Full wwPDB EM Validation Report ⓘ

Jul 21, 2021 – 02:29 pm BST

PDB ID	:	7OBR
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 Full wwPDB EM Validation 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 following versions of software and data (see references ⓘ) were used in the production of this report:

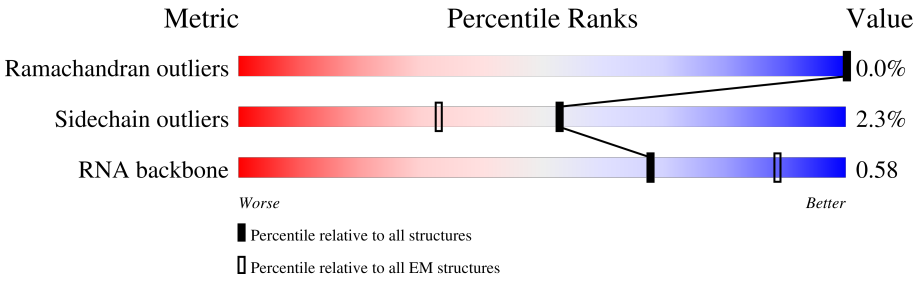
EMDB validation analysis	:	0.0.0.dev84
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.22

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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1	249	98% 79% 20%
2	5	3493	14% 78% 21%
3	7	120	89% 11%
4	8	156	10% 79% 21%
5	A	245	98%
6	B	402	96%
7	C	413	86% 12%
8	D	297	14% 96%

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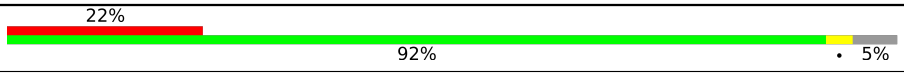
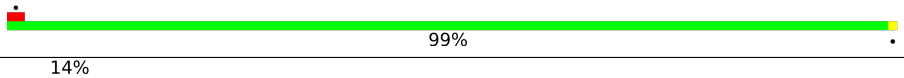
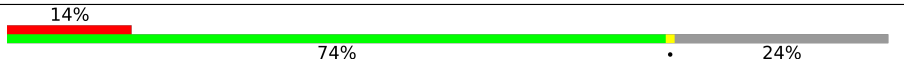
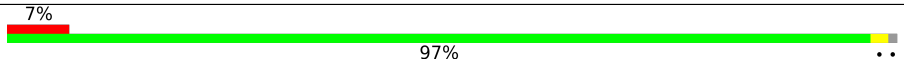
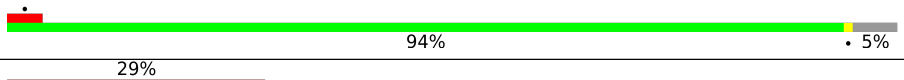
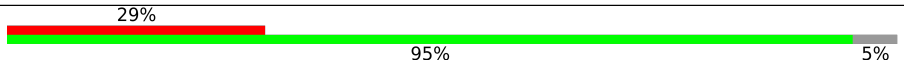
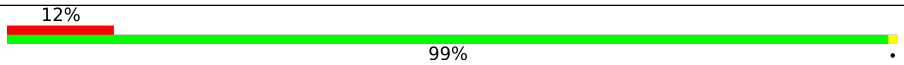
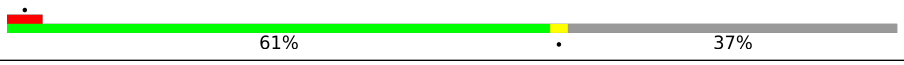
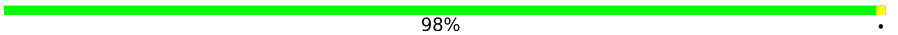
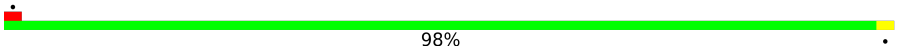
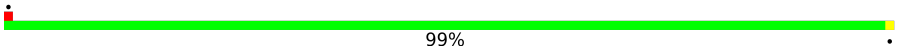
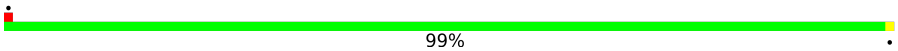
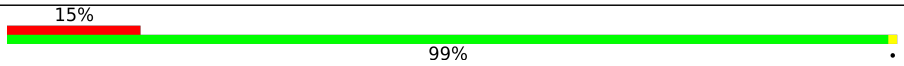
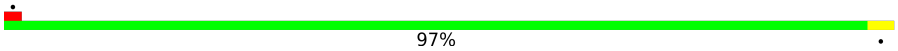
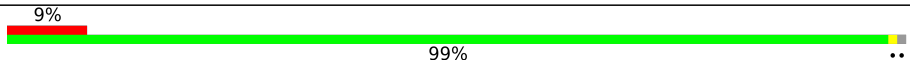
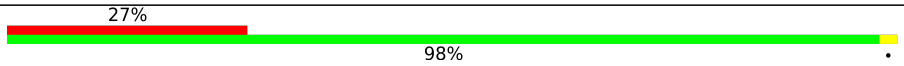
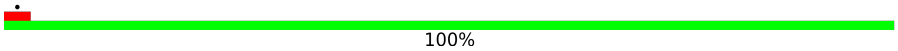
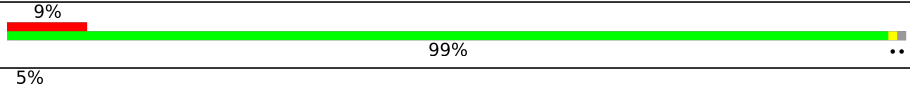
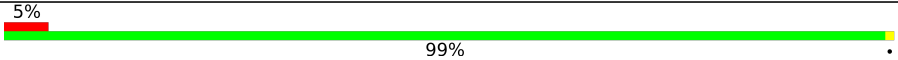
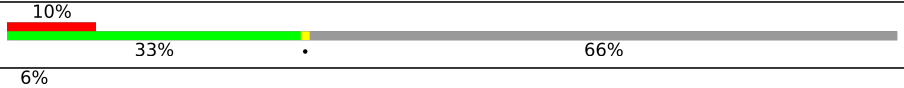
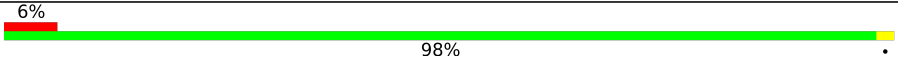
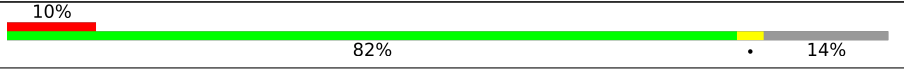
Mol	Chain	Length	Quality of chain
9	E	248	
10	F	225	
11	G	319	
12	H	192	
13	I	214	
14	J	178	
15	L	210	
16	M	218	
17	N	204	
18	O	199	
19	P	153	
20	Q	187	
21	R	180	
22	S	175	
23	T	160	
24	U	99	
25	V	140	
26	W	63	
27	X	156	
28	Y	145	
29	Z	136	
30	a	147	
31	b	223	
32	c	94	
33	d	125	

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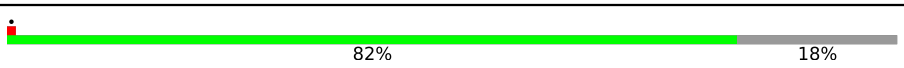
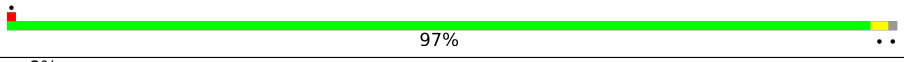
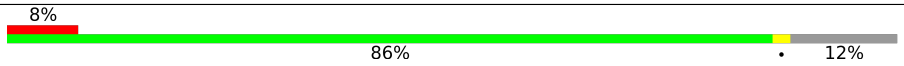
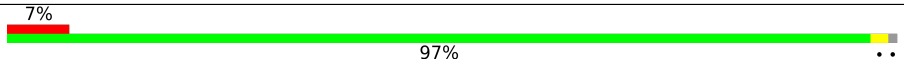
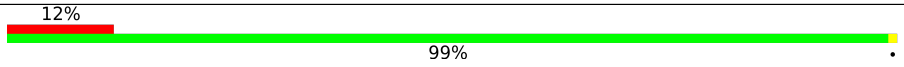
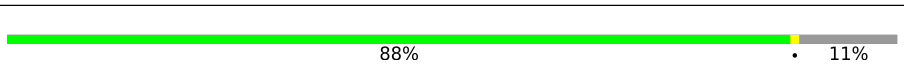
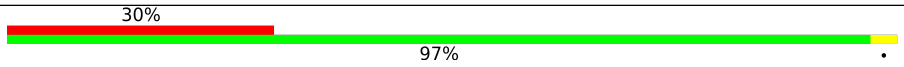
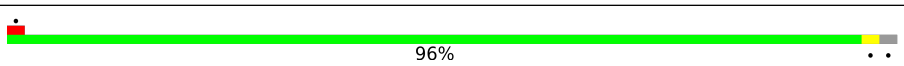
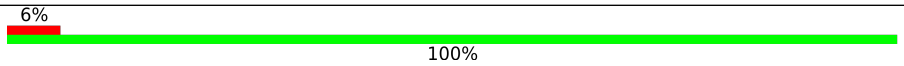
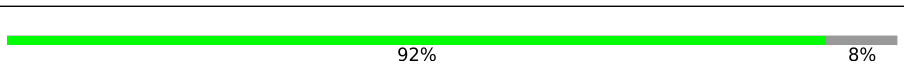
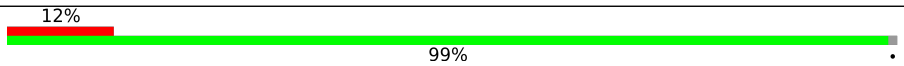
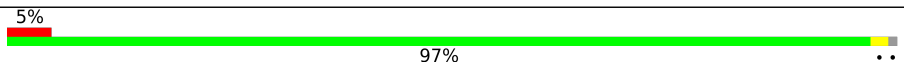
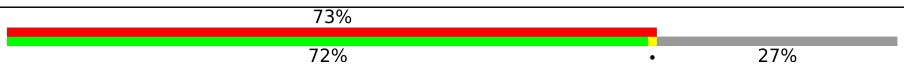
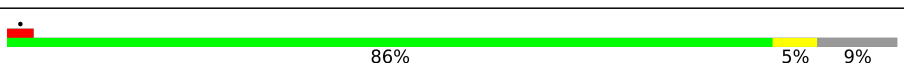
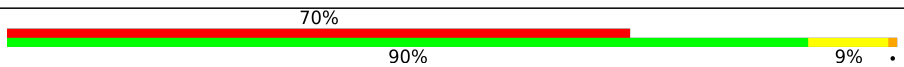
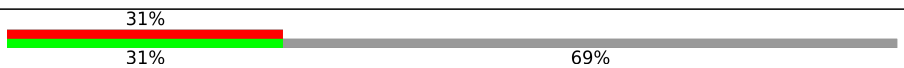
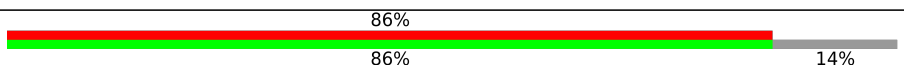
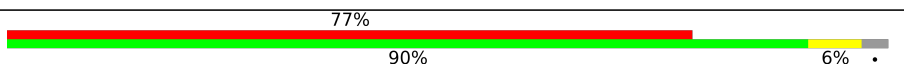
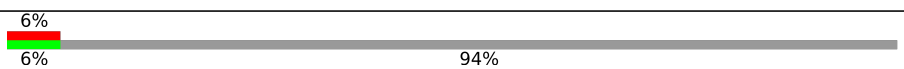
Mol	Chain	Length	Quality of chain
34	e	157	
35	f	110	
36	g	129	
37	h	123	
38	i	102	
39	j	97	
40	k	69	
41	l	51	
42	m	52	
43	n	25	
44	o	105	
45	p	92	
46	q	144	
47	r	137	
48	s	67	
49	t	110	
50	u	622	
51	w	86	
52	x	504	
53	z	671	

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
			Total	C	N	O	P		
1	1	249	5341	2377	977	1738	249	0	0

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

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

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

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

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

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

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

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

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 (three-letter code: MG) (formula: Mg).

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

- Molecule 55 is ZINC ION (three-letter code: 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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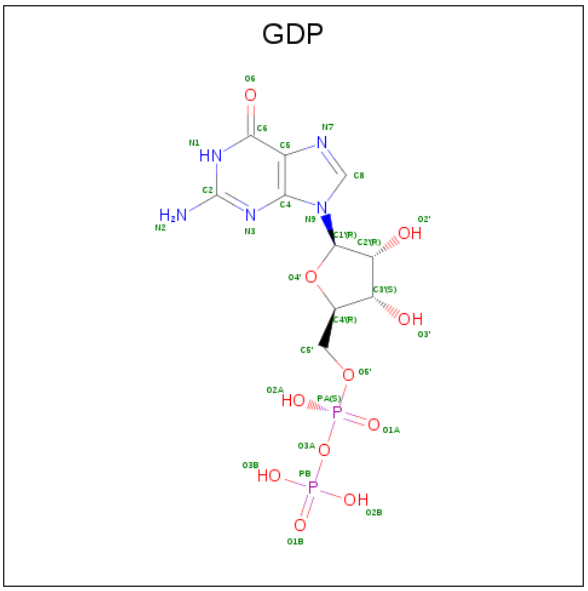
Mol	Chain	Residues	Atoms	AltConf
55	o	1	Total Zn 1 1	0
55	p	1	Total Zn 1 1	0

- Molecule 56 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).



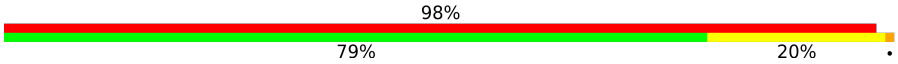
Mol	Chain	Residues	Atoms	AltConf
56	x	1	Total C N O P 28 10 5 11 2	0

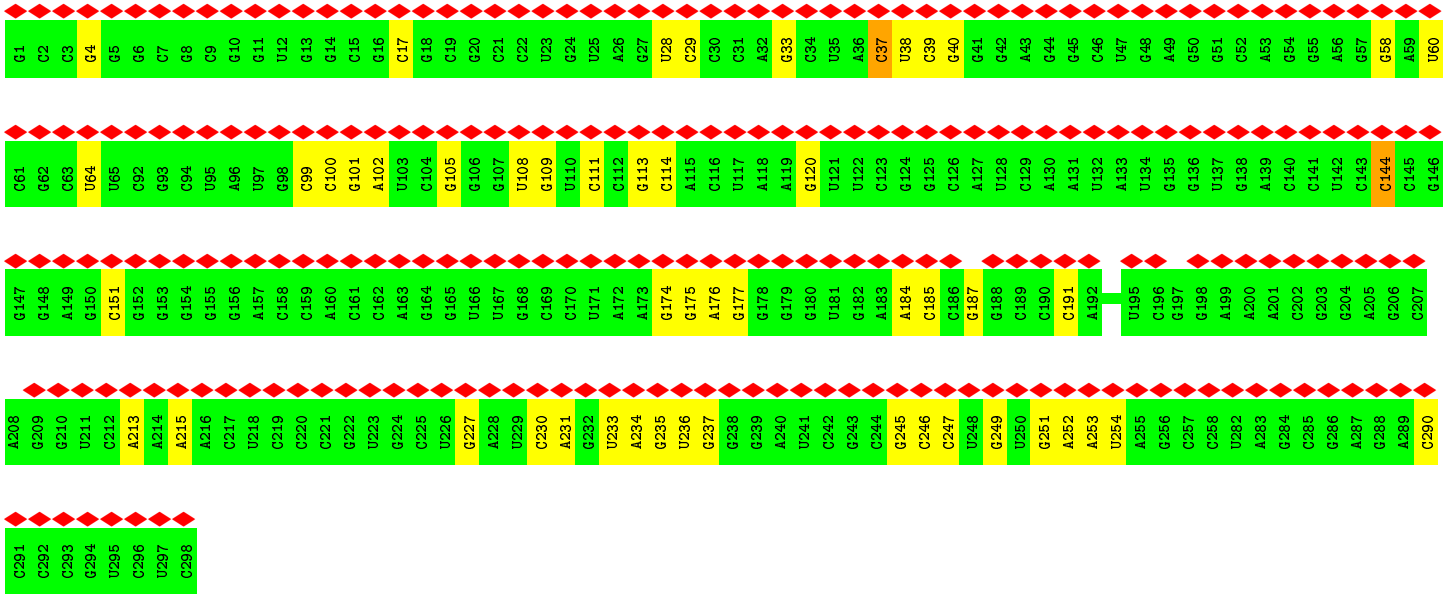
3 Residue-property plots (i)

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: SRP RNA

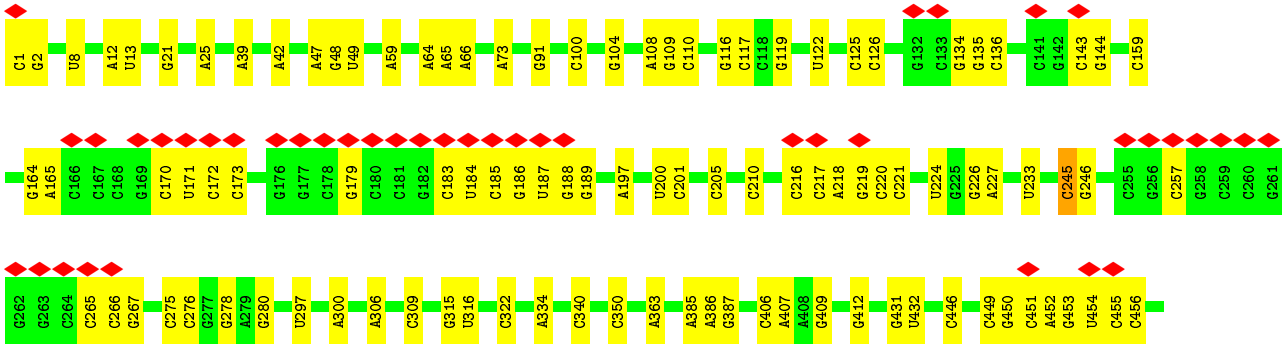
Chain 1:

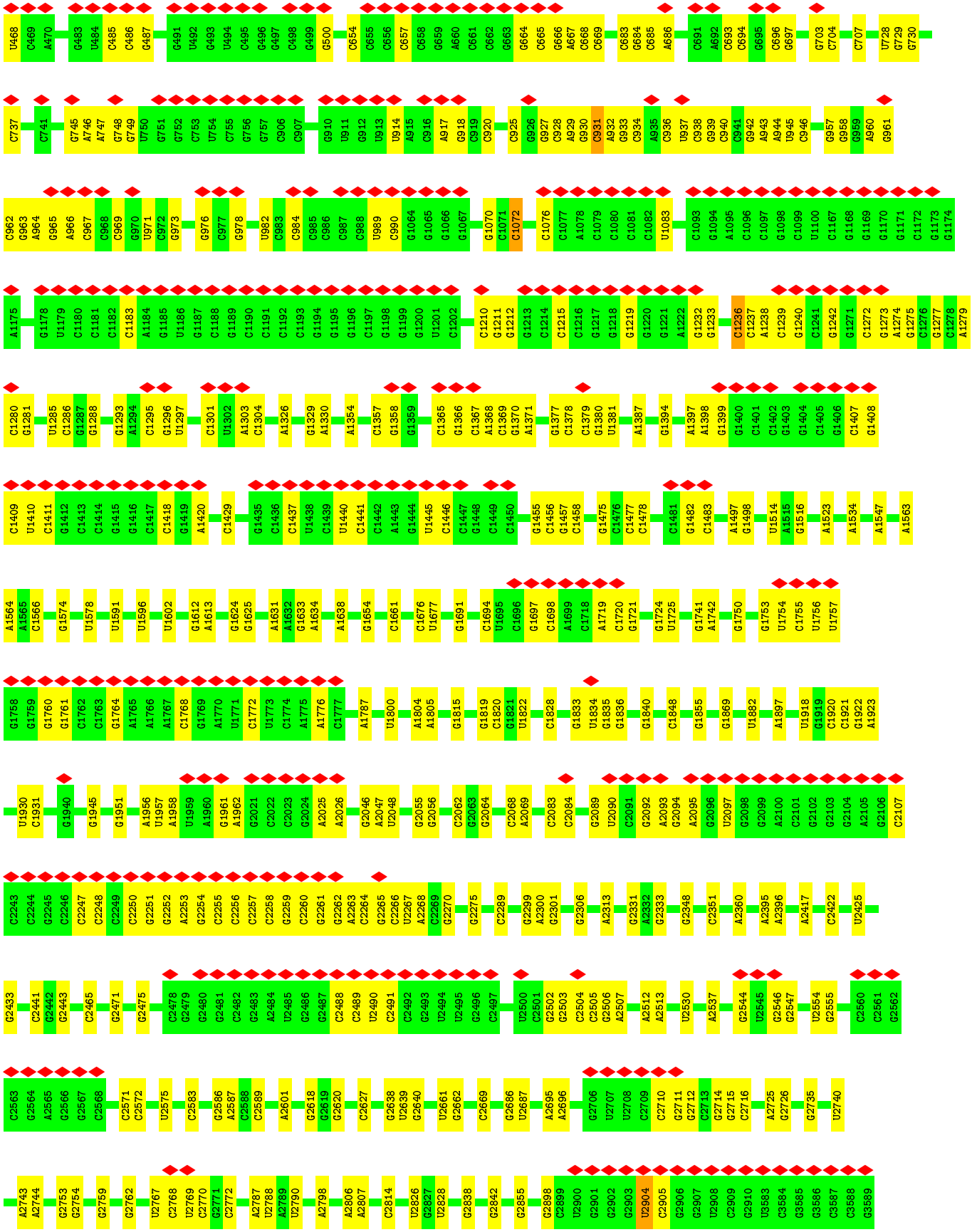




- Molecule 2: 28S rRNA

Chain 5:




U468 C469 A470 G483 U484 C485 C486 G487 G491 U492 G493 U494 C495 G496 G497 C498 G499 G500 C654 C655 C656 C657 C658 G659 A660 C661 C662 G663 G664 C665 G666 A667 C668 C669 C683 G684 C685 A686 C691 A692 C693 C694 G695 C696 G697 G703 C704 C707 U728 G729 G730
C737 C741 G745 A746 A747 G748 G749 U750 G751 G752 C753 U754 C755 G756 C757 C906 C907 G910 U911 G912 U913 U914 A915 C916 A917 G918 C919 C920 C925 G926 G927 C928 A929 G930 G931 A932 G933 C934 A935 C936 U937 C938 G939 C940 G941 G942 A943 A944 U945 C946 G957 G958 G959 A960 G961
C962 G963 A964 G965 A966 C967 G968 C969 G970 U971 G972 G973 G976 G977 G978 U982 C983 C984 C985 C986 G987 G988 U989 C990 G1064 G1065 G1066 G1067 G1070 C1071 C1072 C1076 G1077 A1078 C1079 C1080 C1081 C1082 U1083 C1093 G1094 A1095 C1096 C1097 G1098 C1099 U1100 C1167 G1168 G1169 G1170 G1171 C1172 G1173 G1174
A1175 G1178 U1179 C1180 C1181 C1182 C1183 A1184 G1185 U1186 G1187 C1188 G1189 C1190 C1191 C1192 C1193 G1194 G1195 G1196 C1197 G1198 G1199 G1200 U1201 C1202 C1210 G1211 G1212 G1213 C1214 C1215 C1216 G1217 G1218 G1219 G1220 G1221 A1222 G1232 G1233 C1236 C1237 A1238 C1239 G1240 C1241 G1242 G1271 C1272 G1273 A1274 G1275 C1276 G1277 G1278 A1279
C1280 G1281 U1285 C1286 G1287 G1288 G1293 A1294 C1295 G1296 U1297 C1301 U1302 A1303 C1304 A1326 G1329 A1330 A1354 C1357 G1358 G1359 C1365 G1366 C1367 A1368 C1369 G1370 A1371 G1377 C1378 C1379 G1380 U1381 A1387 G1394 A1397 A1398 G1399 G1400 C1401 C1402 G1403 G1404 C1405 G1406 C1407 G1408
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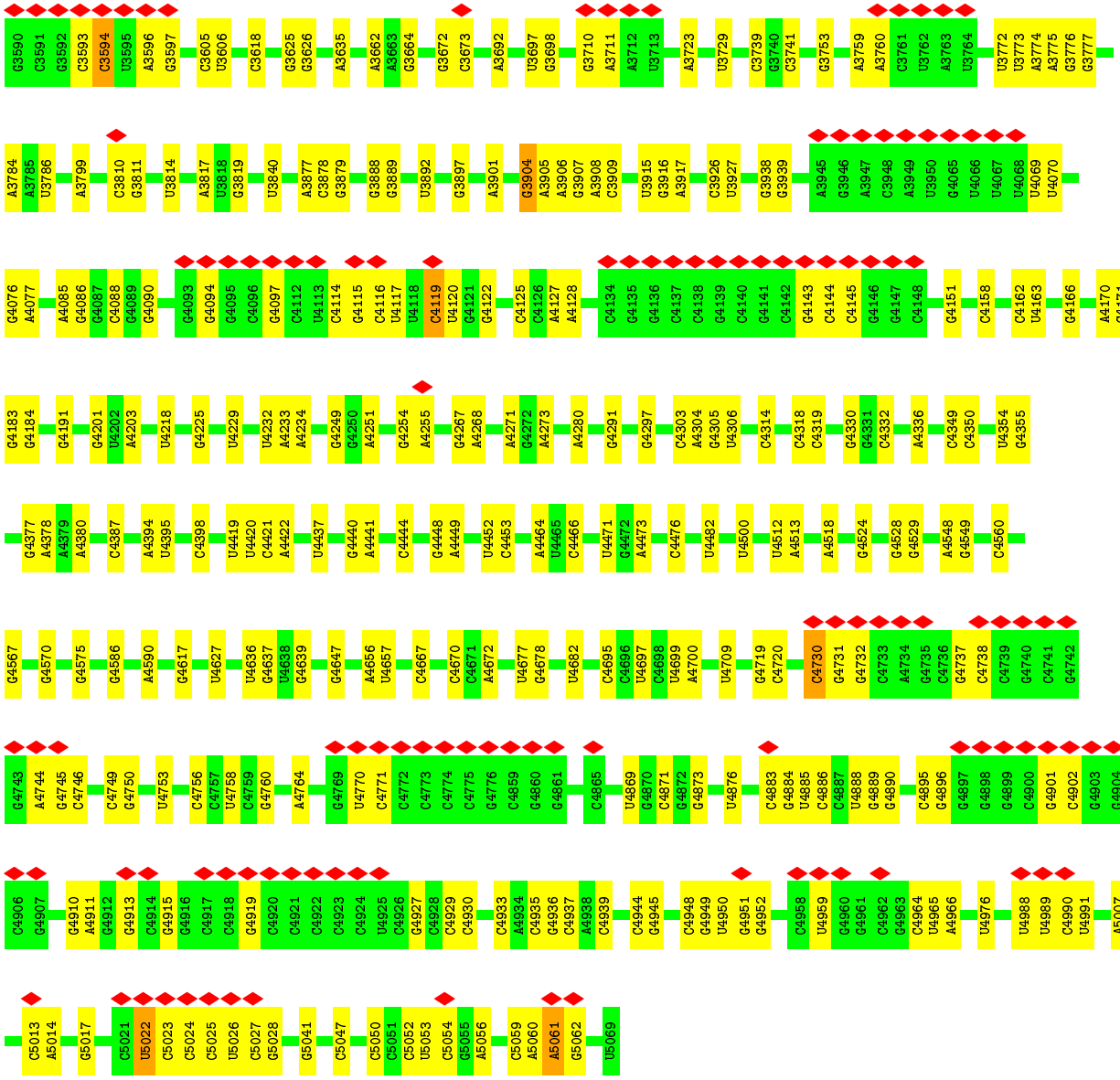
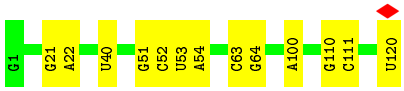
A1564 A1565 C1566 G1574 U1578 U1591 U1596 U1602 G1612 A1613 G1624 G1625 A1631 A1632 G1633 A1634 A1638 G1654 C1661 C1676 U1677 G1691 C1694 U1695 C1696 G1697 C1698 A1699 C1718 A1719 C1720 G1721 G1724 U1725 G1741 A1742 G1750 G1753 U1754 C1755 U1756 U1757
G1758 G1759 G1760 G1761 C1762 C1763 G1764 A1765 A1766 A1767 C1768 G1769 A1770 U1771 C1772 U1773 C1774 A1775 A1776 C1777 A1787 U1800 A1804 A1805 G1815 G1819 C1820 G1821 U1822 C1828 G1833 U1834 G1835 G1836 G1840 C1848 G1855 G1869 U1882 A1897 U1918 G1919 C1920 C1921 G1922 A1923
U1930 C1931 G1940 G1945 G1951 A1956 U1957 A1958 U1959 A1960 G1961 A1962 G2021 C2022 C2023 G2024 A2025 A2026 G2046 A2047 U2048 G2055 G2056 C2062 G2063 G2064 C2068 A2069 C2083 C2084 G2089 U2090 C2091 G2092 A2093 G2094 A2095 G2096 U2097 G2098 G2099 A2100 C2101 G2102 G2103 G2104 A2105 G2106 C2107
C2243 C2244 G2245 C2246 C2247 C2248 C2249 C2250 G2251 G2252 A2253 G2254 C2255 C2256 C2257 C2258 G2259 C2260 G2261 G2262 A2263 C2264 G2265 C2266 U2267 A2268 C2269 G2270 G2275 C2289 G2299 A2300 G2301 G2306 A2313 G2331 A2332 G2333 G2348 C2351 A2360 A2395 A2396 A2417 C2422 U2425
G2433 C2441 G2442 G2443 C2465 G2471 G2475 C2478 G2479 G2480 G2481 C2482 G2483 A2484 U2485 G2486 G2487 C2488 C2489 U2490 C2491 C2492 G2493 U2494 U2495 G2496 C2497 U2500 C2501 G2502 G2503 C2504 C2505 G2506 A2507 A2512 A2513 U2530 A2537 G2544 U2545 G2546 G2547 U2554 G2555 C2560 C2561 G2562
C2563 G2564 A2565 G2566 G2567 C2568 C2571 C2572 U2575 C2583 G2586 A2587 C2588 C2589 A2601 G2618 G2619 G2620 C2627 G2638 U2639 G2640 U2661 G2662 C2669 G2686 U2687 A2695 A2696 G2706 U2707 U2708 C2709 C2710 G2711 G2712 C2713 G2714 G2715 C2716 A2725 G2726 G2735 U2740
A2743 A2744 G2753 G2754 G2759 G2762 U2767 C2768 U2769 C2770 G2771 C2772 A2787 U2788 A2789 U2790 A2798 A2806 A2807 C2814 U2826 G2827 U2828 G2838 G2842 G2855 G2898 C2899 U2900 G2901 G2902 G2903 U2904 C2905 G2906 G2907 U2908 C2909 G2910 U3583 C3584 G3585 G3586 C3587 C3588 G3589



• Molecule 3: 5S ribosomal RNA

Chain 7:

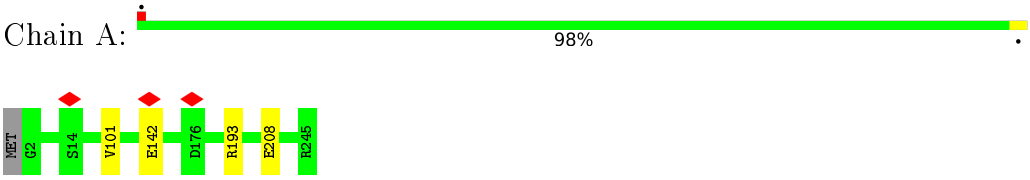


• Molecule 4: 5.8S ribosomal RNA

Chain 8:

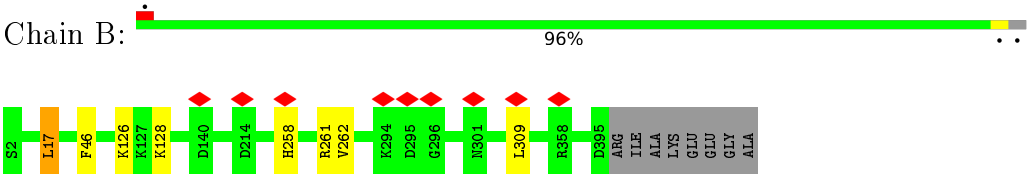
• Molecule 5: 60S ribosomal protein L8

Chain A:



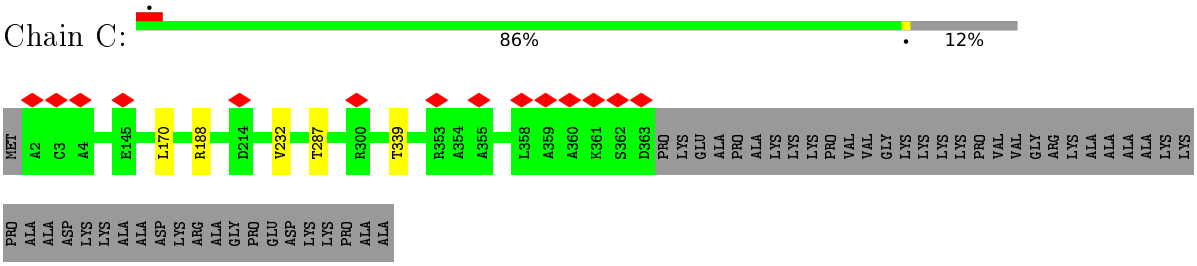
- Molecule 6: uL3

Chain B:



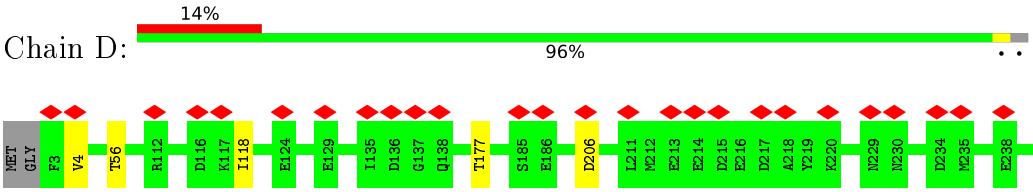
- Molecule 7: 60S ribosomal protein L4

Chain C:



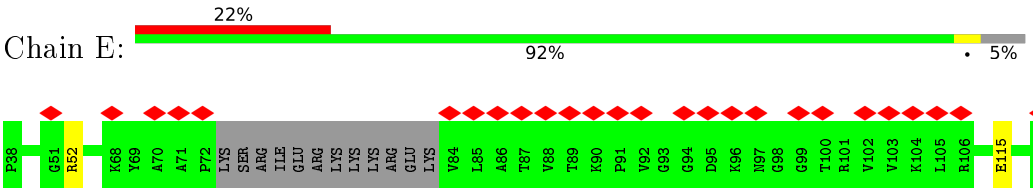
- Molecule 8: 60S ribosomal protein L5

Chain D:



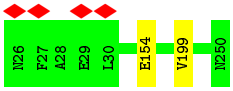
- Molecule 9: 60S ribosomal protein L6

Chain E:



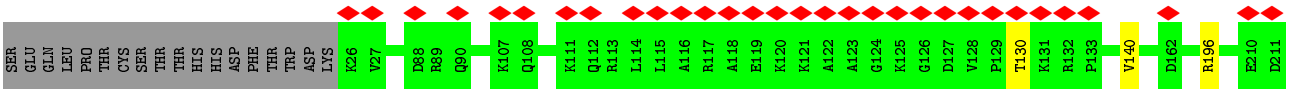
- Molecule 10: uL30

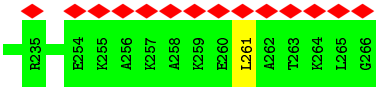
Chain F:



• Molecule 11: 60S ribosomal protein L7a

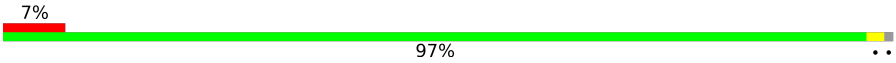
Chain G:

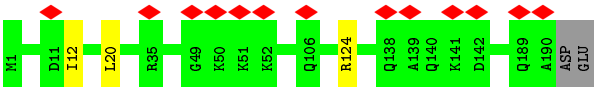




• Molecule 12: 60S ribosomal protein L9

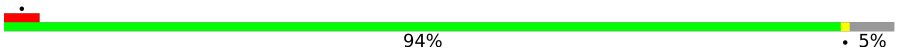
Chain H:

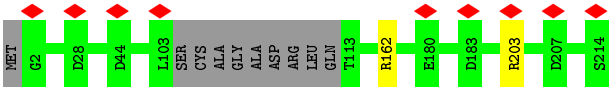




• Molecule 13: 60S ribosomal protein L10

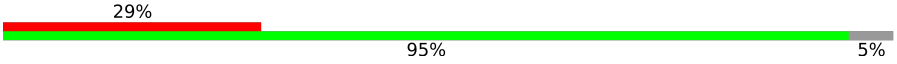
Chain I:

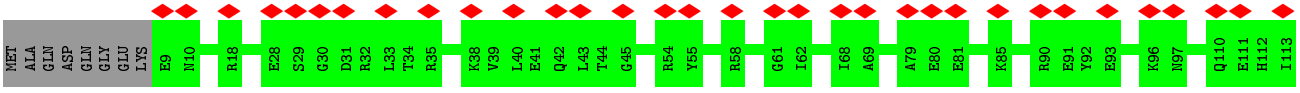


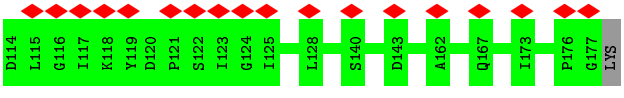


• Molecule 14: Ribosomal protein L11

Chain J:

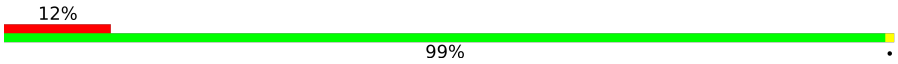


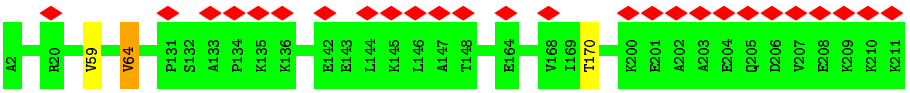




• Molecule 15: 60S ribosomal protein L13

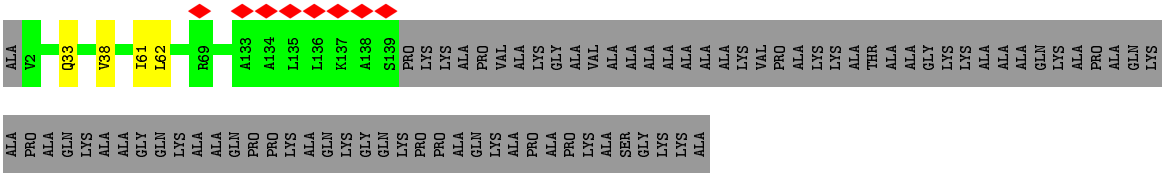
Chain L:





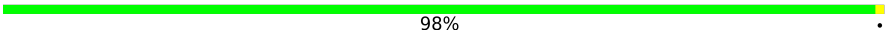
• Molecule 16: 60S ribosomal protein L14

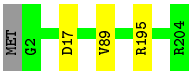
Chain M:



• Molecule 17: Ribosomal protein L15

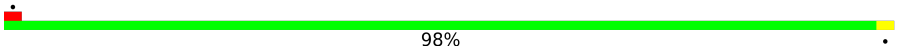
Chain N:

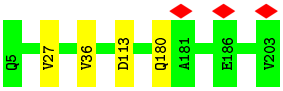




• Molecule 18: 60S ribosomal protein L13a

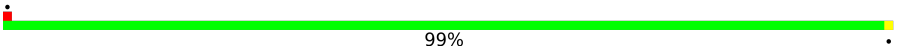
Chain O:

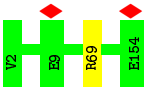




• Molecule 19: uL22

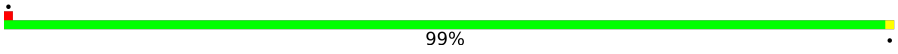
Chain P:

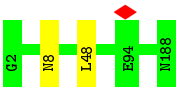




• Molecule 20: eL18

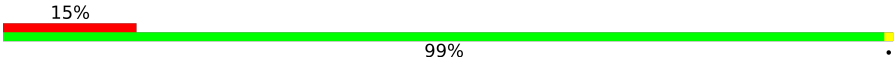
Chain Q:

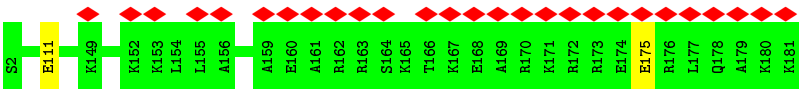




• Molecule 21: 60S RIBOSOMAL PROTEIN EL19

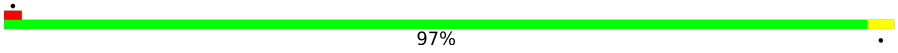
Chain R:

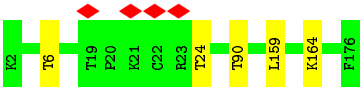




• Molecule 22: 60S ribosomal protein L18a

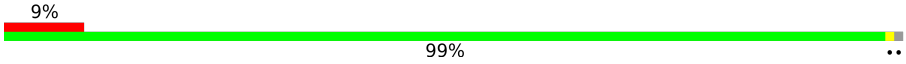
Chain S:

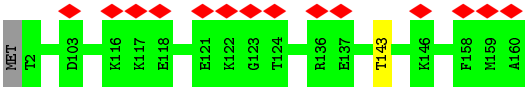




• Molecule 23: eL21

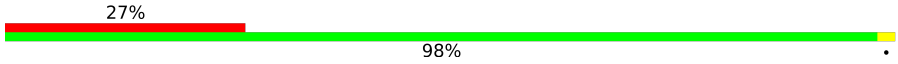
Chain T:

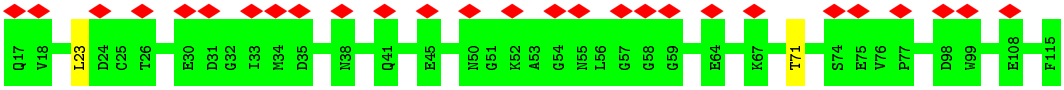




• Molecule 24: Ribosomal protein L22

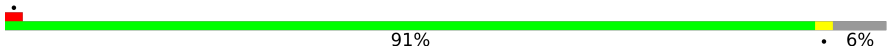
Chain U:

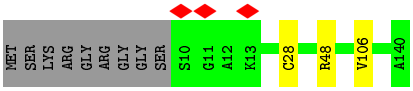




• Molecule 25: Ribosomal protein L23

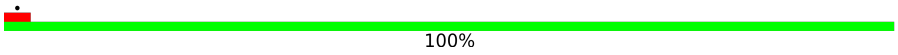
Chain V:





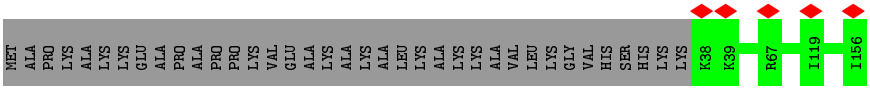
• Molecule 26: Ribosomal protein L24

Chain W:



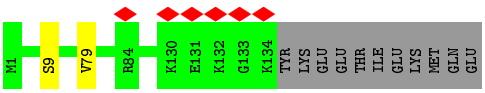
• Molecule 27: uL23

Chain X:



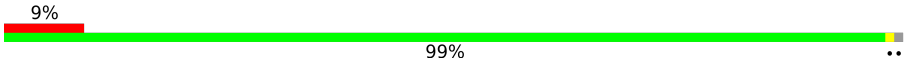
• Molecule 28: Ribosomal protein L26

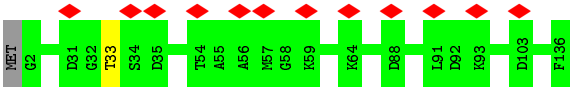
Chain Y:



• Molecule 29: 60S ribosomal protein L27

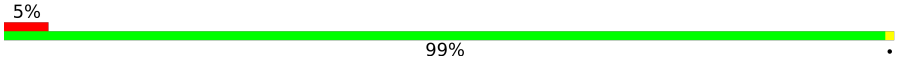
Chain Z:

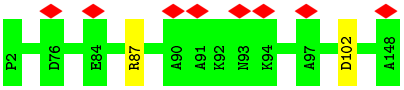




- Molecule 30: uL15

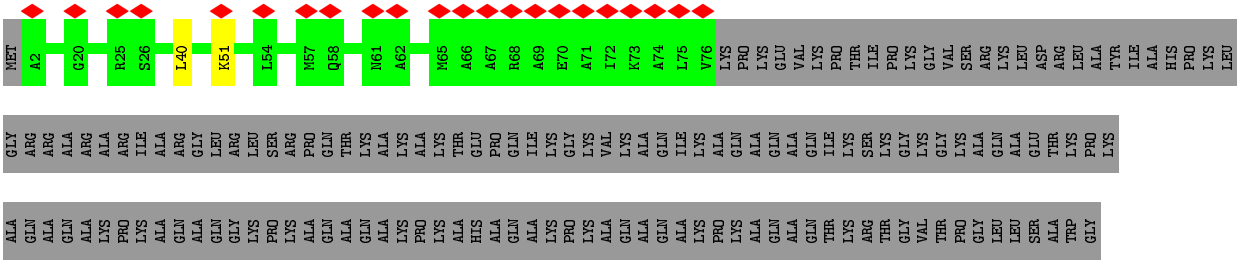
Chain a:





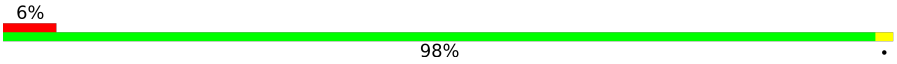
- Molecule 31: 60S ribosomal protein L29

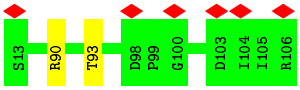
Chain b:



- Molecule 32: 60S ribosomal protein L30

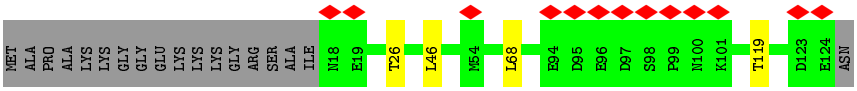
Chain c:





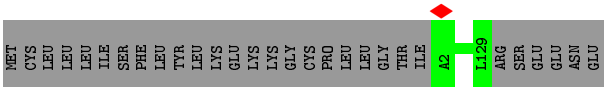
- Molecule 33: eL31

Chain d:



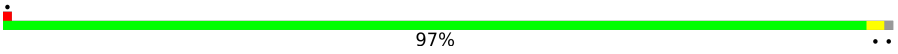
- Molecule 34: eL32

Chain e:



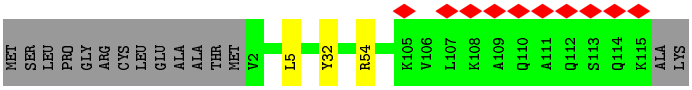
- Molecule 35: eL33

Chain f:



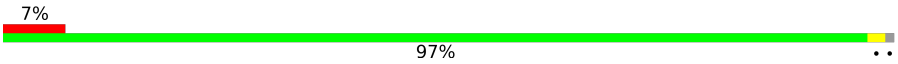
- Molecule 36: 60S ribosomal protein L34

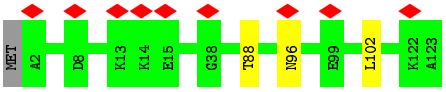
Chain g:



- Molecule 37: uL29

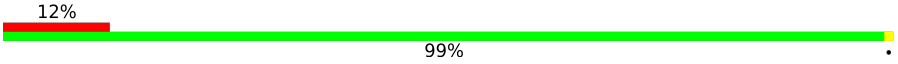
Chain h:

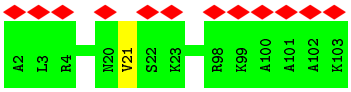




- Molecule 38: 60S ribosomal protein L36

Chain i:



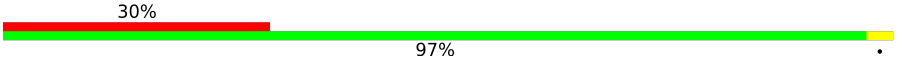


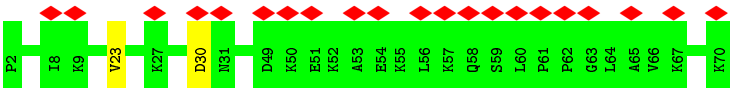
- Molecule 39: Ribosomal protein L37

Chain j:

- Molecule 40: eL38

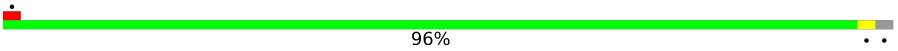
Chain k:

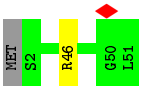




- Molecule 41: eL39

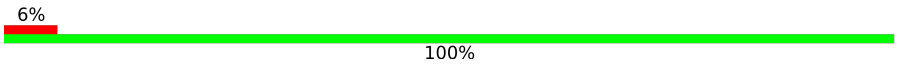
Chain l:

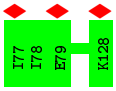




• Molecule 42: 60S RIBOSOMAL PROTEIN EL40

Chain m:



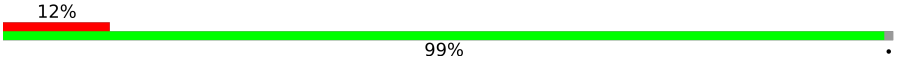


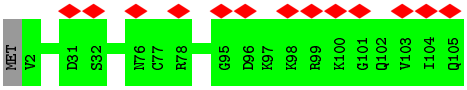
• Molecule 43: 60s ribosomal protein l41

Chain n:

• Molecule 44: eL42

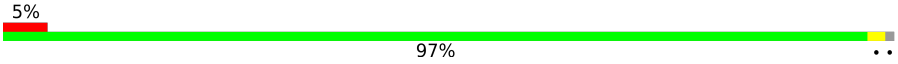
Chain o:

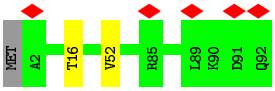




• Molecule 45: eL43

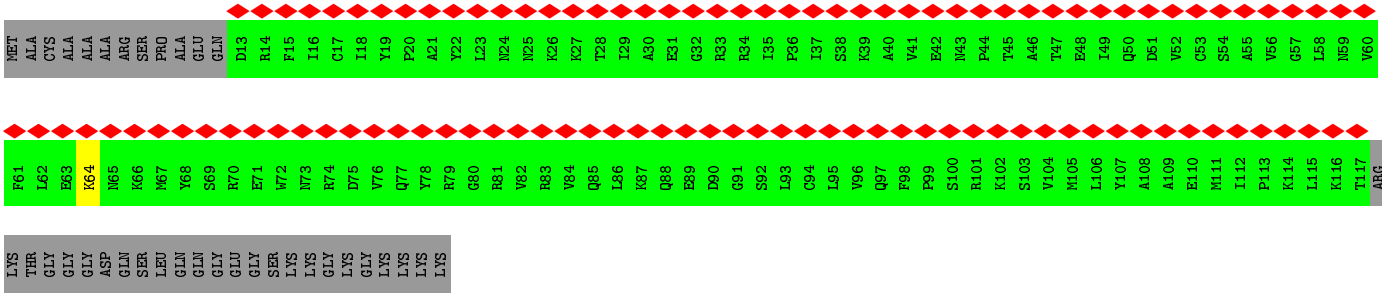
Chain p:





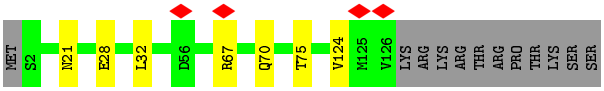
• Molecule 46: Signal recognition particle 19

Chain q:



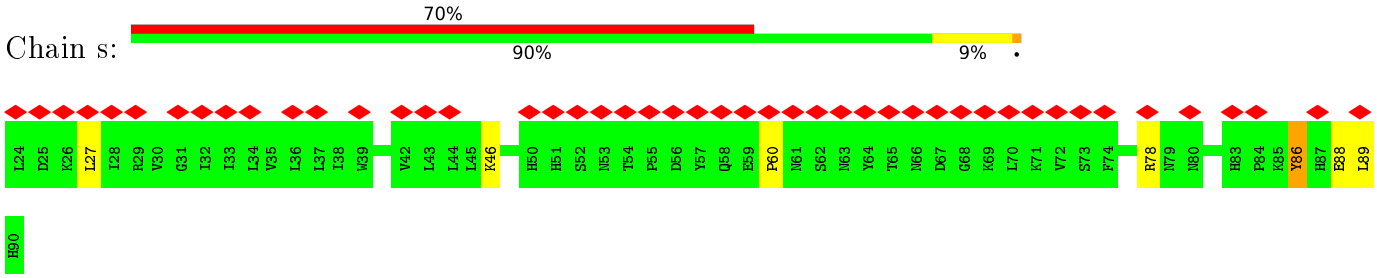
• Molecule 47: eL28

Chain r:



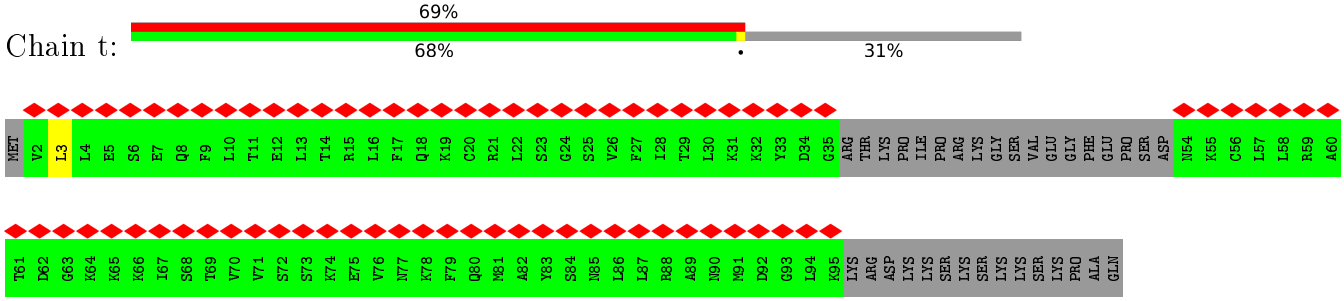
• Molecule 48: Dipeptidyl aminopeptidase B

Chain s:



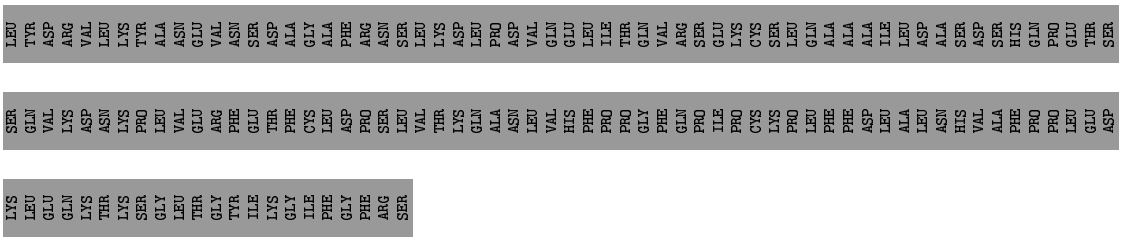
• Molecule 49: Signal recognition particle 14 kDa protein

Chain t:



• Molecule 50: Signal recognition particle subunit SRP68

Chain u:

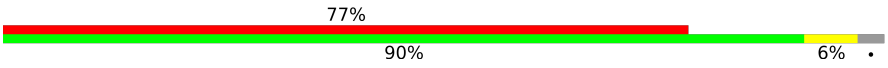


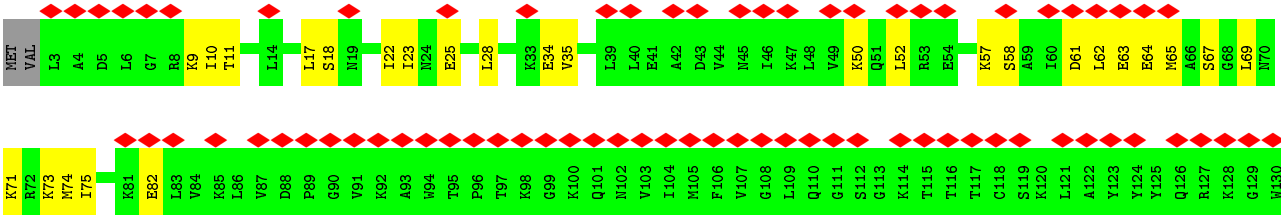
- Molecule 51: Signal recognition particle 9 kDa protein

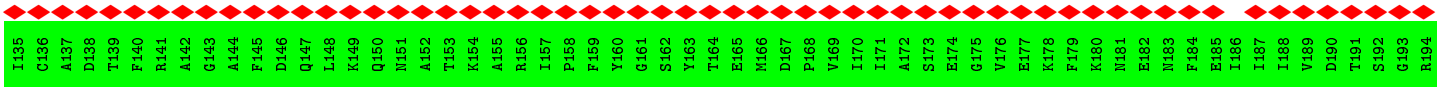
Chain w:

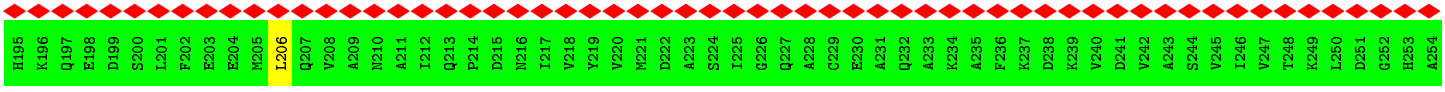
- Molecule 52: Signal recognition particle 54 kDa protein

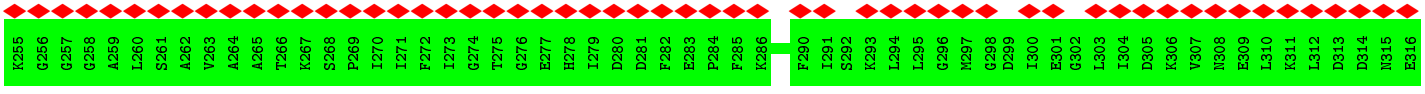
Chain x:

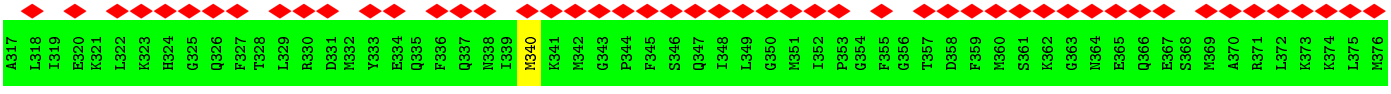


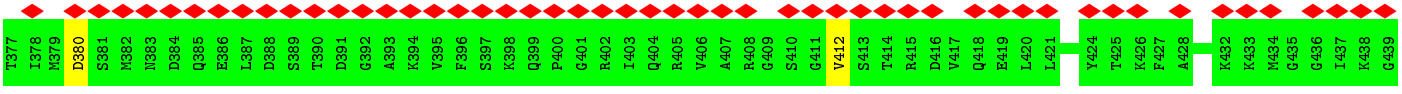


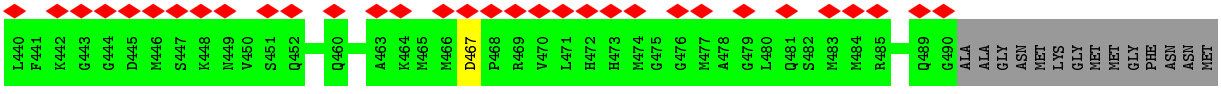






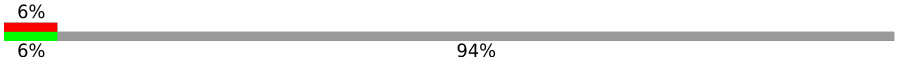






- Molecule 53: Signal recognition particle subunit SRP72

Chain z:



MET ALA SER GLY GLY SER GLY GLY VAL SER VAL PRO ALA LEU TRP SER GLU VAL ASN ARG TYR GLY GLN ASN GLY ASP PHE THR ARG ALA LEU LYS THR VAL ASN LYS ILE LEU GLN ILE ASN LYS ASP ASP VAL THR ALA LEU HIS CYS LYS VAL VAL CYS LEU ILE GLN ASN GLY SER

PHE LYS GLU ALA LEU ASN VAL ILE ASN THR HIS THR LYS VAL LEU ALA ASN ASN SER LEU SER PHE GLU LYS ALA TYR CYS GLU TYR ARG LEU ASN ARG ILE GLU ASN ALA LEU LYS THR ILE GLU SER ALA ASN GLN GLN THR ASP LYS LEU LYS GLU LEU TYR GLY GLN VAL LEU TYR

ARG LEU GLU ARG TYR ASP GLU CYS LEU ALA VAL TYR ARG ASP LEU VAL ARG ASN SER GLN ASP ASP TYR ASP GLU GLU CYS LEU ARG LYS THR ASN LEU SER ALA VAL VAL ALA ALA GLN SER ASN TRP GLU LYS VAL VAL PRO GLU ASN LEU GLY LEU GLN GLU GLY THR HIS GLU LEU CYS TYR

ASN ALA ALA CYS ALA LEU ILE GLY GLN GLY GLN LEU SER GLN ALA MET LYS ILE LEU GLN LYS ALA GLU ASP LEU CYS ARG ARG SER LEU SER GLU ASP SER SER GLY THR GLU GLU ASP PRO GLN ALA GLU LEU ALA ILE ILE HIS GLY GLN MET ALA TYR ILE LEU GLN LEU GLN SER

ARG THR GLU GLU ALA LEU GLN LEU TYR ASN GLN ILE ILE LYS LEU LYS PRO THR ASP VAL GLY LEU LEU ALA VAL ILE ALA ASN ASN ILE ILE THR ILE ASN LYS ASP GLN ASN VAL PHE ASP SER LYS LYS LYS VAL LYS LEU THR ASN ALA GLU GLY ASP LEU LYS

LYS GLN LEU GLN ALA ILE GLU PHE ASN LYS ALA LEU LEU ALA MET TYR THR ASN GLN ALA GLU GLN CYS ARG LYS ILE SER ALA SER LEU GLN SER GLN SER PRO GLU HIS LEU LEU PRO VAL LEU ILE GLN ALA ALA GLN LEU CYS ARG GLU LYS GLN HIS THR LYS ALA ILE GLU LEU

LEU GLN GLU PHE SER ASP GLN HIS PRO GLU ASN ALA ALA GLU ILE LYS LEU THR MET ALA GLN LEU LYS ILE SER GLN LYS ALA CYS LEU ILE LEU ARG SER ILE GLU GLU LEU LYS HIS HIS LYS PRO GLY MET VAL SER ALA LEU VAL THR MET TYR SER HIS GLU GLU

ASP ILE ASP SER ALA ILE GLU VAL PHE THR GLN ALA ILE GLN TRP TYR GLN ASN HIS GLN PRO LYS SER SER ALA HIS LEU SER LEU ILE ARG GLU ALA ASN PHE LYS LEU LYS TYR GLY ARG LYS LYS GLU ALA ILE SER ASP LEU GLU LEU ARG ASN PRO LYS ASP

ILE HIS THR LEU ALA GLN LEU ILE SER ALA TYR SER LEU VAL ASP PRO GLU LYS ALA LYS ALA LEU SER LYS HIS LEU PRO SER SER ASP SER MET SER LEU LYS VAL ASP VAL GLU ALA LEU GLU ASN SER PRO GLY ALA THR TYR ILE ARG LYS LYS GLY GLY LYS VAL ALA GLY ASP

SER GLN PRO LYS GLU GLN GLY GLN GLY ASP LEU LYS LYS LYS LYS LYS LYS LYS | G560 K561 L562 P563 K564 N565 Y566 D567 P568 K569 | V570 | T571 P572 D573 P574 E575 R576 W577 L578 P579 M580 R581 E582 R583 S584 Y585 Y586 R587 G588 R589 K590 K591 G592 K593 K594 K595 D596 Q597 I598 G599 | LYS

GLY THR THR GLN GLY ALA THR ALA ALA GLY GLY ALA SER SER GLU LEU ASP ALA SER LYS THR VAL SER SER PRO PRO THR SER PRO ARG PRO GLY SER ALA ALA THR ALA SER ALA SER THR SER ASN ILE ILE PRO PRO ARG HIS GLN LYS PRO ALA GLY ALA PRO ALA THR LYS LYS LYS GLN GLN

GLN LYS LYS LYS LYS GLY GLY LYS GLY GLY TRP

4 Experimental information (i)

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 ($e^-/Å^2$)	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: ZN, GDP, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	1	0.16	0/5971	0.78	8/9308 (0.1%)
2	5	0.19	0/83726	0.78	48/130593 (0.0%)
3	7	0.16	0/2858	0.73	1/4455 (0.0%)
4	8	0.18	0/3701	0.74	0/5766
5	A	0.24	0/1906	0.43	0/2556
6	B	0.24	0/3216	0.43	0/4311
7	C	0.23	0/2937	0.39	0/3946
8	D	0.24	0/2432	0.40	0/3257
9	E	0.24	0/1936	0.46	0/2600
10	F	0.24	0/1905	0.38	0/2539
11	G	0.24	0/1967	0.41	0/2647
12	H	0.23	0/1535	0.42	0/2063
13	I	0.24	0/1693	0.40	0/2260
14	J	0.23	0/1376	0.42	0/1841
15	L	0.23	0/1734	0.41	0/2317
16	M	0.24	0/1158	0.37	0/1547
17	N	0.23	0/1746	0.40	0/2338
18	O	0.24	0/1671	0.38	0/2234
19	P	0.22	0/1268	0.41	0/1700
20	Q	0.23	0/1530	0.42	0/2041
21	R	0.22	0/1524	0.39	0/2013
22	S	0.24	0/1493	0.41	0/2002
23	T	0.24	0/1326	0.40	0/1770
24	U	0.24	0/822	0.41	0/1103
25	V	0.25	0/993	0.42	0/1332
26	W	0.24	0/541	0.39	0/720
27	X	0.23	0/993	0.39	0/1334
28	Y	0.23	0/1132	0.39	0/1504
29	Z	0.24	0/1130	0.43	0/1507
30	a	0.23	0/1191	0.41	0/1590
31	b	0.23	0/619	0.35	0/818
32	c	0.24	0/742	0.39	0/996

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	d	0.23	0/903	0.42	0/1216
34	e	0.23	0/1071	0.39	0/1429
35	f	0.24	0/895	0.44	0/1198
36	g	0.23	0/916	0.40	0/1220
37	h	0.23	0/1021	0.37	0/1348
38	i	0.23	0/841	0.38	0/1112
39	j	0.23	0/720	0.42	0/952
40	k	0.24	0/575	0.44	0/761
41	l	0.22	0/454	0.39	0/599
42	m	0.23	0/435	0.41	0/575
43	n	0.21	0/223	0.31	0/284
44	o	0.23	0/864	0.43	0/1140
45	p	0.23	0/718	0.41	0/953
46	q	0.23	0/858	0.43	0/1156
47	r	0.23	0/1017	0.44	0/1364
48	s	0.25	0/514	0.51	1/702 (0.1%)
49	t	0.23	0/608	0.39	0/808
50	u	0.24	0/1654	0.40	0/2215
51	w	0.23	0/617	0.41	0/829
52	x	0.24	0/3825	0.40	0/5124
53	z	0.23	0/348	0.39	0/463
All	All	0.21	0/157849	0.67	58/232456 (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 (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	37	C	N1-C2-O2	10.08	124.95	118.90
1	1	37	C	N3-C2-O2	-9.31	115.38	121.90
2	5	931	C	C2-N1-C1'	8.92	128.61	118.80
2	5	931	C	N1-C2-O2	8.76	124.16	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	37	C	C2-N1-C1'	8.34	127.98	118.80
2	5	1072	C	C2-N1-C1'	8.29	127.92	118.80
2	5	1072	C	N1-C2-O2	8.00	123.70	118.90
2	5	931	C	N3-C2-O2	-7.30	116.79	121.90
2	5	5061	A	P-O3'-C3'	7.06	128.18	119.70
2	5	1236	C	N3-C2-O2	-6.99	117.01	121.90
2	5	931	C	C6-N1-C2	-6.72	117.61	120.30
2	5	3594	C	N1-C2-O2	6.62	122.87	118.90
2	5	3594	C	C2-N1-C1'	6.52	125.97	118.80
1	1	37	C	C6-N1-C2	-6.34	117.76	120.30
2	5	5022	U	OP1-P-O3'	6.23	118.92	105.20
2	5	5061	A	OP2-P-O3'	6.20	118.85	105.20
2	5	1072	C	C6-N1-C1'	-6.09	113.49	120.80
2	5	100	C	C2-N1-C1'	5.96	125.36	118.80
2	5	1398	A	O4'-C1'-N9	5.90	112.92	108.20
48	s	60	PRO	N-CA-CB	5.88	110.36	103.30
2	5	1418	C	N1-C2-O2	5.88	122.43	118.90
2	5	931	C	C6-N1-C1'	-5.86	113.77	120.80
2	5	3904	G	P-O3'-C3'	5.83	126.69	119.70
2	5	1072	C	N3-C2-O2	-5.81	117.83	121.90
2	5	2904	U	C2-N1-C1'	5.75	124.60	117.70
2	5	657	C	N3-C2-O2	-5.70	117.91	121.90
3	7	52	C	N3-C2-O2	-5.67	117.93	121.90
2	5	3741	C	N3-C2-O2	-5.67	117.93	121.90
2	5	1236	C	N1-C2-O2	5.63	122.28	118.90
2	5	300	A	C6-N1-C2	-5.60	115.24	118.60
1	1	290	C	N3-C2-O2	-5.50	118.05	121.90
2	5	449	C	C2-N1-C1'	5.49	124.84	118.80
1	1	37	C	C6-N1-C1'	-5.48	114.22	120.80
2	5	931	C	C5-C6-N1	5.46	123.73	121.00
2	5	1458	C	C2-N1-C1'	5.45	124.79	118.80
1	1	144	C	C2-N1-C1'	5.41	124.75	118.80
2	5	449	C	N1-C2-O2	5.39	122.14	118.90
2	5	4119	C	C2-N1-C1'	5.39	124.73	118.80
2	5	3594	C	N3-C2-O2	-5.30	118.19	121.90
2	5	4420	U	C2-N1-C1'	5.27	124.03	117.70
2	5	1458	C	N1-C2-O2	5.27	122.06	118.90
2	5	5022	U	P-O3'-C3'	5.22	125.96	119.70
2	5	245	C	C2-N1-C1'	5.20	124.53	118.80
2	5	3904	G	OP1-P-O3'	5.20	116.64	105.20
2	5	4749	C	N1-C2-O2	5.19	122.01	118.90
2	5	4749	C	C2-N1-C1'	5.18	124.50	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	5	4119	C	N1-C2-O2	5.18	122.01	118.90
2	5	245	C	N1-C2-O2	5.18	122.01	118.90
2	5	2465	C	N3-C2-O2	-5.16	118.29	121.90
1	1	290	C	N1-C2-O2	5.12	121.97	118.90
2	5	3594	C	C6-N1-C2	-5.12	118.25	120.30
2	5	2904	U	N1-C2-O2	5.11	126.38	122.80
2	5	2465	C	N1-C2-O2	5.10	121.96	118.90
2	5	3723	A	C6-N1-C2	-5.06	115.56	118.60
2	5	4420	U	N1-C2-O2	5.06	126.34	122.80
2	5	100	C	N1-C2-O2	5.03	121.92	118.90
2	5	4303	C	C2-N1-C1'	5.00	124.31	118.80
2	5	4730	C	N1-C2-O2	5.00	121.90	118.90

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 (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	29	61
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	19	49
48	s	65/67 (97%)	53 (82%)	11 (17%)	1 (2%)	10	33
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
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 (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	
5	A	187/188 (100%)	183 (98%)	4 (2%)	53	84
6	B	336/347 (97%)	328 (98%)	8 (2%)	49	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	C	302/337 (90%)	297 (98%)	5 (2%)	60	87
8	D	247/250 (99%)	241 (98%)	6 (2%)	49	81
9	E	208/221 (94%)	201 (97%)	7 (3%)	37	71
10	F	194/195 (100%)	192 (99%)	2 (1%)	76	93
11	G	206/273 (76%)	202 (98%)	4 (2%)	57	85
12	H	169/171 (99%)	166 (98%)	3 (2%)	59	86
13	I	174/181 (96%)	172 (99%)	2 (1%)	73	92
14	J	142/149 (95%)	142 (100%)	0	100	100
15	L	176/176 (100%)	173 (98%)	3 (2%)	60	87
16	M	117/160 (73%)	113 (97%)	4 (3%)	37	71
17	N	171/172 (99%)	168 (98%)	3 (2%)	59	86
18	O	171/171 (100%)	167 (98%)	4 (2%)	50	82
19	P	134/134 (100%)	133 (99%)	1 (1%)	84	95
20	Q	163/163 (100%)	161 (99%)	2 (1%)	71	92
21	R	159/159 (100%)	157 (99%)	2 (1%)	69	91
22	S	156/156 (100%)	152 (97%)	4 (3%)	46	79
23	T	139/140 (99%)	138 (99%)	1 (1%)	84	95
24	U	89/89 (100%)	87 (98%)	2 (2%)	52	83
25	V	101/107 (94%)	98 (97%)	3 (3%)	41	75
26	W	55/55 (100%)	55 (100%)	0	100	100
27	X	107/134 (80%)	107 (100%)	0	100	100
28	Y	124/135 (92%)	122 (98%)	2 (2%)	62	88
29	Z	117/118 (99%)	116 (99%)	1 (1%)	78	94
30	a	119/119 (100%)	117 (98%)	2 (2%)	60	87
31	b	62/170 (36%)	60 (97%)	2 (3%)	39	73
32	c	79/79 (100%)	77 (98%)	2 (2%)	47	80
33	d	98/110 (89%)	94 (96%)	4 (4%)	30	64
34	e	114/141 (81%)	114 (100%)	0	100	100
35	f	88/89 (99%)	87 (99%)	1 (1%)	73	92
36	g	98/109 (90%)	95 (97%)	3 (3%)	40	74
37	h	109/110 (99%)	106 (97%)	3 (3%)	43	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
38	i	86/86 (100%)	85 (99%)	1 (1%)	71 92
39	j	73/80 (91%)	72 (99%)	1 (1%)	67 90
40	k	64/64 (100%)	62 (97%)	2 (3%)	40 74
41	l	47/48 (98%)	46 (98%)	1 (2%)	53 84
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%)	44 78
46	q	92/121 (76%)	91 (99%)	1 (1%)	73 92
47	r	109/121 (90%)	103 (94%)	6 (6%)	21 52
48	s	51/64 (80%)	45 (88%)	6 (12%)	5 16
49	t	69/100 (69%)	68 (99%)	1 (1%)	67 90
50	u	171/524 (33%)	169 (99%)	2 (1%)	71 92
51	w	66/77 (86%)	66 (100%)	0	100 100
52	x	409/420 (97%)	377 (92%)	32 (8%)	12 35
53	z	36/570 (6%)	35 (97%)	1 (3%)	43 77
All	All	6420/7823 (82%)	6274 (98%)	146 (2%)	53 82

All (146) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	A	101	VAL
5	A	142	GLU
5	A	193	ARG
5	A	208	GLU
6	B	17	LEU
6	B	46	PHE
6	B	126	LYS
6	B	128	LYS
6	B	258	HIS
6	B	261	ARG
6	B	262	VAL
6	B	309	LEU
7	C	170	LEU
7	C	188	ARG
7	C	232	VAL

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Mol	Chain	Res	Type
7	C	287	THR
7	C	339	THR
8	D	4	VAL
8	D	56	THR
8	D	118	ILE
8	D	177	THR
8	D	206	ASP
8	D	282	GLN
9	E	52	ARG
9	E	115	GLU
9	E	141	THR
9	E	171	VAL
9	E	184	ARG
9	E	228	ILE
9	E	274	THR
10	F	154	GLU
10	F	199	VAL
11	G	130	THR
11	G	140	VAL
11	G	196	ARG
11	G	261	LEU
12	H	12	ILE
12	H	20	LEU
12	H	124	ARG
13	I	162	ARG
13	I	203	ARG
15	L	59	VAL
15	L	64	VAL
15	L	170	THR
16	M	33	GLN
16	M	38	VAL
16	M	61	ILE
16	M	62	LEU
17	N	17	ASP
17	N	89	VAL
17	N	195	ARG
18	O	27	VAL
18	O	36	VAL
18	O	113	ASP
18	O	180	GLN
19	P	69	ARG
20	Q	8	ASN

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Mol	Chain	Res	Type
20	Q	48	LEU
21	R	111	GLU
21	R	175	GLU
22	S	6	THR
22	S	24	THR
22	S	90	THR
22	S	159	LEU
23	T	143	THR
24	U	23	LEU
24	U	71	THR
25	V	28	CYS
25	V	48	ARG
25	V	106	VAL
28	Y	9	SER
28	Y	79	VAL
29	Z	33	THR
30	a	87	ARG
30	a	102	ASP
31	b	40	LEU
31	b	51	LYS
32	c	90	ARG
32	c	93	THR
33	d	26	THR
33	d	46	LEU
33	d	68	LEU
33	d	119	THR
35	f	103	VAL
36	g	5	LEU
36	g	32	TYR
36	g	54	ARG
37	h	88	THR
37	h	96	ASN
37	h	102	LEU
38	i	21	VAL
39	j	13	ASN
40	k	23	VAL
40	k	30	ASP
41	l	46	ARG
45	p	16	THR
45	p	52	VAL
46	q	64	LYS
47	r	28	GLU

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Mol	Chain	Res	Type
47	r	32	LEU
47	r	67	ARG
47	r	70	GLN
47	r	75	THR
47	r	124	VAL
48	s	27	LEU
48	s	46	LYS
48	s	78	ARG
48	s	86	TYR
48	s	88	GLU
48	s	89	LEU
49	t	3	LEU
50	u	64	ASN
50	u	140	LEU
52	x	9	LYS
52	x	10	ILE
52	x	11	THR
52	x	17	LEU
52	x	18	SER
52	x	22	ILE
52	x	23	ILE
52	x	25	GLU
52	x	28	LEU
52	x	34	GLU
52	x	35	VAL
52	x	50	LYS
52	x	52	LEU
52	x	57	LYS
52	x	58	SER
52	x	61	ASP
52	x	62	LEU
52	x	63	GLU
52	x	64	GLU
52	x	65	MET
52	x	67	SER
52	x	69	LEU
52	x	71	LYS
52	x	73	LYS
52	x	74	MET
52	x	75	ILE
52	x	82	GLU
52	x	206	LEU

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Mol	Chain	Res	Type
52	x	340	MET
52	x	380	ASP
52	x	412	VAL
52	x	467	ASP
53	z	570	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
6	B	138	GLN
6	B	167	GLN
6	B	184	GLN
7	C	299	GLN
10	F	112	GLN
12	H	79	ASN
14	J	42	GLN
19	P	25	HIS
20	Q	8	ASN
30	a	66	ASN
30	a	120	GLN
37	h	30	GLN
47	r	6	GLN
49	t	18	GLN
49	t	90	ASN
50	u	13	GLN
52	x	101	GLN
52	x	423	GLN
52	x	488	GLN

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%)

All (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
1	1	33	G
1	1	38	U
1	1	39	C
1	1	40	G
1	1	58	G
1	1	60	U
1	1	64	U
1	1	99	C
1	1	100	C
1	1	101	G
1	1	102	A
1	1	105	G
1	1	108	U
1	1	109	G
1	1	111	C
1	1	113	G
1	1	114	C
1	1	120	G
1	1	144	C
1	1	151	C
1	1	174	G
1	1	175	G
1	1	176	A
1	1	177	G
1	1	184	A
1	1	185	C
1	1	187	G
1	1	191	C
1	1	213	A
1	1	215	A
1	1	227	G
1	1	230	C
1	1	231	A
1	1	233	U
1	1	235	G
1	1	236	U
1	1	237	G
1	1	245	G
1	1	246	C

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Mol	Chain	Res	Type
1	1	247	C
1	1	249	G
1	1	251	G
1	1	252	A
1	1	253	A
1	1	254	U
2	5	2	G
2	5	8	U
2	5	12	A
2	5	13	U
2	5	21	G
2	5	25	A
2	5	39	A
2	5	42	A
2	5	48	G
2	5	49	U
2	5	59	A
2	5	64	A
2	5	65	A
2	5	66	A
2	5	73	A
2	5	91	G
2	5	104	G
2	5	108	A
2	5	109	G
2	5	110	C
2	5	116	G
2	5	117	C
2	5	119	G
2	5	122	U
2	5	126	C
2	5	134	G
2	5	135	G
2	5	136	C
2	5	143	C
2	5	144	G
2	5	159	C
2	5	164	G
2	5	165	A
2	5	171	U
2	5	172	C
2	5	173	C

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Mol	Chain	Res	Type
2	5	179	G
2	5	183	C
2	5	184	U
2	5	185	C
2	5	186	G
2	5	187	U
2	5	188	G
2	5	189	G
2	5	197	A
2	5	200	U
2	5	201	C
2	5	205	C
2	5	210	C
2	5	216	C
2	5	217	C
2	5	218	A
2	5	219	G
2	5	220	C
2	5	221	C
2	5	224	U
2	5	227	A
2	5	233	U
2	5	246	G
2	5	257	C
2	5	265	C
2	5	266	C
2	5	267	G
2	5	276	C
2	5	278	G
2	5	280	G
2	5	297	U
2	5	306	A
2	5	309	C
2	5	315	G
2	5	316	U
2	5	322	C
2	5	334	A
2	5	340	C
2	5	350	C
2	5	363	A
2	5	386	A
2	5	387	G

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Mol	Chain	Res	Type
2	5	407	A
2	5	409	G
2	5	412	G
2	5	431	G
2	5	432	U
2	5	446	C
2	5	450	G
2	5	451	C
2	5	452	A
2	5	453	G
2	5	454	U
2	5	455	C
2	5	456	C
2	5	468	U
2	5	485	C
2	5	486	C
2	5	487	G
2	5	500	G
2	5	654	C
2	5	664	G
2	5	665	C
2	5	666	G
2	5	667	A
2	5	668	C
2	5	669	C
2	5	683	C
2	5	684	G
2	5	685	C
2	5	686	A
2	5	694	C
2	5	696	C
2	5	697	G
2	5	703	G
2	5	704	C
2	5	707	C
2	5	729	G
2	5	730	G
2	5	737	C
2	5	745	G
2	5	746	A
2	5	747	A
2	5	748	G

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Mol	Chain	Res	Type
2	5	749	G
2	5	914	U
2	5	918	G
2	5	920	C
2	5	925	C
2	5	927	G
2	5	928	C
2	5	929	A
2	5	930	G
2	5	931	C
2	5	932	A
2	5	933	G
2	5	934	C
2	5	936	C
2	5	937	U
2	5	938	C
2	5	939	G
2	5	940	C
2	5	942	G
2	5	944	A
2	5	945	U
2	5	946	C
2	5	957	G
2	5	958	G
2	5	960	A
2	5	961	G
2	5	962	C
2	5	963	G
2	5	964	A
2	5	965	G
2	5	966	A
2	5	967	C
2	5	969	C
2	5	971	U
2	5	973	G
2	5	976	G
2	5	978	G
2	5	982	U
2	5	984	C
2	5	989	U
2	5	990	C
2	5	1070	G

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Mol	Chain	Res	Type
2	5	1072	C
2	5	1076	C
2	5	1083	U
2	5	1183	C
2	5	1210	C
2	5	1211	G
2	5	1212	G
2	5	1215	C
2	5	1219	G
2	5	1233	G
2	5	1236	C
2	5	1237	C
2	5	1238	A
2	5	1239	C
2	5	1240	G
2	5	1242	G
2	5	1272	C
2	5	1273	G
2	5	1274	A
2	5	1275	G
2	5	1277	G
2	5	1279	A
2	5	1280	C
2	5	1281	G
2	5	1285	U
2	5	1286	C
2	5	1288	G
2	5	1293	G
2	5	1295	C
2	5	1296	G
2	5	1297	U
2	5	1301	C
2	5	1303	A
2	5	1304	C
2	5	1326	A
2	5	1330	A
2	5	1354	A
2	5	1358	G
2	5	1366	G
2	5	1367	C
2	5	1369	C
2	5	1370	G

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Mol	Chain	Res	Type
2	5	1371	A
2	5	1377	G
2	5	1378	C
2	5	1379	C
2	5	1380	G
2	5	1381	U
2	5	1387	A
2	5	1394	G
2	5	1397	A
2	5	1399	G
2	5	1407	C
2	5	1408	G
2	5	1409	C
2	5	1410	U
2	5	1411	C
2	5	1420	A
2	5	1429	C
2	5	1437	C
2	5	1440	U
2	5	1441	C
2	5	1445	U
2	5	1446	C
2	5	1456	C
2	5	1457	G
2	5	1475	G
2	5	1478	C
2	5	1482	G
2	5	1483	C
2	5	1497	A
2	5	1498	G
2	5	1514	U
2	5	1516	G
2	5	1523	A
2	5	1534	A
2	5	1547	A
2	5	1563	A
2	5	1564	A
2	5	1566	C
2	5	1574	G
2	5	1578	U
2	5	1591	U
2	5	1596	U

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Mol	Chain	Res	Type
2	5	1602	U
2	5	1612	G
2	5	1613	A
2	5	1624	G
2	5	1625	G
2	5	1631	A
2	5	1633	G
2	5	1634	A
2	5	1638	A
2	5	1654	G
2	5	1661	C
2	5	1676	C
2	5	1677	U
2	5	1691	G
2	5	1694	C
2	5	1697	G
2	5	1698	C
2	5	1719	A
2	5	1720	C
2	5	1721	G
2	5	1724	G
2	5	1725	U
2	5	1741	G
2	5	1742	A
2	5	1750	G
2	5	1753	G
2	5	1754	U
2	5	1755	C
2	5	1756	U
2	5	1757	U
2	5	1760	G
2	5	1761	G
2	5	1764	G
2	5	1768	C
2	5	1772	C
2	5	1776	A
2	5	1787	A
2	5	1800	U
2	5	1804	A
2	5	1805	A
2	5	1815	G
2	5	1819	G

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Mol	Chain	Res	Type
2	5	1820	C
2	5	1822	U
2	5	1828	C
2	5	1833	G
2	5	1834	U
2	5	1835	G
2	5	1836	G
2	5	1840	G
2	5	1848	C
2	5	1855	G
2	5	1869	G
2	5	1882	U
2	5	1897	A
2	5	1918	U
2	5	1920	C
2	5	1921	C
2	5	1922	G
2	5	1923	A
2	5	1930	U
2	5	1931	C
2	5	1945	G
2	5	1951	G
2	5	1956	A
2	5	1957	U
2	5	1958	A
2	5	1961	G
2	5	1962	A
2	5	2025	A
2	5	2026	A
2	5	2047	A
2	5	2048	U
2	5	2055	G
2	5	2056	G
2	5	2062	C
2	5	2064	G
2	5	2069	A
2	5	2084	C
2	5	2089	G
2	5	2090	U
2	5	2092	G
2	5	2093	A
2	5	2094	G

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Mol	Chain	Res	Type
2	5	2095	A
2	5	2097	U
2	5	2107	C
2	5	2247	C
2	5	2248	C
2	5	2250	C
2	5	2251	G
2	5	2252	G
2	5	2253	A
2	5	2254	G
2	5	2255	C
2	5	2257	C
2	5	2258	C
2	5	2259	G
2	5	2260	C
2	5	2261	G
2	5	2263	A
2	5	2264	C
2	5	2265	G
2	5	2266	C
2	5	2267	U
2	5	2268	A
2	5	2270	G
2	5	2275	G
2	5	2289	C
2	5	2299	G
2	5	2300	A
2	5	2301	G
2	5	2306	G
2	5	2313	A
2	5	2331	G
2	5	2333	G
2	5	2348	G
2	5	2351	C
2	5	2360	A
2	5	2395	A
2	5	2396	A
2	5	2417	A
2	5	2422	C
2	5	2425	U
2	5	2433	G
2	5	2441	C

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Mol	Chain	Res	Type
2	5	2443	G
2	5	2471	G
2	5	2475	G
2	5	2488	C
2	5	2489	C
2	5	2490	U
2	5	2491	C
2	5	2503	G
2	5	2504	C
2	5	2505	C
2	5	2506	G
2	5	2507	A
2	5	2512	A
2	5	2513	A
2	5	2530	U
2	5	2537	A
2	5	2544	G
2	5	2546	G
2	5	2547	G
2	5	2554	U
2	5	2555	G
2	5	2571	C
2	5	2572	C
2	5	2575	U
2	5	2583	C
2	5	2586	G
2	5	2587	A
2	5	2589	C
2	5	2601	A
2	5	2618	G
2	5	2620	G
2	5	2627	C
2	5	2638	G
2	5	2640	G
2	5	2661	U
2	5	2662	G
2	5	2669	C
2	5	2686	G
2	5	2687	U
2	5	2695	A
2	5	2696	A
2	5	2710	C

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Mol	Chain	Res	Type
2	5	2711	G
2	5	2712	G
2	5	2714	G
2	5	2715	G
2	5	2716	C
2	5	2725	A
2	5	2726	G
2	5	2735	G
2	5	2740	U
2	5	2743	A
2	5	2744	A
2	5	2753	G
2	5	2754	G
2	5	2759	G
2	5	2762	G
2	5	2767	U
2	5	2768	C
2	5	2769	U
2	5	2770	C
2	5	2772	C
2	5	2787	A
2	5	2788	U
2	5	2790	U
2	5	2798	A
2	5	2806	A
2	5	2807	A
2	5	2814	C
2	5	2826	U
2	5	2828	U
2	5	2838	G
2	5	2842	G
2	5	2855	G
2	5	2898	G
2	5	2904	U
2	5	2905	C
2	5	3593	C
2	5	3594	C
2	5	3596	A
2	5	3597	G
2	5	3605	C
2	5	3606	U
2	5	3618	C

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Mol	Chain	Res	Type
2	5	3625	G
2	5	3626	G
2	5	3635	A
2	5	3662	A
2	5	3664	G
2	5	3672	G
2	5	3673	C
2	5	3692	A
2	5	3698	G
2	5	3710	G
2	5	3711	A
2	5	3729	U
2	5	3739	C
2	5	3753	G
2	5	3759	A
2	5	3760	A
2	5	3772	U
2	5	3773	U
2	5	3774	A
2	5	3775	A
2	5	3776	G
2	5	3777	G
2	5	3784	A
2	5	3786	U
2	5	3799	A
2	5	3810	C
2	5	3811	G
2	5	3814	U
2	5	3817	A
2	5	3819	G
2	5	3840	U
2	5	3877	A
2	5	3878	C
2	5	3879	G
2	5	3889	G
2	5	3892	U
2	5	3897	G
2	5	3901	A
2	5	3905	A
2	5	3906	A
2	5	3907	G
2	5	3908	A

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Mol	Chain	Res	Type
2	5	3909	C
2	5	3915	U
2	5	3916	G
2	5	3917	A
2	5	3926	C
2	5	3927	U
2	5	3938	G
2	5	3939	G
2	5	4069	U
2	5	4070	U
2	5	4076	G
2	5	4077	A
2	5	4085	A
2	5	4086	G
2	5	4088	C
2	5	4090	G
2	5	4094	G
2	5	4097	G
2	5	4114	C
2	5	4115	G
2	5	4116	C
2	5	4117	U
2	5	4119	C
2	5	4120	U
2	5	4122	G
2	5	4125	C
2	5	4127	A
2	5	4128	A
2	5	4143	G
2	5	4144	C
2	5	4145	C
2	5	4151	G
2	5	4158	C
2	5	4162	C
2	5	4163	U
2	5	4166	G
2	5	4170	A
2	5	4171	C
2	5	4183	G
2	5	4184	G
2	5	4191	G
2	5	4201	G

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Mol	Chain	Res	Type
2	5	4203	A
2	5	4218	U
2	5	4225	G
2	5	4229	U
2	5	4233	A
2	5	4234	A
2	5	4249	G
2	5	4251	A
2	5	4254	G
2	5	4255	A
2	5	4267	G
2	5	4268	A
2	5	4271	A
2	5	4273	A
2	5	4280	A
2	5	4291	G
2	5	4297	G
2	5	4304	A
2	5	4305	G
2	5	4306	U
2	5	4314	C
2	5	4318	C
2	5	4319	C
2	5	4330	G
2	5	4332	C
2	5	4336	A
2	5	4349	C
2	5	4350	C
2	5	4354	U
2	5	4355	G
2	5	4377	G
2	5	4378	A
2	5	4380	A
2	5	4387	C
2	5	4394	A
2	5	4395	U
2	5	4398	C
2	5	4419	U
2	5	4421	C
2	5	4422	A
2	5	4437	U
2	5	4440	G

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Mol	Chain	Res	Type
2	5	4441	A
2	5	4444	C
2	5	4448	G
2	5	4449	A
2	5	4452	U
2	5	4453	C
2	5	4464	A
2	5	4466	C
2	5	4471	U
2	5	4473	A
2	5	4476	C
2	5	4482	U
2	5	4500	U
2	5	4512	U
2	5	4513	A
2	5	4518	A
2	5	4524	G
2	5	4528	G
2	5	4529	G
2	5	4548	A
2	5	4549	G
2	5	4560	C
2	5	4567	G
2	5	4570	G
2	5	4575	G
2	5	4586	G
2	5	4590	A
2	5	4617	G
2	5	4627	U
2	5	4636	U
2	5	4637	G
2	5	4639	G
2	5	4647	G
2	5	4656	A
2	5	4657	U
2	5	4667	C
2	5	4670	C
2	5	4672	A
2	5	4677	U
2	5	4678	G
2	5	4682	U
2	5	4695	C

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Mol	Chain	Res	Type
2	5	4697	U
2	5	4700	A
2	5	4709	U
2	5	4719	G
2	5	4720	C
2	5	4730	C
2	5	4731	G
2	5	4732	G
2	5	4737	G
2	5	4738	C
2	5	4744	A
2	5	4745	G
2	5	4746	C
2	5	4750	G
2	5	4753	U
2	5	4756	C
2	5	4758	U
2	5	4760	G
2	5	4764	A
2	5	4770	U
2	5	4771	C
2	5	4869	U
2	5	4871	C
2	5	4873	G
2	5	4876	U
2	5	4883	C
2	5	4884	G
2	5	4886	C
2	5	4889	G
2	5	4890	G
2	5	4895	C
2	5	4896	G
2	5	4901	G
2	5	4902	C
2	5	4910	G
2	5	4911	A
2	5	4913	G
2	5	4915	G
2	5	4919	G
2	5	4927	G
2	5	4929	C
2	5	4930	C

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Mol	Chain	Res	Type
2	5	4933	C
2	5	4936	G
2	5	4937	C
2	5	4939	C
2	5	4944	C
2	5	4945	G
2	5	4948	C
2	5	4949	G
2	5	4950	U
2	5	4951	G
2	5	4952	G
2	5	4959	U
2	5	4964	C
2	5	4965	U
2	5	4966	A
2	5	4976	U
2	5	4988	U
2	5	4989	U
2	5	4990	C
2	5	4991	U
2	5	5007	A
2	5	5013	C
2	5	5014	A
2	5	5017	G
2	5	5023	C
2	5	5024	C
2	5	5025	C
2	5	5026	U
2	5	5027	C
2	5	5028	G
2	5	5041	G
2	5	5047	C
2	5	5050	C
2	5	5052	C
2	5	5053	U
2	5	5054	C
2	5	5056	A
2	5	5060	A
2	5	5061	A
2	5	5062	G
3	7	21	G
3	7	22	A

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Mol	Chain	Res	Type
3	7	40	U
3	7	51	G
3	7	53	U
3	7	54	A
3	7	63	C
3	7	64	G
3	7	100	A
3	7	110	G
3	7	111	C
3	7	120	U
4	8	2	G
4	8	23	C
4	8	34	U
4	8	35	C
4	8	38	U
4	8	39	G
4	8	59	A
4	8	62	A
4	8	63	U
4	8	75	G
4	8	77	A
4	8	79	G
4	8	80	A
4	8	81	C
4	8	82	A
4	8	83	C
4	8	84	A
4	8	85	U
4	8	86	U
4	8	87	G
4	8	94	G
4	8	103	A
4	8	105	C
4	8	109	C
4	8	110	U
4	8	111	U
4	8	114	G
4	8	123	U
4	8	125	C
4	8	126	C
4	8	127	U
4	8	128	C

All (90) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	37	C
1	1	38	U
1	1	39	C
1	1	234	A
1	1	236	U
2	5	1	C
2	5	12	A
2	5	47	A
2	5	48	G
2	5	125	C
2	5	134	G
2	5	170	C
2	5	187	U
2	5	216	C
2	5	218	A
2	5	226	G
2	5	245	C
2	5	265	C
2	5	275	C
2	5	385	A
2	5	406	C
2	5	451	C
2	5	454	U
2	5	684	G
2	5	693	C
2	5	728	U
2	5	917	A
2	5	930	G
2	5	932	A
2	5	943	A
2	5	957	G
2	5	965	G
2	5	1211	G
2	5	1232	G
2	5	1236	C
2	5	1238	A
2	5	1239	C
2	5	1296	G
2	5	1329	G
2	5	1357	C
2	5	1365	C
2	5	1368	A

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Mol	Chain	Res	Type
2	5	1380	G
2	5	1407	C
2	5	1440	U
2	5	1455	G
2	5	1477	C
2	5	1633	G
2	5	1720	C
2	5	1804	A
2	5	1835	G
2	5	2046	G
2	5	2068	C
2	5	2083	C
2	5	2089	G
2	5	2093	A
2	5	2256	C
2	5	2257	C
2	5	2260	C
2	5	2262	G
2	5	2265	G
2	5	2502	G
2	5	2506	G
2	5	2639	U
2	5	2661	U
2	5	2695	A
2	5	3625	G
2	5	3697	U
2	5	3888	G
2	5	3904	G
2	5	4069	U
2	5	4119	C
2	5	4170	A
2	5	4232	U
2	5	4448	G
2	5	4528	G
2	5	4656	A
2	5	4699	U
2	5	4719	G
2	5	4885	U
2	5	4888	U
2	5	4889	G
2	5	4935	C
2	5	4948	C

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Mol	Chain	Res	Type
2	5	5022	U
2	5	5027	C
2	5	5059	C
2	5	5060	A
2	5	5061	A
4	8	124	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 monosaccharides 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	-	24,30,30	1.19	2 (8%)	31,47,47	2.00	8 (25%)

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	-	-	0/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	x	601	GDP	C6-C5	4.22	1.48	1.41
56	x	601	GDP	C5-C4	2.45	1.47	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
56	x	601	GDP	C2-N3-C4	4.93	120.99	115.36
56	x	601	GDP	C6-N1-C2	4.00	122.29	115.93
56	x	601	GDP	C5-C6-N1	-3.97	118.01	123.43
56	x	601	GDP	PA-O3A-PB	-3.71	120.09	132.83
56	x	601	GDP	C6-C5-C4	-3.71	117.26	120.80
56	x	601	GDP	N3-C2-N1	-3.25	122.89	127.22
56	x	601	GDP	C3'-C2'-C1'	3.13	105.69	100.98
56	x	601	GDP	C4-C5-N7	-2.76	106.52	109.40

There are no chirality outliers.

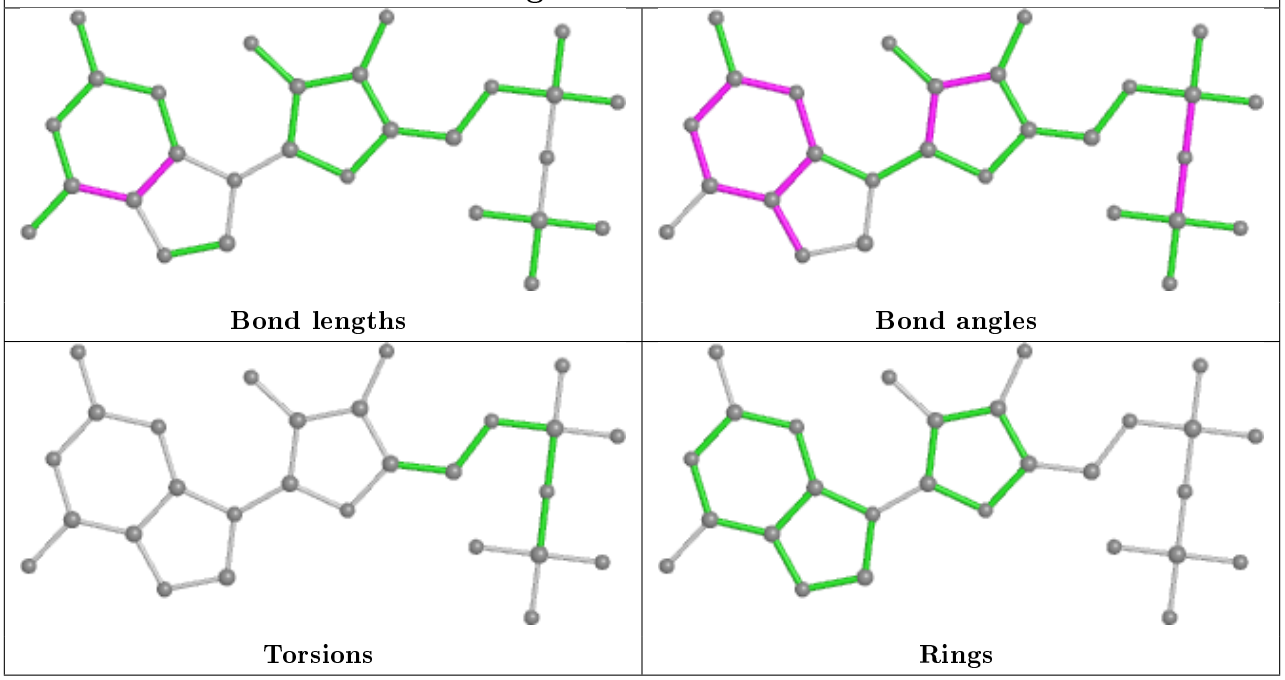
There are no torsion outliers.

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 x 601



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

All 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
1	5	757:G	O3'	906:C	P	17.40
1	5	2910:G	O3'	3583:U	P	16.72
1	5	990:C	O3'	1064:G	P	16.04
1	5	500:G	O3'	652:G	P	15.94
1	5	3950:U	O3'	4065:G	P	14.72

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2107:C	O3'	2243:C	P	13.48
1	5	1962:A	O3'	2021:G	P	13.43
1	5	1242:G	O3'	1271:G	P	12.04
1	5	1699:A	O3'	1718:C	P	5.02
1	5	1840:G	O3'	1842:G	P	4.62
1	1	105:G	O3'	106:G	P	4.57
1	5	1222:A	O3'	1232:G	P	4.31
1	5	1100:U	O3'	1167:C	P	3.76

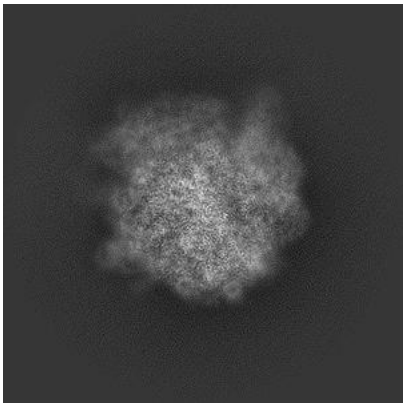
6 Map visualisation

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.

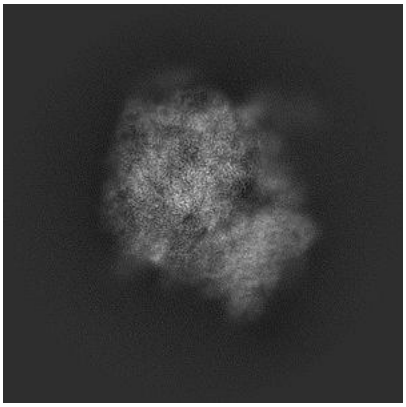
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

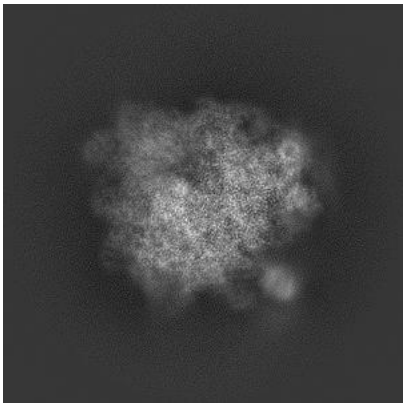
6.1.1 Primary map



X



Y

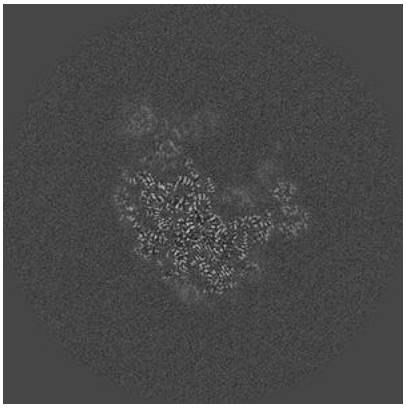


Z

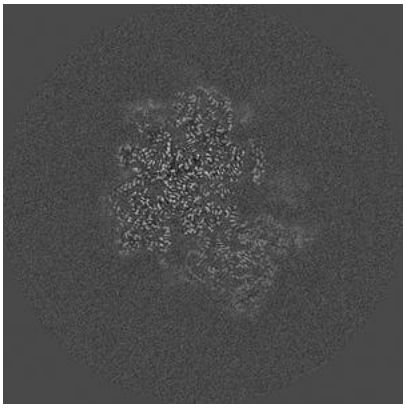
The images above show the map projected in three orthogonal directions.

6.2 Central slices

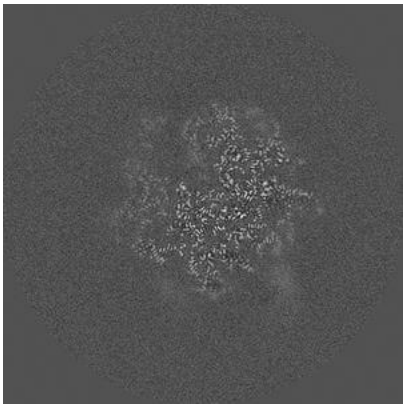
6.2.1 Primary map



X Index: 224



Y Index: 224

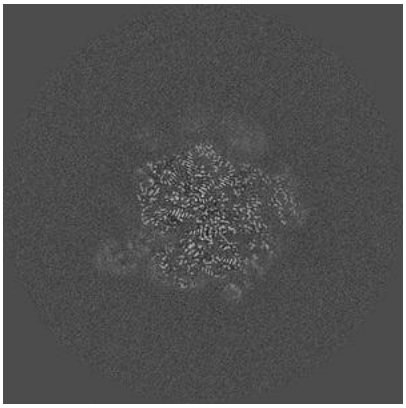


Z Index: 224

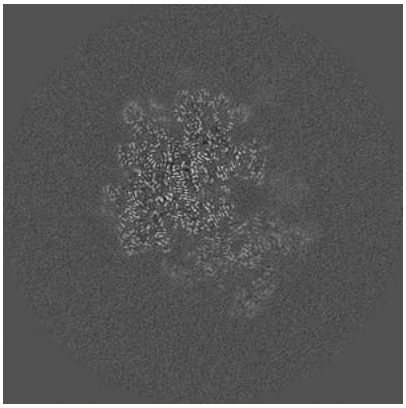
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

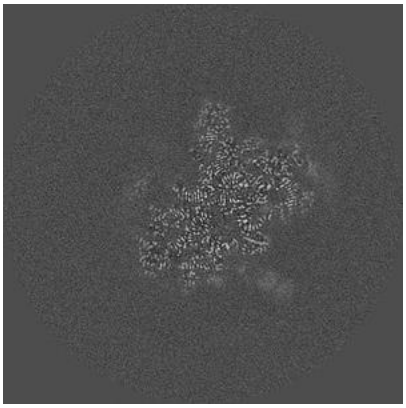
6.3.1 Primary map



X Index: 259



Y Index: 228

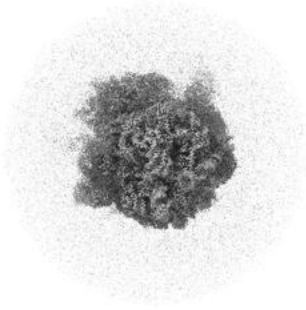


Z Index: 195

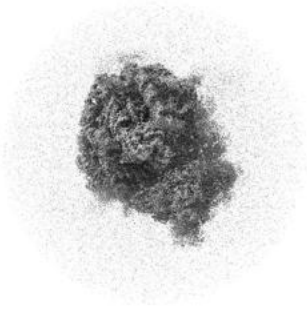
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

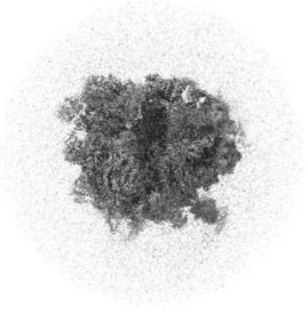
6.4.1 Primary map



X



Y



Z

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.

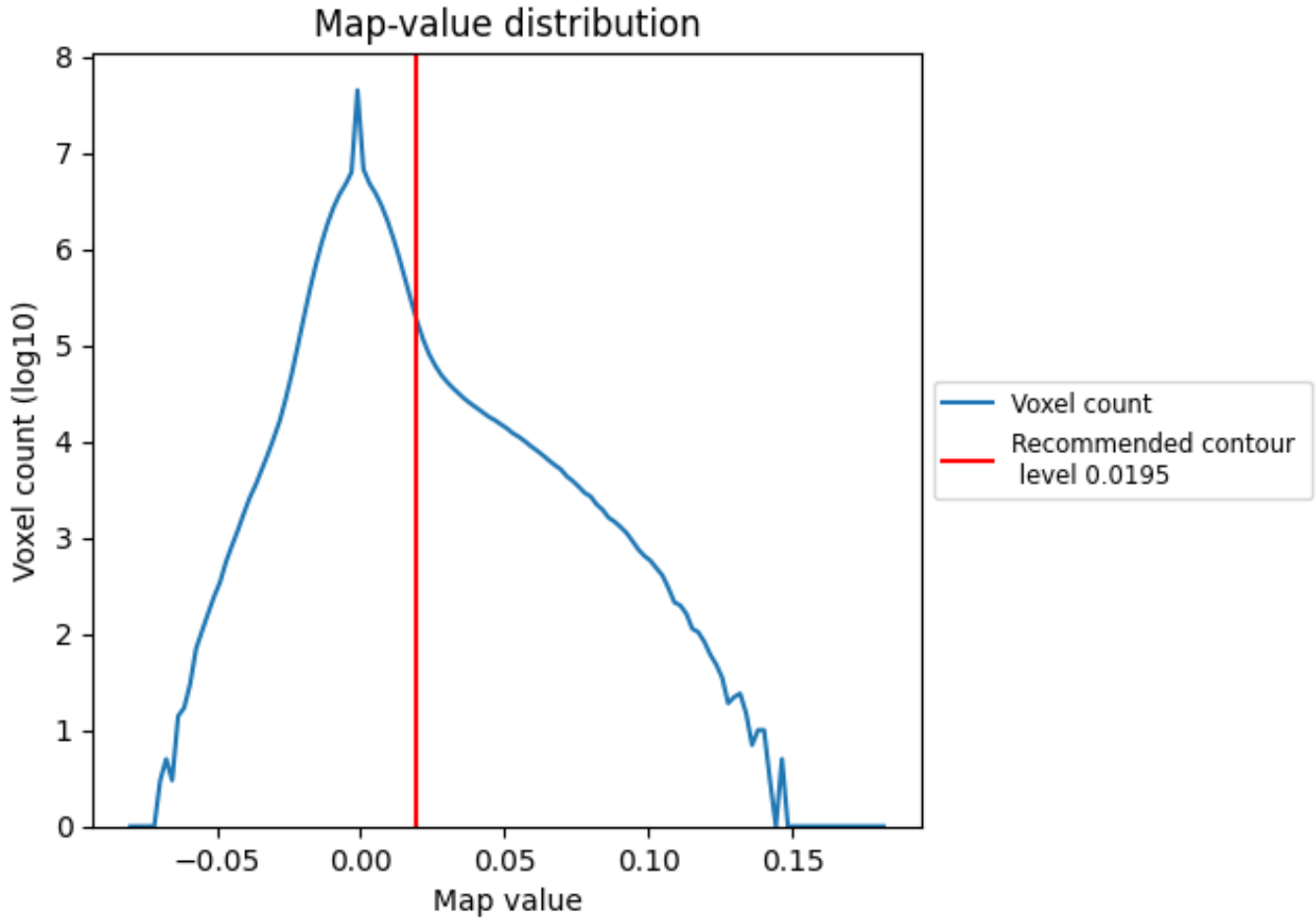
6.5 Mask visualisation (i)

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

7 Map analysis

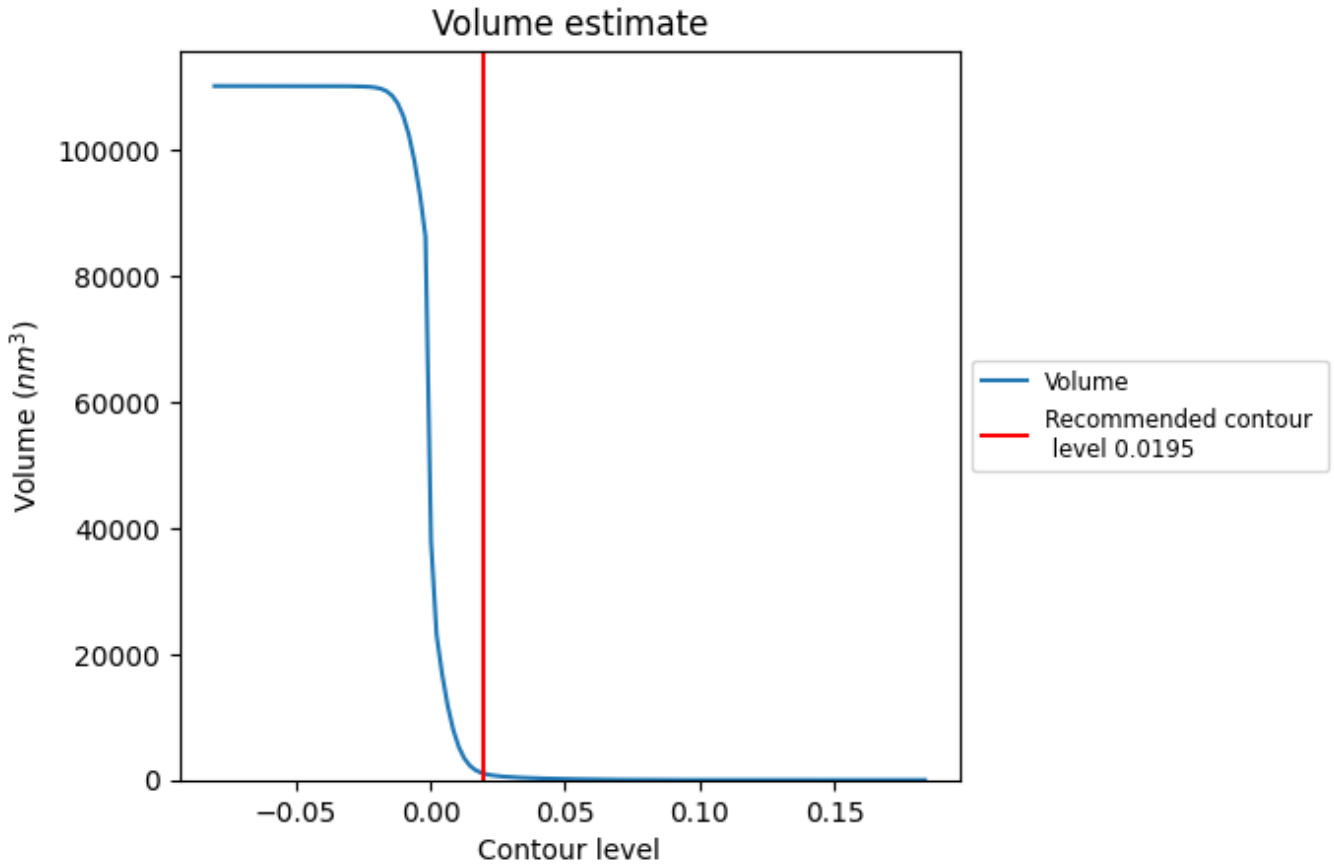
This section contains the results of statistical analysis of the map.

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.

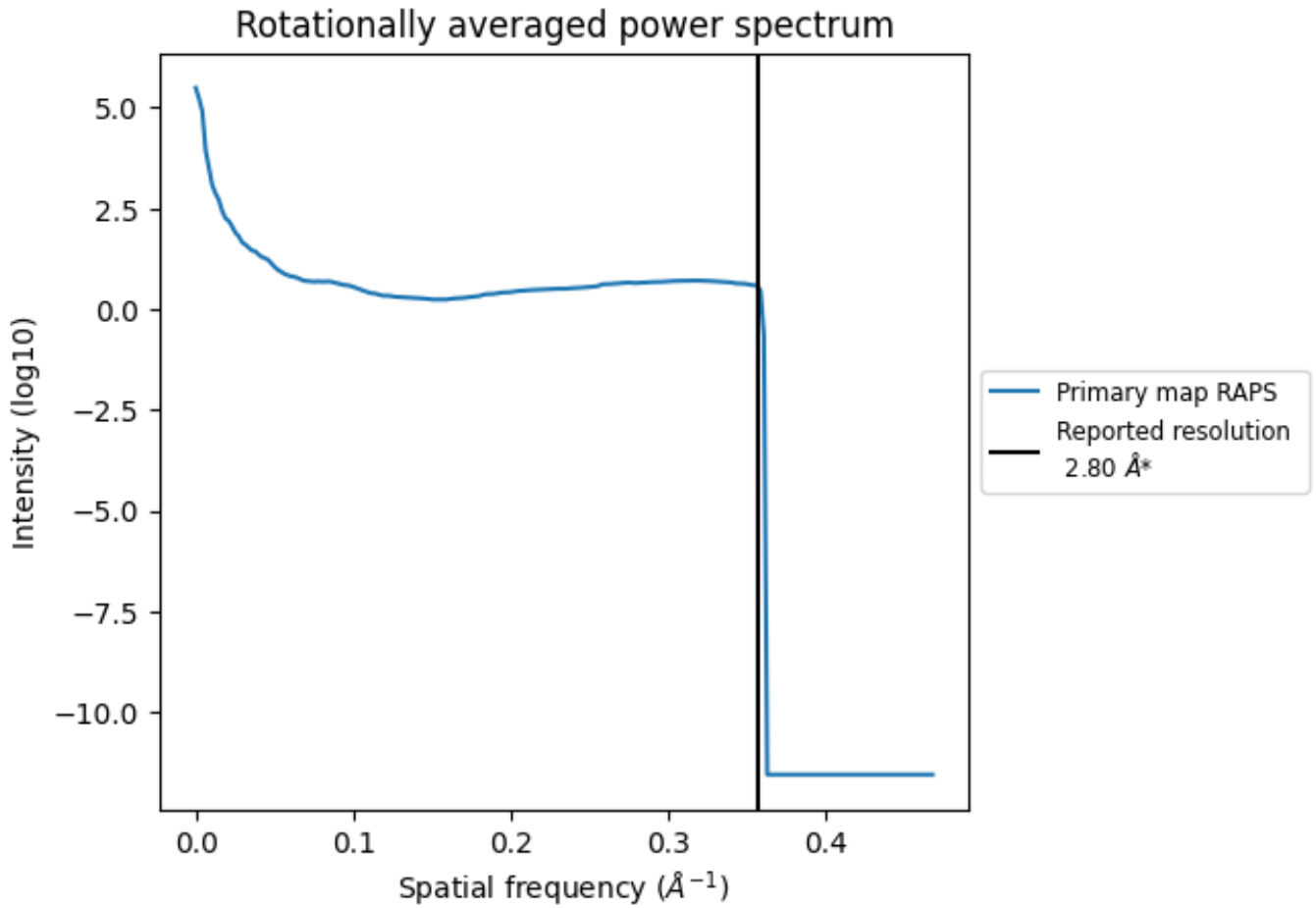
7.2 Volume estimate



The volume at the recommended contour level is 1075 nm^3; 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 (i)



*Reported resolution corresponds to spatial frequency of 0.357 $Å^{-1}$

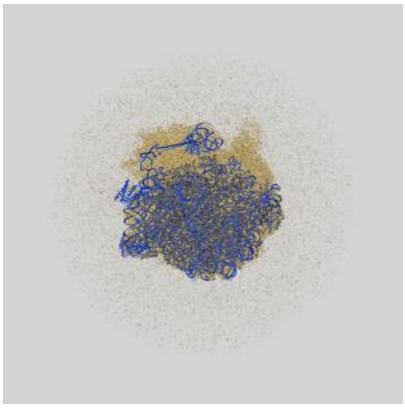
8 Fourier-Shell correlation

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

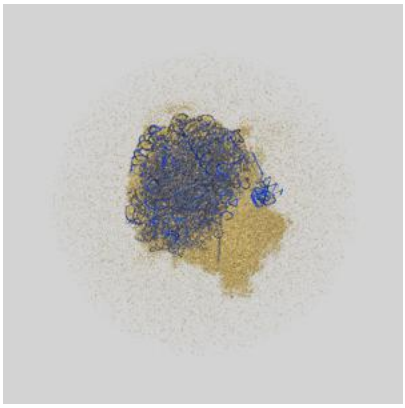
9 Map-model fit

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

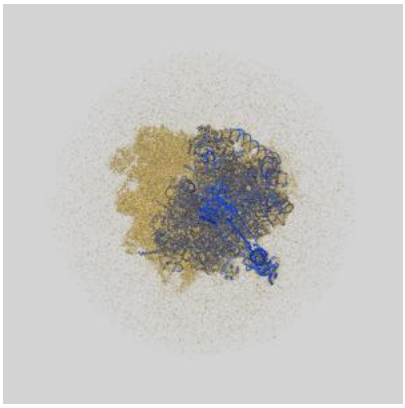
9.1 Map-model overlay



X



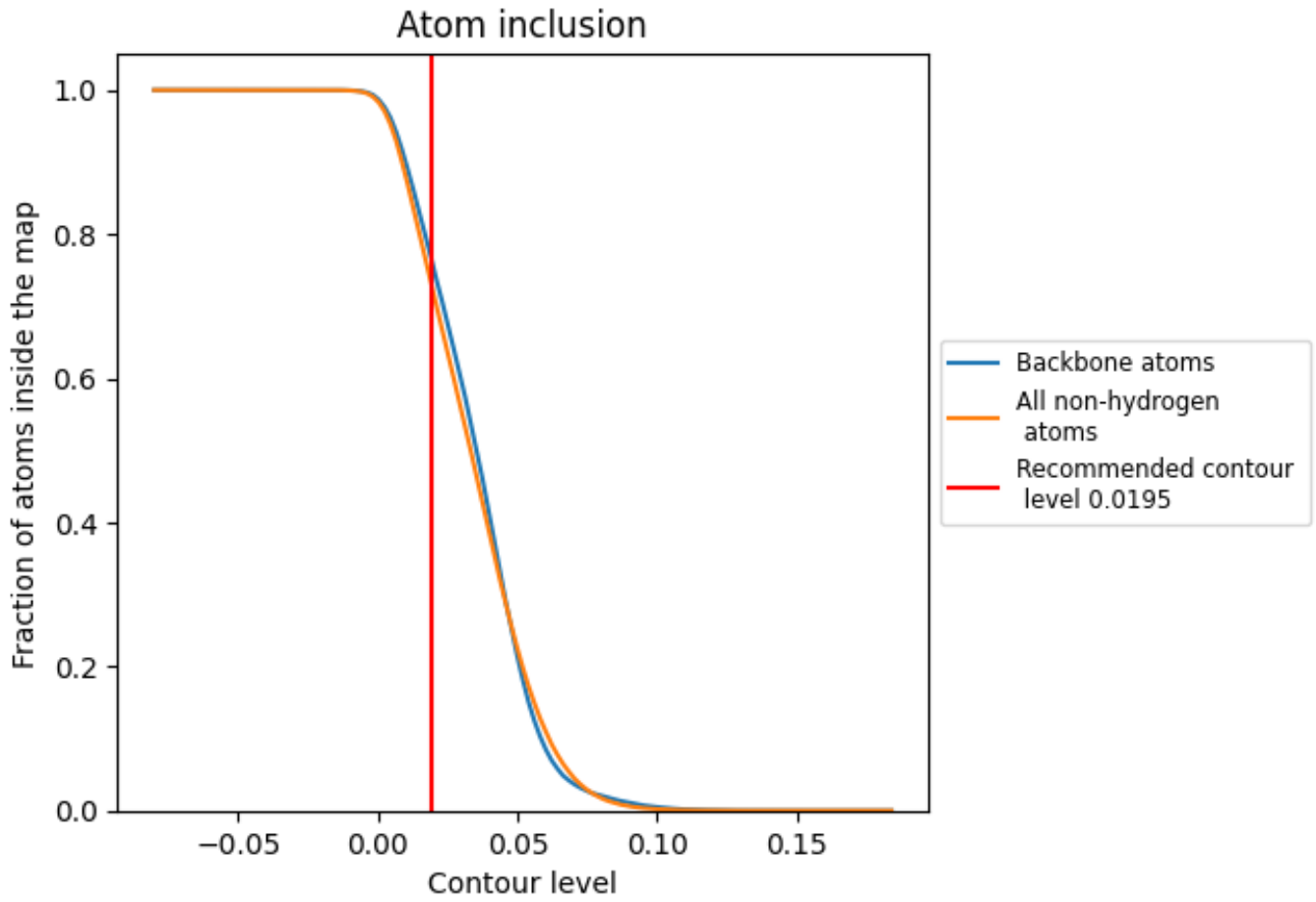
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0195 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 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.