



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:24 AM UTC

PDB ID : 7OBR / pdb_00007obr
EMDB ID : EMD-12801
Title : RNC-SRP early complex
Authors : Jomaa, A.; Ban, N.
Deposited on : 2021-04-23
Resolution : 2.80 Å(reported)
Based on initial model : 6FRK

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

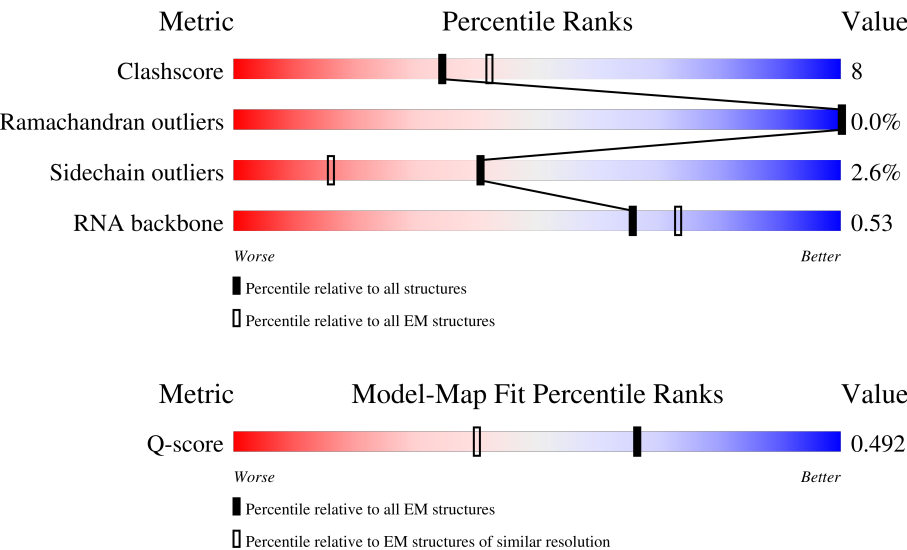
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.80 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.



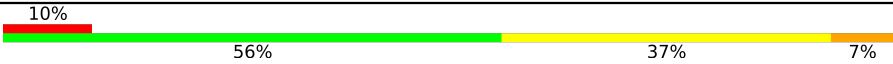
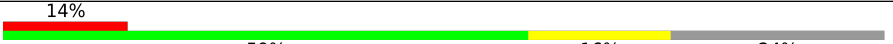
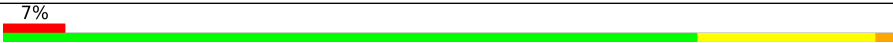
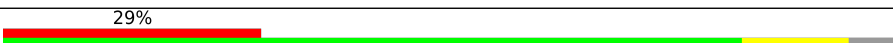
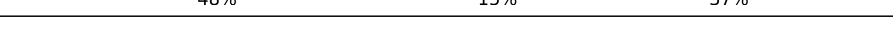
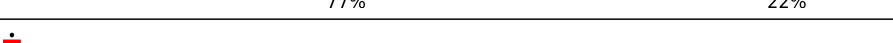
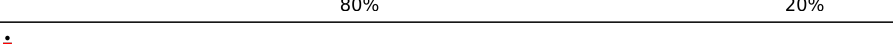
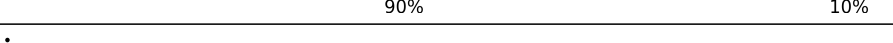
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	1	249	
2	5	3493	
3	7	120	

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Mol	Chain	Length	Quality of chain
4	8	156	
5	A	245	
6	B	402	
7	C	413	
8	D	297	
9	E	248	
10	F	225	
11	G	319	
12	H	192	
13	I	214	
14	J	178	
15	L	210	
16	M	218	
17	N	204	
18	O	199	
19	P	153	
20	Q	187	
21	R	180	
22	S	175	
23	T	160	
24	U	99	
25	V	140	
26	W	63	
27	X	156	
28	Y	145	

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Mol	Chain	Length	Quality of chain
29	Z	136	
30	a	147	
31	b	223	
32	c	94	
33	d	125	
34	e	157	
35	f	110	
36	g	129	
37	h	123	
38	i	102	
39	j	97	
40	k	69	
41	l	51	
42	m	52	
43	n	25	
44	o	105	
45	p	92	
46	q	144	
47	r	137	
48	s	67	
49	t	110	
50	u	622	
51	w	86	
52	x	504	
53	z	671	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 146701 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 RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	249	Total	C	N	O	P	0	0
			5341	2377	977	1738	249		

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	3493	Total	C	N	O	P	0	0
			74854	33335	13681	24346	3492		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 4 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	LYS	-	insertion	UNP A0A5F9D5B2
A	47	ASP	-	insertion	UNP A0A5F9D5B2
A	48	ILE	-	insertion	UNP A0A5F9D5B2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	49	ILE	-	insertion	UNP A0A5F9D5B2
A	50	HIS	-	insertion	UNP A0A5F9D5B2
A	51	ASP	-	insertion	UNP A0A5F9D5B2
A	52	PRO	-	insertion	UNP A0A5F9D5B2
A	53	GLY	-	insertion	UNP A0A5F9D5B2
A	54	ARG	-	insertion	UNP A0A5F9D5B2
A	55	GLY	-	insertion	UNP A0A5F9D5B2
A	56	ALA	-	insertion	UNP A0A5F9D5B2
A	57	PRO	-	insertion	UNP A0A5F9D5B2
A	58	LEU	-	insertion	UNP A0A5F9D5B2
A	59	ALA	-	insertion	UNP A0A5F9D5B2
A	60	LYS	-	insertion	UNP A0A5F9D5B2
A	61	VAL	-	insertion	UNP A0A5F9D5B2
A	62	VAL	-	insertion	UNP A0A5F9D5B2
A	63	PHE	-	insertion	UNP A0A5F9D5B2
A	64	ARG	-	insertion	UNP A0A5F9D5B2
A	65	ASP	-	insertion	UNP A0A5F9D5B2
A	66	PRO	-	insertion	UNP A0A5F9D5B2
A	67	TYR	-	insertion	UNP A0A5F9D5B2
A	68	ARG	-	insertion	UNP A0A5F9D5B2
A	69	PHE	-	insertion	UNP A0A5F9D5B2

- Molecule 6 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	394	Total	C	N	O	S	0	0
			3148	2007	591	537	13		

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	292	Total	C	N	O	S	0	0
			2386	1509	437	426	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	initiating methionine	UNP G1SYJ6

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	236	Total	C	N	O	S	0	0
			1898	1215	362	318	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	126	ARG	LYS	conflict	UNP G1SKF7
E	217	GLN	LYS	conflict	UNP G1SKF7

- Molecule 10 is a protein called uL30.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	175	ALA	THR	conflict	UNP G1SV32
F	185	GLY	ASN	conflict	UNP G1SV32
F	202	ARG	HIS	conflict	UNP G1SV32
F	233	GLU	GLY	conflict	UNP G1SV32

- Molecule 11 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	241	Total	C	N	O	S	0	0
			1934	1233	371	326	4		

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 13 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	204	Total	C	N	O	S	0	0
			1655	1051	319	272	13		

- Molecule 14 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	210	Total	C	N	O	S	0	0
			1703	1065	354	280	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	SER	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0
L	55	LEU	-	insertion	UNP G1TPV0

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 17 is a protein called Ribosomal protein L15.

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

- Molecule 18 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	199	Total	C	N	O	S	0	0
			1638	1056	321	256	5		

- Molecule 19 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 20 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	6	ARG	LEU	conflict	UNP G1TX70
Q	14	ARG	TRP	conflict	UNP G1TX70
Q	23	ILE	MET	conflict	UNP G1TX70
Q	24	TYR	CYS	conflict	UNP G1TX70
Q	38	ARG	HIS	conflict	UNP G1TX70
Q	57	ASN	LYS	conflict	UNP G1TX70
Q	66	MET	VAL	conflict	UNP G1TX70
Q	74	GLY	ASP	conflict	UNP G1TX70
Q	75	ARG	PRO	conflict	UNP G1TX70
Q	77	GLY	ASN	conflict	UNP G1TX70
Q	106	SER	THR	conflict	UNP G1TX70
Q	110	ARG	HIS	conflict	UNP G1TX70
Q	117	GLY	GLU	conflict	UNP G1TX70
Q	124	ASP	HIS	conflict	UNP G1TX70
Q	134	CYS	ARG	conflict	UNP G1TX70
Q	150	ARG	GLN	conflict	UNP G1TX70
Q	172	ARG	GLY	conflict	UNP G1TX70
Q	184	ARG	TRP	conflict	UNP G1TX70

- Molecule 21 is a protein called 60S RIBOSOMAL PROTEIN EL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 22 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	18	PRO	-	insertion	UNP G1TTY7
S	19	THR	-	insertion	UNP G1TTY7
S	20	PRO	SER	conflict	UNP G1TTY7
S	22	CYS	SER	conflict	UNP G1TTY7
S	23	ARG	PRO	conflict	UNP G1TTY7
S	24	THR	ALA	conflict	UNP G1TTY7
S	49	SER	LEU	conflict	UNP G1TTY7
S	50	GLN	GLU	conflict	UNP G1TTY7
S	95	ARG	HIS	conflict	UNP G1TTY7
S	101	THR	ILE	conflict	UNP G1TTY7
S	102	THR	MET	conflict	UNP G1TTY7
S	104	GLY	SER	conflict	UNP G1TTY7
S	126	ILE	VAL	conflict	UNP G1TTY7
S	132	ILE	MET	conflict	UNP G1TTY7
S	135	SER	ALA	conflict	UNP G1TTY7
S	136	LYS	ARG	conflict	UNP G1TTY7
S	138	ARG	PRO	conflict	UNP G1TTY7
S	149	LYS	ARG	conflict	UNP G1TTY7
S	151	LYS	ARG	conflict	UNP G1TTY7
S	168	THR	TYR	conflict	UNP G1TTY7
S	169	THR	ALA	conflict	UNP G1TTY7
S	176	PHE	-	insertion	UNP G1TTY7

- Molecule 23 is a protein called eL21.

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

- Molecule 24 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	32	GLY	ARG	variant	UNP G1TSG1
U	36	ALA	GLU	variant	UNP G1TSG1
U	39	PHE	SER	variant	UNP G1TSG1
U	54	GLY	ARG	variant	UNP G1TSG1
U	60	VAL	ALA	variant	UNP G1TSG1
U	97	ARG	HIS	variant	UNP G1TSG1

- Molecule 25 is a protein called Ribosomal protein L23.

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

- Molecule 26 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 27 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 28 is a protein called Ribosomal protein L26.

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

- Molecule 29 is a protein called 60S ribosomal protein L27.

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

- Molecule 30 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	75	Total	C	N	O	S	0	0
			609	378	130	98	3		

- Molecule 32 is a protein called 60S ribosomal protein L30.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	34	THR	SER	conflict	UNP G1TDL2
c	95	ALA	SER	conflict	UNP G1TDL2

- Molecule 33 is a protein called eL31.

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

- Molecule 34 is a protein called eL32.

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

- Molecule 35 is a protein called eL33.

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

- Molecule 36 is a protein called 60S ribosomal protein L34.

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

- Molecule 37 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 38 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 39 is a protein called Ribosomal protein L37.

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

- Molecule 40 is a protein called eL38.

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

- Molecule 41 is a protein called eL39.

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

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN EL40.

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

- Molecule 43 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 44 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 45 is a protein called eL43.

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

- Molecule 46 is a protein called Signal recognition particle 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	105	Total	C	N	O	S	0	0
			844	534	152	152	6		

- Molecule 47 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	125	Total	C	N	O	S	0	0
			1001	621	206	168	6		

- Molecule 48 is a protein called Dipeptidyl aminopeptidase B.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	s	67	Total	C	N	O	0	0
			502	329	91	82		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	83	HIS	GLN	conflict	UNP P18962
s	90	HIS	GLN	conflict	UNP P18962

- Molecule 49 is a protein called Signal recognition particle 14 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	76	Total	C	N	O	S	0	0
			604	384	105	111	4		

- Molecule 50 is a protein called Signal recognition particle subunit SRP68.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	194	Total	C	N	O	S	0	0
			1626	1022	305	291	8		

- Molecule 51 is a protein called Signal recognition particle 9 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w	74	Total	C	N	O	S	0	0
			607	386	106	110	5		

- Molecule 52 is a protein called Signal recognition particle 54 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	x	488	Total	C	N	O	S	0	0
			3773	2377	650	713	33		

- Molecule 53 is a protein called Signal recognition particle subunit SRP72.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	40	Total	C	N	O	S	0	0
			339	215	66	57	1		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	5	97	Total	Mg	0
			97	97	

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

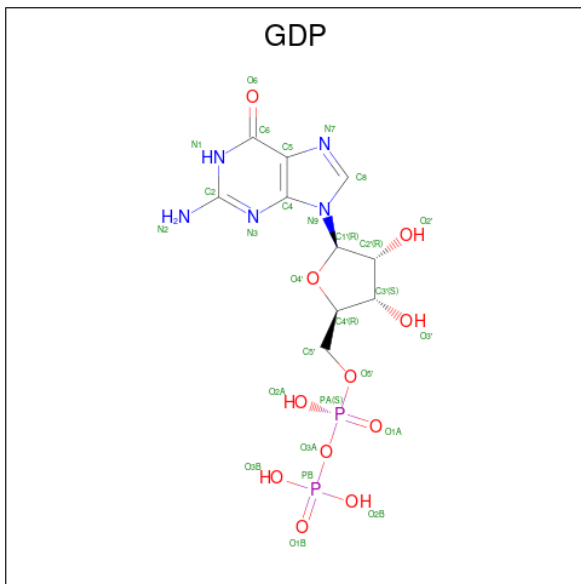
Mol	Chain	Residues	Atoms		AltConf
55	g	1	Total	Zn	0
			1	1	
55	j	1	Total	Zn	0
			1	1	
55	m	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
55	o	1	Total Zn 1 1	0
55	p	1	Total Zn 1 1	0

- Molecule 56 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{11}\text{P}_2$) (labeled as "Ligand of Interest" by depositor).

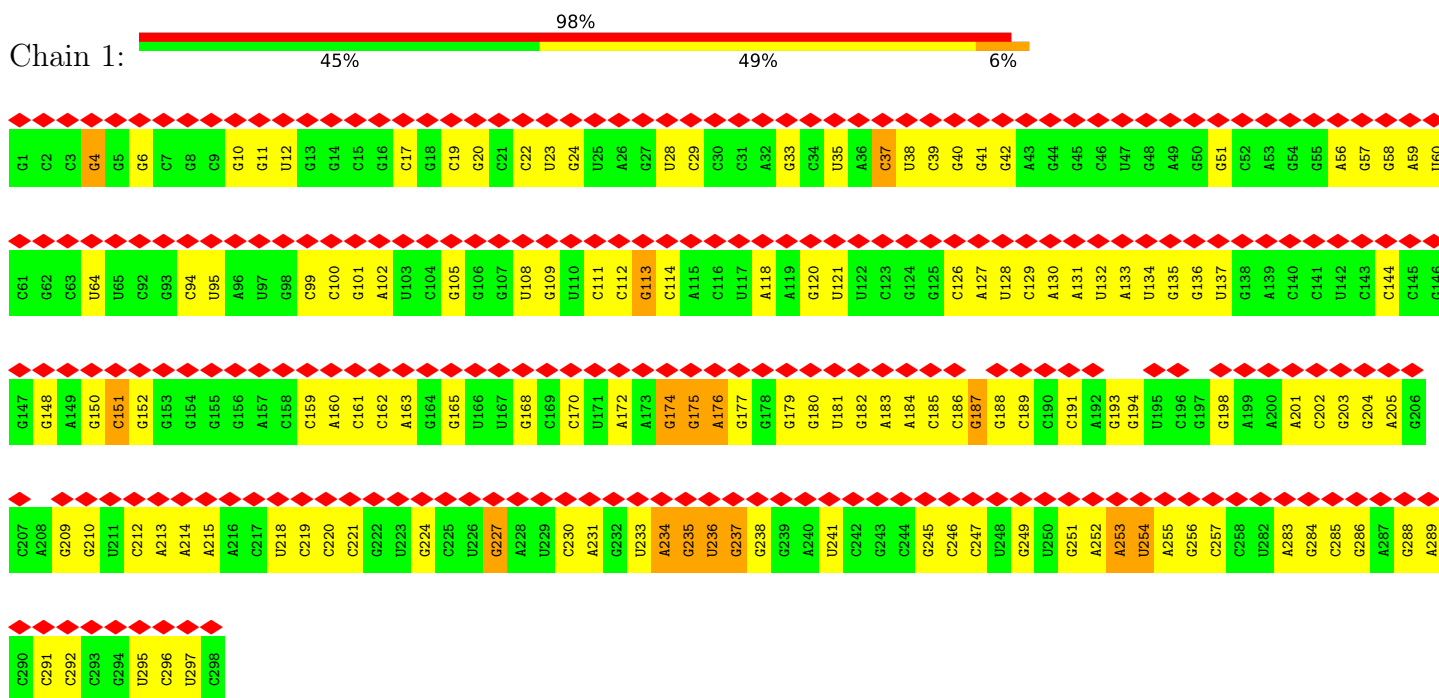


Mol	Chain	Residues	Atoms					AltConf
56	x	1	Total	C	N	O	P	0
			28	10	5	11	2	

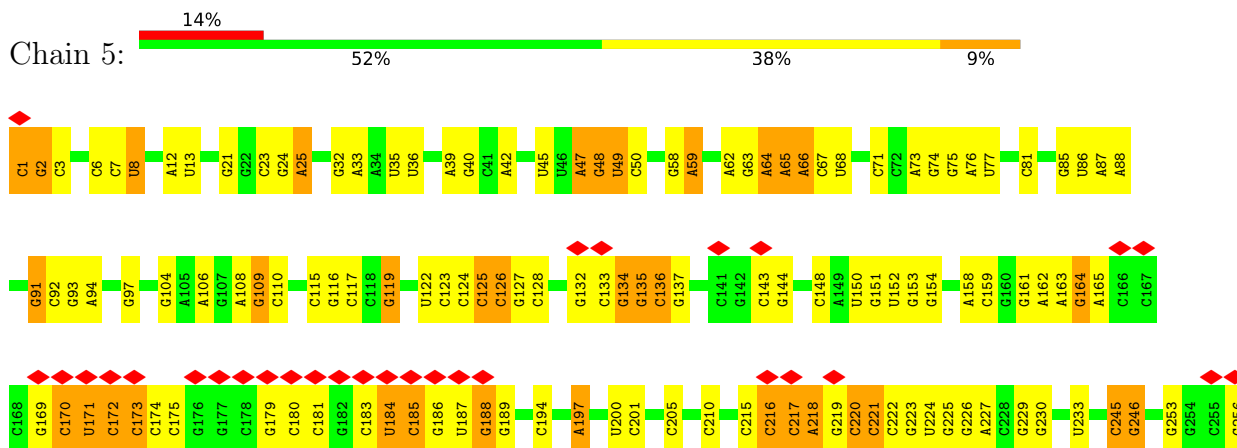
3 Residue-property plots

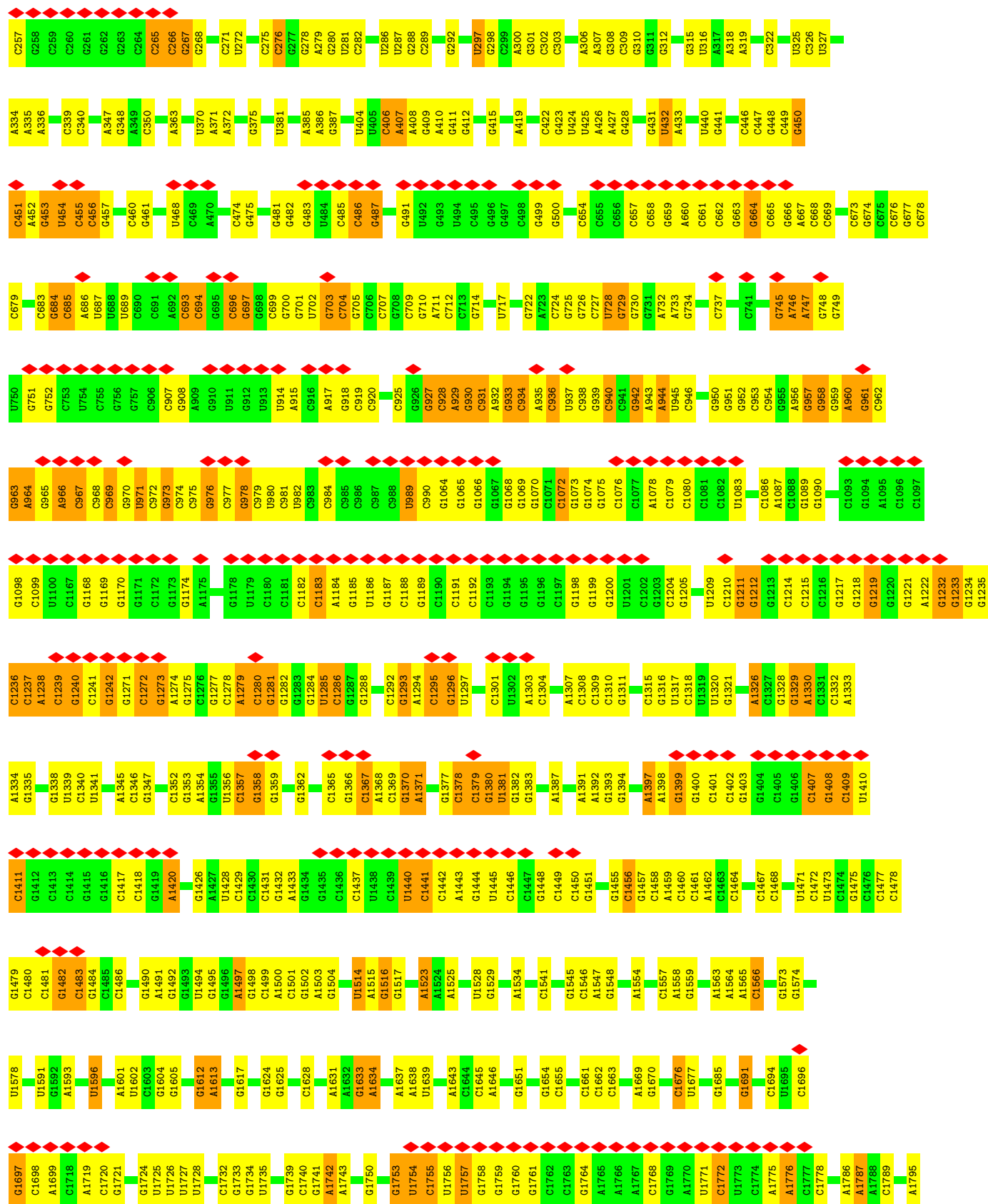
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

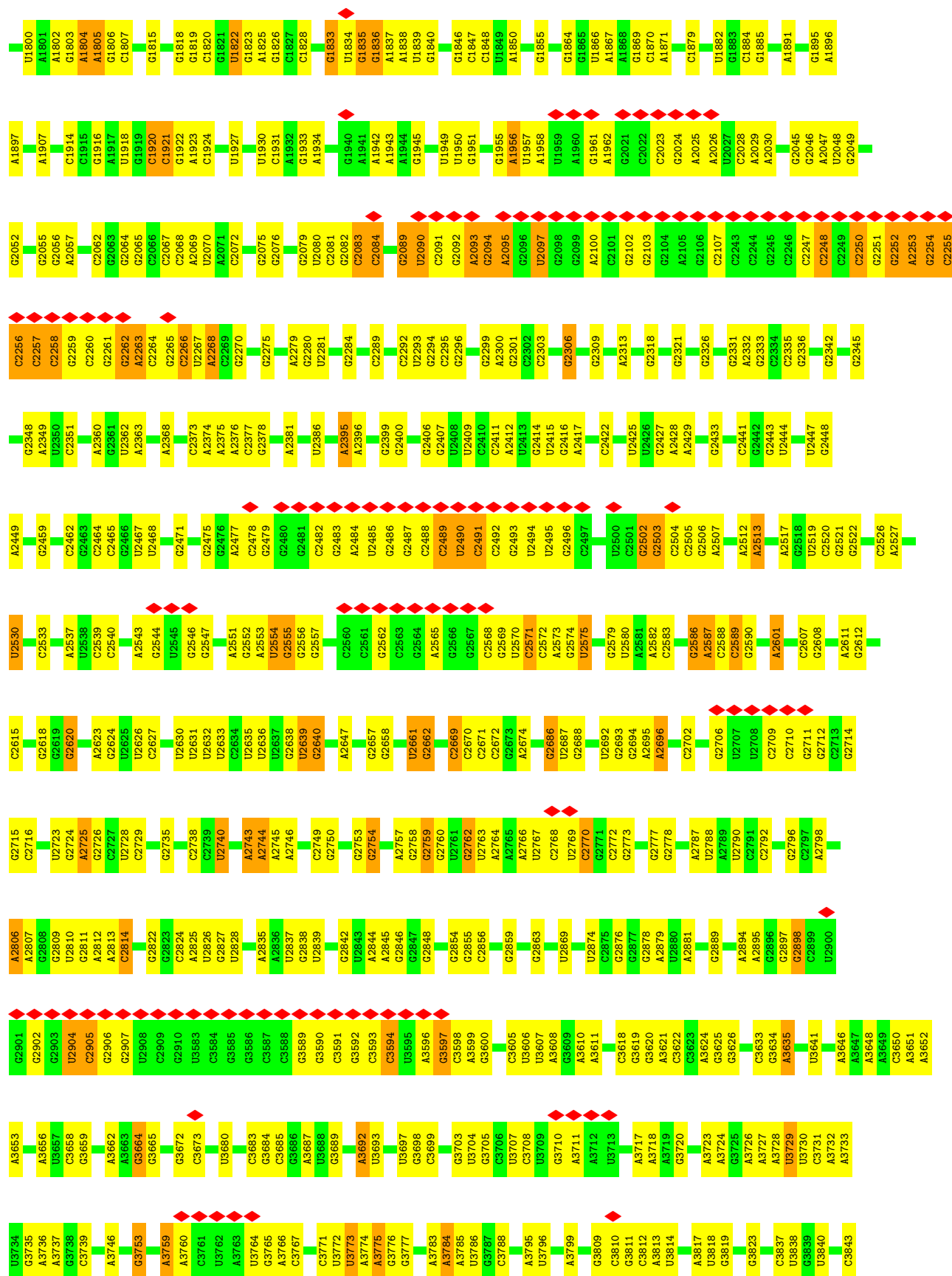
• Molecule 1: SRP RNA

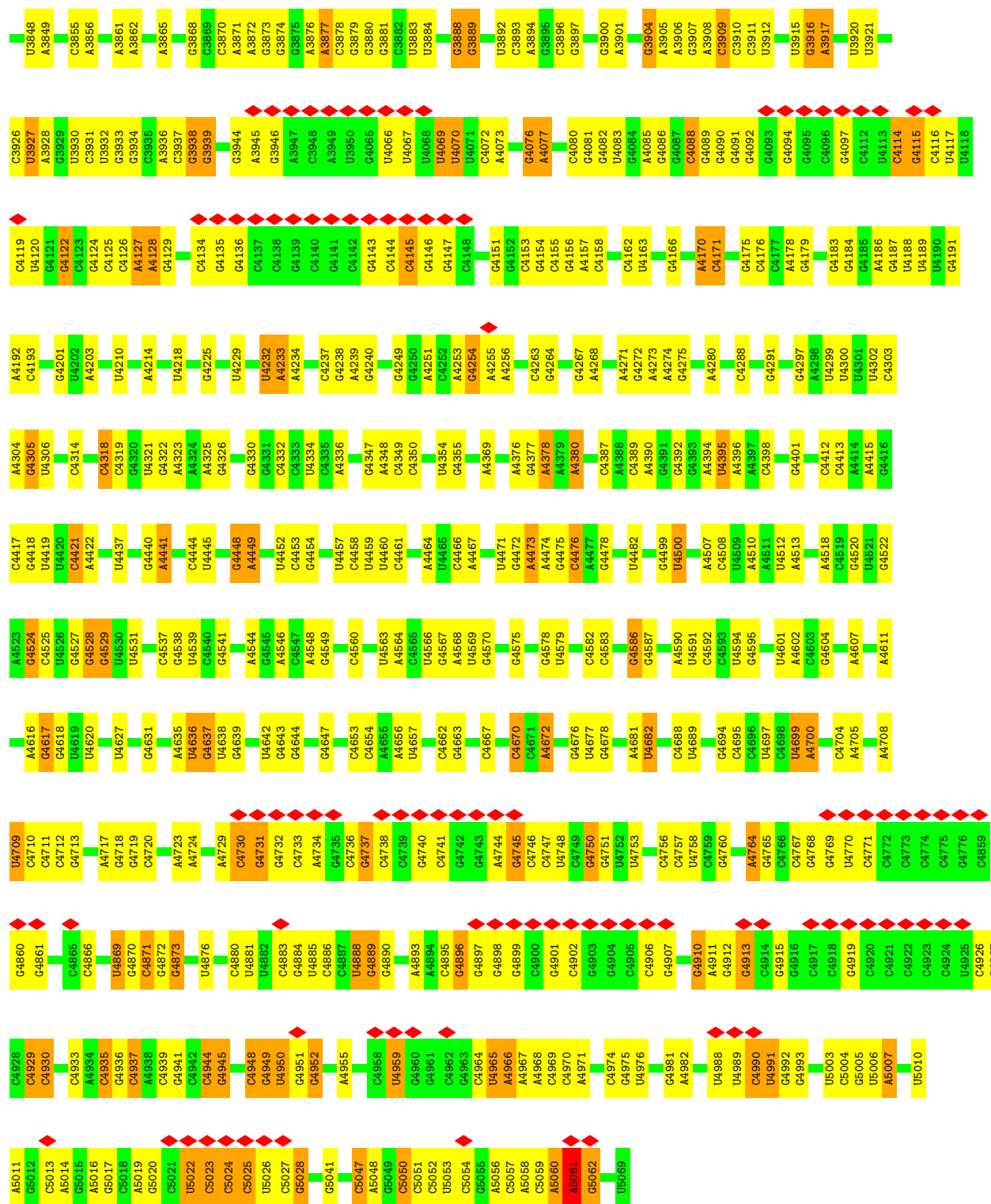


• Molecule 2: 28S rRNA



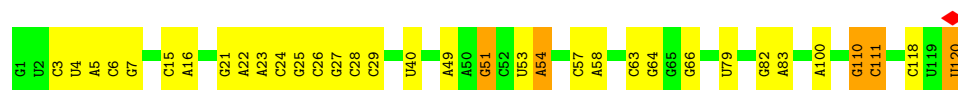




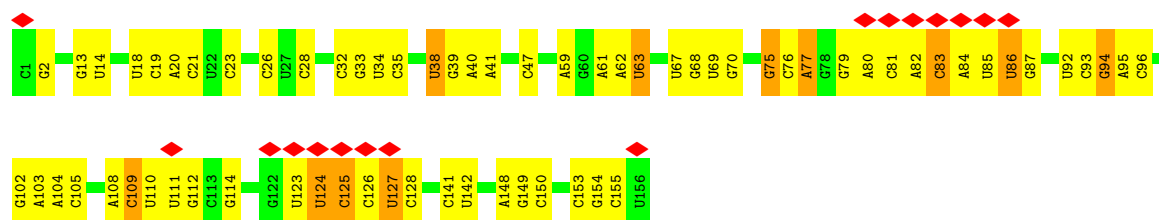


• Molecule 3: 5S ribosomal RNA

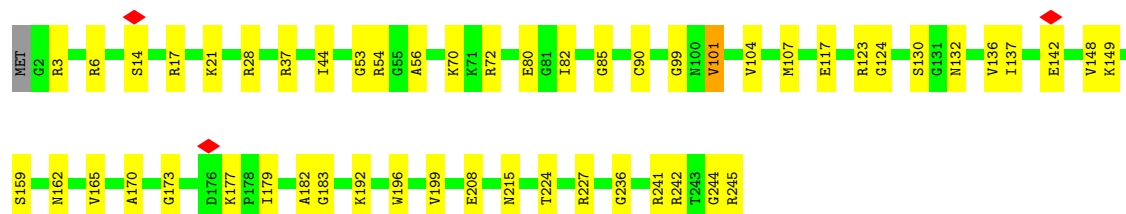
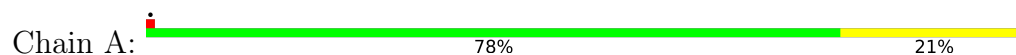




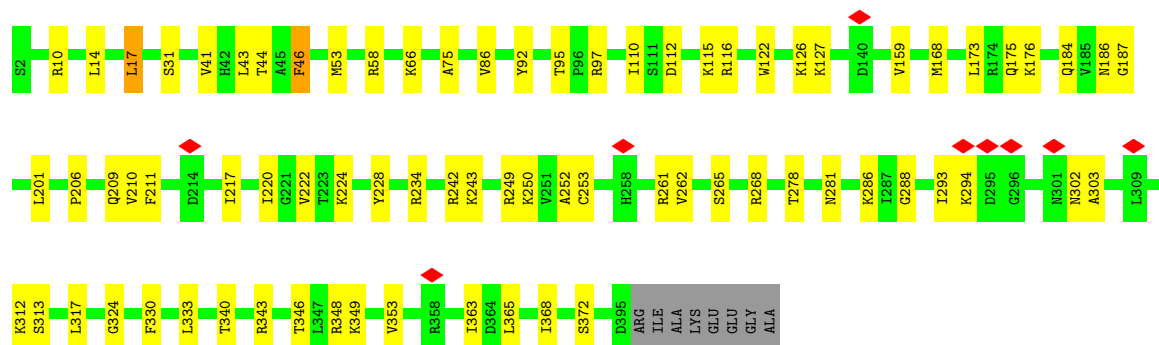
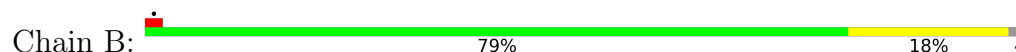
• Molecule 4: 5.8S ribosomal RNA



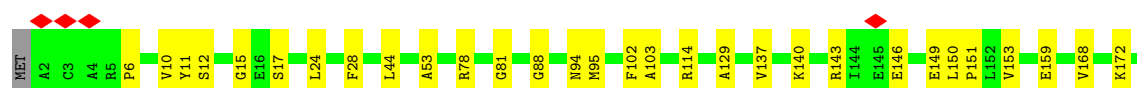
• Molecule 5: 60S ribosomal protein L8

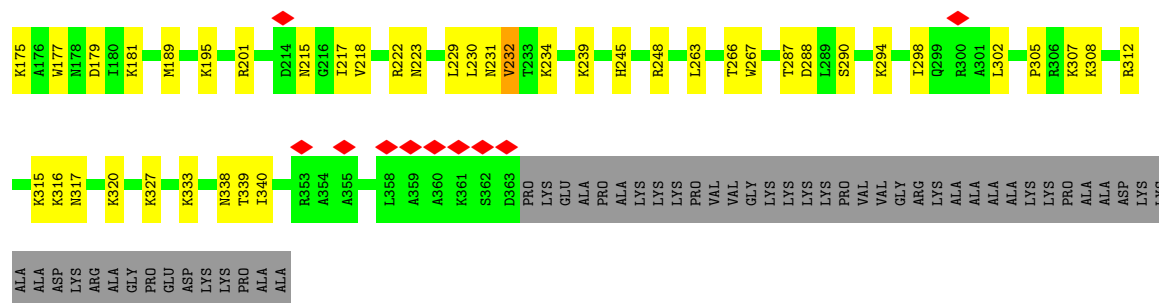


• Molecule 6: uL3

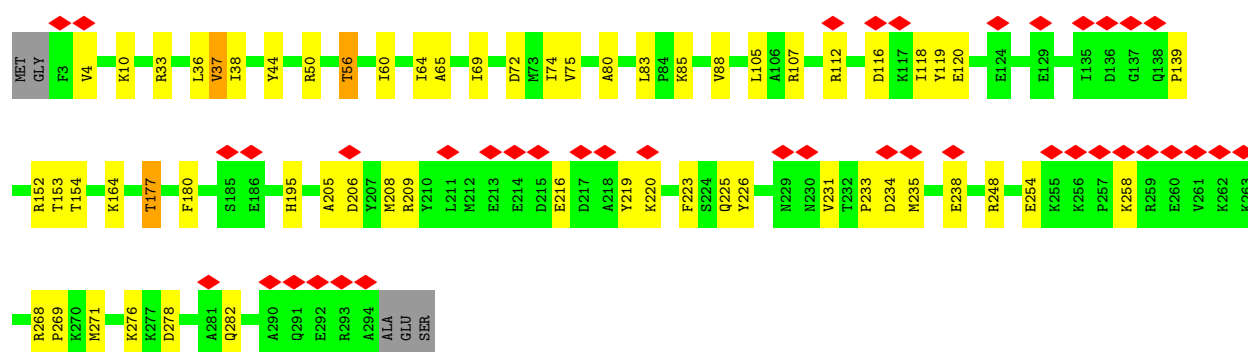
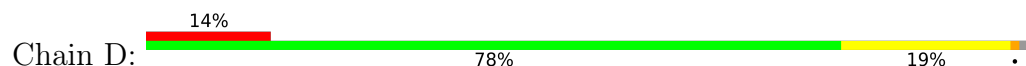


• Molecule 7: 60S ribosomal protein L4

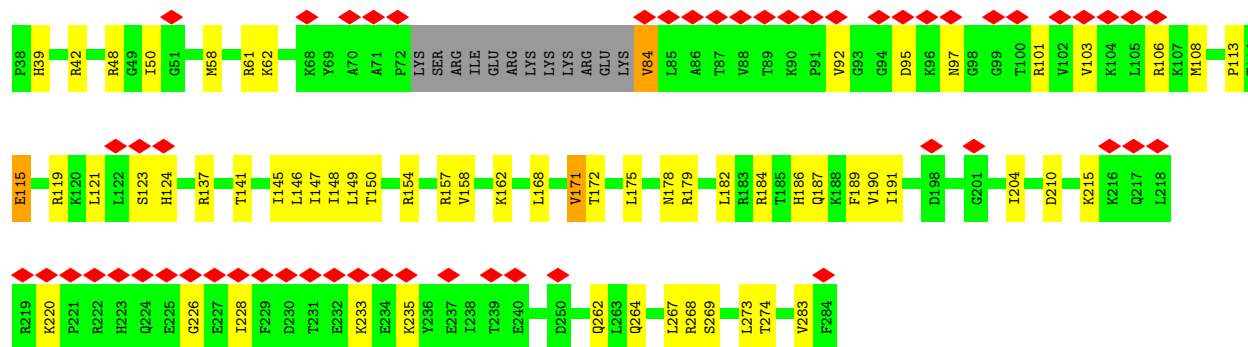




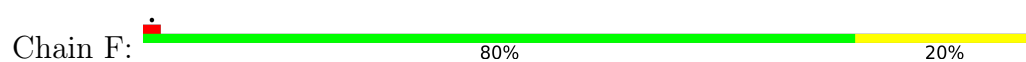
• Molecule 8: 60S ribosomal protein L5



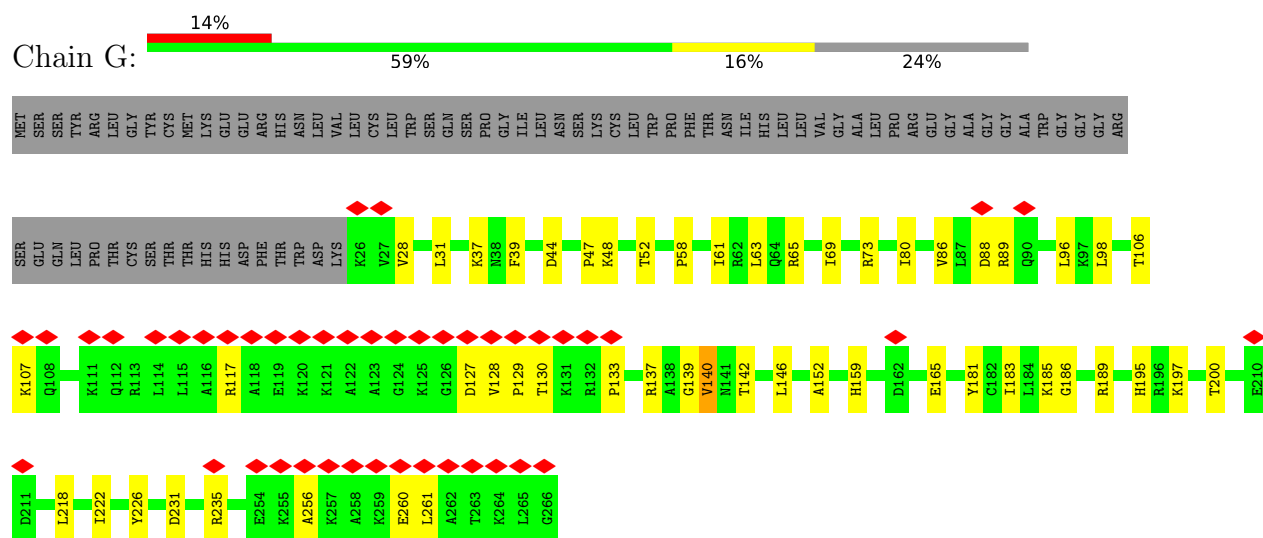
• Molecule 9: 60S ribosomal protein L6



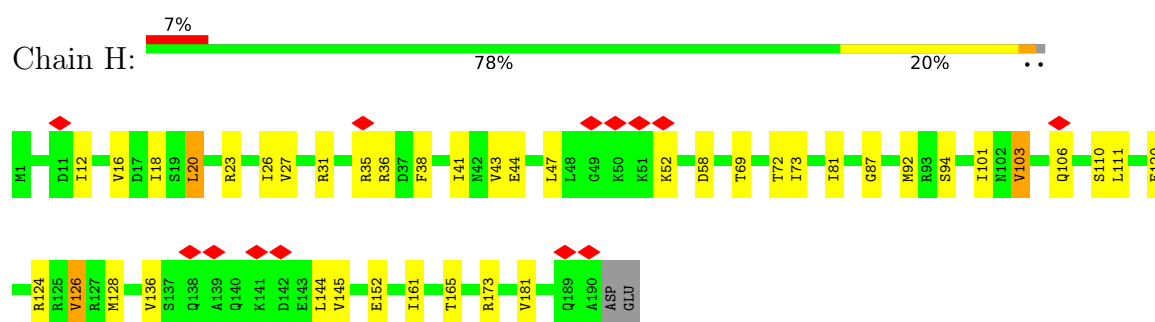
• Molecule 10: uL30



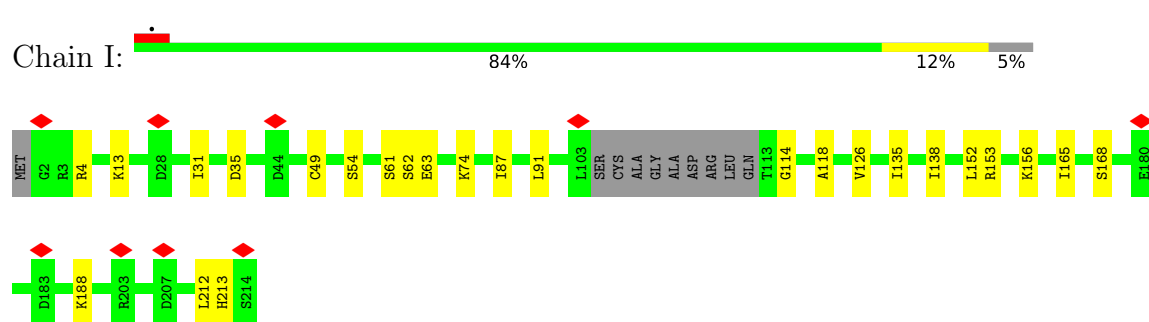
- Molecule 11: 60S ribosomal protein L7a



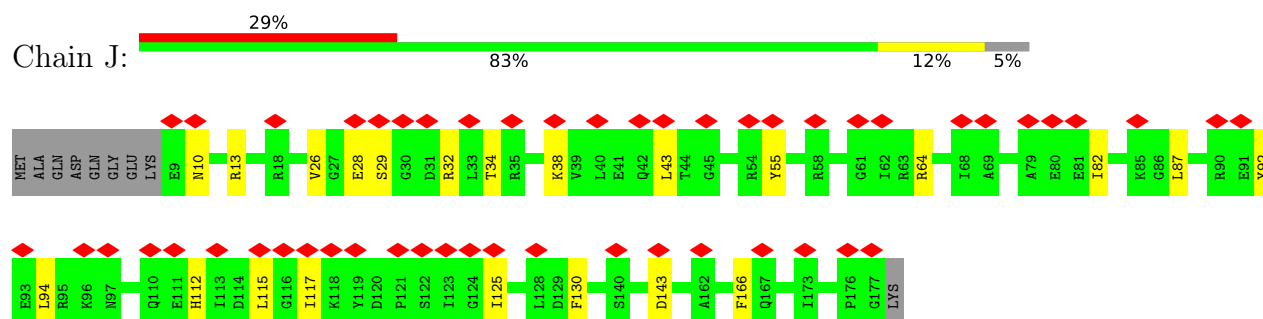
- Molecule 12: 60S ribosomal protein L9



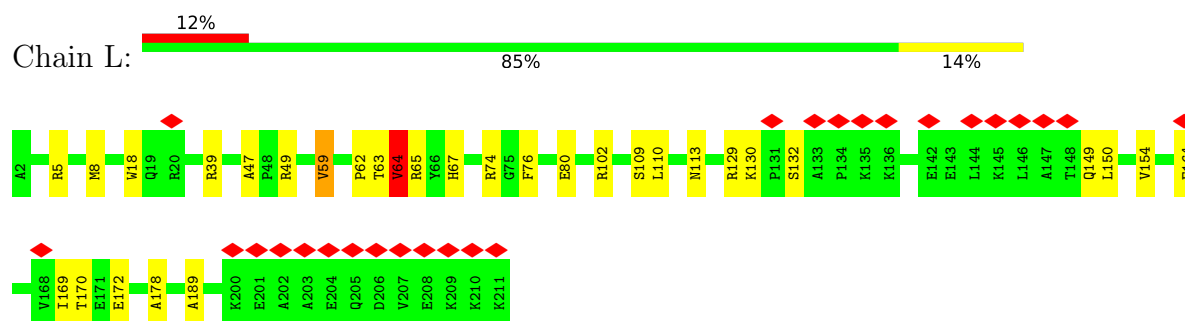
- Molecule 13: 60S ribosomal protein L10



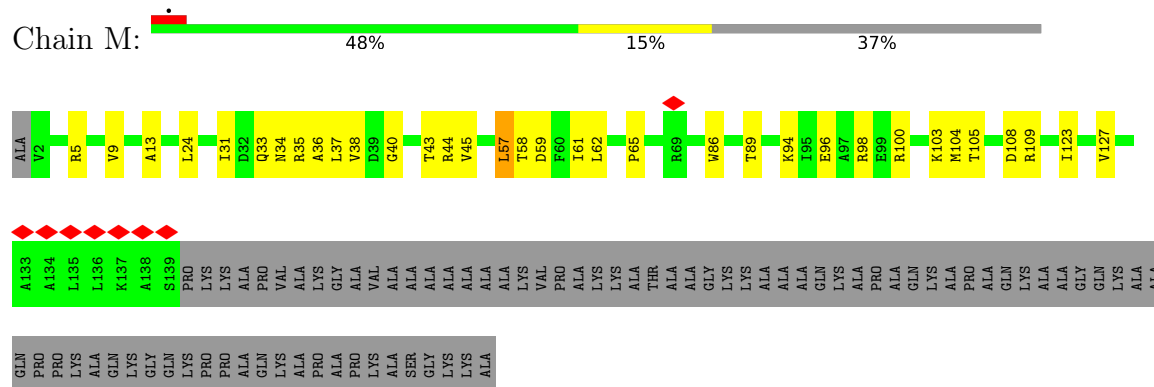
- Molecule 14: Ribosomal protein L11



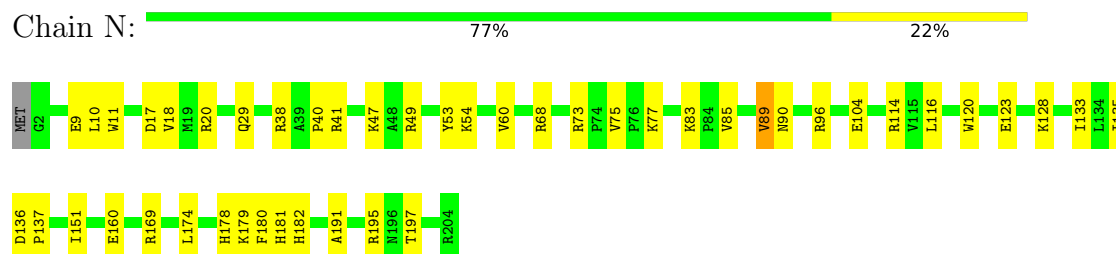
- Molecule 15: 60S ribosomal protein L13



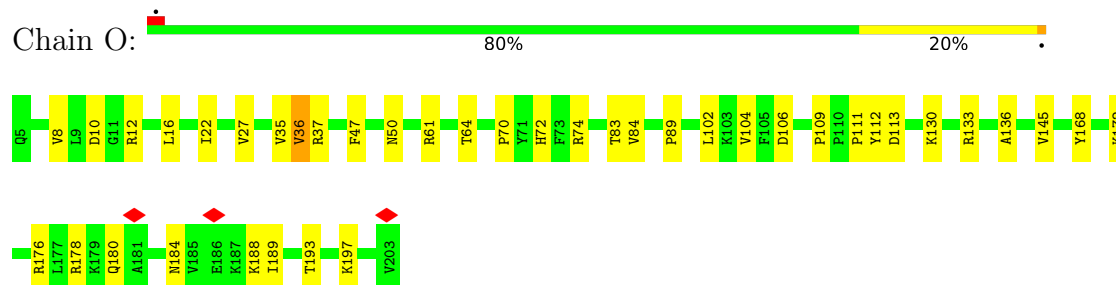
- Molecule 16: 60S ribosomal protein L14



- Molecule 17: Ribosomal protein L15



- Molecule 18: 60S ribosomal protein L13a

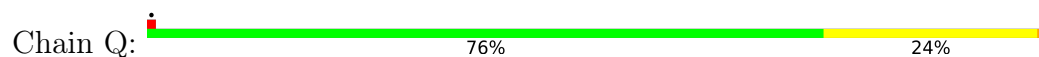


- Molecule 19: uL22

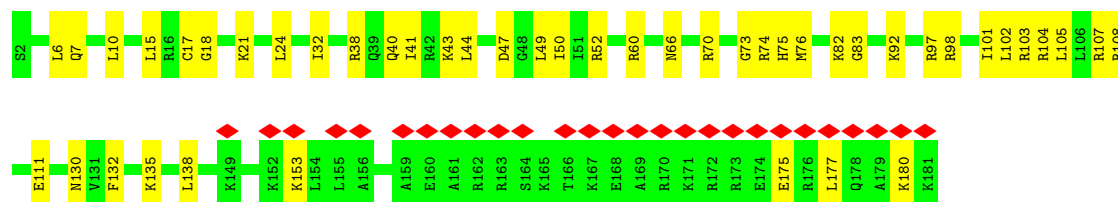
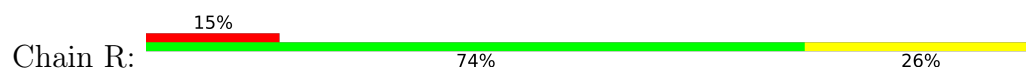




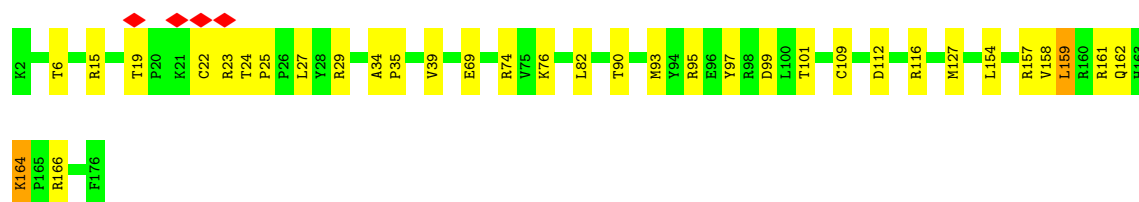
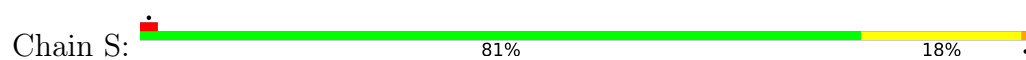
• Molecule 20: eL18



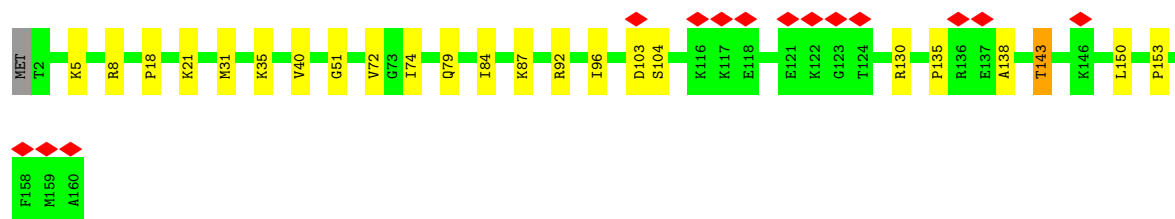
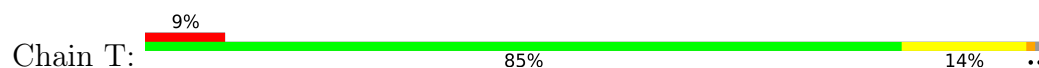
• Molecule 21: 60S RIBOSOMAL PROTEIN EL19



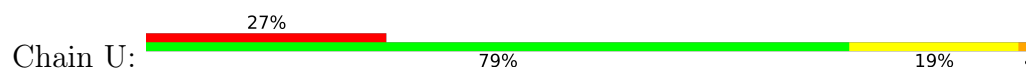
• Molecule 22: 60S ribosomal protein L18a

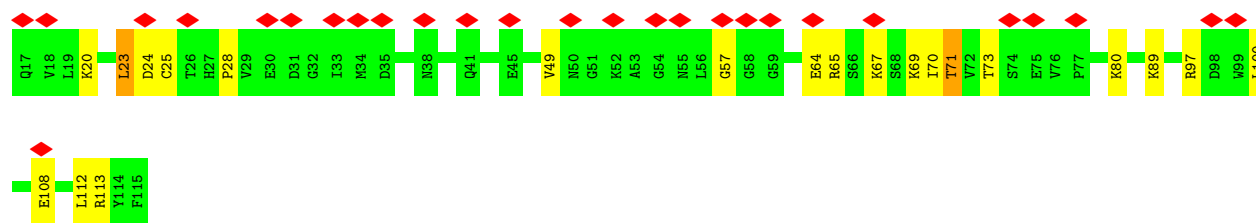


• Molecule 23: eL21

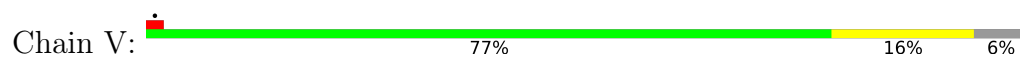


• Molecule 24: Ribosomal protein L22

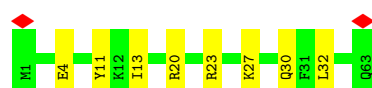
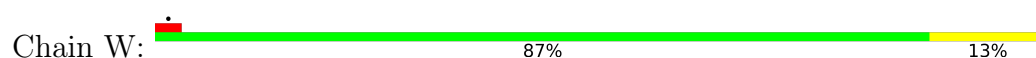




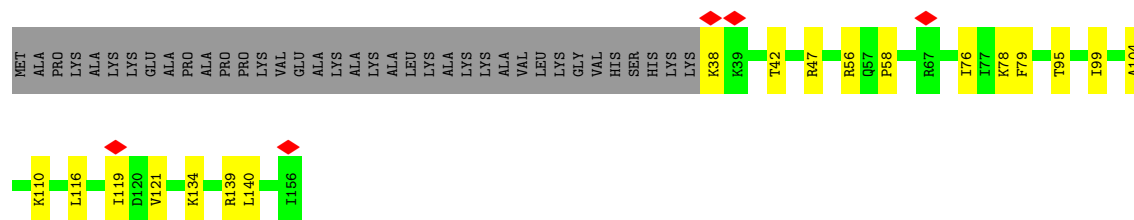
- Molecule 25: Ribosomal protein L23



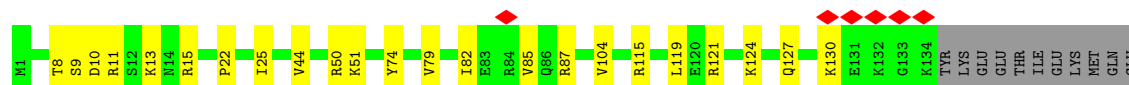
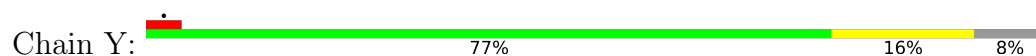
- Molecule 26: Ribosomal protein L24



- Molecule 27: uL23

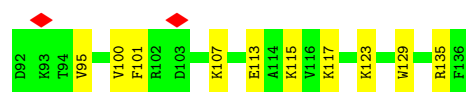


- Molecule 28: Ribosomal protein L26

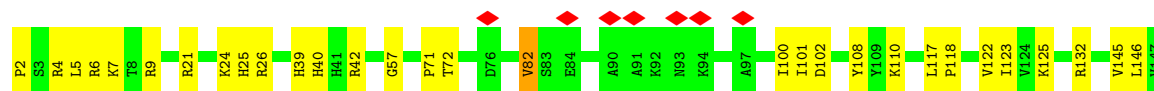
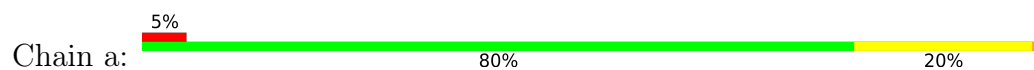


- Molecule 29: 60S ribosomal protein L27

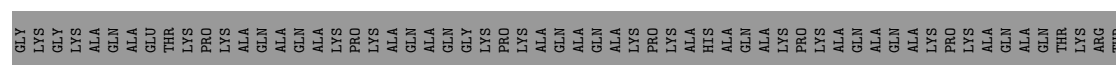
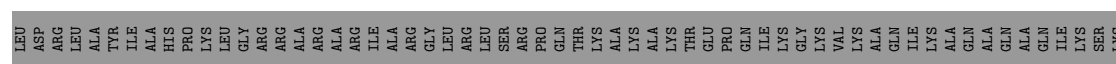
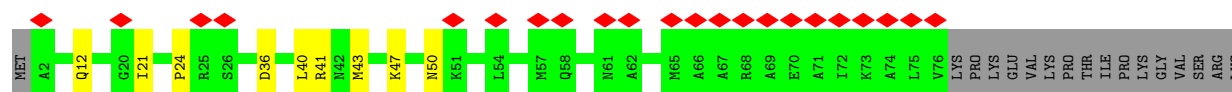




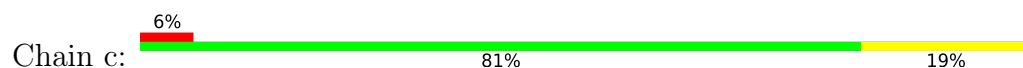
• Molecule 30: uL15



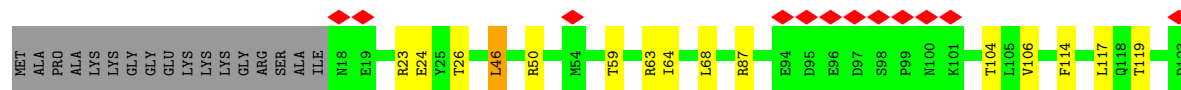
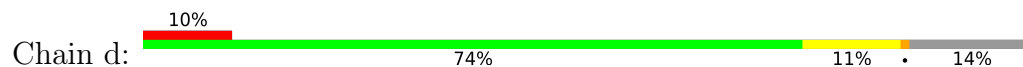
• Molecule 31: 60S ribosomal protein L29



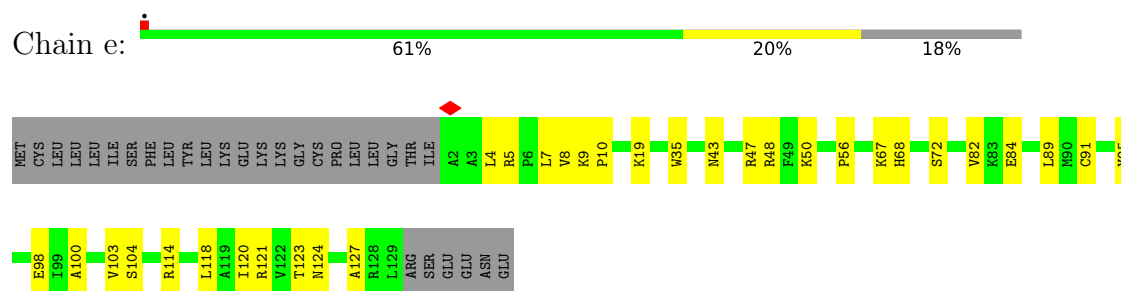
• Molecule 32: 60S ribosomal protein L30



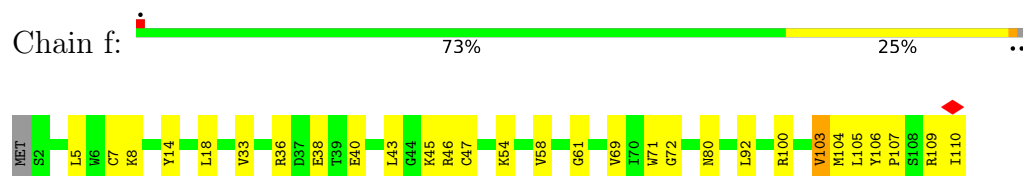
• Molecule 33: eL31



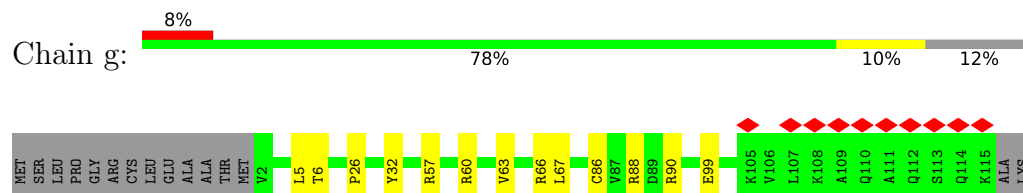
• Molecule 34: eL32



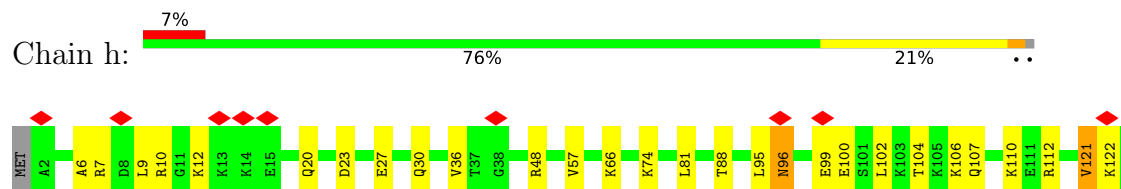
- Molecule 35: eL33



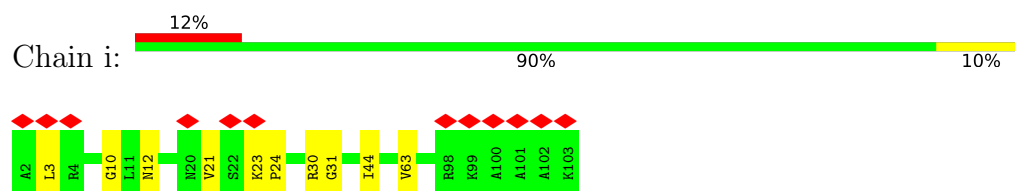
- Molecule 36: 60S ribosomal protein L34



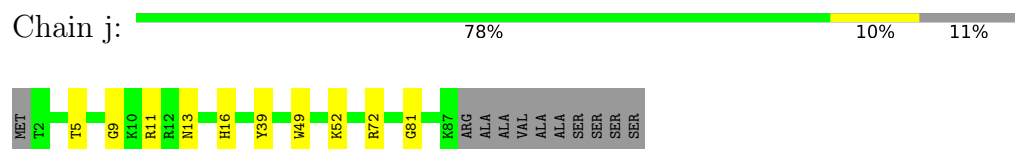
- Molecule 37: uL29



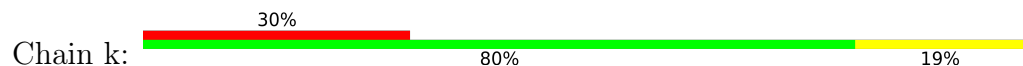
- Molecule 38: 60S ribosomal protein L36

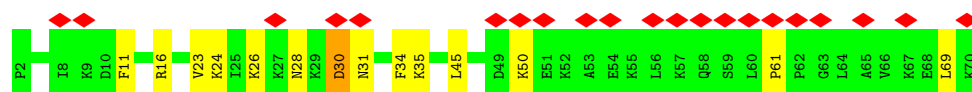


- Molecule 39: Ribosomal protein L37

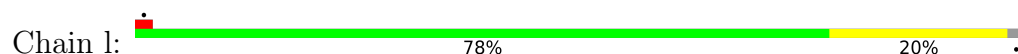


- Molecule 40: eL38

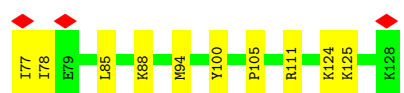
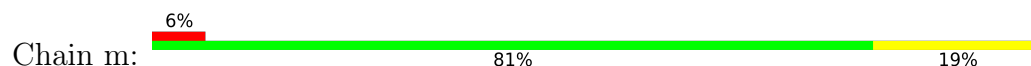




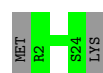
- Molecule 41: eL39



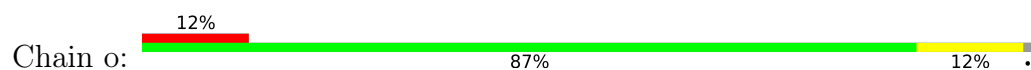
- Molecule 42: 60S RIBOSOMAL PROTEIN EL40



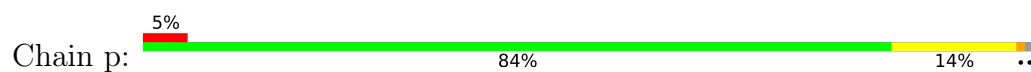
- Molecule 43: 60s ribosomal protein l41



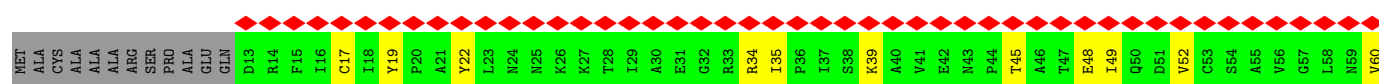
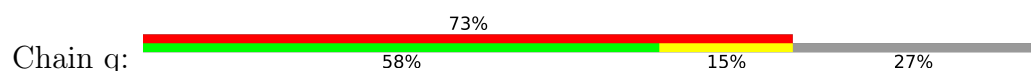
- Molecule 44: eL42



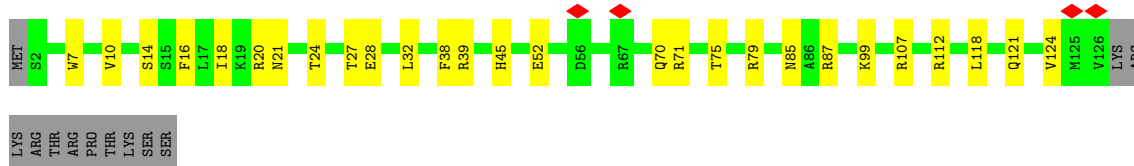
- Molecule 45: eL43



- Molecule 46: Signal recognition particle 19



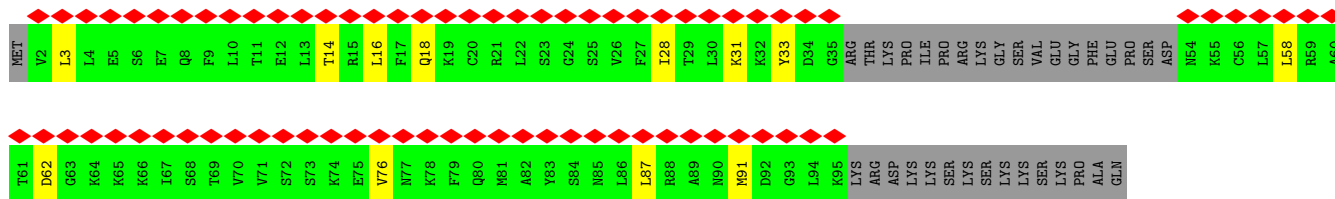
- Molecule 47: eL28



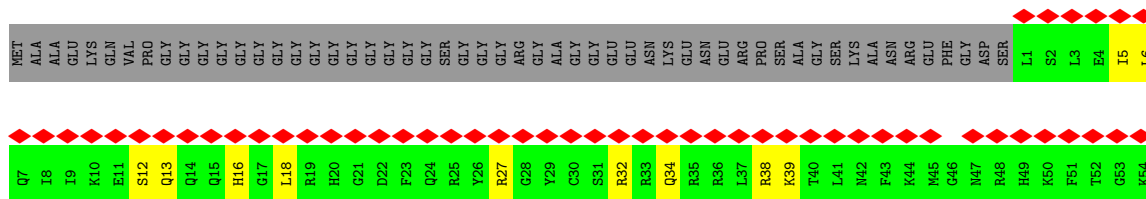
- Molecule 48: Dipeptidyl aminopeptidase B



- Molecule 49: Signal recognition particle 14 kDa protein



- Molecule 50: Signal recognition particle subunit SRP68







GLY	THR	GLN	GLY	ALA	THR	ALA	GLY	ALA	GLY	ALA	GLY	GLY	TRP
GLN	LYS	LYS	LYS	LYS	GLY	GLY	LYS	GLY	GLY	GLY	GLY	GLY	TRP

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43135	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.184	Depositor
Minimum map value	-0.080	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0195	Depositor
Map size (Å)	479.36002, 479.36002, 479.36002	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, 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	1	0.08	0/5971	0.23	0/9308
2	5	0.10	0/83726	0.25	1/130593 (0.0%)
3	7	0.08	0/2858	0.19	0/4455
4	8	0.09	0/3701	0.22	0/5766
5	A	0.10	0/1906	0.33	0/2556
6	B	0.09	0/3216	0.29	0/4311
7	C	0.10	0/2937	0.31	0/3946
8	D	0.10	0/2432	0.30	0/3257
9	E	0.13	0/1936	0.41	0/2600
10	F	0.11	0/1905	0.31	0/2539
11	G	0.12	0/1967	0.33	0/2647
12	H	0.09	0/1535	0.30	0/2063
13	I	0.10	0/1693	0.28	0/2260
14	J	0.10	0/1376	0.32	0/1841
15	L	0.11	0/1734	0.36	0/2317
16	M	0.11	0/1158	0.30	0/1547
17	N	0.11	0/1746	0.34	0/2338
18	O	0.11	0/1671	0.30	0/2234
19	P	0.10	0/1268	0.30	0/1700
20	Q	0.12	0/1530	0.33	0/2041
21	R	0.12	0/1524	0.35	0/2013
22	S	0.10	0/1493	0.31	0/2002
23	T	0.09	0/1326	0.29	0/1770
24	U	0.10	0/822	0.31	0/1103
25	V	0.09	0/993	0.29	0/1332
26	W	0.09	0/541	0.28	0/720
27	X	0.09	0/993	0.27	0/1334
28	Y	0.10	0/1132	0.28	0/1504
29	Z	0.11	0/1130	0.36	0/1507
30	a	0.10	0/1191	0.31	0/1590
31	b	0.10	0/619	0.28	0/818
32	c	0.09	0/742	0.24	0/996

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.11	0/903	0.31	0/1216
34	e	0.09	0/1071	0.28	0/1429
35	f	0.10	0/895	0.36	0/1198
36	g	0.10	0/916	0.32	0/1220
37	h	0.11	0/1021	0.31	0/1348
38	i	0.12	0/841	0.36	0/1112
39	j	0.11	0/720	0.35	0/952
40	k	0.11	0/575	0.31	0/761
41	l	0.13	0/454	0.33	0/599
42	m	0.11	0/435	0.35	0/575
43	n	0.14	0/223	0.37	0/284
44	o	0.10	0/864	0.34	0/1140
45	p	0.10	0/718	0.32	0/953
46	q	0.10	0/858	0.30	0/1156
47	r	0.13	0/1017	0.38	0/1364
48	s	0.29	0/514	0.72	2/702 (0.3%)
49	t	0.08	0/608	0.24	0/808
50	u	0.11	0/1654	0.29	0/2215
51	w	0.11	0/617	0.30	0/829
52	x	0.14	0/3825	0.36	0/5124
53	z	0.12	0/348	0.34	0/463
All	All	0.10	0/157849	0.28	3/232456 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	B	0	1
22	S	0	1
35	f	0	1
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	s	60	PRO	N-CA-CB	7.13	110.36	103.51
2	5	5061	A	P-O3'-C3'	5.32	128.18	120.20
48	s	30	VAL	CB-CA-C	-5.13	105.22	112.14

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	B	17	LEU	Peptide
22	S	164	LYS	Peptide
35	f	106	TYR	Peptide

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	1	5341	0	2701	86	0
2	5	74854	0	37828	1067	0
3	7	2558	0	1296	22	0
4	8	3314	0	1683	43	0
5	A	1868	0	1959	37	0
6	B	3148	0	3267	51	0
7	C	2883	0	3053	59	0
8	D	2386	0	2419	36	0
9	E	1898	0	2035	49	0
10	F	1870	0	1994	29	0
11	G	1934	0	2085	38	0
12	H	1516	0	1597	22	0
13	I	1655	0	1704	18	0
14	J	1353	0	1386	14	0
15	L	1703	0	1820	23	0
16	M	1137	0	1211	22	0
17	N	1701	0	1749	38	0
18	O	1638	0	1777	27	0
19	P	1242	0	1274	11	0
20	Q	1506	0	1623	35	0
21	R	1508	0	1664	37	0
22	S	1454	0	1496	26	0
23	T	1298	0	1366	20	0
24	U	808	0	831	12	0
25	V	979	0	1039	15	0
26	W	528	0	541	5	0
27	X	976	0	1053	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	Y	1115	0	1205	15	0
29	Z	1107	0	1182	25	0
30	a	1162	0	1209	22	0
31	b	609	0	650	7	0
32	c	732	0	769	11	0
33	d	888	0	930	8	0
34	e	1053	0	1147	21	0
35	f	876	0	912	19	0
36	g	906	0	998	10	0
37	h	1013	0	1147	23	0
38	i	830	0	916	8	0
39	j	705	0	737	11	0
40	k	569	0	637	8	0
41	l	444	0	483	8	0
42	m	429	0	465	8	0
43	n	222	0	264	0	0
44	o	851	0	920	9	0
45	p	708	0	756	9	0
46	q	844	0	861	16	0
47	r	1001	0	1060	16	0
48	s	502	0	492	65	0
49	t	604	0	642	8	0
50	u	1626	0	1645	21	0
51	w	607	0	617	13	0
52	x	3773	0	3855	189	0
53	z	339	0	353	8	0
54	5	97	0	0	0	0
55	g	1	0	0	0	0
55	j	1	0	0	0	0
55	m	1	0	0	0	0
55	o	1	0	0	0	0
55	p	1	0	0	0	0
56	x	28	0	12	1	0
All	All	146701	0	107315	2003	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 8.

The worst 5 of 2003 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)
48:s:43:LEU:CD2	52:x:312:LEU:HD23	1.28	1.57
48:s:44:LEU:HD11	52:x:319:ILE:CG1	1.40	1.49
52:x:9:LYS:NZ	52:x:38:ALA:CB	1.83	1.39
52:x:9:LYS:HZ1	52:x:38:ALA:CA	1.37	1.37
52:x:9:LYS:HZ3	52:x:38:ALA:CB	1.34	1.34

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	
5	A	242/245 (99%)	227 (94%)	15 (6%)	0	100	100
6	B	392/402 (98%)	384 (98%)	8 (2%)	0	100	100
7	C	360/413 (87%)	348 (97%)	12 (3%)	0	100	100
8	D	290/297 (98%)	275 (95%)	15 (5%)	0	100	100
9	E	232/248 (94%)	199 (86%)	33 (14%)	0	100	100
10	F	223/225 (99%)	216 (97%)	7 (3%)	0	100	100
11	G	239/319 (75%)	223 (93%)	16 (7%)	0	100	100
12	H	188/192 (98%)	181 (96%)	7 (4%)	0	100	100
13	I	200/214 (94%)	195 (98%)	5 (2%)	0	100	100
14	J	167/178 (94%)	154 (92%)	13 (8%)	0	100	100
15	L	208/210 (99%)	191 (92%)	16 (8%)	1 (0%)	24	55
16	M	136/218 (62%)	133 (98%)	3 (2%)	0	100	100
17	N	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
18	O	197/199 (99%)	195 (99%)	2 (1%)	0	100	100
19	P	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
20	Q	185/187 (99%)	180 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	R	178/180 (99%)	173 (97%)	5 (3%)	0	100	100
22	S	173/175 (99%)	166 (96%)	7 (4%)	0	100	100
23	T	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
24	U	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
25	V	129/140 (92%)	126 (98%)	3 (2%)	0	100	100
26	W	61/63 (97%)	61 (100%)	0	0	100	100
27	X	117/156 (75%)	112 (96%)	5 (4%)	0	100	100
28	Y	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
29	Z	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
30	a	145/147 (99%)	135 (93%)	10 (7%)	0	100	100
31	b	73/223 (33%)	70 (96%)	3 (4%)	0	100	100
32	c	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
33	d	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
34	e	126/157 (80%)	121 (96%)	5 (4%)	0	100	100
35	f	107/110 (97%)	101 (94%)	6 (6%)	0	100	100
36	g	112/129 (87%)	112 (100%)	0	0	100	100
37	h	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
38	i	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
39	j	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
40	k	67/69 (97%)	60 (90%)	7 (10%)	0	100	100
41	l	48/51 (94%)	41 (85%)	7 (15%)	0	100	100
42	m	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
43	n	21/25 (84%)	21 (100%)	0	0	100	100
44	o	102/105 (97%)	94 (92%)	8 (8%)	0	100	100
45	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
46	q	103/144 (72%)	100 (97%)	3 (3%)	0	100	100
47	r	123/137 (90%)	111 (90%)	11 (9%)	1 (1%)	16	44
48	s	65/67 (97%)	53 (82%)	11 (17%)	1 (2%)	8	28
49	t	72/110 (66%)	72 (100%)	0	0	100	100
50	u	192/622 (31%)	189 (98%)	3 (2%)	0	100	100
51	w	72/86 (84%)	65 (90%)	7 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	x	486/504 (96%)	463 (95%)	23 (5%)	0	100	100
53	z	38/671 (6%)	32 (84%)	6 (16%)	0	100	100
All	All	7380/9200 (80%)	7034 (95%)	343 (5%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	L	64	VAL
48	s	86	TYR
47	r	21	ASN

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	
5	A	187/188 (100%)	184 (98%)	3 (2%)	55	83
6	B	336/347 (97%)	332 (99%)	4 (1%)	63	87
7	C	302/337 (90%)	298 (99%)	4 (1%)	61	86
8	D	247/250 (99%)	239 (97%)	8 (3%)	34	70
9	E	208/221 (94%)	199 (96%)	9 (4%)	26	60
10	F	194/195 (100%)	192 (99%)	2 (1%)	68	88
11	G	206/273 (76%)	201 (98%)	5 (2%)	43	77
12	H	169/171 (99%)	163 (96%)	6 (4%)	31	66
13	I	174/181 (96%)	174 (100%)	0	100	100
14	J	142/149 (95%)	141 (99%)	1 (1%)	76	91
15	L	176/176 (100%)	173 (98%)	3 (2%)	53	83
16	M	117/160 (73%)	111 (95%)	6 (5%)	21	54
17	N	171/172 (99%)	168 (98%)	3 (2%)	51	82
18	O	171/171 (100%)	167 (98%)	4 (2%)	44	78
19	P	134/134 (100%)	134 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	Q	163/163 (100%)	159 (98%)	4 (2%)	42	76
21	R	159/159 (100%)	157 (99%)	2 (1%)	61	86
22	S	156/156 (100%)	151 (97%)	5 (3%)	34	70
23	T	139/140 (99%)	138 (99%)	1 (1%)	76	91
24	U	89/89 (100%)	86 (97%)	3 (3%)	32	68
25	V	101/107 (94%)	99 (98%)	2 (2%)	48	80
26	W	55/55 (100%)	55 (100%)	0	100	100
27	X	107/134 (80%)	104 (97%)	3 (3%)	38	73
28	Y	124/135 (92%)	121 (98%)	3 (2%)	43	77
29	Z	117/118 (99%)	114 (97%)	3 (3%)	40	75
30	a	119/119 (100%)	116 (98%)	3 (2%)	42	76
31	b	62/170 (36%)	60 (97%)	2 (3%)	34	70
32	c	79/79 (100%)	78 (99%)	1 (1%)	61	86
33	d	98/110 (89%)	93 (95%)	5 (5%)	21	54
34	e	114/141 (81%)	113 (99%)	1 (1%)	70	89
35	f	88/89 (99%)	86 (98%)	2 (2%)	44	78
36	g	98/109 (90%)	96 (98%)	2 (2%)	48	80
37	h	109/110 (99%)	105 (96%)	4 (4%)	30	65
38	i	86/86 (100%)	84 (98%)	2 (2%)	44	78
39	j	73/80 (91%)	72 (99%)	1 (1%)	59	85
40	k	64/64 (100%)	62 (97%)	2 (3%)	35	70
41	l	47/48 (98%)	46 (98%)	1 (2%)	47	79
42	m	48/48 (100%)	48 (100%)	0	100	100
43	n	22/24 (92%)	22 (100%)	0	100	100
44	o	92/93 (99%)	92 (100%)	0	100	100
45	p	74/75 (99%)	72 (97%)	2 (3%)	39	74
46	q	92/121 (76%)	92 (100%)	0	100	100
47	r	109/121 (90%)	104 (95%)	5 (5%)	24	58
48	s	51/64 (80%)	44 (86%)	7 (14%)	3	13
49	t	69/100 (69%)	69 (100%)	0	100	100
50	u	171/524 (33%)	168 (98%)	3 (2%)	51	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	w	66/77 (86%)	66 (100%)	0	100	100
52	x	409/420 (97%)	373 (91%)	36 (9%)	9	29
53	z	36/570 (6%)	35 (97%)	1 (3%)	38	73
All	All	6420/7823 (82%)	6256 (97%)	164 (3%)	41	75

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	r	75	THR
52	x	60	ILE
48	s	46	LYS
52	x	15	ARG
52	x	71	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
49	t	77	ASN
52	x	488	GLN
50	u	13	GLN
52	x	102	ASN
18	O	63	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	245/249 (98%)	49 (20%)	5 (2%)
2	5	3478/3493 (99%)	706 (20%)	84 (2%)
3	7	119/120 (99%)	12 (10%)	0
4	8	155/156 (99%)	32 (20%)	1 (0%)
All	All	3997/4018 (99%)	799 (19%)	90 (2%)

5 of 799 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	4	G
1	1	17	C
1	1	28	U
1	1	29	C

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Mol	Chain	Res	Type
1	1	33	G

5 of 90 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	5	2257	C
2	5	4119	C
2	5	2262	G
2	5	2695	A
2	5	4528	G

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 103 ligands modelled in this entry, 102 are monoatomic - leaving 1 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	$\# Z > 2$
56	GDP	x	601	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)

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
56	GDP	x	601	-	-	0/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	x	601	GDP	C5-C4	3.15	1.47	1.38
56	x	601	GDP	C6-N1	-2.41	1.34	1.38
56	x	601	GDP	C5-N7	-2.02	1.35	1.39

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	x	601	GDP	C5-C4-N3	-6.17	118.57	128.39
56	x	601	GDP	C2-N3-C4	5.04	120.99	112.30
56	x	601	GDP	N9-C4-N3	4.51	134.97	125.95
56	x	601	GDP	C6-C5-N7	3.26	136.22	130.29
56	x	601	GDP	C4-C5-N7	-2.62	106.52	110.67

There are no chirality outliers.

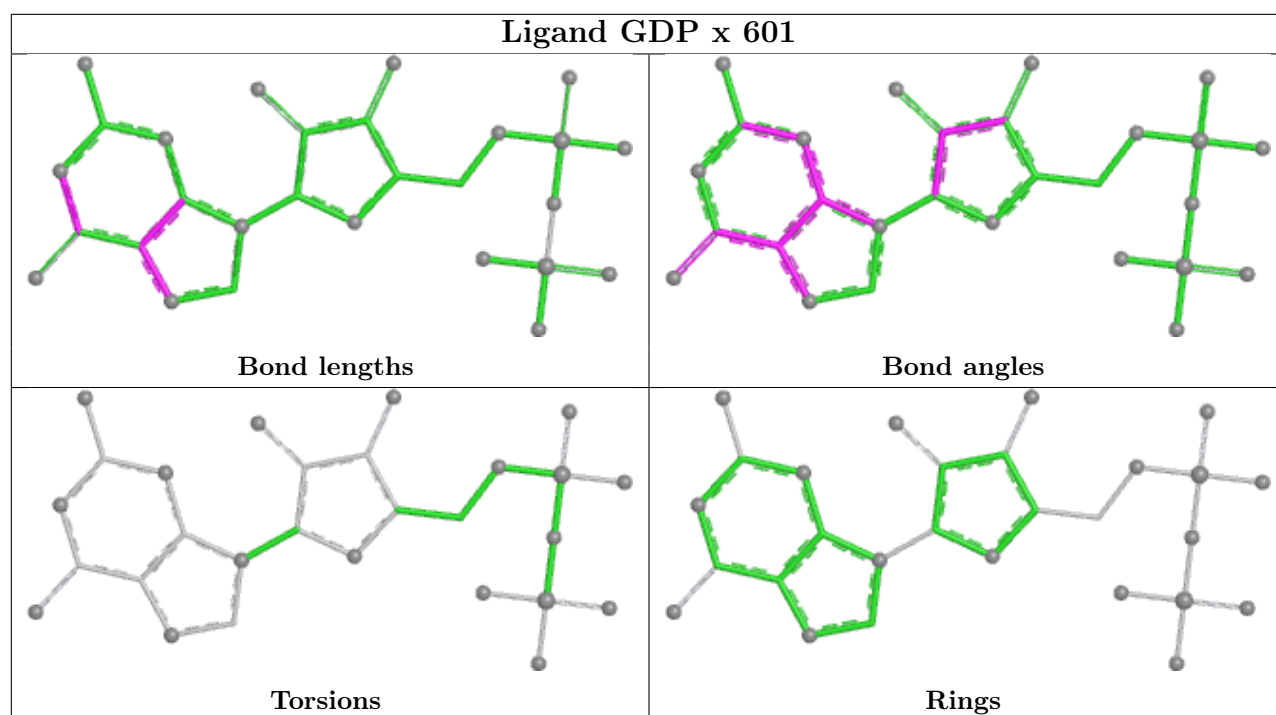
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	x	601	GDP	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	5	15
1	1	3

The worst 5 of 18 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	65:U	O3'	92:C	P	57.10
1	1	258:C	O3'	282:U	P	50.27
1	5	462:G	O3'	467:U	P	20.95
1	5	4776:G	O3'	4859:C	P	17.67
1	5	4097:G	O3'	4112:C	P	17.47

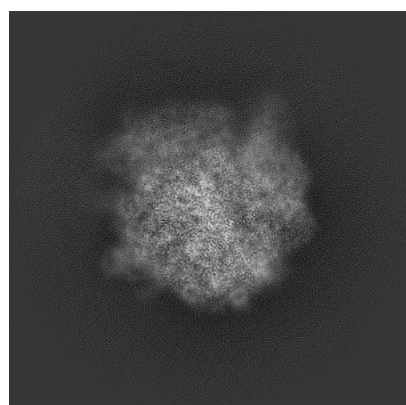
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12801. These allow visual inspection of the internal detail of the map and identification of artifacts.

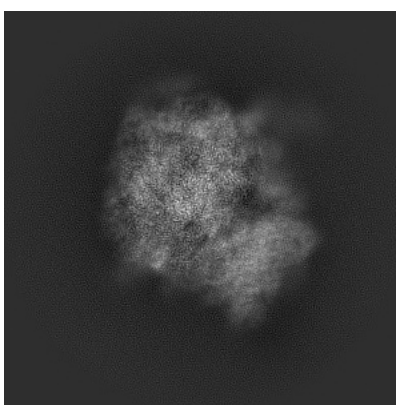
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

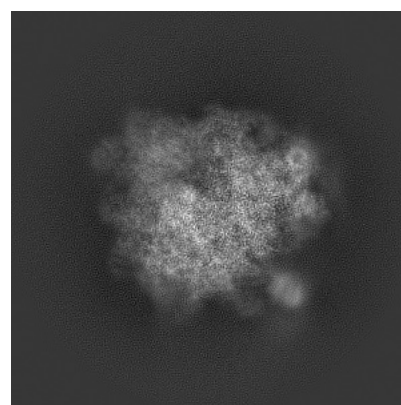
6.1.1 Primary map



X



Y

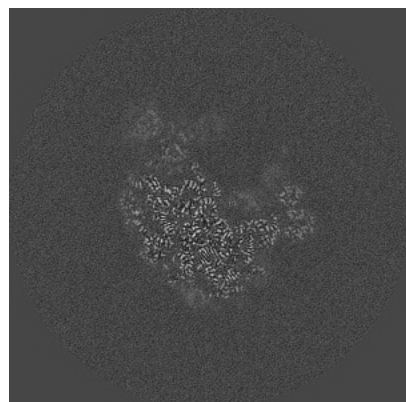


Z

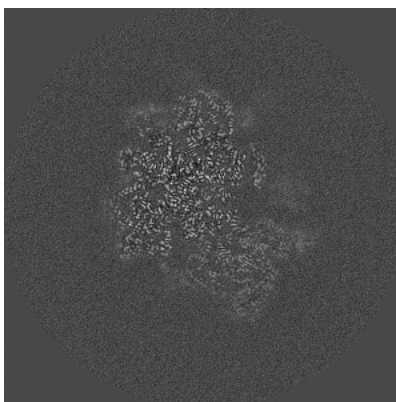
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

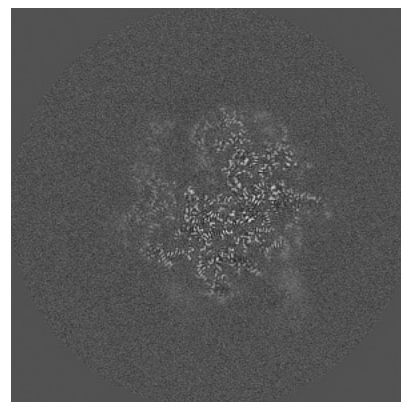
6.2.1 Primary map



X Index: 224



Y Index: 224

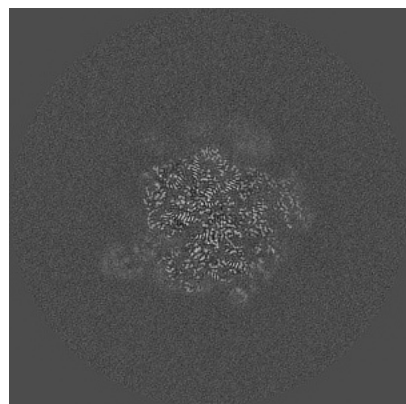


Z Index: 224

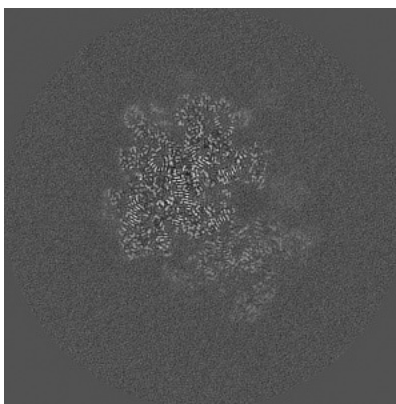
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

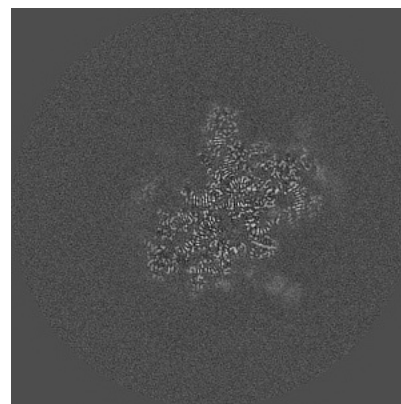
6.3.1 Primary map



X Index: 259



Y Index: 228

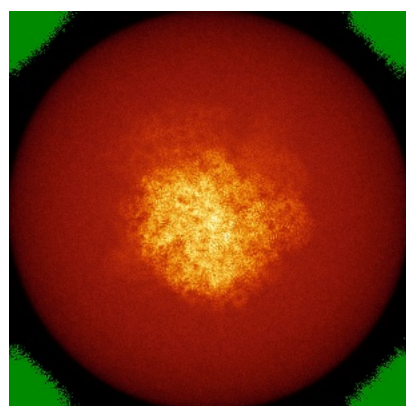


Z Index: 195

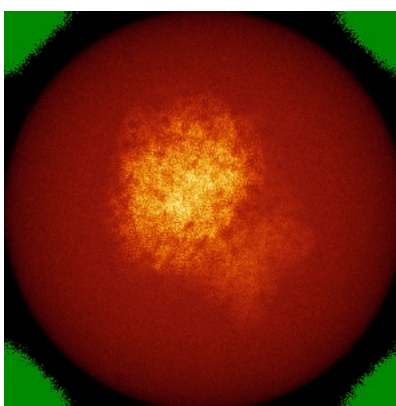
The images above show the largest variance slices of the map in three orthogonal directions.

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

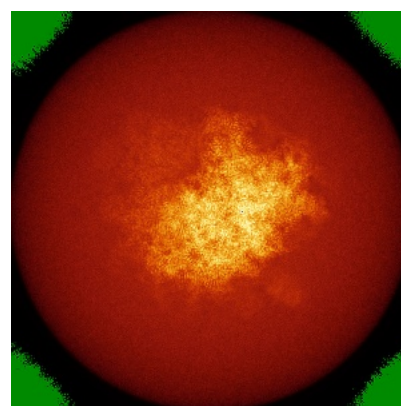
6.4.1 Primary map



X



Y

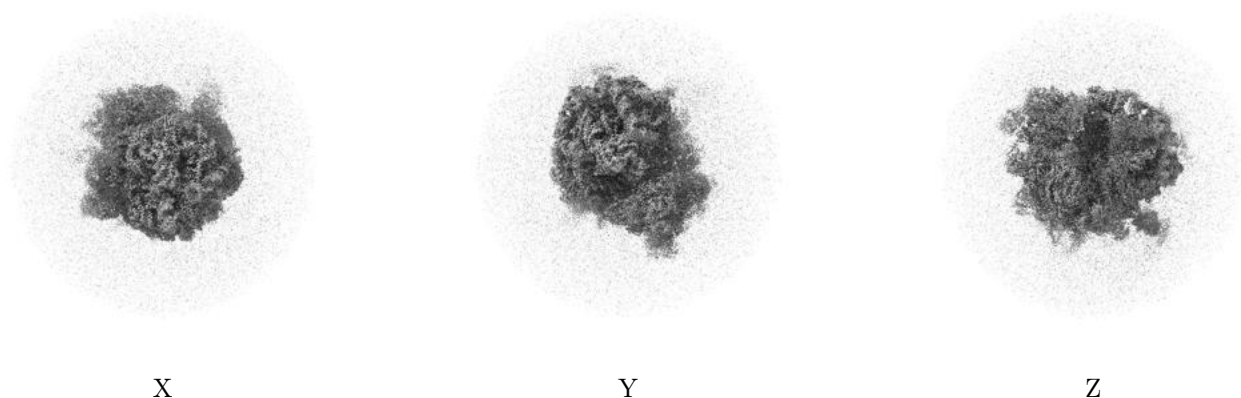


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0195. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

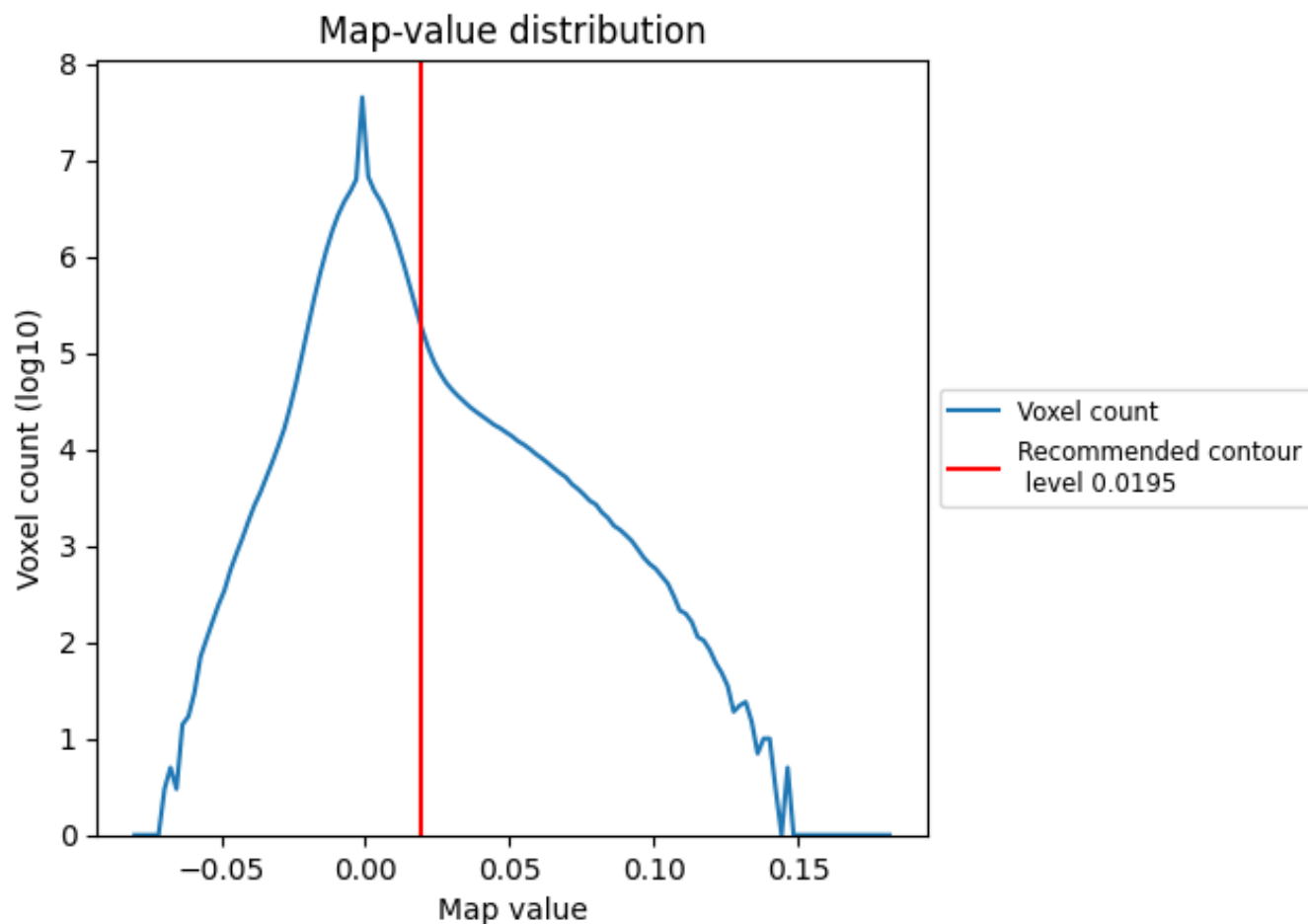
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

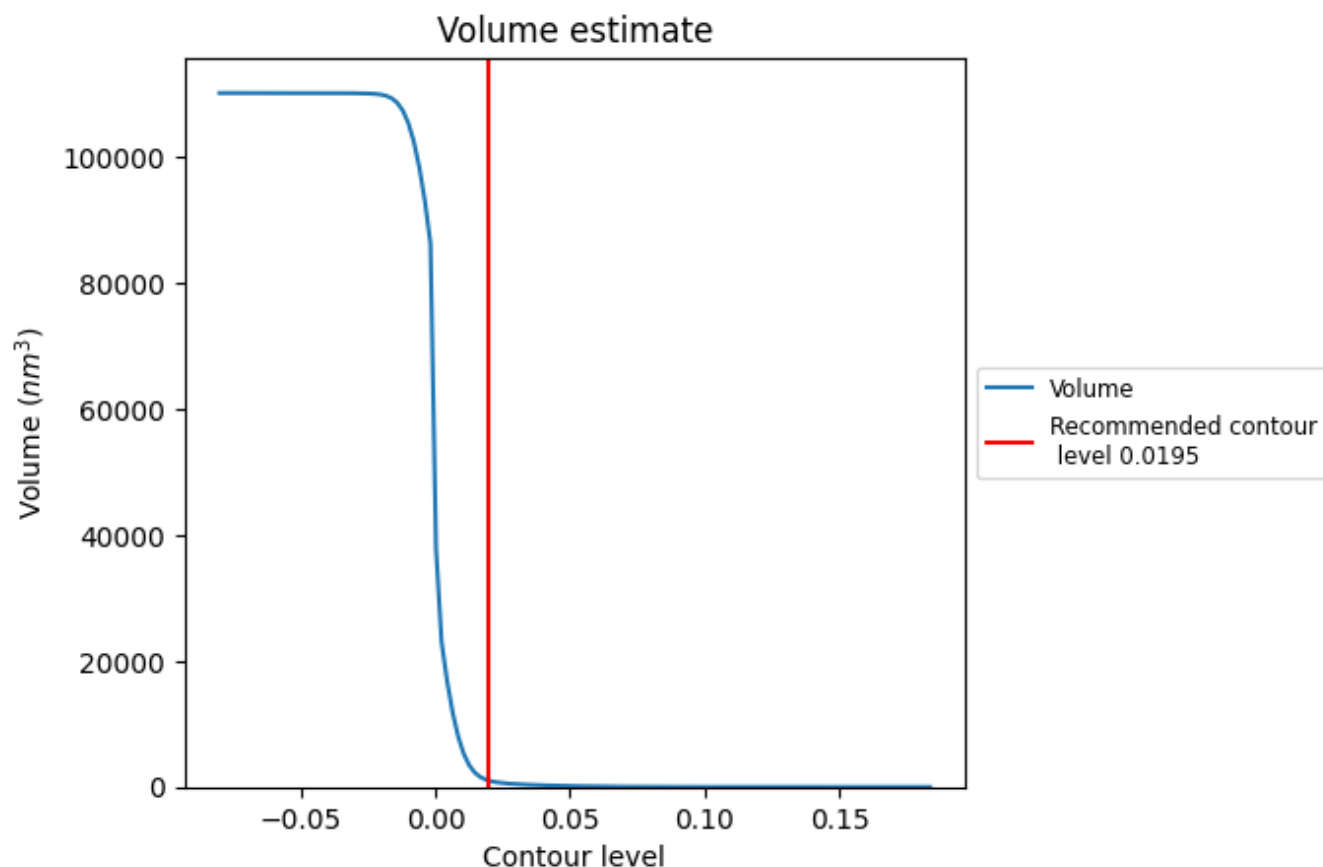
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

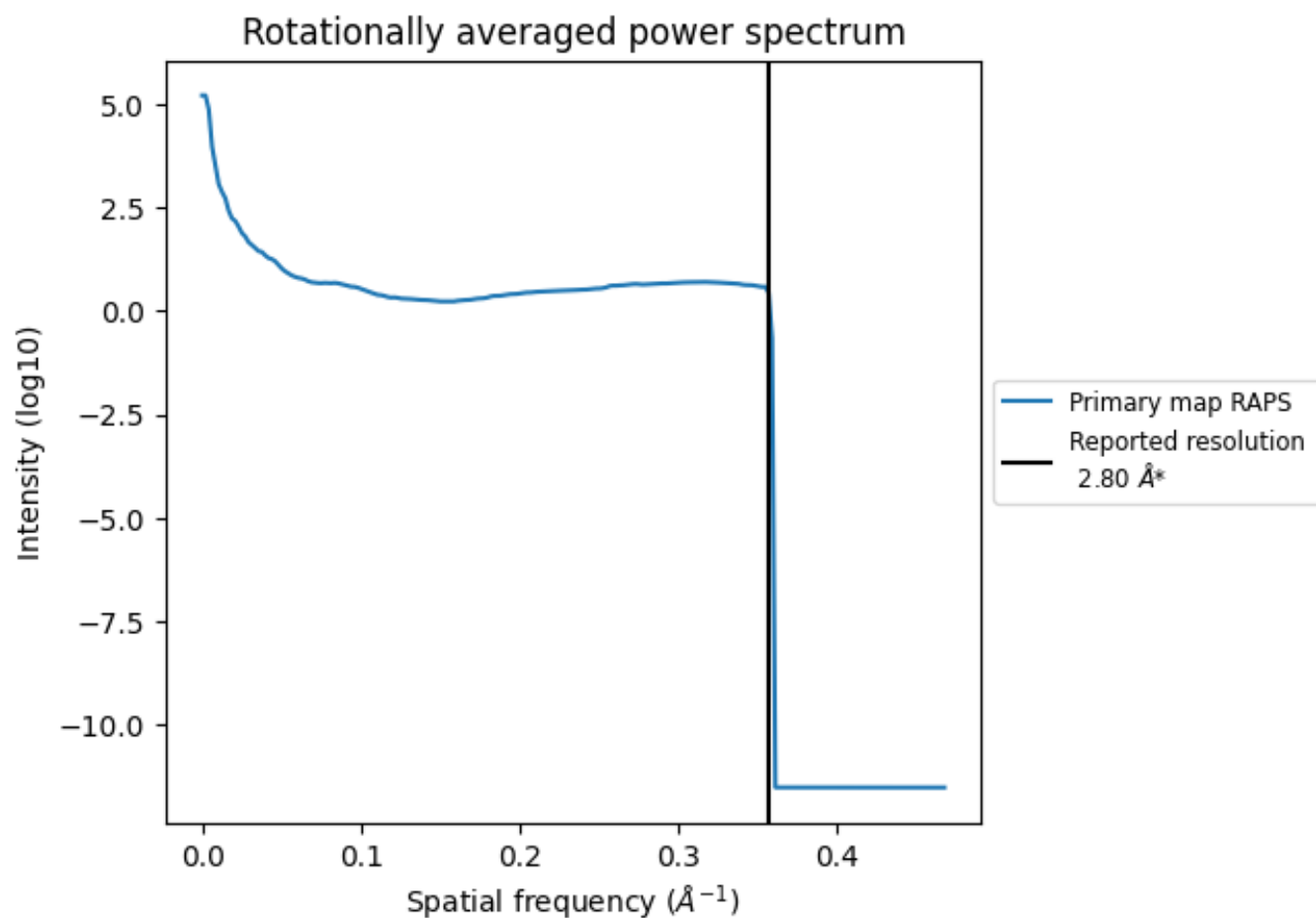
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 10750 nm³; this corresponds to an approximate mass of 971 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 0.357 $\text{\AA}^{-1}$

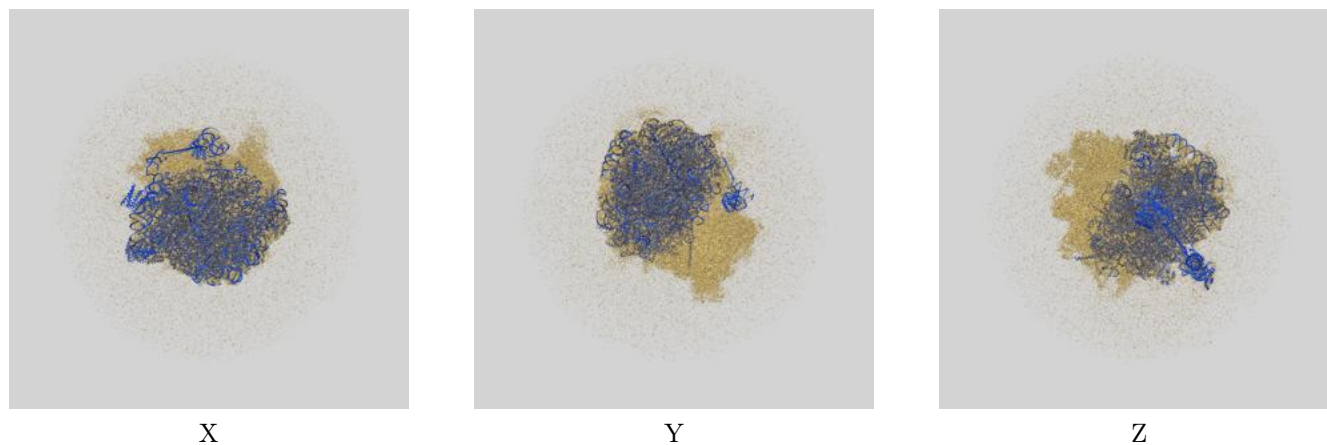
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

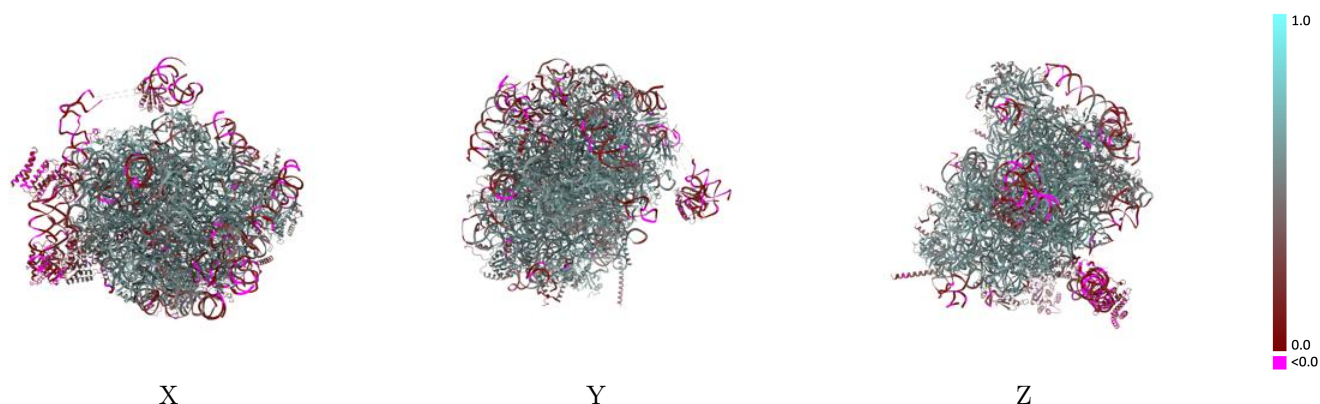
This section contains information regarding the fit between EMDB map EMD-12801 and PDB model 7OBR. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



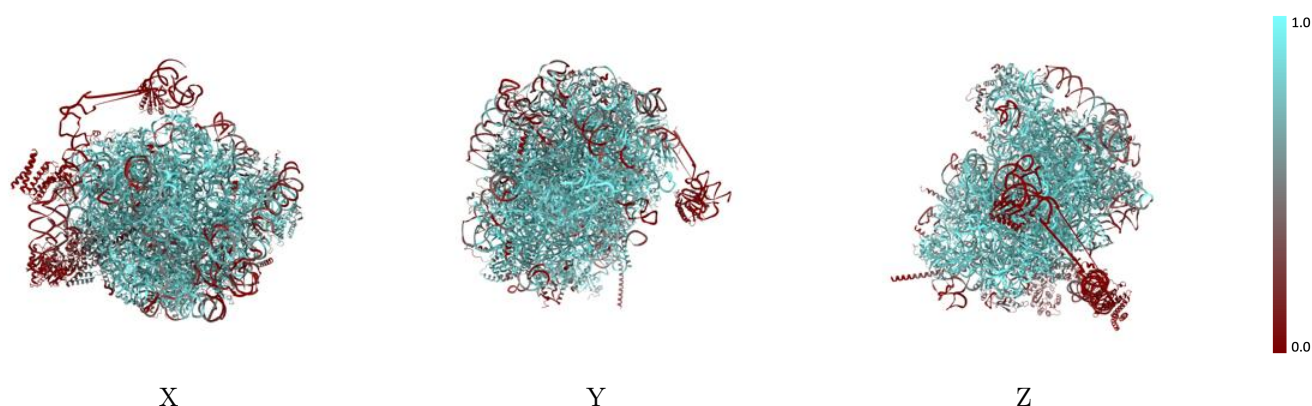
The images above show the 3D surface view of the map at the recommended contour level 0.0195 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



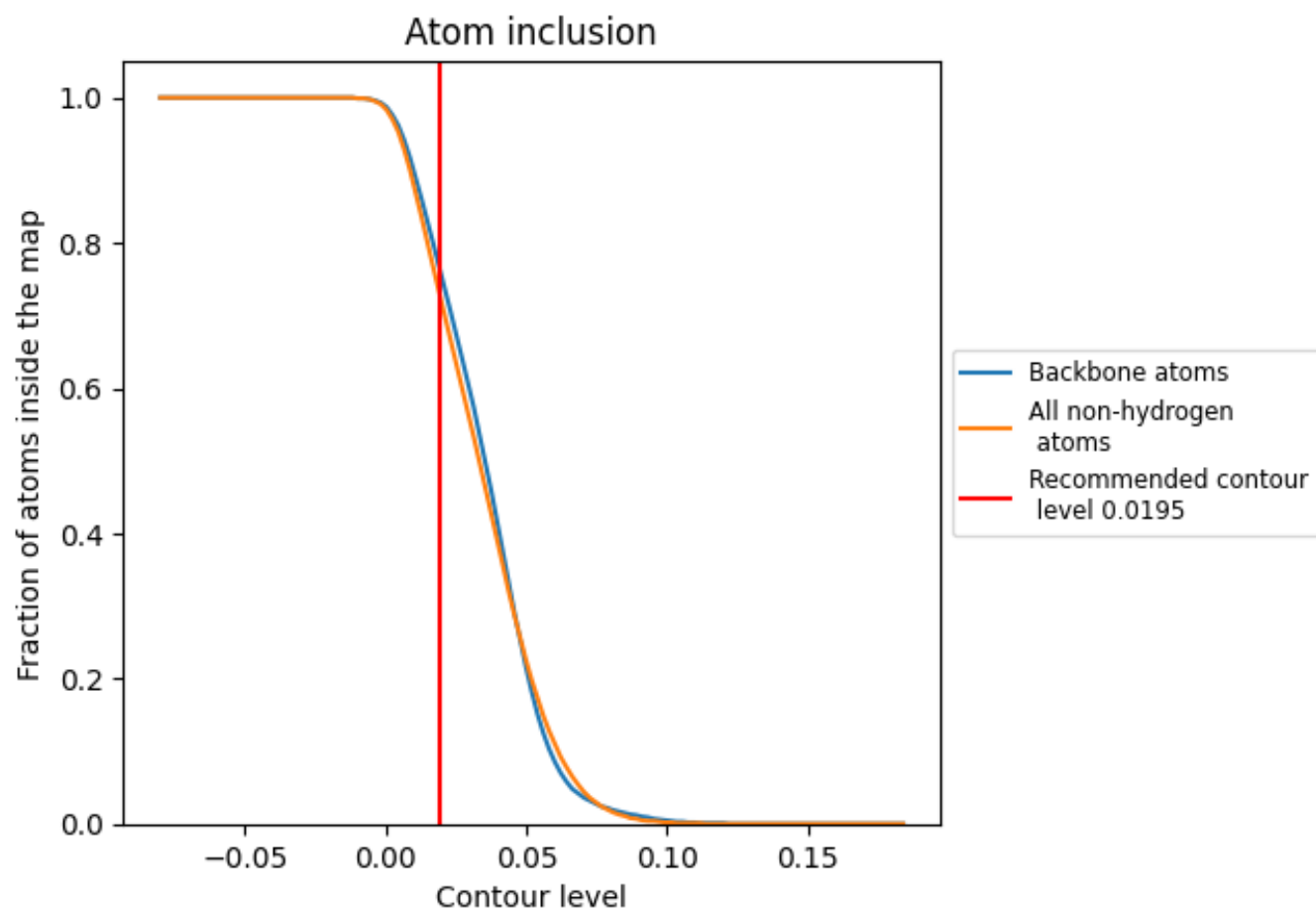
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0195).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 72% 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 (0.0195) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7240	 0.4920
1	 0.0770	 0.0730
5	 0.7880	 0.5050
7	 0.8960	 0.5740
8	 0.8380	 0.5380
A	 0.8680	 0.6060
B	 0.8390	 0.5920
C	 0.8260	 0.5720
D	 0.6920	 0.5080
E	 0.6190	 0.4500
F	 0.8350	 0.5890
G	 0.6570	 0.4850
H	 0.7400	 0.5440
I	 0.7950	 0.5740
J	 0.5490	 0.4640
L	 0.7300	 0.5310
M	 0.7780	 0.5450
N	 0.8880	 0.6030
O	 0.8570	 0.5930
P	 0.8470	 0.5990
Q	 0.8460	 0.5890
R	 0.7220	 0.5320
S	 0.8400	 0.5810
T	 0.7570	 0.5470
U	 0.5620	 0.4520
V	 0.8330	 0.5880
W	 0.8430	 0.5870
X	 0.7680	 0.5490
Y	 0.7880	 0.5690
Z	 0.7370	 0.5280
a	 0.8470	 0.5830
b	 0.6390	 0.4930
c	 0.7830	 0.5550
d	 0.7530	 0.5440
e	 0.8560	 0.6060



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Chain	Atom inclusion	Q-score
f	 0.8760	 0.6040
g	 0.7920	 0.5680
h	 0.7450	 0.5520
i	 0.7290	 0.5280
j	 0.8680	 0.5930
k	 0.5690	 0.4440
l	 0.8110	 0.5650
m	 0.7880	 0.5520
n	 0.6770	 0.5350
o	 0.7450	 0.5580
p	 0.8130	 0.5910
q	 0.0590	 0.1270
r	 0.8130	 0.5590
s	 0.3020	 0.3100
t	 0.0440	 0.2170
u	 0.0200	 0.1110
w	 0.0220	 0.1990
x	 0.2340	 0.2740
z	 0.0120	 0.0950