



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:38 AM UTC

PDB ID : 9YPO / pdb_00009ypo
EMDB ID : EMD-73302
Title : GTPBP1*GCP*Phe-tRNA*ribosome in the open state, Structure IIa
Authors : Susorov, D.; Korostelev, A.A.
Deposited on : 2025-10-14
Resolution : 3.00 Å(reported)
Based on initial model : 5LZS

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

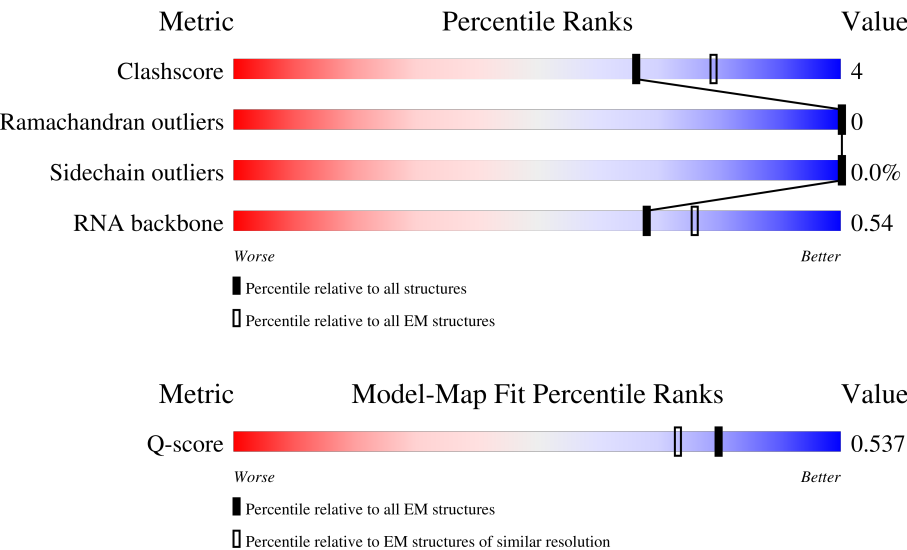
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	5	3601	
2	7	120	
3	8	156	

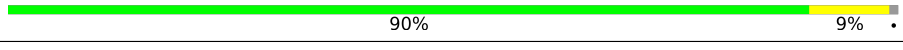
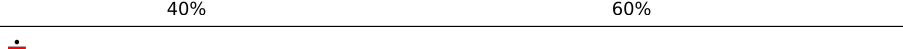
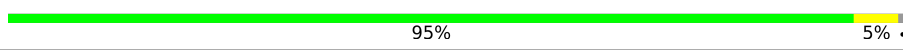
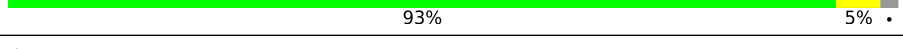
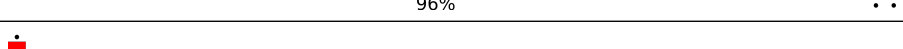
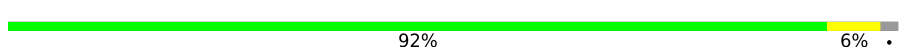
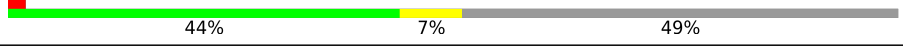
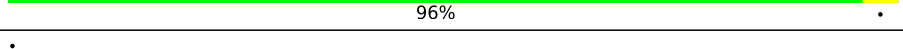
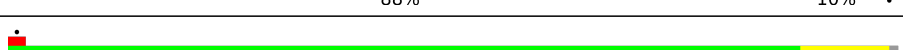
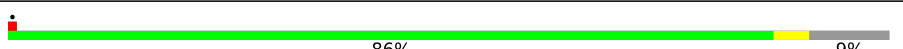
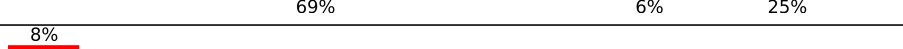
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	9	1869	
5	A	257	
6	B	403	
7	C	425	
8	D	297	
9	E	291	
10	G	319	
11	H	192	
12	I	214	
13	J	178	
14	K	247	
15	L	211	
16	M	218	
17	N	204	
18	O	203	
19	P	184	
20	Q	188	
21	R	196	
22	S	176	
23	T	160	
24	U	128	
25	V	140	
26	W	157	
27	X	156	
28	Y	145	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	Z	136	
30	a	148	
31	b	245	
32	c	115	
33	d	125	
34	e	135	
35	f	110	
36	g	116	
37	h	123	
38	i	105	
39	k	70	
40	l	51	
41	m	102	
42	n	25	
43	o	106	
44	p	92	
45	r	137	
46	AA	295	
47	BB	264	
48	CC	293	
49	DD	243	
50	EE	263	
51	FF	204	
52	GG	249	
53	HH	194	

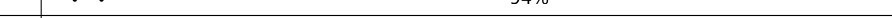
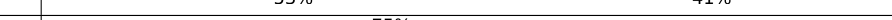
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	II	208	
55	JJ	194	
56	KK	165	
57	LL	158	
58	MM	132	
59	NN	151	
60	OO	168	
61	PP	145	
62	QQ	146	
63	RR	135	
64	SS	152	
65	TT	145	
66	UU	119	
67	VV	83	
68	WW	130	
69	XX	143	
70	YY	130	
71	ZZ	125	
72	aa	115	
73	bb	84	
74	cc	69	
75	dd	56	
76	ee	133	
77	ff	156	
78	gg	317	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	10	185	 94%
80	12	76	 53%41%5%
81	11	75	 75%39%52%8%
81	13	75	 12%68%24%7%
82	j	97	 77%11%11%
83	jj	703	 17%64%9%27%

2 Entry composition

There are 92 unique types of molecules in this entry. The entry contains 219555 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3601	Total	C	N	O	P	0	0
			77221	34390	14143	25087	3601		

There are 59 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	1	C	N	conflict	GB 5LZS_5
5	3948	C	-	insertion	GB 5LZS_5
5	3949	A	-	insertion	GB 5LZS_5
5	3950	U	-	insertion	GB 5LZS_5
5	3951	G	-	insertion	GB 5LZS_5
5	3952	A	-	insertion	GB 5LZS_5
5	3953	G	-	insertion	GB 5LZS_5
5	3954	A	-	insertion	GB 5LZS_5
5	3955	G	-	insertion	GB 5LZS_5
5	3956	G	-	insertion	GB 5LZS_5
5	3957	U	-	insertion	GB 5LZS_5
5	3958	G	-	insertion	GB 5LZS_5
5	3959	U	-	insertion	GB 5LZS_5
5	3960	A	-	insertion	GB 5LZS_5
5	3961	G	-	insertion	GB 5LZS_5
5	3962	A	-	insertion	GB 5LZS_5
5	3963	A	-	insertion	GB 5LZS_5
5	3964	U	-	insertion	GB 5LZS_5
5	3965	A	-	insertion	GB 5LZS_5
5	3966	A	-	insertion	GB 5LZS_5
5	3967	G	-	insertion	GB 5LZS_5
5	3968	U	-	insertion	GB 5LZS_5
5	3969	G	-	insertion	GB 5LZS_5
5	3970	G	-	insertion	GB 5LZS_5
5	3971	G	-	insertion	GB 5LZS_5
5	3972	A	-	insertion	GB 5LZS_5
5	3973	G	-	insertion	GB 5LZS_5
5	3974	G	-	insertion	GB 5LZS_5

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
5	3975	C	-	insertion	GB 5LZS_5
5	3976	C	-	insertion	GB 5LZS_5
5	4035	G	-	insertion	GB 5LZS_5
5	4036	G	-	insertion	GB 5LZS_5
5	4037	C	-	insertion	GB 5LZS_5
5	4038	C	-	insertion	GB 5LZS_5
5	4039	G	-	insertion	GB 5LZS_5
5	4040	C	-	insertion	GB 5LZS_5
5	4041	C	-	insertion	GB 5LZS_5
5	4042	G	-	insertion	GB 5LZS_5
5	4043	G	-	insertion	GB 5LZS_5
5	4044	U	-	insertion	GB 5LZS_5
5	4045	G	-	insertion	GB 5LZS_5
5	4046	A	-	insertion	GB 5LZS_5
5	4047	A	-	insertion	GB 5LZS_5
5	4048	A	-	insertion	GB 5LZS_5
5	4049	U	-	insertion	GB 5LZS_5
5	4050	A	-	insertion	GB 5LZS_5
5	4051	C	-	insertion	GB 5LZS_5
5	4052	C	-	insertion	GB 5LZS_5
5	4053	A	-	insertion	GB 5LZS_5
5	4054	C	-	insertion	GB 5LZS_5
5	4055	U	-	insertion	GB 5LZS_5
5	4056	A	-	insertion	GB 5LZS_5
5	4057	C	-	insertion	GB 5LZS_5
5	4058	U	-	insertion	GB 5LZS_5
5	4059	C	-	insertion	GB 5LZS_5
5	4060	U	-	insertion	GB 5LZS_5
5	4061	G	-	insertion	GB 5LZS_5
5	4062	A	-	insertion	GB 5LZS_5
5	4063	U	-	insertion	GB 5LZS_5

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	120	U	-	insertion	GB XR_011385821

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	1	C	-	insertion	GB XR_011385890
8	155	C	-	insertion	GB XR_011385890
8	156	U	-	insertion	GB XR_011385890

- Molecule 4 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 5 is a protein called Ribosomal protein L8.

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

- Molecule 6 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	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		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	378	LYS	-	insertion	UNP G1SVW5
C	379	VAL	-	insertion	UNP G1SVW5
C	380	LYS	-	insertion	UNP G1SVW5
C	381	LYS	-	insertion	UNP G1SVW5

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	382	PRO	-	insertion	UNP G1SVW5
C	383	ARG	-	insertion	UNP G1SVW5
C	384	ALA	-	insertion	UNP G1SVW5
C	385	VAL	-	insertion	UNP G1SVW5
C	386	GLY	-	insertion	UNP G1SVW5
C	387	ILE	-	insertion	UNP G1SVW5
C	388	LYS	-	insertion	UNP G1SVW5
C	389	GLN	-	insertion	UNP G1SVW5

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 11 is a protein called 60S ribosomal protein L9.

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

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 13 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 14 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	61	ARG	GLY	conflict	UNP G1TUB1
K	93	ARG	GLY	conflict	UNP G1TUB1
K	131	MET	VAL	conflict	UNP G1TUB1
K	153	ILE	VAL	conflict	UNP G1TUB1

- 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
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0
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	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	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 Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 19 is a protein called Large ribosomal subunit protein 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 Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	4	ASP	ASN	conflict	UNP G1TFE0
Q	14	ARG	TRP	conflict	UNP G1TFE0
Q	53	MET	LEU	conflict	UNP G1TFE0
Q	58	ARG	TRP	conflict	UNP G1TFE0
Q	75	ARG	GLN	conflict	UNP G1TFE0
Q	80	ALA	PRO	conflict	UNP G1TFE0
Q	86	VAL	ILE	conflict	UNP G1TFE0
Q	104	ARG	HIS	conflict	UNP G1TFE0
Q	110	ARG	CYS	conflict	UNP G1TFE0
Q	137	VAL	GLY	conflict	UNP G1TFE0
Q	157	GLY	ARG	conflict	UNP G1TFE0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 21 is a protein called Ribosomal protein L19.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3
R	94	THR	LYS	conflict	UNP G1TJR3

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	1	MET	THR	conflict	UNP G1TTY7
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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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 eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1
U	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 25 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 26 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 27 is a protein called eL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 28 is a protein called uL24.

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 60S ribosomal protein L27a.

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 Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	98	Total	C	N	O	S	0	0
			806	498	182	123	3		

- Molecule 32 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- 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 Ribosomal protein L32.

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 Large ribosomal subunit protein eL34.

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 eL35.

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 eL38.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	3	ARG	GLN	conflict	UNP G1U3J0
k	38	CYS	TYR	conflict	UNP G1U3J0
k	48	THR	MET	conflict	UNP G1U3J0
k	66	VAL	MET	conflict	UNP G1U3J0

- Molecule 40 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 41 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

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

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	1	MET	-	insertion	UNP P0DXC2
m	2	GLY	-	insertion	UNP P0DXC2
m	3	ASP	-	insertion	UNP P0DXC2
m	4	PRO	-	insertion	UNP P0DXC2
m	5	GLU	-	insertion	UNP P0DXC2
m	6	SER	-	insertion	UNP P0DXC2
m	7	GLY	-	insertion	UNP P0DXC2
m	8	GLY	-	insertion	UNP P0DXC2
m	9	CYS	-	insertion	UNP P0DXC2

- Molecule 42 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 43 is a protein called Large ribosomal subunit protein eL42.

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

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
o	101	GLY	-	insertion	UNP G1T040
o	102	GLN	-	insertion	UNP G1T040
o	103	VAL	-	insertion	UNP G1T040
o	104	ILE	-	insertion	UNP G1T040
o	105	GLN	-	insertion	UNP G1T040
o	106	PHE	-	insertion	UNP G1T040

- Molecule 44 is a protein called eL43.

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

- Molecule 45 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 46 is a protein called uS2 (SA).

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AA	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	114	THR	ALA	conflict	UNP G1TLT8

- Molecule 47 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 48 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CC	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CC	13	ASP	GLY	conflict	UNP G1SWM1
CC	19	ILE	MET	conflict	UNP G1SWM1
CC	33	VAL	ILE	conflict	UNP G1SWM1
CC	97	PHE	CYS	conflict	UNP G1SWM1
CC	101	SER	ALA	conflict	UNP G1SWM1
CC	141	VAL	LEU	conflict	UNP G1SWM1
CC	181	PRO	LEU	conflict	UNP G1SWM1
CC	191	VAL	-	insertion	UNP G1SWM1
CC	215	MET	LEU	conflict	UNP G1SWM1
CC	271	ASP	ASN	conflict	UNP G1SWM1
CC	274	VAL	MET	conflict	UNP G1SWM1

- Molecule 49 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	DD	224	Total	C	N	O	S	0	0
			1739	1108	313	311	7		

- Molecule 50 is a protein called eS4 (S4 X isoform).

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	25	GLY	SER	conflict	UNP G1TK17
EE	51	ARG	LYS	conflict	UNP G1TK17
EE	78	THR	ALA	conflict	UNP G1TK17
EE	156	VAL	MET	conflict	UNP G1TK17

- Molecule 51 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	FF	184	Total	C	N	O	S	0	0
			1460	915	273	265	7		

- Molecule 52 is a protein called 40S ribosomal protein S6.

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

- Molecule 53 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	HH	185	Total	C	N	O	S	0	0
			1489	952	271	265	1		

- Molecule 54 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	II	198	Total	C	N	O	S	0	0
			1628	1021	322	280	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 55 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
55	JJ	181	Total	C	N	O	S	0	0
			1508	960	302	244	2		

- Molecule 56 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 57 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LL	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 58 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	MM	112	Total	C	N	O	S	0	0
			871	551	155	158	7		

- Molecule 59 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 60 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	OO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 61 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	PP	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 62 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	QQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 63 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 64 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SS	140	Total	C	N	O	S	0	0
			1157	728	231	197	1		

- Molecule 65 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	TT	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 66 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	UU	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 67 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	VV	83	Total	C	N	O	S	0	0
			637	393	117	122	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VV	3	ASN	SER	conflict	UNP G1TM82
VV	4	ASP	ASN	conflict	UNP G1TM82
VV	33	GLN	PRO	conflict	UNP G1TM82
VV	50	PHE	SER	conflict	UNP G1TM82
VV	75	ALA	SER	conflict	UNP G1TM82
VV	76	ASP	HIS	conflict	UNP G1TM82
VV	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 68 is a protein called Ribosomal protein S15a.

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

- Molecule 69 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	XX	140	Total	C	N	O	S	0	0
			1087	687	215	182	3		

- Molecule 70 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	YY	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 71 is a protein called eS25.

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

- Molecule 72 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
aa	28	ARG	CYS	conflict	UNP G1TFE8
aa	56	ALA	VAL	conflict	UNP G1TFE8
aa	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 73 is a protein called 40S ribosomal protein S27.

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

- Molecule 74 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	cc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 75 is a protein called eS29.

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

- Molecule 76 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	ee	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 77 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	ff	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 78 is a protein called RACK1.

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

- Molecule 79 is a RNA chain called MF mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	10	11	Total	C	N	O	P	0	0
			234	105	41	77	11		

- Molecule 80 is a RNA chain called Phe-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	12	75	Total	C	N	O	P	0	0
			1599	714	286	524	75		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
12	37	C	G	conflict	GB 176419

- Molecule 81 is a RNA chain called Met-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	13	74	Total	C	N	O	P	0	0
			1585	707	293	511	74		
81	11	74	Total	C	N	O	P	0	0
			1585	707	293	511	74		

- Molecule 82 is a protein called Ribosomal protein L37.

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

- Molecule 83 is a protein called GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	jj	513	Total	C	N	O	S	0	0
			3982	2508	702	748	24		

There are 34 discrepancies between the modelled and reference sequences:

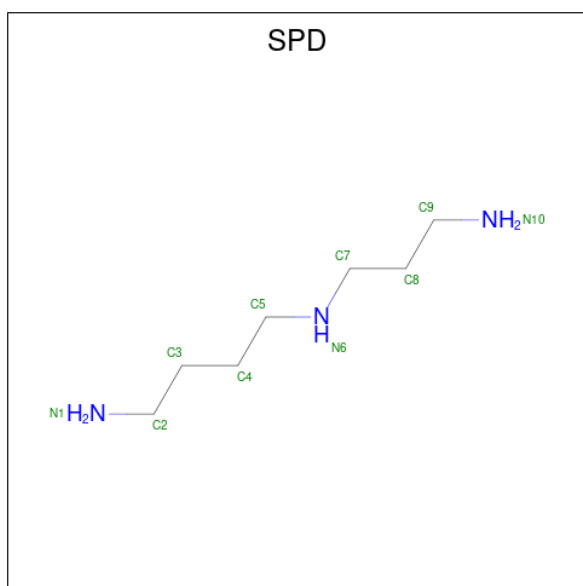
Chain	Residue	Modelled	Actual	Comment	Reference
jj	-33	MET	-	expression tag	UNP O00178
jj	-32	GLY	-	expression tag	UNP O00178
jj	-31	SER	-	expression tag	UNP O00178
jj	-30	SER	-	expression tag	UNP O00178
jj	-29	HIS	-	expression tag	UNP O00178
jj	-28	HIS	-	expression tag	UNP O00178
jj	-27	HIS	-	expression tag	UNP O00178
jj	-26	HIS	-	expression tag	UNP O00178
jj	-25	HIS	-	expression tag	UNP O00178
jj	-24	HIS	-	expression tag	UNP O00178
jj	-23	SER	-	expression tag	UNP O00178
jj	-22	SER	-	expression tag	UNP O00178
jj	-21	GLY	-	expression tag	UNP O00178
jj	-20	LEU	-	expression tag	UNP O00178
jj	-19	VAL	-	expression tag	UNP O00178
jj	-18	PRO	-	expression tag	UNP O00178
jj	-17	ARG	-	expression tag	UNP O00178
jj	-16	GLY	-	expression tag	UNP O00178
jj	-15	SER	-	expression tag	UNP O00178
jj	-14	HIS	-	expression tag	UNP O00178
jj	-13	MET	-	expression tag	UNP O00178
jj	-12	ALA	-	expression tag	UNP O00178
jj	-11	SER	-	expression tag	UNP O00178

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
jj	-10	MET	-	expression tag	UNP O00178
jj	-9	THR	-	expression tag	UNP O00178
jj	-8	GLY	-	expression tag	UNP O00178
jj	-7	GLY	-	expression tag	UNP O00178
jj	-6	GLN	-	expression tag	UNP O00178
jj	-5	GLN	-	expression tag	UNP O00178
jj	-4	MET	-	expression tag	UNP O00178
jj	-3	GLY	-	expression tag	UNP O00178
jj	-2	ARG	-	expression tag	UNP O00178
jj	-1	GLY	-	expression tag	UNP O00178
jj	0	SER	-	expression tag	UNP O00178

- Molecule 84 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			AltConf
84	5	1	Total	C	N	0
			10	7	3	

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

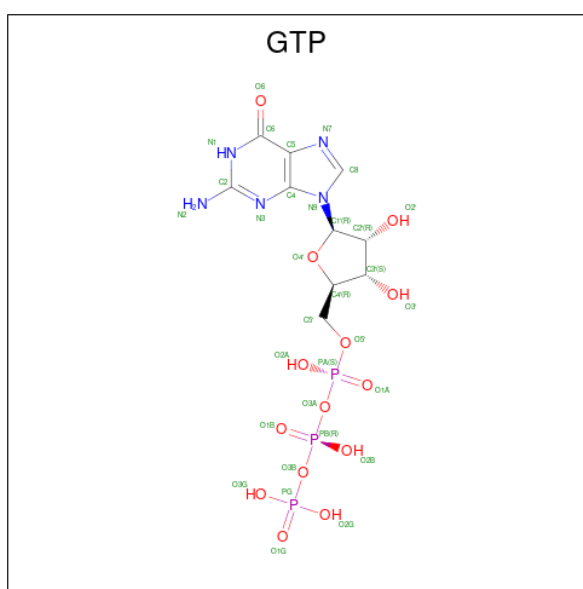
Mol	Chain	Residues	Atoms		AltConf
85	g	1	Total	Zn	0
			1	1	
85	m	1	Total	Zn	0
			1	1	

Continued on next page...

Continued from previous page...

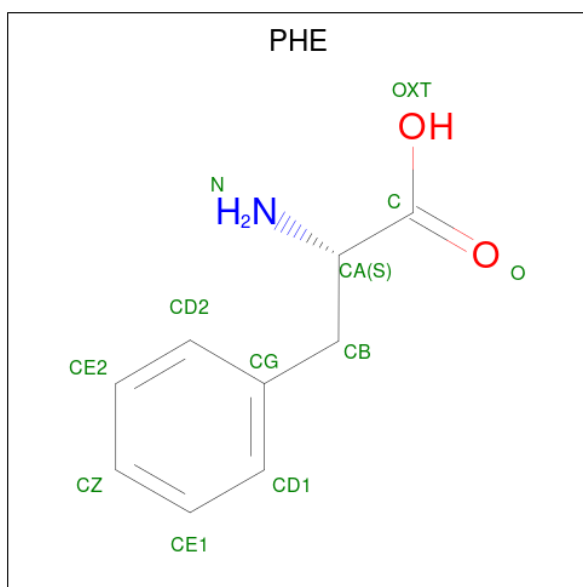
Mol	Chain	Residues	Atoms		AltConf
85	o	1	Total	Zn	0
			1	1	
85	p	1	Total	Zn	0
			1	1	
85	dd	1	Total	Zn	0
			1	1	
85	j	1	Total	Zn	0
			1	1	

- Molecule 86 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



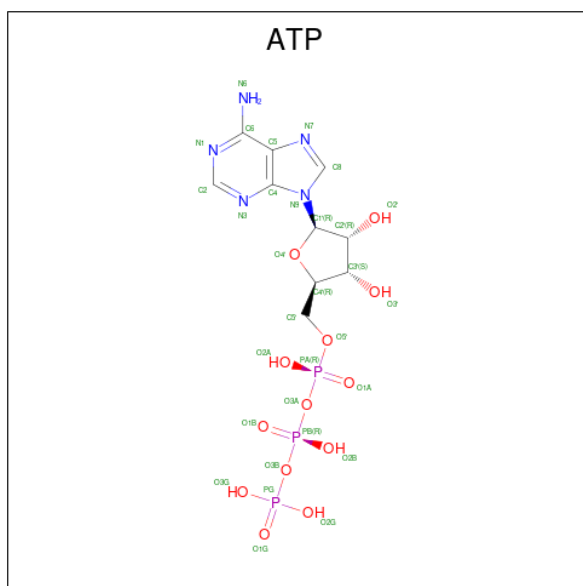
Mol	Chain	Residues	Atoms					AltConf
86	12	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 87 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



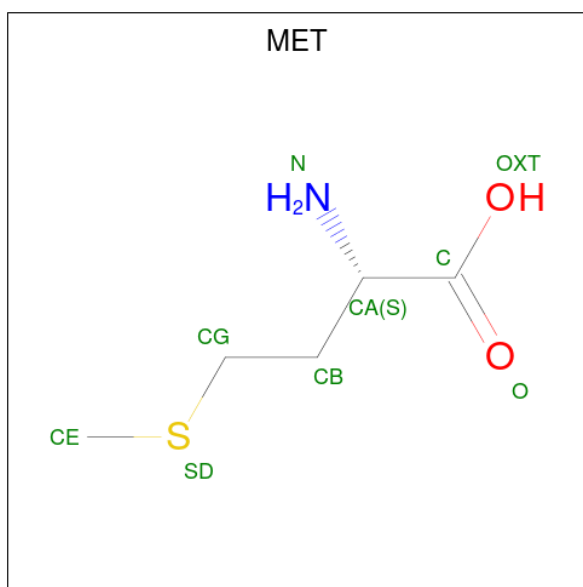
Mol	Chain	Residues	Atoms				AltConf
87	12	1	Total	C	N	O	0
			11	9	1	1	

- Molecule 88 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



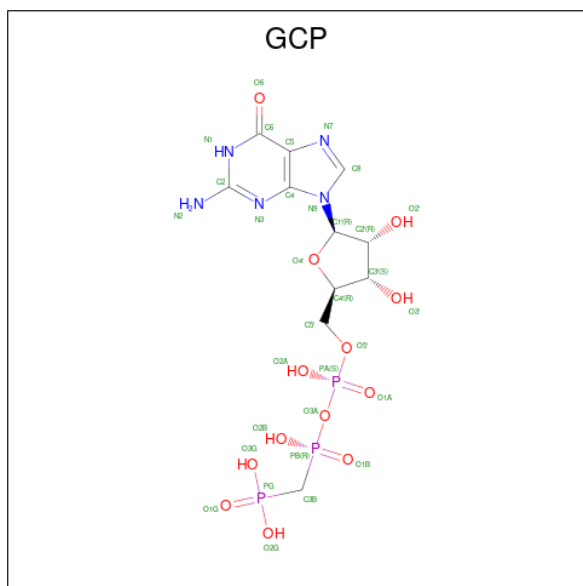
Mol	Chain	Residues	Atoms					AltConf
88	13	1	Total	C	N	O	P	0
			31	10	5	13	3	
88	11	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 89 is METHIONINE (CCD ID: MET) (formula: C₅H₁₁NO₂S).



Mol	Chain	Residues	Atoms					AltConf
89	13	1	Total	C	N	O	S	0
			8	5	1	1	1	

- Molecule 90 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
90	jj	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 91 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
91	jj	1	Total	Mg	0
			1	1	

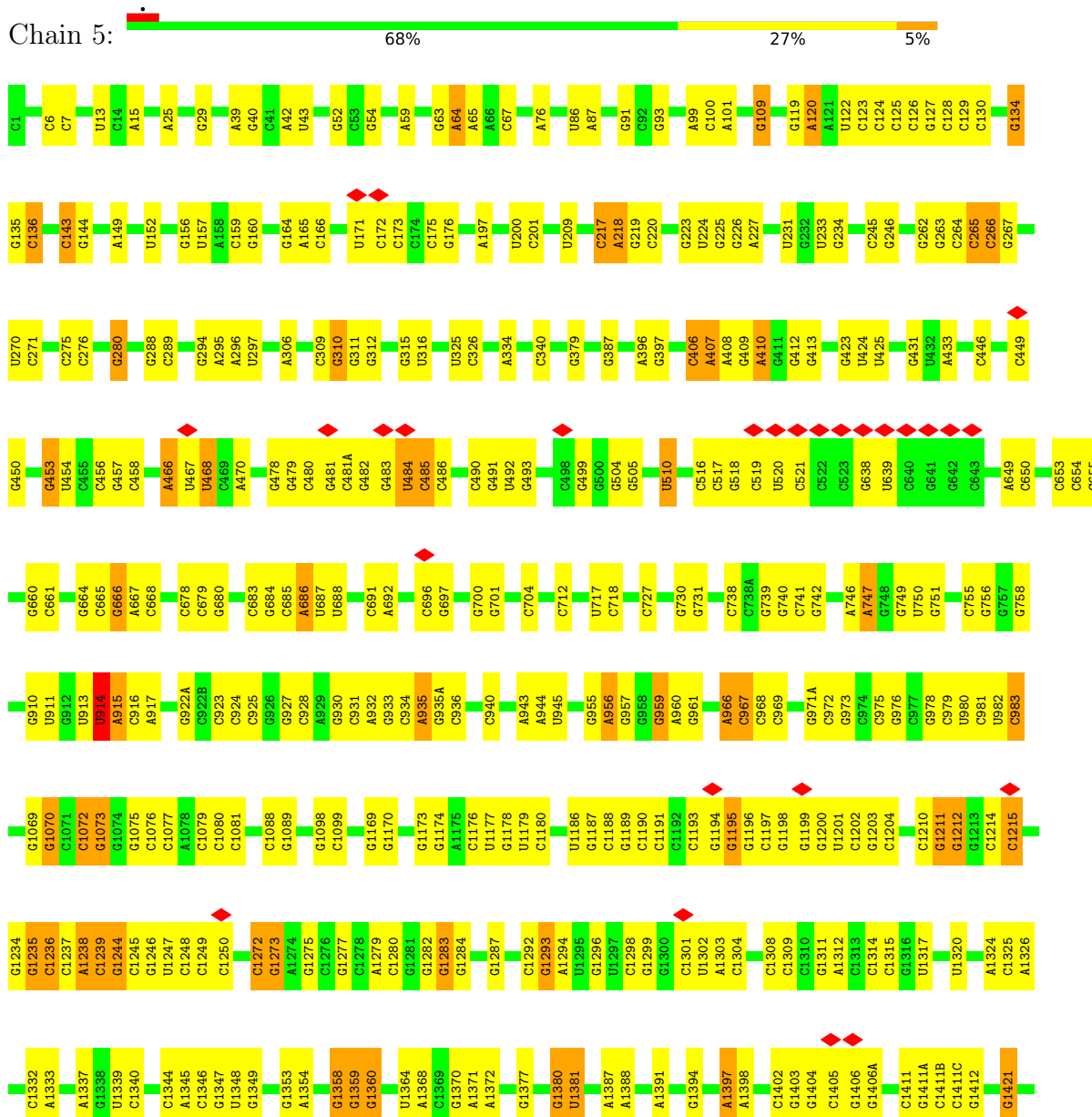
- Molecule 92 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
92	jj	1	Total	K	0
			1	1	

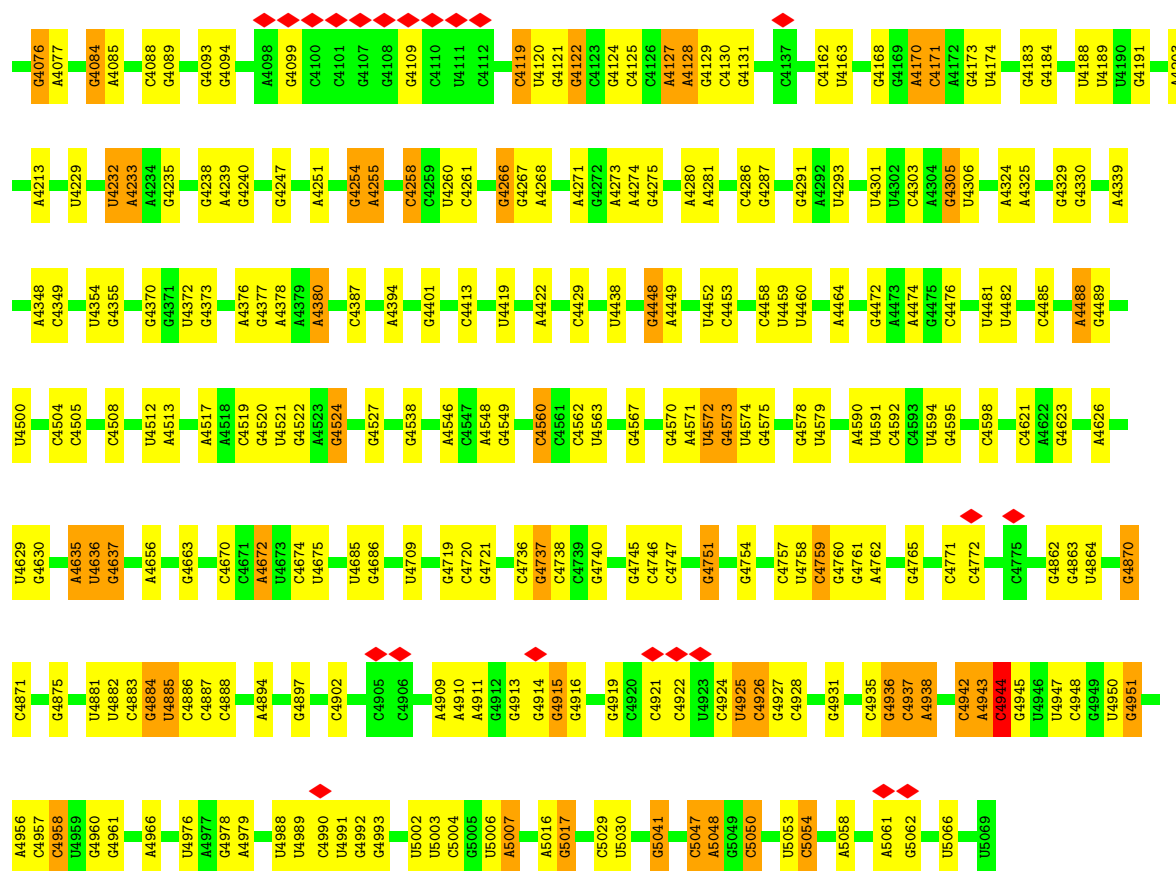
3 Residue-property plots

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

• Molecule 1: 28S ribosomal RNA



G3953	G3954	G3955	G3956	G3957	U3959	A3960	G3961	A3962	A3963	U3964	A3965	A3966	G3967	U3968	G3969	G3970	G3971	A3972	G3973	G3974	A3975	G3976	G4035	G4036	C4037	C4038	G4039	C4040	C4041	G4042	G4043	U4044	G4045	A4046	A4047	A4048	U4049	A4050	C4051	C4052	A4053	C4054	U4055	U4056	C4057	U4058	U4059	U4060	A4061	A4062	U4063	C4064	G4065	U4066	U4067	U4068	U4069	U4070																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
U3709	G3710	A3711	A3712	A3717	A3718	A3719	G3720	A3723	A3724	G3725	A3726	A3727	A3728	A3732	A3733	U3734	G3735	A3736	A3737	G3740	A3748	C3749	G3750	G3753	U3770	C3771	G3777	A3783	A3784	U3785	U3786	G3787	C3788	A3799	C3810	G3811	C3812	A3813	A3817	U3818	G3819	G3823	A3827	G3828	A3829	G3832	A3833	A3834	A3835	A3836	A3837	A3838	A3839	A3840	A3841	A3842	A3843	A3844	A3845	A3846	A3847	A3848	A3849	A3850	A3851	A3852	A3853	A3854	A3855	A3856	A3857	A3858	A3859	A3860	A3861	A3862	A3863	A3864	A3865	A3866	A3867	A3868	A3869	A3870	A3871	A3872	A3873	A3874	A3875	A3876	A3877	A3878	A3879	A3880	A3881	A3882	A3883	A3884	A3885	A3886	A3887	A3888	A3889	A3890	A3891	A3892	A3893	A3894	A3895	A3896	A3897	A3898	A3899	A3900	A3901	A3902	A3903	A3904	A3905	A3906	A3907	A3908	A3909	A3910	A3911	A3912	A3913	A3914	A3915	A3916	A3917	A3918	A3919	A3920	A3921	A3922	A3923	A3924	A3925	A3926	A3927	A3928	A3929	A3930	A3931	A3932	A3933	A3934	A3935	A3936	A3937	A3938	A3939	A3940	A3941	A3942	A3943	A3944	A3945	A3946	A3947	A3948	A3949	A3950	A3951	A3952	A3953	A3954	A3955	A3956	A3957	A3958	A3959	A3960	A3961	A3962	A3963	A3964	A3965	A3966	A3967	A3968	A3969	A3970	A3971	A3972	A3973	A3974	A3975	A3976	A3977	A3978	A3979	A3980	A3981	A3982	A3983	A3984	A3985	A3986	A3987	A3988	A3989	A3990	A3991	A3992	A3993	A3994	A3995	A3996	A3997	A3998	A3999	A4000	A4001	A4002	A4003	A4004	A4005	A4006	A4007	A4008	A4009	A4010	A4011	A4012	A4013	A4014	A4015	A4016	A4017	A4018	A4019	A4020	A4021	A4022	A4023	A4024	A4025	A4026	A4027	A4028	A4029	A4030	A4031	A4032	A4033	A4034	A4035	A4036	A4037	A4038	A4039	A4040	A4041	A4042	A4043	A4044	A4045	A4046	A4047	A4048	A4049	A4050	A4051	A4052	A4053	A4054	A4055	A4056	A4057	A4058	A4059	A4060	A4061	A4062	A4063	A4064	A4065	A4066	A4067	A4068	A4069	A4070																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
U2874	C2875	C2876	A2881	A2885	G2886	C2889	C2890	C2891	C2892	C2893	C2894	C2895	C2896	C2897	C2898	C2899	C2900	C2901	C2902	C2903	C2904	C2905	C2906	C2907	C2908	C2909	C2910	C2911	C2912	C2913	C2914	C2915	C2916	C2917	C2918	C2919	C2920	C2921	C2922	C2923	C2924	C2925	C2926	C2927	C2928	C2929	C2930	C2931	C2932	C2933	C2934	C2935	C2936	C2937	C2938	C2939	C2940	C2941	C2942	C2943	C2944	C2945	C2946	C2947	C2948	C2949	C2950	C2951	C2952	C2953	C2954	C2955	C2956	C2957	C2958	C2959	C2960	C2961	C2962	C2963	C2964	C2965	C2966	C2967	C2968	C2969	C2970	C2971	C2972	C2973	C2974	C2975	C2976	C2977	C2978	C2979	C2980	C2981	C2982	C2983	C2984	C2985	C2986	C2987	C2988	C2989	C2990	C2991	C2992	C2993	C2994	C2995	C2996	C2997	C2998	C2999	C3000	C3001	C3002	C3003	C3004	C3005	C3006	C3007	C3008	C3009	C3010	C3011	C3012	C3013	C3014	C3015	C3016	C3017	C3018	C3019	C3020	C3021	C3022	C3023	C3024	C3025	C3026	C3027	C3028	C3029	C3030	C3031	C3032	C3033	C3034	C3035	C3036	C3037	C3038	C3039	C3040	C3041	C3042	C3043	C3044	C3045	C3046	C3047	C3048	C3049	C3050	C3051	C3052	C3053	C3054	C3055	C3056	C3057	C3058	C3059	C3060	C3061	C3062	C3063	C3064	C3065	C3066	C3067	C3068	C3069	C3070	C3071	C3072	C3073	C3074	C3075	C3076	C3077	C3078	C3079	C3080	C3081	C3082	C3083	C3084	C3085	C3086	C3087	C3088	C3089	C3090	C3091	C3092	C3093	C3094	C3095	C3096	C3097	C3098	C3099	C3100	C3101	C3102	C3103	C3104	C3105	C3106	C3107	C3108	C3109	C3110	C3111	C3112	C3113	C3114	C3115	C3116	C3117	C3118	C3119	C3120	C3121	C3122	C3123	C3124	C3125	C3126	C3127	C3128	C3129	C3130	C3131	C3132	C3133	C3134	C3135	C3136	C3137	C3138	C3139	C3140	C3141	C3142	C3143	C3144	C3145	C3146	C3147	C3148	C3149	C3150	C3151	C3152	C3153	C3154	C3155	C3156	C3157	C3158	C3159	C3160	C3161	C3162	C3163	C3164	C3165	C3166	C3167	C3168	C3169	C3170	C3171	C3172	C3173	C3174	C3175	C3176	C3177	C3178	C3179	C3180	C3181	C3182	C3183	C3184	C3185	C3186	C3187	C3188	C3189	C3190	C3191	C3192	C3193	C3194	C3195	C3196	C3197	C3198	C3199	C3200	C3201	C3202	C3203	C3204	C3205	C3206	C3207	C3208	C3209	C3210	C3211	C3212	C3213	C3214	C3215	C3216	C3217	C3218	C3219	C3220	C3221	C3222	C3223	C3224	C3225	C3226	C3227	C3228	C3229	C3230	C3231	C3232	C3233	C3234	C3235	C3236	C3237	C3238	C3239	C3240	C3241	C3242	C3243	C3244	C3245	C3246	C3247	C3248	C3249	C3250	C3251	C3252	C3253	C3254	C3255	C3256	C3257	C3258	C3259	C3260	C3261	C3262	C3263	C3264	C3265	C3266	C3267	C3268	C3269	C3270	C3271	C3272	C3273	C3274	C3275	C3276	C3277	C3278	C3279	C3280	C3281	C3282	C3283	C3284	C3285	C3286	C3287	C3288	C3289	C3290	C3291	C3292	C3293	C3294	C3295	C3296	C3297	C3298	C3299	C3300	C3301	C3302	C3303	C3304	C3305	C3306	C3307	C3308	C3309	C3310	C3311	C3312	C3313	C3314	C3315	C3316	C3317	C3318	C3319	C3320	C3321	C3322	C3323	C3324	C3325	C3326	C3327	C3328	C3329	C3330	C3331	C3332	C3333	C3334	C3335	C3336	C3337	C3338	C3339	C3340	C3341	C3342	C3343	C3344	C3345	C3346	C3347	C3348	C3349	C3350	C3351	C3352	C3353	C3354	C3355	C3356	C3357	C3358	C3359	C3360	C3361	C3362	C3363	C3364	C3365	C3366	C3367	C3368	C3369	C3370	C3371	C3372	C3373	C3374	C3375	C3376	C3377	C3378	C3379	C3380	C3381	C3382	C3383	C3384	C3385	C3386	C3387	C3388	C3389	C3390	C3391	C3392	C3393	C3394	C3395	C3396	C3397	C3398	C3399	C3400	C3401	C3402	C3403	C3404	C3405	C3406	C3407	C3408	C3409	C3410	C3411	C3412	C3413	C3414	C3415	C3416	C3417	C3418	C3419	C3420	C3421	C3422	C3423	C3424	C3425	C3426	C3427	C3428	C3429	C3430	C3431	C3432	C3433	C3434	C3435	C3436	C3437	C3438	C3439	C3440	C3441	C3442	C3443	C3444	C3445	C3446	C3447	C3448	C3449	C3450	C3451	C3452	C3453	C3454	C3455	C3456	C3457	C3458	C3459	C3460	C3461	C3462	C3463	C3464	C3465	C3466	C3467	C3468	C3469	C3470	C3471	C3472	C3473	C3474	C3475	C3476	C3477	C3478	C3479	C3480	C3481	C3482	C3483	C3484	C3485	C3486	C3487	C3488	C3489	C3490	C3491	C3492	C3493	C3494	C3495	C3496	C3497	C3498	C3499	C3500	C3501	C3502	C3503	C3504	C3505	C3506	C3507	C3508	C3509	C3510	C3511	C3512	C3513	C3514	C3515	C3516	C3517	C3518	C3519	C3520	C3521	C3522	C3523	C3524	C3525	C3526	C3527	C3528	C3529	C3530	C3531	C3532	C3533	C3534	C3535	C3536	C3537	C3538	C3539	C3540	C3541	C3542	C3543	C3544	C3545	C3546	C3547	C3548	C3549	C3550	C3551	C3552	C3553	C3554	C3555	C3556	C3557	C3558	C3559	C3560	C3561	C3562	C3563	C3564	C3565	C3566	C3567	C3568	C3569	C3570	C3571	C3572	C3573	C3574	C3575	C3576	C3577	C3578	C3579	C3580	C3581	C3582	C3583	C3584	C3585	C3586	C3587	C3588	C3589	C3590	C3591	C3592	C3593	C3594	C3595	C3596	C3597	C3598	C3599	C3600	C3601	C3602	C3603	C3604	C3605	C3606	C3607	C3608	C3609	C3610	C3611	C3612	C3613	C3614	C3615	C3616	C3617	C3618	C3619	C3620	C3621	C3622	C3623	C3624	C3625	C3626	C3627	C3628	C3629	C3630	C3631	C3632	C3633	C3634	C3635	C3636	C3637	C3638	C3639	C3640	C3641	C3642	C3643	C3644	C3645	C3646	C3647	C3648	C3649	C3650	C3651	C3652	C3653	C3654	C3655	C3656	C3657	C3658	C3659	C3660	C3661	C3662	C3663	C3664	C3665	C3666	C3667	C3668	C3669	C3670	C3671	C3672	C3673	C3674	C3675	C3676	C3677	C3678	C3679	C3680	C3681	C3682	C3683	C3684	C3685	C3686	C3687	C3688	C3689	C3690	C3691	C3692	C3693	C3694	C3695	C3696	C3697	C3698	C3699	C3700	C3701	C3702	C3703	C3704	C3705	C3706	C3707	C3708	C3709	C3710	C3711	C3712	C3713	C3714	C3715	C3716	C3717	C3718	C3719	C3720	C3721	C3722	C3723	C3724	C3725	C3726	C3727	C3728	C3729	C3730	C3731	C3732	C3733	C3734	C3735	C3736	C3737	C3738	C3739	C3740	C3741	C3742	C3743	C3744	C3745	C3746	C3747	C3748	C3749	C3750	C3751	C3752	C3753	C3754	C3755	C3756	C3757	C3758	C3759	C3760	C3761	C3762	C3763	C3764	C3765	C3766	C3767	C3768	C3769	C3770	C3771	C3772	C3773	C3774	C3775	C3776	C3777	C3778	C3779	C3780	C3781	C3782	C3783	C3784	C3785	C3786	C3787	C3788	C3789	C3790	C3791	C3792	C3793	C3794	C3795	C3796	C3797	C3798	C3799	C3800	C3801	C3802	C3803	C3804	C3805	C3806	C3807	C3808	C3809	C3810	C3811	C3812	C3813	C3814	C3815	C3816	C3817	C3818	C3819	C3820	C3821	C3822	C3823	C3824	C3825	C3826	C3827	C3828	C3829	C3830	C3831	C3832	C3833	C3834	C3835	C3836	C3837	C3838	C3839	C3840	C3841	C3842	C3843	C3844	C3845	C3846	C3847	C3848	C3849	C3850	C3851	C3852	C3853	C3854	C3855	C3856	C3857	C3858	C3859	C3860	C3861	C3862	C3863	C3864	C3865	C3866	C3867	C3868	C3869	C3870	C3871	C3872	C3873	C3874	C3875	C3876	C3877	C3878	C3879	C3880	C3881	C3882	C3883	C3884	C3885	C3886	C3887	C3888	C3889	C3890	C3891	C3892	C3893	C3894	C3895	C



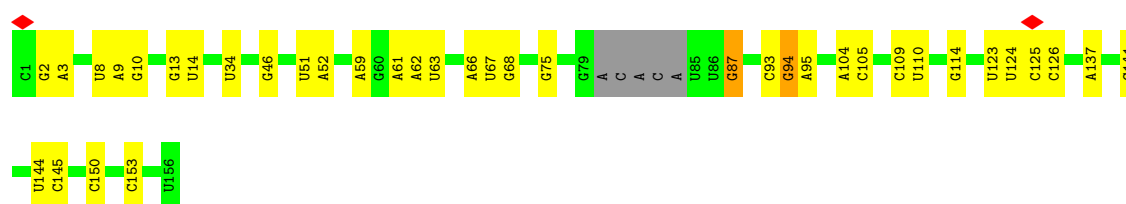
• Molecule 2: 5S ribosomal RNA

Chain 7: 85% 13% ..



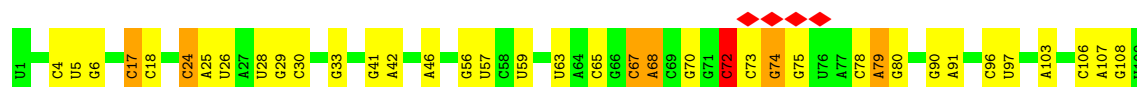
• Molecule 3: 5.8S ribosomal RNA

Chain 8: 72% 23% ..

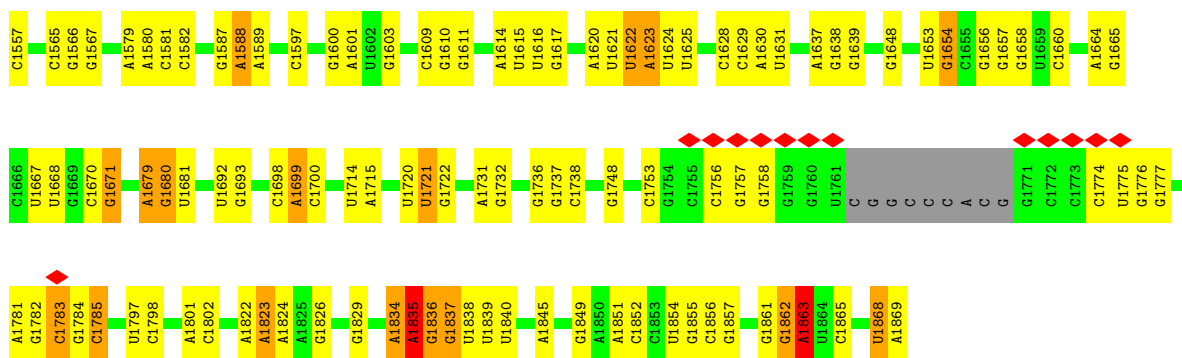


• Molecule 4: 18S ribosomal RNA

Chain 9: 5% 60% 26% 9%







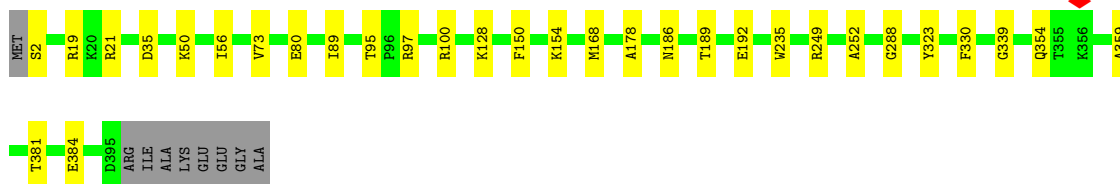
• Molecule 5: Ribosomal protein L8

Chain A: 88% 9% .



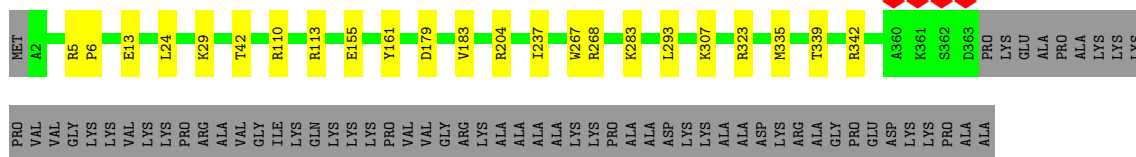
• Molecule 6: Ribosomal protein L3

Chain B: 90% 8% .



• Molecule 7: 60S ribosomal protein L4

Chain C: 80% 5% 15%



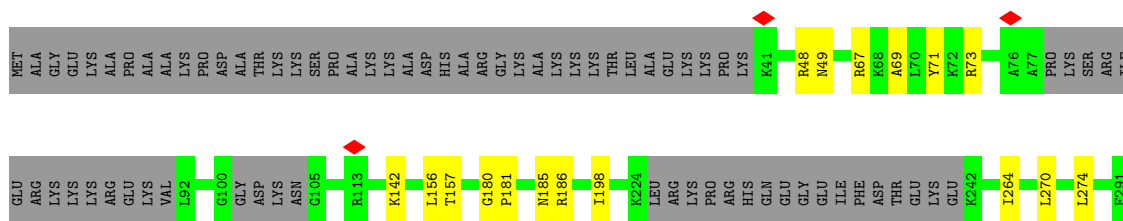
• Molecule 8: Large ribosomal subunit protein uL18

Chain D: 93% 5% ..

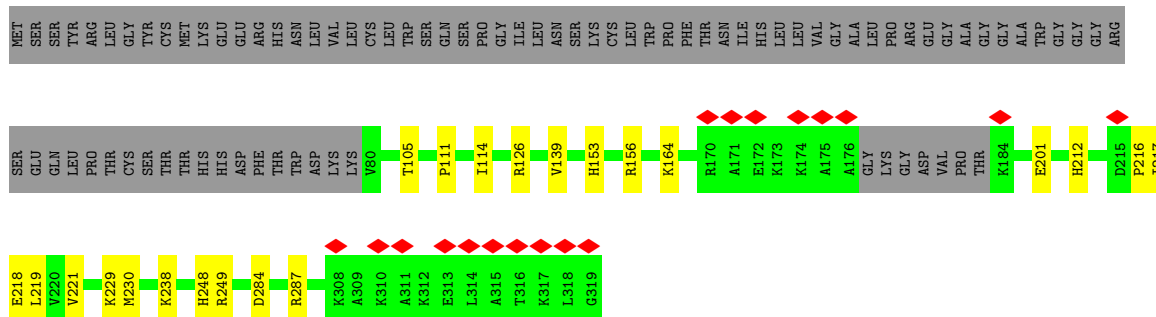


• Molecule 9: 60S ribosomal protein L6

Chain E: 68% 6% 26%



• Molecule 10: 60S ribosomal protein L7a



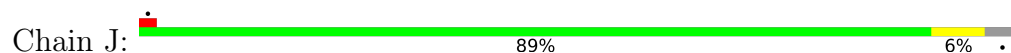
• Molecule 11: 60S ribosomal protein L9



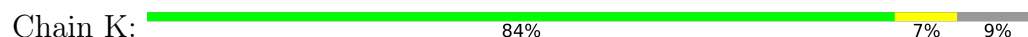
• Molecule 12: 60S ribosomal protein L10



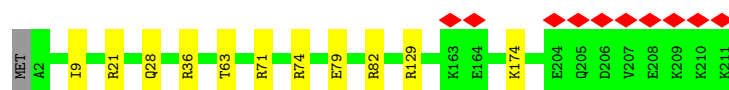
• Molecule 13: Ribosomal protein L11



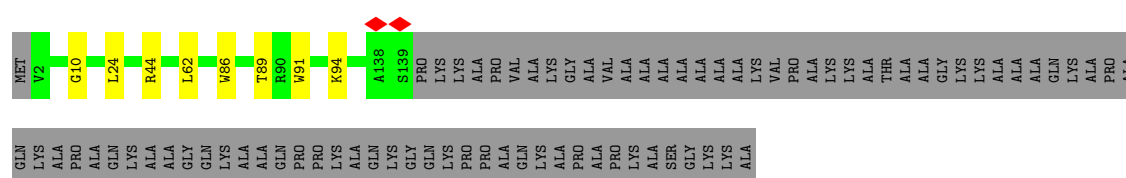
• Molecule 14: 60S ribosomal protein L7



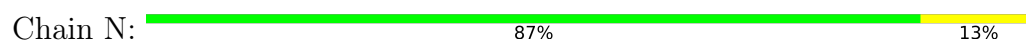
- Molecule 15: 60S ribosomal protein L13



- Molecule 16: 60S ribosomal protein L14



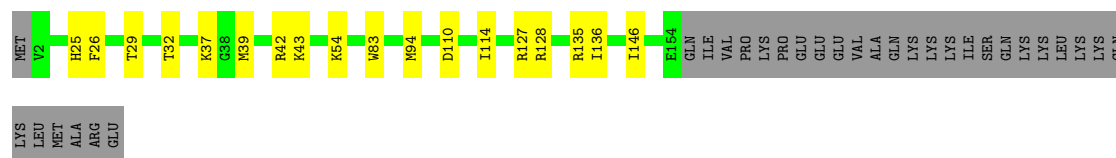
- Molecule 17: Ribosomal protein L15



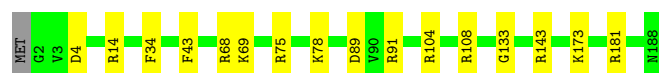
- Molecule 18: Large ribosomal subunit protein uL13



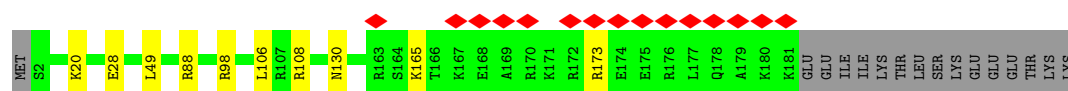
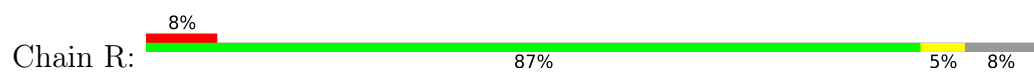
- Molecule 19: Large ribosomal subunit protein uL22



- Molecule 20: Ribosomal protein L18



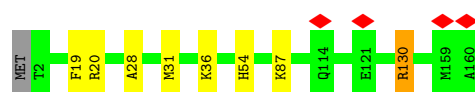
- Molecule 21: Ribosomal protein L19



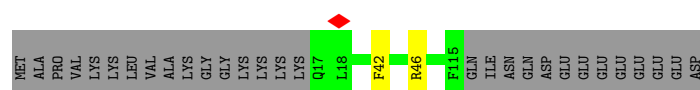
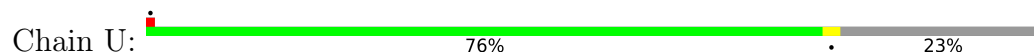
- Molecule 22: 60S ribosomal protein L18a



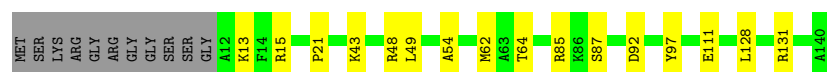
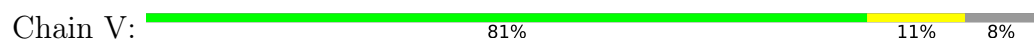
- Molecule 23: eL21



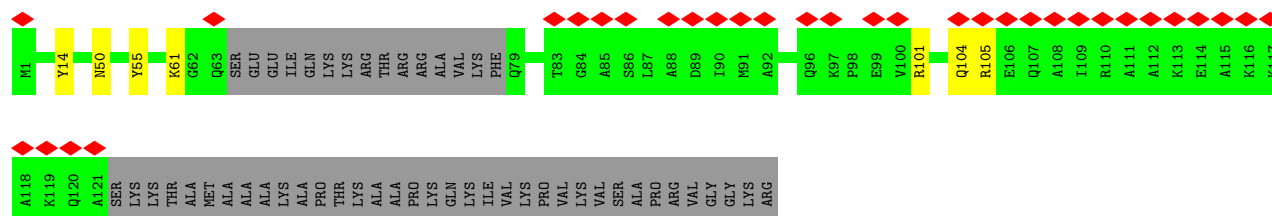
- Molecule 24: eL22



- Molecule 25: Ribosomal protein L23

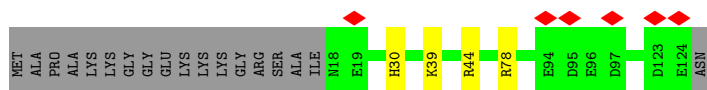


- Molecule 26: eL24



- Molecule 27: eL23





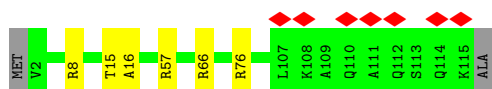
• Molecule 34: Ribosomal protein L32



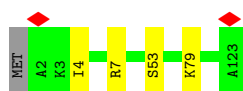
• Molecule 35: eL33



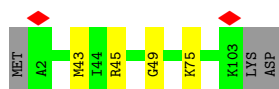
• Molecule 36: Large ribosomal subunit protein eL34



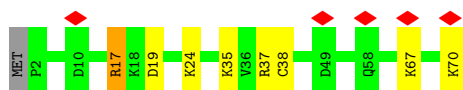
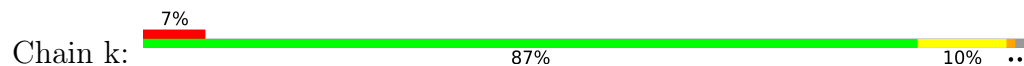
• Molecule 37: eL35



• Molecule 38: 60S ribosomal protein L36



• Molecule 39: eL38

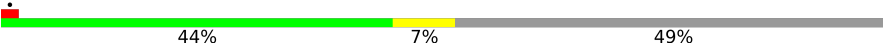


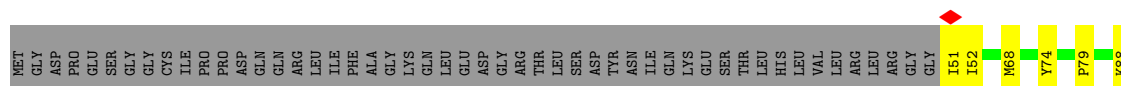
• Molecule 40: eL39

Chain l:  92% 6%

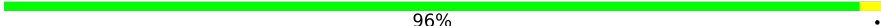


- Molecule 41: Ubiquitin-ribosomal protein eL40 fusion protein

Chain m:  44% 7% 49%



- Molecule 42: eL41

Chain n:  96%



- Molecule 43: Large ribosomal subunit protein eL42

Chain o:  88% 10%



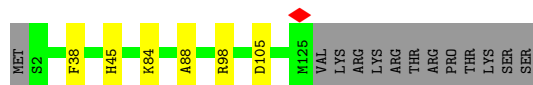
- Molecule 44: eL43

Chain p:  89% 10%



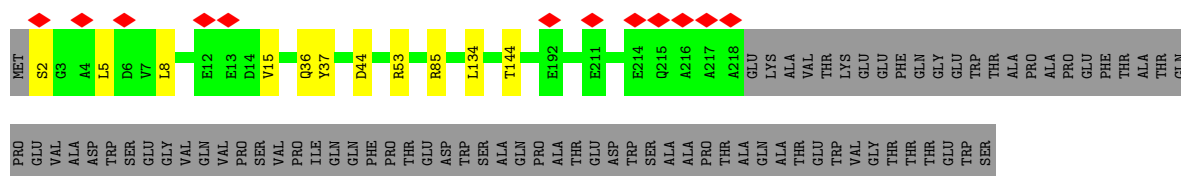
- Molecule 45: eL28

Chain r:  86% 9%

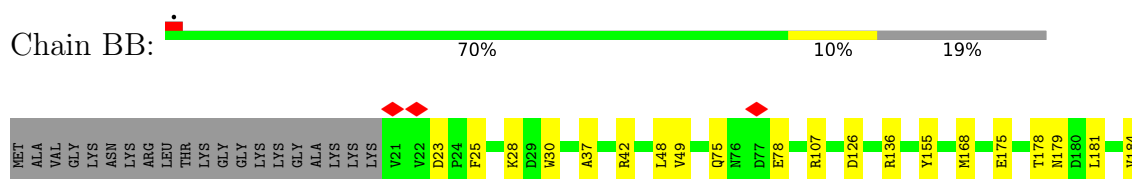


- Molecule 46: uS2 (SA)

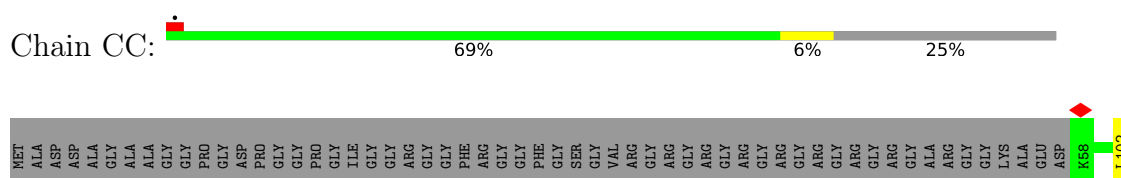
Chain AA:  70% 26%



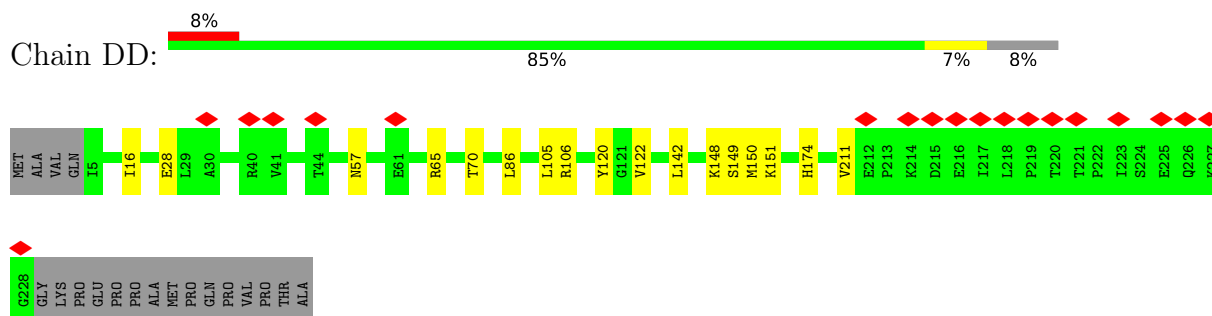
- Molecule 47: 40S ribosomal protein S3a



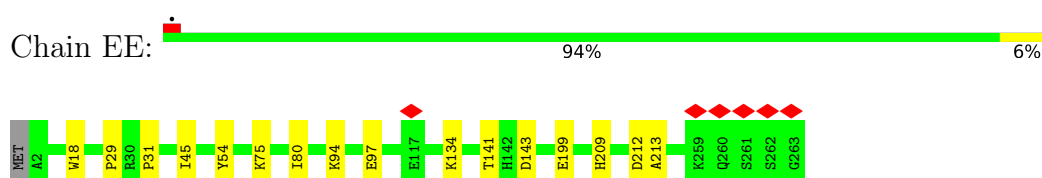
- Molecule 48: Small ribosomal subunit protein uS5



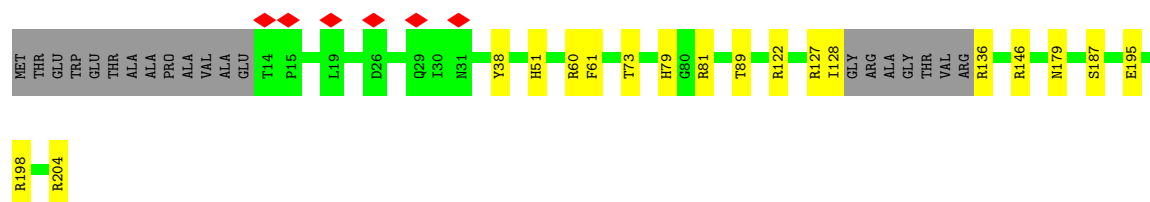
- Molecule 49: Ribosomal protein S3



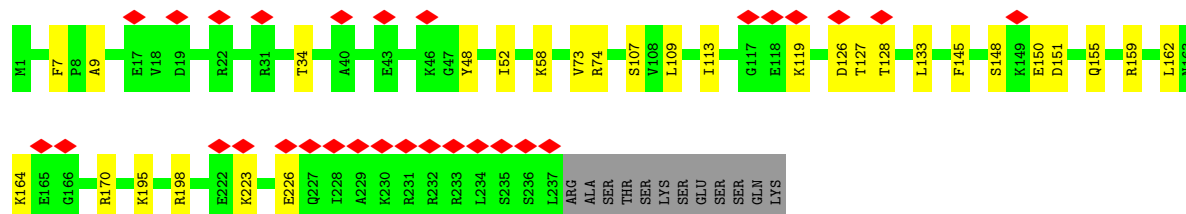
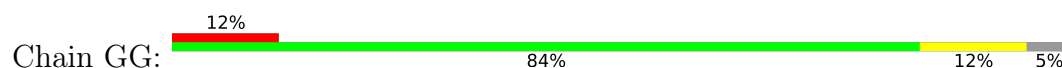
- Molecule 50: eS4 (S4 X isoform)



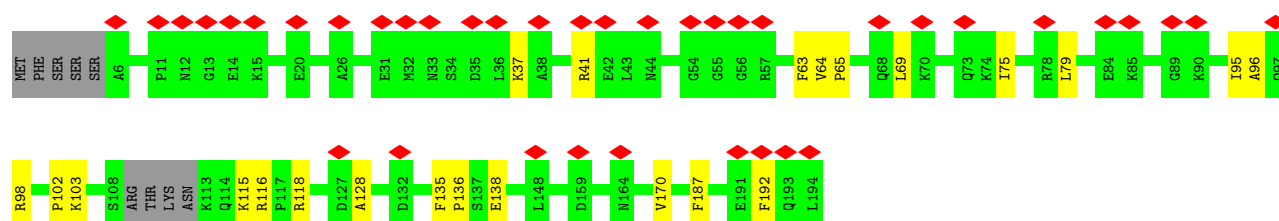
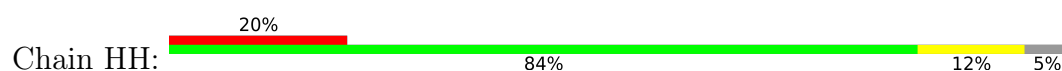
- Molecule 51: Ribosomal protein S5



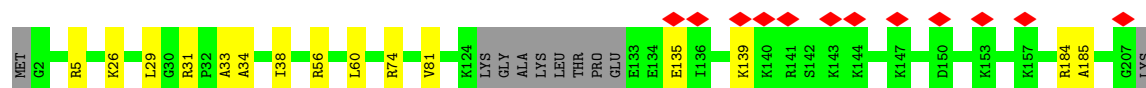
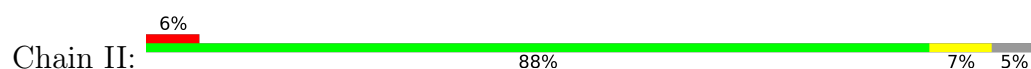
- Molecule 52: 40S ribosomal protein S6



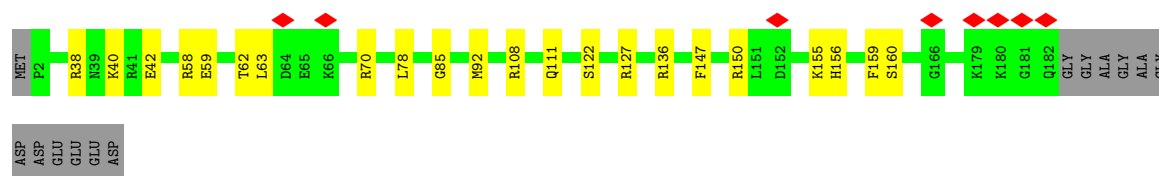
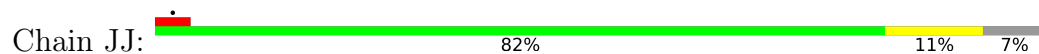
- Molecule 53: 40S ribosomal protein S7



- Molecule 54: 40S ribosomal protein S8



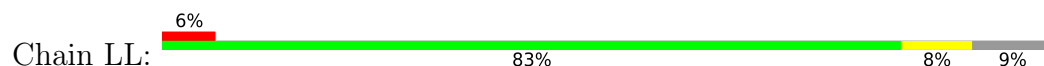
- Molecule 55: Ribosomal protein S9 (Predicted)



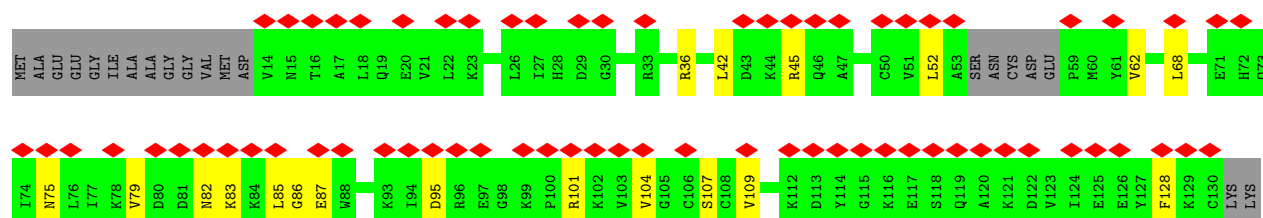
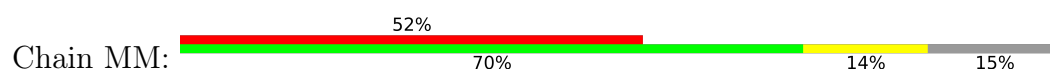
- Molecule 56: Small ribosomal subunit protein eS10



- Molecule 57: Ribosomal protein S11



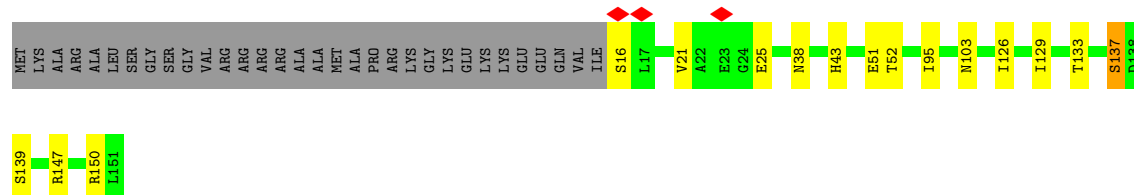
- Molecule 58: 40S ribosomal protein S12



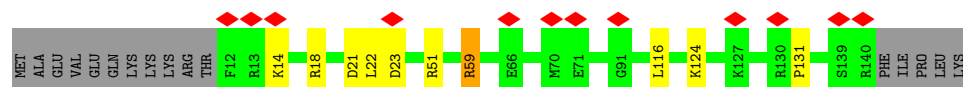
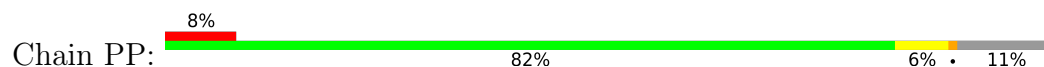
- Molecule 59: Ribosomal protein S13



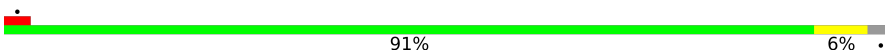
- Molecule 60: Small ribosomal subunit protein uS11

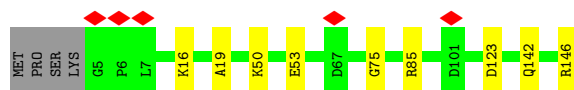


- Molecule 61: uS19



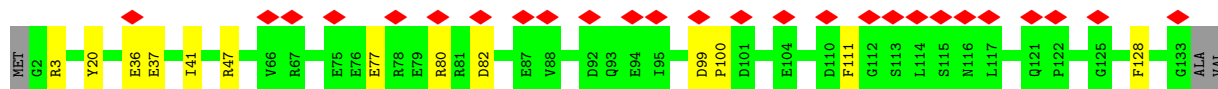
- Molecule 62: uS9

Chain QQ:  91% 6%



- Molecule 63: eS17

Chain RR:  19% 88% 10%



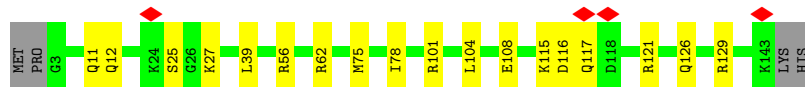
- Molecule 64: uS13

Chain SS:  5% 82% 11% 8%



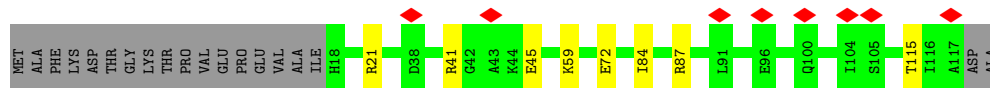
- Molecule 65: eS19

Chain TT:  85% 12%

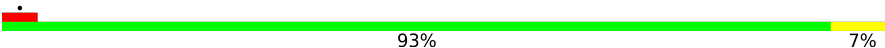


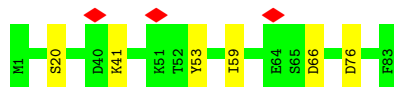
- Molecule 66: uS10

Chain UU:  7% 77% 7% 16%

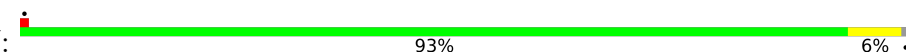


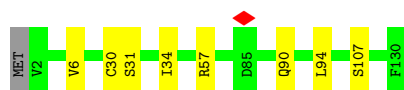
- Molecule 67: eS21

Chain VV:  93% 7%



- Molecule 68: Ribosomal protein S15a

Chain WW:  93% 6%



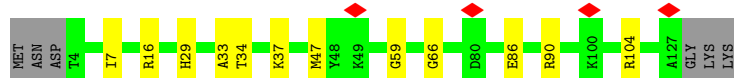
- Molecule 69: uS12

Chain XX: 91% 7% .



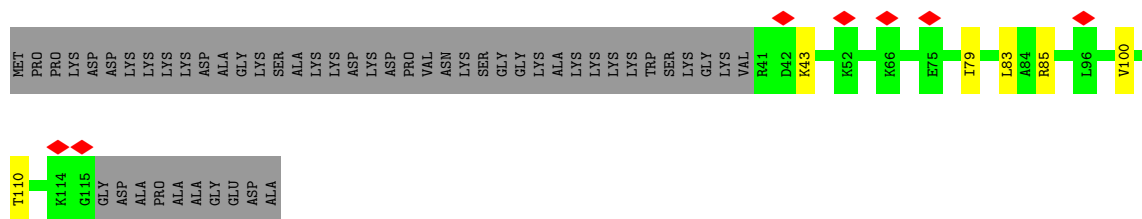
- Molecule 70: 40S ribosomal protein S24

Chain YY: 86% 9% 5%



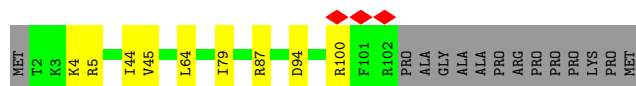
- Molecule 71: eS25

Chain ZZ: 6% 55% 5% 40%



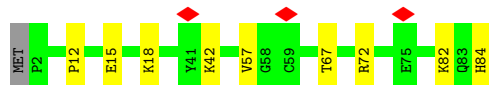
- Molecule 72: 40S ribosomal protein S26

Chain aa: 80% 8% 12%



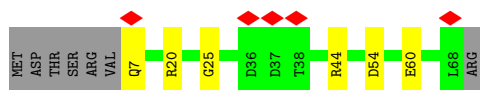
- Molecule 73: 40S ribosomal protein S27

Chain bb: 88% 11% .



- Molecule 74: Ribosomal protein S28

Chain cc: 7% 81% 9% 10%



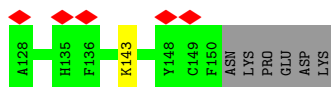
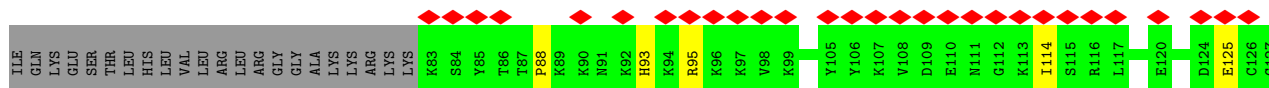
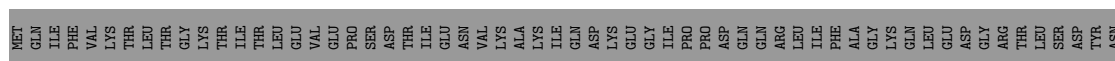
- Molecule 75: eS29



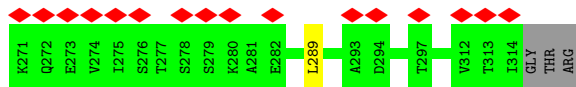
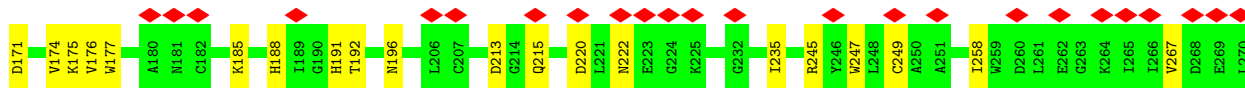
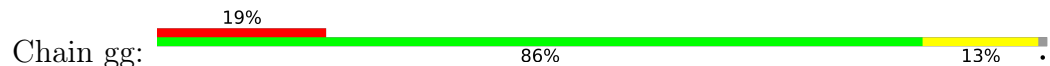
- Molecule 76: 40S ribosomal protein S30



- Molecule 77: Ribosomal protein S27a

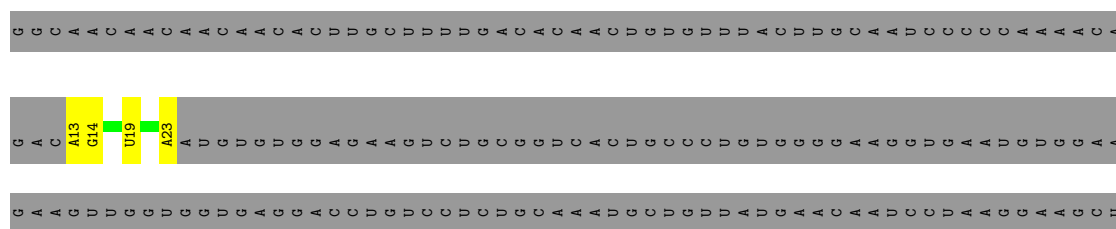


- Molecule 78: RACK1



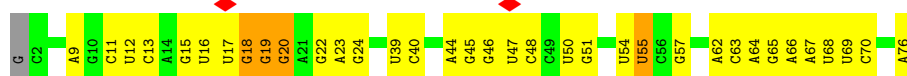
- Molecule 79: MF mRNA

Chain 10:  94%



• Molecule 80: Phe-tRNA

Chain 12:  53% 41% 5%



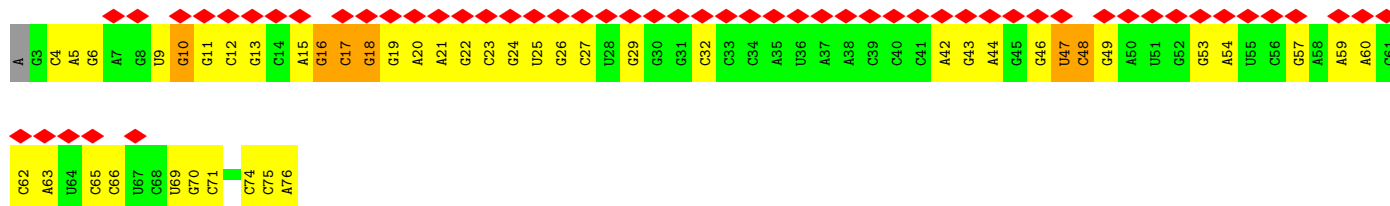
• Molecule 81: Met-tRNA

Chain 13:  12% 68% 24% 7%



• Molecule 81: Met-tRNA

Chain 11:  75% 39% 52% 8%



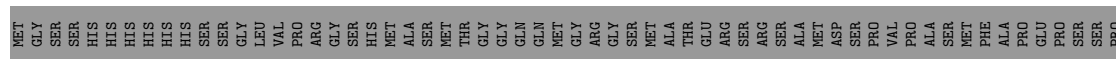
• Molecule 82: Ribosomal protein L37

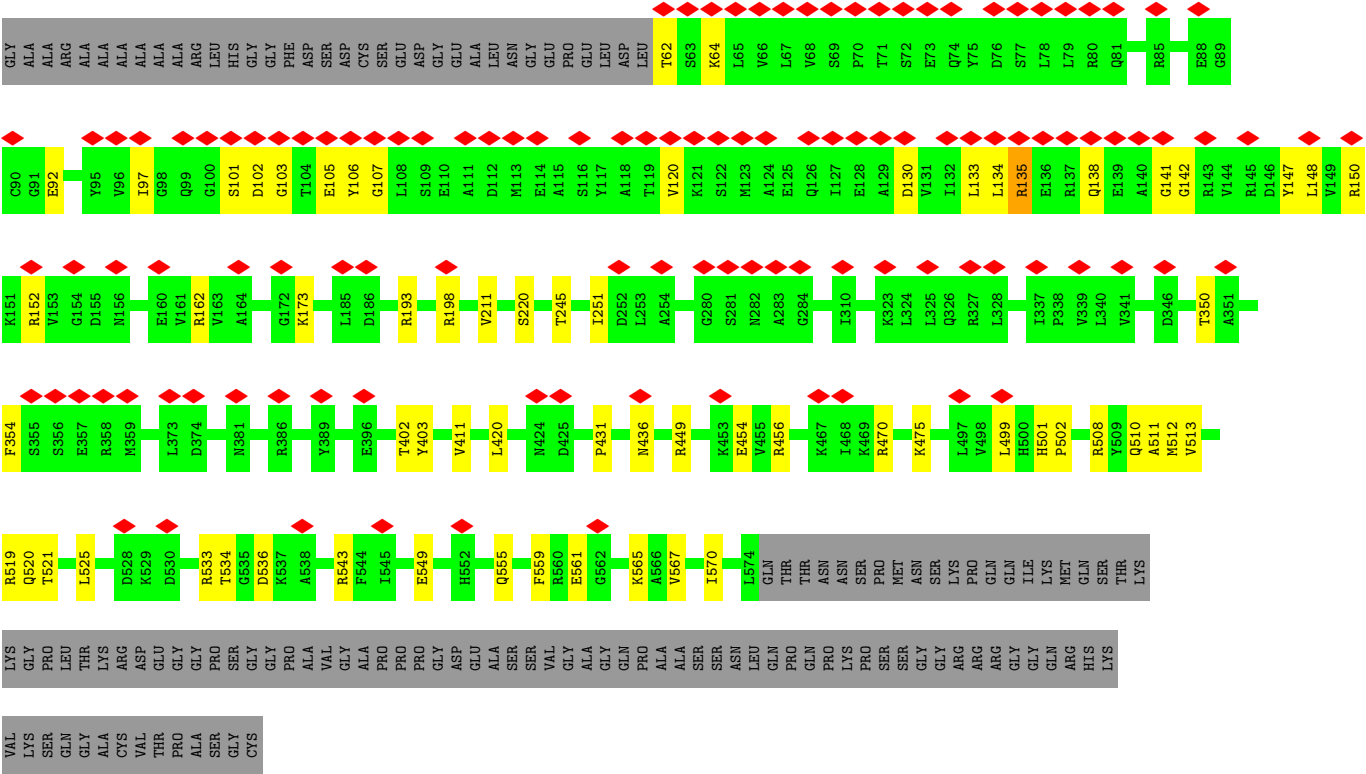
Chain j:  77% 11% 11%



• Molecule 83: GTP-binding protein 1

Chain jj:  17% 64% 9% 27%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8005	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	29.7955	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.100	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	464.8, 464.8, 464.8	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.162, 1.162, 1.162	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: K, MG, SPD, GCP, ATP, GTP, ZN

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	5	0.47	0/86380	0.68	14/134721 (0.0%)
2	7	0.45	0/2836	0.61	0/4421
3	8	0.46	0/3581	0.65	0/5577
4	9	0.41	0/40509	0.66	8/63128 (0.0%)
5	A	0.37	0/1936	0.53	0/2596
6	B	0.34	0/3240	0.53	0/4339
7	C	0.36	0/2937	0.54	0/3946
8	D	0.32	0/2437	0.49	0/3264
9	E	0.30	0/1762	0.54	0/2362
10	G	0.31	0/1910	0.52	0/2569
11	H	0.32	0/1535	0.48	0/2063
12	I	0.33	0/1702	0.48	0/2272
13	J	0.28	0/1385	0.48	0/1852
14	K	0.37	0/1911	0.52	0/2549
15	L	0.33	0/1733	0.50	0/2316
16	M	0.32	0/1158	0.51	0/1547
17	N	0.40	0/1746	0.55	0/2338
18	O	0.37	0/1662	0.55	1/2222 (0.0%)
19	P	0.36	0/1268	0.55	0/1700
20	Q	0.38	0/1539	0.53	0/2054
21	R	0.33	0/1524	0.53	0/2013
22	S	0.36	0/1501	0.49	0/2012
23	T	0.34	0/1326	0.50	0/1770
24	U	0.29	0/823	0.51	0/1104
25	V	0.35	0/983	0.53	0/1319
26	W	0.31	0/873	0.52	0/1158
27	X	0.31	0/984	0.48	0/1323
28	Y	0.33	0/1132	0.49	0/1504
29	Z	0.34	0/1130	0.49	0/1507
30	a	0.38	0/1191	0.56	0/1590
31	b	0.31	0/819	0.54	0/1081
32	c	0.36	0/771	0.53	0/1034

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.37	0/903	0.54	0/1216
34	e	0.39	0/1071	0.58	0/1429
35	f	0.39	0/895	0.49	0/1198
36	g	0.34	0/916	0.52	0/1220
37	h	0.34	0/1021	0.53	0/1348
38	i	0.30	0/841	0.60	0/1112
39	k	0.30	0/575	0.47	0/761
40	l	0.39	0/459	0.57	0/608
41	m	0.34	0/435	0.48	0/575
42	n	0.37	0/241	0.56	0/305
43	o	0.34	0/864	0.49	0/1140
44	p	0.36	0/718	0.59	0/953
45	r	0.35	0/1010	0.56	0/1354
46	AA	0.28	0/1747	0.50	0/2374
47	BB	0.30	0/1756	0.51	0/2350
48	CC	0.31	0/1753	0.52	0/2369
49	DD	0.27	0/1767	0.49	0/2378
50	EE	0.26	0/2118	0.50	0/2849
51	FF	0.27	0/1481	0.50	0/1991
52	GG	0.24	0/1946	0.52	0/2590
53	HH	0.23	0/1511	0.48	0/2022
54	II	0.28	0/1655	0.51	0/2205
55	JJ	0.26	0/1533	0.51	0/2047
56	KK	0.26	0/834	0.46	0/1125
57	LL	0.30	0/1195	0.53	0/1597
58	MM	0.20	0/880	0.57	0/1179
59	NN	0.29	0/1226	0.52	0/1649
60	OO	0.32	0/1029	0.56	0/1380
61	PP	0.24	0/1079	0.55	0/1441
62	QQ	0.27	0/1146	0.51	0/1534
63	RR	0.25	0/1082	0.54	0/1452
64	SS	0.26	0/1175	0.52	0/1575
65	TT	0.25	0/1115	0.53	0/1493
66	UU	0.25	0/805	0.45	0/1081
67	VV	0.27	0/644	0.43	0/860
68	WW	0.34	0/1051	0.50	0/1406
69	XX	0.31	0/1105	0.51	0/1476
70	YY	0.23	0/1028	0.47	0/1366
71	ZZ	0.23	0/604	0.46	0/810
72	aa	0.32	0/828	0.50	0/1109
73	bb	0.25	0/665	0.45	0/891
74	cc	0.25	0/490	0.42	0/656
75	dd	0.32	0/470	0.57	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	ee	0.24	0/462	0.56	0/607
77	ff	0.16	0/567	0.56	0/753
78	gg	0.22	0/2493	0.48	0/3394
79	10	0.38	0/261	0.53	0/404
80	12	0.31	0/1787	0.66	0/2783
81	11	0.26	0/1773	0.67	0/2763
81	13	0.31	0/1773	0.66	0/2763
82	j	0.38	0/720	0.53	0/952
83	jj	0.21	0/4047	0.49	0/5462
All	All	0.40	0/235774	0.62	23/346229 (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
1	5	0	1
5	A	0	1
6	B	0	1
7	C	0	1
8	D	0	3
9	E	0	1
11	H	0	2
15	L	0	1
18	O	0	1
20	Q	0	3
22	S	0	1
23	T	0	1
27	X	0	2
29	Z	0	2
31	b	0	1
34	e	0	1
35	f	0	1
36	g	0	1
39	k	0	1
44	p	0	1
51	FF	0	1
54	II	0	2
60	OO	0	1
61	PP	0	1
77	ff	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
83	jj	0	2
All	All	0	35

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	9	1835	A	C2'-C3'-O3'	7.03	120.04	109.50
1	5	2544	G	C8-N9-C1'	-6.55	107.34	127.00
1	5	1440	U	C2'-C3'-O3'	6.47	119.20	109.50
1	5	914	U	C2'-C3'-O3'	6.09	118.64	109.50
1	5	4119	C	C2'-C3'-O3'	5.97	118.46	109.50

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	2544	G	Sidechain
5	A	123	ARG	Sidechain
6	B	21	ARG	Sidechain
7	C	204	ARG	Sidechain
8	D	24	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	77221	0	39013	600	0
2	7	2538	0	1286	8	0
3	8	3208	0	1629	18	0
4	9	36229	0	18300	326	0
5	A	1898	0	1993	15	0
6	B	3172	0	3310	22	0
7	C	2883	0	3053	17	0
8	D	2391	0	2424	11	0
9	E	1729	0	1887	13	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	G	1879	0	2027	19	0
11	H	1516	0	1597	8	0
12	I	1664	0	1712	6	0
13	J	1362	0	1399	8	0
14	K	1875	0	1995	14	0
15	L	1702	0	1820	9	0
16	M	1137	0	1211	6	0
17	N	1701	0	1749	22	0
18	O	1630	0	1778	9	0
19	P	1242	0	1274	13	0
20	Q	1515	0	1634	12	0
21	R	1508	0	1664	9	0
22	S	1462	0	1508	7	0
23	T	1298	0	1366	6	0
24	U	809	0	833	1	0
25	V	969	0	1031	13	0
26	W	860	0	903	6	0
27	X	967	0	1040	5	0
28	Y	1115	0	1205	3	0
29	Z	1107	0	1182	16	0
30	a	1162	0	1209	12	0
31	b	806	0	866	0	0
32	c	761	0	794	6	0
33	d	888	0	930	4	0
34	e	1053	0	1147	4	0
35	f	876	0	912	2	0
36	g	906	0	998	5	0
37	h	1013	0	1147	4	0
38	i	830	0	916	3	0
39	k	569	0	637	5	0
40	l	447	0	480	3	0
41	m	429	0	465	8	0
42	n	240	0	289	1	0
43	o	851	0	920	7	0
44	p	708	0	756	8	0
45	r	994	0	1051	5	0
46	AA	1710	0	1708	8	0
47	BB	1729	0	1803	17	0
48	CC	1716	0	1806	11	0
49	DD	1739	0	1832	11	0
50	EE	2076	0	2177	10	0
51	FF	1460	0	1509	13	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	GG	1923	0	2089	23	0
53	HH	1489	0	1582	15	0
54	II	1628	0	1706	10	0
55	JJ	1508	0	1626	16	0
56	KK	810	0	836	2	0
57	LL	1175	0	1249	9	0
58	MM	871	0	913	14	0
59	NN	1202	0	1289	6	0
60	OO	1016	0	1039	12	0
61	PP	1058	0	1104	9	0
62	QQ	1128	0	1195	7	0
63	RR	1068	0	1121	10	0
64	SS	1157	0	1213	13	0
65	TT	1097	0	1132	11	0
66	UU	795	0	862	6	0
67	VV	637	0	637	4	0
68	WW	1034	0	1080	5	0
69	XX	1087	0	1154	12	0
70	YY	1011	0	1083	12	0
71	ZZ	598	0	656	4	0
72	aa	814	0	867	7	0
73	bb	651	0	672	6	0
74	cc	488	0	514	4	0
75	dd	459	0	448	3	0
76	ee	457	0	502	6	0
77	ff	555	0	567	4	0
78	gg	2436	0	2393	22	0
79	10	234	0	118	1	0
80	12	1599	0	808	20	0
81	11	1585	0	804	32	0
81	13	1585	0	803	14	0
82	j	705	0	737	9	0
83	jj	3982	0	4069	42	0
84	5	10	0	19	0	0
85	dd	1	0	0	0	0
85	g	1	0	0	0	0
85	j	1	0	0	0	0
85	m	1	0	0	0	0
85	o	1	0	0	0	0
85	p	1	0	0	0	0
86	12	32	0	11	1	0
87	12	11	0	8	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
88	11	31	0	11	1	0
88	13	31	0	11	0	0
89	13	8	0	8	0	0
90	jj	32	0	14	2	0
91	jj	1	0	0	0	0
92	jj	1	0	0	0	0
All	All	219555	0	163125	1457	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 1457 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2638:G:N2	1:5:2697:A:N1	2.09	0.99
1:5:2395:A:O2'	1:5:2806:A:H1'	1.72	0.89
44:p:42:CYS:HB3	44:p:60:CYS:SG	2.15	0.87
1:5:982:U:H3	1:5:1273:G:H1	1.23	0.86
4:9:1272:C:O2'	4:9:1274:G:N2	2.10	0.85

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	A	246/257 (96%)	237 (96%)	9 (4%)	0	100	100
6	B	392/403 (97%)	379 (97%)	13 (3%)	0	100	100
7	C	360/425 (85%)	354 (98%)	6 (2%)	0	100	100
8	D	291/297 (98%)	285 (98%)	6 (2%)	0	100	100
9	E	208/291 (72%)	200 (96%)	8 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	G	229/319 (72%)	222 (97%)	7 (3%)	0	100	100
11	H	188/192 (98%)	182 (97%)	6 (3%)	0	100	100
12	I	201/214 (94%)	196 (98%)	5 (2%)	0	100	100
13	J	168/178 (94%)	166 (99%)	2 (1%)	0	100	100
14	K	223/247 (90%)	217 (97%)	6 (3%)	0	100	100
15	L	208/211 (99%)	203 (98%)	5 (2%)	0	100	100
16	M	136/218 (62%)	134 (98%)	2 (2%)	0	100	100
17	N	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
18	O	197/203 (97%)	190 (96%)	7 (4%)	0	100	100
19	P	151/184 (82%)	147 (97%)	4 (3%)	0	100	100
20	Q	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
21	R	178/196 (91%)	177 (99%)	1 (1%)	0	100	100
22	S	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
23	T	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
24	U	97/128 (76%)	92 (95%)	5 (5%)	0	100	100
25	V	127/140 (91%)	125 (98%)	2 (2%)	0	100	100
26	W	102/157 (65%)	101 (99%)	1 (1%)	0	100	100
27	X	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
28	Y	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
29	Z	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
30	a	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
31	b	94/245 (38%)	92 (98%)	2 (2%)	0	100	100
32	c	96/115 (84%)	93 (97%)	3 (3%)	0	100	100
33	d	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
34	e	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
35	f	107/110 (97%)	105 (98%)	2 (2%)	0	100	100
36	g	112/116 (97%)	112 (100%)	0	0	100	100
37	h	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
38	i	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
39	k	67/70 (96%)	67 (100%)	0	0	100	100
40	l	48/51 (94%)	48 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	m	50/102 (49%)	46 (92%)	4 (8%)	0	100	100
42	n	23/25 (92%)	23 (100%)	0	0	100	100
43	o	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
44	p	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	r	122/137 (89%)	120 (98%)	2 (2%)	0	100	100
46	AA	215/295 (73%)	207 (96%)	8 (4%)	0	100	100
47	BB	211/264 (80%)	203 (96%)	8 (4%)	0	100	100
48	CC	219/293 (75%)	214 (98%)	5 (2%)	0	100	100
49	DD	222/243 (91%)	218 (98%)	4 (2%)	0	100	100
50	EE	260/263 (99%)	253 (97%)	7 (3%)	0	100	100
51	FF	180/204 (88%)	171 (95%)	9 (5%)	0	100	100
52	GG	235/249 (94%)	225 (96%)	10 (4%)	0	100	100
53	HH	181/194 (93%)	178 (98%)	3 (2%)	0	100	100
54	II	194/208 (93%)	193 (100%)	1 (0%)	0	100	100
55	JJ	179/194 (92%)	175 (98%)	4 (2%)	0	100	100
56	KK	94/165 (57%)	92 (98%)	2 (2%)	0	100	100
57	LL	139/158 (88%)	137 (99%)	2 (1%)	0	100	100
58	MM	108/132 (82%)	105 (97%)	3 (3%)	0	100	100
59	NN	147/151 (97%)	144 (98%)	3 (2%)	0	100	100
60	OO	134/168 (80%)	132 (98%)	2 (2%)	0	100	100
61	PP	127/145 (88%)	124 (98%)	3 (2%)	0	100	100
62	QQ	140/146 (96%)	137 (98%)	3 (2%)	0	100	100
63	RR	130/135 (96%)	128 (98%)	2 (2%)	0	100	100
64	SS	138/152 (91%)	134 (97%)	4 (3%)	0	100	100
65	TT	139/145 (96%)	136 (98%)	3 (2%)	0	100	100
66	UU	98/119 (82%)	94 (96%)	4 (4%)	0	100	100
67	VV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
68	WW	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
69	XX	138/143 (96%)	135 (98%)	3 (2%)	0	100	100
70	YY	122/130 (94%)	119 (98%)	3 (2%)	0	100	100
71	ZZ	73/125 (58%)	72 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	aa	99/115 (86%)	96 (97%)	3 (3%)	0	100	100
73	bb	81/84 (96%)	76 (94%)	5 (6%)	0	100	100
74	cc	60/69 (87%)	59 (98%)	1 (2%)	0	100	100
75	dd	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
76	ee	55/133 (41%)	53 (96%)	2 (4%)	0	100	100
77	ff	66/156 (42%)	63 (96%)	3 (4%)	0	100	100
78	gg	311/317 (98%)	297 (96%)	14 (4%)	0	100	100
82	j	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
83	jj	511/703 (73%)	498 (98%)	13 (2%)	0	100	100
All	All	11657/13594 (86%)	11344 (97%)	313 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	A	190/199 (96%)	190 (100%)	0	100	100
6	B	342/348 (98%)	342 (100%)	0	100	100
7	C	302/347 (87%)	302 (100%)	0	100	100
8	D	247/250 (99%)	247 (100%)	0	100	100
9	E	190/251 (76%)	190 (100%)	0	100	100
10	G	200/272 (74%)	200 (100%)	0	100	100
11	H	169/171 (99%)	169 (100%)	0	100	100
12	I	175/181 (97%)	175 (100%)	0	100	100
13	J	143/149 (96%)	143 (100%)	0	100	100
14	K	196/215 (91%)	196 (100%)	0	100	100
15	L	175/176 (99%)	175 (100%)	0	100	100
16	M	117/161 (73%)	117 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	N	171/172 (99%)	171 (100%)	0	100	100
18	O	171/173 (99%)	171 (100%)	0	100	100
19	P	134/163 (82%)	134 (100%)	0	100	100
20	Q	164/165 (99%)	164 (100%)	0	100	100
21	R	159/175 (91%)	159 (100%)	0	100	100
22	S	157/157 (100%)	156 (99%)	1 (1%)	78	88
23	T	139/140 (99%)	139 (100%)	0	100	100
24	U	89/114 (78%)	89 (100%)	0	100	100
25	V	100/107 (94%)	100 (100%)	0	100	100
26	W	86/126 (68%)	86 (100%)	0	100	100
27	X	106/134 (79%)	106 (100%)	0	100	100
28	Y	124/135 (92%)	124 (100%)	0	100	100
29	Z	117/118 (99%)	117 (100%)	0	100	100
30	a	119/120 (99%)	119 (100%)	0	100	100
31	b	80/184 (44%)	80 (100%)	0	100	100
32	c	84/98 (86%)	84 (100%)	0	100	100
33	d	98/110 (89%)	98 (100%)	0	100	100
34	e	114/121 (94%)	114 (100%)	0	100	100
35	f	88/89 (99%)	88 (100%)	0	100	100
36	g	98/99 (99%)	98 (100%)	0	100	100
37	h	109/110 (99%)	109 (100%)	0	100	100
38	i	86/89 (97%)	86 (100%)	0	100	100
39	k	64/65 (98%)	64 (100%)	0	100	100
40	l	47/48 (98%)	47 (100%)	0	100	100
41	m	48/90 (53%)	48 (100%)	0	100	100
42	n	24/24 (100%)	24 (100%)	0	100	100
43	o	92/94 (98%)	92 (100%)	0	100	100
44	p	74/75 (99%)	74 (100%)	0	100	100
45	r	108/121 (89%)	108 (100%)	0	100	100
46	AA	180/245 (74%)	180 (100%)	0	100	100
47	BB	194/231 (84%)	194 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	CC	187/225 (83%)	186 (100%)	1 (0%)	81	89
49	DD	187/202 (93%)	187 (100%)	0	100	100
50	EE	224/225 (100%)	224 (100%)	0	100	100
51	FF	157/170 (92%)	157 (100%)	0	100	100
52	GG	207/218 (95%)	207 (100%)	0	100	100
53	HH	165/174 (95%)	165 (100%)	0	100	100
54	II	172/180 (96%)	172 (100%)	0	100	100
55	JJ	161/168 (96%)	161 (100%)	0	100	100
56	KK	87/136 (64%)	87 (100%)	0	100	100
57	LL	130/142 (92%)	130 (100%)	0	100	100
58	MM	94/108 (87%)	94 (100%)	0	100	100
59	NN	130/131 (99%)	130 (100%)	0	100	100
60	OO	106/130 (82%)	106 (100%)	0	100	100
61	PP	115/130 (88%)	115 (100%)	0	100	100
62	QQ	117/121 (97%)	117 (100%)	0	100	100
63	RR	119/121 (98%)	119 (100%)	0	100	100
64	SS	122/132 (92%)	122 (100%)	0	100	100
65	TT	111/115 (96%)	111 (100%)	0	100	100
66	UU	92/107 (86%)	92 (100%)	0	100	100
67	VV	67/67 (100%)	67 (100%)	0	100	100
68	WW	112/113 (99%)	112 (100%)	0	100	100
69	XX	112/115 (97%)	112 (100%)	0	100	100
70	YY	107/112 (96%)	107 (100%)	0	100	100
71	ZZ	66/103 (64%)	66 (100%)	0	100	100
72	aa	88/98 (90%)	88 (100%)	0	100	100
73	bb	75/76 (99%)	75 (100%)	0	100	100
74	cc	55/62 (89%)	55 (100%)	0	100	100
75	dd	48/49 (98%)	48 (100%)	0	100	100
76	ee	47/106 (44%)	47 (100%)	0	100	100
77	ff	61/140 (44%)	61 (100%)	0	100	100
78	gg	272/275 (99%)	272 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
82	j	73/80 (91%)	73 (100%)	0	100	100
83	jj	445/586 (76%)	445 (100%)	0	100	100
All	All	10181/11529 (88%)	10179 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	S	84	TYR
48	CC	248	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 111 such sidechains are listed below:

Mol	Chain	Res	Type
33	d	30	HIS
83	jj	367	ASN
49	DD	226	GLN
83	jj	138	GLN
72	aa	17	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3580/3601 (99%)	537 (15%)	165 (4%)
2	7	118/120 (98%)	7 (5%)	1 (0%)
3	8	149/156 (95%)	21 (14%)	4 (2%)
4	9	1685/1869 (90%)	233 (13%)	57 (3%)
79	10	10/185 (5%)	2 (20%)	0
80	12	74/76 (97%)	8 (10%)	3 (4%)
81	11	73/75 (97%)	11 (15%)	4 (5%)
81	13	73/75 (97%)	9 (12%)	3 (4%)
All	All	5762/6157 (93%)	828 (14%)	237 (4%)

5 of 828 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	13	U
1	5	15	A
1	5	25	A
1	5	39	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	42	A

5 of 237 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	3625	G
4	9	1679	A
1	5	4448	G
4	9	1638	G
81	11	74	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 8 are monoatomic - leaving 7 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	$\# Z > 2$
88	ATP	11	101	81	32,33,33	0.30	0	48,52,52	0.53	0
86	GTP	12	101	80	33,34,34	0.85	1 (3%)	50,54,54	1.55	8 (16%)
90	GCP	jj	700	91	32,34,34	2.00	2 (6%)	49,54,54	0.96	4 (8%)
87	PHE	12	102	80	10,11,12	0.37	0	8,13,15	0.23	0
84	SPD	5	5101	-	9,9,9	0.35	0	8,8,8	0.81	0
89	MET	13	102	81	6,7,8	0.55	0	2,7,9	0.30	0
88	ATP	13	101	81	32,33,33	0.40	0	48,52,52	0.53	0

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
88	ATP	11	101	81	-	3/22/38/38	0/3/3/3
86	GTP	12	101	80	-	4/22/38/38	0/3/3/3
90	GCP	jj	700	91	-	1/19/38/38	0/3/3/3
87	PHE	12	102	80	-	2/5/6/8	0/1/1/1
84	SPD	5	5101	-	-	1/7/7/7	-
89	MET	13	102	81	-	0/5/6/8	-
88	ATP	13	101	81	-	4/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	jj	700	GCP	PB-O3A	9.95	1.69	1.58
90	jj	700	GCP	PB-O2B	-2.34	1.50	1.56
86	12	101	GTP	C2-N3	2.09	1.38	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	12	101	GTP	C5-C4-N3	-5.08	120.31	128.39
86	12	101	GTP	C2-N3-C4	4.52	120.09	112.30
86	12	101	GTP	N9-C4-N3	3.26	132.48	125.95
90	jj	700	GCP	O2B-PB-C3B	3.25	120.20	106.73
86	12	101	GTP	C2-N1-C6	-3.12	119.45	125.11

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

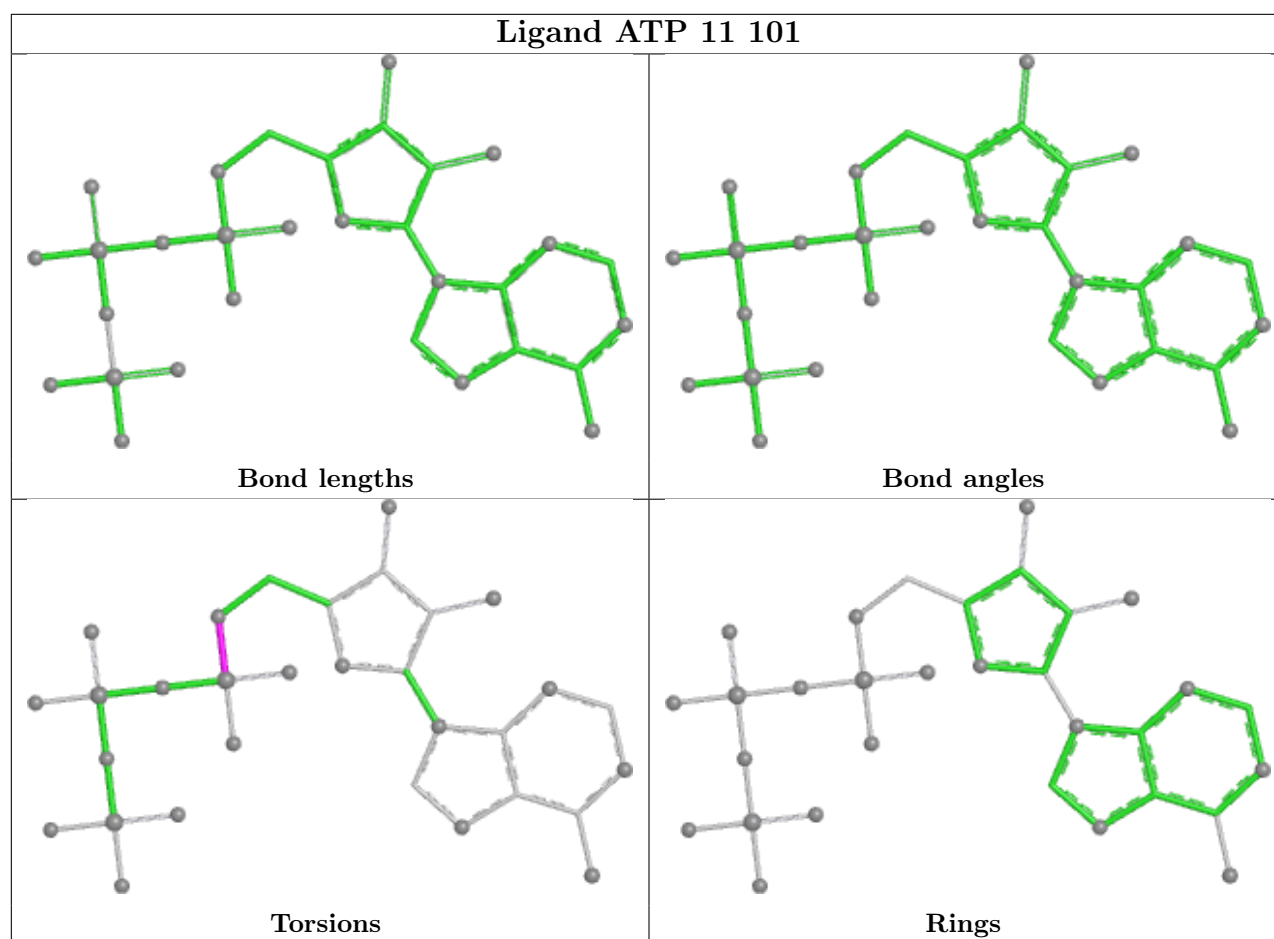
Mol	Chain	Res	Type	Atoms
86	12	101	GTP	PB-O3B-PG-O2G
86	12	101	GTP	C5'-O5'-PA-O2A
88	13	101	ATP	C5'-O5'-PA-O3A
88	11	101	ATP	C5'-O5'-PA-O1A
88	11	101	ATP	C5'-O5'-PA-O2A

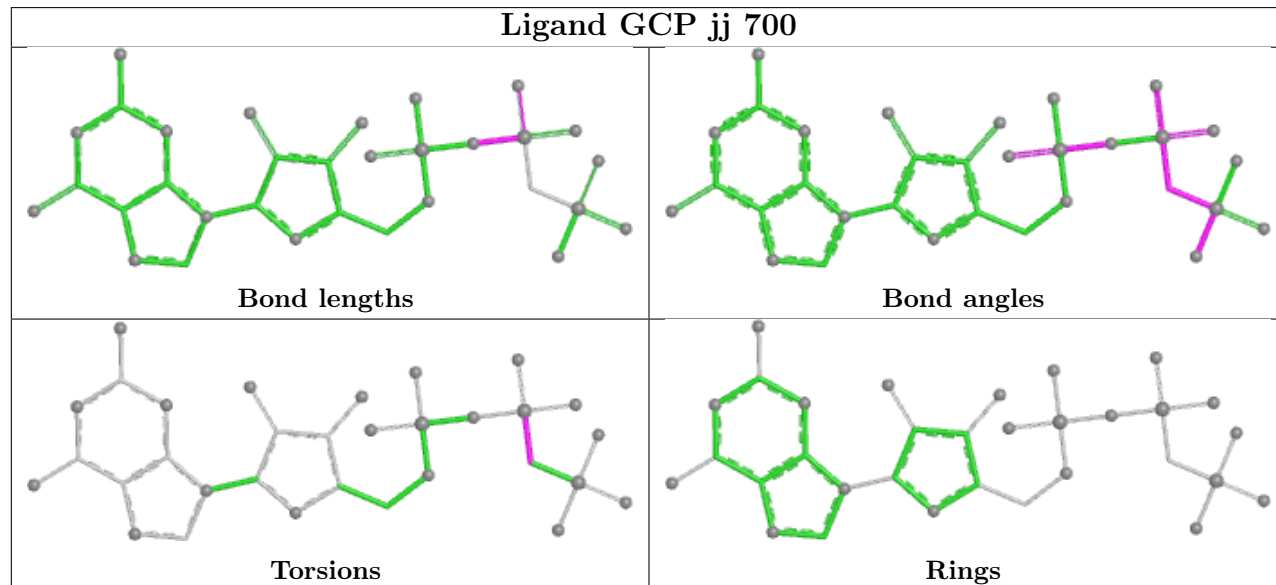
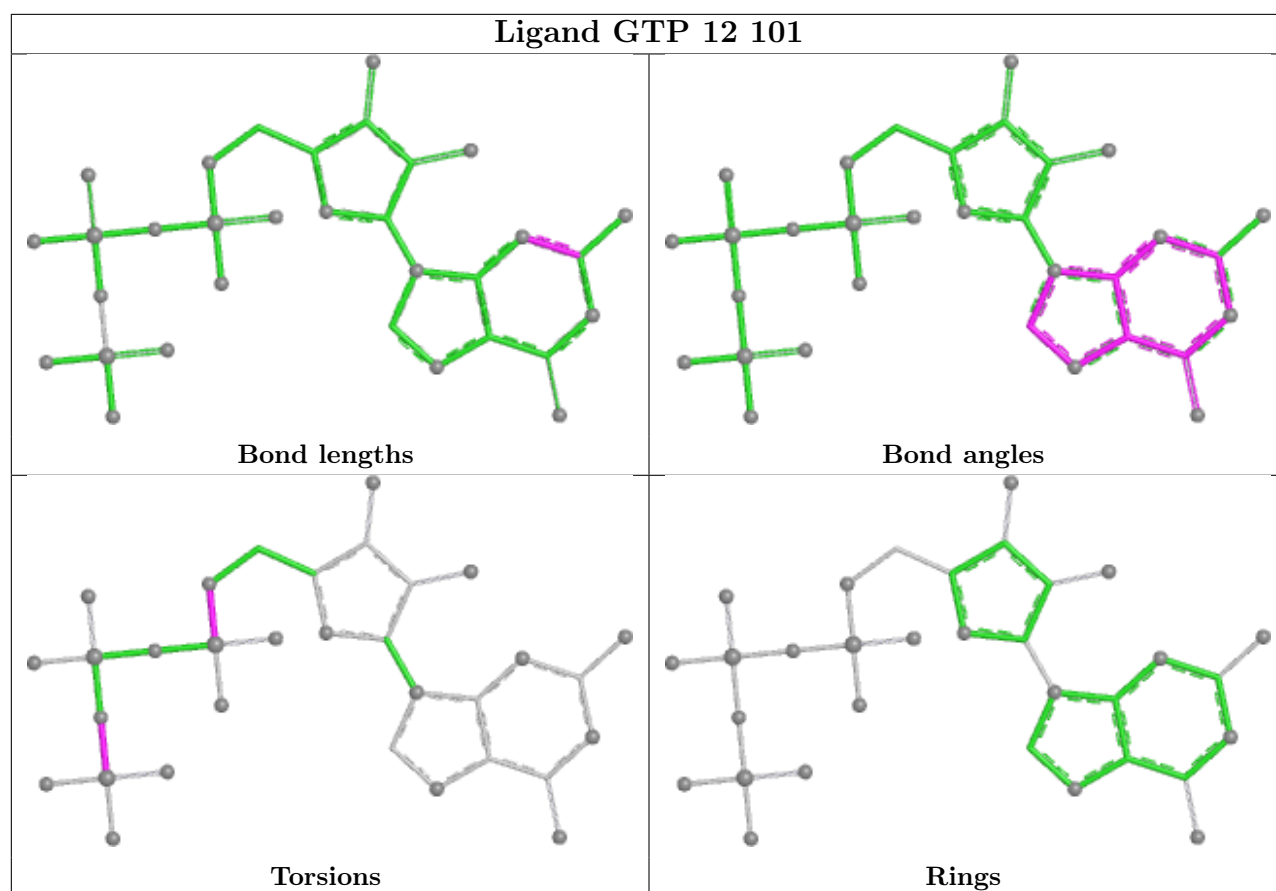
There are no ring outliers.

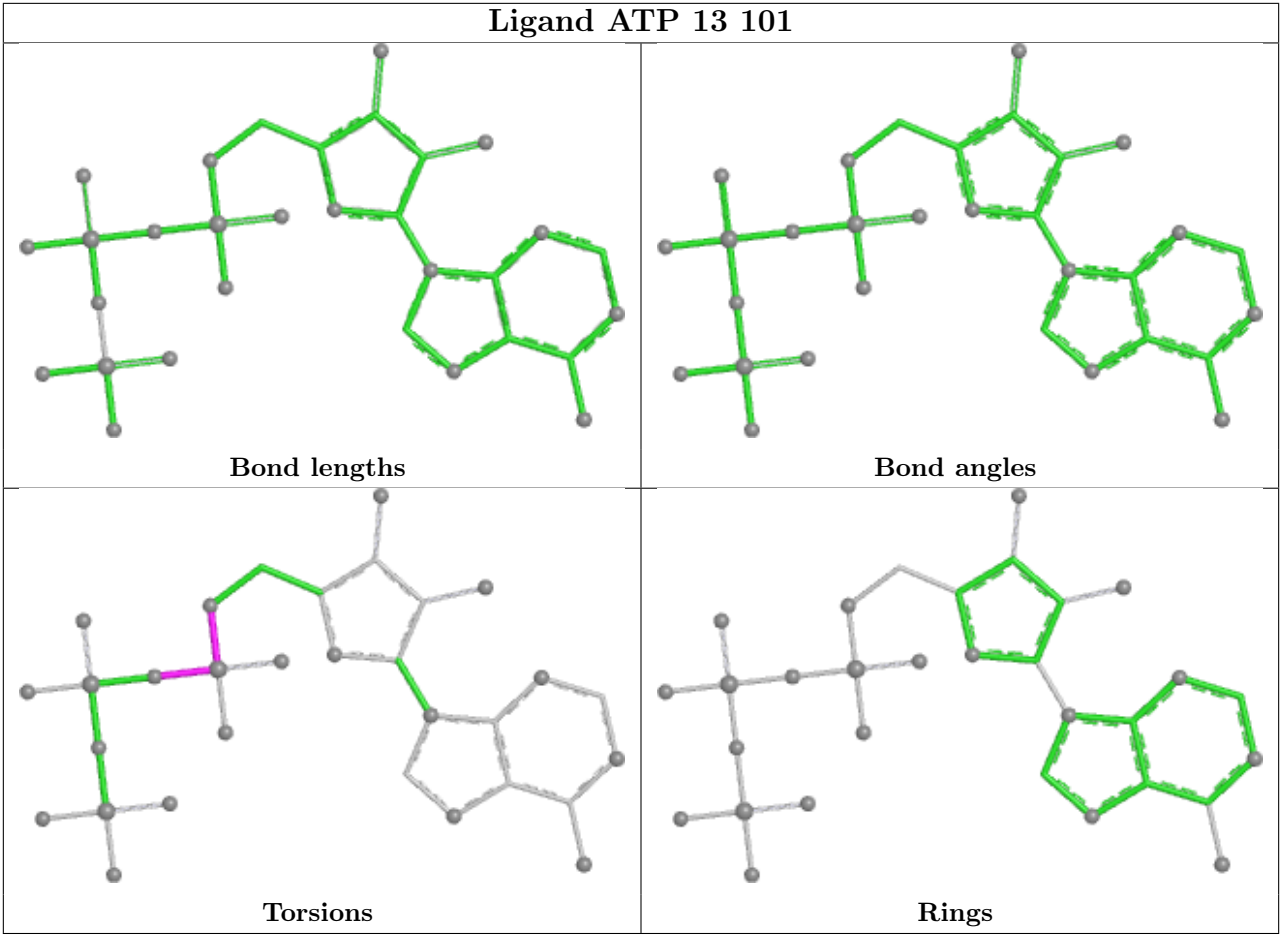
3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	11	101	ATP	1	0
86	12	101	GTP	1	0
90	jj	700	GCP	2	0

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







5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	23

The worst 5 of 23 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	42.08
1	5	1252:C	O3'	1271:G	P	35.85
1	5	1219:G	O3'	1233:G	P	21.05
1	5	1406(C):G	O3'	1411:C	P	17.84
1	5	4101:C	O3'	4107:G	P	17.51

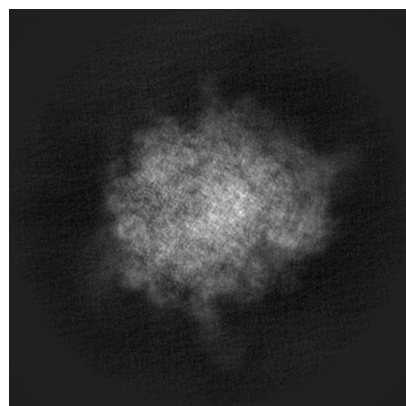
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73302. These allow visual inspection of the internal detail of the map and identification of artifacts.

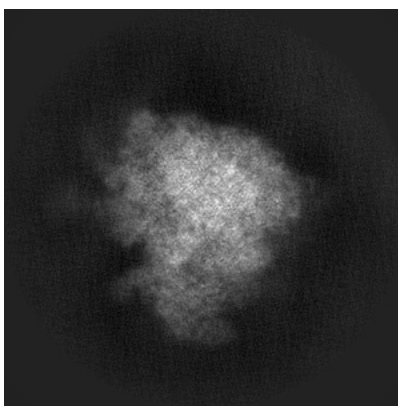
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

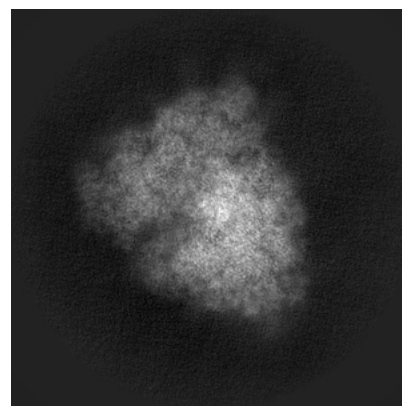
6.1.1 Primary map



X

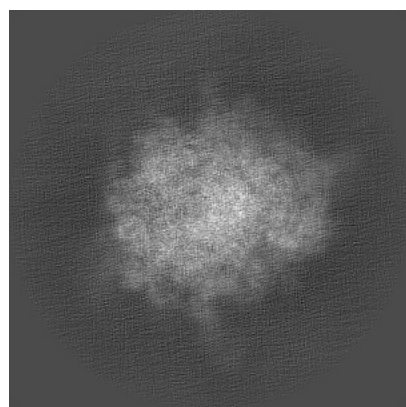


Y

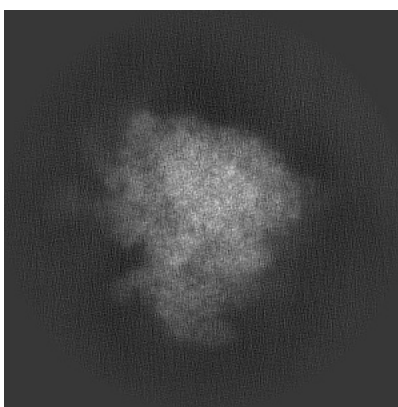


Z

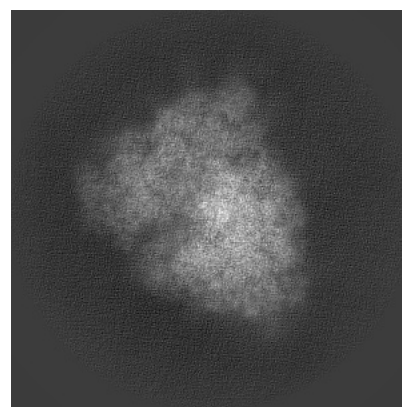
6.1.2 Raw map



X



Y

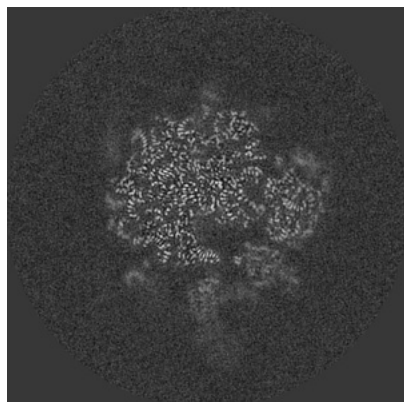


Z

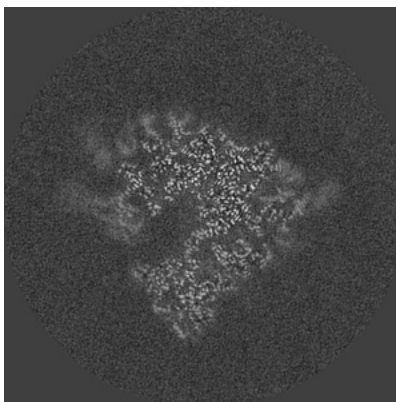
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

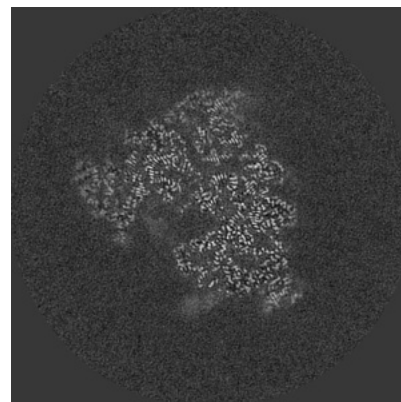
6.2.1 Primary map



X Index: 200

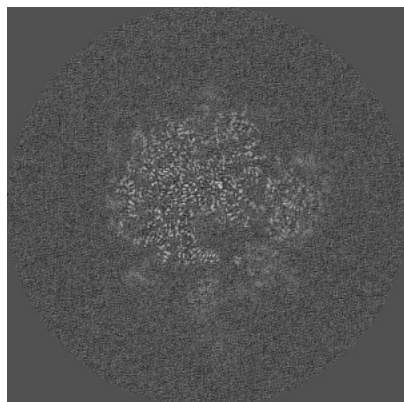


Y Index: 200

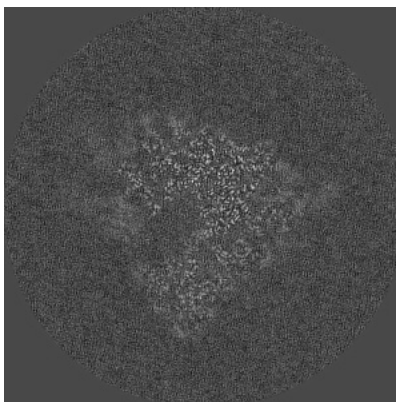


Z Index: 200

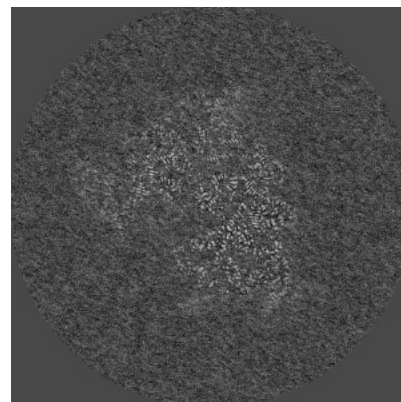
6.2.2 Raw map



X Index: 200



Y Index: 200

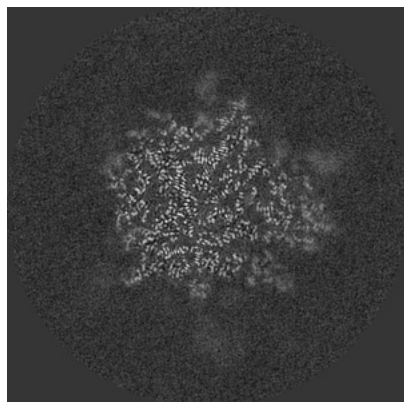


Z Index: 200

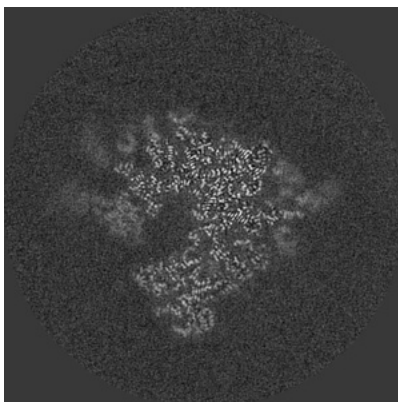
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

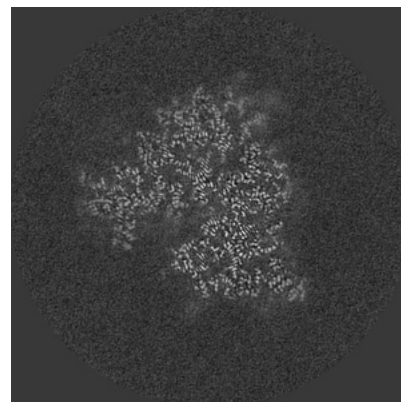
6.3.1 Primary map



X Index: 215

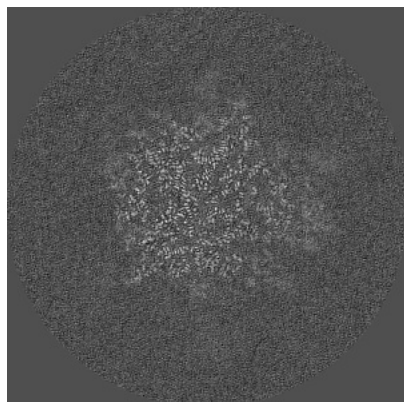


Y Index: 203

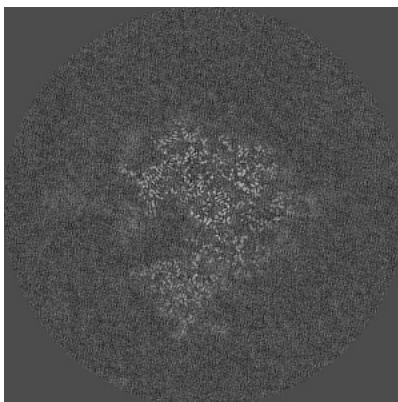


Z Index: 192

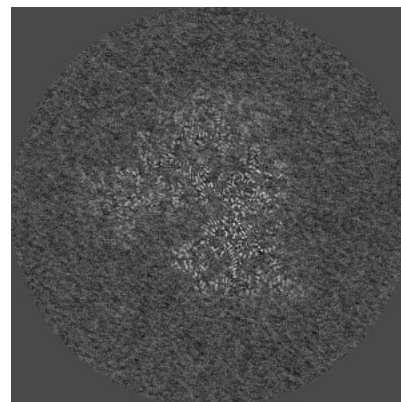
6.3.2 Raw map



X Index: 215



Y Index: 209

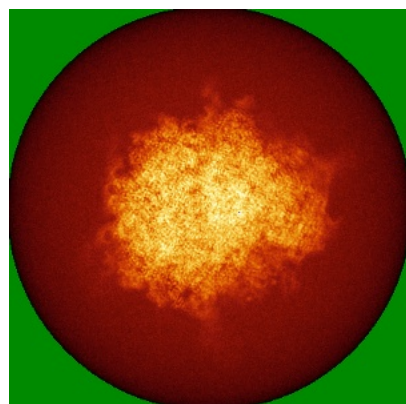


Z Index: 192

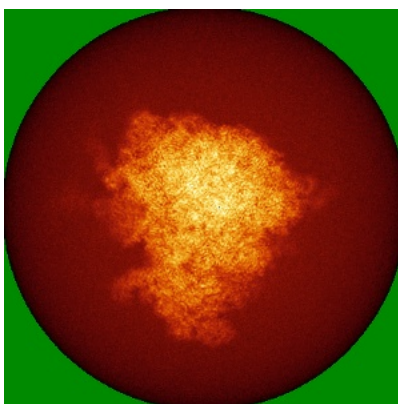
The images above show the largest variance slices of the map in three orthogonal directions.

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

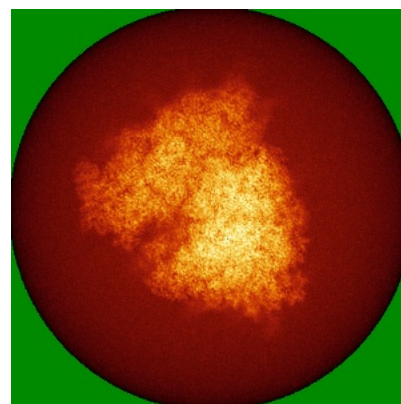
6.4.1 Primary map



X

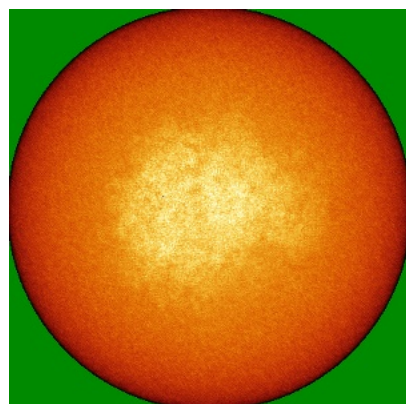


Y

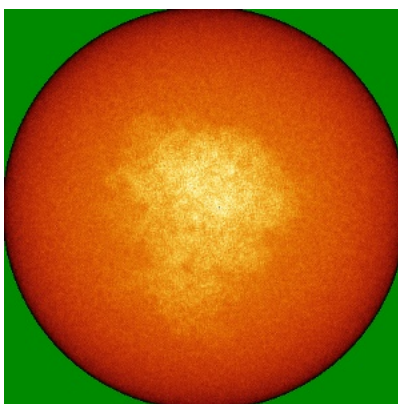


Z

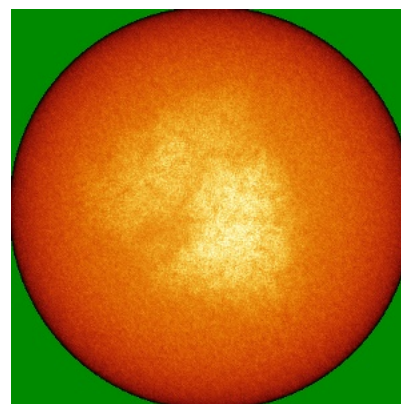
6.4.2 Raw map



X



Y

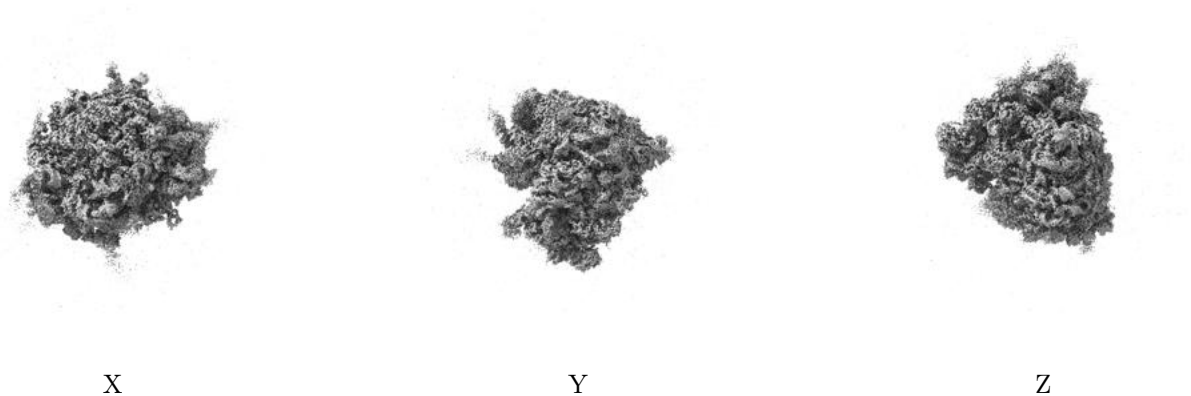


Z

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

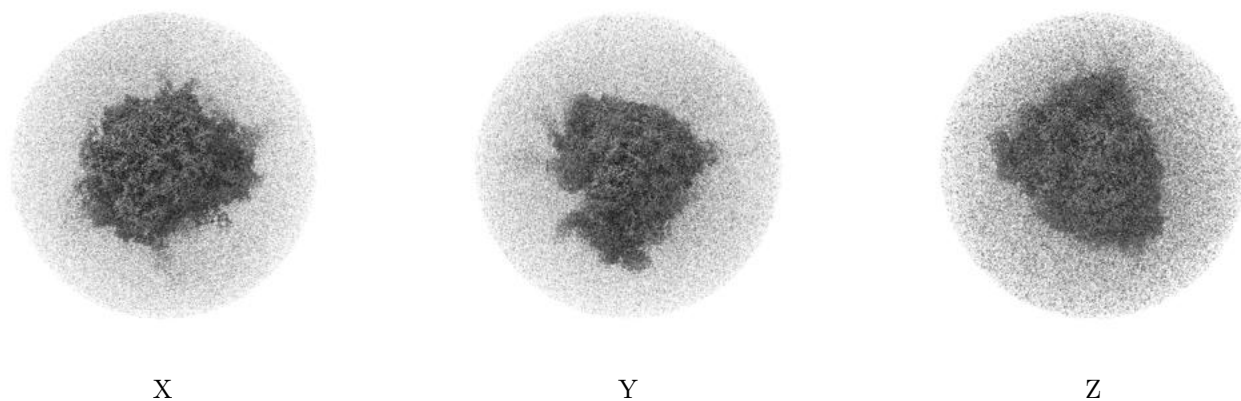
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

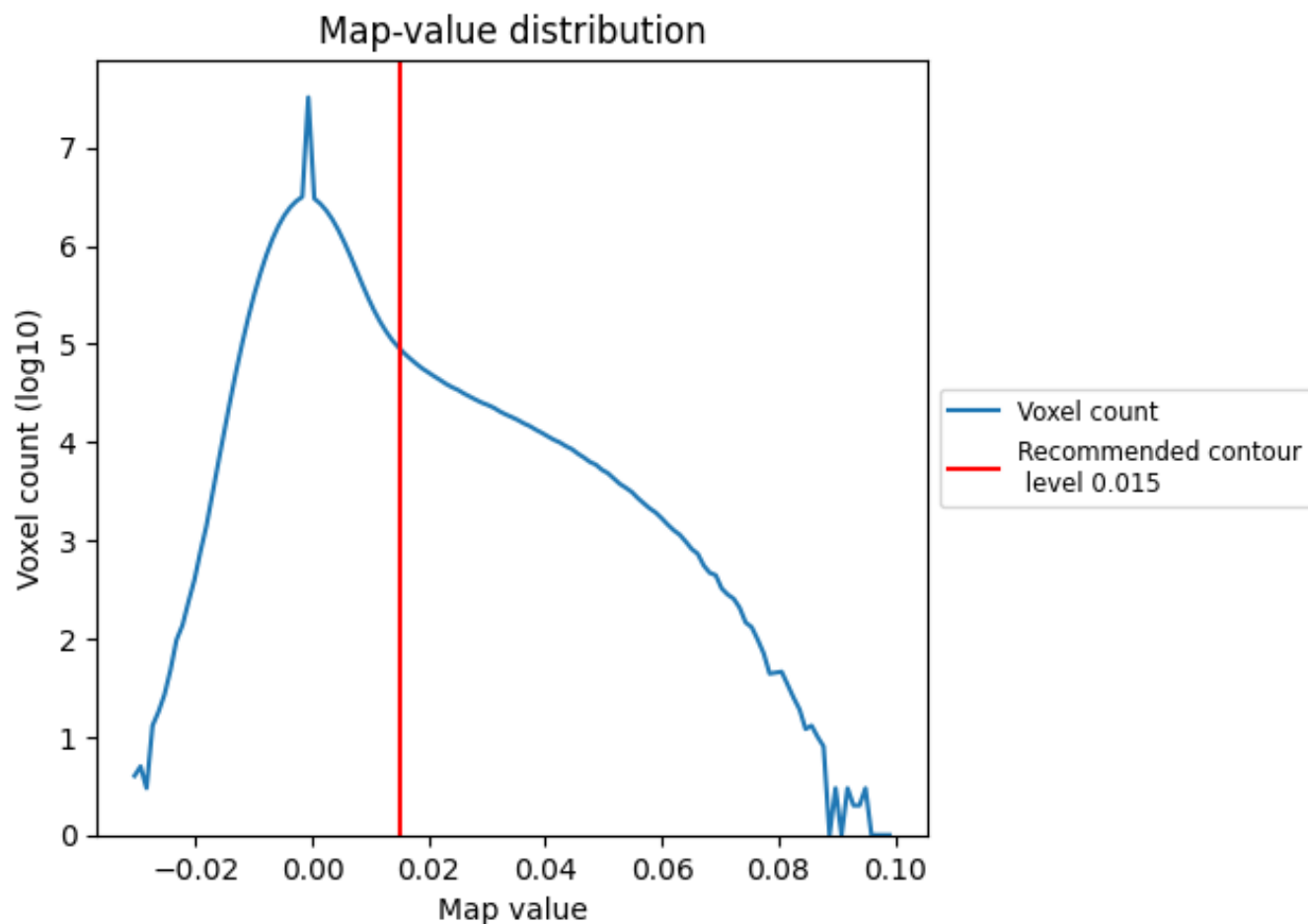
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

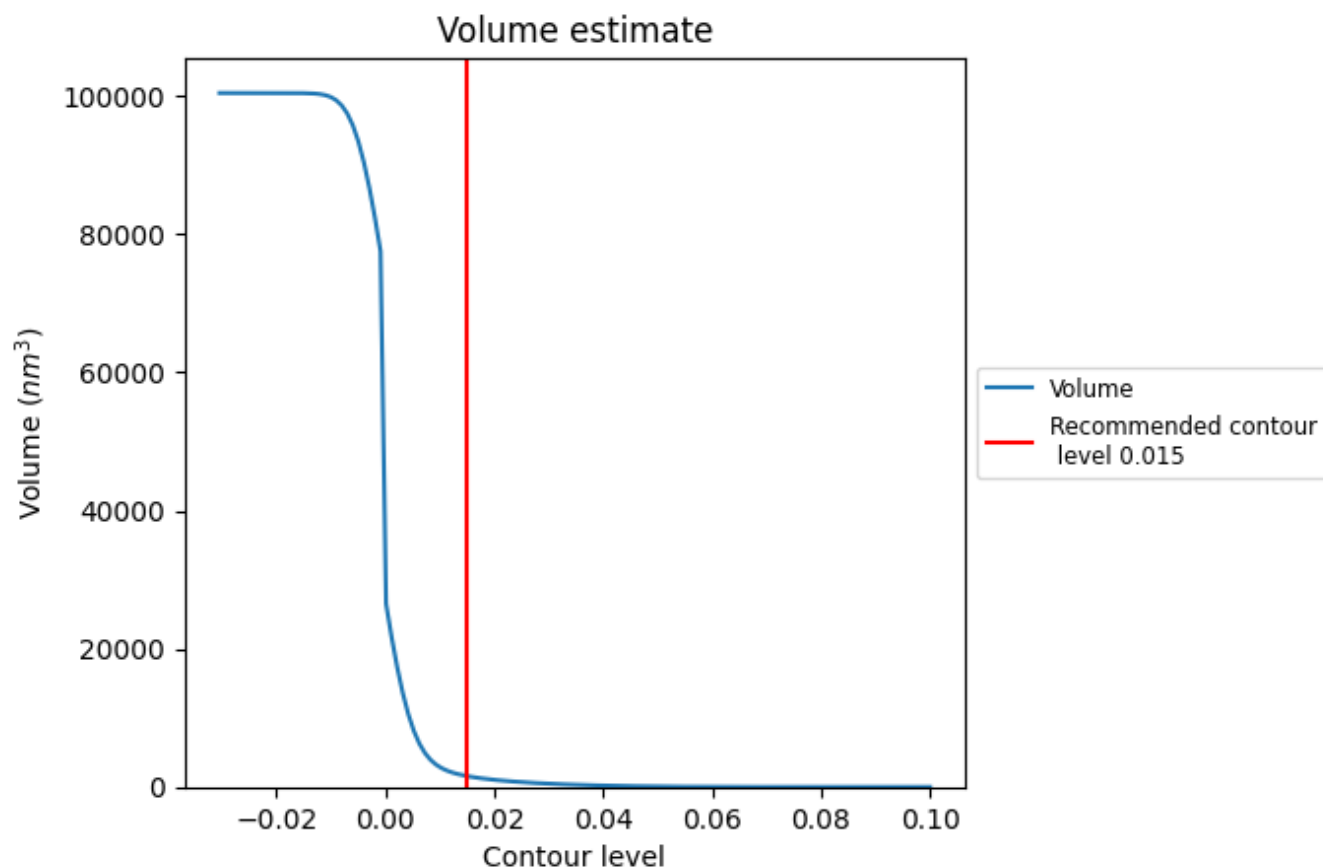
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

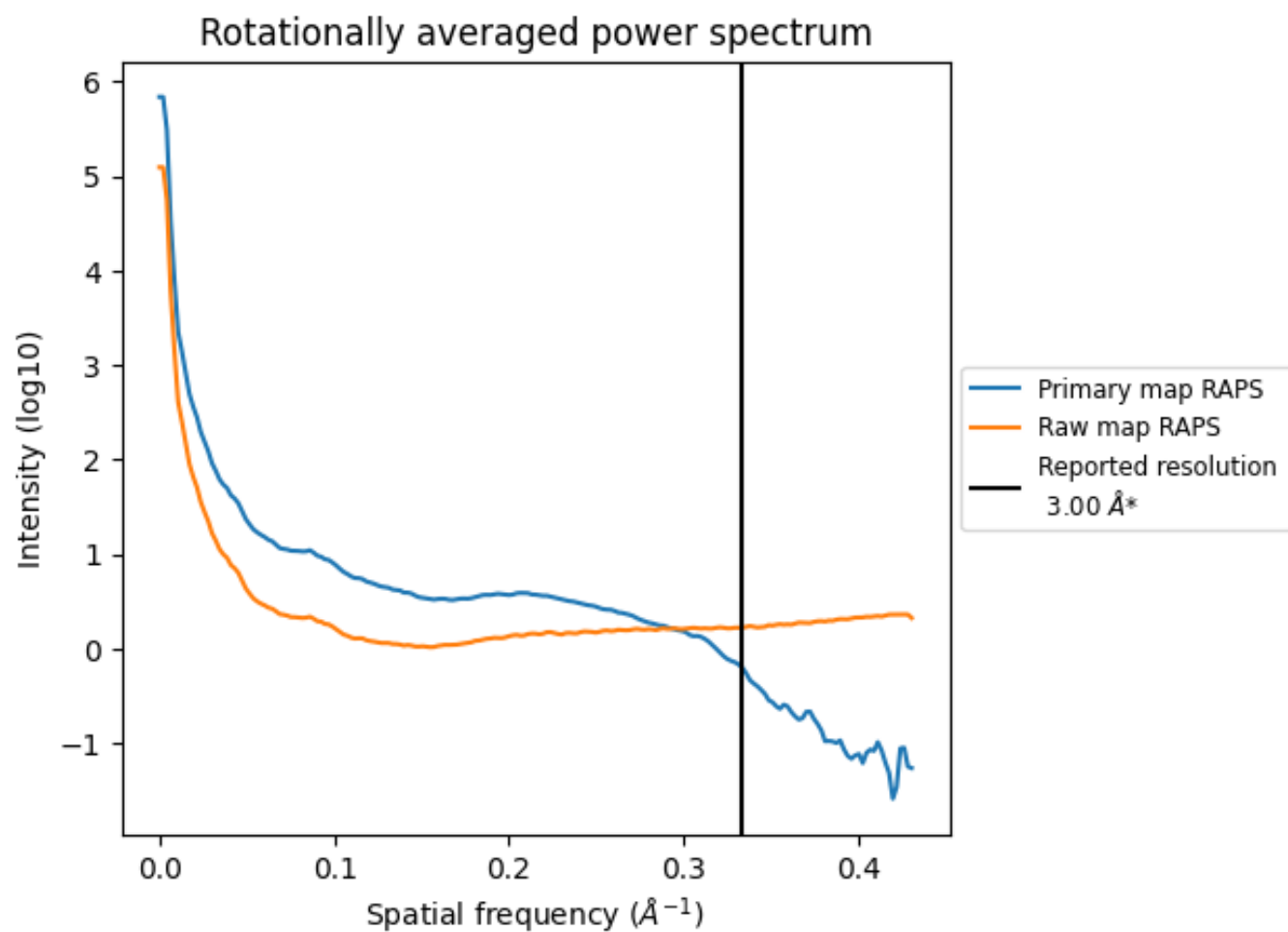
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1580 nm^3 ; this corresponds to an approximate mass of 1427 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

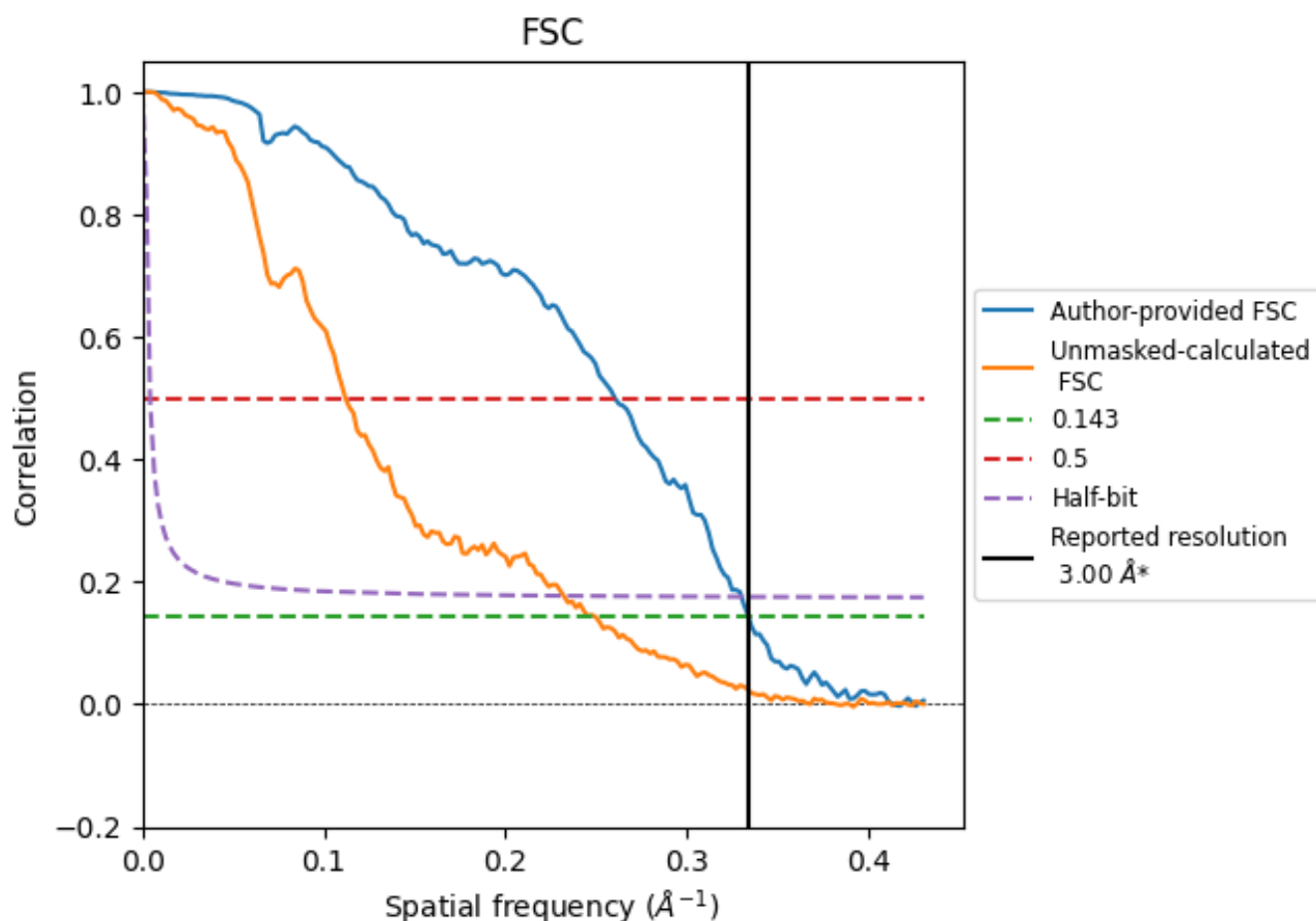


*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

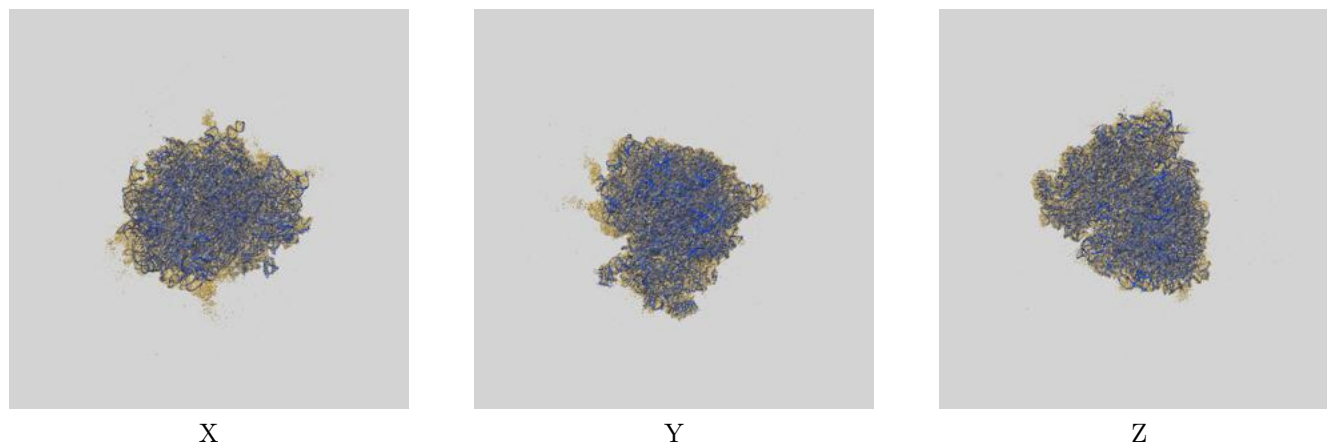
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.99	3.84	3.03
Unmasked-calculated*	4.01	8.94	4.31

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.01 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

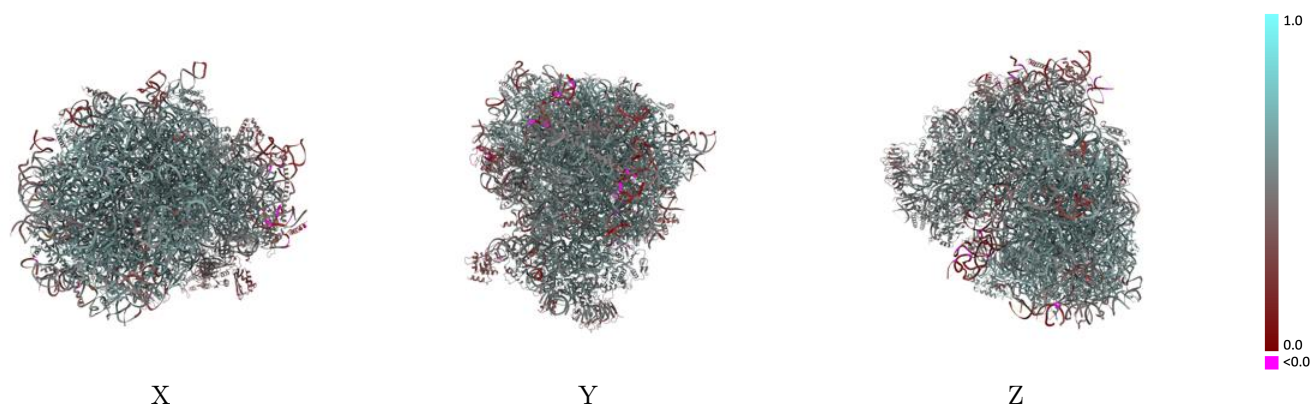
This section contains information regarding the fit between EMDB map EMD-73302 and PDB model 9YPO. Per-residue inclusion information can be found in section [3](#) on page [31](#).

9.1 Map-model overlay [i](#)



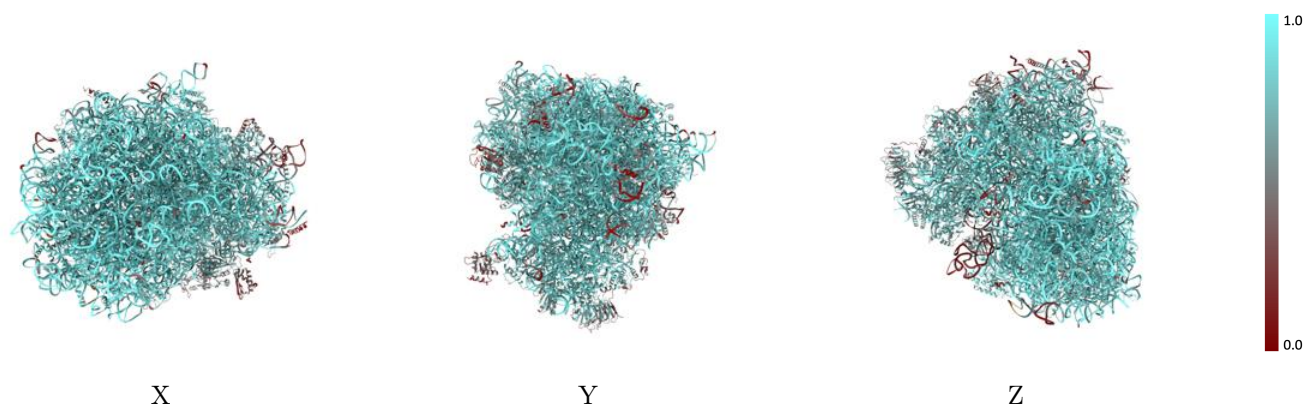
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



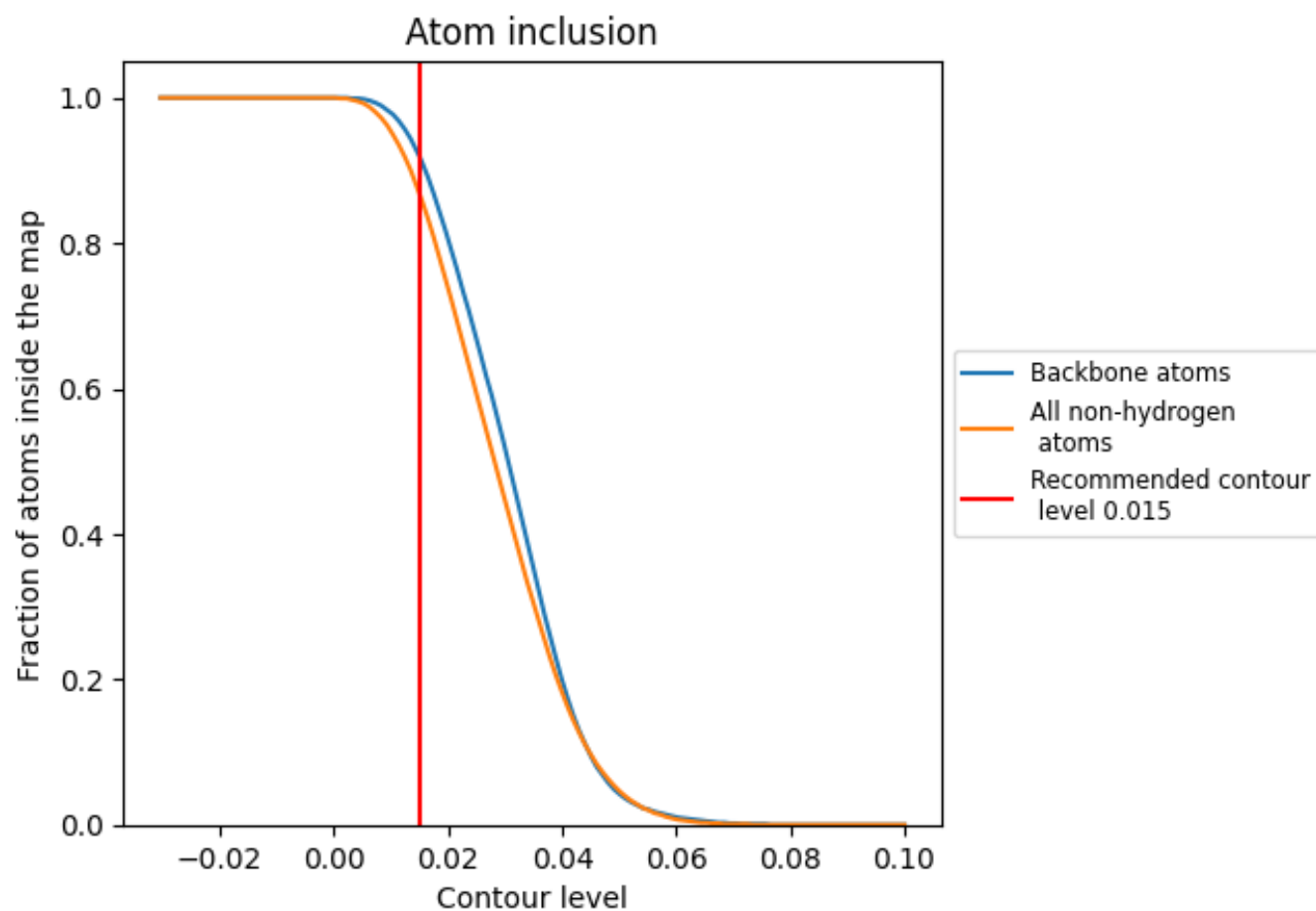
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8680	 0.5370
10	 0.9490	 0.5630
11	 0.3330	 0.2410
12	 0.8810	 0.4700
13	 0.6800	 0.4420
5	 0.9290	 0.5490
7	 0.9910	 0.5970
8	 0.9610	 0.5760
9	 0.9110	 0.5260
A	 0.9390	 0.6060
AA	 0.7690	 0.5270
B	 0.8880	 0.5850
BB	 0.8120	 0.5460
C	 0.9050	 0.5850
CC	 0.8390	 0.5500
D	 0.8500	 0.5530
DD	 0.7450	 0.5110
E	 0.8390	 0.5490
EE	 0.7980	 0.5130
FF	 0.7760	 0.5180
G	 0.7730	 0.5250
GG	 0.6750	 0.4590
H	 0.8350	 0.5640
HH	 0.5990	 0.4650
I	 0.8790	 0.5790
II	 0.7890	 0.5230
J	 0.8050	 0.5320
JJ	 0.7690	 0.4910
K	 0.9110	 0.5900
KK	 0.7560	 0.4890
L	 0.8330	 0.5540
LL	 0.8190	 0.5520
M	 0.8710	 0.5600
MM	 0.3310	 0.3030
N	 0.9480	 0.6020



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
NN	 0.8440	 0.5580
O	 0.9090	 0.5910
OO	 0.8490	 0.5510
P	 0.9050	 0.5930
PP	 0.7160	 0.4860
Q	 0.9050	 0.5920
QQ	 0.7890	 0.5220
R	 0.8280	 0.5460
RR	 0.6490	 0.4930
S	 0.9030	 0.5920
SS	 0.7500	 0.4980
T	 0.8610	 0.5680
TT	 0.7660	 0.5060
U	 0.7650	 0.5000
UU	 0.7160	 0.4820
V	 0.8960	 0.5910
VV	 0.7660	 0.5200
W	 0.6570	 0.4660
WW	 0.8650	 0.5700
X	 0.8610	 0.5630
XX	 0.8720	 0.5690
Y	 0.8640	 0.5700
YY	 0.7320	 0.4860
Z	 0.8580	 0.5590
ZZ	 0.6790	 0.4770
a	 0.9240	 0.5930
aa	 0.8390	 0.5530
b	 0.8160	 0.5390
bb	 0.7620	 0.5220
c	 0.8480	 0.5610
cc	 0.7550	 0.5250
d	 0.8290	 0.5600
dd	 0.8760	 0.5600
e	 0.9230	 0.5990
ee	 0.6960	 0.4700
f	 0.9330	 0.6080
ff	 0.4150	 0.3580
g	 0.8770	 0.5740
gg	 0.6100	 0.4340
h	 0.8490	 0.5530
i	 0.8430	 0.5480
j	 0.9500	 0.6030

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
jj	 0.5690	 0.3990
k	 0.7420	 0.5180
l	 0.9160	 0.5830
m	 0.8680	 0.5780
n	 0.9360	 0.5840
o	 0.8830	 0.5820
p	 0.8720	 0.5780
r	 0.9140	 0.5890