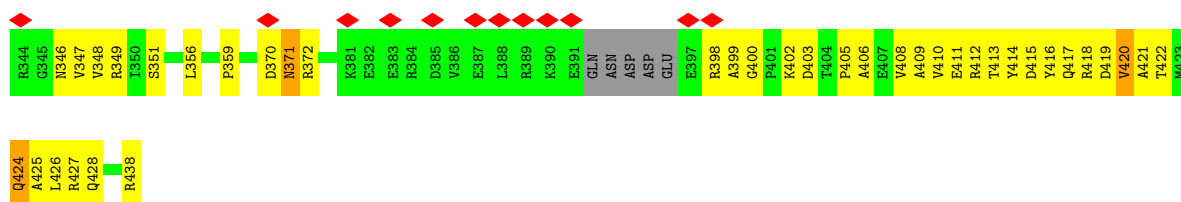


• Molecule 48: Large ribosomal subunit protein mL43

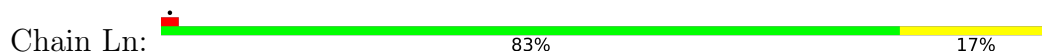


• Molecule 49: Large ribosomal subunit protein uL24c

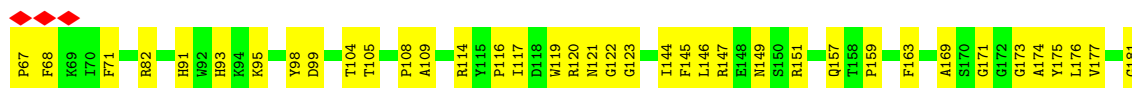




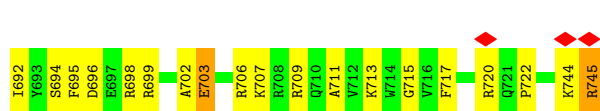
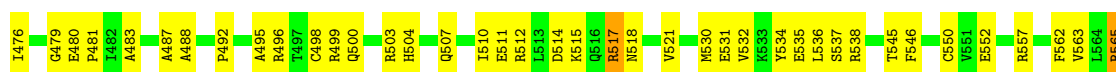
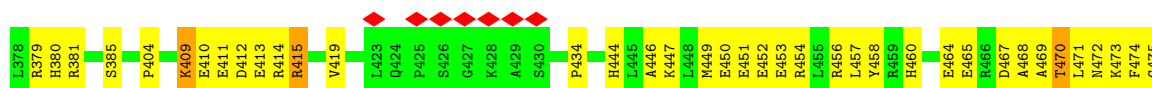
- Molecule 50: mL185



- Molecule 51: Transmembrane protein



- Molecule 52: bL19m

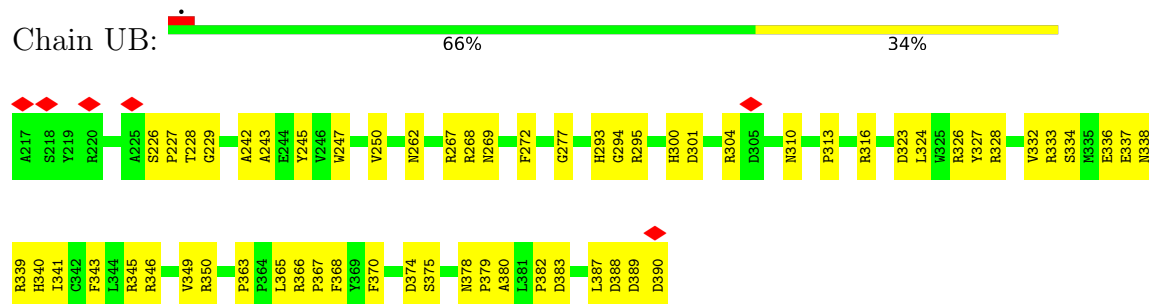


- Molecule 53: RAP domain-containing protein

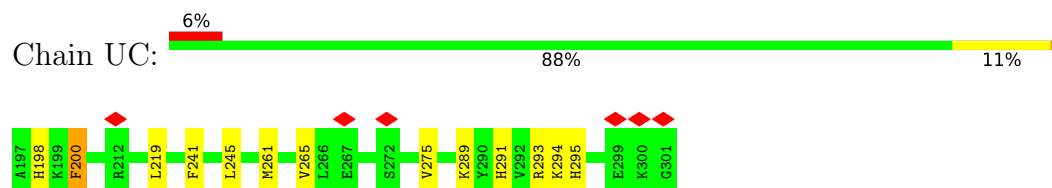




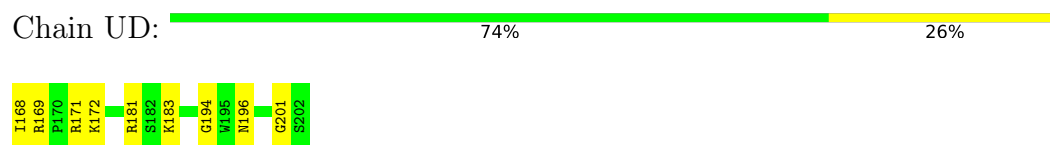
- Molecule 64: bL27m



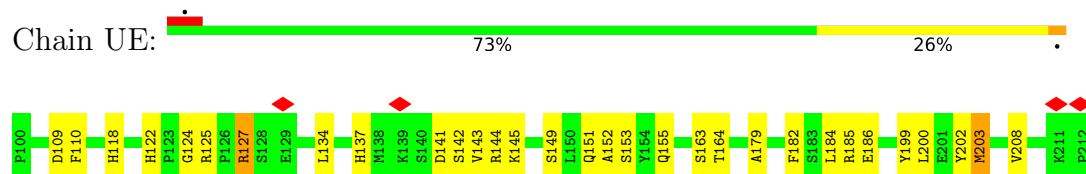
- Molecule 65: mL179



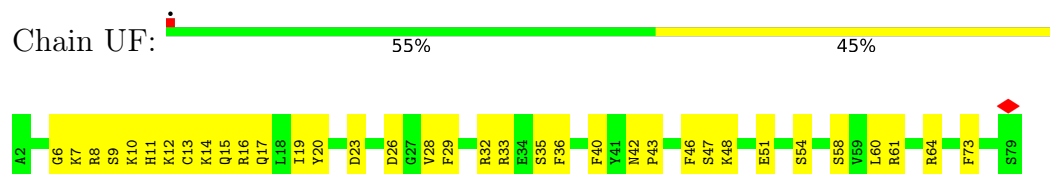
- Molecule 66: Transmembrane protein



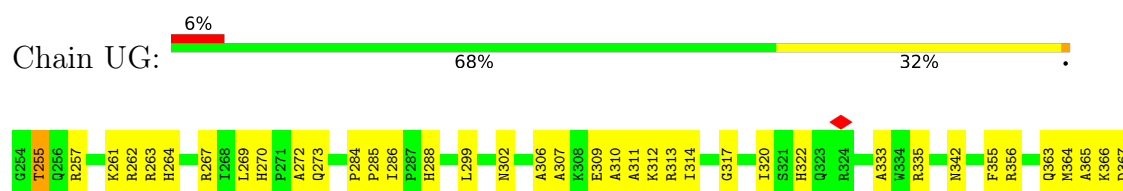
- Molecule 67: mL53

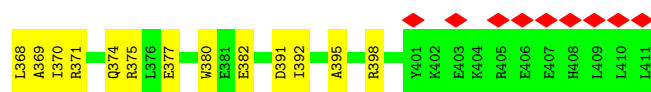


- Molecule 68: bL32m

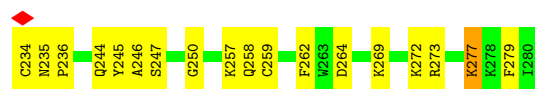


- Molecule 69: AP2 domain transcription factor AP2IV-1

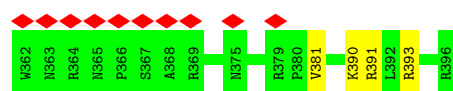
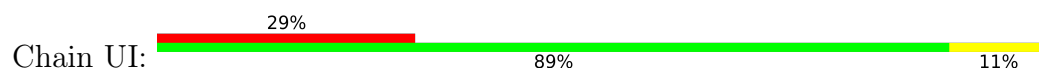




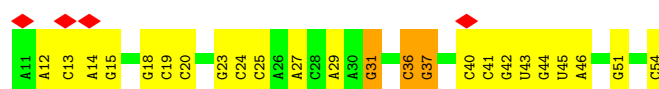
- Molecule 70: mL181



- Molecule 71: mL184



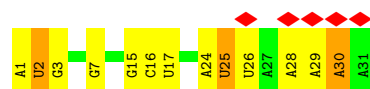
- Molecule 72: RNA23t



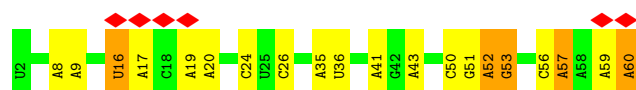
- Molecule 73: RNA29



- Molecule 74: LSUB

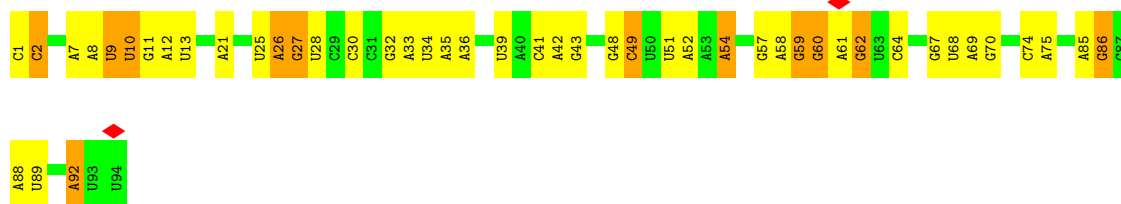


- Molecule 75: RNA6



- Molecule 76: RNA1

Chain 14: 



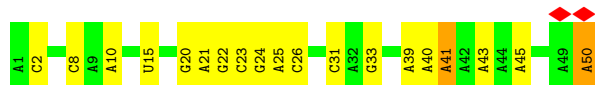
- Molecule 77: RNA31

Chain 15: 



- Molecule 78: RNA14

Chain 16: 



- Molecule 79: RNA11

Chain 17: 



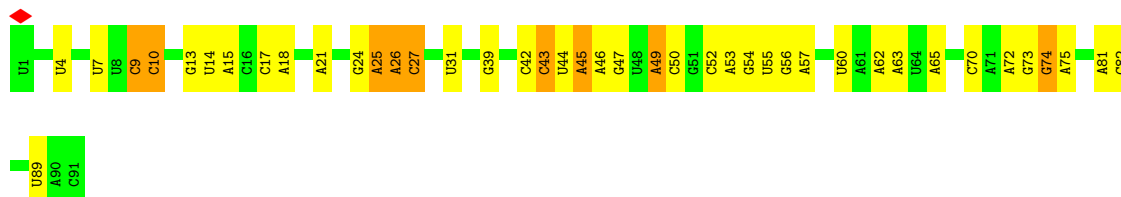
- Molecule 80: RNA36

Chain 18: 



- Molecule 81: RNA3

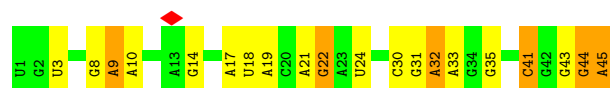
Chain 19: 



- Molecule 82: RNA2



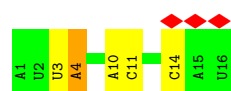
- Molecule 83: RNA38



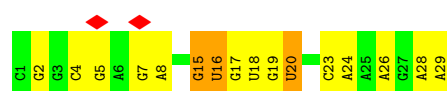
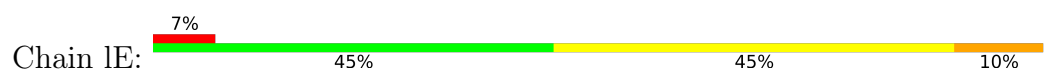
- Molecule 84: RNA35



- Molecule 85: RNA32



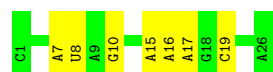
- Molecule 86: RNA15



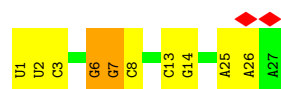
- Molecule 87: RNA10



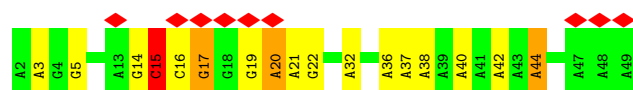
- Molecule 88: LSUC



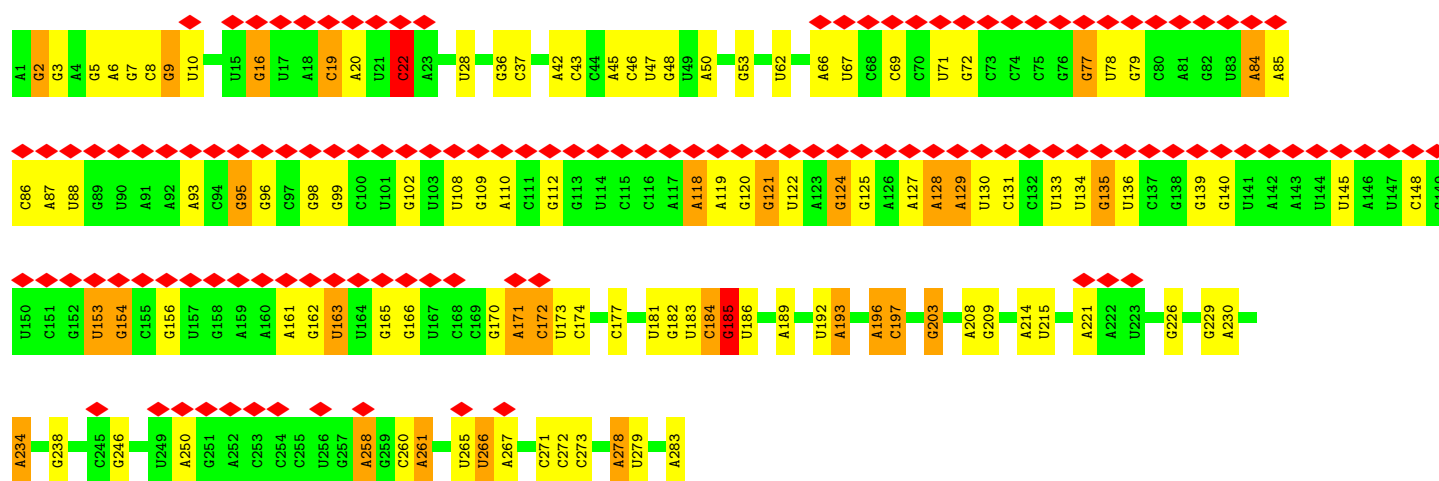
- Molecule 89: RNA16



• Molecule 90: RNA13



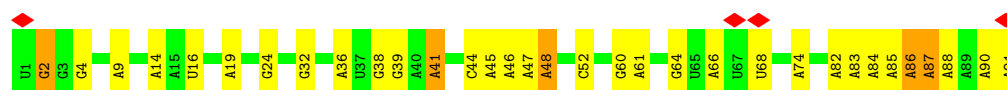
• Molecule 91: LSUD/E



• Molecule 92: SSUF

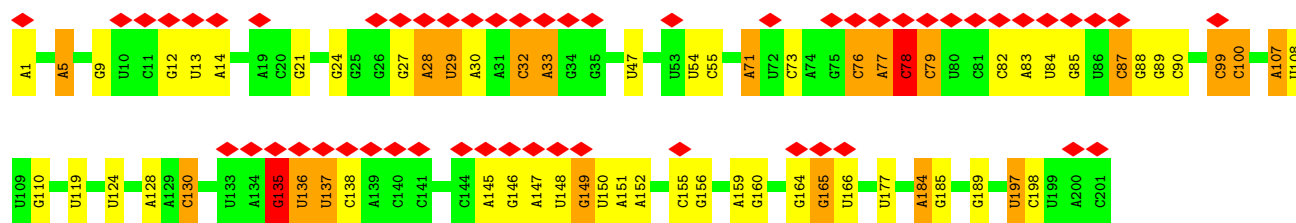


• Molecule 93: RNA7

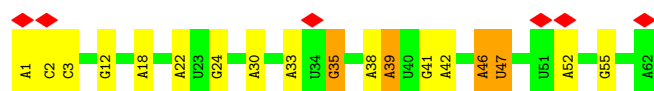
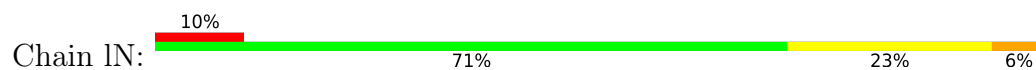


• Molecule 94: LSUF/G

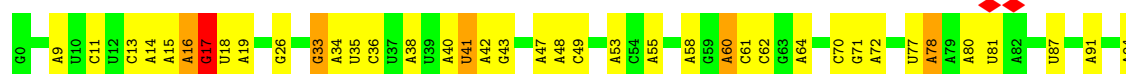




• Molecule 95: RNA37



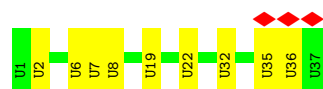
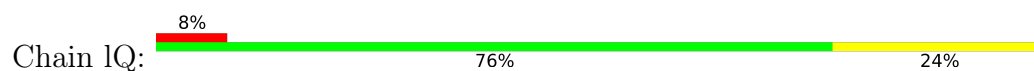
• Molecule 96: LSUA



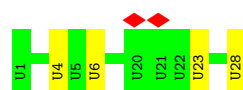
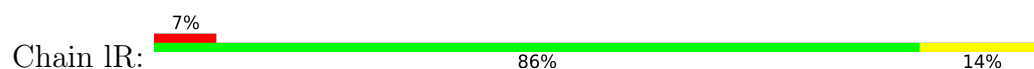
• Molecule 97: ulr1



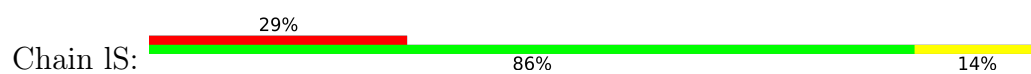
• Molecule 98: ulr2



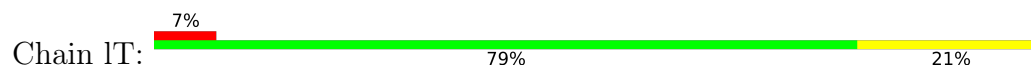
• Molecule 99: ulr3



• Molecule 100: ulr4



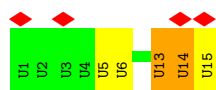
- Molecule 101: ulr5



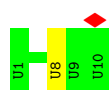
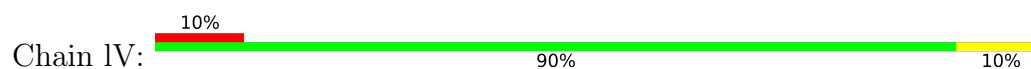
- Molecule 101: ulr5



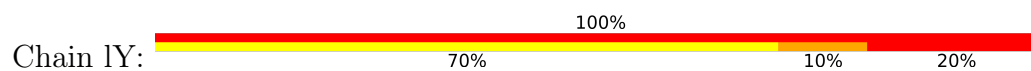
- Molecule 102: ulr6



- Molecule 103: ulr7,ulr8



- Molecule 103: ulr7,ulr8



- Molecule 104: ulr9



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22169	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	59000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.021	Depositor
Minimum map value	-0.059	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	520.785, 520.785, 520.785	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1573, 1.1573, 1.1573	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	L0	2.39	105/3065 (3.4%)	2.22	224/4138 (5.4%)
2	L1	2.13	19/789 (2.4%)	2.03	37/1064 (3.5%)
3	L2	1.81	39/2147 (1.8%)	1.80	99/2899 (3.4%)
4	L3	2.12	57/2259 (2.5%)	2.04	94/3068 (3.1%)
5	L4	1.44	53/3505 (1.5%)	1.35	96/4737 (2.0%)
6	L5	3.00	21/270 (7.8%)	2.60	21/355 (5.9%)
7	L6	1.69	10/491 (2.0%)	1.49	9/664 (1.4%)
8	L7	2.03	30/920 (3.3%)	1.93	47/1230 (3.8%)
9	L8	2.20	70/2066 (3.4%)	1.99	114/2794 (4.1%)
10	L9	1.01	26/3996 (0.7%)	1.01	44/5422 (0.8%)
11	LA	2.28	65/1758 (3.7%)	2.06	97/2387 (4.1%)
12	LB	2.33	37/1059 (3.5%)	2.21	82/1427 (5.7%)
13	LC	2.07	86/2963 (2.9%)	1.97	200/4015 (5.0%)
14	LD	2.18	44/1900 (2.3%)	2.12	123/2566 (4.8%)
15	LE	1.66	36/2172 (1.7%)	1.59	27/2948 (0.9%)
16	LF	1.91	19/757 (2.5%)	1.68	21/1025 (2.0%)
17	LG	1.52	20/1295 (1.5%)	1.45	28/1758 (1.6%)
18	LH	2.14	18/707 (2.5%)	1.97	33/953 (3.5%)
19	LI	1.93	14/628 (2.2%)	1.95	41/840 (4.9%)
20	LJ	2.39	140/3731 (3.8%)	2.23	297/5048 (5.9%)
21	LK	2.02	46/1961 (2.3%)	1.95	87/2643 (3.3%)
22	LL	1.52	66/4945 (1.3%)	1.46	170/6705 (2.5%)
23	LM	2.01	32/1403 (2.3%)	1.95	88/1893 (4.6%)
24	LN	2.67	41/1009 (4.1%)	2.57	101/1346 (7.5%)
25	LO	2.31	104/2708 (3.8%)	2.11	182/3659 (5.0%)
26	LP	2.03	46/1683 (2.7%)	1.86	72/2272 (3.2%)
27	LQ	2.73	33/614 (5.4%)	2.61	66/822 (8.0%)
28	LR	2.49	33/757 (4.4%)	2.28	49/1018 (4.8%)
29	LS	2.00	27/1858 (1.5%)	2.00	103/2522 (4.1%)
30	LT	1.97	25/986 (2.5%)	1.85	40/1317 (3.0%)
31	LU	2.37	19/635 (3.0%)	2.21	43/858 (5.0%)
32	LV	1.90	103/5258 (2.0%)	1.81	258/7127 (3.6%)
33	LW	2.28	79/2500 (3.2%)	2.19	151/3377 (4.5%)
34	LX	2.24	19/797 (2.4%)	2.20	55/1071 (5.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	LY	2.02	62/2977 (2.1%)	1.94	159/3997 (4.0%)
36	LZ	2.18	56/1638 (3.4%)	2.04	105/2217 (4.7%)
37	La	2.27	57/1823 (3.1%)	2.15	113/2471 (4.6%)
38	Lb	2.54	209/5031 (4.2%)	2.41	478/6788 (7.0%)
39	Lc	2.33	135/3872 (3.5%)	2.23	303/5251 (5.8%)
40	Ld	2.00	88/3576 (2.5%)	1.90	216/4852 (4.5%)
41	Le	1.91	77/3118 (2.5%)	1.84	151/4192 (3.6%)
42	Lf	1.79	30/1751 (1.7%)	1.75	71/2364 (3.0%)
43	Lg	2.30	54/1862 (2.9%)	2.23	111/2499 (4.4%)
44	Lh	2.06	87/3781 (2.3%)	1.94	186/5115 (3.6%)
45	Li	1.83	97/3927 (2.5%)	1.65	162/5332 (3.0%)
46	Lj	2.57	50/994 (5.0%)	2.35	89/1333 (6.7%)
47	Lk	1.92	32/1544 (2.1%)	1.95	86/2074 (4.1%)
48	Ll	2.22	55/1618 (3.4%)	2.04	106/2181 (4.9%)
49	Lm	2.21	39/1525 (2.6%)	2.25	133/2043 (6.5%)
50	Ln	1.99	11/457 (2.4%)	1.92	14/624 (2.2%)
51	Lo	2.42	89/2288 (3.9%)	2.23	167/3100 (5.4%)
52	Lp	2.34	120/3153 (3.8%)	2.18	187/4245 (4.4%)
53	Lq	1.77	113/5374 (2.1%)	1.63	203/7299 (2.8%)
54	Lr	1.71	47/2409 (2.0%)	1.65	76/3241 (2.3%)
55	Ls	2.02	85/2617 (3.2%)	1.84	112/3512 (3.2%)
56	Lt	2.42	64/1604 (4.0%)	2.19	134/2174 (6.2%)
57	Lu	2.01	30/1873 (1.6%)	1.98	98/2532 (3.9%)
58	Lv	1.94	13/952 (1.4%)	1.92	46/1286 (3.6%)
59	Lw	1.89	32/1477 (2.2%)	1.81	60/1994 (3.0%)
60	Lx	2.19	26/812 (3.2%)	2.00	37/1093 (3.4%)
61	Ly	2.34	96/2895 (3.3%)	2.21	180/3911 (4.6%)
62	Lz	2.09	26/1021 (2.5%)	1.94	43/1377 (3.1%)
63	UA	1.87	13/728 (1.8%)	1.82	26/976 (2.7%)
64	UB	2.15	49/1489 (3.3%)	2.03	84/2016 (4.2%)
65	UC	1.04	6/890 (0.7%)	0.99	9/1201 (0.7%)
66	UD	1.98	7/316 (2.2%)	1.89	10/416 (2.4%)
67	UE	1.92	20/960 (2.1%)	1.82	53/1289 (4.1%)
68	UF	2.42	23/698 (3.3%)	2.36	60/935 (6.4%)
69	UG	2.27	46/1377 (3.3%)	2.10	80/1856 (4.3%)
70	UH	2.11	5/408 (1.2%)	2.39	30/537 (5.6%)
71	UI	1.71	6/298 (2.0%)	1.66	5/393 (1.3%)
72	l0	1.04	6/1046 (0.6%)	0.80	1/1627 (0.1%)
73	l1	1.44	6/1199 (0.5%)	1.03	2/1866 (0.1%)
74	l2	1.46	6/738 (0.8%)	1.09	1/1147 (0.1%)
75	l3	1.50	8/1403 (0.6%)	1.05	2/2182 (0.1%)
76	l4	1.57	21/2225 (0.9%)	1.11	2/3461 (0.1%)
77	l5	1.34	5/849 (0.6%)	0.97	0/1319

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	l6	1.35	11/1204 (0.9%)	0.98	1/1873 (0.1%)
79	l7	1.42	17/1663 (1.0%)	1.03	0/2589
80	l8	0.71	0/793	0.69	0/1233
81	l9	1.60	25/2152 (1.2%)	1.11	1/3347 (0.0%)
82	lA	1.17	8/1553 (0.5%)	0.89	0/2417
83	lB	1.54	9/1108 (0.8%)	1.07	2/1730 (0.1%)
84	lC	1.04	3/653 (0.5%)	0.86	1/1014 (0.1%)
85	lD	1.78	4/378 (1.1%)	1.17	0/585
86	lE	1.45	5/708 (0.7%)	1.06	0/1103
87	lF	1.32	12/2105 (0.6%)	0.96	0/3278
88	lG	1.04	3/630 (0.5%)	0.77	0/980
89	lH	1.01	0/638	0.84	3/991 (0.3%)
90	lI	1.39	13/1169 (1.1%)	1.00	0/1821
91	lJ	1.36	45/6628 (0.7%)	0.99	7/10319 (0.1%)
92	lK	1.12	4/921 (0.4%)	0.87	1/1435 (0.1%)
93	lL	1.47	25/2185 (1.1%)	1.04	1/3402 (0.0%)
94	lM	1.16	21/4604 (0.5%)	0.87	3/7167 (0.0%)
95	lN	1.29	11/1473 (0.7%)	0.91	1/2290 (0.0%)
96	lO	1.53	36/4302 (0.8%)	1.08	6/6700 (0.1%)
97	lP	1.49	0/637	1.18	0/982
98	lQ	1.38	0/813	1.03	0/1254
99	lR	1.67	0/615	1.26	0/948
100	lS	0.05	0/153	0.14	0/234
101	lT	1.30	0/307	0.91	0/472
101	lW	1.31	0/307	1.02	0/472
102	lU	1.45	0/329	1.11	1/506 (0.2%)
103	lV	1.53	0/219	1.10	0/336
103	lY	0.96	0/219	1.67	3/336 (0.9%)
104	lX	1.10	0/1275	0.90	1/1968 (0.1%)
All	All	1.91	3941/183926 (2.1%)	1.74	7422/258068 (2.9%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	L1	0	1
22	LL	0	1
37	La	0	1
40	Ld	0	1
53	Lq	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
61	Ly	0	1
72	l0	0	1
78	l6	0	1
79	l7	0	1
80	l8	0	1
82	lA	0	2
84	lC	0	3
91	lJ	0	5
92	lK	0	2
94	lM	0	3
95	lN	0	1
96	lO	0	1
97	lP	0	1
101	lW	0	1
103	lY	0	6
104	lX	0	1
All	All	0	36

The worst 5 of 3941 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	Li	677	PRO	CA-CB	-9.90	1.46	1.53
53	Lq	673	ALA	CA-CB	-9.54	1.42	1.53
43	Lg	160	PRO	CA-CB	-9.38	1.47	1.53
17	LG	162	ALA	CA-CB	-9.35	1.41	1.52
23	LM	14	ALA	CA-CB	-9.34	1.43	1.54

The worst 5 of 7422 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	LJ	285	ARG	CA-C-N	11.39	130.79	122.59
20	LJ	285	ARG	C-N-CA	11.39	130.79	122.59
59	Lw	108	PRO	CA-N-CD	-9.73	98.37	112.00
33	LW	305	MET	CA-C-N	9.17	128.51	122.18
33	LW	305	MET	C-N-CA	9.17	128.51	122.18

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	L1	481	TYR	Sidechain

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Mol	Chain	Res	Type	Group
22	LL	296	HIS	Mainchain
37	La	134	TYR	Sidechain
40	Ld	489	SER	Mainchain
53	Lq	765	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L0	2984	0	2988	8	0
2	L1	768	0	774	1	0
3	L2	2111	0	2147	7	0
4	L3	2196	0	2156	5	0
5	L4	3430	0	3454	14	0
6	L5	264	0	288	1	0
7	L6	476	0	503	0	0
8	L7	906	0	973	5	0
9	L8	2008	0	1998	3	0
10	L9	3888	0	3896	15	0
11	LA	1708	0	1745	7	0
12	LB	1033	0	1052	5	0
13	LC	2909	0	2949	14	0
14	LD	1847	0	1840	3	0
15	LE	2118	0	2118	12	0
16	LF	731	0	744	3	0
17	LG	1253	0	1225	11	0
18	LH	693	0	729	0	0
19	LI	613	0	652	1	0
20	LJ	3640	0	3677	23	0
21	LK	1905	0	1879	4	0
22	LL	4847	0	4916	15	0
23	LM	1376	0	1435	5	0
24	LN	986	0	1036	3	0
25	LO	2647	0	2725	9	0
26	LP	1636	0	1577	4	0
27	LQ	600	0	618	3	0
28	LR	738	0	728	1	0
29	LS	1812	0	1884	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	LT	965	0	1013	5	0
31	LU	623	0	665	1	0
32	LV	5149	0	5211	26	0
33	LW	2433	0	2442	13	0
34	LX	779	0	762	2	0
35	LY	2909	0	2976	5	0
36	LZ	1591	0	1608	6	0
37	La	1769	0	1799	5	0
38	Lb	4929	0	5042	19	0
39	Lc	3797	0	3835	5	0
40	Ld	3507	0	3563	17	0
41	Le	3057	0	3083	7	0
42	Lf	1709	0	1711	5	0
43	Lg	1824	0	1879	4	0
44	Lh	3675	0	3687	12	0
45	Li	3833	0	3922	10	0
46	Lj	977	0	1019	8	0
47	Lk	1502	0	1491	2	0
48	Ll	1573	0	1585	3	0
49	Lm	1501	0	1559	5	0
50	Ln	442	0	417	0	0
51	Lo	2219	0	2223	4	0
52	Lp	3074	0	3164	15	0
53	Lq	5268	0	5324	32	0
54	Lr	2342	0	2310	4	0
55	Ls	2565	0	2644	11	0
56	Lt	1556	0	1518	7	0
57	Lu	1834	0	1841	9	0
58	Lv	928	0	960	4	0
59	Lw	1440	0	1483	7	0
60	Lx	796	0	824	3	0
61	Ly	2821	0	2849	8	0
62	Lz	994	0	944	0	0
63	UA	709	0	752	2	0
64	UB	1451	0	1477	3	0
65	UC	864	0	888	4	0
66	UD	308	0	321	1	0
67	UE	935	0	927	3	0
68	UF	672	0	664	0	0
69	UG	1343	0	1341	3	0
70	UH	401	0	427	1	0
71	UI	293	0	320	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	l0	936	0	461	4	0
73	l1	1070	0	494	3	0
74	l2	660	0	300	2	0
75	l3	1254	0	581	5	0
76	l4	1991	0	906	9	0
77	l5	761	0	358	4	0
78	l6	1072	0	503	1	0
79	l7	1481	0	683	3	0
80	l8	707	0	357	0	0
81	l9	1926	0	867	10	0
82	lA	1387	0	666	6	0
83	lB	985	0	433	7	0
84	lC	583	0	283	1	0
85	lD	338	0	152	3	0
86	lE	630	0	285	2	0
87	lF	1880	0	883	9	0
88	lG	561	0	271	0	0
89	lH	572	0	273	1	0
90	lI	1039	0	471	4	0
91	lJ	5929	0	2780	24	0
92	lK	821	0	396	2	0
93	lL	1948	0	890	4	0
94	lM	4121	0	1965	20	0
95	lN	1316	0	619	2	0
96	lO	3841	0	1750	10	0
97	lP	580	0	276	6	0
98	lQ	740	0	355	1	0
99	lR	560	0	262	1	0
100	lS	140	0	71	0	0
101	lT	280	0	135	0	0
101	lW	280	0	136	0	0
102	lU	300	0	144	1	0
103	lV	200	0	95	1	0
103	lY	200	0	101	1	0
104	lX	1160	0	568	4	0
All	All	175729	0	154946	514	0

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

The worst 5 of 514 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)
76:l4:25:U:OP2	76:l4:26:A:O2'	1.88	0.91
94:lM:99:C:O2'	94:lM:100:C:OP1	1.97	0.82
91:lJ:184:C:O2'	91:lJ:185:G:OP1	1.97	0.81
96:lO:161:A:O2'	96:lO:162:A:OP1	2.00	0.80
94:lM:77:A:O2'	94:lM:78:C:OP1	2.00	0.79

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L0	349/405 (86%)	335 (96%)	14 (4%)	0	100	100
2	L1	90/92 (98%)	89 (99%)	1 (1%)	0	100	100
3	L2	268/270 (99%)	263 (98%)	5 (2%)	0	100	100
4	L3	268/331 (81%)	258 (96%)	10 (4%)	0	100	100
5	L4	420/430 (98%)	413 (98%)	7 (2%)	0	100	100
6	L5	28/30 (93%)	26 (93%)	2 (7%)	0	100	100
7	L6	53/57 (93%)	53 (100%)	0	0	100	100
8	L7	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
9	L8	235/246 (96%)	226 (96%)	9 (4%)	0	100	100
10	L9	473/475 (100%)	461 (98%)	12 (2%)	0	100	100
11	LA	215/217 (99%)	206 (96%)	9 (4%)	0	100	100
12	LB	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
13	LC	370/527 (70%)	359 (97%)	11 (3%)	0	100	100
14	LD	221/282 (78%)	213 (96%)	8 (4%)	0	100	100
15	LE	259/338 (77%)	255 (98%)	4 (2%)	0	100	100
16	LF	86/88 (98%)	84 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	LG	146/148 (99%)	139 (95%)	7 (5%)	0	100	100
18	LH	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
19	LI	77/79 (98%)	75 (97%)	2 (3%)	0	100	100
20	LJ	441/443 (100%)	423 (96%)	18 (4%)	0	100	100
21	LK	217/219 (99%)	210 (97%)	6 (3%)	1 (0%)	24	54
22	LL	615/855 (72%)	598 (97%)	17 (3%)	0	100	100
23	LM	175/177 (99%)	167 (95%)	8 (5%)	0	100	100
24	LN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
25	LO	342/344 (99%)	318 (93%)	24 (7%)	0	100	100
26	LP	198/230 (86%)	191 (96%)	7 (4%)	0	100	100
27	LQ	68/70 (97%)	63 (93%)	5 (7%)	0	100	100
28	LR	82/132 (62%)	81 (99%)	1 (1%)	0	100	100
29	LS	226/228 (99%)	219 (97%)	7 (3%)	0	100	100
30	LT	109/117 (93%)	108 (99%)	1 (1%)	0	100	100
31	LU	77/79 (98%)	73 (95%)	4 (5%)	0	100	100
32	LV	642/880 (73%)	629 (98%)	13 (2%)	0	100	100
33	LW	304/306 (99%)	287 (94%)	17 (6%)	0	100	100
34	LX	90/92 (98%)	87 (97%)	3 (3%)	0	100	100
35	LY	344/346 (99%)	337 (98%)	7 (2%)	0	100	100
36	LZ	195/197 (99%)	189 (97%)	6 (3%)	0	100	100
37	La	212/214 (99%)	203 (96%)	9 (4%)	0	100	100
38	Lb	601/733 (82%)	584 (97%)	17 (3%)	0	100	100
39	Lc	469/512 (92%)	442 (94%)	27 (6%)	0	100	100
40	Ld	435/437 (100%)	419 (96%)	16 (4%)	0	100	100
41	Le	374/376 (100%)	366 (98%)	8 (2%)	0	100	100
42	Lf	212/226 (94%)	204 (96%)	8 (4%)	0	100	100
43	Lg	212/214 (99%)	209 (99%)	3 (1%)	0	100	100
44	Lh	437/464 (94%)	428 (98%)	9 (2%)	0	100	100
45	Li	463/602 (77%)	450 (97%)	13 (3%)	0	100	100
46	Lj	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
47	Lk	182/184 (99%)	172 (94%)	10 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	Ll	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
49	Lm	180/189 (95%)	176 (98%)	4 (2%)	0	100	100
50	Ln	58/60 (97%)	51 (88%)	7 (12%)	0	100	100
51	Lo	281/283 (99%)	268 (95%)	13 (5%)	0	100	100
52	Lp	366/368 (100%)	353 (96%)	13 (4%)	0	100	100
53	Lq	677/787 (86%)	649 (96%)	28 (4%)	0	100	100
54	Lr	279/281 (99%)	272 (98%)	7 (2%)	0	100	100
55	Ls	309/311 (99%)	294 (95%)	15 (5%)	0	100	100
56	Lt	184/240 (77%)	180 (98%)	4 (2%)	0	100	100
57	Lu	228/232 (98%)	218 (96%)	10 (4%)	0	100	100
58	Lv	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
59	Lw	177/179 (99%)	168 (95%)	9 (5%)	0	100	100
60	Lx	96/98 (98%)	92 (96%)	4 (4%)	0	100	100
61	Ly	336/404 (83%)	325 (97%)	11 (3%)	0	100	100
62	Lz	118/120 (98%)	118 (100%)	0	0	100	100
63	UA	83/85 (98%)	83 (100%)	0	0	100	100
64	UB	172/174 (99%)	169 (98%)	3 (2%)	0	100	100
65	UC	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
66	UD	33/35 (94%)	32 (97%)	1 (3%)	0	100	100
67	UE	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
68	UF	76/78 (97%)	74 (97%)	2 (3%)	0	100	100
69	UG	156/158 (99%)	156 (100%)	0	0	100	100
70	UH	45/47 (96%)	44 (98%)	1 (2%)	0	100	100
71	UI	33/35 (94%)	29 (88%)	4 (12%)	0	100	100
All	All	16226/17933 (90%)	15694 (97%)	531 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	LK	184	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L0	317/359 (88%)	316 (100%)	1 (0%)	86	96
2	L1	83/83 (100%)	82 (99%)	1 (1%)	63	86
3	L2	227/227 (100%)	227 (100%)	0	100	100
4	L3	232/281 (83%)	231 (100%)	1 (0%)	84	94
5	L4	371/375 (99%)	371 (100%)	0	100	100
6	L5	26/26 (100%)	26 (100%)	0	100	100
7	L6	51/51 (100%)	51 (100%)	0	100	100
8	L7	95/96 (99%)	95 (100%)	0	100	100
9	L8	212/218 (97%)	212 (100%)	0	100	100
10	L9	418/418 (100%)	417 (100%)	1 (0%)	87	96
11	LA	180/180 (100%)	179 (99%)	1 (1%)	78	93
12	LB	105/105 (100%)	104 (99%)	1 (1%)	68	89
13	LC	309/423 (73%)	308 (100%)	1 (0%)	86	96
14	LD	194/241 (80%)	192 (99%)	2 (1%)	68	89
15	LE	222/281 (79%)	222 (100%)	0	100	100
16	LF	78/78 (100%)	78 (100%)	0	100	100
17	LG	131/131 (100%)	130 (99%)	1 (1%)	73	90
18	LH	71/71 (100%)	71 (100%)	0	100	100
19	LI	65/65 (100%)	65 (100%)	0	100	100
20	LJ	381/382 (100%)	381 (100%)	0	100	100
21	LK	199/199 (100%)	199 (100%)	0	100	100
22	LL	523/701 (75%)	520 (99%)	3 (1%)	78	93
23	LM	149/149 (100%)	149 (100%)	0	100	100
24	LN	106/106 (100%)	105 (99%)	1 (1%)	70	90
25	LO	271/272 (100%)	271 (100%)	0	100	100
26	LP	171/195 (88%)	169 (99%)	2 (1%)	63	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	LQ	62/62 (100%)	62 (100%)	0	100	100
28	LR	82/114 (72%)	81 (99%)	1 (1%)	63	86
29	LS	205/205 (100%)	205 (100%)	0	100	100
30	LT	102/106 (96%)	102 (100%)	0	100	100
31	LU	69/69 (100%)	69 (100%)	0	100	100
32	LV	538/705 (76%)	535 (99%)	3 (1%)	78	93
33	LW	262/263 (100%)	261 (100%)	1 (0%)	84	94
34	LX	85/85 (100%)	83 (98%)	2 (2%)	43	75
35	LY	300/302 (99%)	298 (99%)	2 (1%)	76	92
36	LZ	166/166 (100%)	166 (100%)	0	100	100
37	La	193/193 (100%)	193 (100%)	0	100	100
38	Lb	520/626 (83%)	517 (99%)	3 (1%)	78	93
39	Lc	412/450 (92%)	411 (100%)	1 (0%)	87	96
40	Ld	387/388 (100%)	381 (98%)	6 (2%)	55	83
41	Le	311/311 (100%)	310 (100%)	1 (0%)	86	96
42	Lf	174/181 (96%)	174 (100%)	0	100	100
43	Lg	192/192 (100%)	191 (100%)	1 (0%)	81	93
44	Lh	391/406 (96%)	390 (100%)	1 (0%)	86	96
45	Li	421/526 (80%)	421 (100%)	0	100	100
46	Lj	105/105 (100%)	103 (98%)	2 (2%)	50	79
47	Lk	156/156 (100%)	156 (100%)	0	100	100
48	Ll	169/169 (100%)	168 (99%)	1 (1%)	78	93
49	Lm	165/170 (97%)	165 (100%)	0	100	100
50	Ln	44/44 (100%)	44 (100%)	0	100	100
51	Lo	235/236 (100%)	233 (99%)	2 (1%)	70	90
52	Lp	329/330 (100%)	328 (100%)	1 (0%)	86	96
53	Lq	557/637 (87%)	557 (100%)	0	100	100
54	Lr	241/242 (100%)	240 (100%)	1 (0%)	84	94
55	Ls	268/268 (100%)	266 (99%)	2 (1%)	76	92
56	Lt	165/201 (82%)	163 (99%)	2 (1%)	63	86
57	Lu	196/197 (100%)	196 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	Lv	101/101 (100%)	100 (99%)	1 (1%)	68	89
59	Lw	152/152 (100%)	150 (99%)	2 (1%)	61	86
60	Lx	86/86 (100%)	86 (100%)	0	100	100
61	Ly	303/351 (86%)	303 (100%)	0	100	100
62	Lz	103/103 (100%)	103 (100%)	0	100	100
63	UA	76/76 (100%)	76 (100%)	0	100	100
64	UB	159/159 (100%)	159 (100%)	0	100	100
65	UC	95/95 (100%)	95 (100%)	0	100	100
66	UD	30/30 (100%)	30 (100%)	0	100	100
67	UE	103/103 (100%)	102 (99%)	1 (1%)	68	89
68	UF	71/71 (100%)	71 (100%)	0	100	100
69	UG	139/139 (100%)	139 (100%)	0	100	100
70	UH	43/43 (100%)	42 (98%)	1 (2%)	44	76
71	UI	30/30 (100%)	30 (100%)	0	100	100
All	All	14180/15357 (92%)	14126 (100%)	54 (0%)	81	94

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	Lc	231	VAL
41	Le	440	ILE
58	Lv	80	ILE
40	Ld	432	ARG
40	Ld	537	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 110 such sidechains are listed below:

Mol	Chain	Res	Type
37	La	165	ASN
44	Lh	742	HIS
69	UG	343	HIS
61	Ly	298	HIS
38	Lb	690	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
100	IS	6/7 (85%)	1 (16%)	0
101	IT	13/14 (92%)	3 (23%)	0
101	IW	13/14 (92%)	1 (7%)	0
102	IU	14/15 (93%)	4 (28%)	0
103	IV	9/10 (90%)	0	0
103	IY	9/10 (90%)	5 (55%)	0
104	IX	57/58 (98%)	21 (36%)	0
72	I0	43/44 (97%)	12 (27%)	0
73	I1	49/50 (98%)	11 (22%)	0
74	I2	29/31 (93%)	6 (20%)	0
75	I3	58/59 (98%)	12 (20%)	0
76	I4	93/94 (98%)	26 (27%)	0
77	I5	35/36 (97%)	7 (20%)	0
78	I6	46/50 (92%)	6 (13%)	0
79	I7	66/69 (95%)	11 (16%)	0
80	I8	30/33 (90%)	8 (26%)	0
81	I9	90/91 (98%)	15 (16%)	0
82	IA	64/65 (98%)	16 (25%)	0
83	IB	42/45 (93%)	11 (26%)	0
84	IC	25/27 (92%)	4 (16%)	0
85	ID	15/16 (93%)	0	0
86	IE	24/29 (82%)	10 (41%)	0
87	IF	87/88 (98%)	19 (21%)	0
88	IG	25/26 (96%)	4 (16%)	0
89	IH	26/27 (96%)	8 (30%)	0
90	II	43/48 (89%)	4 (9%)	0
91	IJ	277/279 (99%)	58 (20%)	0
92	IK	36/38 (94%)	8 (22%)	0
93	IL	88/91 (96%)	7 (7%)	0
94	IM	192/194 (98%)	41 (21%)	0
95	IN	55/62 (88%)	7 (12%)	0
96	IO	179/180 (99%)	36 (20%)	0
97	IP	28/29 (96%)	11 (39%)	0
98	IQ	36/37 (97%)	8 (22%)	0
99	IR	27/28 (96%)	3 (11%)	0
All	All	1929/1994 (96%)	404 (20%)	0

5 of 404 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
72	I0	12	A
72	I0	13	C
72	I0	14	A
72	I0	15	G

Continued on next page...

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Mol	Chain	Res	Type
72	l0	19	C

There are no RNA pucker outliers to report.

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](#)

There are no ligands in this entry.

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
7	L6	1
57	Lu	1
94	lM	1
91	lJ	1
84	lC	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L6	267:ALA	C	533:ARG	N	44.09
1	Lu	451:GLY	C	462:GLU	N	29.06
1	lM	166:U	O3'	174:G	P	22.23
1	lJ	103:U	O3'	108:U	P	11.87

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1C	26:G	O3'	27:G	P	3.50

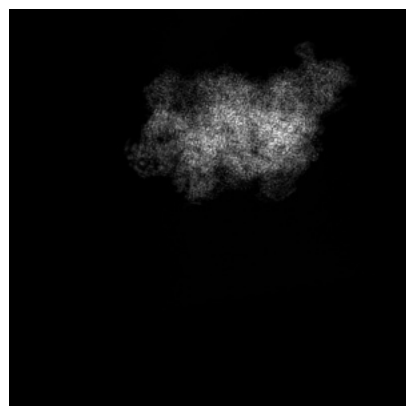
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51104. These allow visual inspection of the internal detail of the map and identification of artifacts.

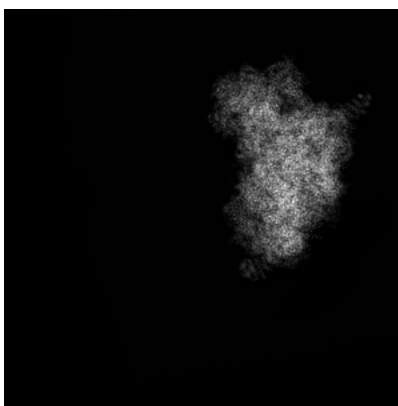
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

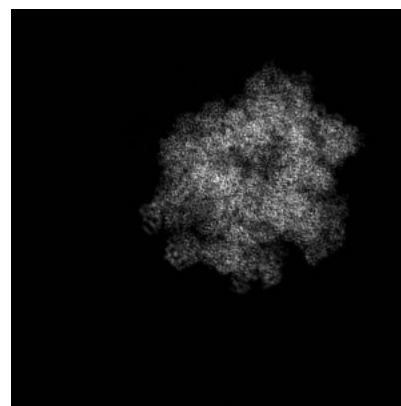
6.1.1 Primary map



X

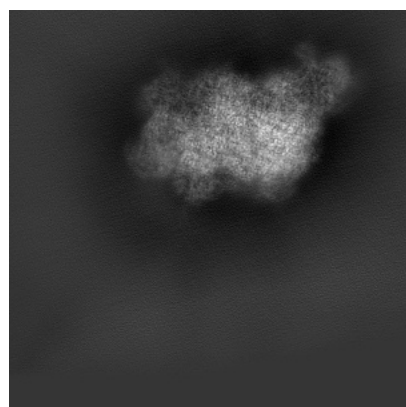


Y

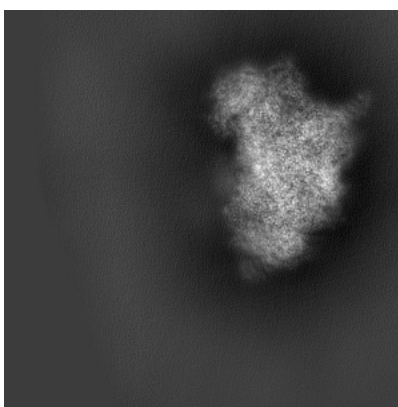


Z

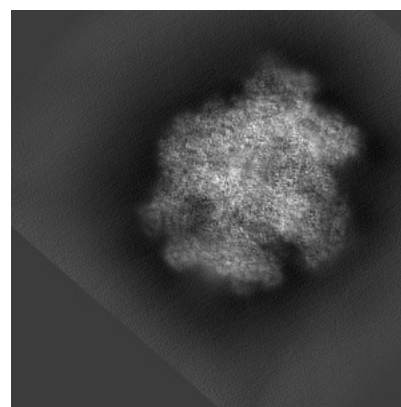
6.1.2 Raw map



X



Y



Z

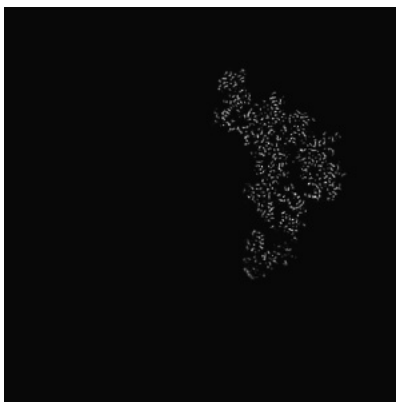
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

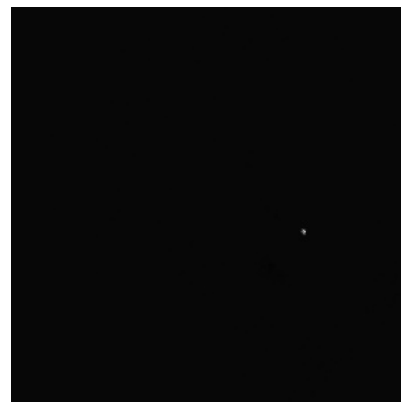
6.2.1 Primary map



X Index: 225

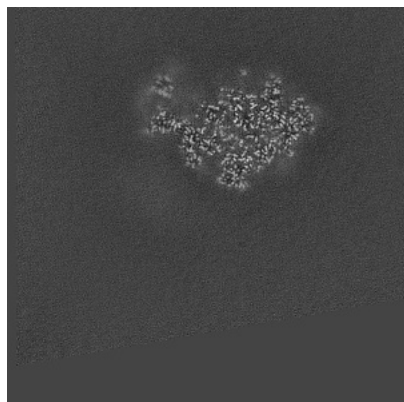


Y Index: 225

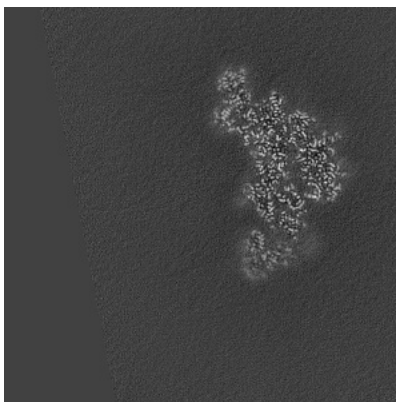


Z Index: 225

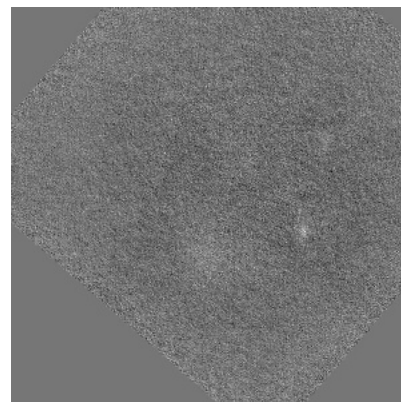
6.2.2 Raw map



X Index: 225



Y Index: 225



Z Index: 225

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: 320

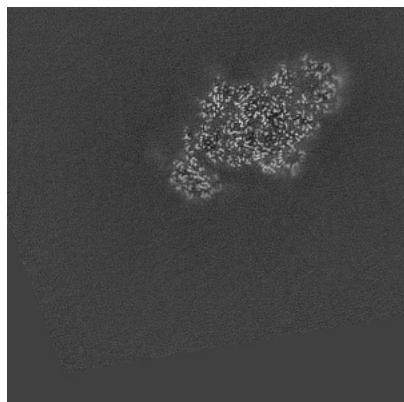


Y Index: 300

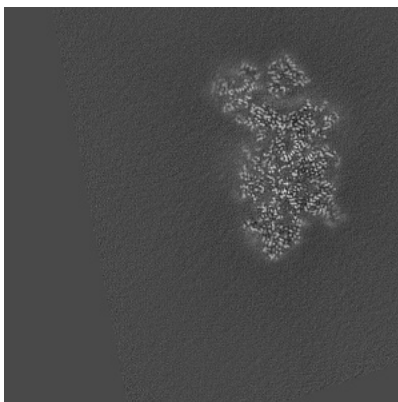


Z Index: 317

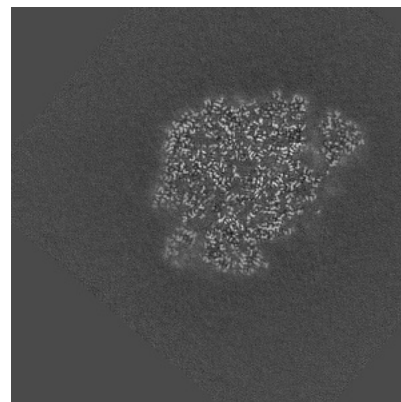
6.3.2 Raw map



X Index: 320



Y Index: 300

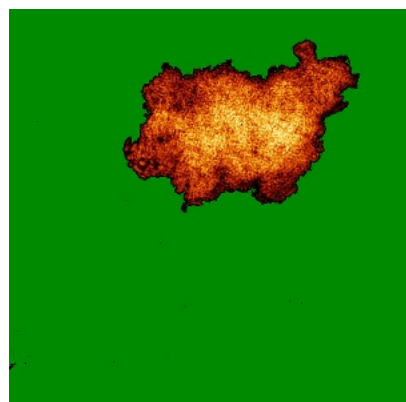


Z Index: 317

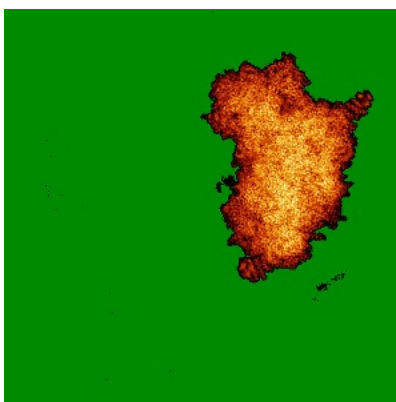
The images above show the largest variance slices of the map in three orthogonal directions.

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

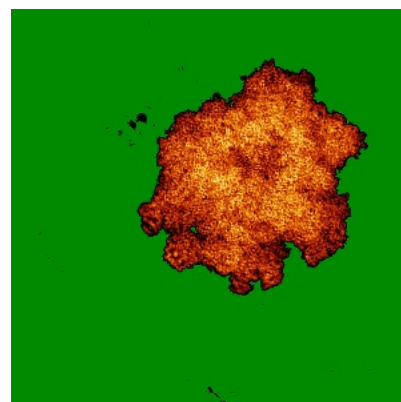
6.4.1 Primary map



X

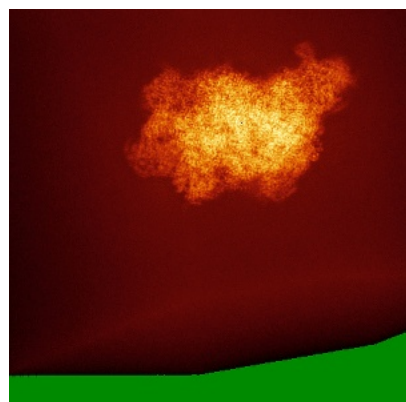


Y

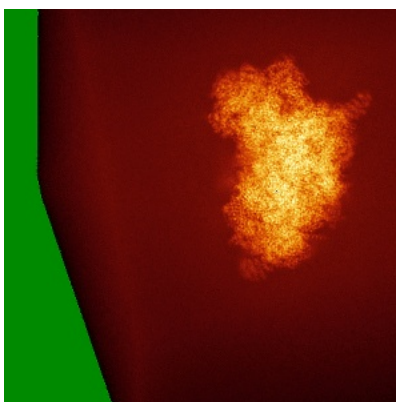


Z

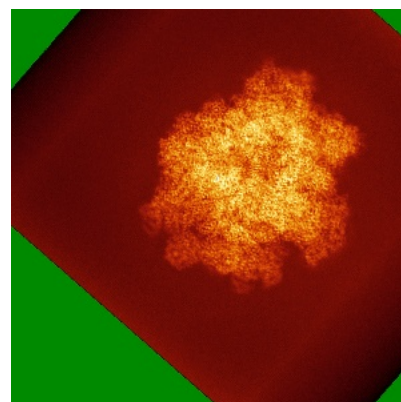
6.4.2 Raw map



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.

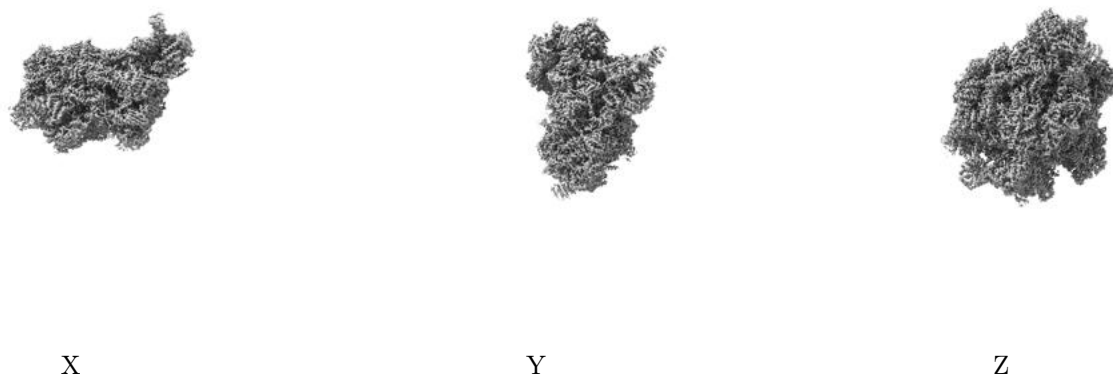
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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



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.

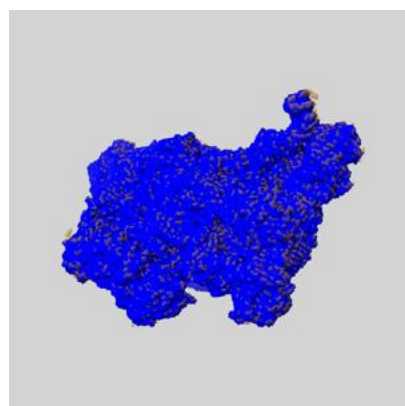
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

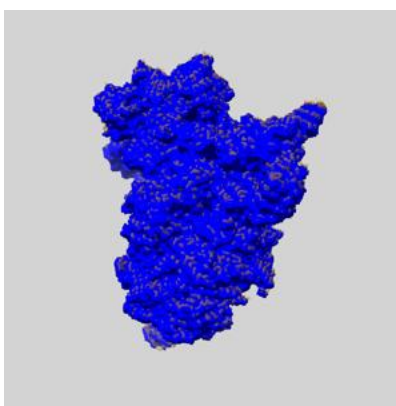
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

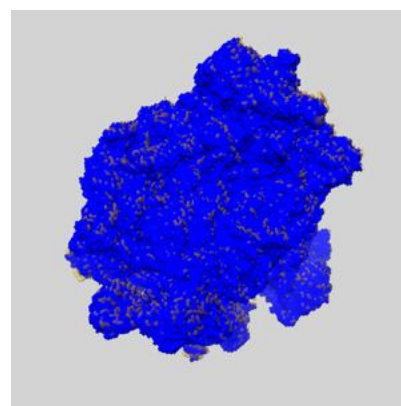
6.6.1 emd_51104_msk_1.map [i](#)



X



Y

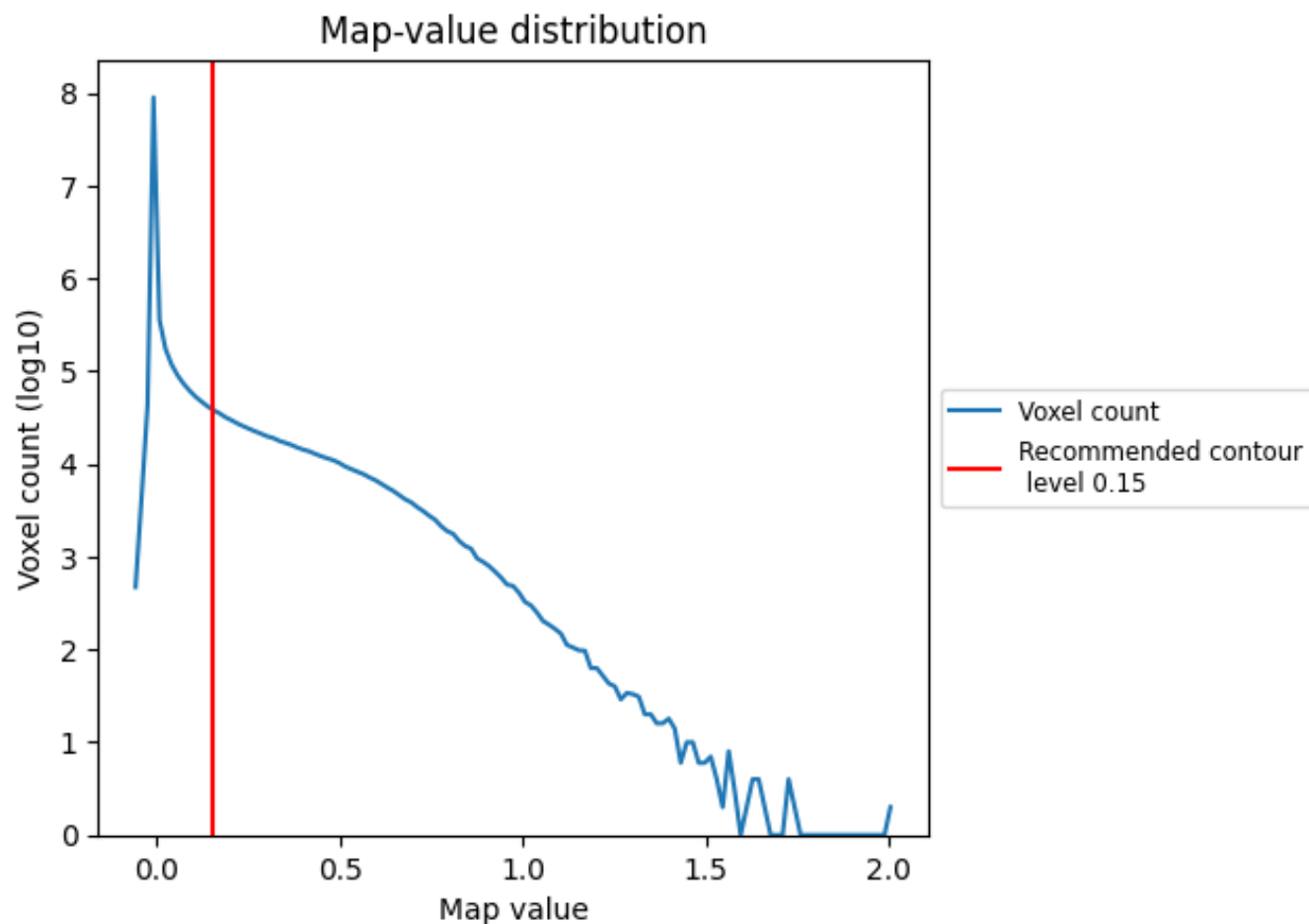


Z

7 Map analysis [i](#)

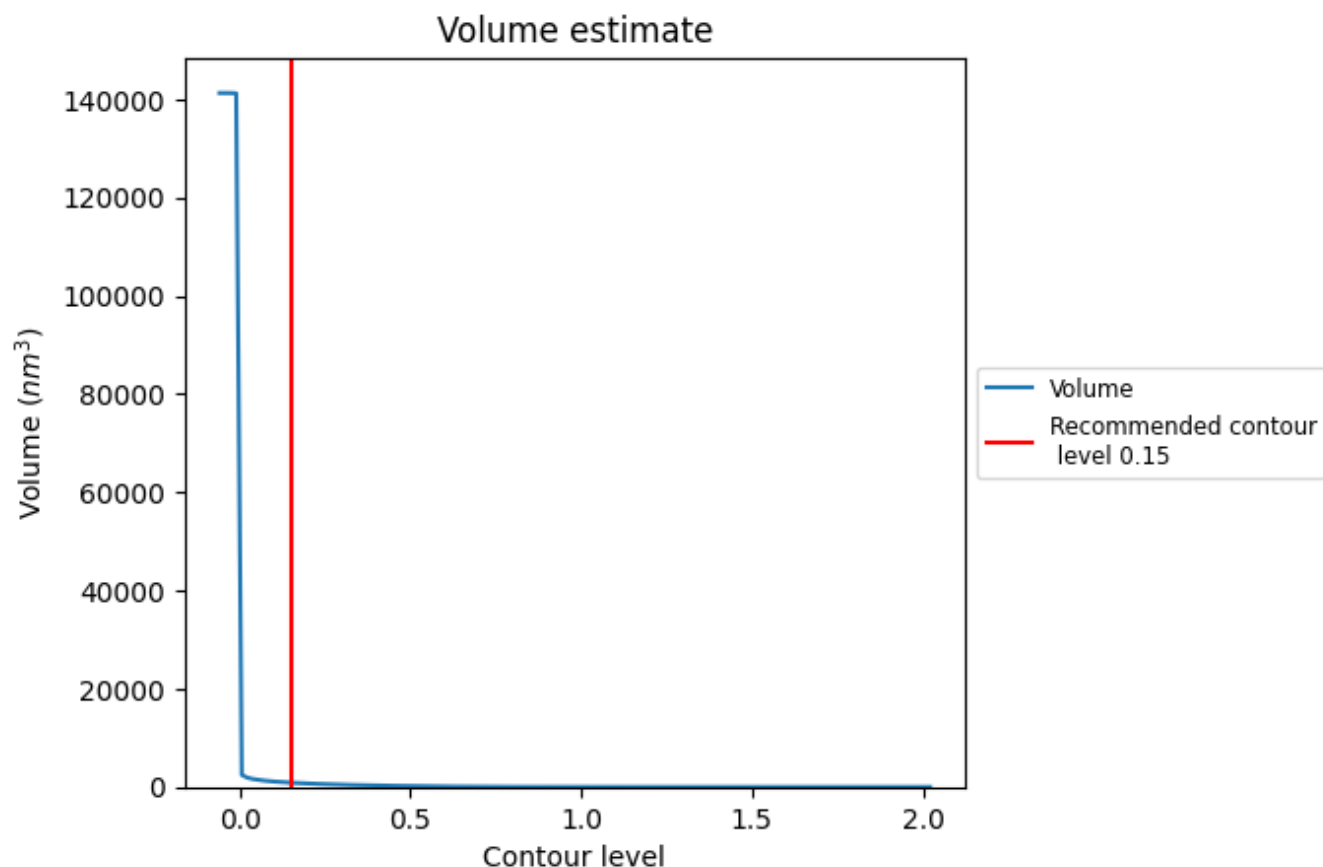
This section contains the results of statistical analysis of the map.

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.

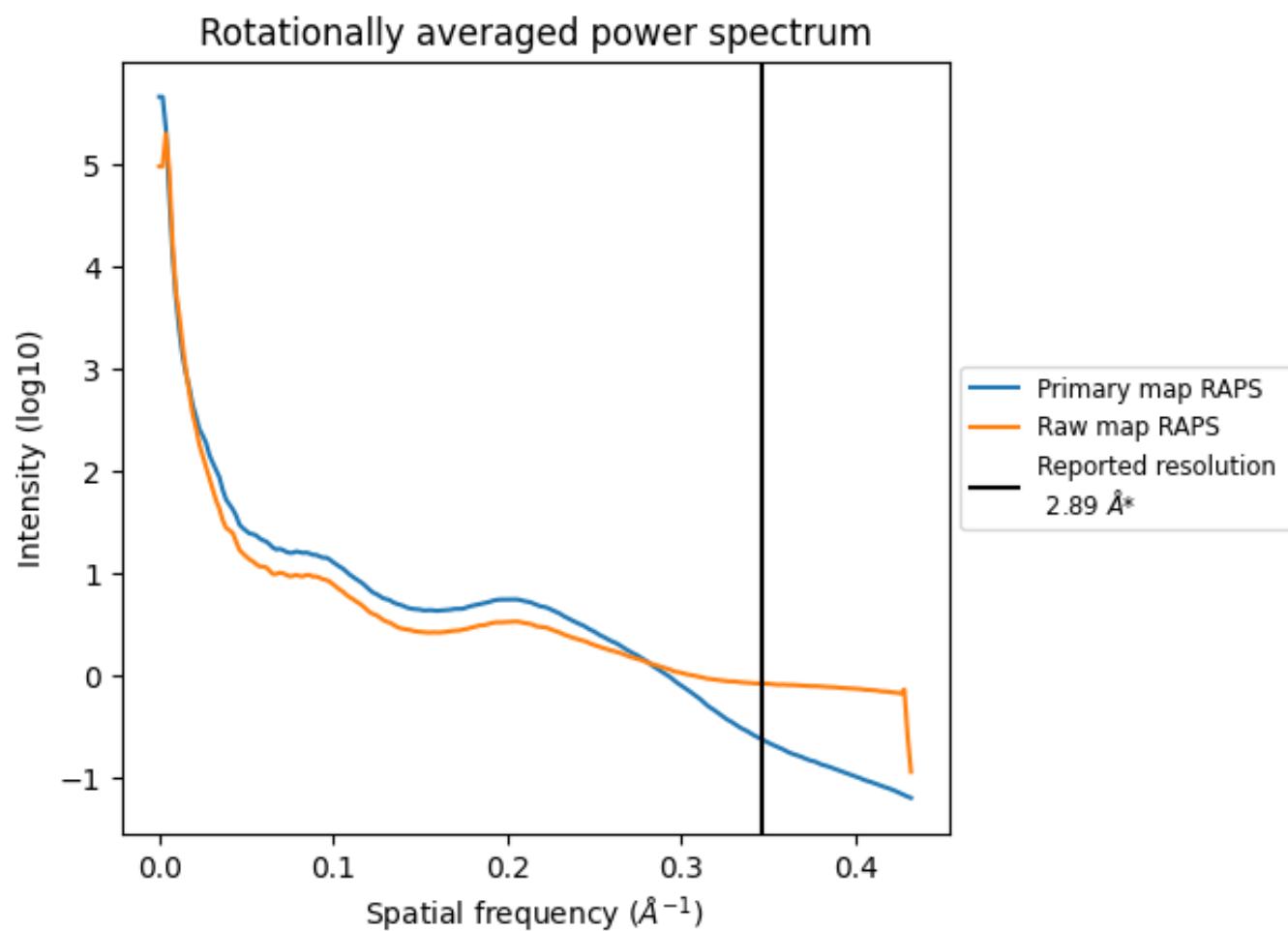
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 871 nm³; this corresponds to an approximate mass of 787 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 ⓘ

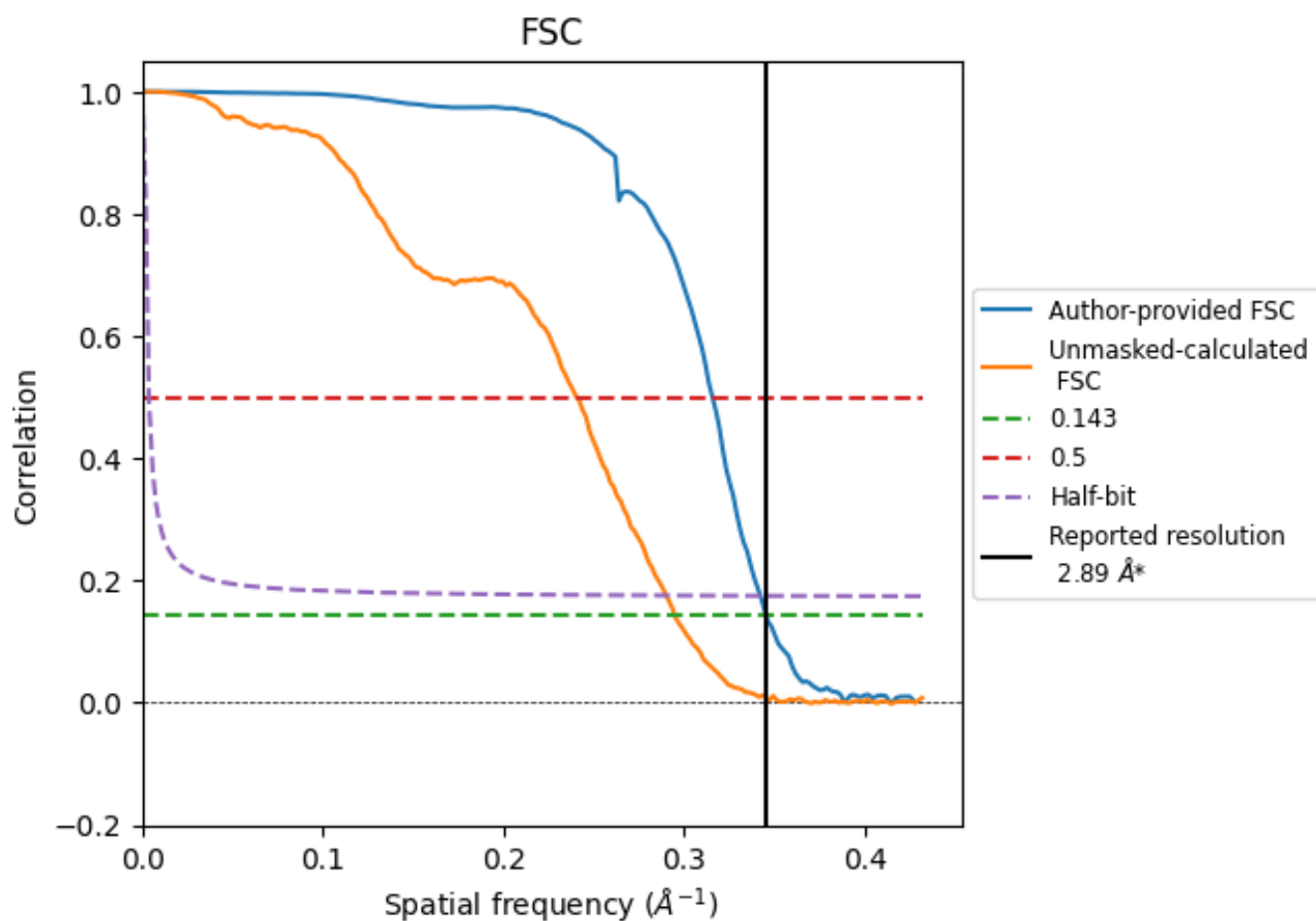


*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

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 0.346 Å⁻¹

8.2 Resolution estimates [i](#)

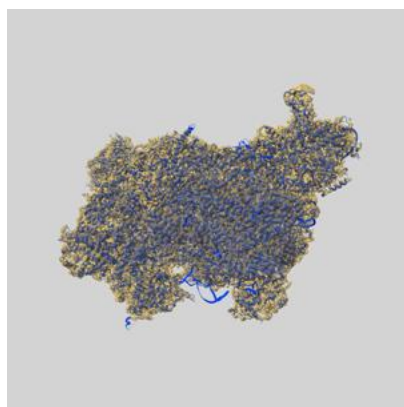
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	2.89	3.17	2.92
Unmasked-calculated*	3.39	4.15	3.44

*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 3.39 differs from the reported value 2.89 by more than 10 %

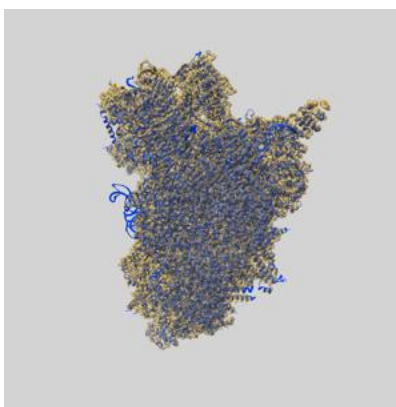
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51104 and PDB model 9G6K. Per-residue inclusion information can be found in [section 3](#) on [page 24](#).

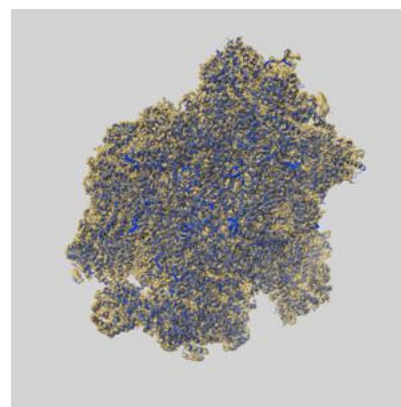
9.1 Map-model overlay [i](#)



X



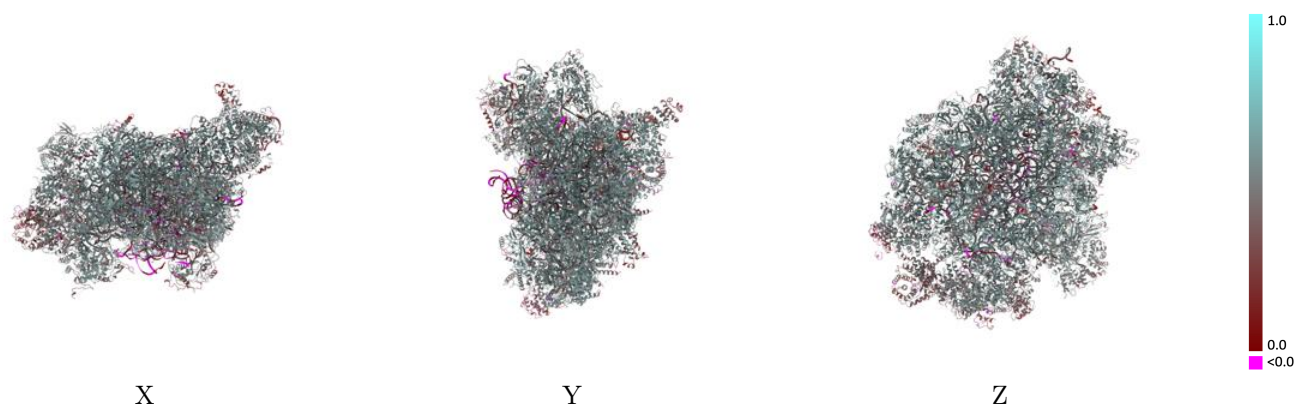
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15 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](#)

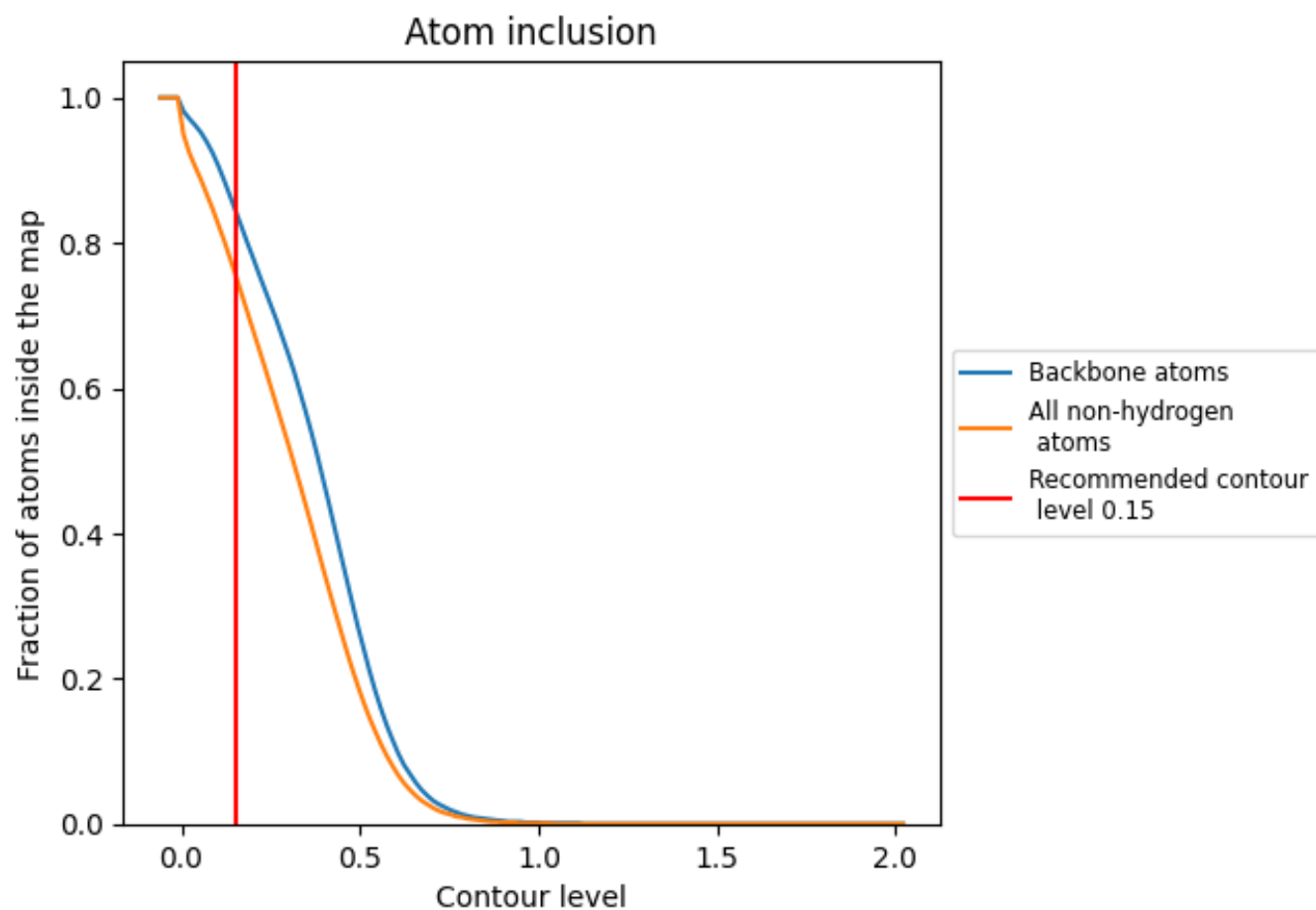


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 85% of all backbone atoms, 76% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7590	 0.4820
L0	 0.7970	 0.5210
L1	 0.7040	 0.4720
L2	 0.7320	 0.4540
L3	 0.8040	 0.5190
L4	 0.7980	 0.5150
L5	 0.7310	 0.4910
L6	 0.6090	 0.4260
L7	 0.6780	 0.4810
L8	 0.8520	 0.5520
L9	 0.7770	 0.4980
LA	 0.8410	 0.5520
LB	 0.8640	 0.5600
LC	 0.7640	 0.4930
LD	 0.7240	 0.4780
LE	 0.7590	 0.5080
LF	 0.8790	 0.5590
LG	 0.8490	 0.5420
LH	 0.7190	 0.4940
LI	 0.7910	 0.5350
LJ	 0.8660	 0.5550
LK	 0.8180	 0.5250
LL	 0.7160	 0.4680
LM	 0.5640	 0.3890
LN	 0.8640	 0.5720
LO	 0.7640	 0.5090
LP	 0.8430	 0.5430
LQ	 0.8480	 0.5480
LR	 0.7570	 0.5260
LS	 0.8330	 0.5430
LT	 0.7210	 0.4830
LU	 0.8450	 0.5600
LV	 0.7500	 0.4880
LW	 0.8170	 0.5450
LX	 0.7530	 0.4910



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Chain	Atom inclusion	Q-score
LY	 0.8260	 0.5450
LZ	 0.8150	 0.5380
La	 0.8570	 0.5640
Lb	 0.8030	 0.5230
Lc	 0.5540	 0.2980
Ld	 0.5930	 0.3190
Le	 0.7060	 0.4890
Lf	 0.7690	 0.5000
Lg	 0.8590	 0.5490
Lh	 0.7570	 0.5050
Li	 0.7330	 0.4750
Lj	 0.7980	 0.5370
Lk	 0.8050	 0.5160
Ll	 0.8040	 0.5280
Lm	 0.7480	 0.5230
Ln	 0.8120	 0.5000
Lo	 0.7970	 0.5100
Lp	 0.8030	 0.5270
Lq	 0.6820	 0.4190
Lr	 0.8440	 0.5550
Ls	 0.7690	 0.5080
Lt	 0.6980	 0.4670
Lu	 0.7490	 0.4960
Lv	 0.6490	 0.4380
Lw	 0.7810	 0.4930
Lx	 0.7390	 0.4940
Ly	 0.8140	 0.5370
Lz	 0.7920	 0.5240
UA	 0.8060	 0.5490
UB	 0.8540	 0.5470
UC	 0.7060	 0.4980
UD	 0.8720	 0.5650
UE	 0.7600	 0.5040
UF	 0.8520	 0.5550
UG	 0.7970	 0.5340
UH	 0.8300	 0.5540
UI	 0.5490	 0.2930
10	 0.8140	 0.4580
11	 0.8700	 0.5130
12	 0.6390	 0.3320
13	 0.8200	 0.4840
14	 0.8620	 0.5000

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Chain	Atom inclusion	Q-score
I5	 0.6660	 0.4220
I6	 0.8520	 0.4920
I7	 0.8570	 0.5200
I8	 0.7570	 0.4220
I9	 0.8690	 0.5050
IA	 0.8420	 0.4720
IB	 0.8270	 0.4510
IC	 0.7670	 0.4090
ID	 0.7100	 0.4240
IE	 0.7630	 0.4360
IF	 0.7700	 0.4700
IG	 0.8130	 0.4690
IH	 0.7590	 0.4380
II	 0.7060	 0.4610
IJ	 0.4820	 0.2990
IK	 0.7530	 0.4470
IL	 0.8490	 0.5110
IM	 0.5990	 0.3750
IN	 0.7970	 0.4960
IO	 0.8230	 0.4950
IP	 0.8170	 0.4200
IQ	 0.7840	 0.4170
IR	 0.8230	 0.4590
IS	 0.6000	 0.4180
IT	 0.8070	 0.4370
IU	 0.5800	 0.3320
IV	 0.8550	 0.4880
IW	 0.8500	 0.4700
IX	 0.7100	 0.3880
IY	 0.1550	 0.0000