



wwPDB EM Validation Summary Report ⓘ

Jun 9, 2026 – 03:41 PM EDT

PDB ID : 9Q1Q / pdb_00009q1q
EMDB ID : EMD-72136
Title : NediV IRES (A site) in complex with Rabbit 80S ribosome
Authors : De, S.; Altomare, C.G.; Abaeva, I.S.; Dadhwal, P.; Garg, P.; Acosta-Reyes, F.; Brown, Z.P.; Pestova, T.V.; Hellen, C.U.T.; Frank, J.
Deposited on : 2025-08-14
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

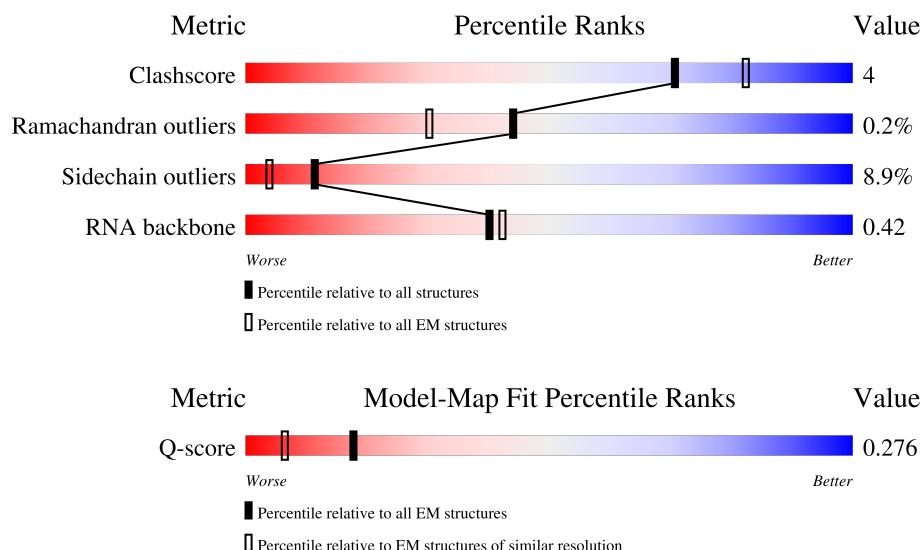
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 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.











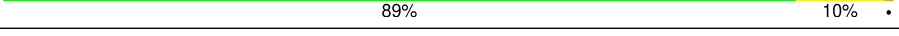

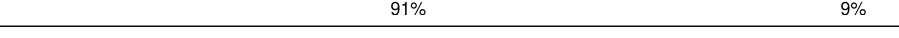
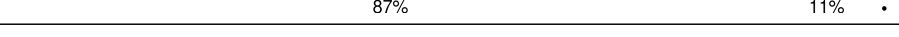

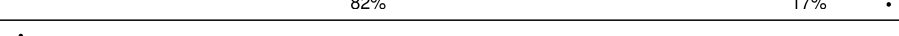


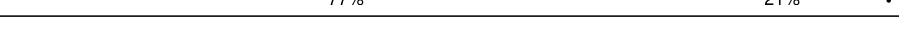

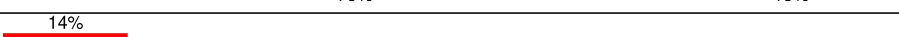






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	7	119	
2	A	248	
3	B	394	



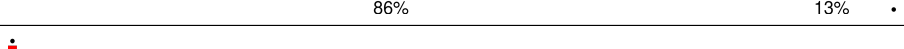
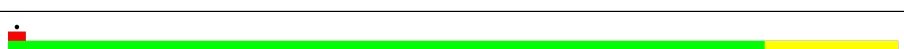



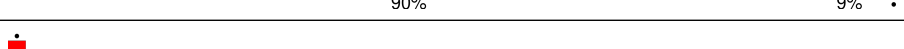



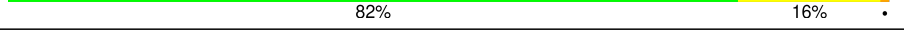

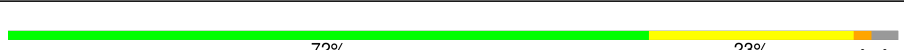










Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	C	362	
5	D	293	
6	E	251	
7	F	225	
8	G	240	
9	H	190	
10	I	213	
11	J	170	
12	L	210	
13	M	138	
14	N	203	
15	O	199	
16	P	153	
17	Q	187	
18	R	180	
19	S	176	
20	T	159	
21	U	99	
22	V	139	
23	W	106	
24	X	118	
25	Y	134	
26	Z	135	
27	a	147	
28	b	104	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	c	98	
30	d	107	
31	e	128	
32	f	109	
33	g	114	
34	h	122	
35	i	102	
36	j	86	
37	k	69	
38	l	50	
39	m	52	
40	n	25	
41	o	104	
42	p	91	
43	r	124	
44	5	3603	
45	8	156	
46	DD	213	
47	FF	191	
48	KK	96	
49	MM	117	
50	PP	129	
51	QQ	142	
52	RR	132	
53	SS	144	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	TT	141	
55	UU	100	
56	ZZ	75	
57	cc	62	
58	dd	55	
59	ff	68	
60	gg	313	
61	9	1696	
62	AA	202	
63	BB	213	
64	CC	221	
65	EE	262	
66	GG	237	
67	HH	189	
68	II	206	
69	JJ	185	
70	LL	151	
71	NN	149	
72	OO	136	
73	VV	83	
74	WW	129	
75	XX	141	
76	YY	124	
77	aa	101	
78	bb	83	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	ee	57	<div><div></div><div>9%</div><div>81%</div><div>19%</div></div>
80	K	212	<div><div></div><div>10%</div><div>65%</div><div>24%</div><div>10%</div><div></div></div>
81	1	165	<div><div></div><div>8%</div><div>34%</div><div>58%</div><div>8%</div><div></div></div>
82	s	196	<div><div></div><div>5%</div><div></div><div>8%</div><div>88%</div></div>
83	t	153	<div><div></div><div>12%</div><div>9%</div><div>9%</div><div>5%</div><div>76%</div></div>

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 216047 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 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 2 is a protein called 60S ribosomal protein L8.

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

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 4 is a protein called 60S ribosomal protein L4.

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

- Molecule 5 is a protein called 60S ribosomal protein L5.

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

- Molecule 6 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 7 is a protein called 60S ribosomal protein L7.

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

- Molecule 8 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	232	Total	C	N	O	S	0	0
			1872	1195	360	313	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 9 is a protein called 60S ribosomal protein L9.

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

- Molecule 10 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	204	Total	C	N	O	S	0	0
			1660	1054	320	273	13		

- Molecule 11 is a protein called 60S ribosomal protein L11.

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

- Molecule 12 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	74	ARG	HIS	conflict	UNP G1TKB3
L	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 13 is a protein called 60S ribosomal protein L14.

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

- Molecule 14 is a protein called 60S ribosomal protein L15.

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

- Molecule 15 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 16 is a protein called 60S ribosomal protein L17.

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

- Molecule 17 is a protein called eL18.

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

- Molecule 18 is a protein called 60S ribosomal protein L19.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	HIS	conflict	UNP G1TYL6
R	151	ARG	HIS	conflict	UNP G1TYL6

- Molecule 19 is a protein called eL20.

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

- Molecule 20 is a protein called 60S ribosomal protein L21.

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

- Molecule 21 is a protein called eL22.

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

- Molecule 22 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 23 is a protein called uL24.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 25 is a protein called 60S ribosomal protein L26.

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

- Molecule 26 is a protein called 60S ribosomal protein L27.

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

- Molecule 27 is a protein called 60S ribosomal protein L27a.

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

- Molecule 28 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	103	Total	C	N	O	S	0	0
			841	522	188	128	3		

- Molecule 29 is a protein called 60S ribosomal protein L30.

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

- Molecule 30 is a protein called 60S ribosomal protein L31.

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

- Molecule 31 is a protein called eL32.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 33 is a protein called 60S ribosomal protein L34.

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

- Molecule 34 is a protein called 60S ribosomal protein L35.

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

- Molecule 35 is a protein called 60S ribosomal protein L36.

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

- Molecule 36 is a protein called 60S ribosomal protein L37.

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

- Molecule 37 is a protein called Large ribosomal subunit protein eL38.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 38 is a protein called 60S ribosomal protein L39.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 40 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 41 is a protein called eL42.

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

- Molecule 42 is a protein called 60S ribosomal protein L37a.

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

- Molecule 43 is a protein called 60S ribosomal protein L28.

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

- Molecule 44 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5	3603	Total	C	N	O	P	0	0
			77244	34401	14135	25105	3603		

- Molecule 45 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 46 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	DD	213	Total	C	N	O	S	0	0
			1653	1054	300	291	8		

- Molecule 47 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	FF	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 48 is a protein called 40S ribosomal protein S10.

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

- Molecule 49 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	MM	98	Total	C	N	O	S	0	0
			754	475	135	137	7		

- Molecule 50 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 51 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 52 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RR	124	Total	C	N	O	S	0	0
			1002	628	190	180	4		

- Molecule 53 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 54 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	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 55 is a protein called 40S ribosomal protein S20.

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

- Molecule 56 is a protein called 40S ribosomal protein S25.

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

- Molecule 57 is a protein called 40S ribosomal protein S28.

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

- Molecule 58 is a protein called 40S ribosomal protein S29.

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

- Molecule 59 is a protein called 40S ribosomal protein S27a.

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

- Molecule 60 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 61 is a RNA chain called 18S RNA (1696-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
61	9	1696	Total	C	N	O	P	0	0
			36209	16162	6504	11848	1695		

- Molecule 62 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AA	202	Total	C	N	O	S	0	0
			1586	1011	280	287	8		

- Molecule 63 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BB	206	Total	C	N	O	S	0	0
			1680	1068	300	298	14		

- Molecule 64 is a protein called 40S ribosomal protein S2.

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

- Molecule 65 is a protein called 40S ribosomal protein S4.

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

- Molecule 66 is a protein called 40S ribosomal protein S6.

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

- Molecule 67 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	HH	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 68 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	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 69 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 70 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 71 is a protein called 40S ribosomal protein S13.

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

- Molecule 72 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 73 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	VV	83	Total	C	N	O	S	0	0
			636	393	117	121	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 74 is a protein called 40S ribosomal protein S15a.

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

- Molecule 75 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	XX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 76 is a protein called 40S ribosomal protein S24.

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

- Molecule 77 is a protein called eS26.

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

There are 2 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

- Molecule 78 is a protein called 40S ribosomal protein S27.

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

- Molecule 79 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 80 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	K	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

- Molecule 81 is a RNA chain called NediV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	1	165	Total	C	N	O	P	0	0
			3496	1564	608	1159	165		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1479	C	U	conflict	GB 403044781
1	1486	C	U	conflict	GB 403044781

- Molecule 82 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	s	23	Total	C	N	O	S	0	0
			173	106	35	29	3		

- Molecule 83 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	t	36	Total	C	N	O	S	0	0
			275	165	55	53	2		

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	7	5	Total	Mg	0
			5	5	
84	P	1	Total	Mg	0
			1	1	
84	V	1	Total	Mg	0
			1	1	
84	a	1	Total	Mg	0
			1	1	
84	g	1	Total	Mg	0
			1	1	
84	j	1	Total	Mg	0
			1	1	
84	5	192	Total	Mg	0
			192	192	
84	8	3	Total	Mg	0
			3	3	
84	9	1	Total	Mg	0
			1	1	

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

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

Continued on next page...


Continued from previous page...

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

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.

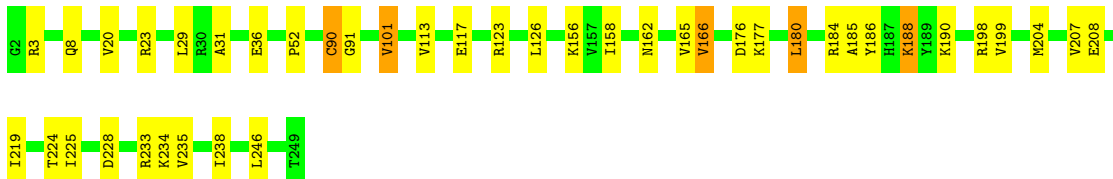
- Molecule 1: 5S rRNA

Chain 7: 




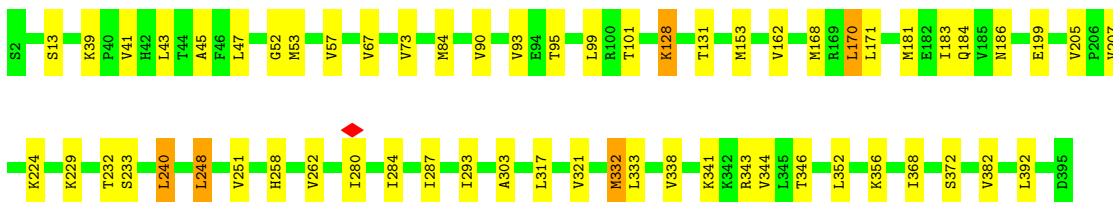
- Molecule 2: 60S ribosomal protein L8

Chain A: 




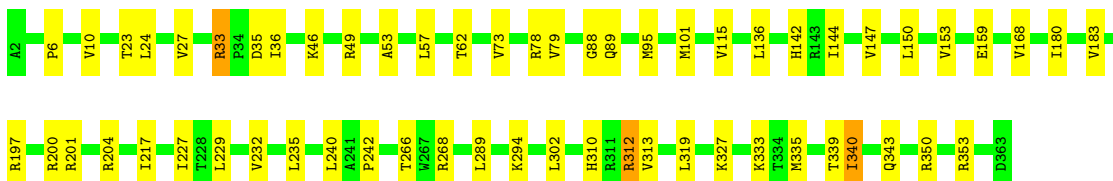
- Molecule 3: 60S ribosomal protein L3

Chain B: 




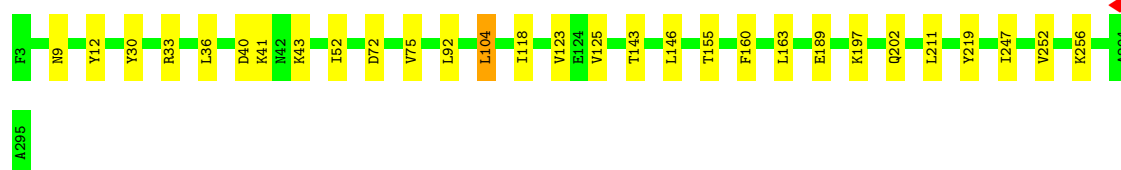
- Molecule 4: 60S ribosomal protein L4

Chain C: 



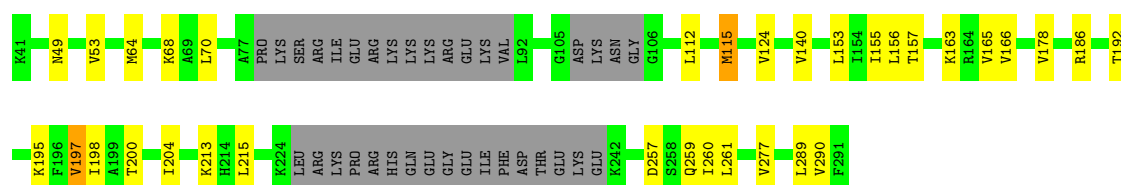
- Molecule 5: 60S ribosomal protein L5

Chain D:  90% 10%




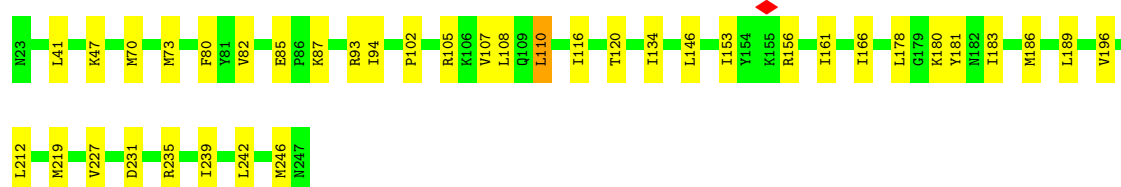
- Molecule 6: Large ribosomal subunit protein eL6

Chain E:  73% 12% 14%




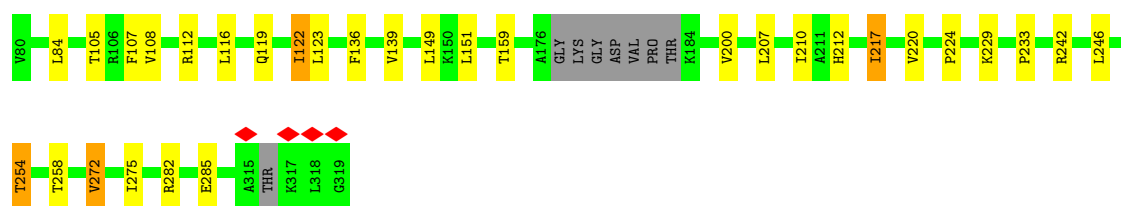
- Molecule 7: 60S ribosomal protein L7

Chain F:  83% 16%




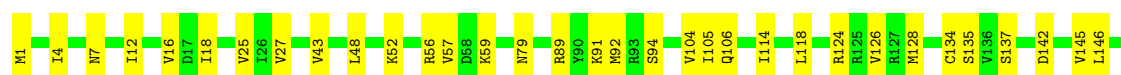
- Molecule 8: Large ribosomal subunit protein eL8

Chain G:  84% 11%



- Molecule 9: 60S ribosomal protein L9

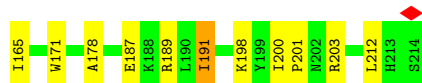
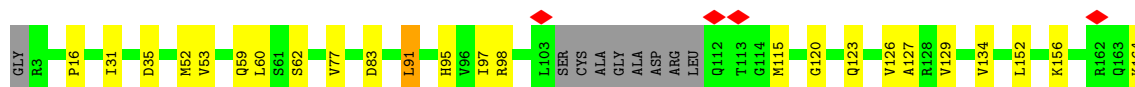
Chain H:  81% 18%





- Molecule 10: Ribosomal protein L10

Chain I: 79% 15% . .



- Molecule 11: 60S ribosomal protein L11

Chain J: 88% 10% .



- Molecule 12: Large ribosomal subunit protein eL13

Chain L: 89% 10% .



- Molecule 13: 60S ribosomal protein L14

Chain M: 89% 11%



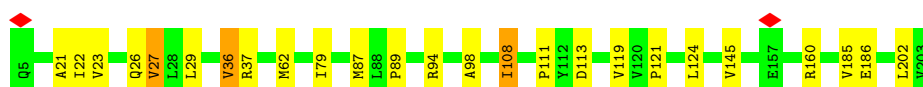
- Molecule 14: 60S ribosomal protein L15

Chain N: 91% 9%




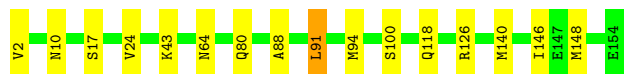
- Molecule 15: Large ribosomal subunit protein uL13

Chain O: 87% 11% .




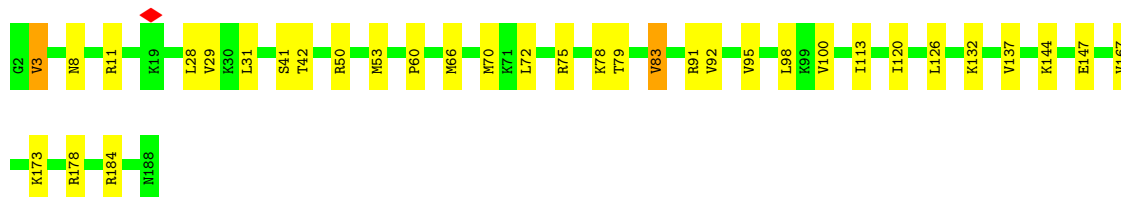
- Molecule 16: 60S ribosomal protein L17

Chain P:  90% 10%




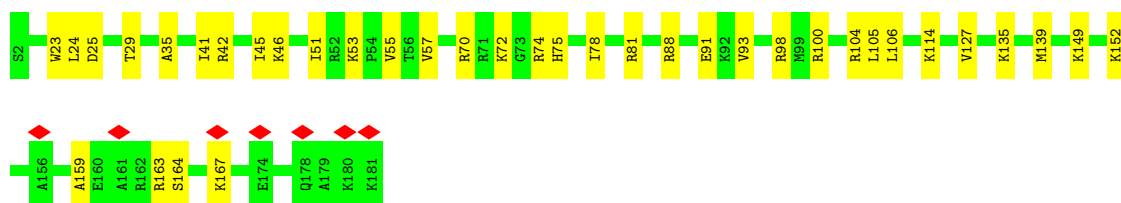
- Molecule 17: eL18

Chain Q:  82% 17%




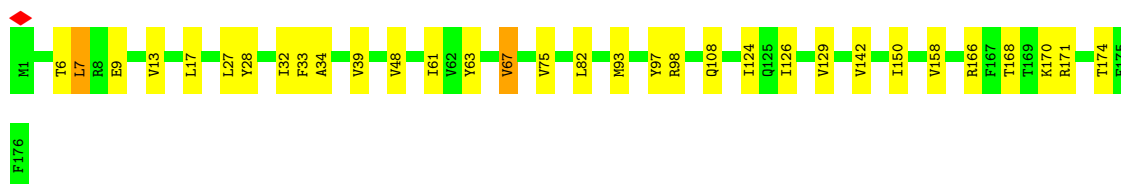
- Molecule 18: 60S ribosomal protein L19

Chain R:  79% 21%



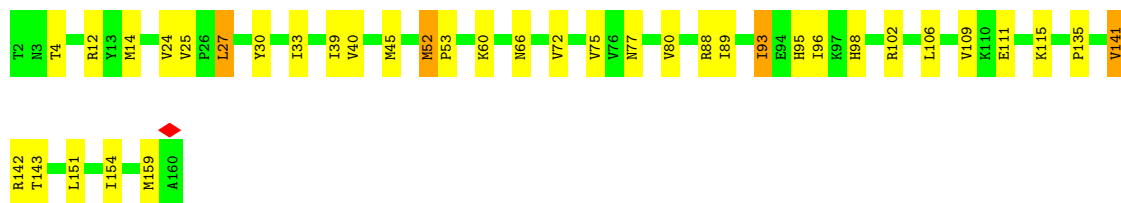
- Molecule 19: eL20

Chain S:  82% 17%




- Molecule 20: 60S ribosomal protein L21

Chain T:  77% 21%




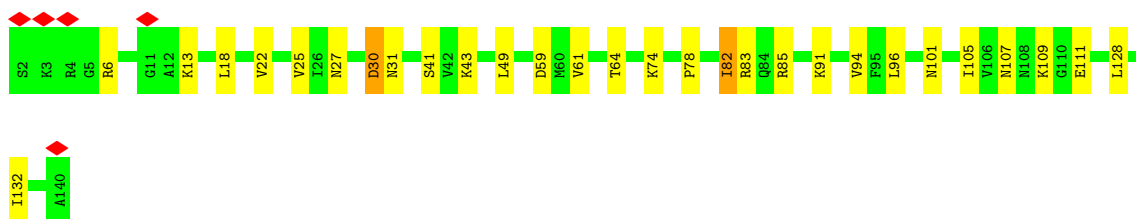
- Molecule 21: eL22

Chain U:  89% 10%



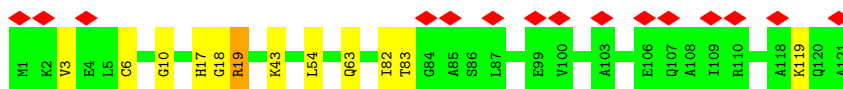
- Molecule 22: Large ribosomal subunit protein uL14

Chain V:  79% 19%



- Molecule 23: uL24

Chain W:  14% 89% 10%




- Molecule 24: Large ribosomal subunit protein uL23

Chain X:  94% 6%




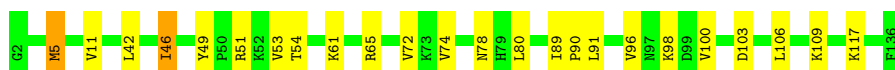
- Molecule 25: 60S ribosomal protein L26

Chain Y:  83% 15%




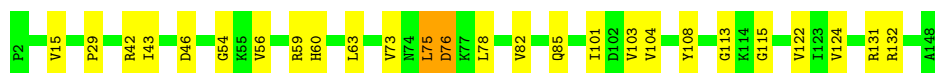
- Molecule 26: 60S ribosomal protein L27

Chain Z:  82% 16%

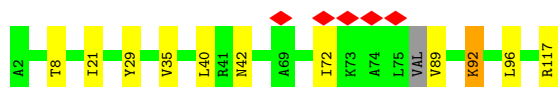
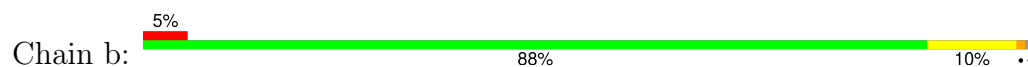


- Molecule 27: 60S ribosomal protein L27a

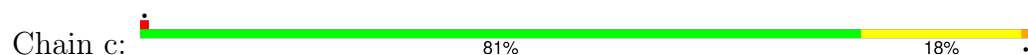
Chain a:  82% 16%



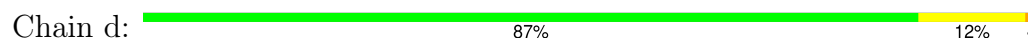
- Molecule 28: eL29



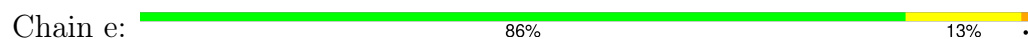
- Molecule 29: 60S ribosomal protein L30



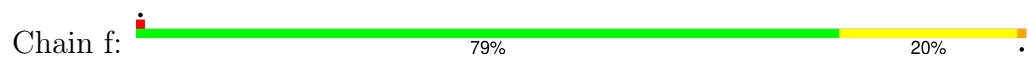
- Molecule 30: 60S ribosomal protein L31



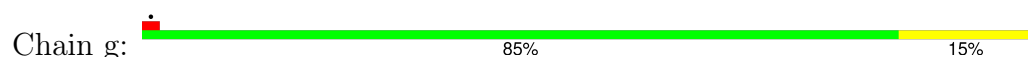
- Molecule 31: eL32



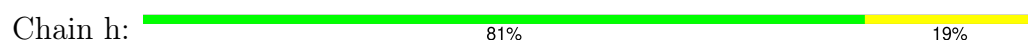
- Molecule 32: Large ribosomal subunit protein eL33



- Molecule 33: 60S ribosomal protein L34

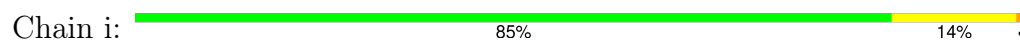


- Molecule 34: 60S ribosomal protein L35

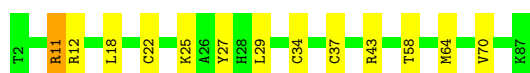
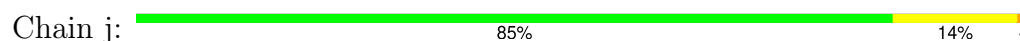




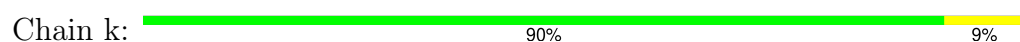
- Molecule 35: 60S ribosomal protein L36



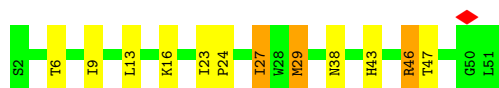
- Molecule 36: 60S ribosomal protein L37



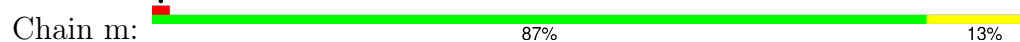
- Molecule 37: Large ribosomal subunit protein eL38



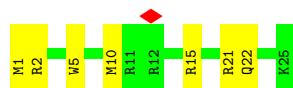
- Molecule 38: 60S ribosomal protein L39



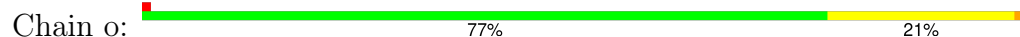
- Molecule 39: Large ribosomal subunit protein eL40



- Molecule 40: eL41



- Molecule 41: eL42





- Molecule 42: 60S ribosomal protein L37a

Chain p: 82% 16%



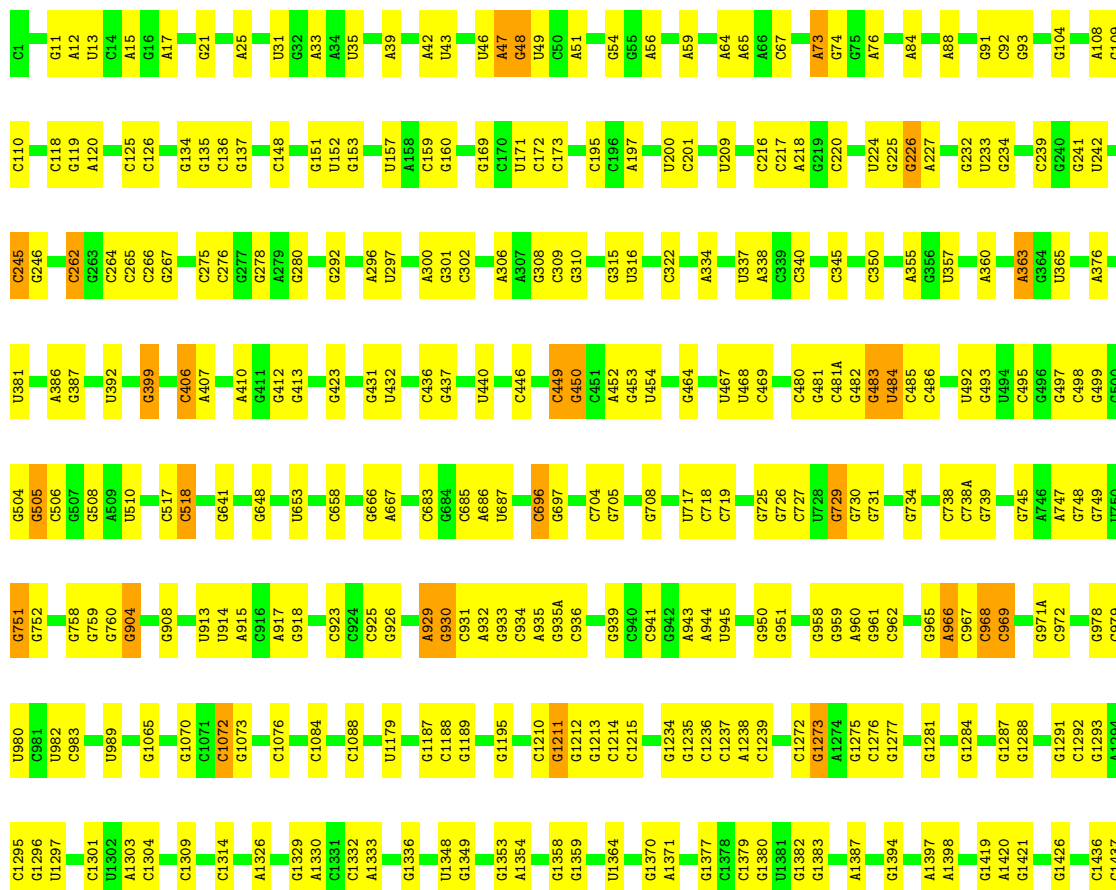
- Molecule 43: 60S ribosomal protein L28

Chain r: 85% 14%

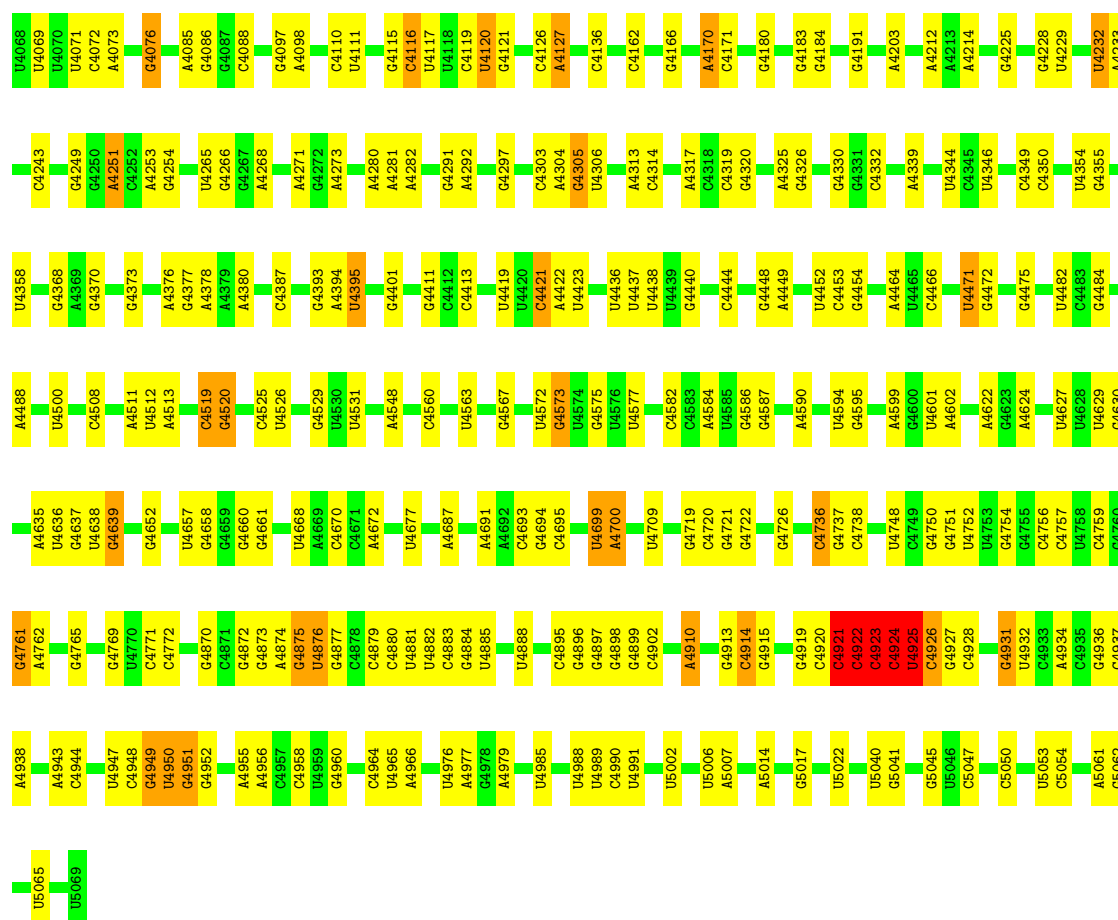


- Molecule 44: 28S rRNA

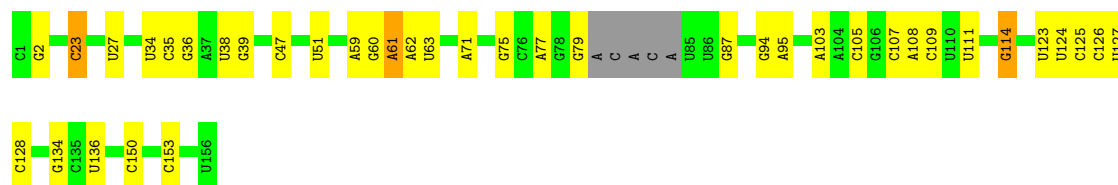
Chain 5: 68% 28%



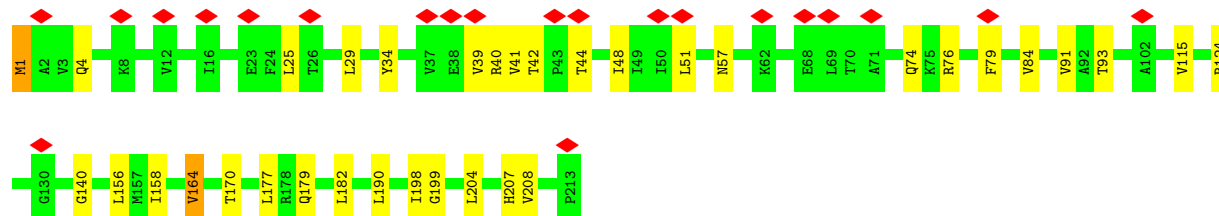
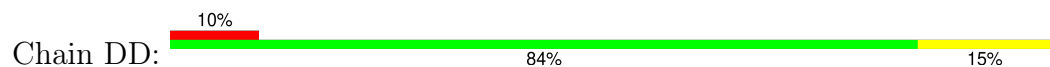
G3918	G3810	G3664	G2814	U2708	G2566	C2441	C2302	A2069	C1978	C1856	G1752	U1438
U3930	G3811	G3665	C2820	C2709	U2570	U2447	C2303	C2070	U1979	C1857	G1753	U1440
G3938	G3812	C3673	G2826	C2710	C2571	G2448	G2306	C2081	U1980	A1858	U1754	C1441
G3939	U3813	G3678	A2825	G2711	C2572	A2449	G2309	C2084	G1982	G1869	U1756	G1444
U3940	U3814	U3679	U2826	G2712	A2573	G2450	G2309	G2084	A1983	U1757	U1578	U1445
G3941	A3817	U3680	U2827	G2713	C2574	A2451	A2313	G2085	A1984	C1884	G1758	C1446
U3818	U3818	U3681	U2828	G2714	U2575	G2452	A2313	A2088	G1985	G1885	G1759	C1447
G3819	G3819	G3682	C2716	G2715	C2583	A2453	G2316	U2089	U1986	A1888	G1760	G1448
G3820	G3820	A3682	U2837	C2716	G2586	G2463	G2316	U2090	G1988	U1888	G1761	G1455
G3946	U3838	A3692	G2842	G2721	G2586	G2463	U2339	C2091	C1989	U1889	G1764	G1456
A3947	G3839	U3695	G2842	G2724	A2587	G2471	G2330	G2092	A1990	G1890	U1597	C1456
U3950	U3840	U3695	A2845	G2724	C2588	G2471	G2330	A2093	C1991	G1897	A1765	G1457
G3951	G3846	C3696	G2846	A2725	C2589	G2475	A2332	C2094	U1991	A1897	U1602	C1458
G3952	U3697	U3697	G2846	G2726	C2590	G2476	G2333	A2095	U1992	C1898	U1607	C1459
A3953	G3698	G3698	G2846	G2726	C2591	G2476	G2333	A2096	U1993	G1899	C1607	C1460
G3954	C3843	G3698	G2846	G2726	C2592	G2476	G2333	G2096	C1994	C1899	C1607	G1465
U3848	U3848	G3705	G2855	C2738	A2601	C2488	G2335	U2097	G1995	U1906	C1772	G1465
A3849	U3849	A3711	G2868	C2739	A2601	C2488	G2336	G2098	C1996	A1907	U1773	G1465
G3855	G3855	G3711	G2875	U2740	G2610	U2490	G2345	C2099	U1997	A1907	U1773	C1477
A3856	A3856	A3711	G2875	A2743	A2611	C2491	C2346	A2101	A1998	G1910	U1776	C1478
U3956	G3857	G3714	U2880	G2751	G2618	G2502	G2347	G2102	G2000	C1914	C1777	G1482
G3957	G3858	A3881	A2882	G2752	C2619	C2504	G2348	A2103	G2001	G1915	U1781	G1483
U3958	A3861	A2882	A2882	G2753	C2620	C2504	A2349	A2104	A2002	G1916	U1781	G1484
G3959	U3869	G3742	U2891	G2754	G2620	G2506	U2350	G2106	U2004	A1917	A1787	G1487
A3960	G3868	G3742	U2891	G2754	G2624	A2507	C2351	C2107	G1919	C1919	A1788	G1487
A3965	G3869	A3747	G2897	G2759	G2624	A2507	A2360	G2108	G1920	C1920	C1789	U1494
A3966	C3870	A3747	G2897	G2760	U2632	U2510	A2360	A2109	G1921	A1921	A1794	U1494
G3969	A3871	G3751	G2898	U2761	U2632	U2510	U2369	G2110	U2008	A1922	A1794	G1495
G3970	A3876	G3752	G2898	G2762	U2636	A2511	A2370	G2259	C2011	G1930	G1803	U1496
A3972	A3877	G3753	C3598	U2763	U2637	A2512	U2370	C2260	A2012	C1931	A1804	G1501
G3973	C3878	G3754	A3604	A2764	C2638	A2513	U2372	G2261	U2020	A1932	A1805	C1502
U4039	G3879	G3755	A3604	U2769	A2647	G2515	C2373	G2262	G2023	G1945	G1815	G1509
C4040	C3882	A3756	C3605	U2769	A2647	G2515	A2382	G2263	G2024	G1948	G1815	G1510
G4041	A3759	A3760	U3606	C2772	G2658	U2519	A2382	C2264	C2024	G1948	G1818	U1514
C4042	G3888	A3760	A3610	G2773	A2659	C2520	A2395	G2265	A2025	G1948	G1819	A1515
G4043	G3889	A3611	A3611	G2773	U2660	C2521	A2396	G2266	A2026	G1948	G1819	G1516
U4044	U4044	G3765	G3615	G2777	A2661	G2522	A2396	U2267	U2027	G1948	C1820	G1517
G4045	U3892	G3765	G3615	G2778	G2662	G2522	G2399	A2268	C2269	G1948	G1821	A1518
A4046	U3770	U3770	U3616	G2778	G2662	A2529	G2399	A2268	A2042	G1948	G1821	G1518
A4047	G3897	G3771	G3620	A2787	C2669	U2530	G2402	G2270	U2043	A1958	U1822	C1676
A4048	G3898	U3772	G3620	U2788	C2670	A2537	G2410	C2274	G2044	U1959	U1822	A1523
U4049	G3899	U3773	G3625	A2789	G2673	A2537	C2411	G2275	U2044	A1960	C1828	A1534
A4050	G3900	A3774	G3625	U2790	G2673	A2543	A2412	G2276	G2046	A1962	G1929	C1535
C4051	A3901	A3775	G3626	U2790	A2674	A2543	A2412	A2277	U2048	C1963	G1930	G1534
C4052	G3776	G3776	A3635	G2793	G2675	G2546	A2417	G2278	A2042	G1968	G1830	C1731
A4053	G3904	C2794	A3636	C2794	A2676	G2546	A2417	A2278	G2062	C1968	U1834	C1732
C4054	A3905	A2795	G3636	A2795	A2676	G2547	C2422	A2279	G2062	C1969	U1834	C1732
U4055	G3906	U3637	U3637	G2796	G2681	G2549	C2422	C2289	G2065	A1970	G1733	G1538
A4056	G3907	G3638	U3638	C2797	G2681	G2549	C2422	C2289	G2065	C1971	G1734	G1539
U4056	A3908	A3784	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539
U4056	A3908	A3785	A3653	A2798	U2686	G2549	U2425	C2289	G2065	C1971	G1734	C1539




• Molecule 45: 5.8S rRNA



• Molecule 46: Small ribosomal subunit protein uS3




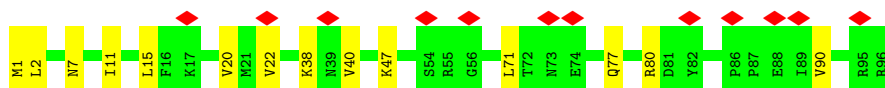
• Molecule 47: Small ribosomal subunit protein uS7

Chain FF:  85% 11% ..




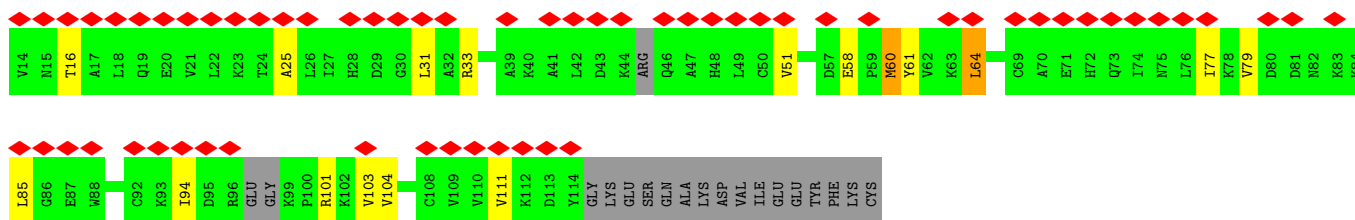
- Molecule 48: 40S ribosomal protein S10

Chain KK:  12% 85% 15%




- Molecule 49: 40S ribosomal protein S12

Chain MM:  53% 69% 13% • 16%




- Molecule 50: Small ribosomal subunit protein uS19

Chain PP:  6% 76% 22% •



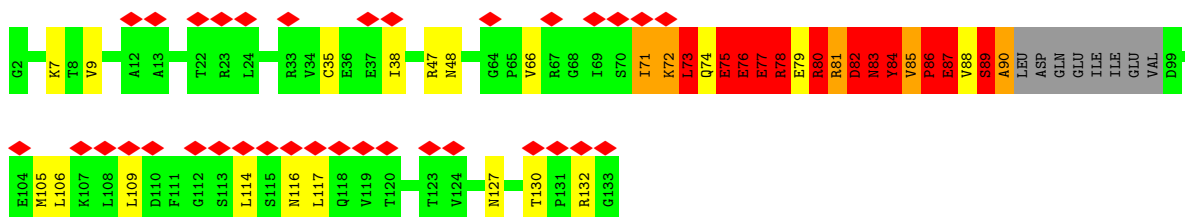
- Molecule 51: Small ribosomal subunit protein uS9

Chain QQ:  11% 87% 13% •




- Molecule 52: 40S ribosomal protein S17

Chain RR:  26% 67% 14% • 9% 6%




- Molecule 53: 40S ribosomal protein S18

Chain SS:  86% 13%




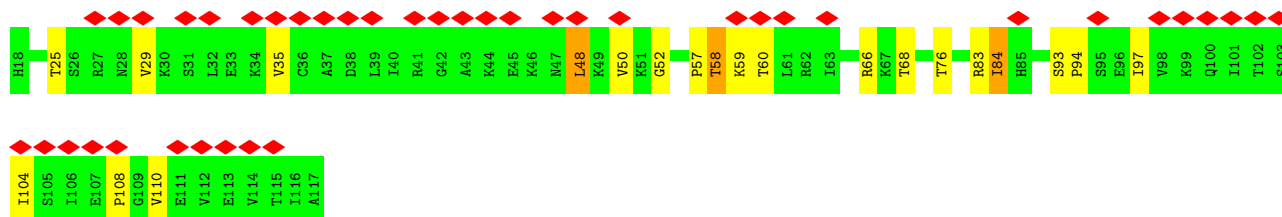
- Molecule 54: Small ribosomal subunit protein eS19

Chain TT:  5% 85% 14%




- Molecule 55: 40S ribosomal protein S20

Chain UU:  41% 79% 18%




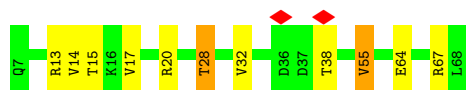
- Molecule 56: 40S ribosomal protein S25

Chain ZZ:  87% 13%




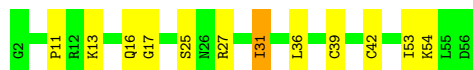
- Molecule 57: 40S ribosomal protein S28

Chain cc:  82% 15%

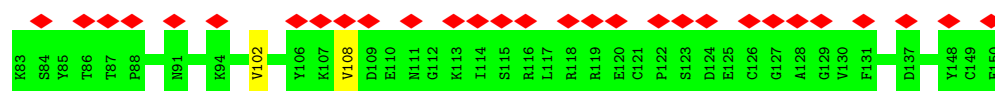


- Molecule 58: 40S ribosomal protein S29

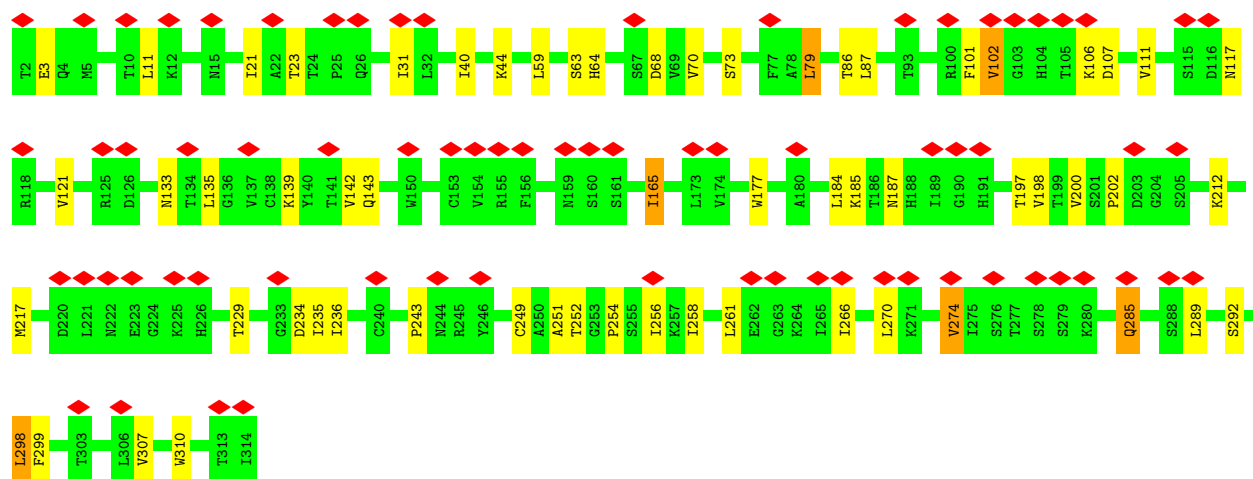
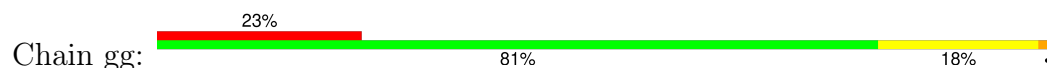
Chain dd:  78% 20%



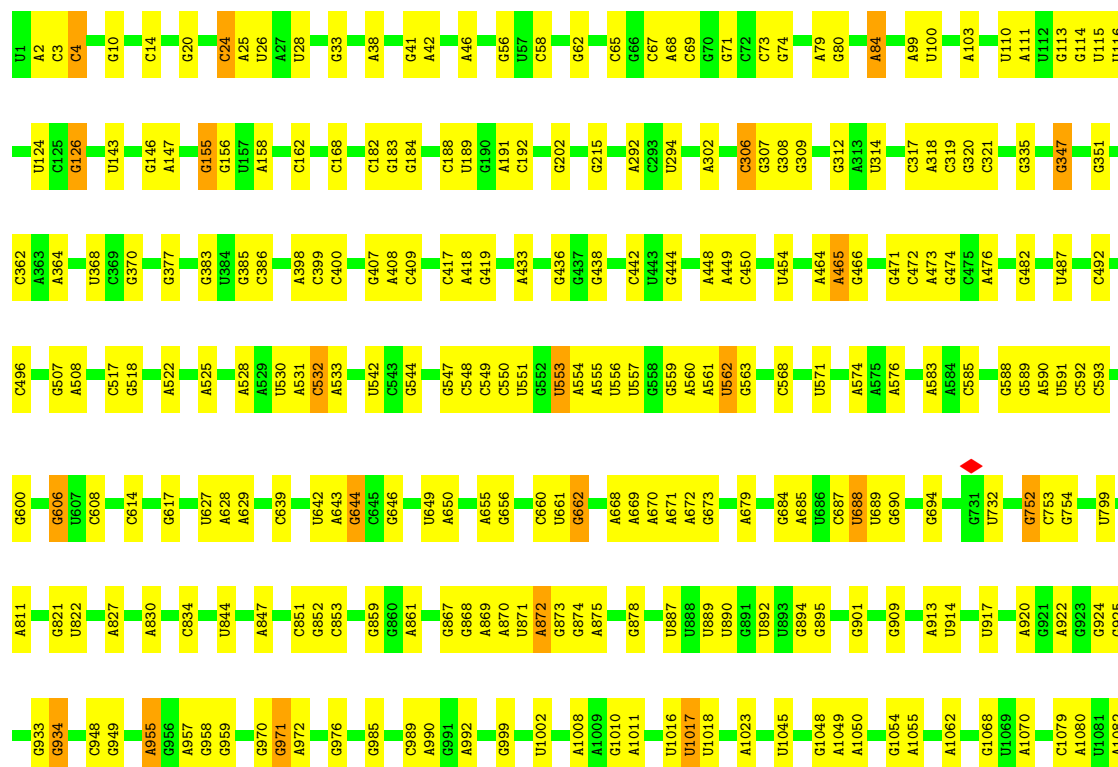
- Molecule 59: 40S ribosomal protein S27a

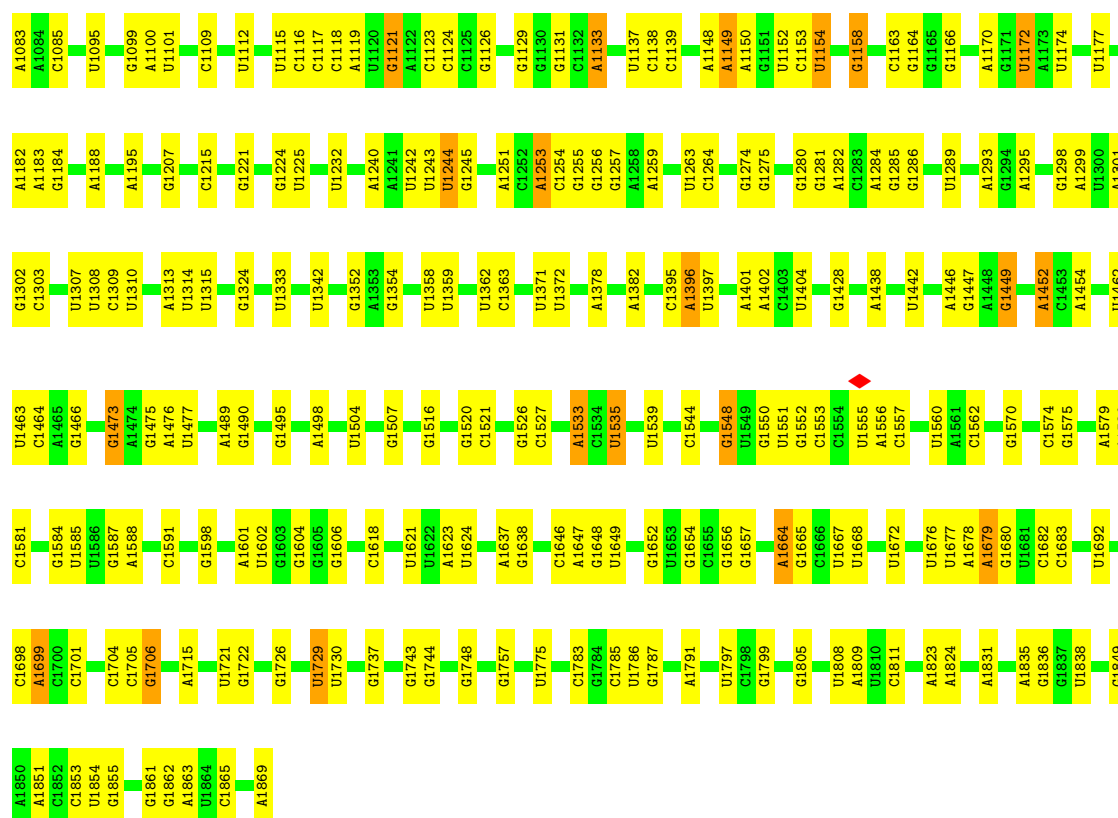


• Molecule 60: Receptor of activated protein C kinase 1

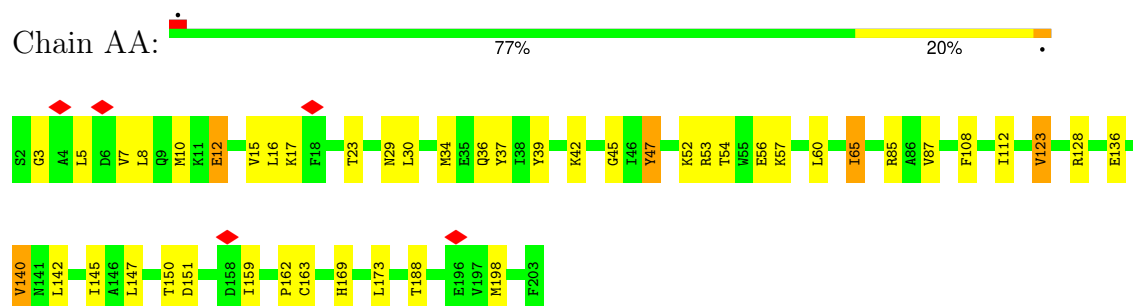


• Molecule 61: 18S RNA (1696-MER)

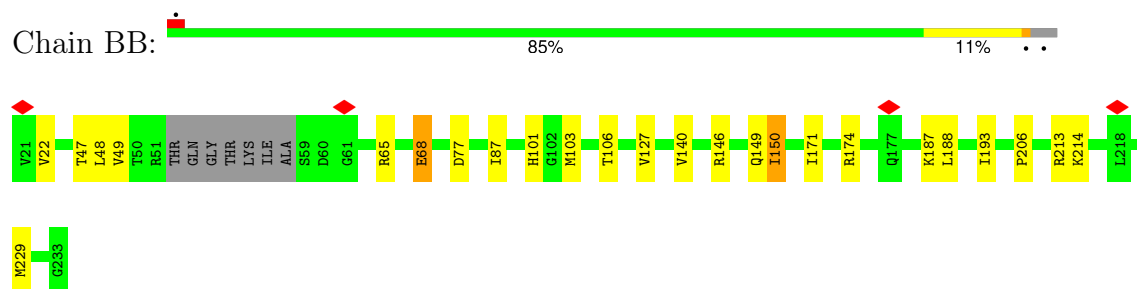




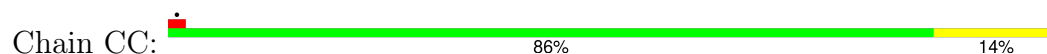
- Molecule 62: 40S ribosomal protein SA

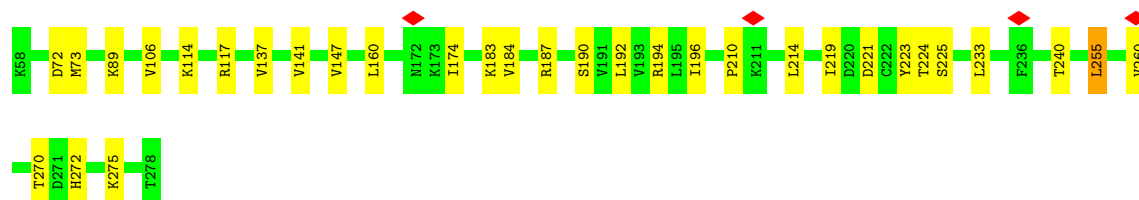


- Molecule 63: 40S ribosomal protein S3a



- Molecule 64: 40S ribosomal protein S2





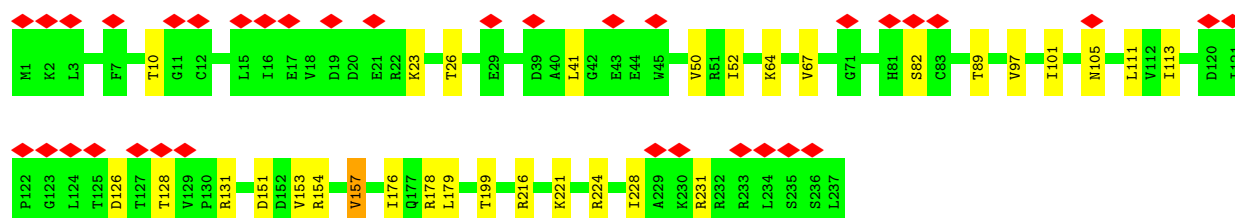
- Molecule 65: 40S ribosomal protein S4

Chain EE: 84% 15% .



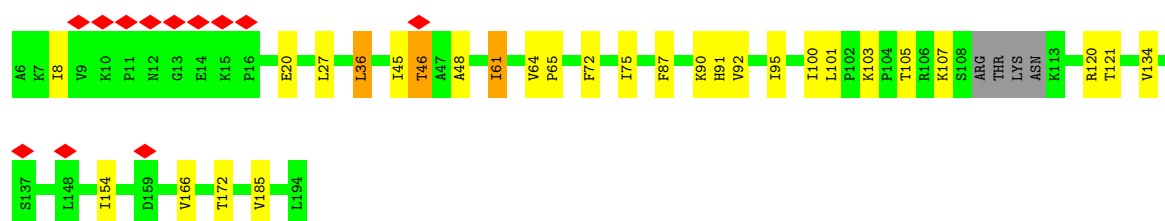
- Molecule 66: 40S ribosomal protein S6

Chain GG: 15% 87% 13%



- Molecule 67: Small ribosomal subunit protein eS7

Chain HH: 6% 83% 14% . .



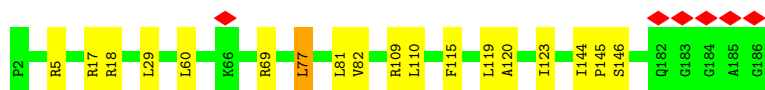
- Molecule 68: 40S ribosomal protein S8

Chain II: 85% 13% .




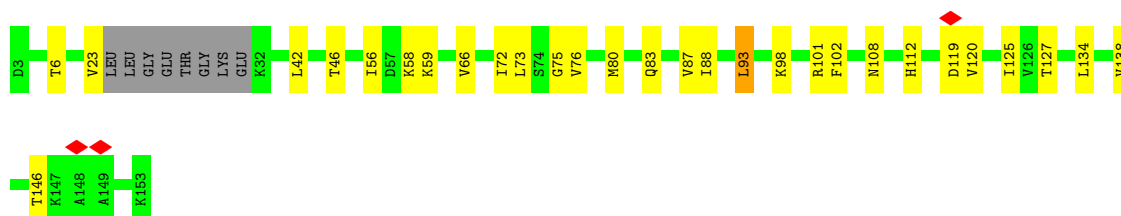
- Molecule 69: 40S ribosomal protein S9

Chain JJ:  90% 9%



- Molecule 70: Small ribosomal subunit protein uS17

Chain LL:  75% 19% 5%



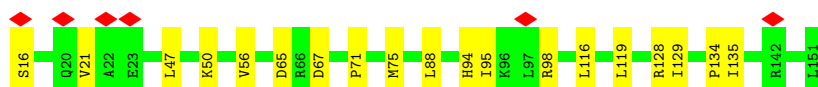
- Molecule 71: 40S ribosomal protein S13

Chain NN:  87% 12%




- Molecule 72: Small ribosomal subunit protein uS11

Chain OO:  86% 14%



- Molecule 73: eS21

Chain VV:  7% 81% 18%

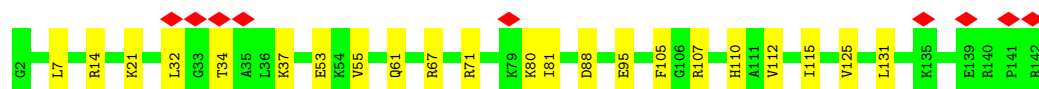
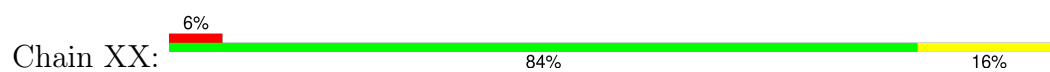


- Molecule 74: 40S ribosomal protein S15a

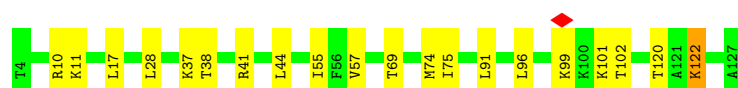
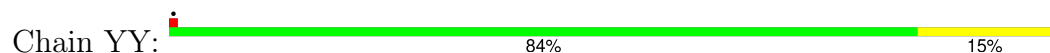
Chain WW:  87% 12%



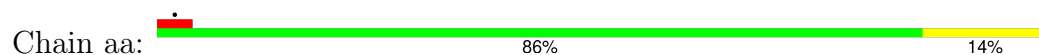
- Molecule 75: 40S ribosomal protein S23



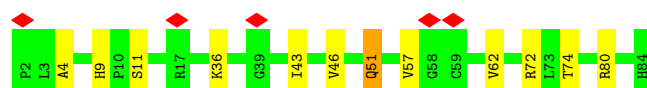
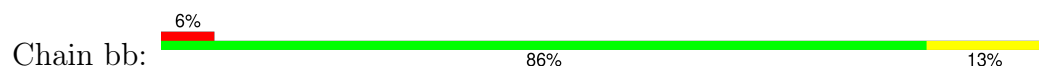
- Molecule 76: 40S ribosomal protein S24



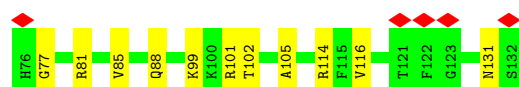
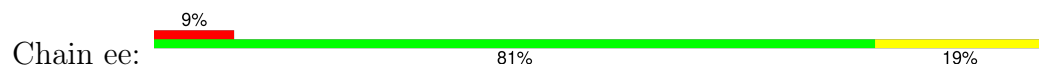
- Molecule 77: eS26



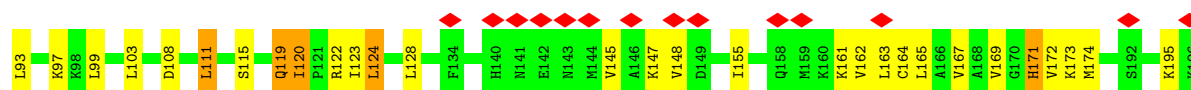
- Molecule 78: 40S ribosomal protein S27



- Molecule 79: Small ribosomal subunit protein eS30



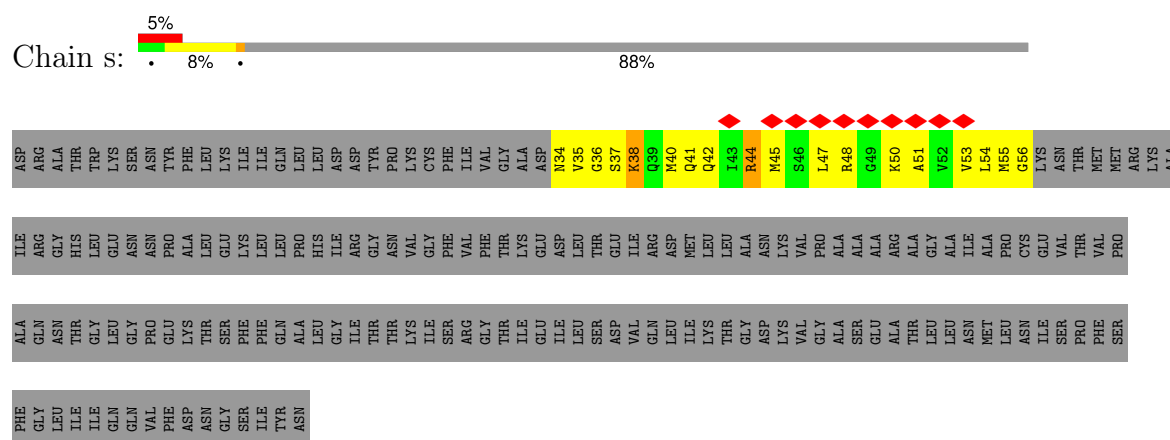
- Molecule 80: Large ribosomal subunit protein uL1



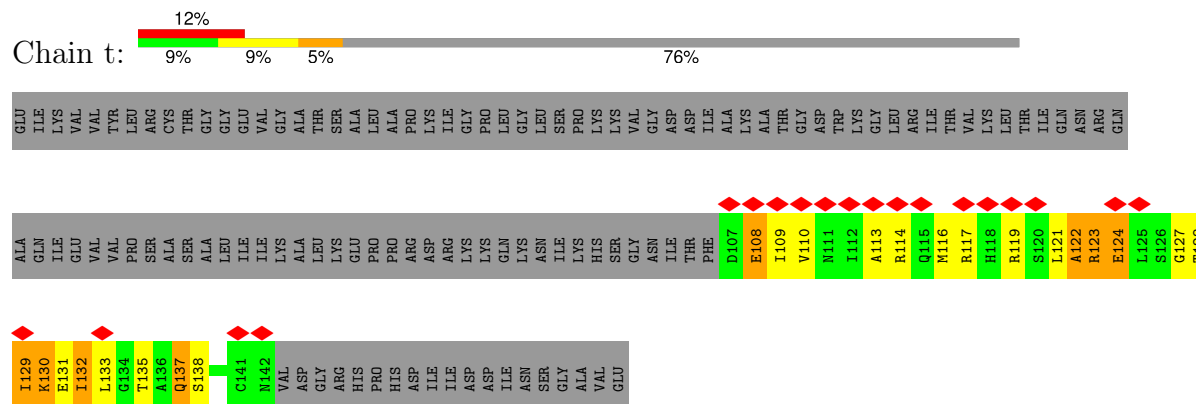
- Molecule 81: NediV IRES



- Molecule 82: 60S acidic ribosomal protein P0



- Molecule 83: uL11



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27739	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.798	Depositor
Minimum map value	-0.800	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.119	Depositor
Recommended contour level	0.2	Depositor
Map size (\AA)	450.0, 450.0, 450.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.25, 1.25, 1.25	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	7	0.22	0/2836	0.39	0/4421
2	A	0.24	0/1936	0.59	0/2596
3	B	0.21	0/3240	0.52	0/4339
4	C	0.21	0/2937	0.54	0/3946
5	D	0.22	0/2437	0.49	0/3264
6	E	0.23	0/1762	0.56	2/2362 (0.1%)
7	F	0.26	0/1911	0.58	0/2549
8	G	0.24	0/1902	0.52	0/2556
9	H	0.25	0/1535	0.59	2/2063 (0.1%)
10	I	0.21	0/1698	0.47	0/2267
11	J	0.22	0/1385	0.51	0/1852
12	L	0.21	0/1733	0.50	0/2316
13	M	0.24	0/1158	0.58	0/1547
14	N	0.21	0/1746	0.50	0/2338
15	O	0.23	0/1662	0.54	0/2222
16	P	0.22	0/1268	0.52	0/1700
17	Q	0.21	0/1539	0.53	0/2054
18	R	0.24	0/1524	0.57	2/2013 (0.1%)
19	S	0.25	0/1501	0.49	0/2012
20	T	0.20	0/1326	0.51	0/1770
21	U	0.26	0/823	0.68	0/1104
22	V	0.21	0/1048	0.53	0/1402
23	W	0.21	0/873	0.51	0/1158
24	X	0.20	0/984	0.49	0/1323
25	Y	0.22	0/1132	0.52	0/1504
26	Z	0.23	0/1130	0.50	0/1507
27	a	0.21	0/1191	0.49	0/1590
28	b	0.20	0/854	0.48	0/1128
29	c	0.22	0/771	0.54	0/1034
30	d	0.24	0/903	0.60	0/1216
31	e	0.21	0/1071	0.57	0/1429
32	f	0.20	0/895	0.49	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.24	0/916	0.56	0/1220
34	h	0.23	0/1021	0.48	0/1348
35	i	0.23	0/841	0.51	0/1112
36	j	0.24	0/720	0.57	0/952
37	k	0.20	0/575	0.49	0/761
38	l	0.23	0/459	0.52	0/608
39	m	0.20	0/435	0.53	0/575
40	n	0.22	0/240	0.53	0/305
41	o	0.20	0/864	0.44	0/1140
42	p	0.25	0/718	0.65	0/953
43	r	0.24	0/1010	0.61	0/1354
44	5	0.25	9/86397 (0.0%)	0.47	33/134736 (0.0%)
45	8	0.25	0/3581	0.46	0/5577
46	DD	0.23	0/1679	0.54	0/2258
47	FF	0.21	0/1492	0.58	2/2005 (0.1%)
48	KK	0.20	0/834	0.54	2/1125 (0.2%)
49	MM	0.23	0/760	0.57	0/1021
50	PP	0.21	0/1079	0.53	0/1441
51	QQ	0.21	0/1146	0.53	2/1534 (0.1%)
52	RR	0.97	12/1015 (1.2%)	1.20	17/1359 (1.3%)
53	SS	0.22	0/1208	0.56	0/1618
54	TT	0.20	0/1115	0.47	0/1493
55	UU	0.20	0/805	0.48	0/1081
56	ZZ	0.23	0/604	0.56	0/810
57	cc	0.17	0/490	0.44	0/656
58	dd	0.22	0/470	0.54	0/623
59	ff	0.21	0/567	0.48	0/753
60	gg	0.21	0/2493	0.50	2/3394 (0.1%)
61	9	0.24	0/40486	0.47	11/63090 (0.0%)
62	AA	0.22	0/1621	0.57	0/2204
63	BB	0.21	0/1706	0.51	0/2281
64	CC	0.22	0/1753	0.49	0/2369
65	EE	0.21	0/2118	0.50	2/2849 (0.1%)
66	GG	0.19	0/1946	0.48	0/2590
67	HH	0.24	0/1510	0.53	1/2022 (0.0%)
68	II	0.23	0/1715	0.57	0/2287
69	JJ	0.21	0/1550	0.53	0/2069
70	LL	0.24	0/1195	0.55	0/1597
71	NN	0.20	0/1226	0.46	0/1649
72	OO	0.19	0/1029	0.45	0/1380
73	VV	0.20	0/643	0.54	0/860
74	WW	0.22	0/1051	0.52	0/1406
75	XX	0.25	0/1116	0.56	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	YY	0.20	0/1028	0.49	0/1366
77	aa	0.22	0/828	0.51	0/1109
78	bb	0.22	0/665	0.45	0/891
79	ee	0.17	0/462	0.38	0/607
80	K	0.52	3/1733 (0.2%)	1.05	7/2324 (0.3%)
81	1	0.34	0/3904	0.78	12/6077 (0.2%)
82	s	0.54	0/172	0.92	0/225
83	t	0.71	0/275	1.04	1/367 (0.3%)
All	All	0.25	24/231977 (0.0%)	0.51	98/340701 (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
3	B	0	1
25	Y	0	1
32	f	0	1
52	RR	0	1
75	XX	0	1
81	1	1	0
All	All	1	5

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	RR	87	GLU	CA-C	8.27	1.63	1.52
52	RR	87	GLU	N-CA	7.39	1.55	1.46
52	RR	80	ARG	CA-C	-7.15	1.43	1.52
52	RR	84	TYR	CA-C	-7.02	1.43	1.52
52	RR	73	LEU	CA-C	-7.00	1.43	1.52

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	K	77	ALA	N-CA-C	-23.05	80.91	112.25
80	K	72	GLN	N-CA-C	-18.34	73.50	107.98
52	RR	88	VAL	CB-CA-C	-12.57	90.68	111.29
44	5	4921	C	C1'-C2'-O2'	-11.42	94.67	111.80
52	RR	89	SER	N-CA-C	-11.09	87.17	110.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
81	1	1435	G	C1'

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	258	HIS	Peptide
52	RR	72	LYS	Mainchain
75	XX	61	GLN	Peptide
25	Y	121	ARG	Sidechain
32	f	106	TYR	Peptide

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	7	2538	0	1286	9	0
2	A	1898	0	1993	18	0
3	B	3172	0	3310	21	0
4	C	2883	0	3053	21	0
5	D	2391	0	2424	12	0
6	E	1729	0	1887	12	0
7	F	1875	0	1995	13	0
8	G	1872	0	2019	10	0
9	H	1516	0	1597	15	0
10	I	1660	0	1709	12	0
11	J	1362	0	1399	7	0
12	L	1702	0	1820	9	0
13	M	1137	0	1211	2	0
14	N	1701	0	1749	7	0
15	O	1630	0	1778	12	0
16	P	1242	0	1274	7	0
17	Q	1515	0	1634	16	0
18	R	1508	0	1664	13	0
19	S	1462	0	1508	12	0
20	T	1298	0	1366	14	0
21	U	809	0	833	5	0
22	V	1034	0	1097	10	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	W	860	0	903	5	0
24	X	967	0	1040	2	0
25	Y	1115	0	1205	9	0
26	Z	1107	0	1182	10	0
27	a	1162	0	1209	9	0
28	b	841	0	911	3	0
29	c	761	0	794	6	0
30	d	888	0	930	2	0
31	e	1053	0	1147	9	0
32	f	876	0	912	8	0
33	g	906	0	998	4	0
34	h	1013	0	1147	12	0
35	i	830	0	916	5	0
36	j	705	0	737	5	0
37	k	569	0	637	3	0
38	l	447	0	480	7	0
39	m	429	0	465	4	0
40	n	239	0	289	3	0
41	o	851	0	920	11	0
42	p	708	0	756	9	0
43	r	994	0	1051	11	0
44	5	77244	0	39022	418	0
45	8	3208	0	1629	6	0
46	DD	1653	0	1747	12	0
47	FF	1471	0	1522	7	0
48	KK	810	0	836	6	0
49	MM	754	0	790	6	0
50	PP	1058	0	1104	14	0
51	QQ	1128	0	1195	7	0
52	RR	1002	0	1054	74	0
53	SS	1190	0	1249	11	0
54	TT	1097	0	1132	7	0
55	UU	795	0	862	11	0
56	ZZ	598	0	656	3	0
57	cc	488	0	514	3	0
58	dd	459	0	448	6	0
59	ff	555	0	563	0	0
60	gg	2436	0	2393	24	0
61	9	36209	0	18290	113	0
62	AA	1586	0	1598	33	0
63	BB	1680	0	1748	12	0
64	CC	1716	0	1806	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
65	EE	2076	0	2177	15	0
66	GG	1923	0	2089	11	0
67	HH	1488	0	1582	8	0
68	II	1686	0	1772	12	0
69	JJ	1525	0	1640	10	0
70	LL	1175	0	1249	5	0
71	NN	1202	0	1289	8	0
72	OO	1016	0	1039	9	0
73	VV	636	0	637	8	0
74	WW	1034	0	1080	7	0
75	XX	1098	0	1167	8	0
76	YY	1011	0	1083	10	0
77	aa	814	0	863	3	0
78	bb	651	0	672	4	0
79	ee	457	0	502	6	0
80	K	1705	0	1810	99	0
81	1	3496	0	1771	15	0
82	s	173	0	192	46	0
83	t	275	0	283	57	0
84	5	192	0	0	0	0
84	7	5	0	0	0	0
84	8	3	0	0	0	0
84	9	1	0	0	0	0
84	P	1	0	0	0	0
84	V	1	0	0	0	0
84	a	1	0	0	0	0
84	g	1	0	0	0	0
84	j	1	0	0	0	0
85	aa	1	0	0	0	0
85	dd	1	0	0	0	0
85	ff	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
All	All	216047	0	160290	1291	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 1291 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)
80:K:65:VAL:HG23	80:K:81:ASP:OD1	1.37	1.18
80:K:74:CYS:SG	80:K:82:ILE:HD11	1.92	1.08
80:K:74:CYS:SG	80:K:84:HIS:HB3	1.94	1.06
44:5:169:G:N2	44:5:267:G:C6	2.23	1.04
52:RR:72:LYS:HA	52:RR:75:GLU:HB3	1.35	1.04

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	
2	A	246/248 (99%)	226 (92%)	20 (8%)	0	100	100
3	B	392/394 (100%)	370 (94%)	22 (6%)	0	100	100
4	C	360/362 (99%)	343 (95%)	17 (5%)	0	100	100
5	D	291/293 (99%)	276 (95%)	14 (5%)	1 (0%)	36	67
6	E	208/251 (83%)	197 (95%)	11 (5%)	0	100	100
7	F	223/225 (99%)	210 (94%)	12 (5%)	1 (0%)	30	62
8	G	226/240 (94%)	212 (94%)	14 (6%)	0	100	100
9	H	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
10	I	200/213 (94%)	184 (92%)	16 (8%)	0	100	100
11	J	168/170 (99%)	163 (97%)	5 (3%)	0	100	100
12	L	208/210 (99%)	200 (96%)	8 (4%)	0	100	100
13	M	136/138 (99%)	126 (93%)	10 (7%)	0	100	100
14	N	201/203 (99%)	191 (95%)	10 (5%)	0	100	100
15	O	197/199 (99%)	190 (96%)	7 (4%)	0	100	100
16	P	151/153 (99%)	144 (95%)	7 (5%)	0	100	100
17	Q	185/187 (99%)	178 (96%)	7 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	R	178/180 (99%)	171 (96%)	7 (4%)	0	100	100
19	S	174/176 (99%)	162 (93%)	11 (6%)	1 (1%)	21	54
20	T	157/159 (99%)	150 (96%)	7 (4%)	0	100	100
21	U	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
22	V	137/139 (99%)	129 (94%)	8 (6%)	0	100	100
23	W	102/106 (96%)	95 (93%)	7 (7%)	0	100	100
24	X	116/118 (98%)	106 (91%)	10 (9%)	0	100	100
25	Y	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
26	Z	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	16	49
27	a	145/147 (99%)	131 (90%)	14 (10%)	0	100	100
28	b	99/104 (95%)	94 (95%)	4 (4%)	1 (1%)	12	44
29	c	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
30	d	105/107 (98%)	97 (92%)	7 (7%)	1 (1%)	12	44
31	e	126/128 (98%)	118 (94%)	8 (6%)	0	100	100
32	f	107/109 (98%)	99 (92%)	7 (6%)	1 (1%)	14	47
33	g	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
34	h	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
35	i	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
36	j	84/86 (98%)	78 (93%)	6 (7%)	0	100	100
37	k	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
38	l	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
39	m	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
40	n	23/25 (92%)	23 (100%)	0	0	100	100
41	o	102/104 (98%)	95 (93%)	7 (7%)	0	100	100
42	p	89/91 (98%)	83 (93%)	6 (7%)	0	100	100
43	r	122/124 (98%)	114 (93%)	8 (7%)	0	100	100
46	DD	211/213 (99%)	205 (97%)	4 (2%)	2 (1%)	14	47
47	FF	181/191 (95%)	169 (93%)	11 (6%)	1 (1%)	21	54
48	KK	94/96 (98%)	91 (97%)	3 (3%)	0	100	100
49	MM	92/117 (79%)	84 (91%)	8 (9%)	0	100	100
50	PP	127/129 (98%)	120 (94%)	7 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	QQ	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
52	RR	120/132 (91%)	98 (82%)	15 (12%)	7 (6%)	1	13
53	SS	142/144 (99%)	133 (94%)	9 (6%)	0	100	100
54	TT	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
55	UU	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
56	ZZ	73/75 (97%)	70 (96%)	3 (4%)	0	100	100
57	cc	60/62 (97%)	56 (93%)	4 (7%)	0	100	100
58	dd	53/55 (96%)	49 (92%)	4 (8%)	0	100	100
59	ff	66/68 (97%)	59 (89%)	7 (11%)	0	100	100
60	gg	311/313 (99%)	281 (90%)	30 (10%)	0	100	100
62	AA	200/202 (99%)	185 (92%)	15 (8%)	0	100	100
63	BB	202/213 (95%)	193 (96%)	9 (4%)	0	100	100
64	CC	219/221 (99%)	208 (95%)	11 (5%)	0	100	100
65	EE	260/262 (99%)	237 (91%)	23 (9%)	0	100	100
66	GG	235/237 (99%)	222 (94%)	13 (6%)	0	100	100
67	HH	181/189 (96%)	173 (96%)	8 (4%)	0	100	100
68	II	204/206 (99%)	187 (92%)	17 (8%)	0	100	100
69	JJ	183/185 (99%)	177 (97%)	6 (3%)	0	100	100
70	LL	139/151 (92%)	129 (93%)	10 (7%)	0	100	100
71	NN	147/149 (99%)	139 (95%)	8 (5%)	0	100	100
72	OO	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
73	VV	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
74	WW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
75	XX	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
76	YY	122/124 (98%)	114 (93%)	8 (7%)	0	100	100
77	aa	99/101 (98%)	90 (91%)	9 (9%)	0	100	100
78	bb	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
79	ee	55/57 (96%)	52 (94%)	3 (6%)	0	100	100
80	K	210/212 (99%)	168 (80%)	32 (15%)	10 (5%)	2	16
82	s	21/196 (11%)	18 (86%)	3 (14%)	0	100	100
83	t	34/153 (22%)	30 (88%)	3 (9%)	1 (3%)	3	26

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	11381/11962 (95%)	10661 (94%)	692 (6%)	28 (0%)	44	74

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	d	96	GLU
46	DD	93	THR
52	RR	83	ASN
52	RR	86	PRO
52	RR	87	GLU

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	
2	A	190/190 (100%)	172 (90%)	18 (10%)	8	31
3	B	342/342 (100%)	308 (90%)	34 (10%)	7	29
4	C	302/302 (100%)	272 (90%)	30 (10%)	7	29
5	D	247/247 (100%)	237 (96%)	10 (4%)	28	54
6	E	190/223 (85%)	171 (90%)	19 (10%)	7	28
7	F	196/196 (100%)	179 (91%)	17 (9%)	9	33
8	G	199/205 (97%)	181 (91%)	18 (9%)	9	32
9	H	169/169 (100%)	158 (94%)	11 (6%)	15	42
10	I	175/180 (97%)	161 (92%)	14 (8%)	11	35
11	J	143/143 (100%)	131 (92%)	12 (8%)	10	34
12	L	175/175 (100%)	161 (92%)	14 (8%)	11	35
13	M	117/117 (100%)	105 (90%)	12 (10%)	7	28
14	N	171/171 (100%)	164 (96%)	7 (4%)	27	53
15	O	171/171 (100%)	160 (94%)	11 (6%)	16	42
16	P	134/134 (100%)	128 (96%)	6 (4%)	24	50
17	Q	164/164 (100%)	146 (89%)	18 (11%)	6	26

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	R	159/159 (100%)	144 (91%)	15 (9%)	8	31
19	S	157/157 (100%)	141 (90%)	16 (10%)	7	28
20	T	139/139 (100%)	119 (86%)	20 (14%)	3	18
21	U	89/89 (100%)	86 (97%)	3 (3%)	32	57
22	V	106/106 (100%)	89 (84%)	17 (16%)	2	14
23	W	86/86 (100%)	80 (93%)	6 (7%)	14	39
24	X	106/106 (100%)	101 (95%)	5 (5%)	23	49
25	Y	124/124 (100%)	114 (92%)	10 (8%)	11	35
26	Z	117/117 (100%)	107 (92%)	10 (8%)	10	34
27	a	119/119 (100%)	104 (87%)	15 (13%)	4	21
28	b	83/84 (99%)	75 (90%)	8 (10%)	8	30
29	c	84/84 (100%)	75 (89%)	9 (11%)	6	27
30	d	98/98 (100%)	86 (88%)	12 (12%)	5	22
31	e	114/114 (100%)	107 (94%)	7 (6%)	17	43
32	f	88/88 (100%)	78 (89%)	10 (11%)	5	24
33	g	98/98 (100%)	85 (87%)	13 (13%)	4	20
34	h	109/109 (100%)	104 (95%)	5 (5%)	24	50
35	i	86/86 (100%)	76 (88%)	10 (12%)	5	24
36	j	73/73 (100%)	67 (92%)	6 (8%)	10	34
37	k	64/64 (100%)	61 (95%)	3 (5%)	23	49
38	l	47/47 (100%)	41 (87%)	6 (13%)	4	21
39	m	48/48 (100%)	47 (98%)	1 (2%)	47	66
40	n	24/24 (100%)	20 (83%)	4 (17%)	2	13
41	o	92/92 (100%)	82 (89%)	10 (11%)	6	26
42	p	74/74 (100%)	70 (95%)	4 (5%)	20	46
43	r	108/108 (100%)	102 (94%)	6 (6%)	19	46
46	DD	176/176 (100%)	162 (92%)	14 (8%)	11	35
47	FF	158/161 (98%)	147 (93%)	11 (7%)	14	39
48	KK	87/87 (100%)	84 (97%)	3 (3%)	32	57
49	MM	83/99 (84%)	73 (88%)	10 (12%)	5	23
50	PP	115/115 (100%)	102 (89%)	13 (11%)	5	25

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	QQ	117/117 (100%)	107 (92%)	10 (8%)	10	34
52	RR	111/119 (93%)	96 (86%)	15 (14%)	4	20
53	SS	125/125 (100%)	121 (97%)	4 (3%)	34	59
54	TT	111/111 (100%)	99 (89%)	12 (11%)	6	26
55	UU	92/92 (100%)	84 (91%)	8 (9%)	9	33
56	ZZ	66/66 (100%)	61 (92%)	5 (8%)	12	37
57	cc	55/55 (100%)	48 (87%)	7 (13%)	4	21
58	dd	48/48 (100%)	44 (92%)	4 (8%)	10	34
59	ff	61/61 (100%)	59 (97%)	2 (3%)	33	58
60	gg	272/272 (100%)	246 (90%)	26 (10%)	8	30
62	AA	168/169 (99%)	148 (88%)	20 (12%)	5	23
63	BB	189/194 (97%)	179 (95%)	10 (5%)	20	47
64	CC	187/187 (100%)	170 (91%)	17 (9%)	9	32
65	EE	224/224 (100%)	206 (92%)	18 (8%)	11	35
66	GG	207/207 (100%)	192 (93%)	15 (7%)	13	38
67	HH	165/169 (98%)	150 (91%)	15 (9%)	9	32
68	II	178/178 (100%)	162 (91%)	16 (9%)	9	32
69	JJ	161/161 (100%)	153 (95%)	8 (5%)	22	48
70	LL	130/136 (96%)	109 (84%)	21 (16%)	2	14
71	NN	130/130 (100%)	122 (94%)	8 (6%)	16	43
72	OO	106/106 (100%)	99 (93%)	7 (7%)	15	41
73	VV	67/67 (100%)	62 (92%)	5 (8%)	12	37
74	WW	112/112 (100%)	104 (93%)	8 (7%)	13	38
75	XX	113/113 (100%)	103 (91%)	10 (9%)	9	32
76	YY	107/107 (100%)	100 (94%)	7 (6%)	15	42
77	aa	88/88 (100%)	79 (90%)	9 (10%)	7	28
78	bb	75/75 (100%)	67 (89%)	8 (11%)	6	27
79	ee	47/47 (100%)	45 (96%)	2 (4%)	26	51
80	K	190/191 (100%)	149 (78%)	41 (22%)	1	6
82	s	19/164 (12%)	15 (79%)	4 (21%)	1	6
83	t	30/126 (24%)	23 (77%)	7 (23%)	1	5

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	9947/10277 (97%)	9065 (91%)	882 (9%)	11	32

5 of 882 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	o	4	VAL
54	TT	110	LEU
83	t	123	ARG
75	XX	95	GLU
43	r	10	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 226 such sidechains are listed below:

Mol	Chain	Res	Type
38	l	19	GLN
80	K	119	GLN
51	QQ	142	GLN
79	ee	110	GLN
72	OO	83	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	7	118/119 (99%)	11 (9%)	0
44	5	3580/3603 (99%)	872 (24%)	60 (1%)
45	8	149/156 (95%)	33 (22%)	1 (0%)
61	9	1684/1696 (99%)	380 (22%)	16 (0%)
81	1	164/165 (99%)	101 (61%)	10 (6%)
All	All	5695/5739 (99%)	1397 (24%)	87 (1%)

5 of 1397 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	7	3	C
1	7	11	A
1	7	22	A
1	7	53	U
1	7	54	A

5 of 87 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	5	4925	U
61	9	872	A
44	5	4947	U
61	9	553	U
61	9	1664	A

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 214 ligands modelled in this entry, 214 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
44	5	26
61	9	12
23	W	1
6	E	1

The worst 5 of 40 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	41.18
1	W	63:GLN	C	79:GLN	N	40.60
1	5	1252:C	O3'	1271:G	P	36.81
1	5	1219:G	O3'	1233:G	P	19.65
1	9	130:G	O3'	141:A	P	18.46

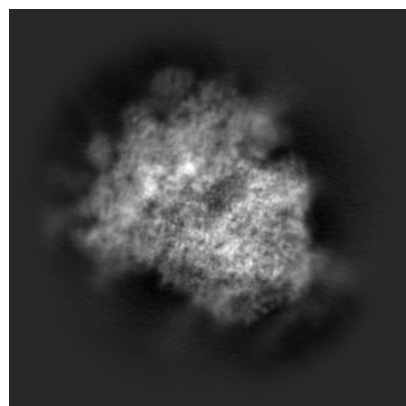
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72136. These allow visual inspection of the internal detail of the map and identification of artifacts.

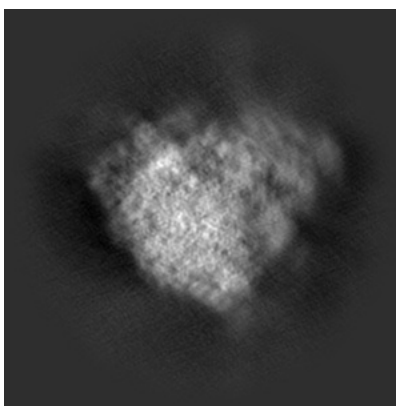
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

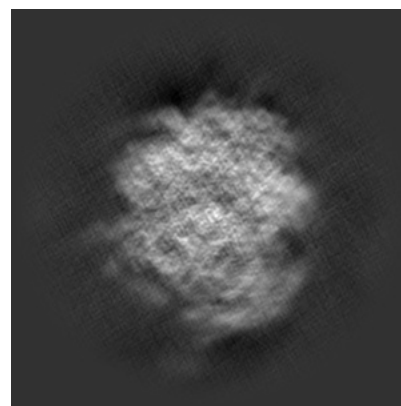
6.1.1 Primary map



X

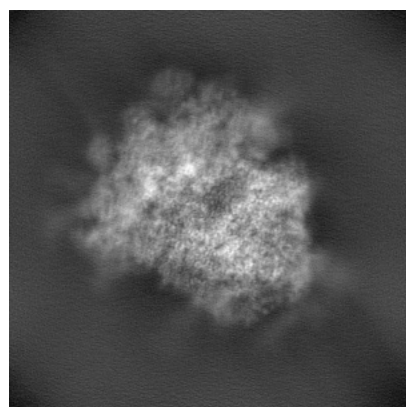


Y

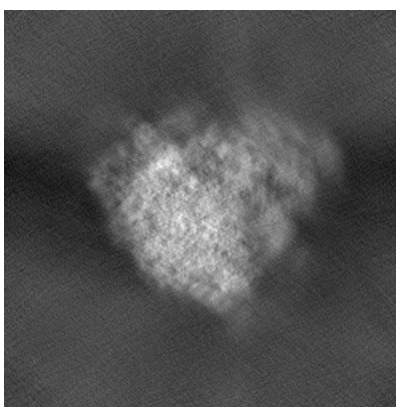


Z

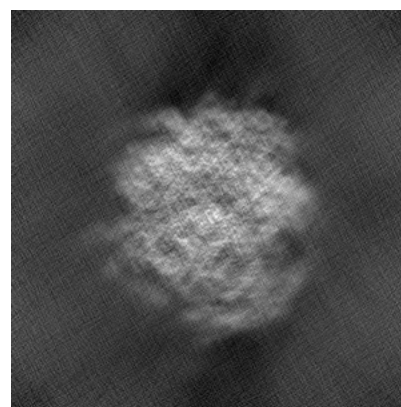
6.1.2 Raw map



X



Y

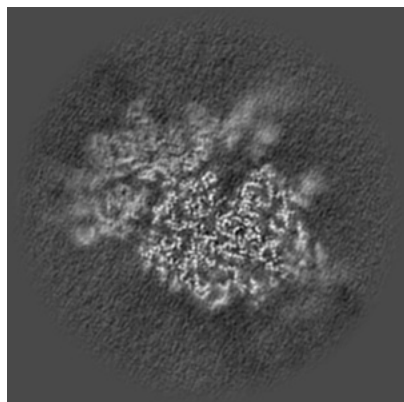


Z

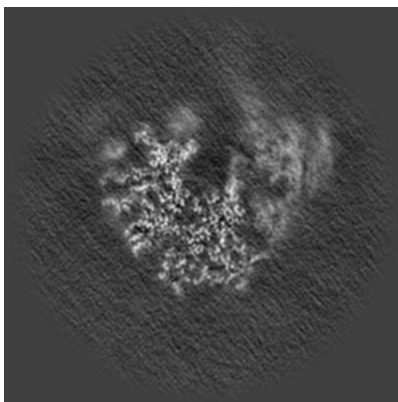
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

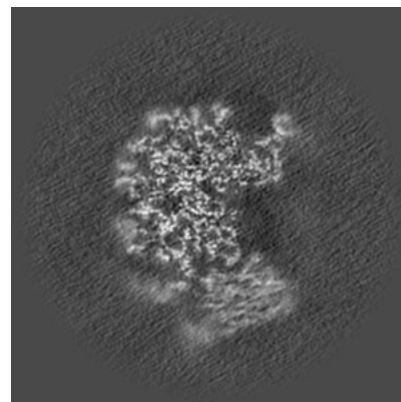
6.2.1 Primary map



X Index: 180

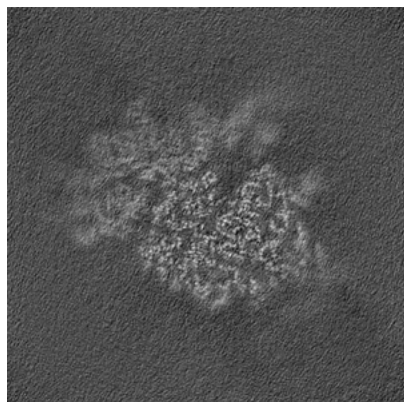


Y Index: 180

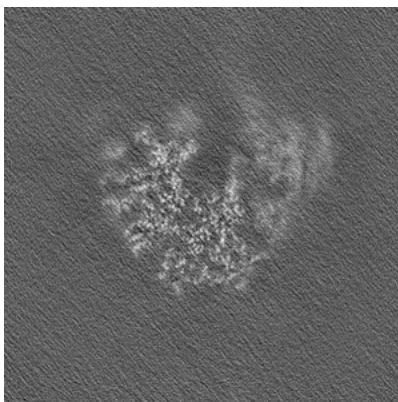


Z Index: 180

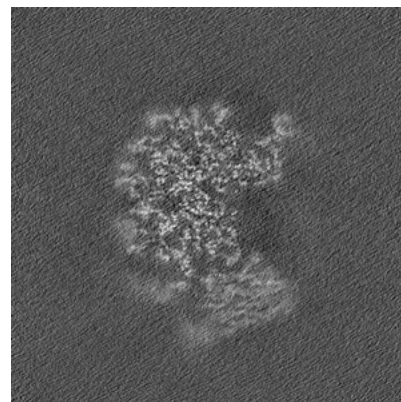
6.2.2 Raw map



X Index: 180



Y Index: 180

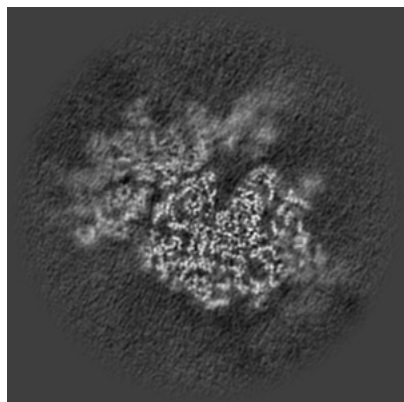


Z Index: 180

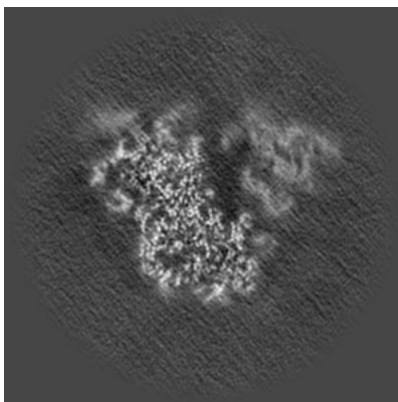
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

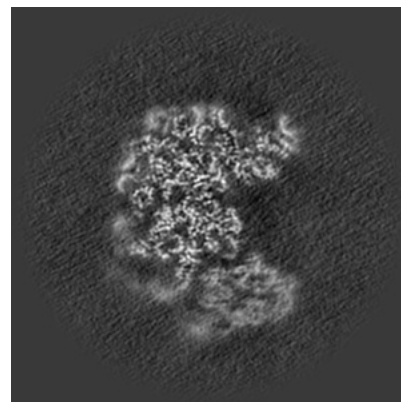
6.3.1 Primary map



X Index: 182

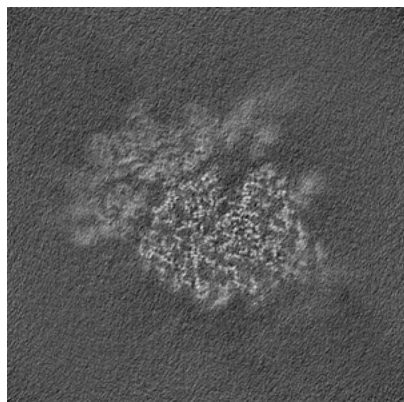


Y Index: 198

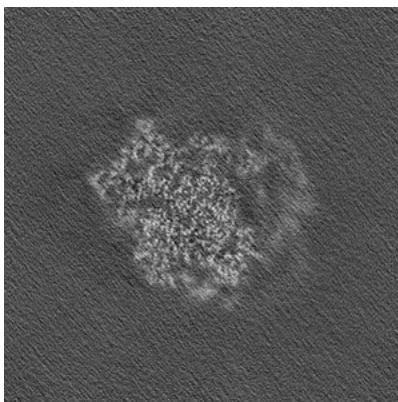


Z Index: 184

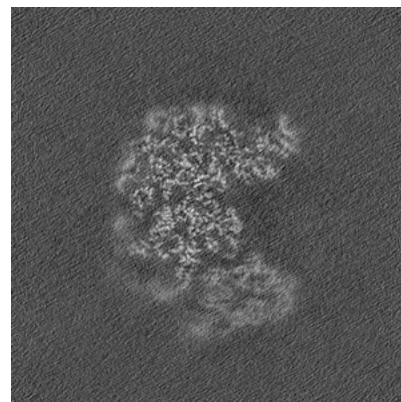
6.3.2 Raw map



X Index: 179



Y Index: 217

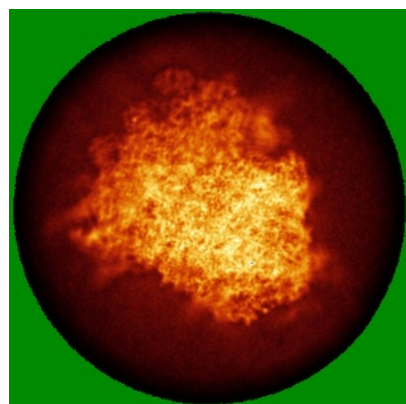


Z Index: 184

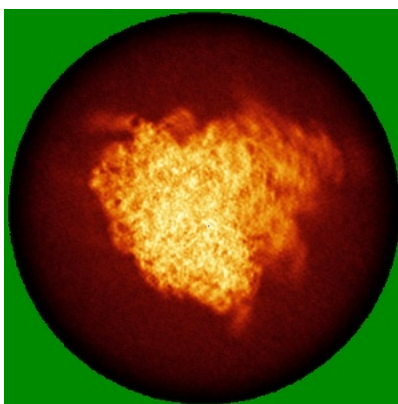
The images above show the largest variance slices of the map in three orthogonal directions.

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

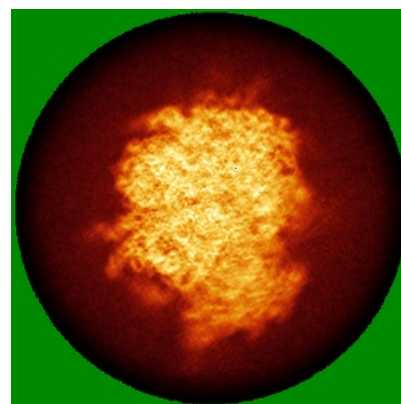
6.4.1 Primary map



X

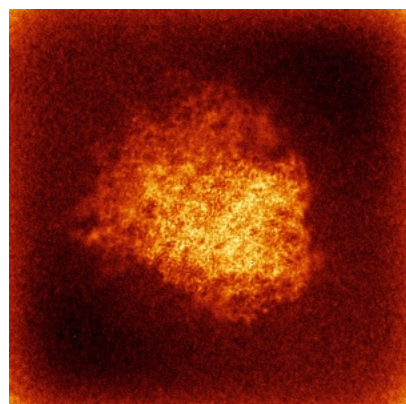


Y

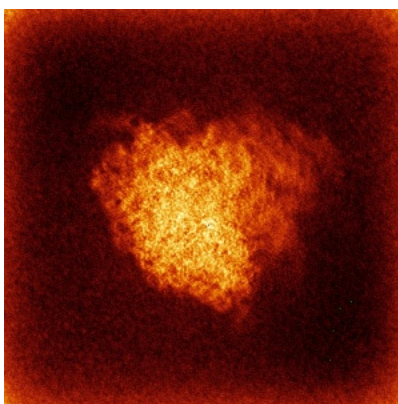


Z

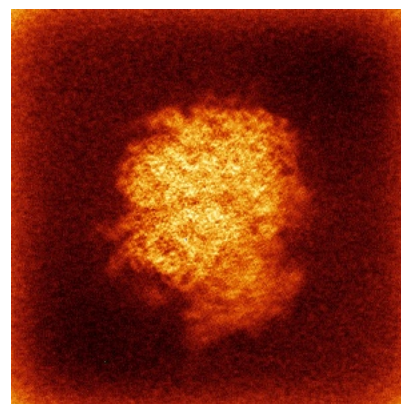
6.4.2 Raw map



X



Y

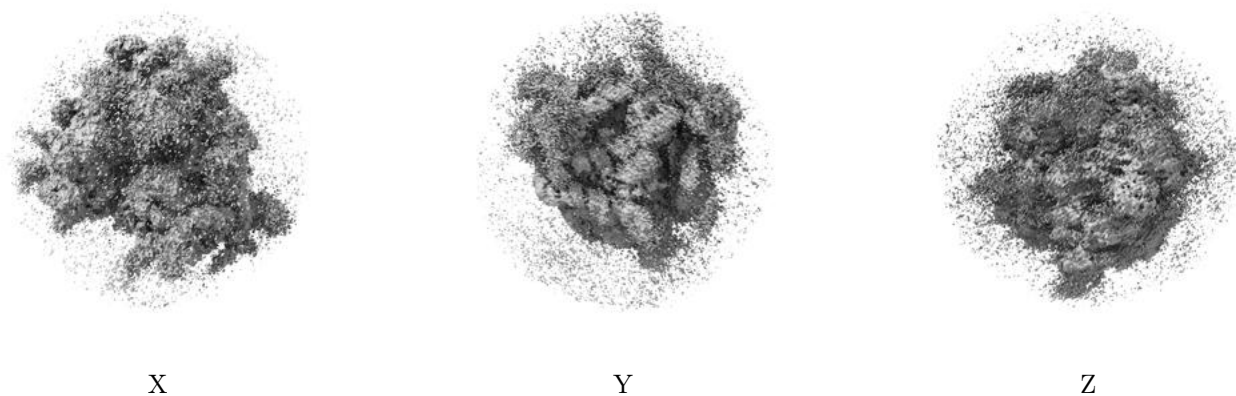


Z

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.

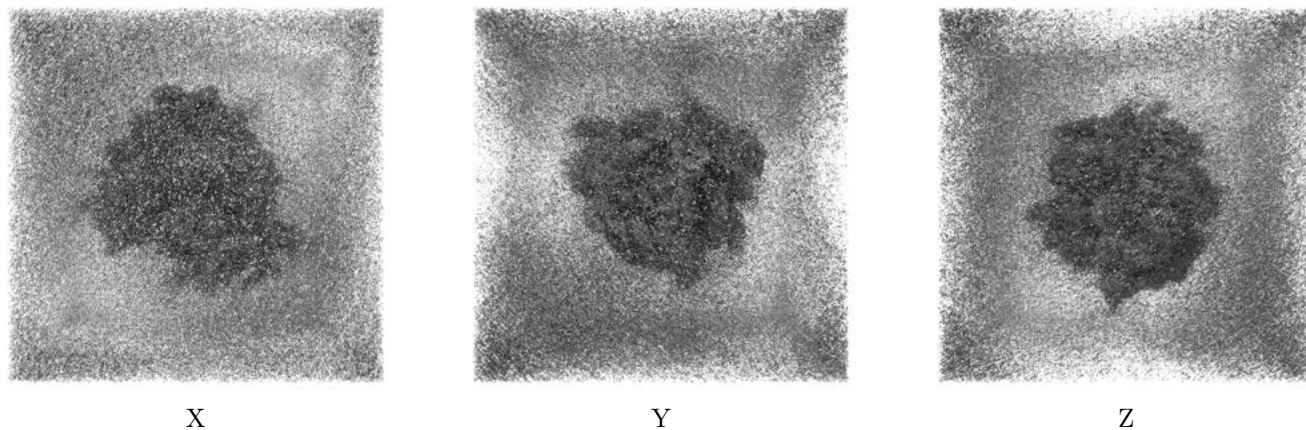
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. 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.

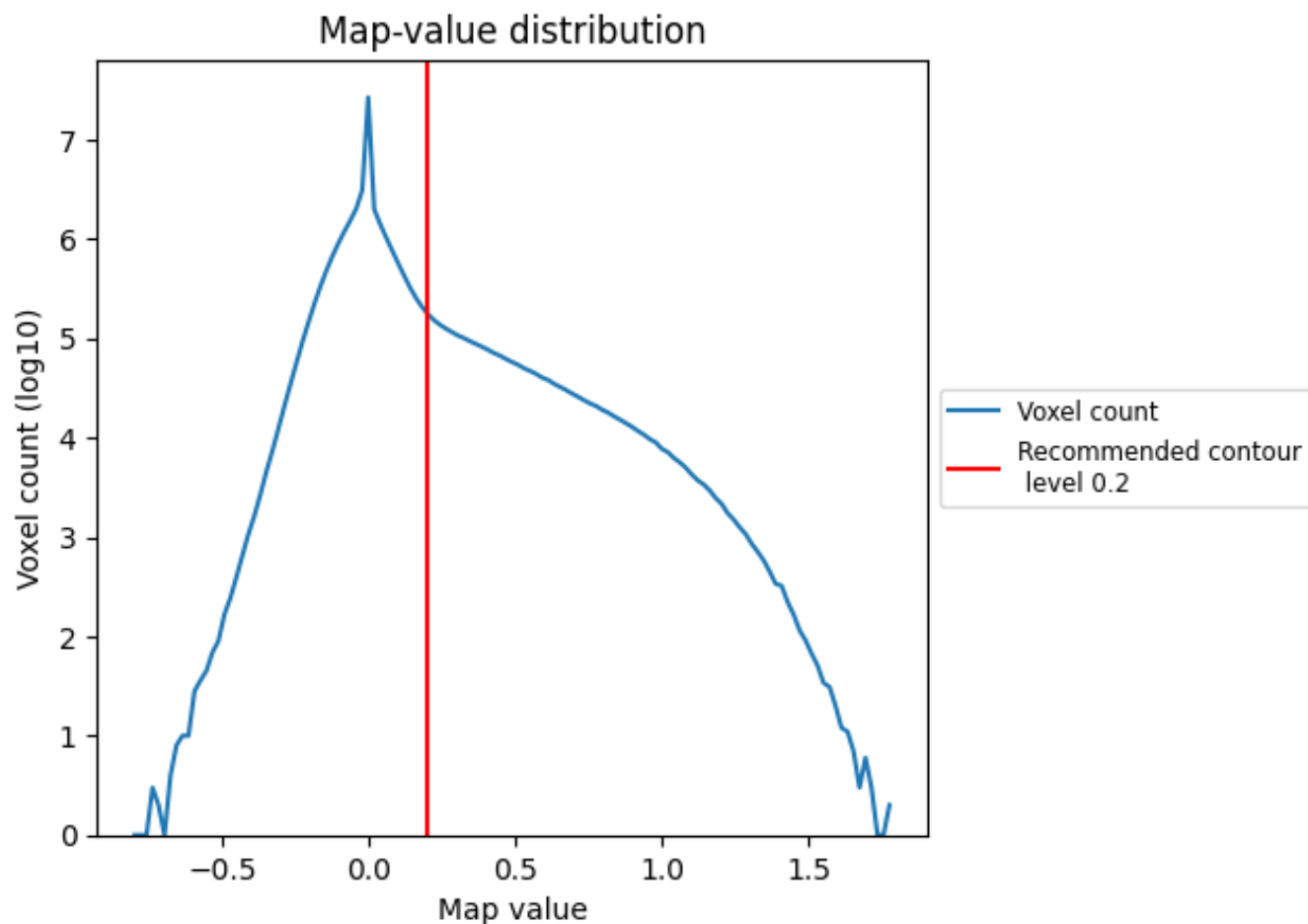
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

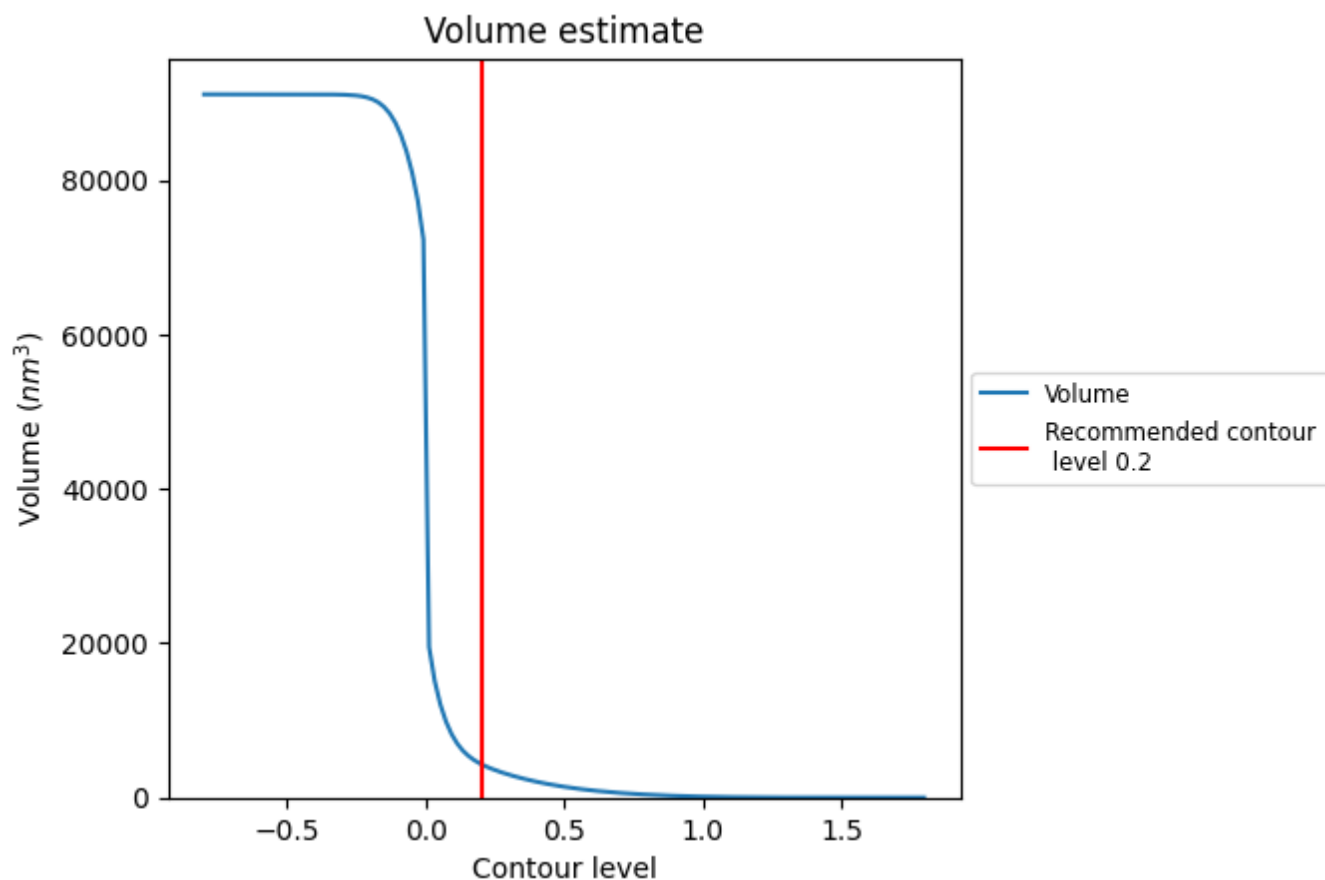
This section contains the results of statistical analysis of the map.

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.

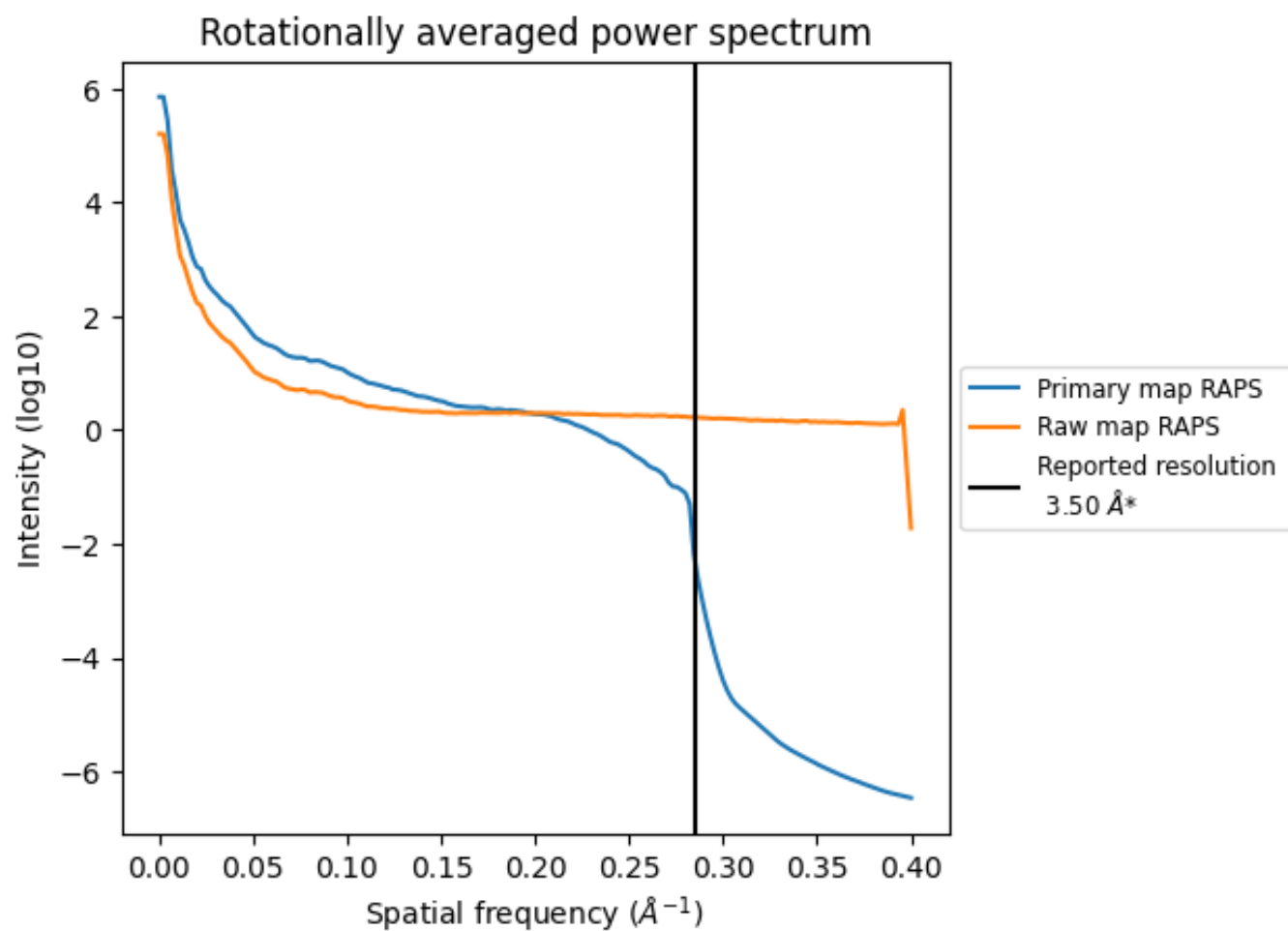
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4338 nm³; this corresponds to an approximate mass of 3918 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 ⓘ

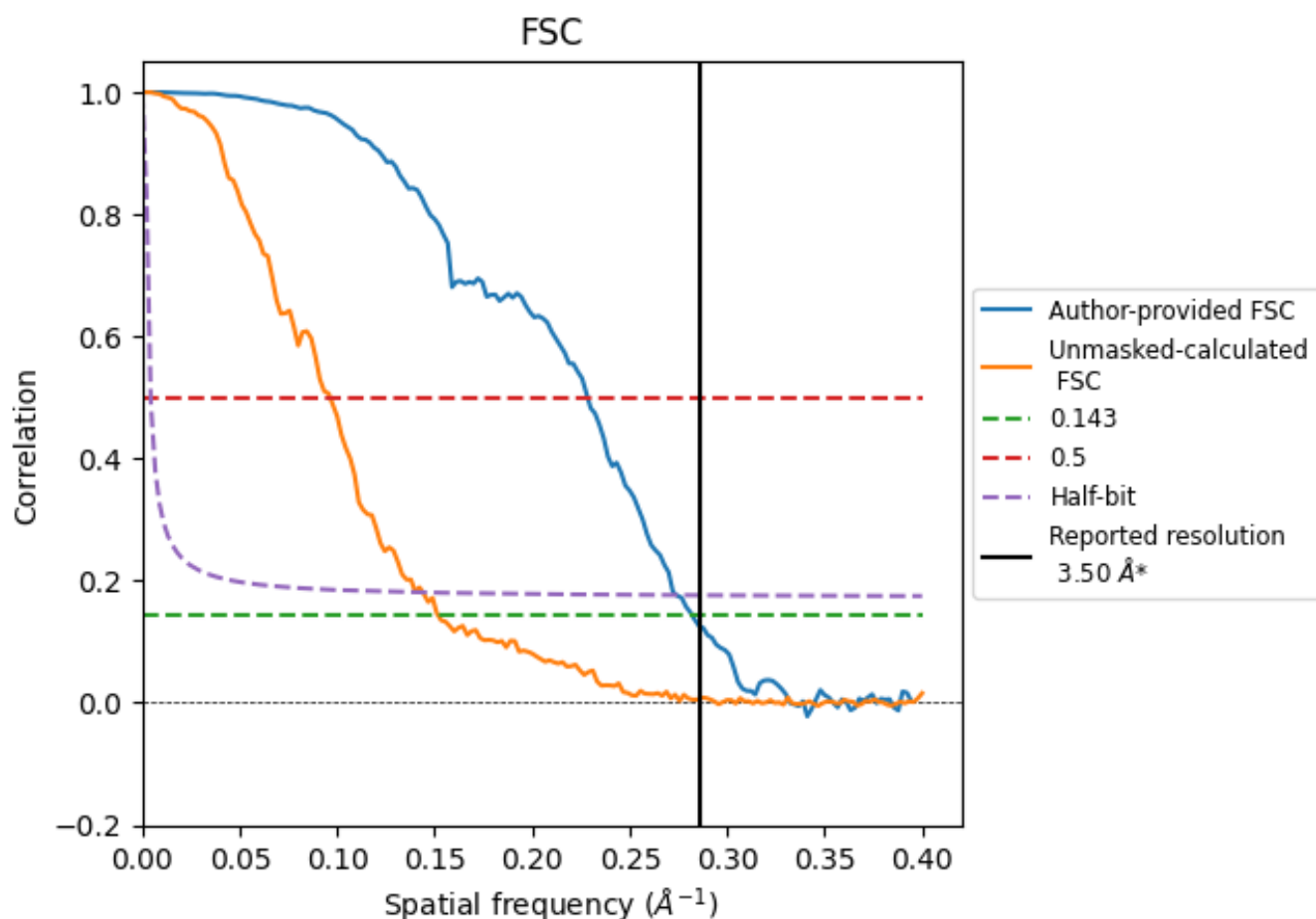


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 \AA^{-1}

8.2 Resolution estimates [i](#)

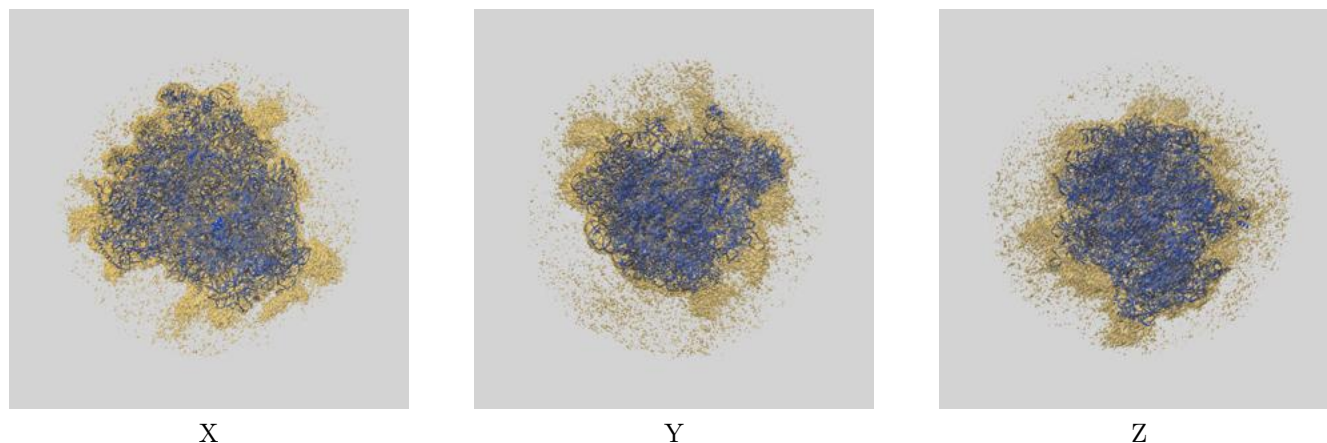
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.54	4.38	3.65
Unmasked-calculated*	6.59	10.38	6.94

*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 6.59 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

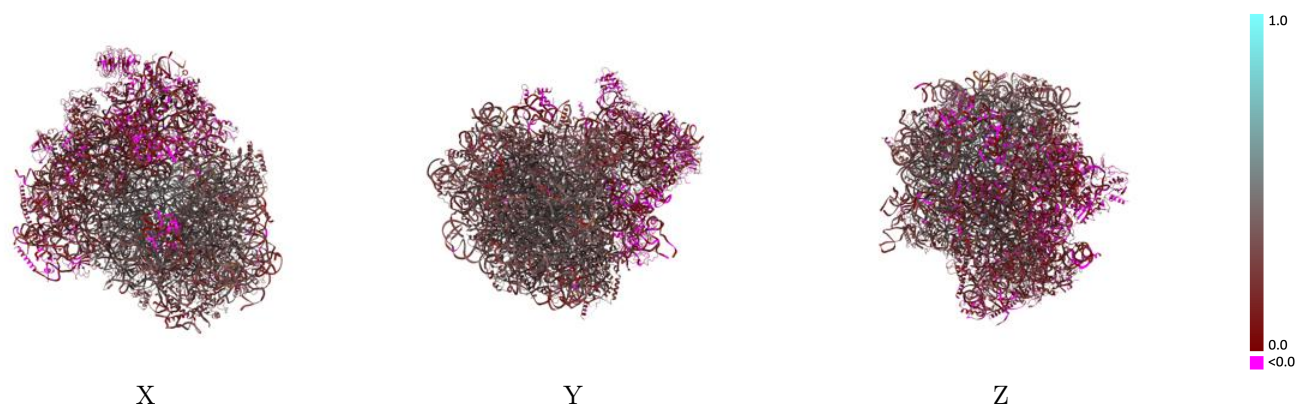
This section contains information regarding the fit between EMDB map EMD-72136 and PDB model 9Q1Q. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)



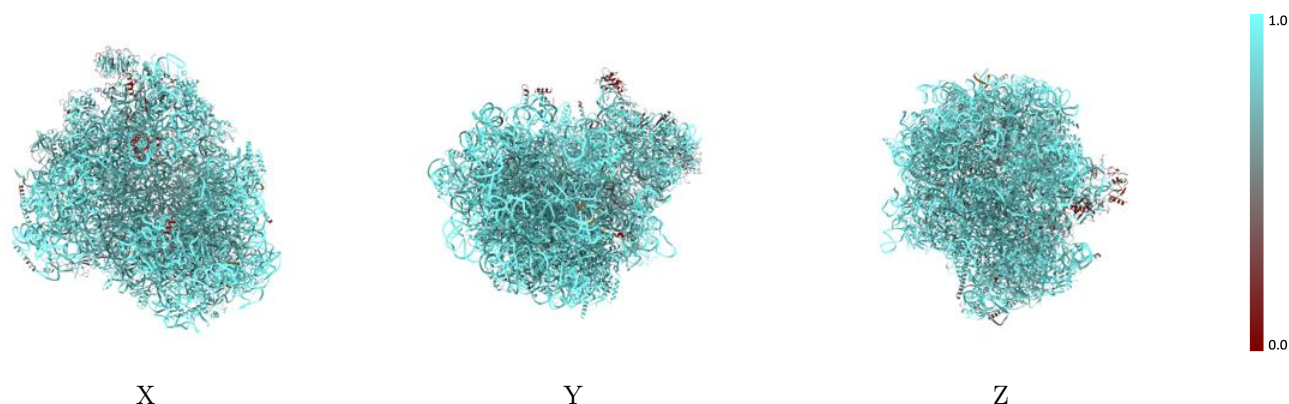
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



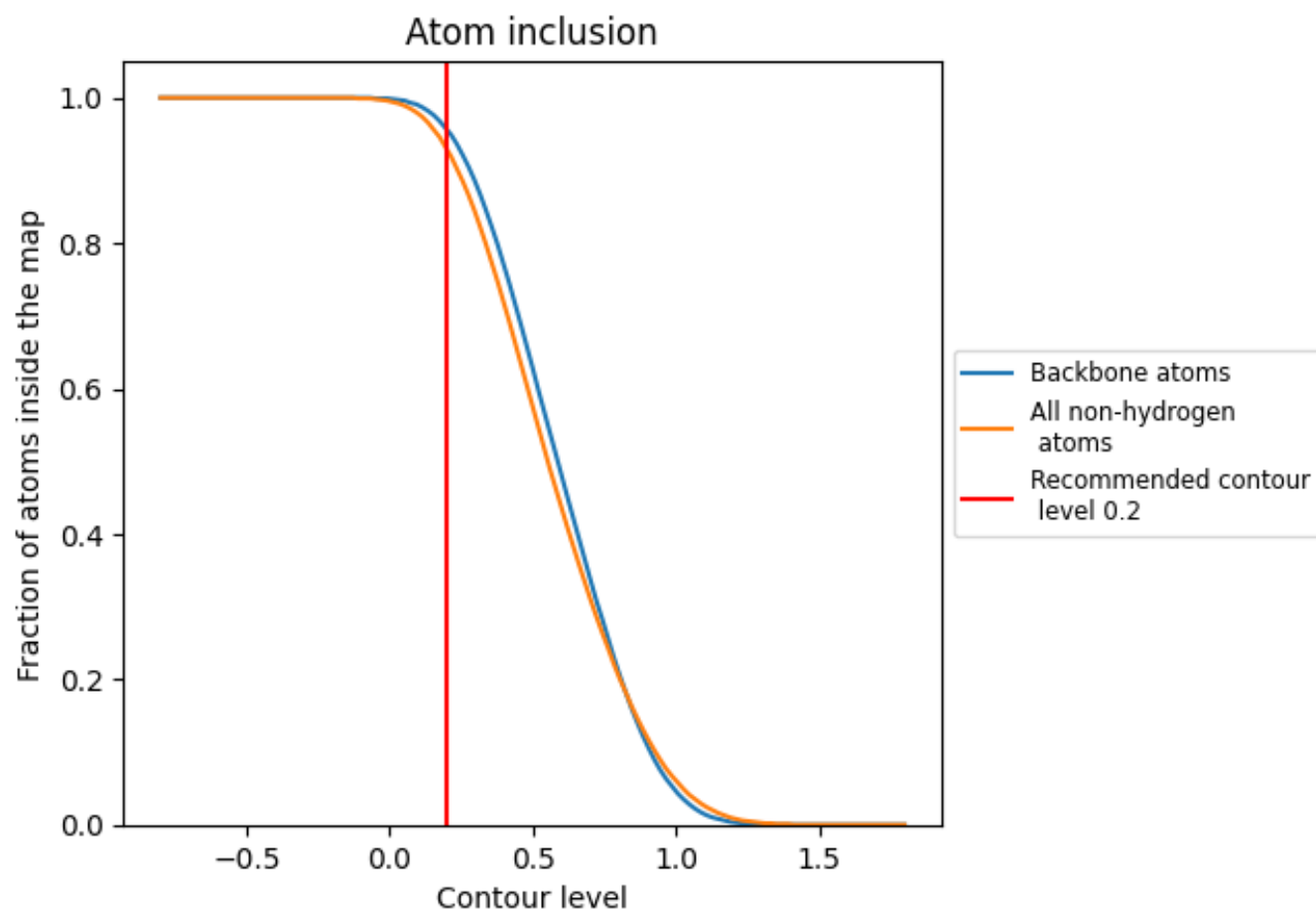
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9290	 0.2760
1	 0.8170	 0.0860
5	 0.9850	 0.3420
7	 0.9950	 0.3480
8	 0.9860	 0.3510
9	 0.9660	 0.2200
A	 0.8910	 0.3490
AA	 0.8280	 0.1810
B	 0.8740	 0.3680
BB	 0.8870	 0.1390
C	 0.9260	 0.3540
CC	 0.9020	 0.2060
D	 0.9610	 0.2930
DD	 0.7740	 0.1070
E	 0.8990	 0.2990
EE	 0.9270	 0.1970
F	 0.8810	 0.3140
FF	 0.8810	 0.1390
G	 0.9190	 0.2740
GG	 0.7820	 0.1220
H	 0.9380	 0.2960
HH	 0.8010	 0.1720
I	 0.9060	 0.3140
II	 0.9170	 0.1630
J	 0.8870	 0.2640
JJ	 0.9190	 0.1630
K	 0.8360	 0.0470
KK	 0.7410	 0.0890
L	 0.9220	 0.3260
LL	 0.8680	 0.2420
M	 0.9400	 0.2780
MM	 0.3140	 0.0320
N	 0.9200	 0.3520
NN	 0.8610	 0.2070
O	 0.8690	 0.3280

















Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
OO	 0.8770	 0.1340
P	 0.9500	 0.3740
PP	 0.8880	 0.1630
Q	 0.9200	 0.3620
QQ	 0.8040	 0.1110
R	 0.9070	 0.3000
RR	 0.6170	 0.1300
S	 0.9200	 0.3130
SS	 0.8530	 0.1670
T	 0.8910	 0.3380
TT	 0.8380	 0.1250
U	 0.9620	 0.2780
UU	 0.5180	 0.0690
V	 0.8040	 0.3380
VV	 0.8200	 0.2190
W	 0.7170	 0.1760
WW	 0.8470	 0.2580
X	 0.8960	 0.3190
XX	 0.8080	 0.2120
Y	 0.9490	 0.3210
YY	 0.9460	 0.1280
Z	 0.9580	 0.2540
ZZ	 0.9430	 0.1640
a	 0.9580	 0.3800
aa	 0.8630	 0.1850
b	 0.8860	 0.2790
bb	 0.8890	 0.1590
c	 0.9490	 0.2840
cc	 0.8910	 0.1220
d	 0.9360	 0.3520
dd	 0.8620	 0.1230
e	 0.8920	 0.3660
ee	 0.8480	 0.1400
f	 0.8730	 0.3450
ff	 0.4750	 0.0360
g	 0.9120	 0.3050
gg	 0.6530	 0.0810
h	 0.9410	 0.3030
i	 0.9250	 0.3190
j	 0.9210	 0.3620
k	 0.9370	 0.2830
l	 0.8780	 0.3170

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
m	 0.9450	 0.3130
n	 0.8300	 0.2910
o	 0.8680	 0.3320
p	 0.9140	 0.3300
r	 0.9160	 0.3500
s	 0.5090	 0.0270
t	 0.4160	 0.0220