wwPDB EM Validation Summary Report (i)

Nov 9, 2026 – 05:38 pm GMT

PDB ID	:	9QES / pdb_00009qes
EMDB ID	:	EMD-53091
Title	:	Human pre-60S - State 2
Authors	:	Thoms, M.; Denk, T.; Beckmann, R.
Deposited on	:	2025-03-11
Resolution	:	3.10 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

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

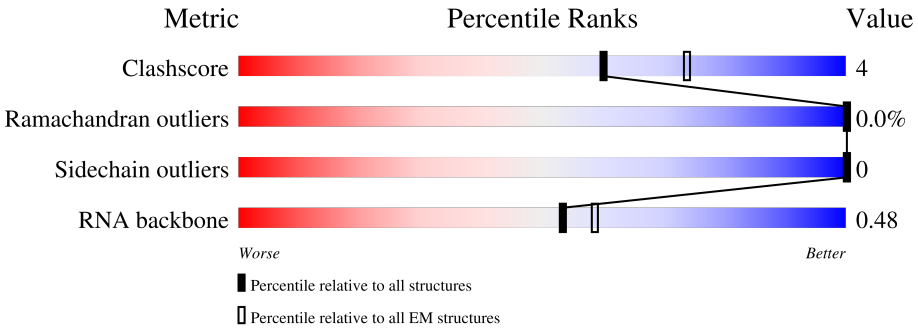
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.51

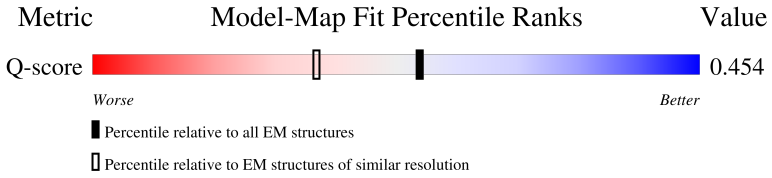
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	CA	245	86% 14%
2	CB	731	6% 54% 7% 40%
3	CC	549	6% 13% 85%

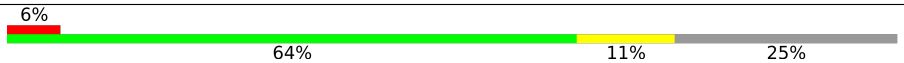
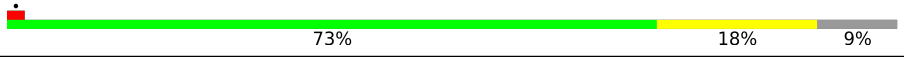
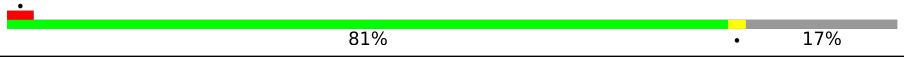
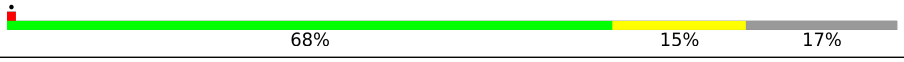
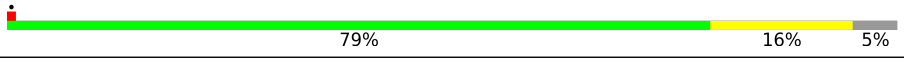
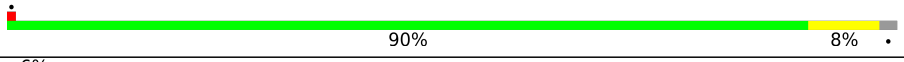
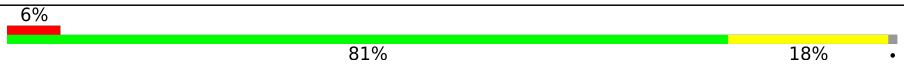
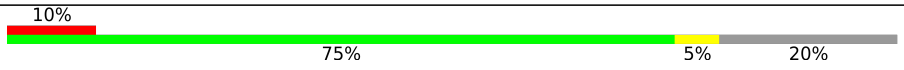
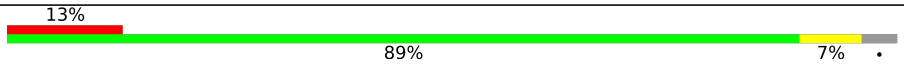
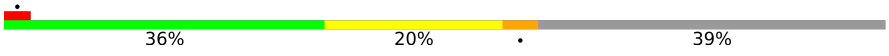
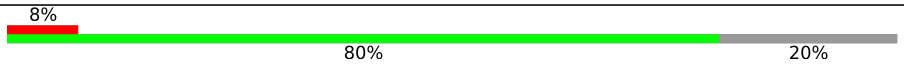
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Mol	Chain	Length	Quality of chain
4	CD	634	13% 78% 11% 11%
5	CE	129	50% 47%
6	CF	239	80% 11% 9%
7	CG	485	6% 88% 9%
8	CH	260	85% 12%
9	CI	163	72% 12% 16%
10	CJ	306	76% 14% 10%
11	CK	365	5% 45% 8% 47%
12	L7	121	68% 26% 6%
13	LA	257	47% 14% 39%
14	LB	403	82% 12% 5%
15	LC	427	76% 9% 15%
16	LD	297	65% 12% 23%
17	LE	288	64% 8% 28%
18	LF	248	79% 9% 12%
19	LG	266	71% 9% 20%
20	LH	192	88% 11%
21	LJ	178	86% 10%
22	LL	211	83% 8% 9%
23	LM	215	54% 9% 37%
24	LN	204	77% 13% 10%
25	LO	203	85% 14%
26	LP	184	74% 8% 17%
27	LQ	188	75% 5% 20%
28	LR	196	54% 5% 41%

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Mol	Chain	Length	Quality of chain
29	LS	176	
30	LT	160	
31	LV	140	
32	LX	156	
33	LY	145	
34	LZ	136	
35	La	148	
36	Lc	115	
37	Ld	125	
38	Le	135	
39	Lf	110	
40	Lg	117	
41	Lh	123	
42	Li	105	
43	Lj	97	
44	Ll	51	
45	Lp	92	
46	Lr	137	
47	Lt	165	
48	L8	157	
49	L5	5070	
50	LU	128	

2 Entry composition (i)

There are 53 unique types of molecules in this entry. The entry contains 136109 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 Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CA	245	Total	C	N	O	S	0	0
			1860	1153	319	375	13		

- Molecule 2 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CB	441	Total	C	N	O	S	0	0
			3189	2019	579	582	9		

- Molecule 3 is a protein called Guanine nucleotide-binding protein-like 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CC	80	Total	C	N	O	S	0	0
			571	355	123	90	3		

- Molecule 4 is a protein called GTP-binding protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CD	566	Total	C	N	O	S	0	0
			4304	2722	771	791	20		

- Molecule 5 is a protein called Protein LLP homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CE	69	Total	C	N	O	S	0	0
			490	308	100	80	2		

- Molecule 6 is a protein called mRNA turnover protein 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CF	218	Total	C	N	O	S	0	0
			1775	1131	312	321	11		

- Molecule 7 is a protein called Notchless protein homolog 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CG	471	Total	C	N	O	S	0	0
			3449	2149	641	648	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CG	85	ALA	GLU	engineered mutation	UNP Q9NVX2

- Molecule 8 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CH	252	Total	C	N	O	S	0	0
			2023	1290	381	343	9		

- Molecule 9 is a protein called Probable ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CI	137	Total	C	N	O	S	0	0
			1105	701	213	182	9		

- Molecule 10 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CJ	274	Total	C	N	O	S	0	0
			2137	1368	371	387	11		

- Molecule 11 is a protein called Ribosome biogenesis regulatory protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CK	195	Total	C	N	O	S	0	0
			1405	886	262	256	1		

- Molecule 12 is a RNA chain called 5S rRNA.

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

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LA	157	Total	C	N	O	S	0	0
			1191	751	229	207	4		

- Molecule 14 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LB	381	Total	C	N	O	S	0	0
			3030	1927	563	527	13		

- Molecule 15 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LC	362	Total	C	N	O	S	0	0
			2861	1800	573	475	13		

- Molecule 16 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LD	229	Total	C	N	O	S	0	0
			1870	1186	336	335	13		

- Molecule 17 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LE	208	Total	C	N	O	S	0	0
			1639	1055	309	271	4		

- Molecule 18 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LF	219	Total	C	N	O	S	0	0
			1773	1135	339	291	8		

- Molecule 19 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LG	213	Total	C	N	O	S	0	0
			1676	1068	321	283	4		

- Molecule 20 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

- Molecule 21 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LJ	170	Total	C	N	O	S	0	0
			1299	820	242	231	6		

- Molecule 22 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LL	192	Total	C	N	O	S	0	0
			1480	929	308	240	3		

- Molecule 23 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LM	135	Total	C	N	O	S	0	0
			1105	707	213	178	7		

- Molecule 24 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LN	183	Total	C	N	O	S	0	0
			1542	972	324	242	4		

- Molecule 25 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LO	201	Total	C	N	O	S	0	0
			1642	1058	320	259	5		

- Molecule 26 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LP	152	Total	C	N	O	S	0	0
			1222	765	235	213	9		

- Molecule 27 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LQ	151	Total	C	N	O	S	0	0
			1217	765	244	203	5		

- Molecule 28 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LR	115	Total	C	N	O	S	0	0
			775	482	153	138	2		

- Molecule 29 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LS	176	Total	C	N	O	S	0	0
			1453	924	282	236	11		

- Molecule 30 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LT	120	Total	C	N	O	S	0	0
			906	577	171	157	1		

- Molecule 31 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LV	136	Total	C	N	O	S	0	0
			986	619	186	176	5		

- Molecule 32 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LX	119	Total	C	N	O	S	0	0
			964	615	180	168	1		

- Molecule 33 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LY	132	Total	C	N	O	S	0	0
			1098	689	222	184	3		

- Molecule 34 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LZ	135	Total	C	N	O	S	0	0
			916	592	171	152	1		

- Molecule 35 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	La	105	Total	C	N	O	S	0	0
			823	524	160	136	3		

- Molecule 36 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lc	95	Total	C	N	O	S	0	0
			558	356	99	102	1		

- Molecule 37 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ld	104	Total	C	N	O	S	0	0
			849	541	167	139	2		

- Molecule 38 is a protein called 60S ribosomal protein L32.

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

- Molecule 39 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		

- Molecule 40 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lg	31	Total	C	N	O	S	0	0
			203	125	41	36	1		

- Molecule 41 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lh	121	Total	C	N	O	S	0	0
			1006	635	203	167	1		

- Molecule 42 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Li	104	Total	C	N	O	S	0	0
			787	490	165	128	4		

- Molecule 43 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lj	74	Total	C	N	O	S	0	0
			611	377	134	95	5		

- Molecule 44 is a protein called 60S ribosomal protein L39.

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

- Molecule 45 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lp	74	Total	C	N	O	S	0	0
			458	280	86	86	6		

- Molecule 46 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lr	123	Total	C	N	O	S	0	0
			976	605	203	164	4		

- Molecule 47 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lt	159	Total	C	N	O	S	0	0
			955	594	186	173	2		

- Molecule 48 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	L8	146	Total	C	N	O	P	0	0
			3110	1388	556	1021	145		

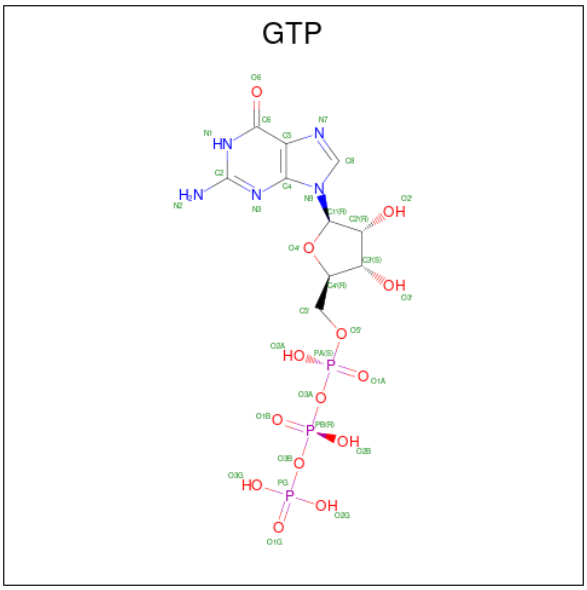
- Molecule 49 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	L5	3068	Total	C	N	O	P	0	0
			65809	29300	12068	21374	3067		

- Molecule 50 is a protein called 60S ribosomal protein L22.

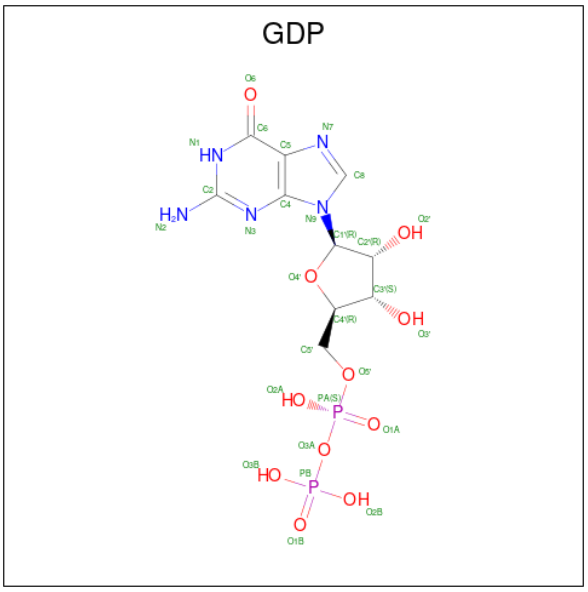
Mol	Chain	Residues	Atoms				AltConf	Trace
50	LU	102	Total	C	N	O	0	0
			508	304	102	102		

- Molecule 51 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
51	CB	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 52 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
52	CD	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

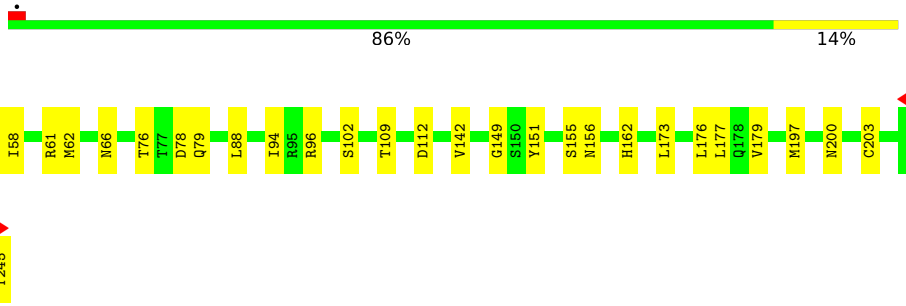
Mol	Chain	Residues	Atoms		AltConf
53	CI	1	Total	Zn	0
			1	1	
53	Lj	1	Total	Zn	0
			1	1	
53	Lp	1	Total	Zn	0
			1	1	

3 Residue-property plots (i)

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

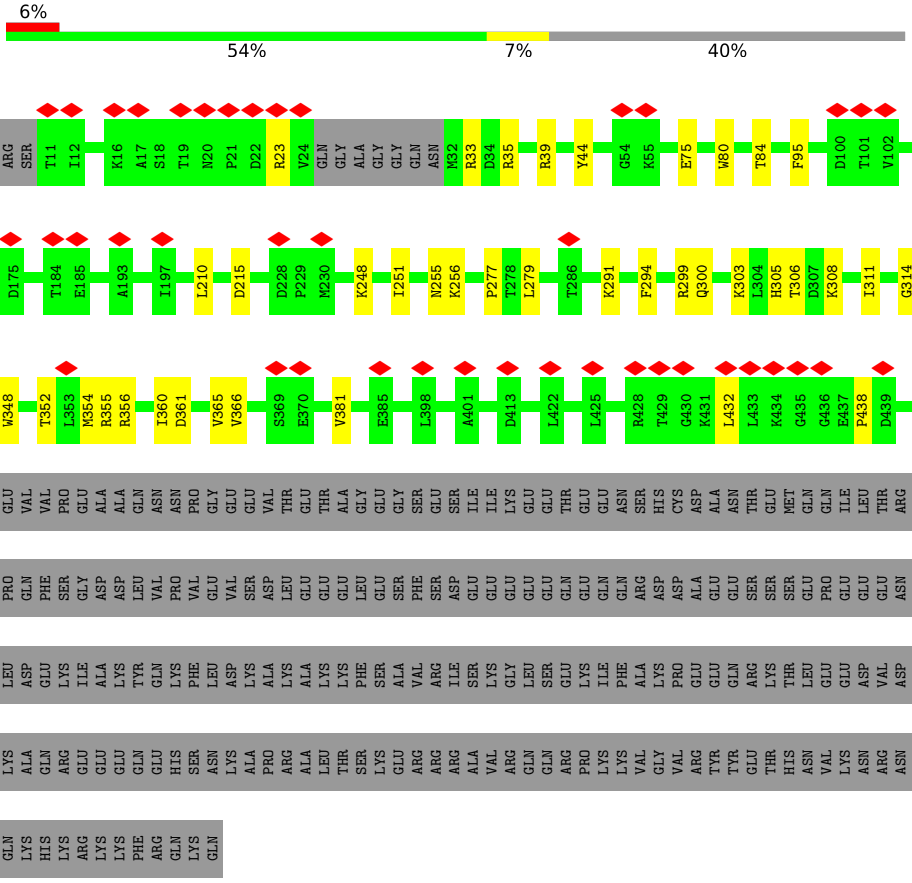
• Molecule 1: Eukaryotic translation initiation factor 6

Chain CA:



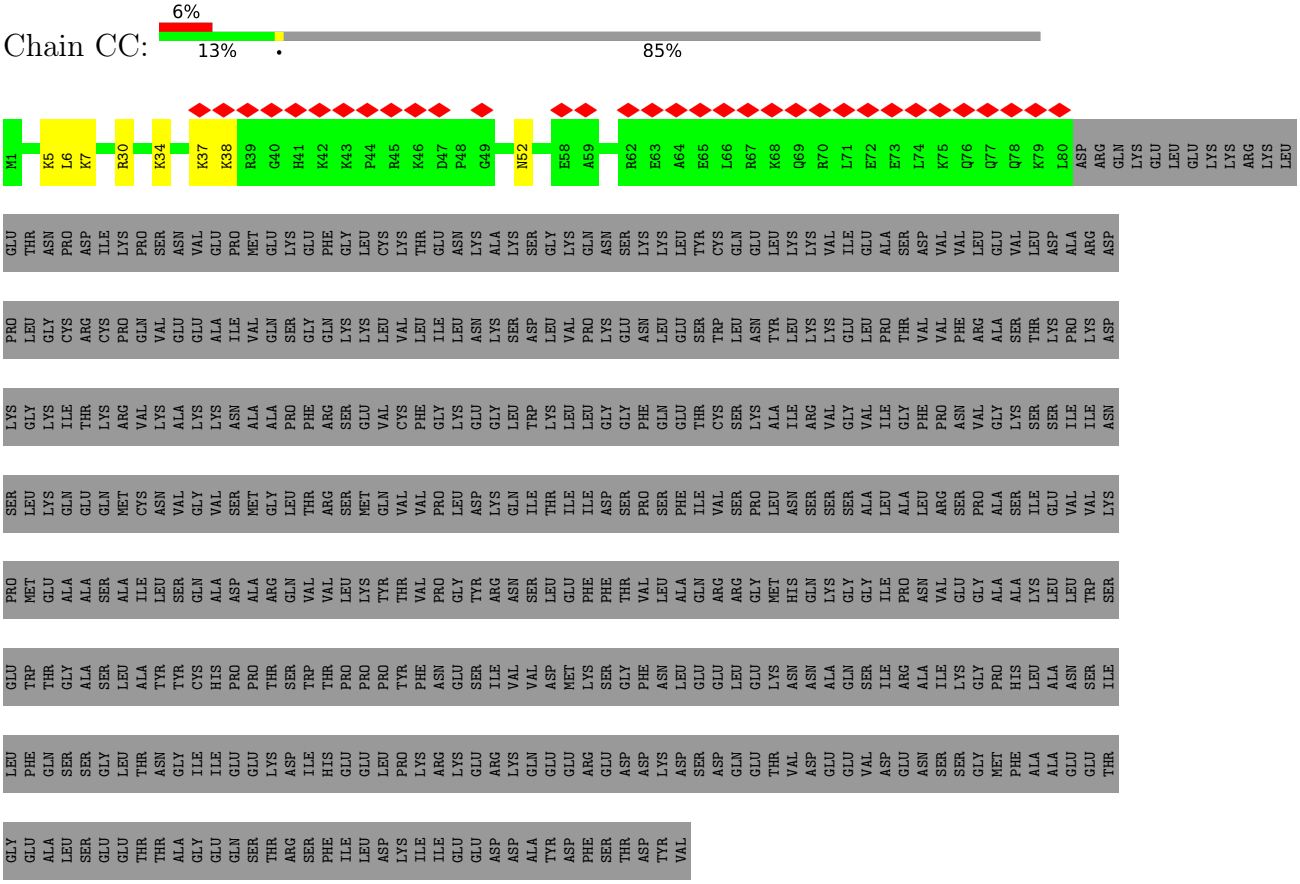
• Molecule 2: Nucleolar GTP-binding protein 2

Chain CB:



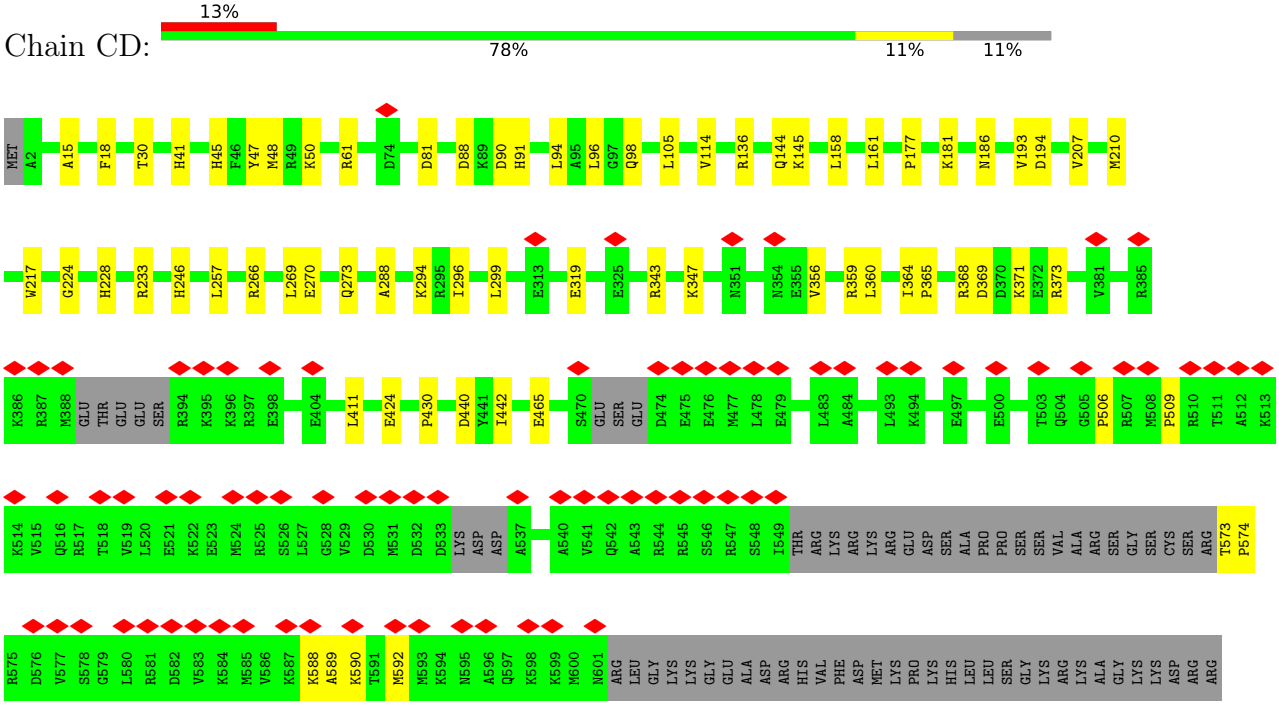
• Molecule 3: Guanine nucleotide-binding protein-like 3

Chain CC:



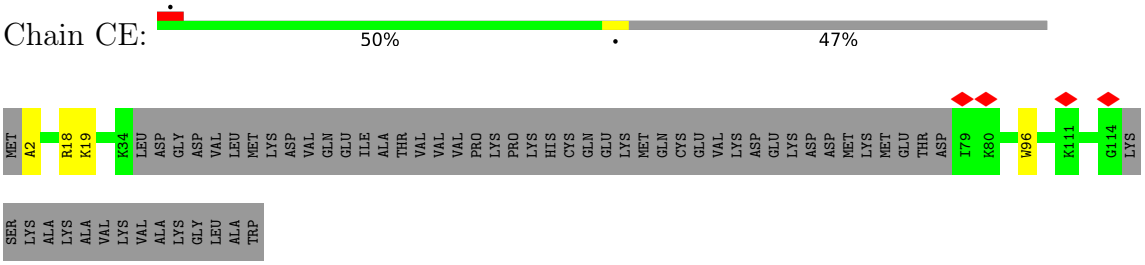
• Molecule 4: GTP-binding protein 4

Chain CD:



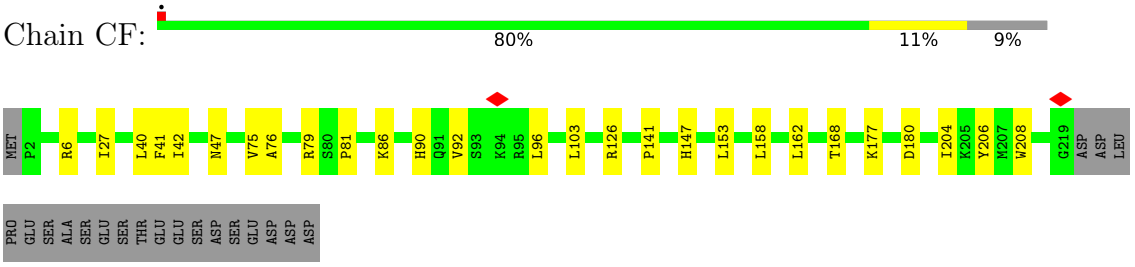
• Molecule 5: Protein LLP homolog

Chain CE:



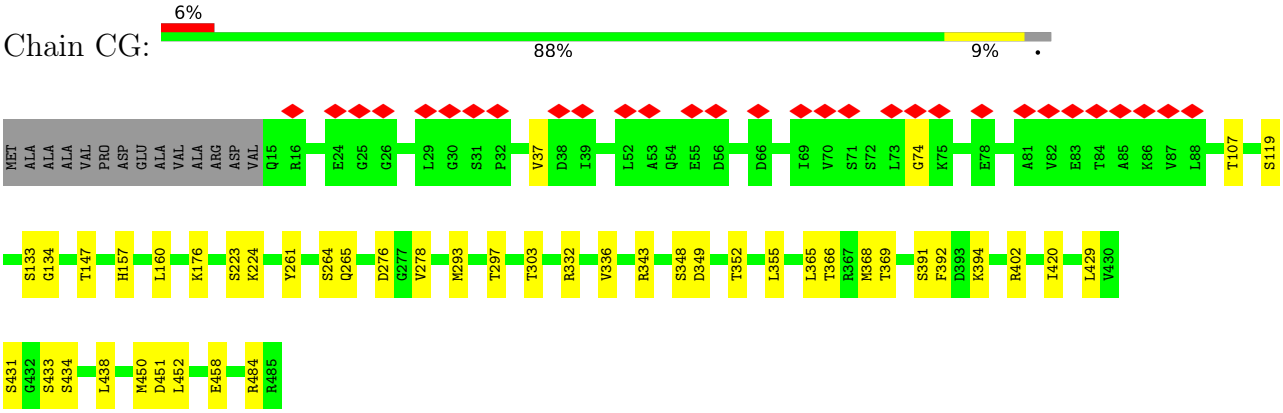
• Molecule 6: mRNA turnover protein 4 homolog

Chain CF:



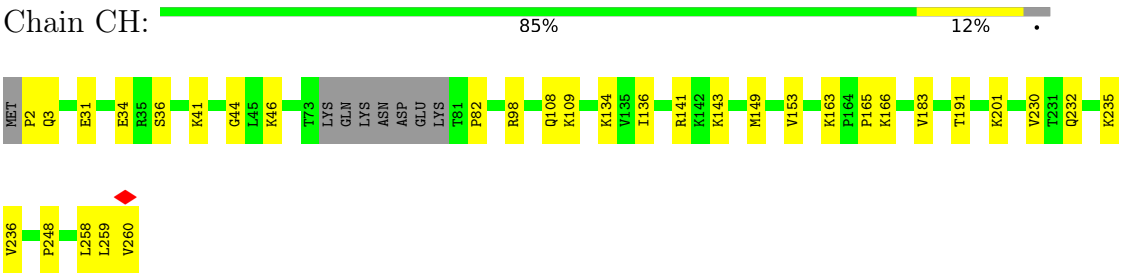
• Molecule 7: Notchless protein homolog 1

Chain CG:



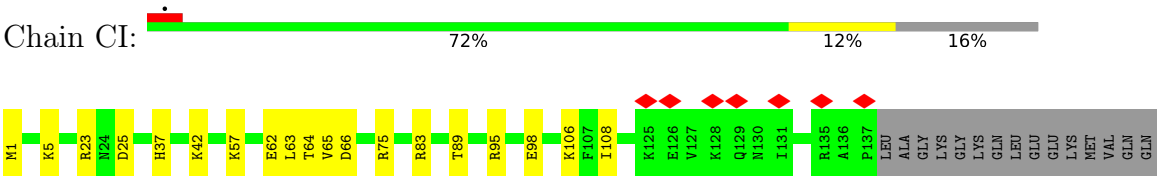
• Molecule 8: Ribosome biogenesis protein NSA2 homolog

Chain CH:



• Molecule 9: Probable ribosome biogenesis protein RLP24

Chain CI:

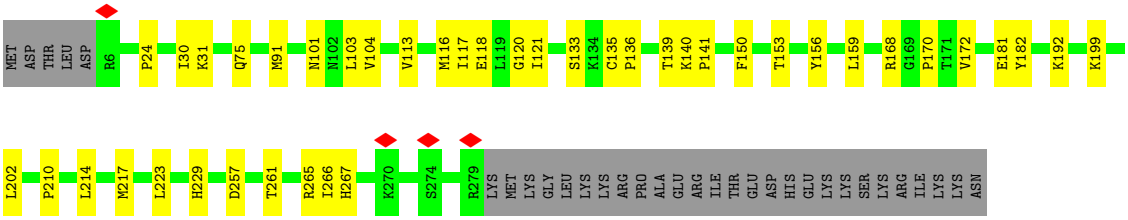




• Molecule 10: Ribosome production factor 2 homolog

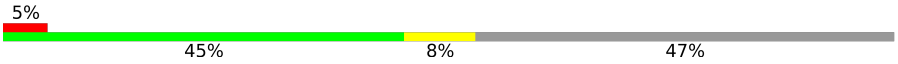
Chain CJ:

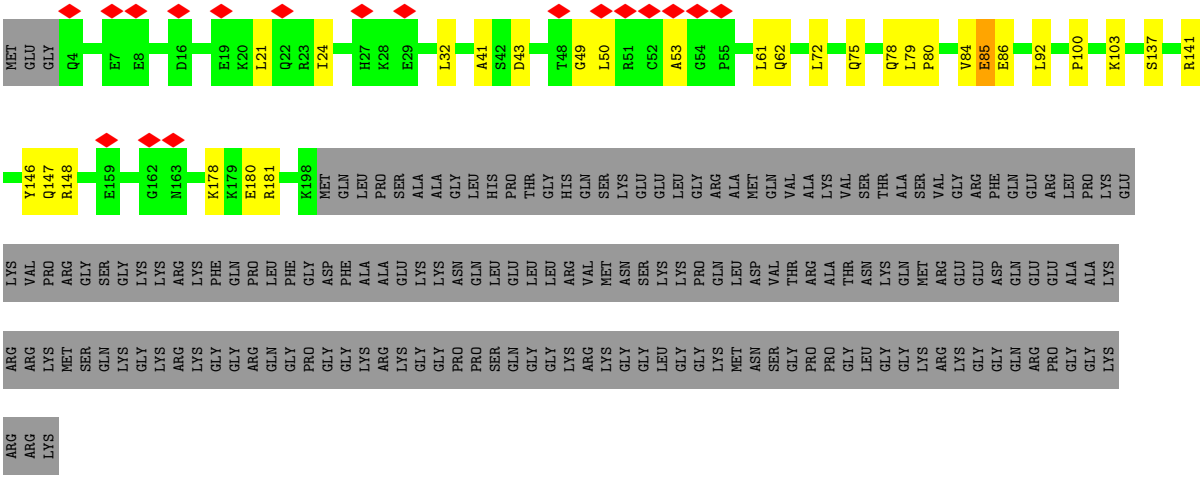




• Molecule 11: Ribosome biogenesis regulatory protein homolog

Chain CK:

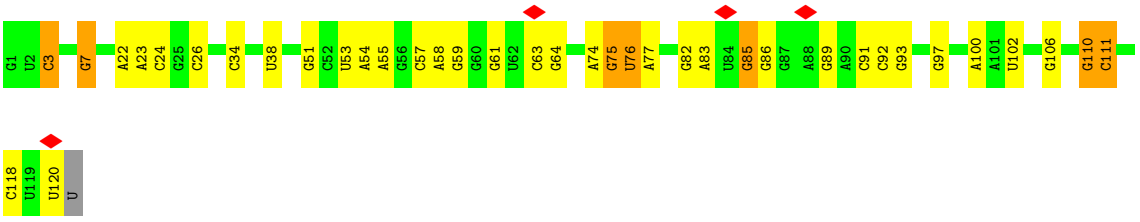




• Molecule 12: 5S rRNA

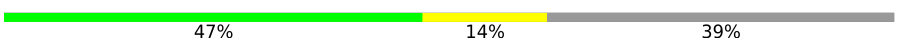
Chain L7:

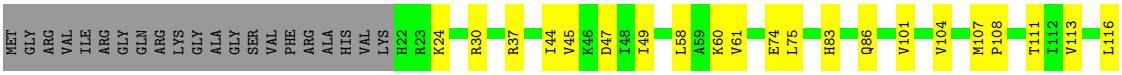


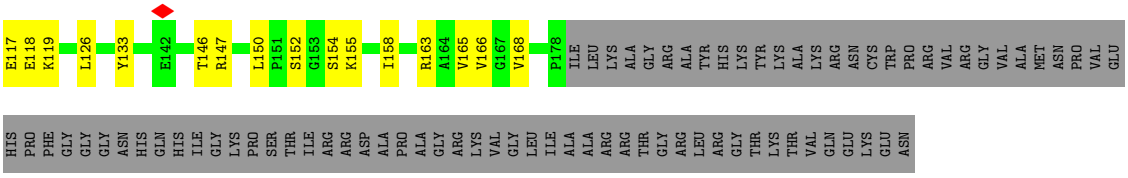


• Molecule 13: 60S ribosomal protein L8

Chain LA:



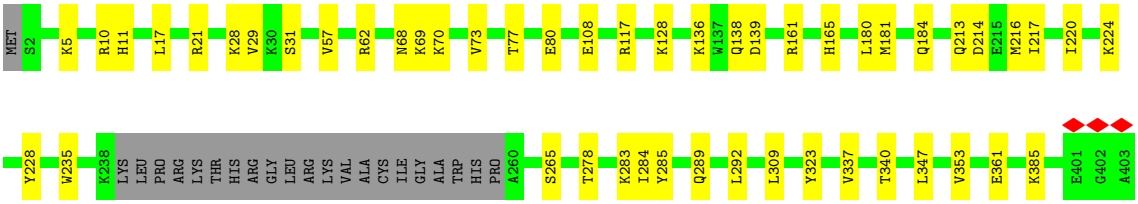




• Molecule 14: 60S ribosomal protein L3

Chain LB:

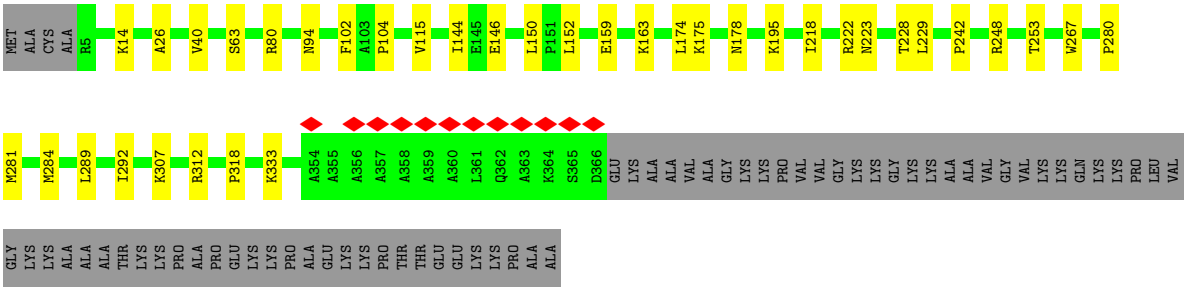




• Molecule 15: 60S ribosomal protein L4

Chain LC:

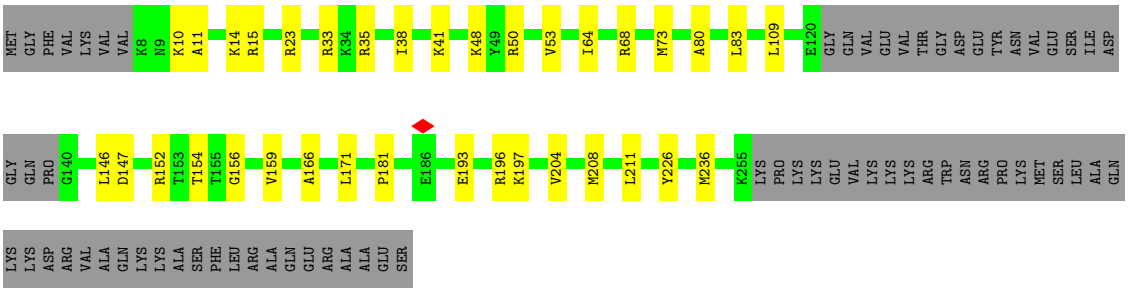




• Molecule 16: 60S ribosomal protein L5

Chain LD:



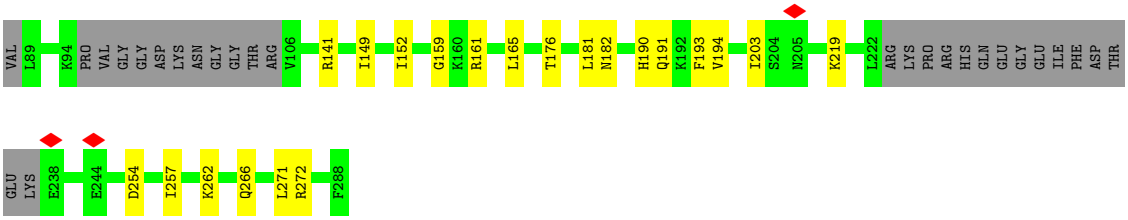


• Molecule 17: Large ribosomal subunit protein eL6

Chain LE:



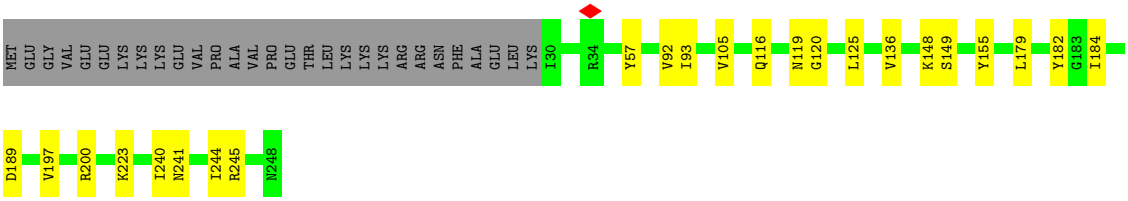




• Molecule 18: Large ribosomal subunit protein uL30

Chain LF:

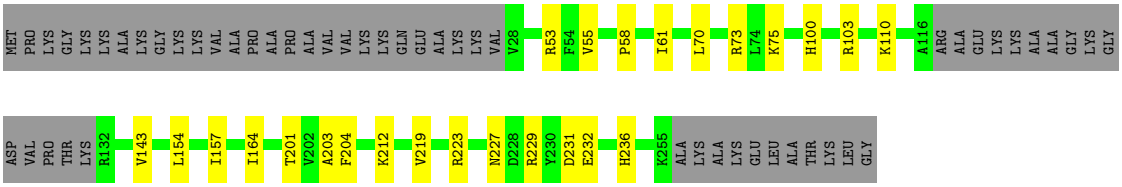




• Molecule 19: 60S ribosomal protein L7a

Chain LG:





• Molecule 20: 60S ribosomal protein L9

Chain LH:

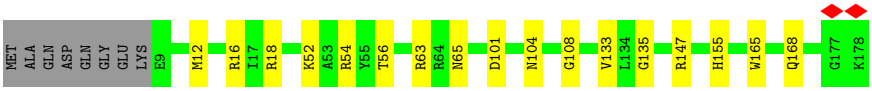




• Molecule 21: 60S ribosomal protein L11

Chain LJ:





• Molecule 22: 60S ribosomal protein L13

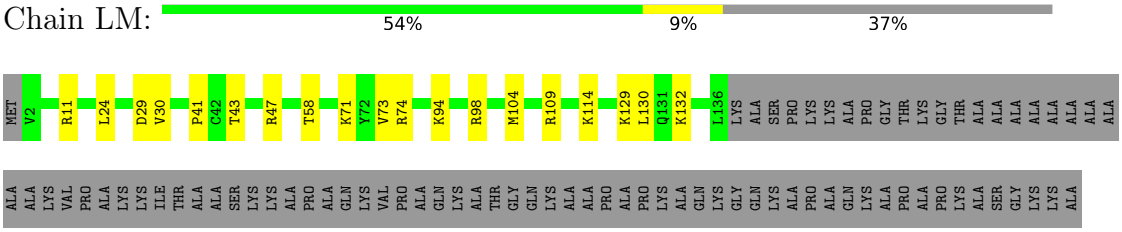
Chain LL:





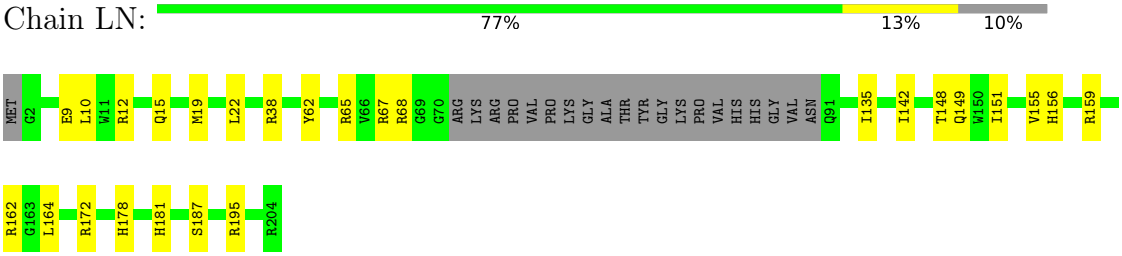
• Molecule 23: 60S ribosomal protein L14

Chain LM:



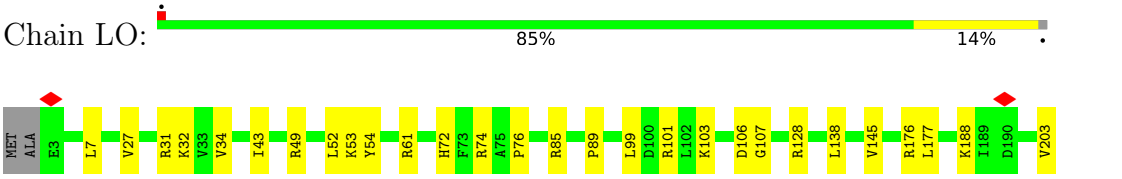
• Molecule 24: 60S ribosomal protein L15

Chain LN:



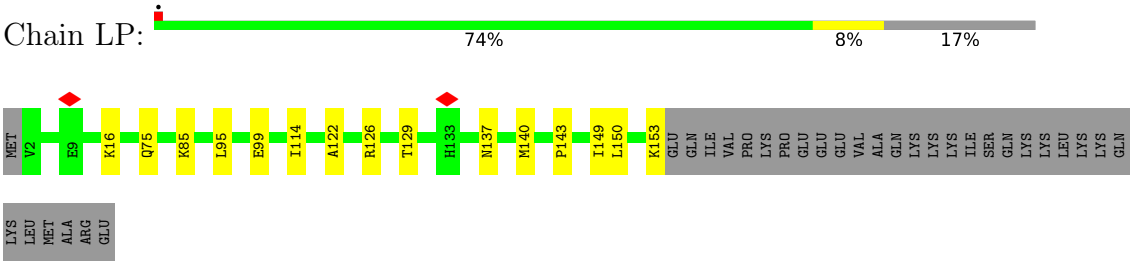
• Molecule 25: 60S ribosomal protein L13a

Chain LO:



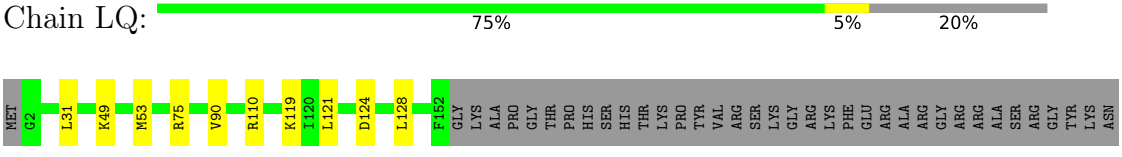
• Molecule 26: 60S ribosomal protein L17

Chain LP:



• Molecule 27: 60S ribosomal protein L18

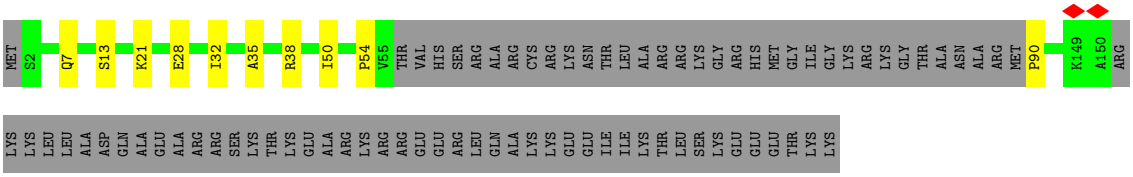
Chain LQ:



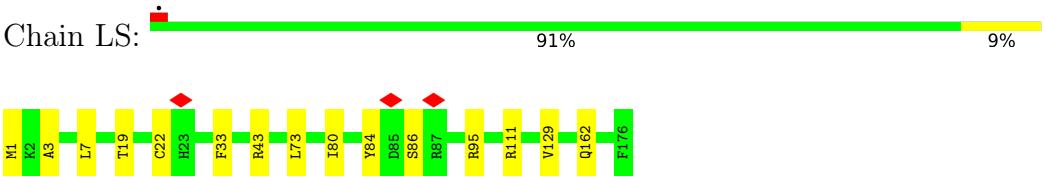
• Molecule 28: 60S ribosomal protein L19

Chain LR:

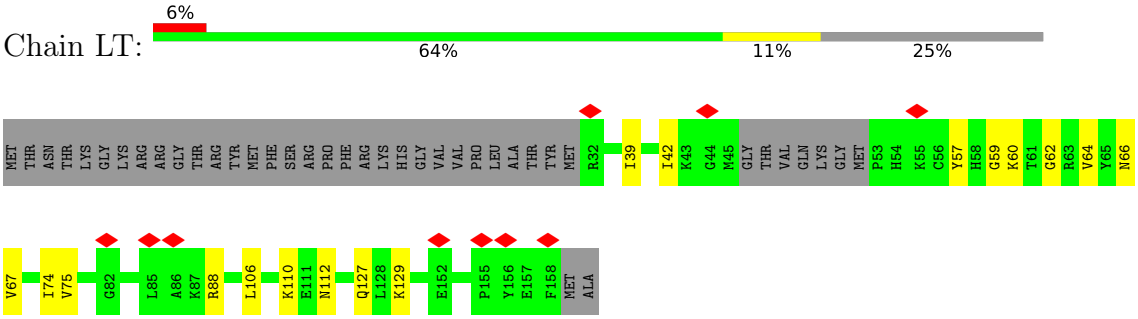




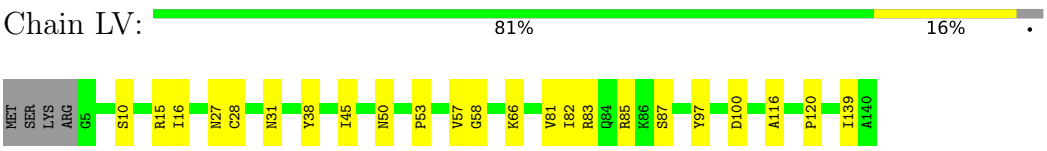
• Molecule 29: 60S ribosomal protein L18a



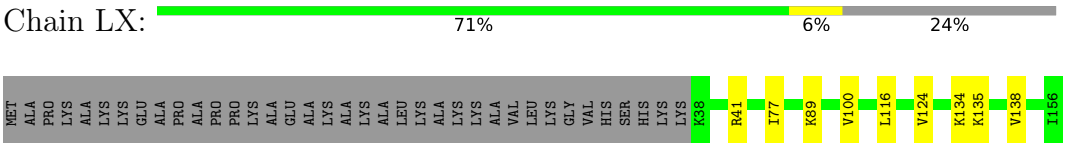
• Molecule 30: 60S ribosomal protein L21



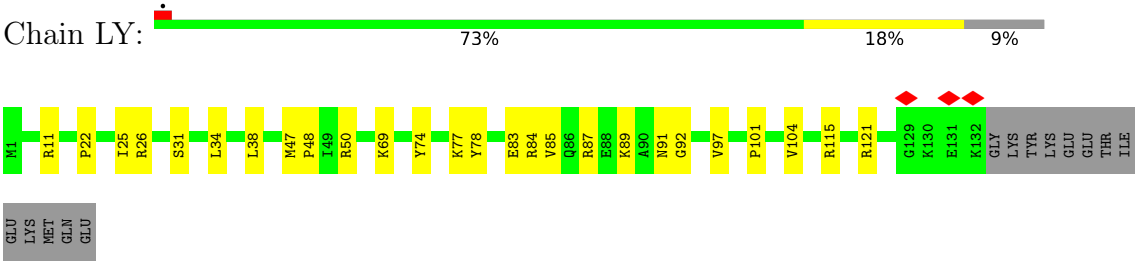
• Molecule 31: 60S ribosomal protein L23



• Molecule 32: 60S ribosomal protein L23a

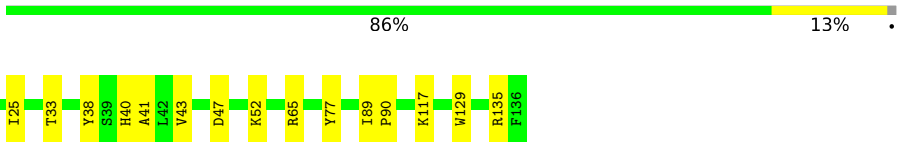


• Molecule 33: 60S ribosomal protein L26



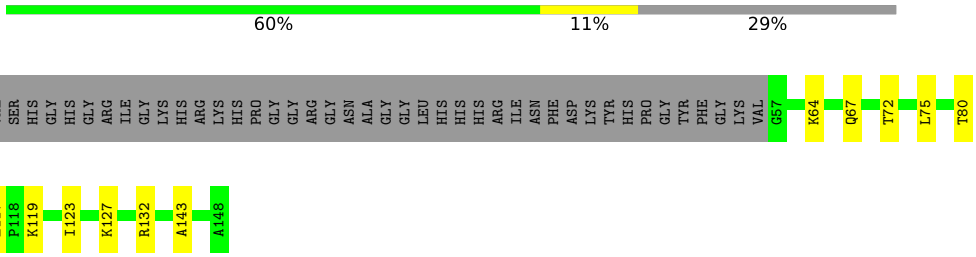
• Molecule 34: 60S ribosomal protein L27

Chain LZ:



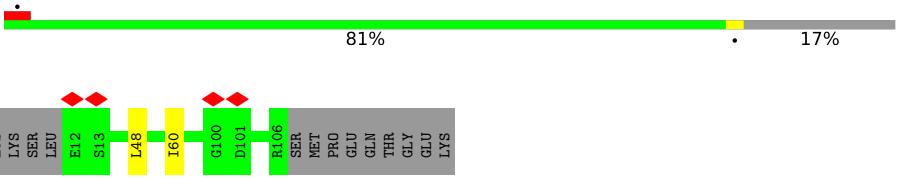
• Molecule 35: 60S ribosomal protein L27a

Chain La:



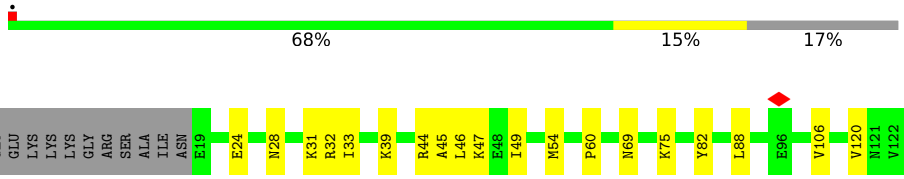
• Molecule 36: 60S ribosomal protein L30

Chain Lc:



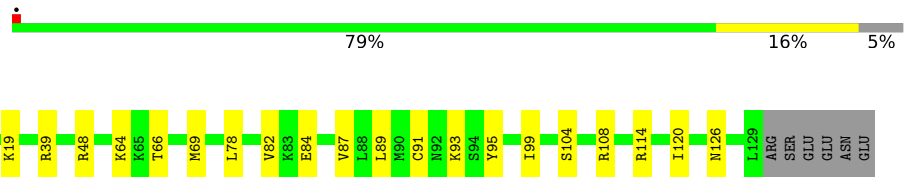
• Molecule 37: 60S ribosomal protein L31

Chain Ld:



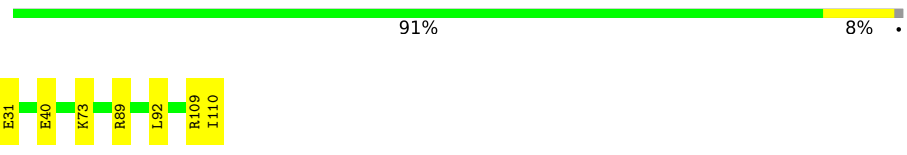
• Molecule 38: 60S ribosomal protein L32

Chain Le:



• Molecule 39: 60S ribosomal protein L35a

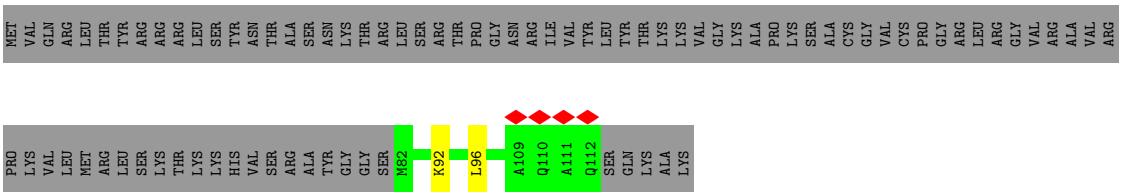
Chain Lf:



• Molecule 40: 60S ribosomal protein L34

Chain Lg:

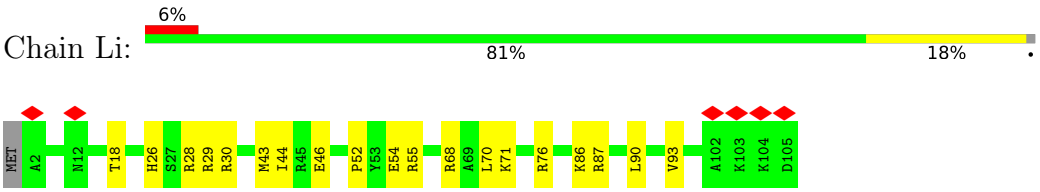




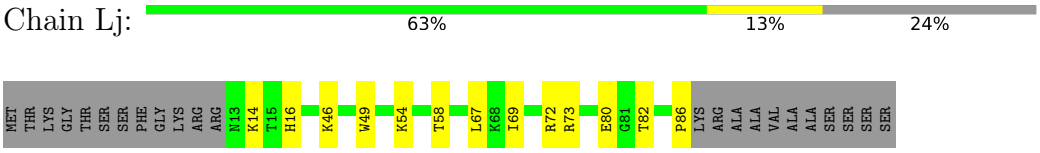
• Molecule 41: 60S ribosomal protein L35



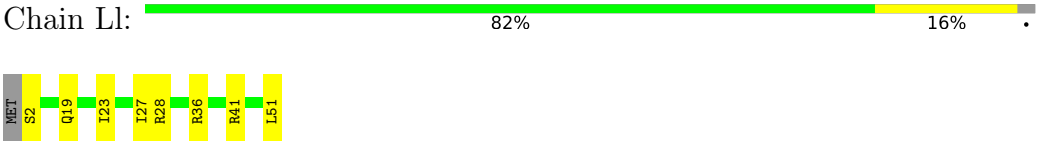
• Molecule 42: 60S ribosomal protein L36



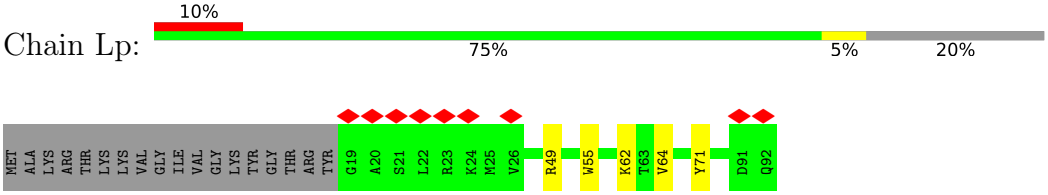
• Molecule 43: Large ribosomal subunit protein eL37



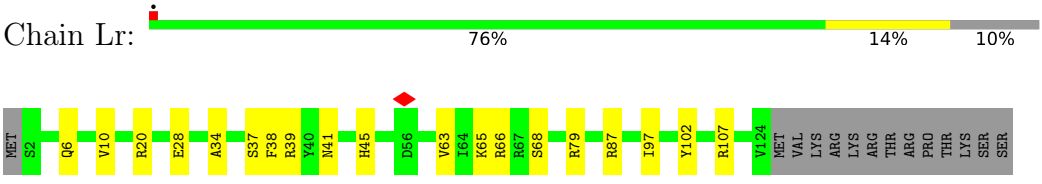
• Molecule 44: 60S ribosomal protein L39



• Molecule 45: 60S ribosomal protein L37a

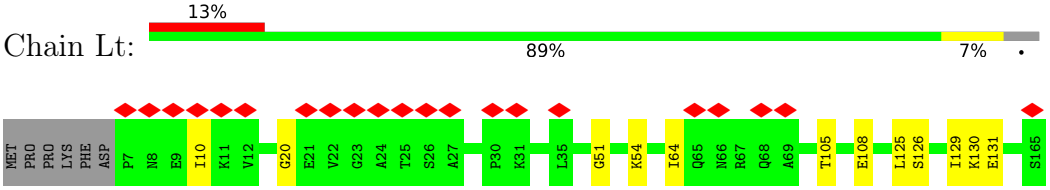


• Molecule 46: 60S ribosomal protein L28



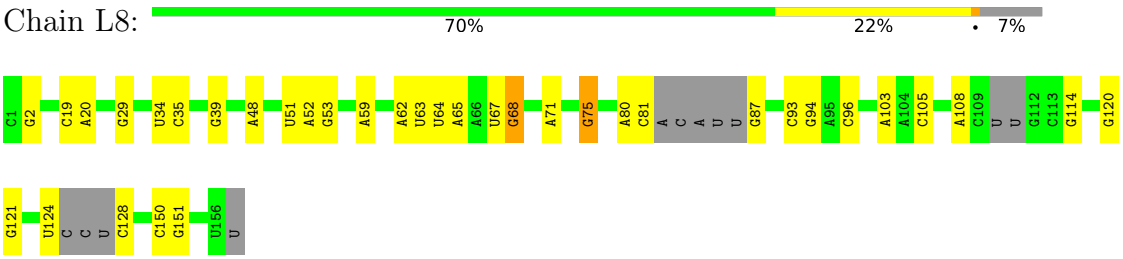
• Molecule 47: Large ribosomal subunit protein uL11

Chain Lt:



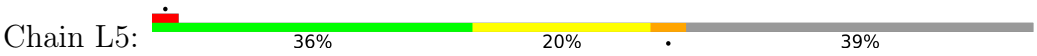
• Molecule 48: 5.8S rRNA

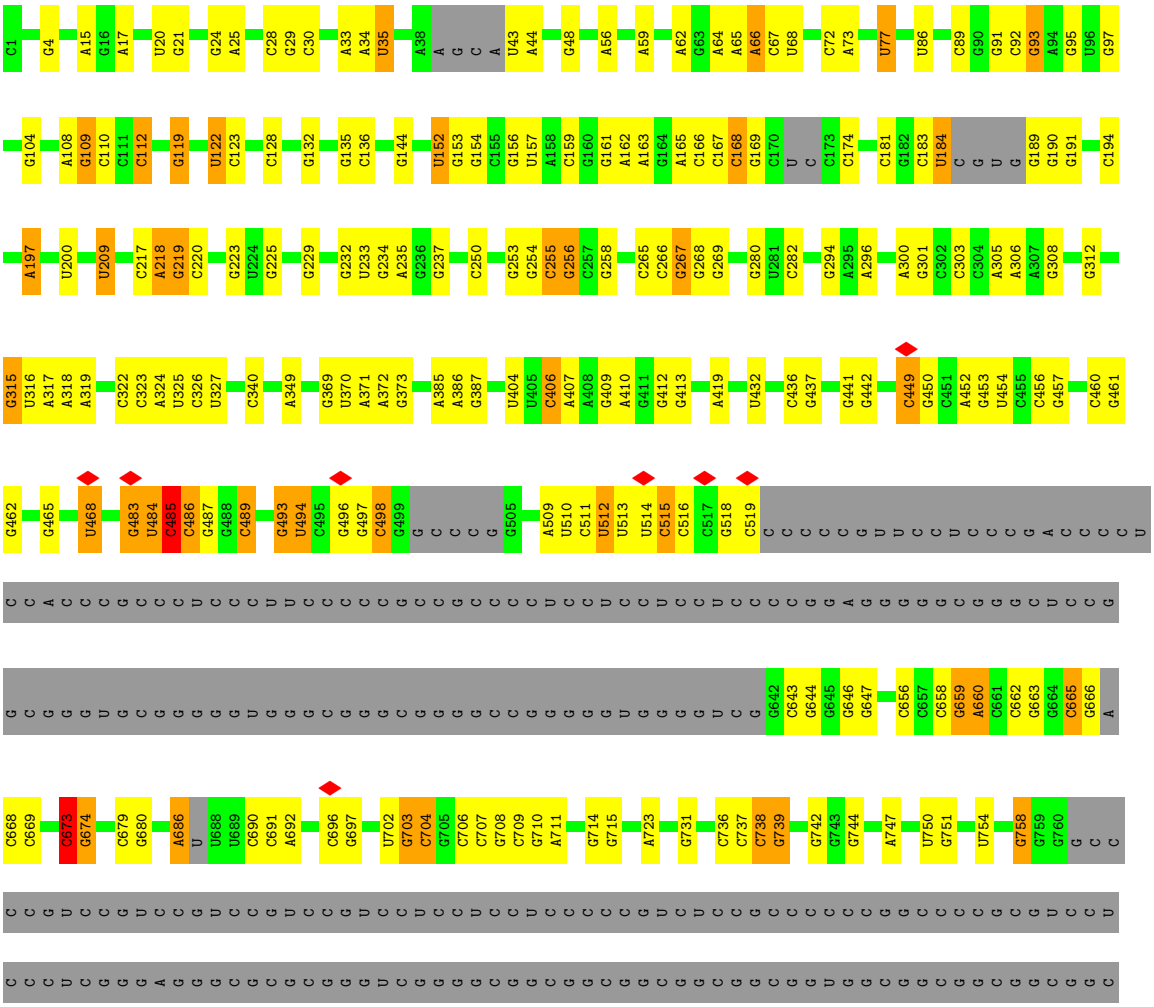
Chain L8:

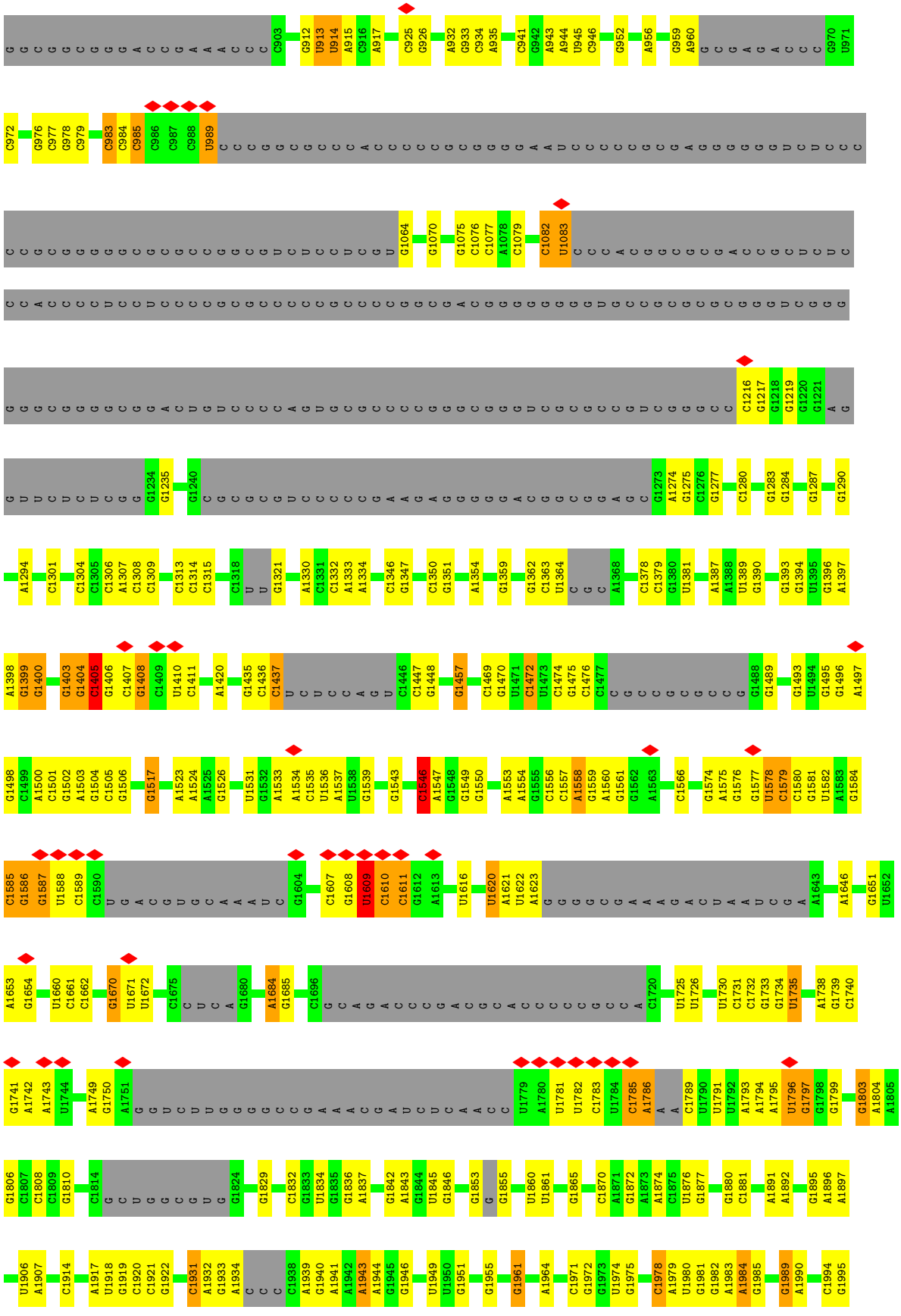


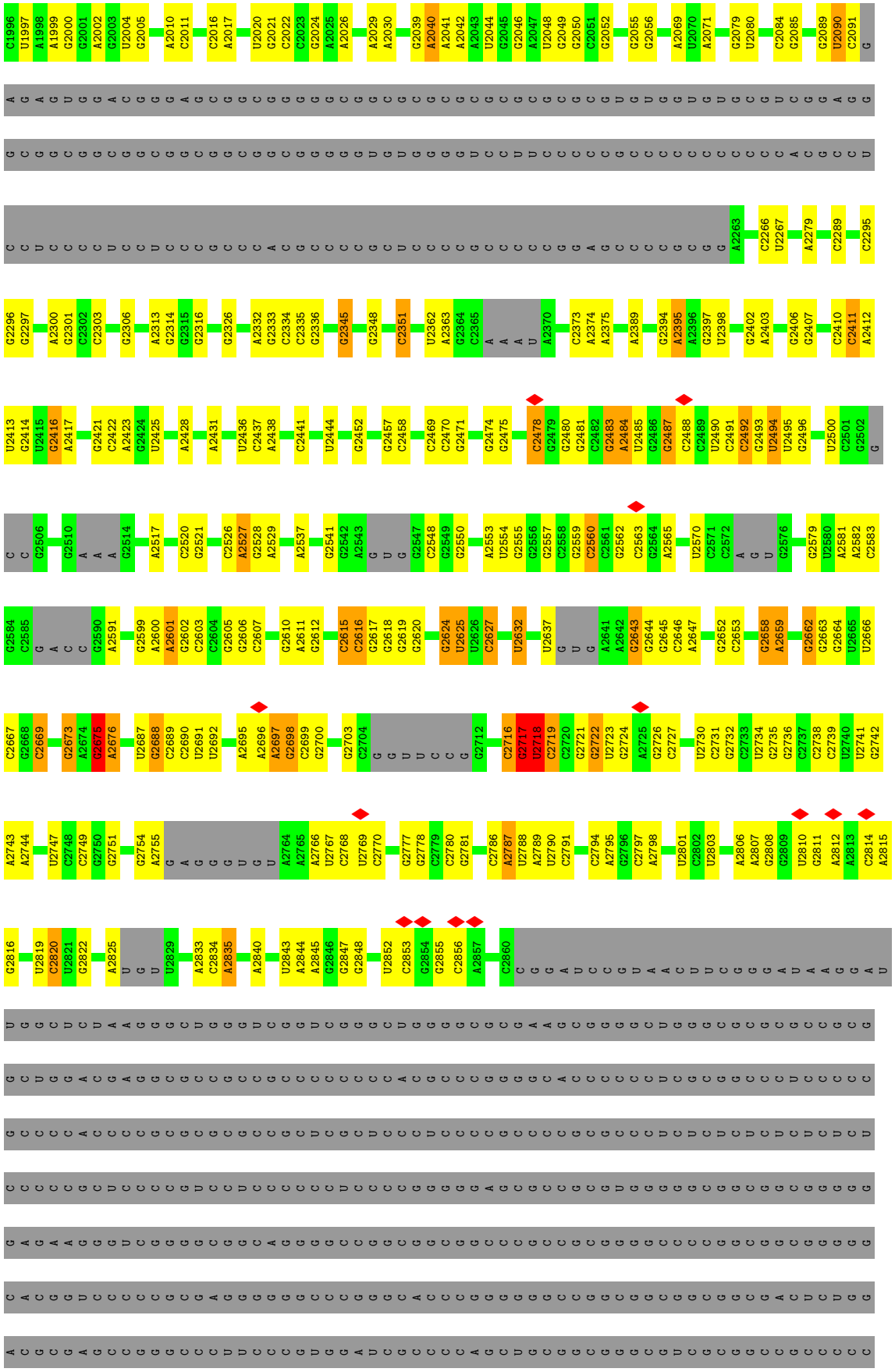
• Molecule 49: 28S rRNA

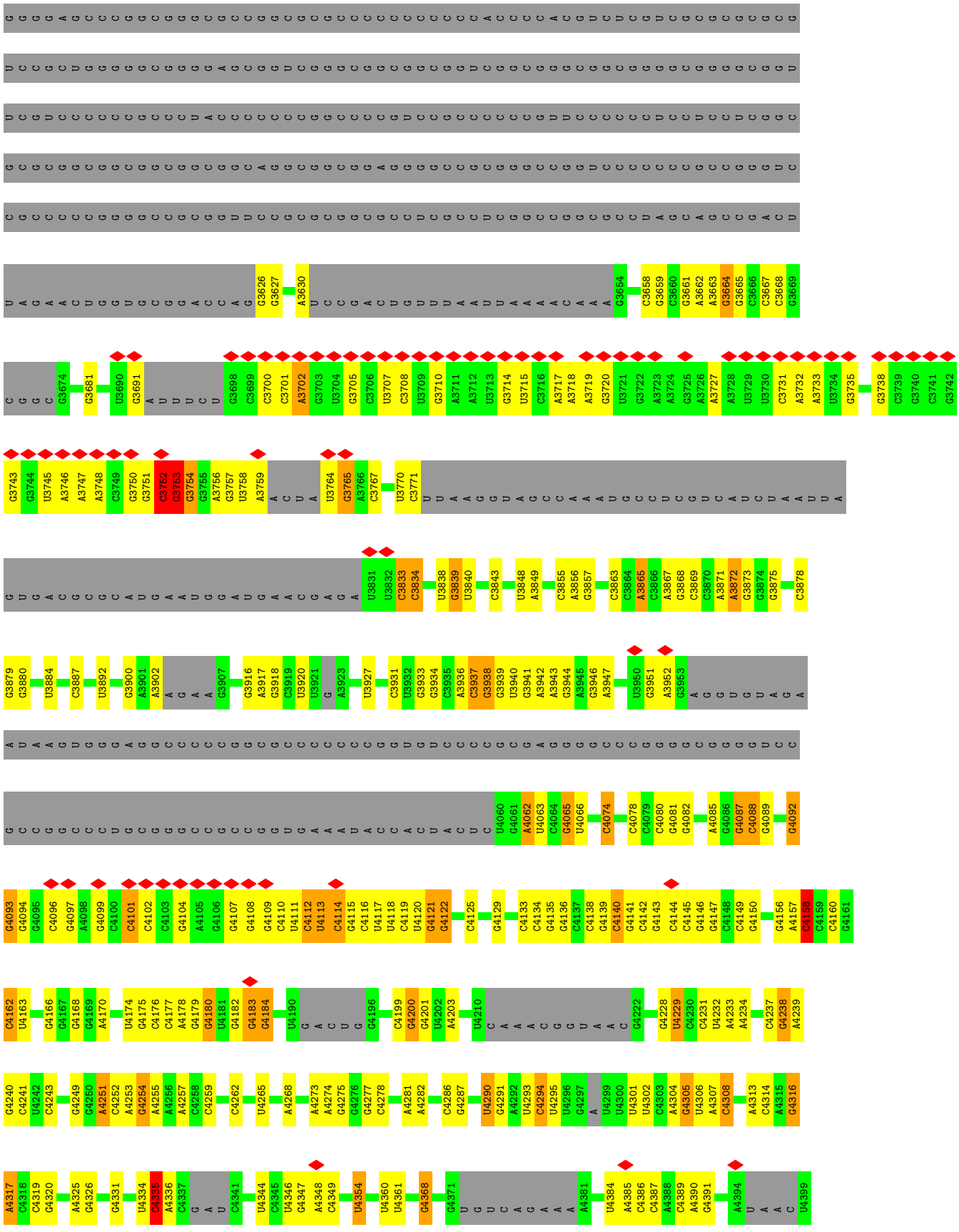
Chain L5:

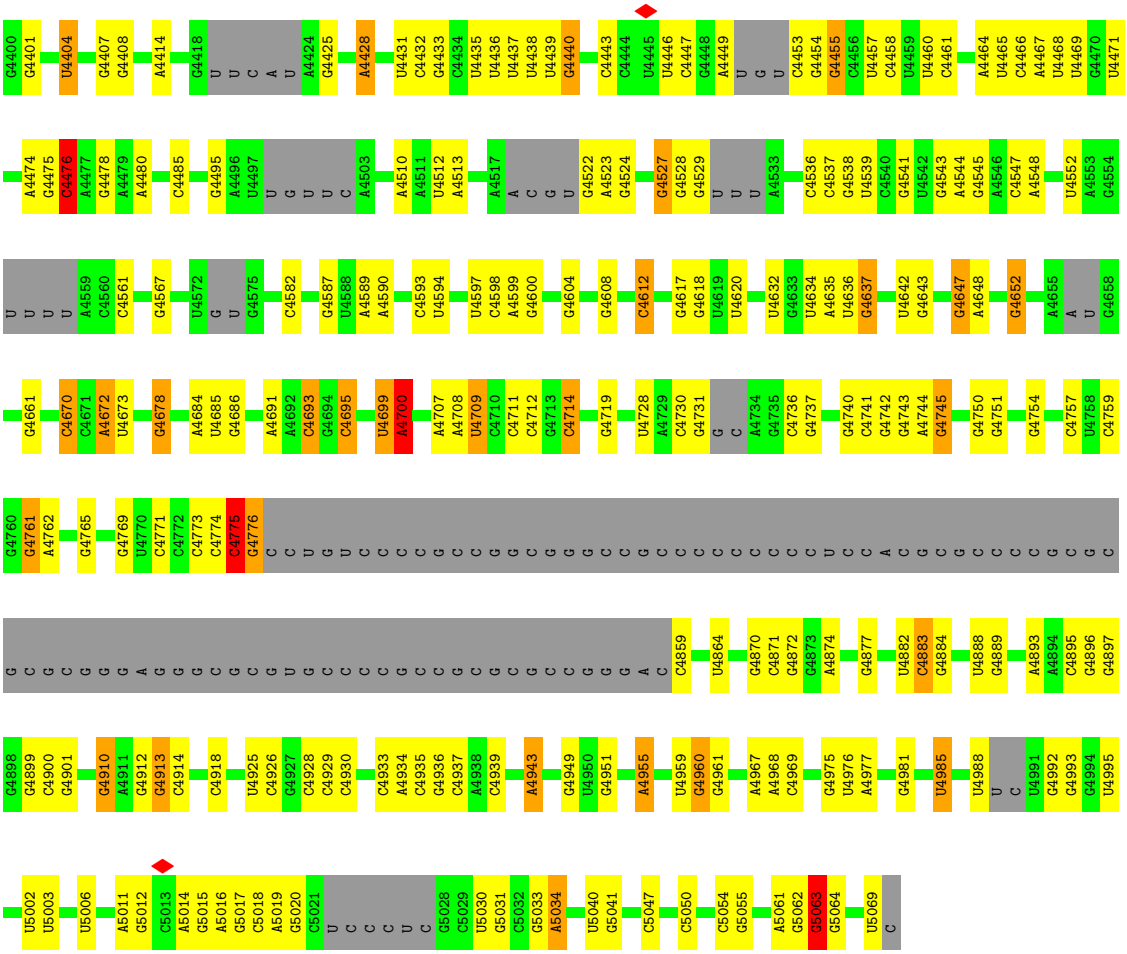








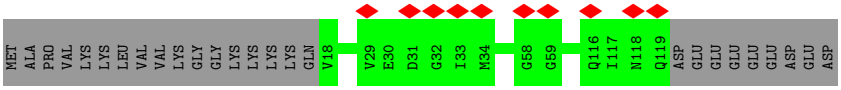




• Molecule 50: 60S ribosomal protein L22

Chain LU:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32928	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	43.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.634	Depositor
Minimum map value	-0.095	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	522.5, 522.5, 522.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	CA	0.18	0/1885	0.47	0/2564
2	CB	0.17	0/3253	0.45	1/4432 (0.0%)
3	CC	0.15	0/579	0.39	0/771
4	CD	0.19	0/4380	0.47	1/5936 (0.0%)
5	CE	0.17	0/496	0.43	0/662
6	CF	0.21	0/1810	0.50	0/2425
7	CG	0.16	0/3526	0.40	0/4799
8	CH	0.18	0/2062	0.43	0/2758
9	CI	0.18	0/1127	0.45	0/1500
10	CJ	0.16	0/2179	0.42	0/2937
11	CK	0.22	0/1436	0.56	1/1975 (0.1%)
12	L7	0.27	0/2861	0.89	4/4459 (0.1%)
13	LA	0.19	0/1213	0.51	0/1630
14	LB	0.16	0/3091	0.41	0/4139
15	LC	0.17	0/2915	0.41	0/3918
16	LD	0.15	0/1907	0.40	0/2555
17	LE	0.16	0/1671	0.43	1/2248 (0.0%)
18	LF	0.18	0/1806	0.44	0/2416
19	LG	0.17	0/1707	0.43	0/2310
20	LH	0.18	0/1529	0.43	0/2058
21	LJ	0.16	0/1320	0.42	0/1771
22	LL	0.15	0/1509	0.39	0/2034
23	LM	0.18	0/1127	0.44	0/1508
24	LN	0.16	0/1580	0.41	0/2112
25	LO	0.16	0/1674	0.38	0/2241
26	LP	0.16	0/1247	0.43	0/1674
27	LQ	0.18	0/1233	0.43	0/1651
28	LR	0.36	1/784 (0.1%)	0.73	3/1065 (0.3%)
29	LS	0.16	0/1493	0.41	0/2005
30	LT	0.21	0/926	0.56	0/1255
31	LV	0.16	0/1000	0.43	0/1345
32	LX	0.16	0/981	0.46	0/1322

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	LY	0.16	0/1115	0.42	0/1484
34	LZ	0.17	0/938	0.46	0/1281
35	La	0.16	0/837	0.42	0/1118
36	Lc	0.11	0/565	0.33	0/781
37	Ld	0.18	0/864	0.47	0/1164
38	Le	0.16	0/1071	0.45	0/1429
39	Lf	0.14	0/891	0.35	0/1194
40	Lg	0.16	0/203	0.50	0/275
41	Lh	0.17	0/1014	0.45	0/1340
42	Li	0.17	0/798	0.41	0/1065
43	Lj	0.15	0/625	0.41	0/829
44	Ll	0.17	0/454	0.45	0/599
45	Lp	0.15	0/465	0.42	0/636
46	Lr	0.17	0/991	0.45	0/1332
47	Lt	0.16	0/970	0.38	0/1334
48	L8	0.28	0/3472	0.85	2/5404 (0.0%)
49	L5	0.28	0/73568	0.90	154/114640 (0.1%)
50	LU	0.13	0/509	0.37	0/709
All	All	0.24	1/145657 (0.0%)	0.74	167/213089 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	LR	90	PRO	CG-CD	-5.95	1.30	1.50

The worst 5 of 167 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
49	L5	485	C	C2-N1-C1'	13.30	133.43	118.80
28	LR	90	PRO	CA-N-CD	-13.16	93.58	112.00
49	L5	485	C	C6-N1-C1'	-10.13	108.64	120.80
4	CD	506	PRO	CA-N-CD	-10.06	97.92	112.00
28	LR	90	PRO	N-CD-CG	-9.47	88.99	103.20

There are no chirality outliers.

There are no planarity outliers.

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	CA	1860	0	1835	24	0
2	CB	3189	0	2904	34	0
3	CC	571	0	545	7	0
4	CD	4304	0	4078	46	0
5	CE	490	0	454	7	0
6	CF	1775	0	1813	16	0
7	CG	3449	0	3178	27	0
8	CH	2023	0	2143	25	0
9	CI	1105	0	1093	14	0
10	CJ	2137	0	2120	27	0
11	CK	1405	0	1258	20	0
12	L7	2561	0	1295	16	0
13	LA	1191	0	1246	22	0
14	LB	3030	0	3113	34	0
15	LC	2861	0	3007	27	0
16	LD	1870	0	1874	22	0
17	LE	1639	0	1710	17	0
18	LF	1773	0	1842	14	0
19	LG	1676	0	1727	17	0
20	LH	1510	0	1579	12	0
21	LJ	1299	0	1284	12	0
22	LL	1480	0	1513	13	0
23	LM	1105	0	1156	14	0
24	LN	1542	0	1579	20	0
25	LO	1642	0	1779	22	0
26	LP	1222	0	1247	9	0
27	LQ	1217	0	1319	8	0
28	LR	775	0	650	8	0
29	LS	1453	0	1480	10	0
30	LT	906	0	865	13	0
31	LV	986	0	1018	19	0
32	LX	964	0	1020	6	0
33	LY	1098	0	1178	18	0
34	LZ	916	0	769	12	0
35	La	823	0	879	12	0
36	Lc	558	0	394	1	0
37	Ld	849	0	902	13	0
38	Le	1053	0	1147	16	0
39	Lf	872	0	901	6	0
40	Lg	203	0	164	1	0
41	Lh	1006	0	1132	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	Li	787	0	786	12	0
43	Lj	611	0	633	12	0
44	Ll	444	0	483	6	0
45	Lp	458	0	334	4	0
46	Lr	976	0	1026	12	0
47	Lt	955	0	750	7	0
48	L8	3110	0	1581	14	0
49	L5	65809	0	33302	494	0
50	LU	508	0	231	0	0
51	CB	32	0	12	0	0
52	CD	28	0	12	0	0
53	CI	1	0	0	0	0
53	Lj	1	0	0	0	0
53	Lp	1	0	0	0	0
All	All	136109	0	100340	1020	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 4.

The worst 5 of 1020 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)
49:L5:3702:A:H62	49:L5:3750:G:H21	1.02	1.02
49:L5:3702:A:H62	49:L5:3750:G:N2	1.62	0.97
49:L5:4745:G:H1	49:L5:4955:A:H61	1.10	0.93
49:L5:2845:A:H61	49:L5:3843:C:N4	1.64	0.92
49:L5:2810:U:H3	49:L5:2816:G:H1	0.96	0.91

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	CA	243/245 (99%)	233 (96%)	10 (4%)	0	100	100
2	CB	435/731 (60%)	428 (98%)	7 (2%)	0	100	100
3	CC	78/549 (14%)	77 (99%)	1 (1%)	0	100	100
4	CD	556/634 (88%)	547 (98%)	9 (2%)	0	100	100
5	CE	65/129 (50%)	65 (100%)	0	0	100	100
6	CF	216/239 (90%)	207 (96%)	9 (4%)	0	100	100
7	CG	469/485 (97%)	454 (97%)	15 (3%)	0	100	100
8	CH	248/260 (95%)	241 (97%)	7 (3%)	0	100	100
9	CI	135/163 (83%)	134 (99%)	1 (1%)	0	100	100
10	CJ	272/306 (89%)	266 (98%)	6 (2%)	0	100	100
11	CK	193/365 (53%)	186 (96%)	6 (3%)	1 (0%)	24	57
13	LA	155/257 (60%)	148 (96%)	7 (4%)	0	100	100
14	LB	377/403 (94%)	368 (98%)	8 (2%)	1 (0%)	36	67
15	LC	360/427 (84%)	350 (97%)	10 (3%)	0	100	100
16	LD	225/297 (76%)	217 (96%)	8 (4%)	0	100	100
17	LE	200/288 (69%)	193 (96%)	7 (4%)	0	100	100
18	LF	217/248 (88%)	212 (98%)	4 (2%)	1 (0%)	24	57
19	LG	209/266 (79%)	205 (98%)	4 (2%)	0	100	100
20	LH	188/192 (98%)	184 (98%)	4 (2%)	0	100	100
21	LJ	168/178 (94%)	167 (99%)	1 (1%)	0	100	100
22	LL	190/211 (90%)	187 (98%)	3 (2%)	0	100	100
23	LM	133/215 (62%)	127 (96%)	6 (4%)	0	100	100
24	LN	179/204 (88%)	174 (97%)	5 (3%)	0	100	100
25	LO	199/203 (98%)	196 (98%)	3 (2%)	0	100	100
26	LP	150/184 (82%)	146 (97%)	4 (3%)	0	100	100
27	LQ	149/188 (79%)	145 (97%)	4 (3%)	0	100	100
28	LR	111/196 (57%)	111 (100%)	0	0	100	100
29	LS	174/176 (99%)	171 (98%)	3 (2%)	0	100	100
30	LT	116/160 (72%)	114 (98%)	2 (2%)	0	100	100
31	LV	134/140 (96%)	129 (96%)	5 (4%)	0	100	100
32	LX	117/156 (75%)	116 (99%)	1 (1%)	0	100	100
33	LY	130/145 (90%)	126 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	LZ	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
35	La	101/148 (68%)	98 (97%)	3 (3%)	0	100	100
36	Lc	93/115 (81%)	92 (99%)	1 (1%)	0	100	100
37	Ld	102/125 (82%)	101 (99%)	1 (1%)	0	100	100
38	Le	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
39	Lf	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
40	Lg	29/117 (25%)	29 (100%)	0	0	100	100
41	Lh	119/123 (97%)	116 (98%)	3 (2%)	0	100	100
42	Li	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
43	Lj	72/97 (74%)	72 (100%)	0	0	100	100
44	Ll	48/51 (94%)	48 (100%)	0	0	100	100
45	Lp	72/92 (78%)	71 (99%)	1 (1%)	0	100	100
46	Lr	121/137 (88%)	119 (98%)	2 (2%)	0	100	100
47	Lt	157/165 (95%)	155 (99%)	2 (1%)	0	100	100
50	LU	100/128 (78%)	98 (98%)	2 (2%)	0	100	100
All	All	8273/10624 (78%)	8085 (98%)	185 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	CK	85	GLU
14	LB	29	VAL
18	LF	197	VAL

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	CA	213/213 (100%)	213 (100%)	0	100	100
2	CB	291/654 (44%)	291 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CC	45/485 (9%)	45 (100%)	0	100	100
4	CD	421/574 (73%)	421 (100%)	0	100	100
5	CE	37/115 (32%)	37 (100%)	0	100	100
6	CF	194/214 (91%)	194 (100%)	0	100	100
7	CG	327/403 (81%)	327 (100%)	0	100	100
8	CH	215/228 (94%)	215 (100%)	0	100	100
9	CI	109/149 (73%)	109 (100%)	0	100	100
10	CJ	225/279 (81%)	225 (100%)	0	100	100
11	CK	119/300 (40%)	119 (100%)	0	100	100
13	LA	123/199 (62%)	123 (100%)	0	100	100
14	LB	321/349 (92%)	321 (100%)	0	100	100
15	LC	294/348 (84%)	294 (100%)	0	100	100
16	LD	192/250 (77%)	192 (100%)	0	100	100
17	LE	172/252 (68%)	172 (100%)	0	100	100
18	LF	178/215 (83%)	178 (100%)	0	100	100
19	LG	171/223 (77%)	171 (100%)	0	100	100
20	LH	167/171 (98%)	167 (100%)	0	100	100
21	LJ	127/149 (85%)	127 (100%)	0	100	100
22	LL	142/177 (80%)	142 (100%)	0	100	100
23	LM	113/161 (70%)	113 (100%)	0	100	100
24	LN	154/172 (90%)	154 (100%)	0	100	100
25	LO	171/174 (98%)	171 (100%)	0	100	100
26	LP	131/163 (80%)	131 (100%)	0	100	100
27	LQ	135/165 (82%)	135 (100%)	0	100	100
28	LR	56/175 (32%)	56 (100%)	0	100	100
29	LS	155/157 (99%)	155 (100%)	0	100	100
30	LT	87/140 (62%)	87 (100%)	0	100	100
31	LV	98/107 (92%)	98 (100%)	0	100	100
32	LX	104/133 (78%)	104 (100%)	0	100	100
33	LY	122/135 (90%)	122 (100%)	0	100	100
34	LZ	62/118 (52%)	62 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	La	87/121 (72%)	87 (100%)	0	100	100
36	Lc	23/97 (24%)	23 (100%)	0	100	100
37	Ld	91/110 (83%)	91 (100%)	0	100	100
38	Le	114/121 (94%)	114 (100%)	0	100	100
39	Lf	87/89 (98%)	87 (100%)	0	100	100
40	Lg	12/100 (12%)	12 (100%)	0	100	100
41	Lh	108/110 (98%)	108 (100%)	0	100	100
42	Li	70/89 (79%)	70 (100%)	0	100	100
43	Lj	63/80 (79%)	63 (100%)	0	100	100
44	Ll	47/48 (98%)	47 (100%)	0	100	100
45	Lp	27/75 (36%)	27 (100%)	0	100	100
46	Lr	104/121 (86%)	104 (100%)	0	100	100
47	Lt	54/137 (39%)	54 (100%)	0	100	100
50	LU	2/115 (2%)	2 (100%)	0	100	100
All	All	6360/9160 (69%)	6360 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
32	LX	111	GLN
33	LY	61	HIS
44	Ll	20	ASN
15	LC	38	ASN
14	LB	328	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	L7	119/121 (98%)	22 (18%)	1 (0%)
48	L8	142/157 (90%)	20 (14%)	0
49	L5	3003/5070 (59%)	721 (24%)	29 (0%)
All	All	3264/5348 (61%)	763 (23%)	30 (0%)

5 of 763 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	L7	3	C
12	L7	7	G
12	L7	22	A
12	L7	24	C
12	L7	38	U

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	L5	2554	U
49	L5	4647	G
49	L5	2716	C
49	L5	4913	G
49	L5	4334	U

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 3 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	$\#\|Z\| > 2$
52	GDP	CD	801	-	28,30,30	1.14	3 (10%)	44,47,47	1.85	8 (18%)
51	GTP	CB	1001	-	30,34,34	0.83	1 (3%)	46,54,54	1.68	11 (23%)

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
52	GDP	CD	801	-	-	5/16/32/32	0/3/3/3
51	GTP	CB	1001	-	-	5/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	CD	801	GDP	C5-C4	3.08	1.47	1.38
52	CD	801	GDP	C6-N1	-2.48	1.34	1.38
51	CB	1001	GTP	C2-N3	2.23	1.38	1.33
52	CD	801	GDP	C5-N7	-2.12	1.35	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
52	CD	801	GDP	C5-C4-N3	-6.08	118.60	128.46
51	CB	1001	GTP	C5-C4-N3	-5.05	120.27	128.46
52	CD	801	GDP	C2-N3-C4	4.87	120.97	112.30
52	CD	801	GDP	N9-C4-N3	4.52	135.02	125.94
51	CB	1001	GTP	C2-N3-C4	4.44	120.22	112.30

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
51	CB	1001	GTP	PB-O3A-PA-O5'
51	CB	1001	GTP	C5'-O5'-PA-O1A
52	CD	801	GDP	C5'-O5'-PA-O1A
52	CD	801	GDP	C5'-O5'-PA-O2A
52	CD	801	GDP	O4'-C4'-C5'-O5'

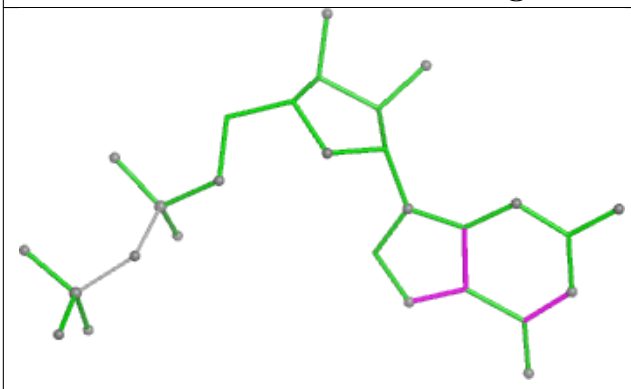
There are no ring outliers.

No monomer is involved in short contacts.

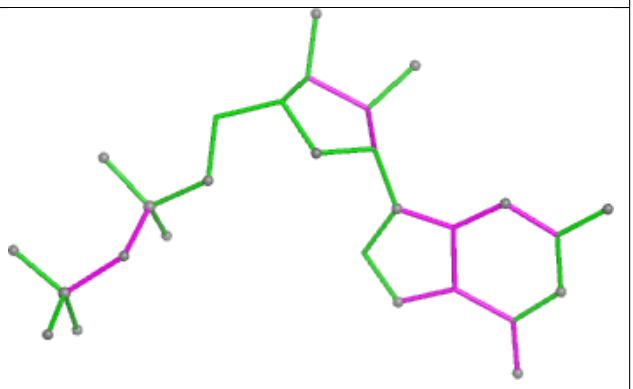
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

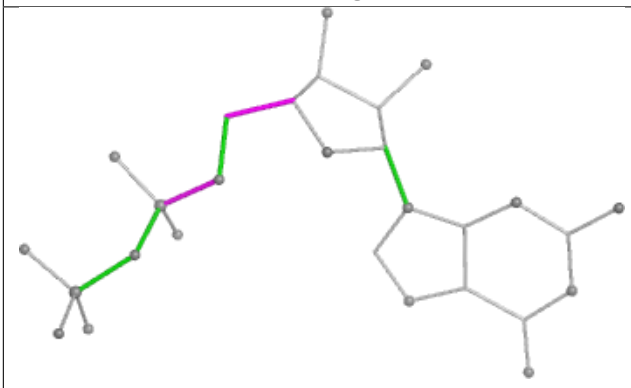
Ligand GDP CD 801



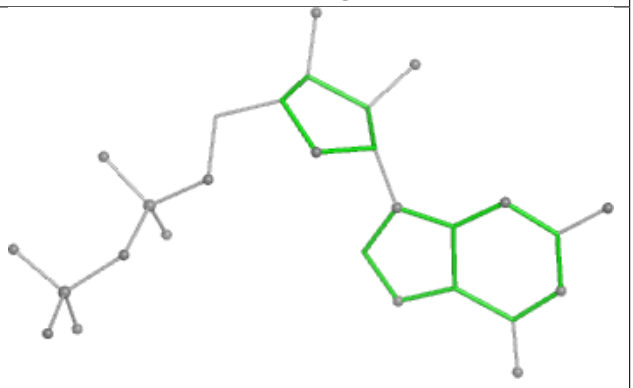
Bond lengths



Bond angles

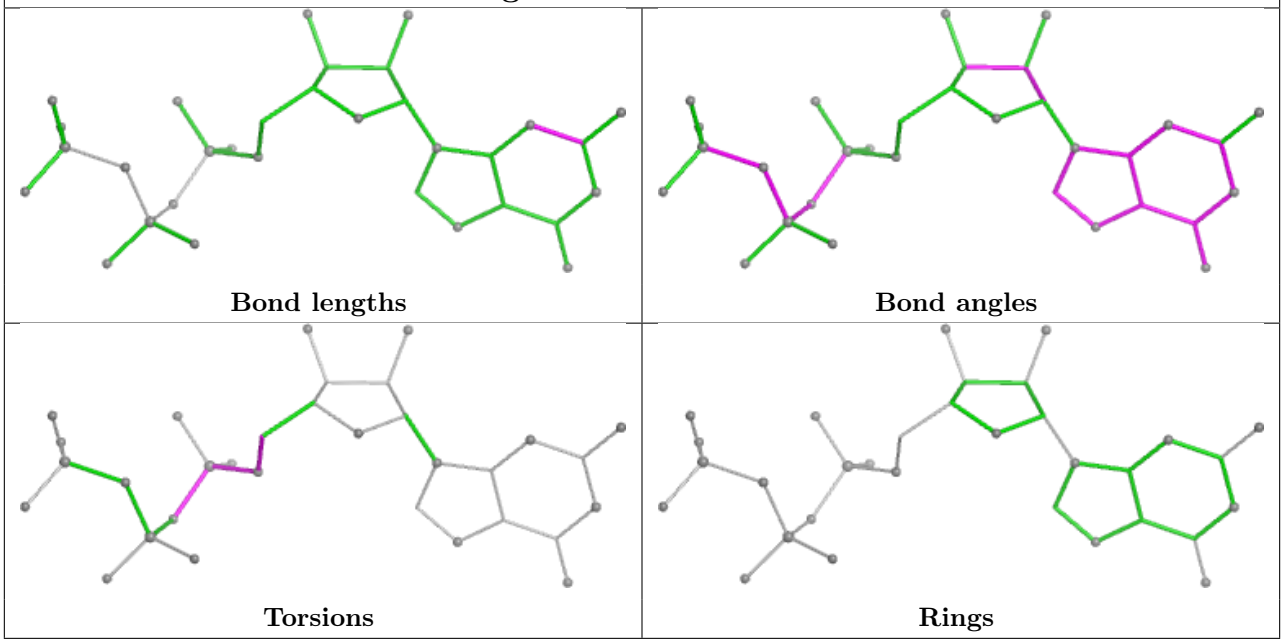


Torsions



Rings

Ligand GTP CB 1001



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

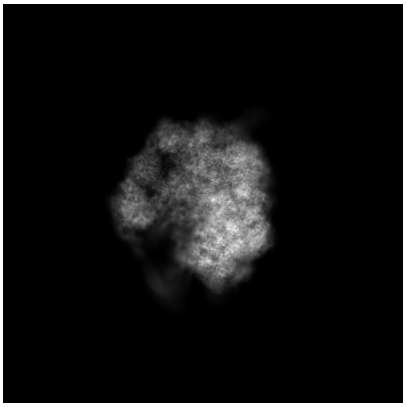
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-53091. These allow visual inspection of the internal detail of the map and identification of artifacts.

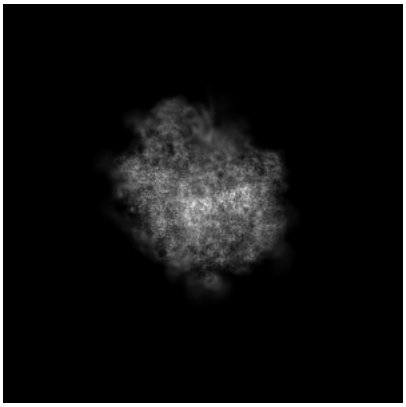
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

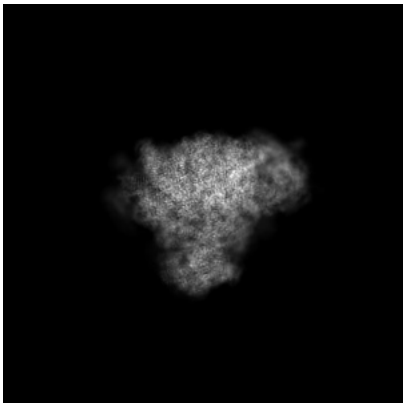
6.1.1 Primary map



X



Y

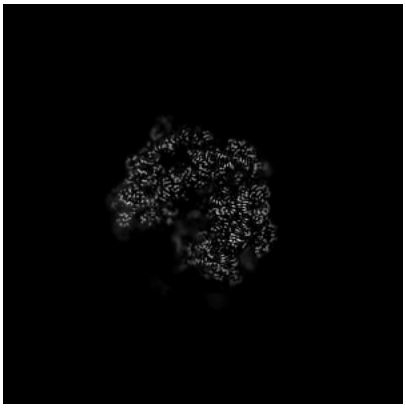


Z

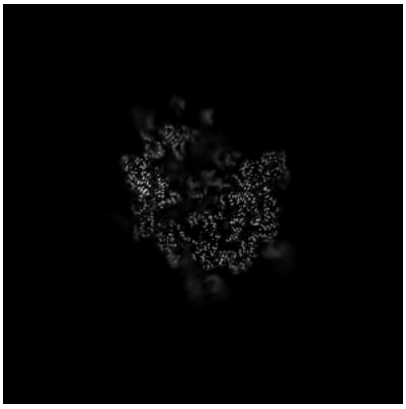
The images above show the map projected in three orthogonal directions.

6.2 Central slices

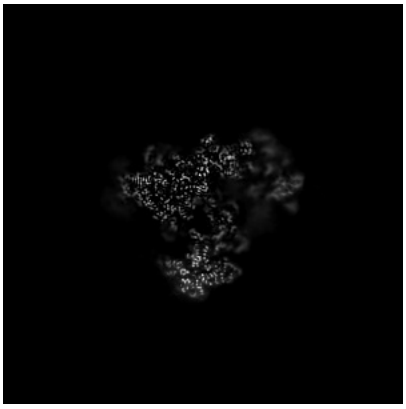
6.2.1 Primary map



X Index: 250



Y Index: 250

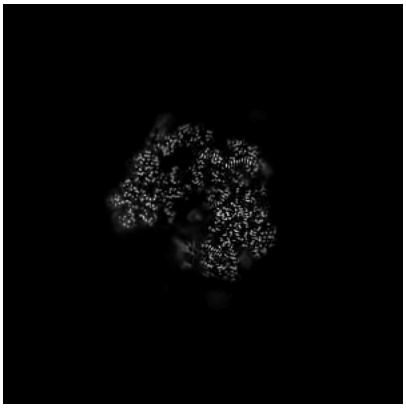


Z Index: 250

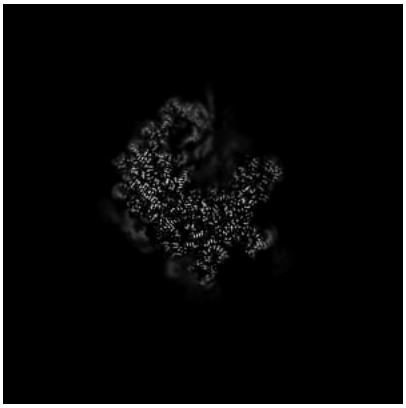
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

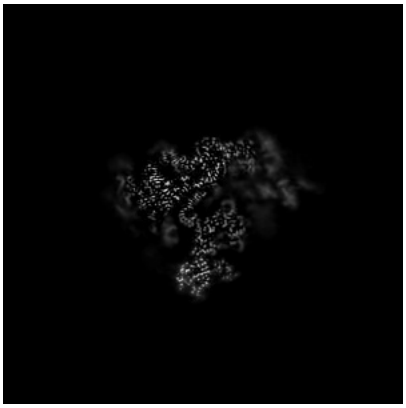
6.3.1 Primary map



X Index: 246



Y Index: 271

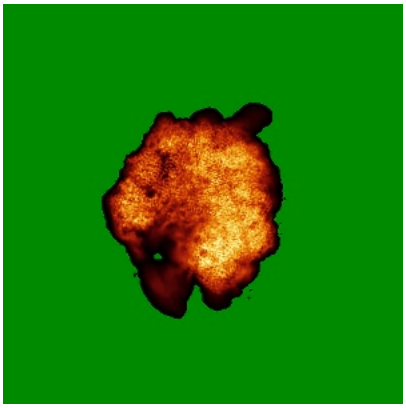


Z Index: 258

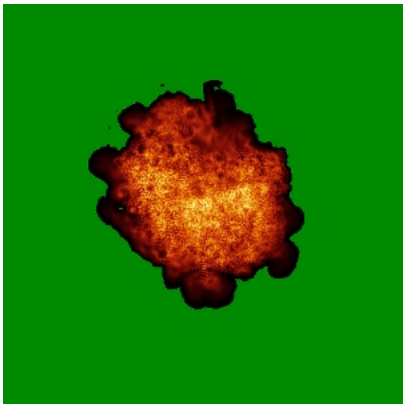
The images above show the largest variance slices of the map in three orthogonal directions.

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

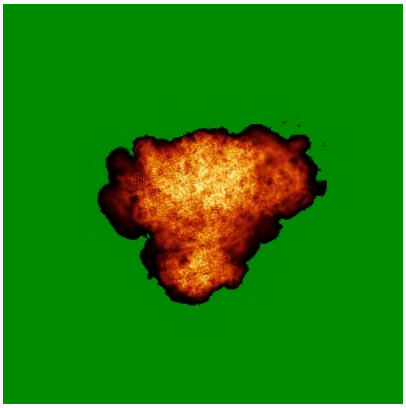
6.4.1 Primary map



X



Y

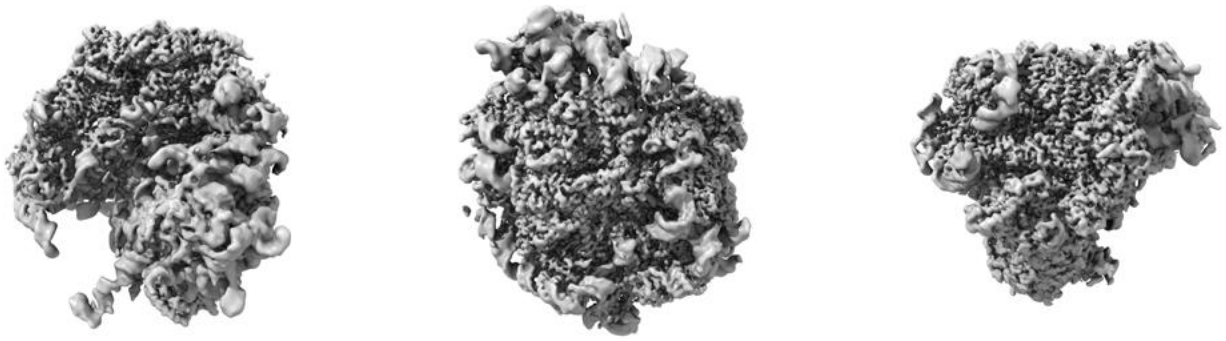


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

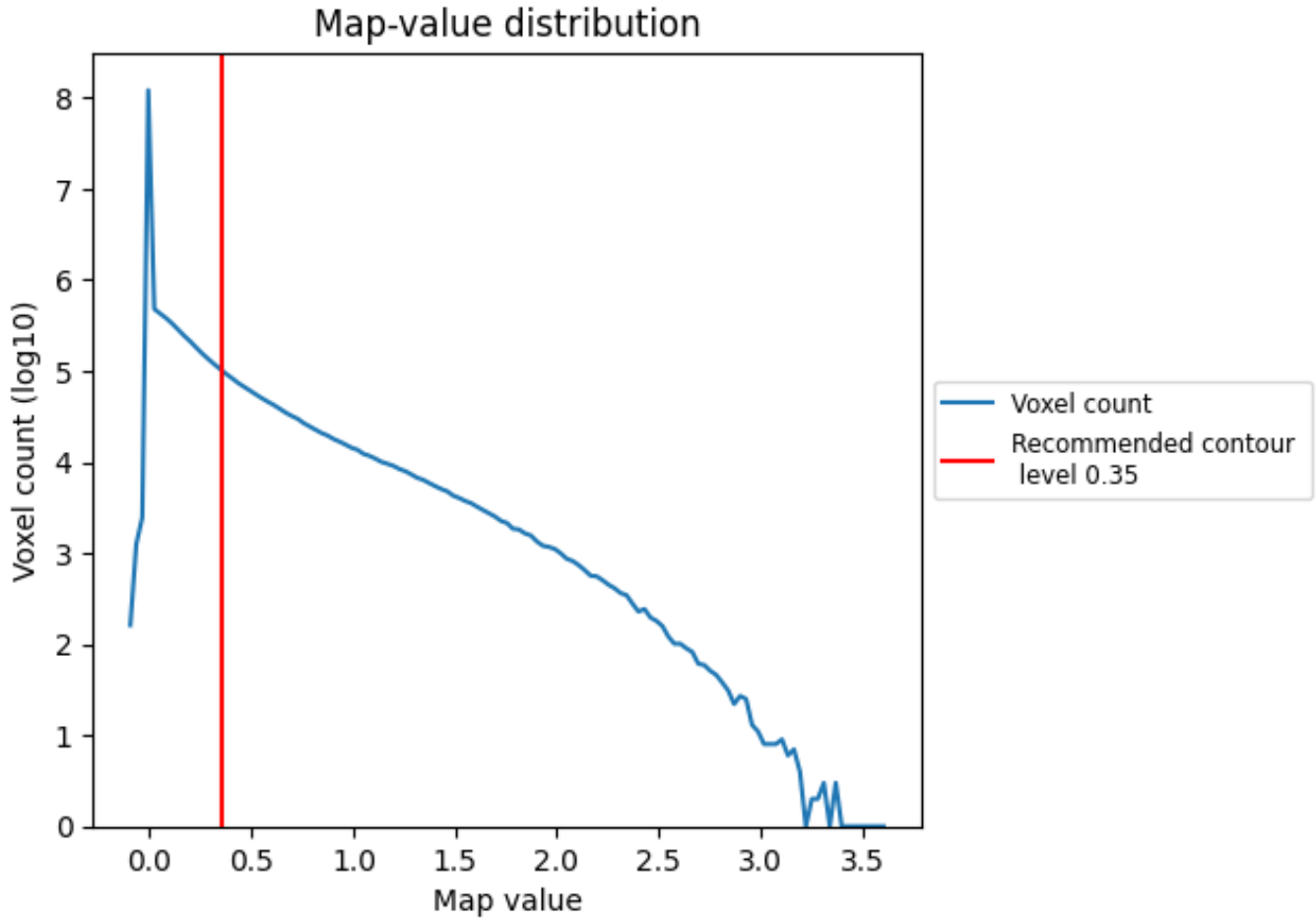
6.6 Mask visualisation (i)

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

7 Map analysis

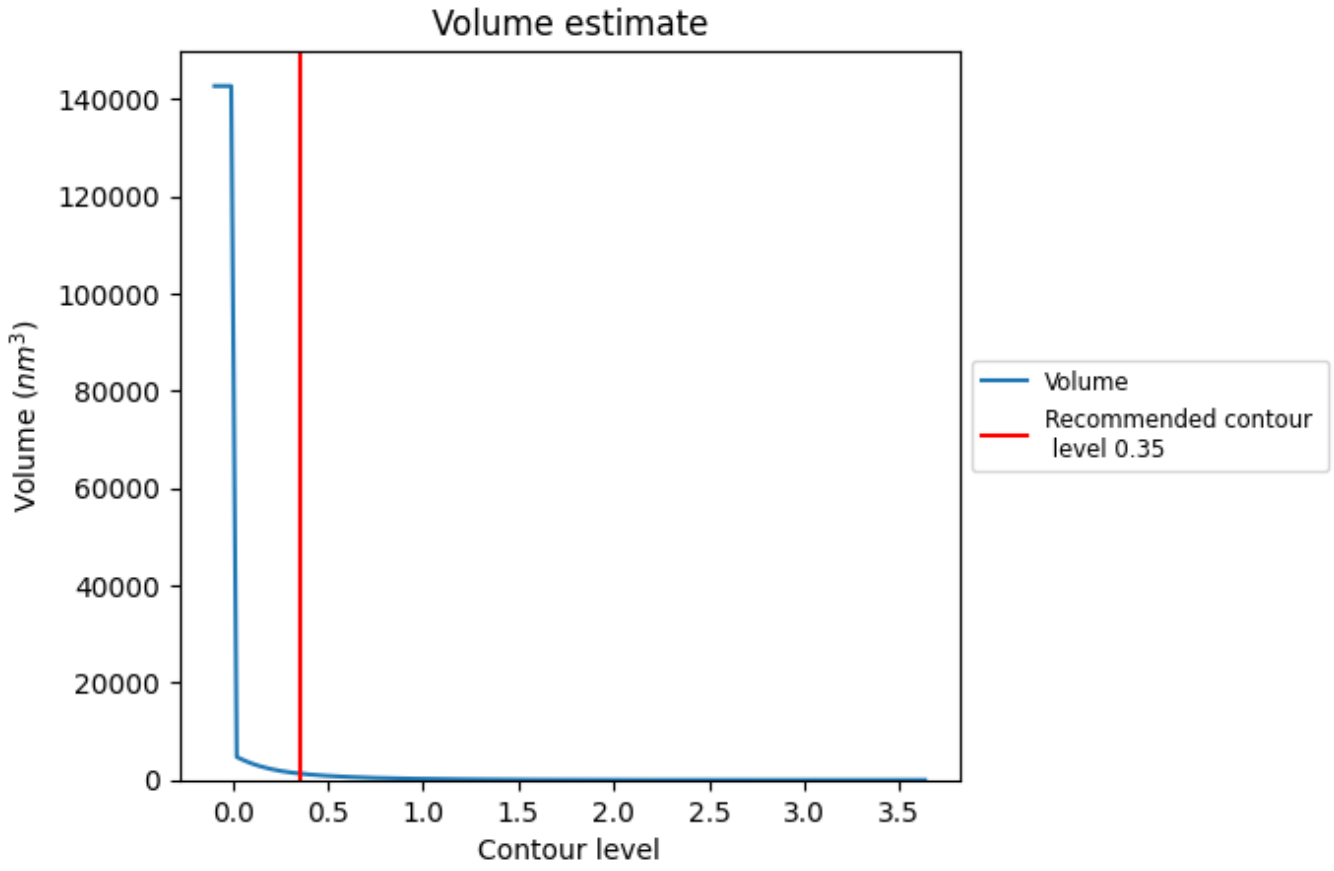
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

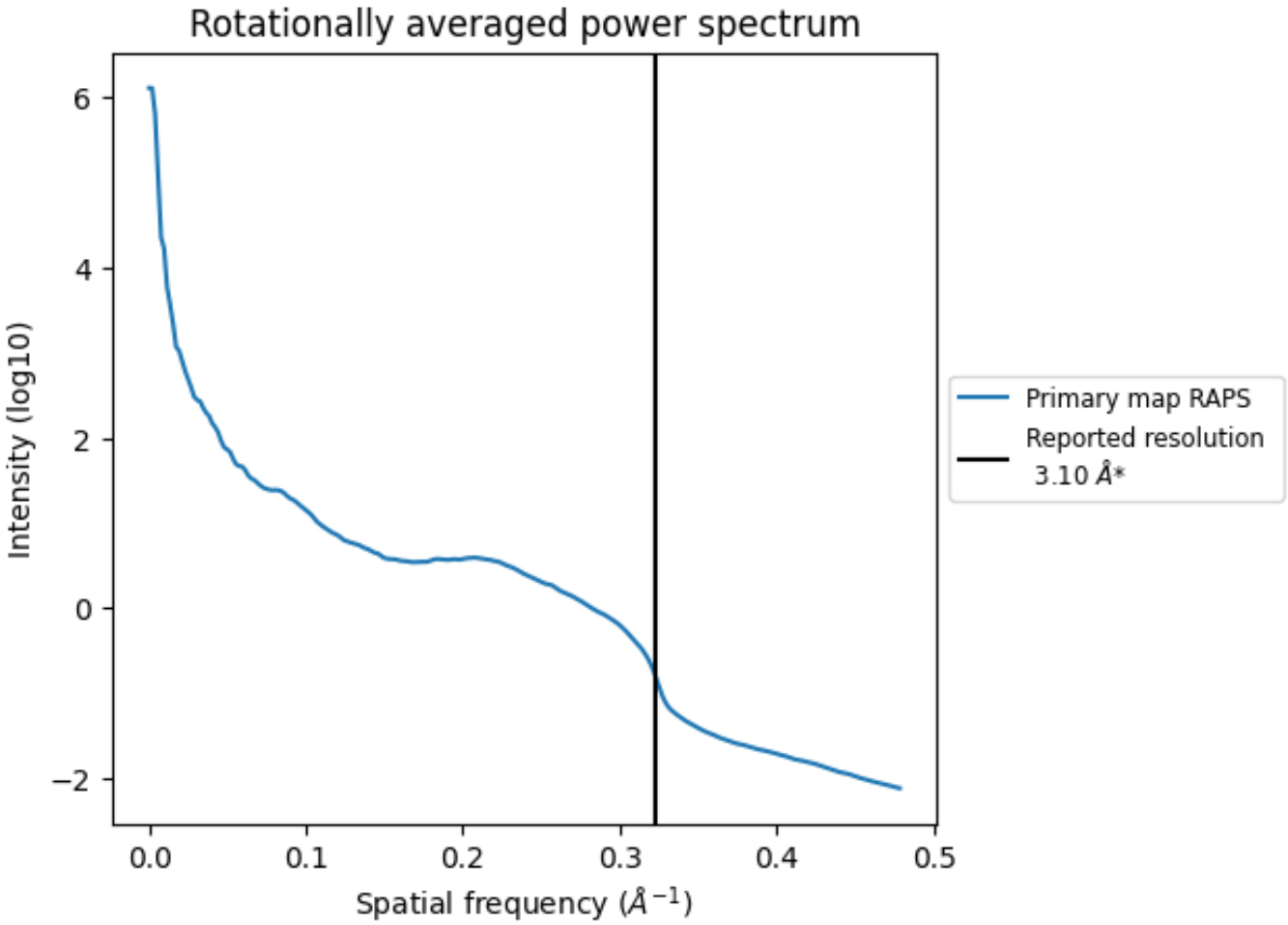
7.2 Volume estimate (i)



The volume at the recommended contour level is 1327 nm^3; this corresponds to an approximate mass of 1199 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.323 $Å^{-1}$

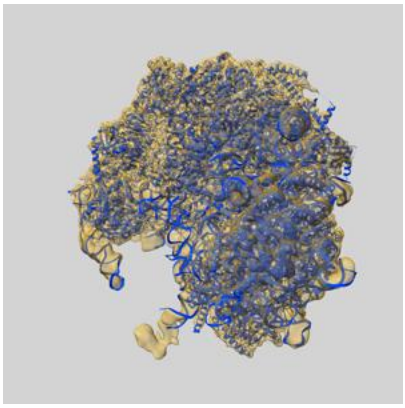
8 Fourier-Shell correlation (i)

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

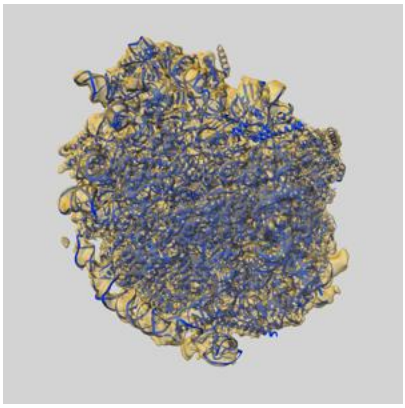
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-53091 and PDB model 9QES. Per-residue inclusion information can be found in section 3 on page 14.

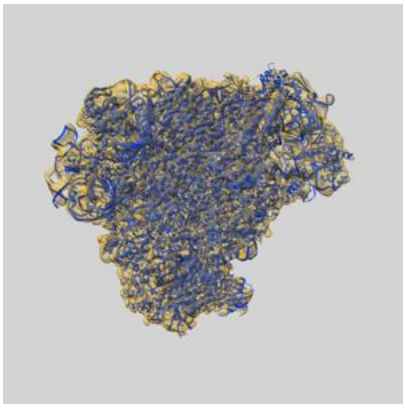
9.1 Map-model overlay



X



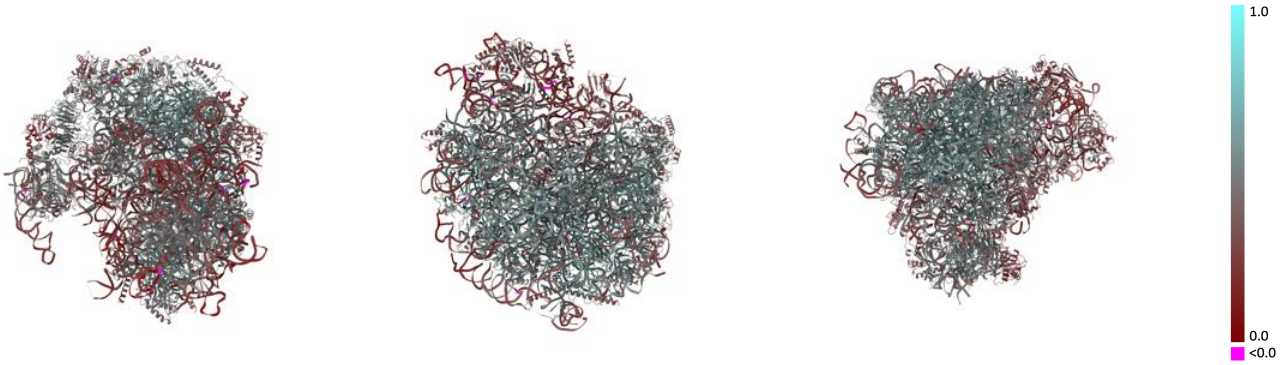
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

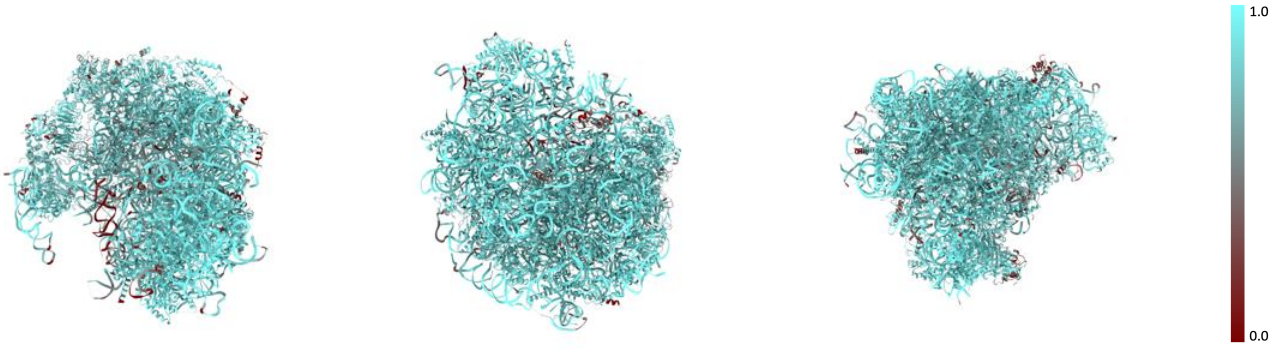
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

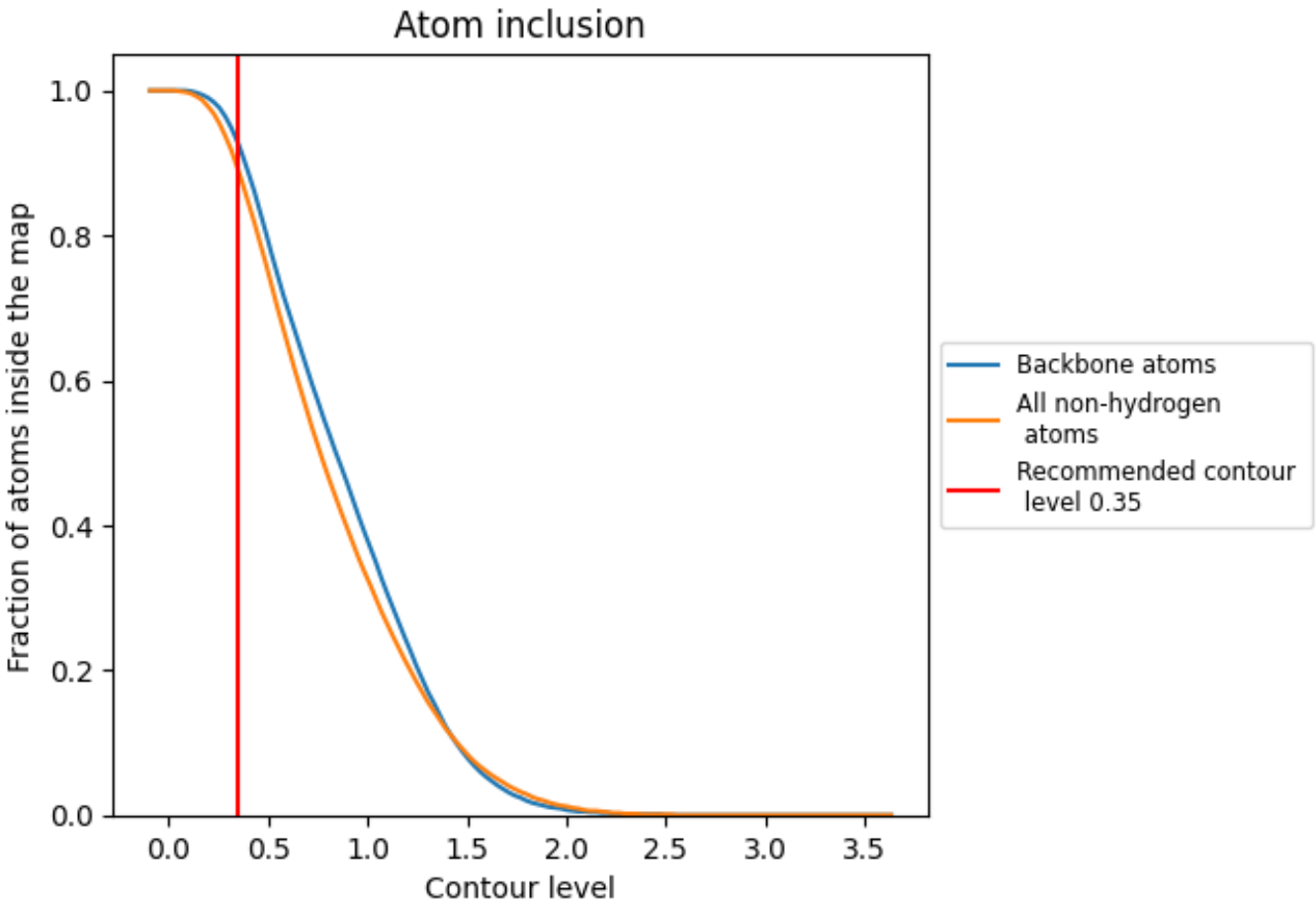
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.35).

9.4 Atom inclusion (i)



At the recommended contour level, 93% of all backbone atoms, 89% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8890	0.4540
CA	0.8320	0.4620
CB	0.7580	0.4110
CC	0.5900	0.4370
CD	0.7610	0.4400
CE	0.8220	0.4660
CF	0.8300	0.4280
CG	0.8980	0.4730
CH	0.8670	0.5140
CI	0.8800	0.4670
CJ	0.8690	0.4270
CK	0.7490	0.3550
L5	0.9020	0.4260
L7	0.9330	0.3740
L8	0.9830	0.5330
LA	0.8570	0.4540
LB	0.9260	0.5470
LC	0.8880	0.5420
LD	0.9250	0.4800
LE	0.8780	0.5060
LF	0.8970	0.5360
LG	0.9260	0.4830
LH	0.8890	0.5280
LJ	0.8950	0.4010
LL	0.8790	0.4920
LM	0.9200	0.5350
LN	0.9800	0.5780
LO	0.9130	0.5580
LP	0.9090	0.5500
LQ	0.8810	0.5340
LR	0.8990	0.3780
LS	0.8890	0.5410
LT	0.7430	0.4020
LU	0.8600	0.3050
LV	0.8840	0.5210



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Chain	Atom inclusion	Q-score
LX	0.9090	0.5080
LY	0.8820	0.5070
LZ	0.9570	0.3860
La	0.8800	0.4780
Lc	0.8940	0.3820
Ld	0.9080	0.4980
Le	0.8960	0.5540
Lf	0.9500	0.5970
Lg	0.8380	0.3930
Lh	0.8910	0.4870
Li	0.8790	0.4660
Lj	0.9500	0.5580
Ll	0.8700	0.5160
Lp	0.8270	0.3960
Lr	0.9030	0.5440
Lt	0.8440	0.3840