



wwPDB EM Validation Summary Report ⓘ

Apr 23, 2024 – 06:24 am BST

PDB ID : 6ZVK
EMDB ID : EMD-11459
Title : The Halastavi arva virus (HalV) intergenic region IRES promotes translation by the simplest possible initiation mechanism
Authors : Abaeva, I.S.; Vicens, Q.; Bochler, A.; Soufari, H.; Simonetti, A.; Pestova, T.; Hashem, Y.; Hellen, C.U.T.
Deposited on : 2020-07-24
Resolution : 3.49 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:

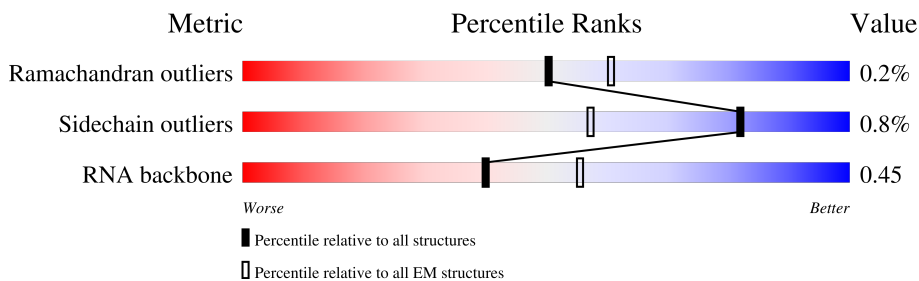
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

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 3.49 Å.

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



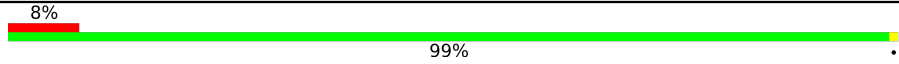
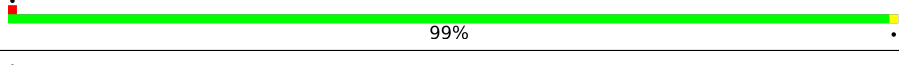
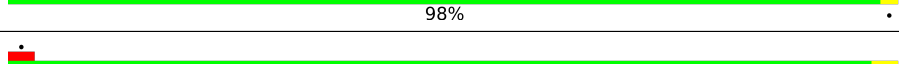
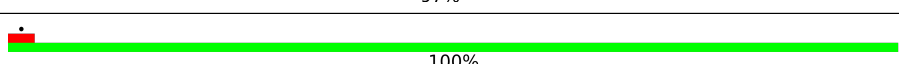
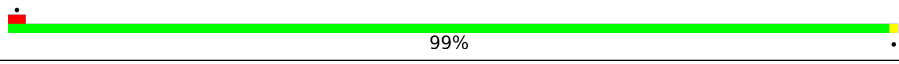
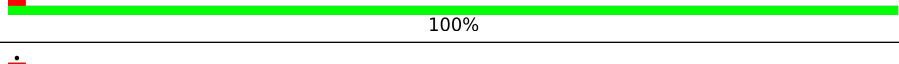
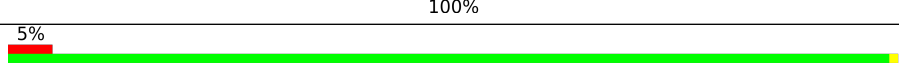
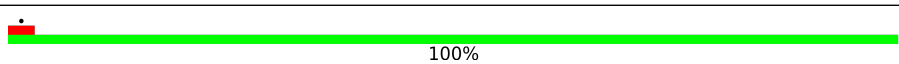
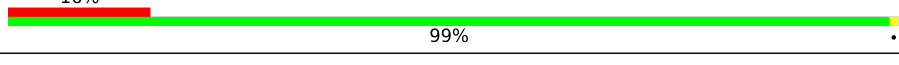
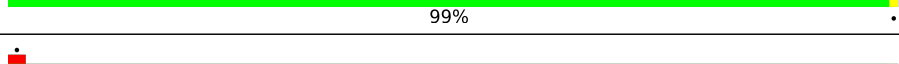
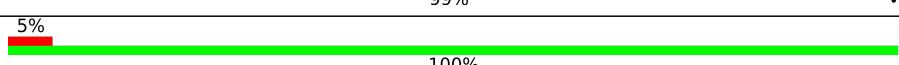
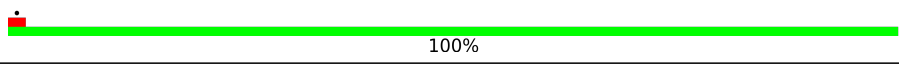
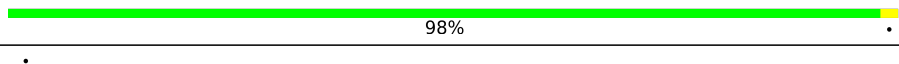
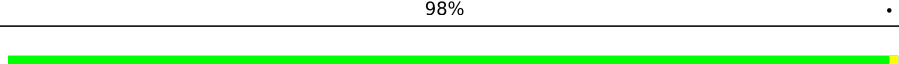
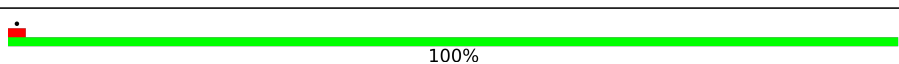
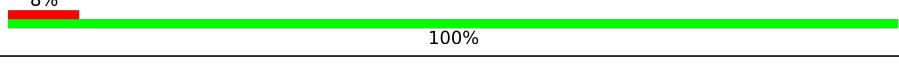
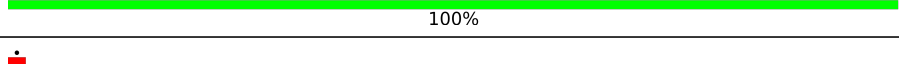
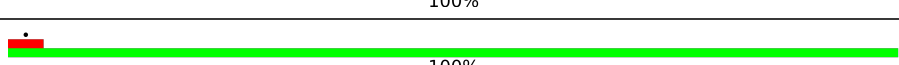
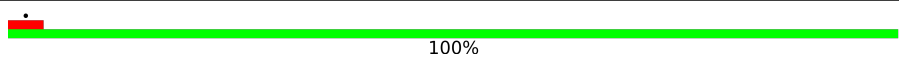
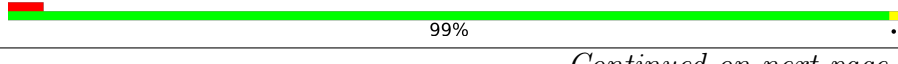



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	Z2	138	
2	e2	3920	
3	d2	120	
4	h2	156	
5	p2	69	
6	w2	199	
7	H2	153	
8	S2	187	

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Mol	Chain	Length	Quality of chain
9	32	180	 8% 99%
10	52	394	 99%
11	62	175	 98%
12	72	159	 97%
13	82	99	 100%
14	k2	131	 99%
15	l2	63	 100%
16	m2	119	 100%
17	o2	134	 5% 99%
18	q2	147	 100%
19	r2	75	 16% 99%
20	13	94	 99%
21	t2	362	 99%
22	u2	107	 5% 100%
23	v2	128	 100%
24	x2	109	 98%
25	y2	114	 98%
26	92	244	 99%
27	A2	122	 100%
28	B2	102	 8% 100%
29	C2	86	 100%
30	D2	50	 100%
31	E2	52	 100%
32	F2	104	100%
33	G2	292	99%

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Mol	Chain	Length	Quality of chain
34	I2	91	100%
35	J2	125	100%
36	K2	198	99%
37	L2	102	100%
38	M2	163	92%
39	R2	35	100%
40	T2	201	98%
41	U2	225	100%
42	V2	241	96%
43	W2	190	97%
44	X2	102	98%
45	Y2	169	99%
46	a7	210	96%
47	12	203	100%
48	22	135	99%
49	42	217	100%
50	E1	153	75% 36% 63%
51	I3	104	99%
52	s3	43	100%
53	G3	153	94% 5%
54	f3	64	100%
55	K3	1869	71% 28%
56	P3	189	100%
57	a5	136	99%
58	A3	127	95% 5%

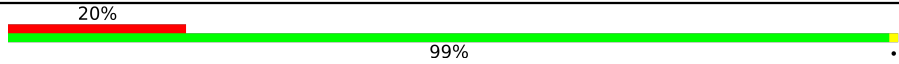
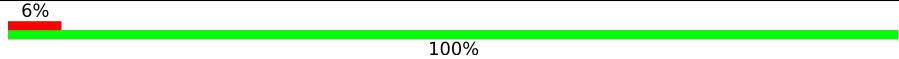
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Mol	Chain	Length	Quality of chain
59	B3	141	9% 99%
60	C3	129	16% 98%
61	D3	83	11% 95%
62	G5	137	12% 96%
63	H5	141	13% 96%
64	J5	129	98%
65	I5	126	6% 99%
66	L3	83	8% 100%
67	M3	75	23% 100%
68	O3	98	98%
69	Q3	69	71% 91% 9%
70	a3	313	25% 100%
71	T3	141	99%
72	U3	208	6% 99%
73	V3	213	100%
74	W3	218	96%
75	X3	23	100%
76	Y3	227	15% 99%
77	j3	262	5% 98%
78	N3	191	9% 100%
79	b3	237	12% 99%
80	c3	206	10% 99%
81	d3	185	5% 100%
82	e3	124	77% 100%
83	F3	150	100%

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Mol	Chain	Length	Quality of chain
84	E3	98	 20% 99%
85	H3	53	 6% 100%

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 228291 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	Z2	138	1138	727	221	183	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	e2	3920	83971	37399	15349	27313	3910	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	d2	120	2558	1141	456	842	119	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	h2	156	3314	1480	585	1094	155	0	0

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN EL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	p2	69	568	364	103	100	1	0	0

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN UL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	w2	199	1630	1051	319	255	5	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w2	174	LEU	ILE	conflict	UNP G5B8P1
w2	194	ASP	GLU	conflict	UNP G5B8P1

- Molecule 7 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	H2	153	1243	777	241	216	9	0	0

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN EL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	S2	187	1513	944	314	250	5	0	0

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN EL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	32	180	1509	933	328	239	9	0	0

- Molecule 10 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	52	394	3173	2020	597	543	13	0	0

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN EL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	62	175	1453	925	283	235	10	0	0

- Molecule 12 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	72	159	1298	823	252	217	6	0	0

- Molecule 13 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	82	99	809	518	141	148	2	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
82	32	GLY	ARG	conflict	UNP G1TSG1
82	36	ALA	GLU	conflict	UNP G1TSG1
82	39	PHE	SER	conflict	UNP G1TSG1
82	54	GLY	ARG	conflict	UNP G1TSG1
82	60	VAL	ALA	conflict	UNP G1TSG1
82	97	ARG	HIS	conflict	UNP G1TSG1

- Molecule 14 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	k2	131	979	618	184	172	5	0	0

- Molecule 15 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	l2	63	529	337	103	86	3	0	0

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN UL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	m2	119	976	624	183	168	1	0	0

- Molecule 17 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	o2	134	1116	700	226	187	3	0	0

- Molecule 18 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	q2	147	1162	734	239	185	4	0	0

- Molecule 19 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	r2	75	610	378	130	99	3	0	0

- Molecule 20 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	13	94	733	464	130	133	6	0	0

- Molecule 21 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	t2	362	2884	1812	577	481	14	0	0

- Molecule 22 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	u2	107	889	560	171	156	2	0	0

- Molecule 23 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	v2	128	1054	667	216	166	5	0	0

- Molecule 24 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	x2	109	876	555	174	143	4	0	0

- Molecule 25 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	y2	114	907	566	187	148	6	0	0

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN UL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	92	244	1869	1171	382	310	6	0	0

- Molecule 27 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	A2	122	1013	640	204	168	1	0	0

- Molecule 28 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	B2	102	831	520	176	130	5	0	0

- Molecule 29 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	C2	86	706	434	155	112	5	0	0

- Molecule 30 is a protein called ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	D2	50	444	281	98	64	1	0	0

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN EL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	E2	52	429	266	90	67	6	0	0

- Molecule 32 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	F2	104	852	533	174	139	6	0	0

- Molecule 33 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	G2	292	2387	1509	437	427	14	0	0

- Molecule 34 is a protein called ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	I2	91	708	445	136	120	7	0	0

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN EL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	J2	125	1002	621	206	169	6	0	0

- Molecule 36 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	K2	198	1524	969	265	281	9	0	0

- Molecule 37 is a protein called Ribosomal protein L10 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	L2	102	834	527	161	137	9	0	0

- Molecule 38 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	M2	156	1183	738	221	219	5	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M2	49	GLY	ALA	conflict	UNP G1SMR7

- Molecule 39 is a protein called Ribosomal_L6e_N domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R2	35	Total	C	N	O	S	0	0
			285	179	59	45	2		

- Molecule 40 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	T2	201	Total	C	N	O	S	0	0
			1614	1039	301	273	1		

- Molecule 41 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	U2	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN EL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	V2	233	Total	C	N	O	S	0	0
			1872	1193	361	314	4		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN UL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	W2	190	Total	C	N	O	S	0	0
			1517	954	284	273	6		

- Molecule 44 is a protein called Ribosomal protein L10 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
44	X2	102	Total	C	N	O	S	0	0
			822	524	158	136	4		

- Molecule 45 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Y2	169	Total	C	N	O	S	0	0
			1354	855	252	241	6		

- Molecule 46 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	a7	210	1702	1065	354	279	4	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a7	47	ALA	-	insertion	UNP G1TPV0
a7	48	PRO	-	insertion	UNP G1TPV0
a7	49	ARG	-	insertion	UNP G1TPV0
a7	50	PRO	-	insertion	UNP G1TPV0
a7	51	ALA	-	insertion	UNP G1TPV0
a7	52	ALA	-	insertion	UNP G1TPV0
a7	53	GLY	-	insertion	UNP G1TPV0
a7	54	PRO	-	insertion	UNP G1TPV0
a7	55	ILE	-	insertion	UNP G1TPV0

- Molecule 47 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	12	203	1701	1072	359	266	4	0	0

- Molecule 48 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	22	135	1107	714	208	182	3	0	0

- Molecule 49 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	42	217	1744	1114	314	307	9	0	0

- Molecule 50 is a RNA chain called INTERNAL RIBOSOME ENTRY SITE.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
50	E1	153	3208	1443	529	1083	153	0	0

- Molecule 51 is a protein called Ribosomal_S10 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	I3	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 52 is a protein called 40S RIBOSOMAL PROTEIN ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s3	43	Total	C	N	O	S	0	0
			350	215	80	54	1		

- Molecule 53 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	G3	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 54 is a protein called ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	f3	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 55 is a RNA chain called 18S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	K3	1869	Total	C	N	O	P	0	0
			39862	17789	7142	13063	1868		

- Molecule 56 is a protein called 40S RIBOSOMAL PROTEIN ES7.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	P3	189	Total	C	N	O	S	0	0
			1522	969	280	272	1		

- Molecule 57 is a protein called 40S RIBOSOMAL PROTEIN US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	a5	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 58 is a protein called ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	A3	127	1061	673	201	180	7	0	0

- Molecule 59 is a protein called 40S RIBOSOMAL PROTEIN US9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	B3	141	1124	715	212	194	3	0	0

- Molecule 60 is a protein called 40S RIBOSOMAL PROTEIN ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	C3	129	1048	658	193	192	5	0	0

- Molecule 61 is a protein called 40S RIBOSOMAL PROTEIN ES21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	D3	83	631	387	118	121	5	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D3	3	SER	ASN	conflict	UNP A0A1Z5KTU7
D3	4	ASN	ASP	conflict	UNP A0A1Z5KTU7
D3	33	PRO	GLN	conflict	UNP A0A1Z5KTU7
D3	50	SER	PHE	conflict	UNP A0A1Z5KTU7
D3	76	HIS	ASP	conflict	UNP A0A1Z5KTU7

- Molecule 62 is a protein called ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	G5	137	1140	714	231	194	1	0	0

- Molecule 63 is a protein called 40S RIBOSOMAL PROTEIN ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	H5	141	1113	701	213	196	3	0	0

- Molecule 64 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	J5	129	1034	659	193	176	6	0	0

- Molecule 65 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	I5	126	1024	646	200	173	5	0	0

- Molecule 66 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	L3	83	651	408	121	115	7	0	0

- Molecule 67 is a protein called ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	M3	75	599	382	111	105	1	0	0

- Molecule 68 is a protein called 40S RIBOSOMAL PROTEIN ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	O3	98	782	486	161	130	5	0	0

- Molecule 69 is a protein called 40S RIBOSOMAL PROTEIN ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Q3	63	528	336	99	87	6	0	0

- Molecule 70 is a protein called ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	a3	313	2437	1535	424	466	12	0	0

- Molecule 71 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	T3	141	Total	C	N	O	S	0	0
			1099	693	219	184	3		

- Molecule 72 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	U3	208	Total	C	N	O	S	0	0
			1645	1046	289	302	8		

- Molecule 73 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	V3	213	Total	C	N	O	S	0	0
			1730	1098	309	309	14		

- Molecule 74 is a protein called S5 DRBM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	W3	218	Total	C	N	O	S	0	0
			1691	1094	289	298	10		

- Molecule 75 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	X3	23	Total	C	N	O	S	0	0
			223	134	61	26	2		

- Molecule 76 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Y3	227	Total	C	N	O	S	0	0
			1765	1124	317	316	8		

- Molecule 77 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	j3	262	Total	C	N	O	S	0	0
			2075	1324	384	358	9		

- Molecule 78 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	N3	191	1509	943	286	273	7	0	0

- Molecule 79 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	b3	237	1924	1200	387	330	7	0	0

- Molecule 80 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	c3	206	1687	1058	332	292	5	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c3	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 81 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
81	d3	185	1526	969	306	249	2	0	0

- Molecule 82 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
82	e3	124	958	600	170	179	9	0	0

- Molecule 83 is a protein called ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
83	F3	150	1208	773	229	205	1	0	0

- Molecule 84 is a protein called S10_ plectin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
84	E3	98	828	539	148	135	6	0	0

- Molecule 85 is a protein called ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
85	H3	53	445	278	90	72	5	0	0

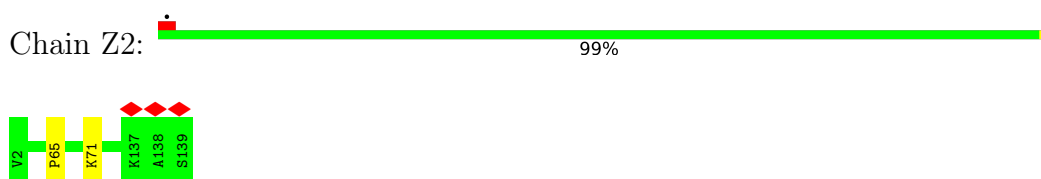
- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	C2	1	Total	Zn	0
			1	1	
86	E2	1	Total	Zn	0
			1	1	
86	F2	1	Total	Zn	0
			1	1	
86	I2	1	Total	Zn	0
			1	1	
86	O3	1	Total	Zn	0
			1	1	
86	H3	1	Total	Zn	0
			1	1	

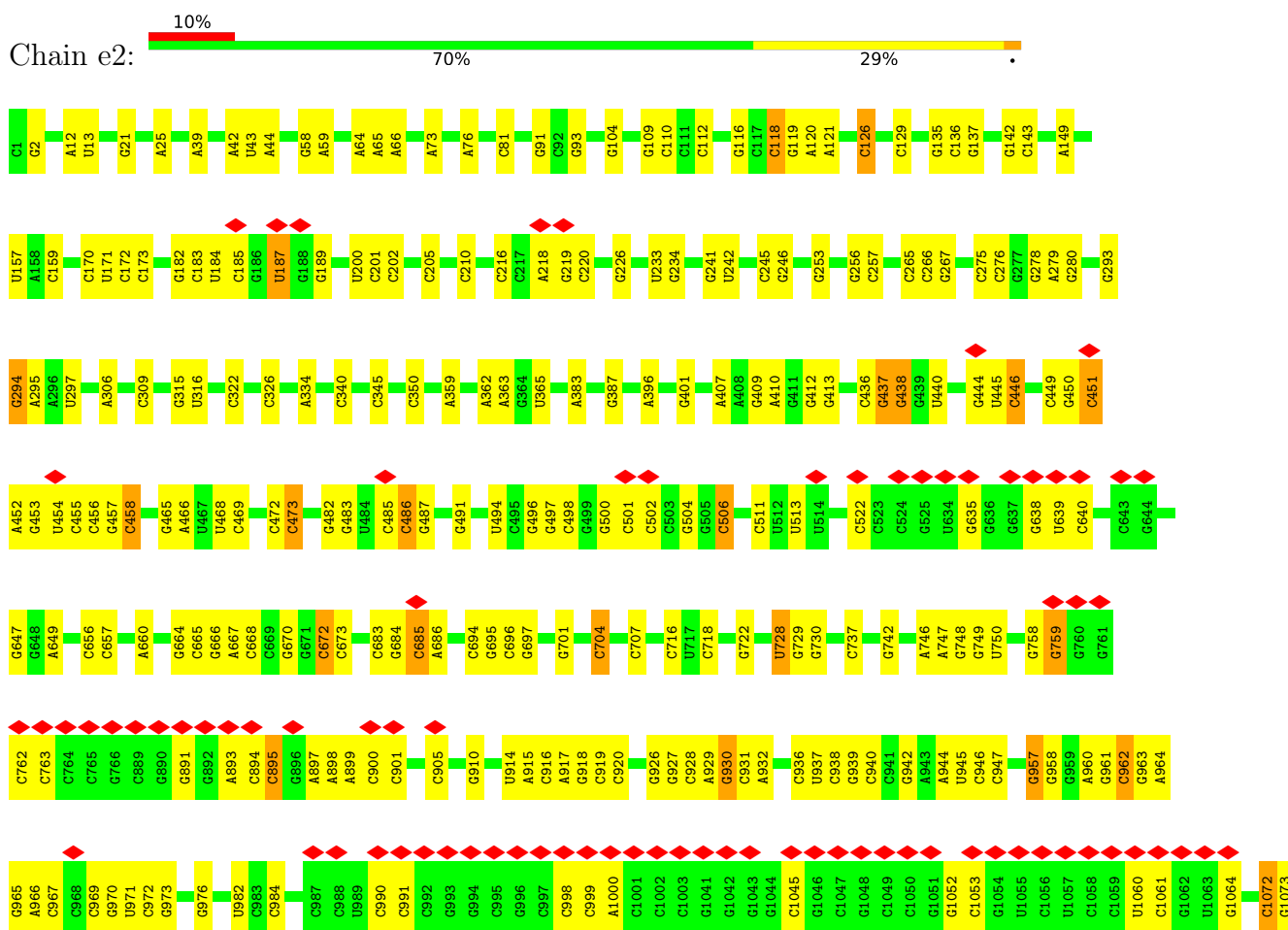
3 Residue-property plots

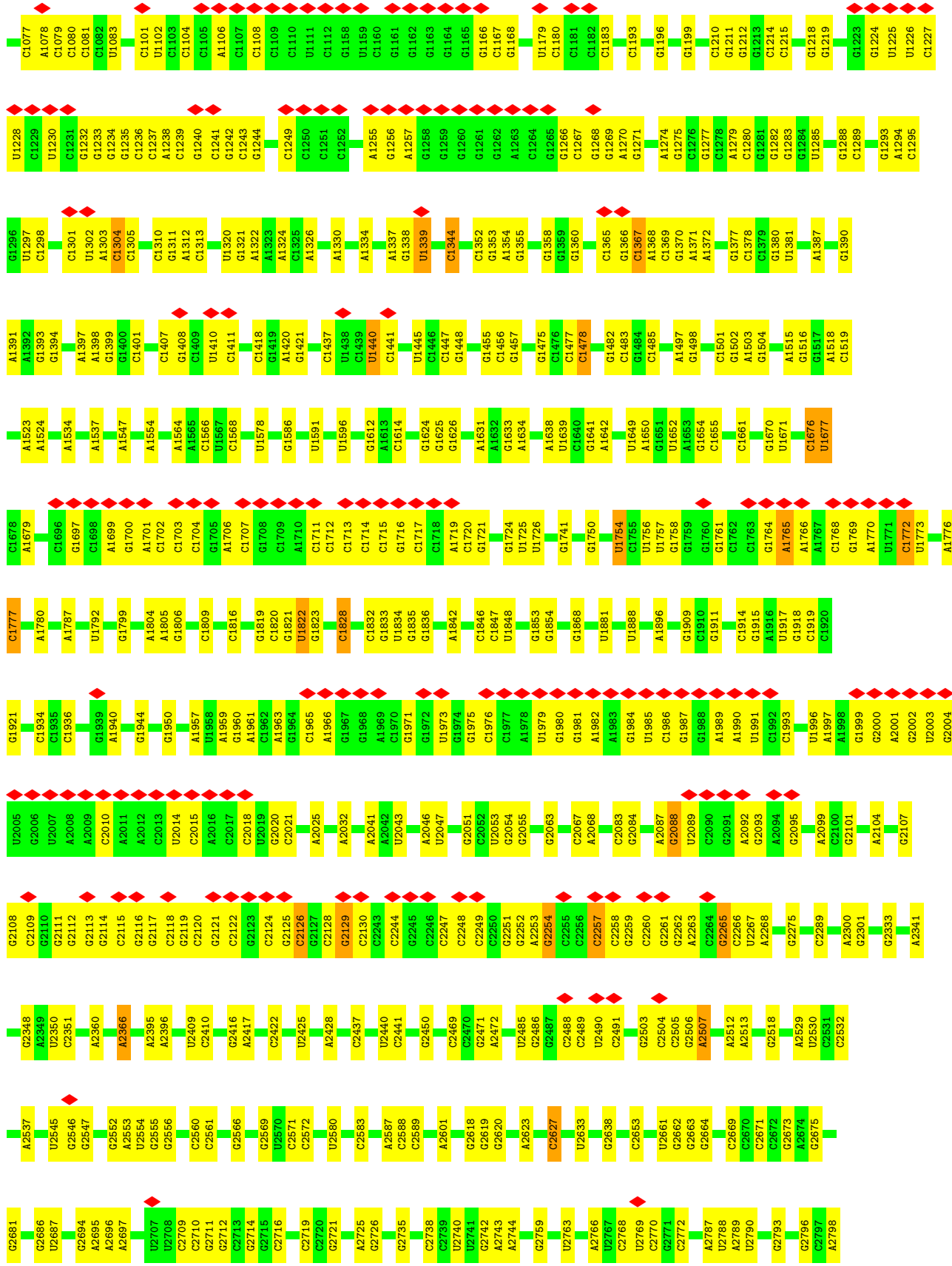
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

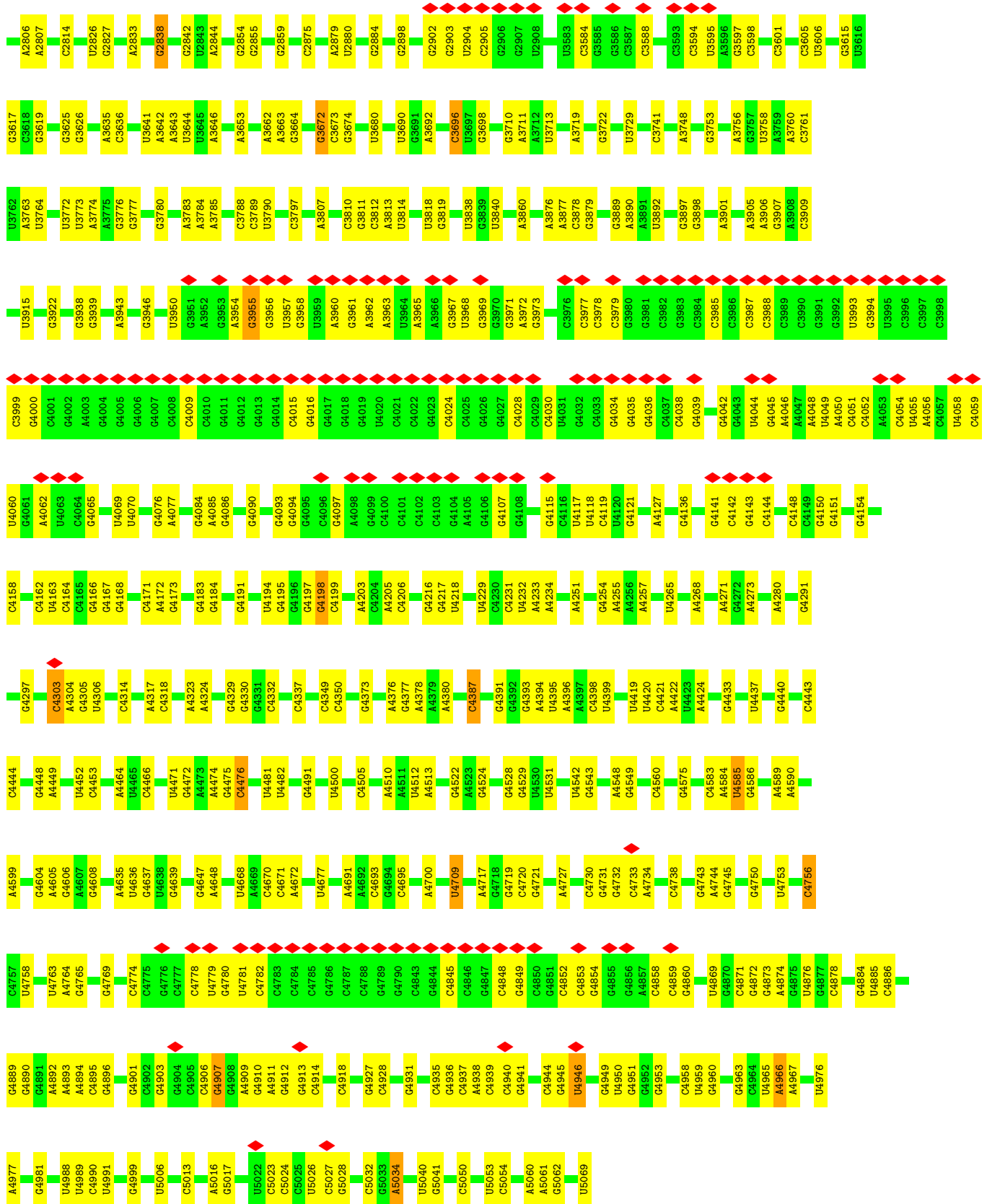
- Molecule 1: Ribosomal protein L14




- Molecule 2: 28S RIBOSOMAL RNA

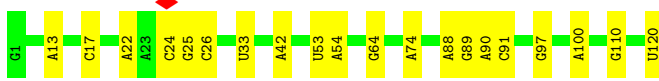







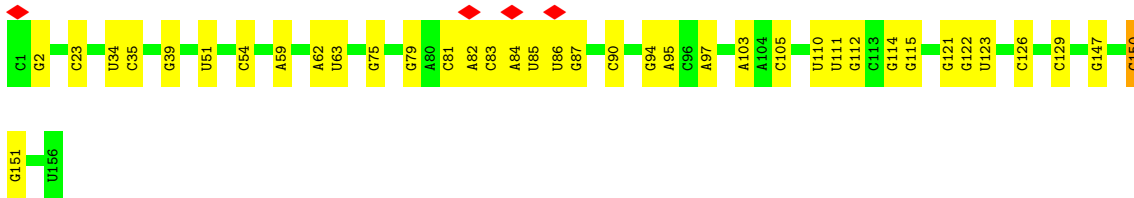
- Molecule 3: 5S RIBOSOMAL RNA

Chain d2:  83% 17%



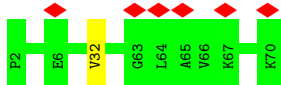
- Molecule 4: 5.8S RIBOSOMAL RNA

Chain h2:  76% 24%



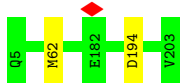
- Molecule 5: 60S RIBOSOMAL PROTEIN EL38

Chain p2:  9% 99%



- Molecule 6: 60S RIBOSOMAL PROTEIN UL13

Chain w2:  99%



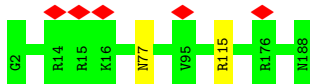
- Molecule 7: uL22

Chain H2:  99%



- Molecule 8: 60S RIBOSOMAL PROTEIN EL18

Chain S2:  99%

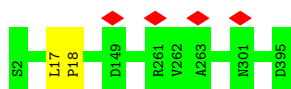


- Molecule 9: 60S RIBOSOMAL PROTEIN EL19

Chain 32:  8% 99%



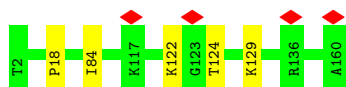
- Molecule 10: uL3



- Molecule 11: 60S RIBOSOMAL PROTEIN EL20



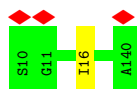
- Molecule 12: eL21



- Molecule 13: Ribosomal protein L22



- Molecule 14: eL14



- Molecule 15: Ribosomal protein L24



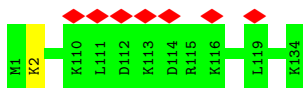
- Molecule 16: 60S RIBOSOMAL PROTEIN UL23

Chain m2:  100%



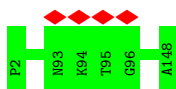
- Molecule 17: Ribosomal protein L26

Chain o2:  99%



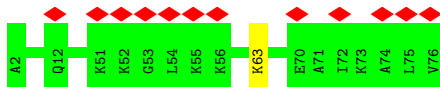
- Molecule 18: uL15

Chain q2:  100%



- Molecule 19: 60S ribosomal protein L29

Chain r2:  99%



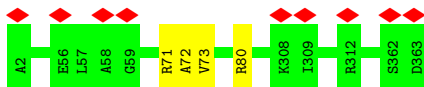
- Molecule 20: Ribosomal protein L30

Chain 13:  99%



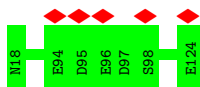
- Molecule 21: uL4

Chain t2:  99%



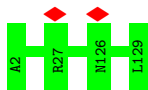
- Molecule 22: eL31

Chain u2:  100%



- Molecule 23: eL32

Chain v2:  100%



- Molecule 24: eL33

Chain x2:  98%



- Molecule 25: eL34

Chain y2:  98%



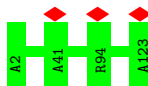
- Molecule 26: 60S RIBOSOMAL PROTEIN UL2

Chain 92:  99%



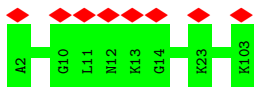
- Molecule 27: uL29

Chain A2:  100%



- Molecule 28: 60S ribosomal protein L36

Chain B2:  8% 100%



- Molecule 29: Ribosomal protein L37

Chain C2:  100%

There are no outlier residues recorded for this chain.

- Molecule 30: ribosomal protein eL39

Chain D2:  100%



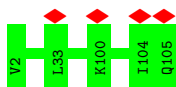
- Molecule 31: 60S RIBOSOMAL PROTEIN EL40

Chain E2:  100%



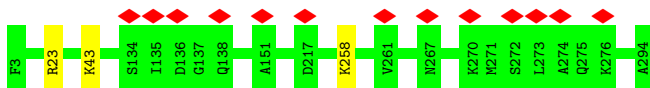
- Molecule 32: eL42

Chain F2:  100%



- Molecule 33: 60S ribosomal protein L5

Chain G2:  99%



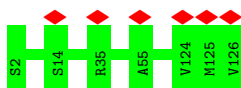
- Molecule 34: ribosomal protein eL43

Chain I2:  100%




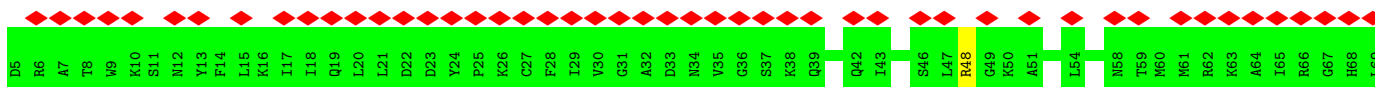
- Molecule 35: 60S RIBOSOMAL PROTEIN EL28

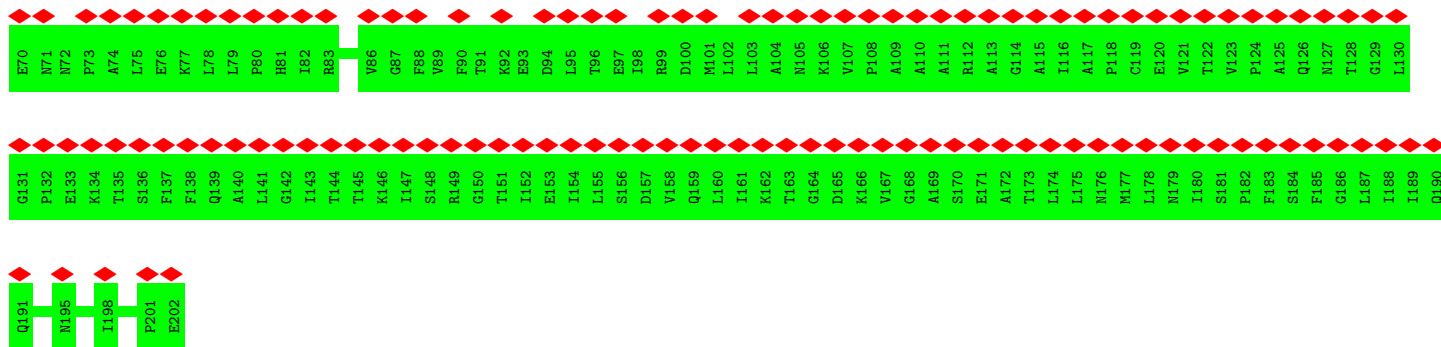
Chain J2:  5%



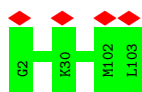
- Molecule 36: 60S acidic ribosomal protein P0

Chain K2:  84%

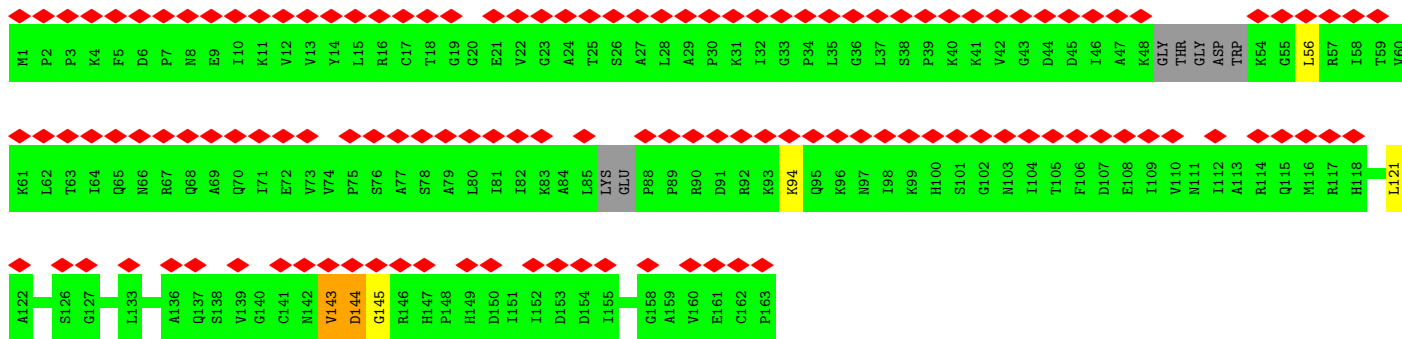
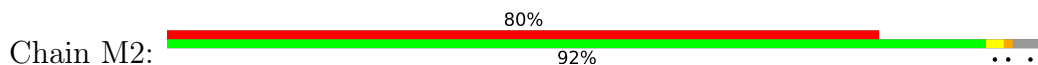




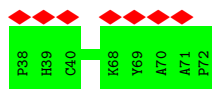
- Molecule 37: Ribosomal protein L10 (Predicted)



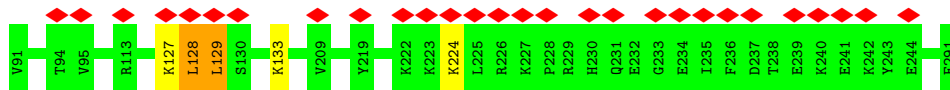
- Molecule 38: Uncharacterized protein



- Molecule 39: Ribosomal_L6e_N domain-containing protein

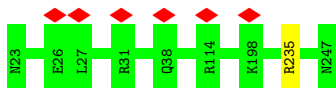


- Molecule 40: 60S ribosomal protein L6



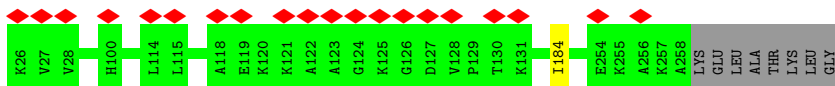
- Molecule 41: uL30

Chain U2:  100%



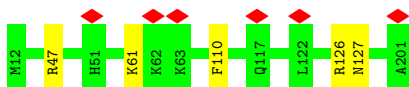
- Molecule 42: 60S RIBOSOMAL PROTEIN EL8

Chain V2:  96%



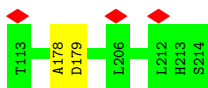
- Molecule 43: 60S RIBOSOMAL PROTEIN UL6

Chain W2:  97%



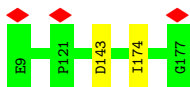
- Molecule 44: Ribosomal protein L10 (Predicted)

Chain X2:  98%



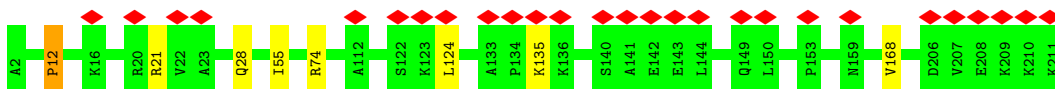
- Molecule 45: Ribosomal protein L11

Chain Y2:  99%



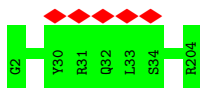
- Molecule 46: 60S ribosomal protein L13

Chain a7:  96%

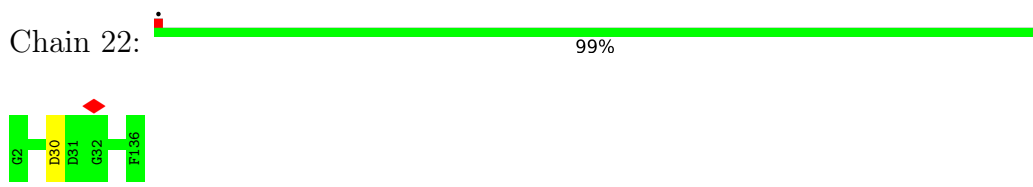


- Molecule 47: Ribosomal protein L15

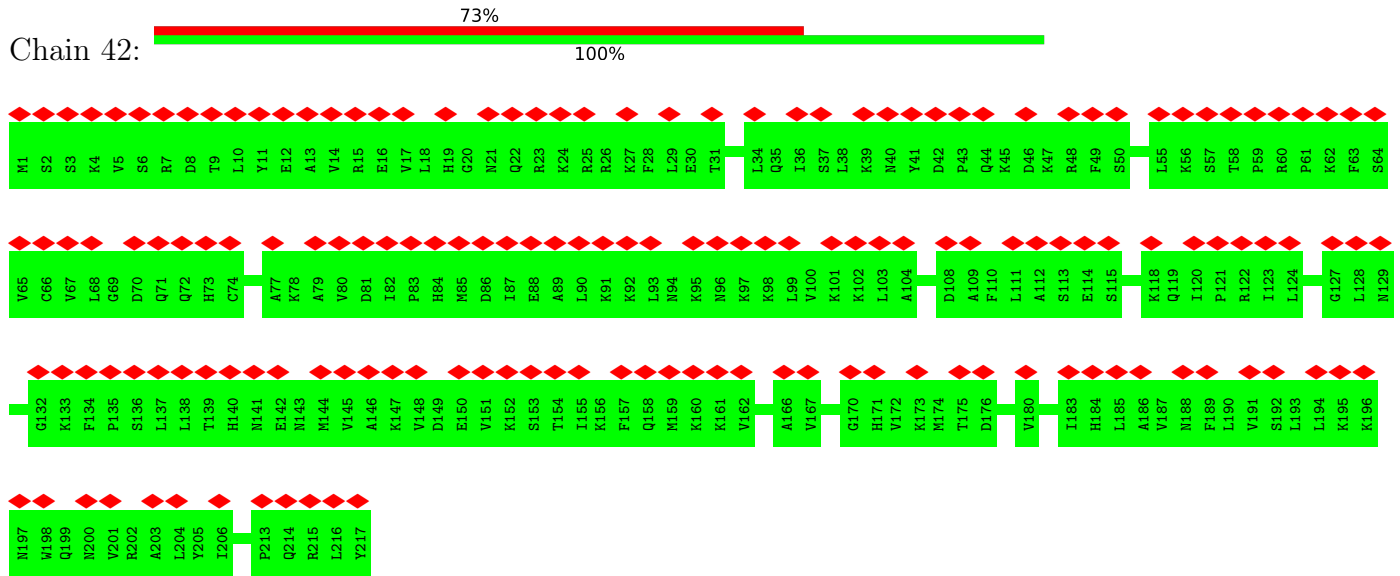
Chain 12:  100%



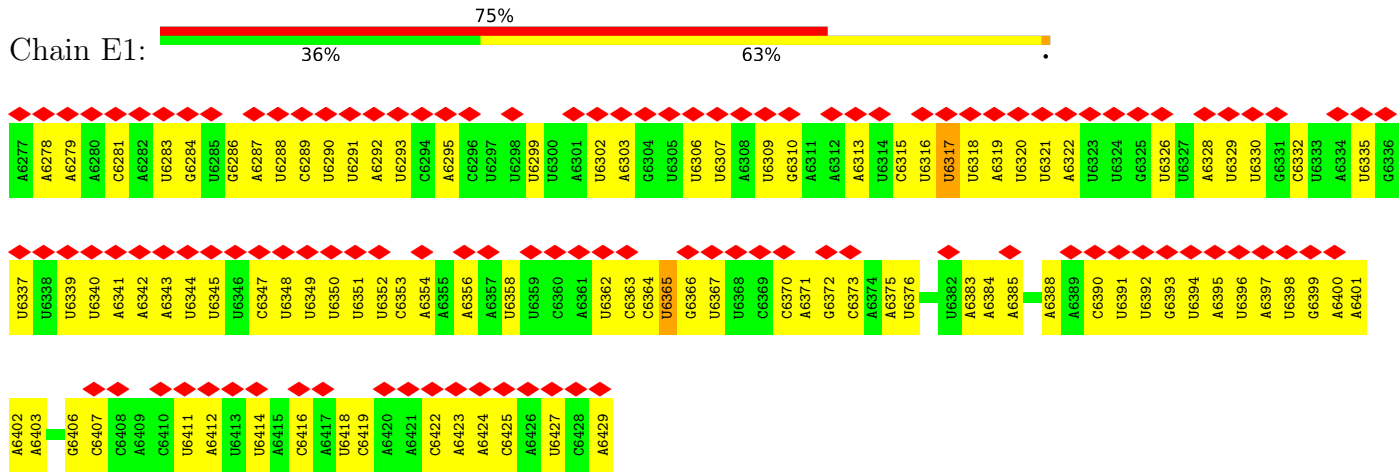
• Molecule 48: 60S ribosomal protein L27



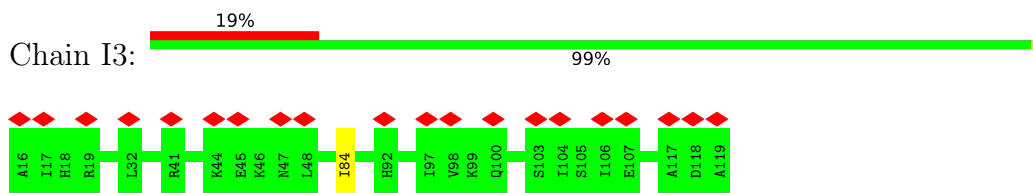
• Molecule 49: Ribosomal protein



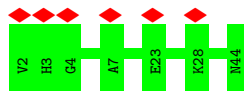
• Molecule 50: INTERNAL RIBOSOME ENTRY SITE



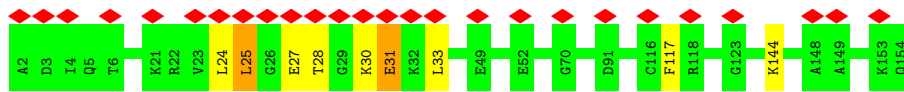
• Molecule 51: Ribosomal_S10 domain-containing protein



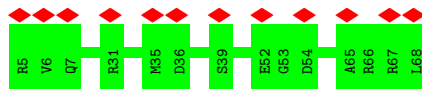
• Molecule 52: 40S RIBOSOMAL PROTEIN ES30



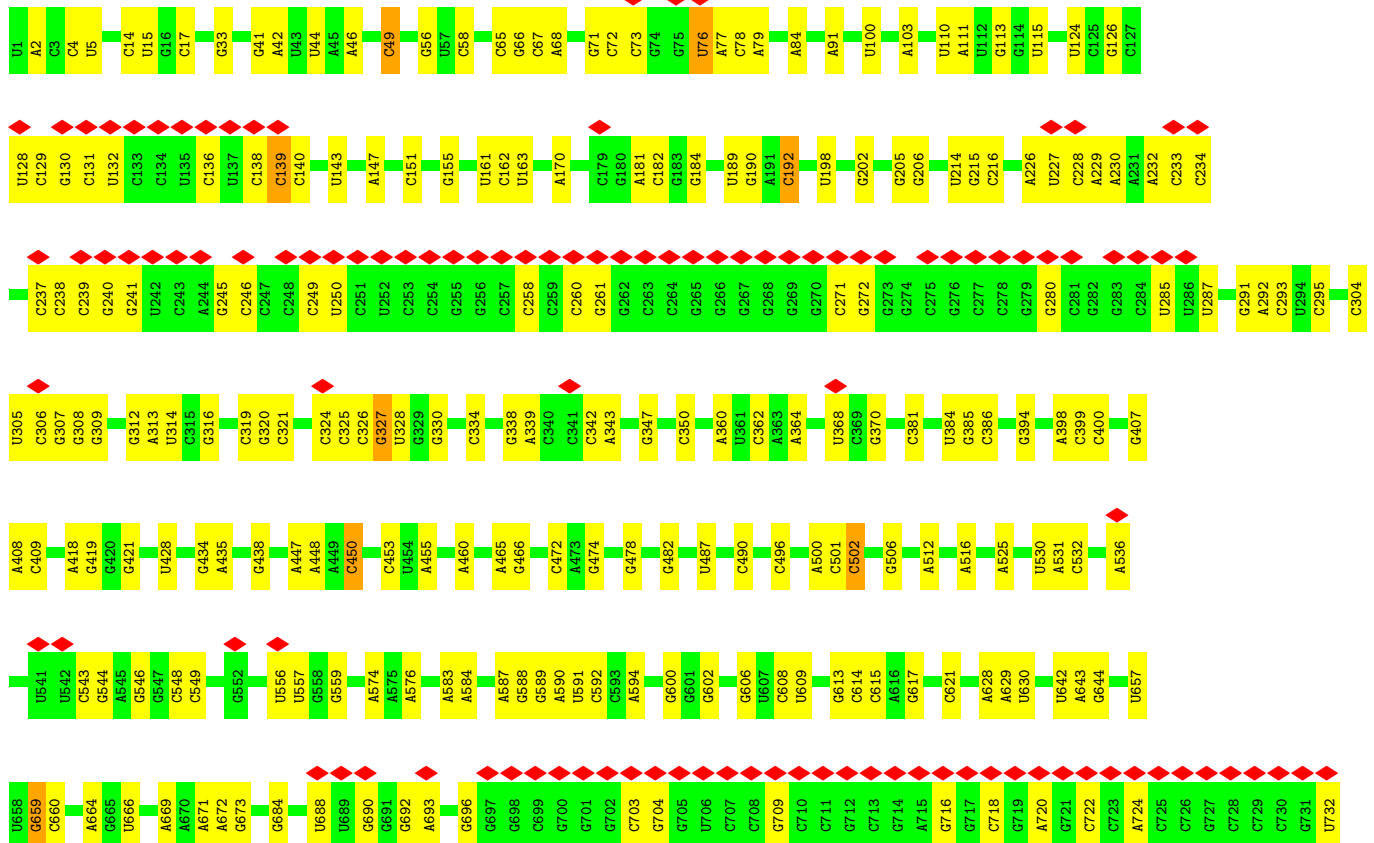
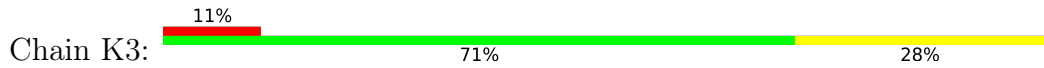
• Molecule 53: Ribosomal protein S11

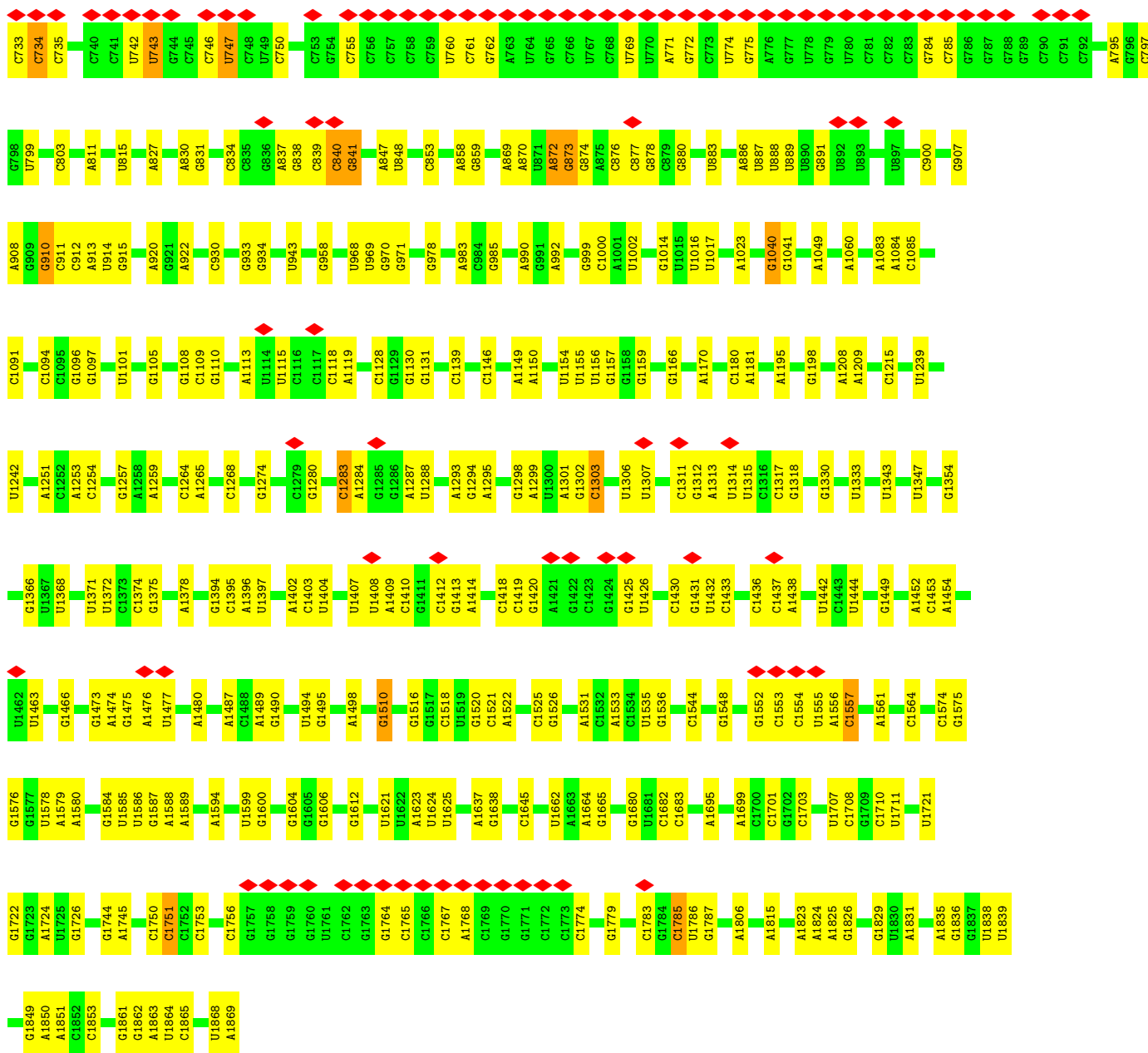


• Molecule 54: ribosomal protein eS28

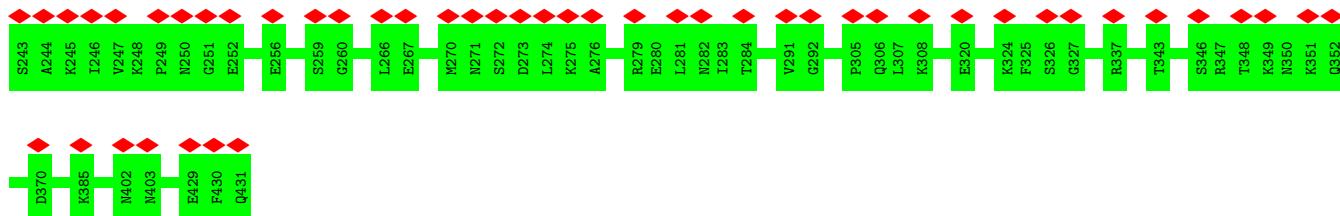


• Molecule 55: 18S RIBOSOMAL RNA

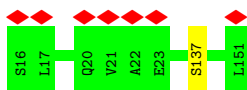




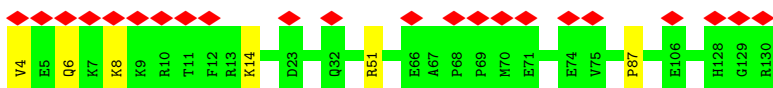
• Molecule 56: 40S RIBOSOMAL PROTEIN ES7



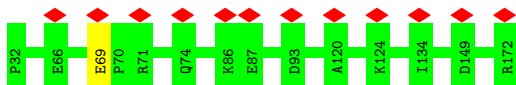
• Molecule 57: 40S RIBOSOMAL PROTEIN US11



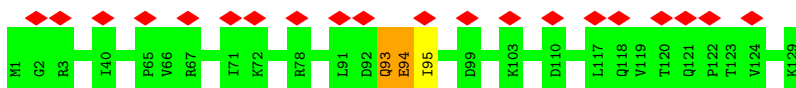
- Molecule 58: ribosomal protein uS19



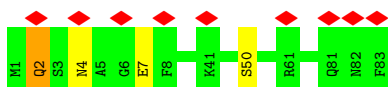
- Molecule 59: 40S RIBOSOMAL PROTEIN US9



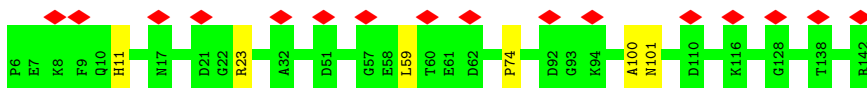
- Molecule 60: 40S RIBOSOMAL PROTEIN ES17



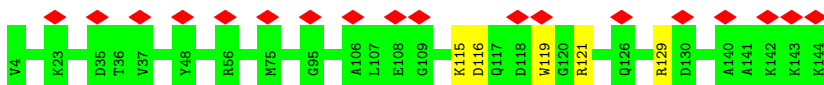
- Molecule 61: 40S RIBOSOMAL PROTEIN ES21



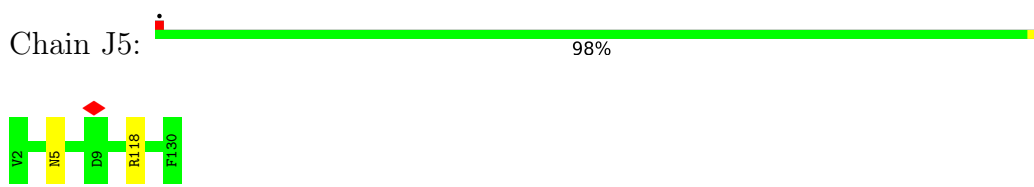
- Molecule 62: ribosomal protein uS13



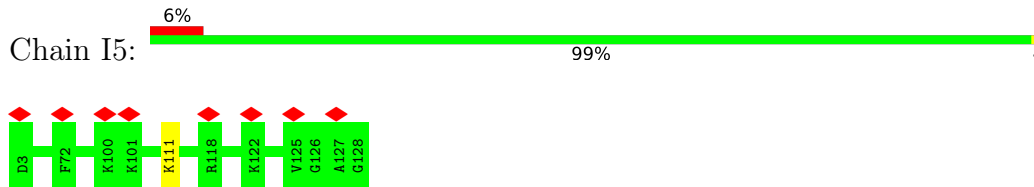
- Molecule 63: 40S RIBOSOMAL PROTEIN ES19



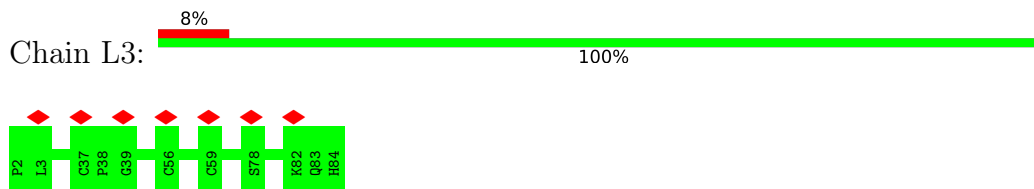
- Molecule 64: Ribosomal protein S15a



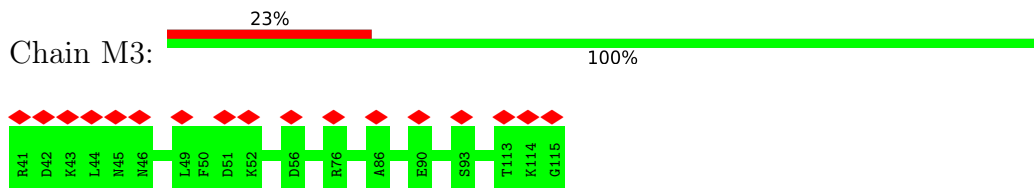
- Molecule 65: 40S ribosomal protein S24



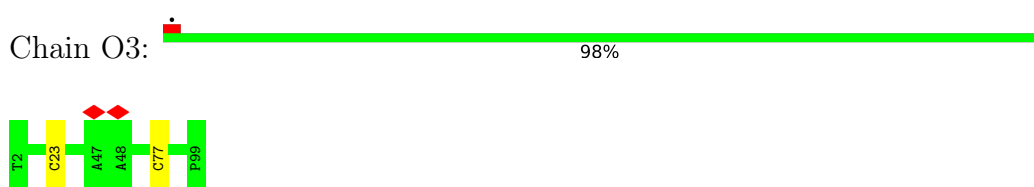
- Molecule 66: 40S ribosomal protein S27



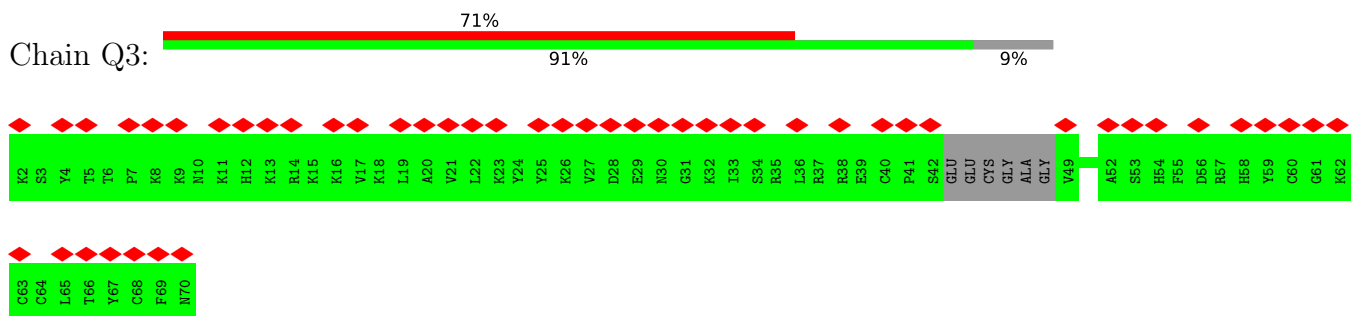
- Molecule 67: ribosomal protein eS25



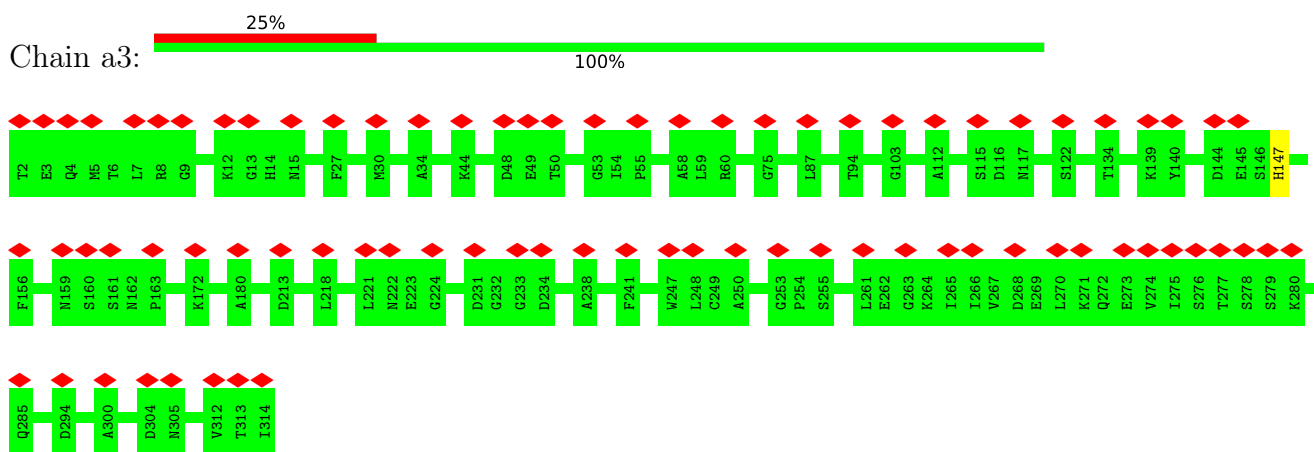
- Molecule 68: 40S RIBOSOMAL PROTEIN ES26



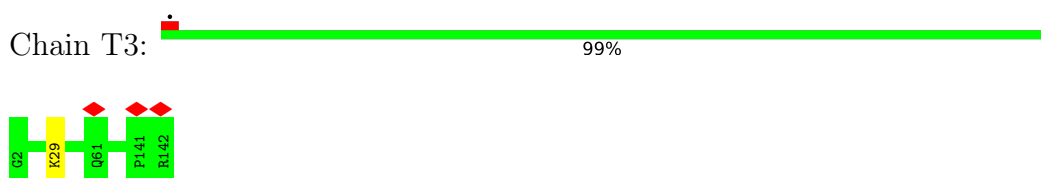
- Molecule 69: 40S RIBOSOMAL PROTEIN ES31



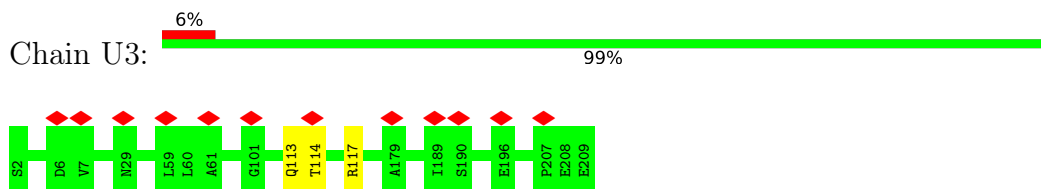
- Molecule 70: ribosomal protein RACK1



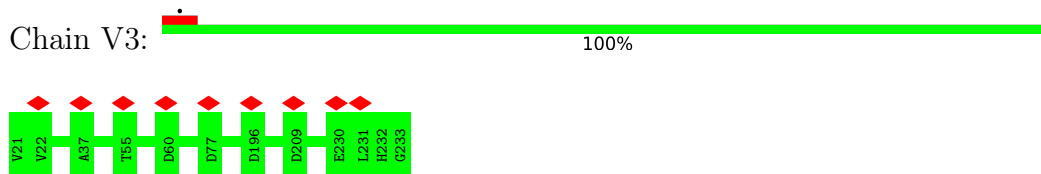
- Molecule 71: Ribosomal protein S23



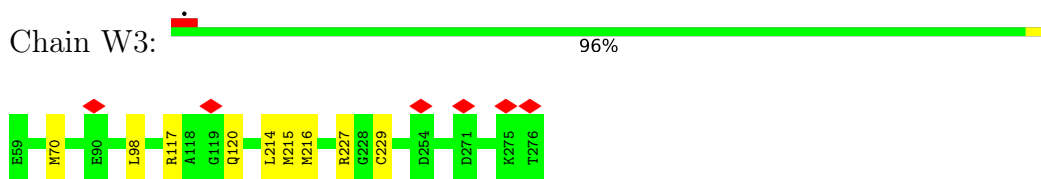
- Molecule 72: 40S_SA_C domain-containing protein



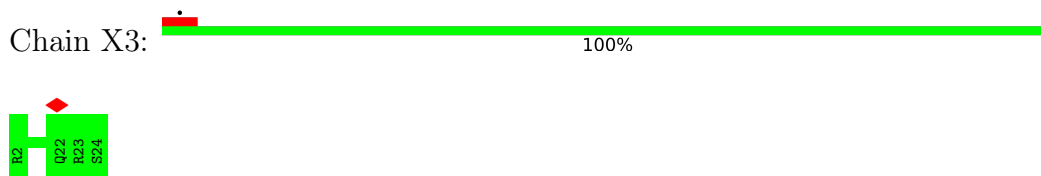
- Molecule 73: 40S ribosomal protein S3a



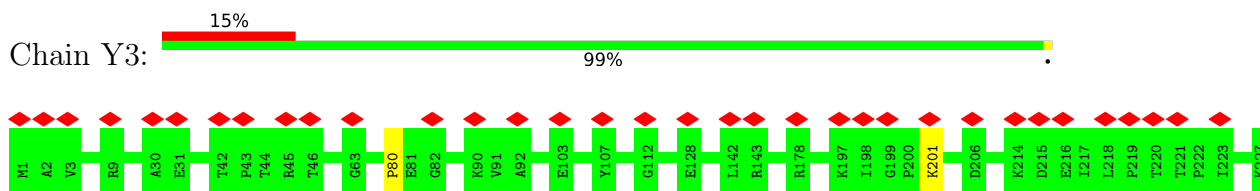
- Molecule 74: S5 DRBM domain-containing protein



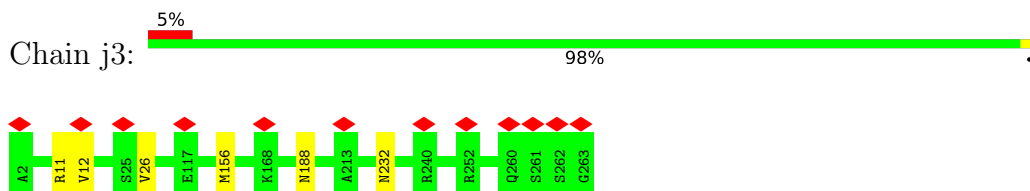
- Molecule 75: 60s ribosomal protein l41



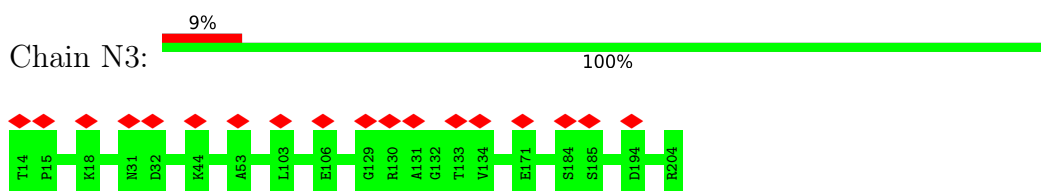
- Molecule 76: Ribosomal protein S3



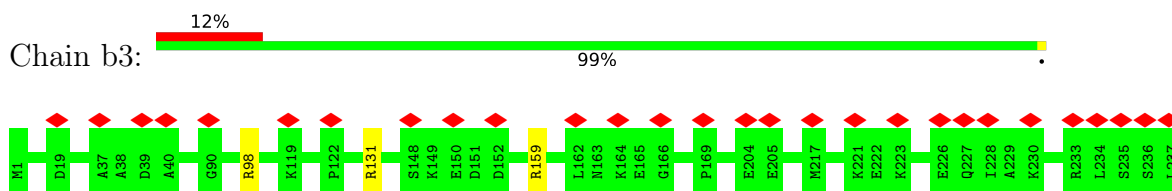
- Molecule 77: 40S ribosomal protein S4



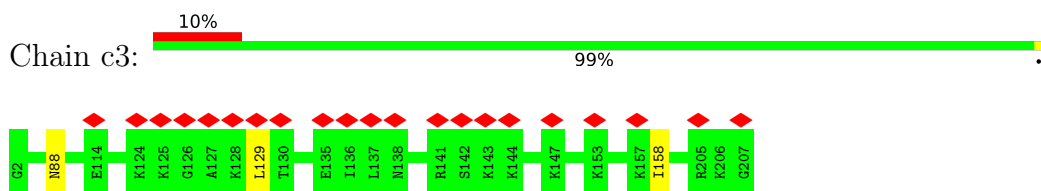
- Molecule 78: Ribosomal protein S5



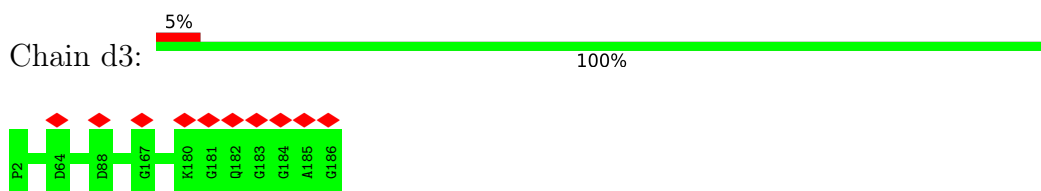
- Molecule 79: 40S ribosomal protein S6



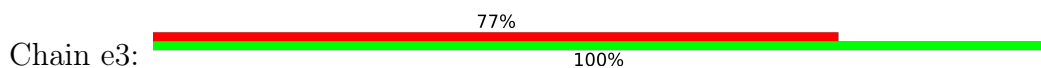
- Molecule 80: 40S ribosomal protein S8

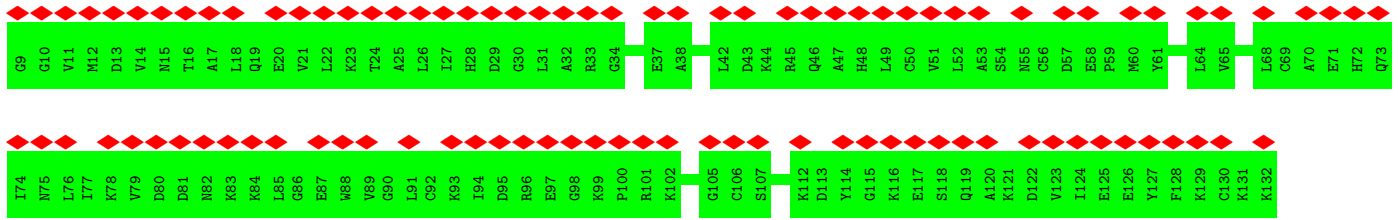


- Molecule 81: Ribosomal protein S9 (Predicted)

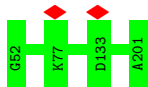


- Molecule 82: 40S ribosomal protein S12

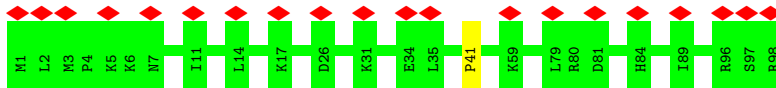




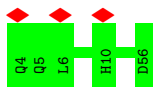
- Molecule 83: ribosomal protein uS15



- Molecule 84: S10_pectin domain-containing protein



- Molecule 85: ribosomal protein uS14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55589	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.250	Depositor
Minimum map value	-0.153	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.027	Depositor
Map size (\AA)	396.0, 396.0, 396.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section:
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	Z2	0.33	0/1159	0.46	0/1547
2	e2	0.62	0/93920	1.02	221/146521 (0.2%)
3	d2	0.55	0/2858	0.92	0/4455
4	h2	0.59	0/3701	0.92	1/5766 (0.0%)
5	p2	0.33	0/574	0.60	0/761
6	w2	0.38	0/1662	0.50	1/2222 (0.0%)
7	H2	0.39	0/1269	0.51	0/1700
8	S2	0.40	0/1537	0.53	0/2052
9	32	0.34	0/1525	0.49	0/2013
10	52	0.39	0/3241	0.53	0/4339
11	62	0.41	0/1493	0.49	0/2003
12	72	0.42	0/1326	0.52	0/1770
13	82	0.33	0/823	0.50	0/1103
14	k2	0.42	0/993	0.50	0/1332
15	l2	0.41	0/542	0.48	0/720
16	m2	0.35	0/993	0.49	0/1334
17	o2	0.35	0/1133	0.48	0/1504
18	q2	0.41	0/1191	0.53	0/1590
19	r2	0.34	0/620	0.59	0/818
20	l3	0.40	0/743	0.49	0/995
21	t2	0.39	0/2938	0.54	0/3946
22	u2	0.40	0/904	0.50	0/1216
23	v2	0.39	0/1072	0.53	0/1429
24	x2	0.42	0/895	0.55	0/1198
25	y2	0.42	0/917	0.54	0/1220
26	92	0.44	0/1907	0.54	0/2556
27	A2	0.32	0/1021	0.47	0/1348
28	B2	0.33	0/842	0.50	0/1112
29	C2	0.43	0/721	0.53	0/952
30	D2	0.36	0/454	0.53	0/599
31	E2	0.35	0/435	0.46	0/575
32	F2	0.39	0/865	0.55	0/1140

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	G2	0.34	0/2433	0.51	0/3257
34	I2	0.43	0/718	0.51	0/953
35	J2	0.37	0/1018	0.49	0/1364
36	K2	0.27	0/1548	0.48	0/2088
37	L2	0.39	0/853	0.50	0/1137
38	M2	0.28	0/1198	0.57	1/1611 (0.1%)
39	R2	0.31	0/292	0.50	0/388
40	T2	0.31	0/1646	0.58	1/2213 (0.0%)
41	U2	0.40	0/1911	0.51	0/2549
42	V2	0.35	0/1905	0.50	0/2566
43	W2	0.34	0/1536	0.53	0/2063
44	X2	0.36	0/841	0.51	0/1123
45	Y2	0.32	0/1377	0.50	1/1841 (0.1%)
46	a7	0.35	0/1733	0.55	2/2316 (0.1%)
47	12	0.45	0/1746	0.55	0/2338
48	22	0.37	0/1130	0.57	0/1507
49	42	0.26	0/1772	0.56	0/2375
50	E1	0.31	0/3579	0.91	2/5560 (0.0%)
51	I3	0.27	0/832	0.55	0/1117
52	s3	0.29	0/353	0.53	0/462
53	G3	0.40	0/1268	0.56	1/1696 (0.1%)
54	f3	0.36	0/508	0.70	0/680
55	K3	0.50	0/44567	0.99	151/69476 (0.2%)
56	P3	0.31	0/1545	0.52	0/2068
57	a5	0.33	0/1029	0.52	0/1380
58	A3	0.51	1/1080 (0.1%)	0.77	3/1437 (0.2%)
59	B3	0.32	0/1142	0.51	0/1528
60	C3	0.29	0/1061	0.50	0/1421
61	D3	0.35	0/639	0.53	0/855
62	G5	0.29	0/1158	0.52	1/1548 (0.1%)
63	H5	0.31	0/1133	0.54	0/1517
64	J5	0.36	0/1051	0.51	0/1406
65	I5	0.29	0/1041	0.47	0/1382
66	L3	0.29	0/665	0.46	0/891
67	M3	0.27	0/605	0.52	0/810
68	O3	0.36	0/795	0.49	0/1065
69	Q3	0.27	0/539	0.48	0/713
70	a3	0.27	0/2494	0.52	0/3394
71	T3	0.35	0/1117	0.50	0/1490
72	U3	0.32	0/1682	0.49	0/2286
73	V3	0.31	0/1757	0.49	0/2350
74	W3	0.40	0/1727	0.55	0/2332
75	X3	0.32	0/224	0.51	0/284

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Y3	0.43	1/1793 (0.1%)	0.68	2/2412 (0.1%)
77	j3	0.32	0/2117	0.50	0/2846
78	N3	0.29	0/1531	0.49	0/2059
79	b3	0.28	0/1947	0.46	0/2590
80	c3	0.32	0/1716	0.51	1/2287 (0.0%)
81	d3	0.30	0/1551	0.48	0/2069
82	e3	0.25	0/968	0.49	0/1296
83	F3	0.31	0/1232	0.51	0/1656
84	E3	0.36	0/852	0.64	2/1147 (0.2%)
85	H3	0.33	0/455	0.46	0/603
All	All	0.50	2/245684 (0.0%)	0.86	391/361638 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	w2	0	1
10	52	0	1
11	62	0	2
12	72	0	2
21	t2	0	2
24	x2	0	1
25	y2	0	1
33	G2	0	1
36	K2	0	1
38	M2	0	2
40	T2	0	2
41	U2	0	1
43	W2	0	1
44	X2	0	2
46	a7	0	2
48	22	0	1
53	G3	0	3
57	a5	0	1
59	B3	0	1
60	C3	0	2
62	G5	0	2
70	a3	0	1
76	Y3	0	1
All	All	0	34

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	A3	87	PRO	CG-CD	-13.00	1.07	1.50
76	Y3	80	PRO	CG-CD	-12.29	1.10	1.50

The worst 5 of 391 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	Y3	80	PRO	N-CD-CG	-17.51	76.94	103.20
58	A3	87	PRO	N-CD-CG	-16.22	78.87	103.20
76	Y3	80	PRO	CA-CB-CG	-11.31	82.51	104.00
2	e2	1676	C	N3-C2-O2	-11.30	113.99	121.90
2	e2	2571	C	N3-C2-O2	-10.87	114.29	121.90

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	52	17	LEU	Peptide
11	62	145	PHE	Peptide
11	62	164	LYS	Peptide
12	72	18	PRO	Peptide
6	w2	62	MET	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	Z2	136/138 (99%)	126 (93%)	9 (7%)	1 (1%)	22 61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	p2	67/69 (97%)	55 (82%)	11 (16%)	1 (2%)	10	45
6	w2	197/199 (99%)	184 (93%)	13 (7%)	0	100	100
7	H2	151/153 (99%)	139 (92%)	12 (8%)	0	100	100
8	S2	185/187 (99%)	173 (94%)	11 (6%)	1 (0%)	29	68
9	32	178/180 (99%)	169 (95%)	9 (5%)	0	100	100
10	52	392/394 (100%)	351 (90%)	40 (10%)	1 (0%)	41	75
11	62	173/175 (99%)	154 (89%)	19 (11%)	0	100	100
12	72	157/159 (99%)	141 (90%)	16 (10%)	0	100	100
13	82	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
14	k2	129/131 (98%)	116 (90%)	13 (10%)	0	100	100
15	l2	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
16	m2	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
17	o2	132/134 (98%)	121 (92%)	11 (8%)	0	100	100
18	q2	145/147 (99%)	124 (86%)	21 (14%)	0	100	100
19	r2	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
20	13	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
21	t2	360/362 (99%)	305 (85%)	54 (15%)	1 (0%)	41	75
22	u2	105/107 (98%)	96 (91%)	9 (9%)	0	100	100
23	v2	126/128 (98%)	112 (89%)	14 (11%)	0	100	100
24	x2	107/109 (98%)	95 (89%)	12 (11%)	0	100	100
25	y2	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
26	92	242/244 (99%)	203 (84%)	37 (15%)	2 (1%)	19	58
27	A2	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
28	B2	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
29	C2	84/86 (98%)	74 (88%)	10 (12%)	0	100	100
30	D2	48/50 (96%)	40 (83%)	8 (17%)	0	100	100
31	E2	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
32	F2	102/104 (98%)	89 (87%)	13 (13%)	0	100	100
33	G2	290/292 (99%)	264 (91%)	26 (9%)	0	100	100
34	I2	89/91 (98%)	82 (92%)	7 (8%)	0	100	100
35	J2	123/125 (98%)	109 (89%)	14 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	K2	196/198 (99%)	177 (90%)	19 (10%)	0	100	100
37	L2	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
38	M2	150/163 (92%)	108 (72%)	39 (26%)	3 (2%)	7	39
39	R2	33/35 (94%)	28 (85%)	5 (15%)	0	100	100
40	T2	199/201 (99%)	161 (81%)	36 (18%)	2 (1%)	15	54
41	U2	223/225 (99%)	207 (93%)	16 (7%)	0	100	100
42	V2	231/241 (96%)	208 (90%)	23 (10%)	0	100	100
43	W2	188/190 (99%)	175 (93%)	13 (7%)	0	100	100
44	X2	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
45	Y2	167/169 (99%)	157 (94%)	10 (6%)	0	100	100
46	a7	208/210 (99%)	183 (88%)	24 (12%)	1 (0%)	29	68
47	12	201/203 (99%)	177 (88%)	24 (12%)	0	100	100
48	22	133/135 (98%)	115 (86%)	18 (14%)	0	100	100
49	42	215/217 (99%)	175 (81%)	40 (19%)	0	100	100
51	I3	102/104 (98%)	92 (90%)	10 (10%)	0	100	100
52	s3	41/43 (95%)	34 (83%)	7 (17%)	0	100	100
53	G3	151/153 (99%)	129 (85%)	21 (14%)	1 (1%)	22	61
54	f3	62/64 (97%)	47 (76%)	15 (24%)	0	100	100
56	P3	187/189 (99%)	164 (88%)	23 (12%)	0	100	100
57	a5	134/136 (98%)	110 (82%)	24 (18%)	0	100	100
58	A3	125/127 (98%)	112 (90%)	11 (9%)	2 (2%)	9	43
59	B3	139/141 (99%)	125 (90%)	14 (10%)	0	100	100
60	C3	127/129 (98%)	113 (89%)	11 (9%)	3 (2%)	6	35
61	D3	81/83 (98%)	74 (91%)	6 (7%)	1 (1%)	13	50
62	G5	135/137 (98%)	117 (87%)	16 (12%)	2 (2%)	10	45
63	H5	139/141 (99%)	127 (91%)	12 (9%)	0	100	100
64	J5	127/129 (98%)	113 (89%)	14 (11%)	0	100	100
65	I5	124/126 (98%)	110 (89%)	14 (11%)	0	100	100
66	L3	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
67	M3	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
68	O3	96/98 (98%)	85 (88%)	11 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	Q3	59/69 (86%)	52 (88%)	7 (12%)	0	100	100
70	a3	311/313 (99%)	278 (89%)	33 (11%)	0	100	100
71	T3	139/141 (99%)	121 (87%)	18 (13%)	0	100	100
72	U3	206/208 (99%)	189 (92%)	17 (8%)	0	100	100
73	V3	211/213 (99%)	190 (90%)	21 (10%)	0	100	100
74	W3	216/218 (99%)	193 (89%)	23 (11%)	0	100	100
75	X3	21/23 (91%)	21 (100%)	0	0	100	100
76	Y3	225/227 (99%)	208 (92%)	17 (8%)	0	100	100
77	j3	260/262 (99%)	235 (90%)	23 (9%)	2 (1%)	19	58
78	N3	189/191 (99%)	174 (92%)	15 (8%)	0	100	100
79	b3	235/237 (99%)	224 (95%)	11 (5%)	0	100	100
80	c3	204/206 (99%)	181 (89%)	23 (11%)	0	100	100
81	d3	183/185 (99%)	167 (91%)	16 (9%)	0	100	100
82	e3	122/124 (98%)	103 (84%)	19 (16%)	0	100	100
83	F3	148/150 (99%)	135 (91%)	13 (9%)	0	100	100
84	E3	96/98 (98%)	79 (82%)	17 (18%)	0	100	100
85	H3	51/53 (96%)	44 (86%)	7 (14%)	0	100	100
All	All	11684/11871 (98%)	10427 (89%)	1233 (11%)	24 (0%)	50	81

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	t2	72	ALA
38	M2	143	VAL
38	M2	144	ASP
53	G3	25	LEU
58	A3	6	GLN

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Z2	117/117 (100%)	116 (99%)	1 (1%)	78	90
5	p2	64/64 (100%)	64 (100%)	0	100	100
6	w2	171/171 (100%)	171 (100%)	0	100	100
7	H2	134/134 (100%)	133 (99%)	1 (1%)	84	93
8	S2	164/164 (100%)	163 (99%)	1 (1%)	86	94
9	32	159/159 (100%)	157 (99%)	2 (1%)	69	86
10	52	342/342 (100%)	342 (100%)	0	100	100
11	62	156/156 (100%)	155 (99%)	1 (1%)	86	94
12	72	139/139 (100%)	136 (98%)	3 (2%)	52	78
13	82	89/89 (100%)	89 (100%)	0	100	100
14	k2	101/101 (100%)	100 (99%)	1 (1%)	76	88
15	l2	55/55 (100%)	55 (100%)	0	100	100
16	m2	107/107 (100%)	107 (100%)	0	100	100
17	o2	124/124 (100%)	123 (99%)	1 (1%)	81	91
18	q2	119/119 (100%)	119 (100%)	0	100	100
19	r2	62/62 (100%)	61 (98%)	1 (2%)	62	83
20	l3	80/80 (100%)	79 (99%)	1 (1%)	69	86
21	t2	302/302 (100%)	301 (100%)	1 (0%)	92	97
22	u2	98/98 (100%)	98 (100%)	0	100	100
23	v2	114/114 (100%)	114 (100%)	0	100	100
24	x2	88/88 (100%)	87 (99%)	1 (1%)	73	88
25	y2	98/98 (100%)	97 (99%)	1 (1%)	76	88
26	92	187/187 (100%)	186 (100%)	1 (0%)	88	94
27	A2	109/109 (100%)	109 (100%)	0	100	100
28	B2	86/86 (100%)	86 (100%)	0	100	100
29	C2	73/73 (100%)	73 (100%)	0	100	100
30	D2	47/47 (100%)	47 (100%)	0	100	100
31	E2	48/48 (100%)	48 (100%)	0	100	100
32	F2	92/92 (100%)	92 (100%)	0	100	100
33	G2	247/247 (100%)	245 (99%)	2 (1%)	81	91
34	I2	74/74 (100%)	74 (100%)	0	100	100
35	J2	109/109 (100%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	K2	166/166 (100%)	166 (100%)	0	100	100
37	L2	89/89 (100%)	89 (100%)	0	100	100
38	M2	131/136 (96%)	129 (98%)	2 (2%)	65	84
39	R2	29/29 (100%)	29 (100%)	0	100	100
40	T2	180/180 (100%)	178 (99%)	2 (1%)	73	88
41	U2	196/196 (100%)	196 (100%)	0	100	100
42	V2	199/205 (97%)	198 (100%)	1 (0%)	88	94
43	W2	169/169 (100%)	165 (98%)	4 (2%)	49	76
44	X2	85/85 (100%)	85 (100%)	0	100	100
45	Y2	142/142 (100%)	141 (99%)	1 (1%)	84	93
46	a7	175/175 (100%)	171 (98%)	4 (2%)	50	77
47	12	171/171 (100%)	171 (100%)	0	100	100
48	22	117/117 (100%)	117 (100%)	0	100	100
49	42	196/196 (100%)	196 (100%)	0	100	100
51	I3	94/94 (100%)	93 (99%)	1 (1%)	73	88
52	s3	35/35 (100%)	35 (100%)	0	100	100
53	G3	137/137 (100%)	131 (96%)	6 (4%)	28	62
54	f3	57/57 (100%)	57 (100%)	0	100	100
56	P3	169/169 (100%)	169 (100%)	0	100	100
57	a5	106/106 (100%)	106 (100%)	0	100	100
58	A3	116/116 (100%)	113 (97%)	3 (3%)	46	74
59	B3	117/117 (100%)	117 (100%)	0	100	100
60	C3	117/117 (100%)	117 (100%)	0	100	100
61	D3	68/68 (100%)	64 (94%)	4 (6%)	19	53
62	G5	119/119 (100%)	118 (99%)	1 (1%)	81	91
63	H5	113/113 (100%)	108 (96%)	5 (4%)	28	62
64	J5	112/112 (100%)	110 (98%)	2 (2%)	59	81
65	I5	108/108 (100%)	107 (99%)	1 (1%)	78	90
66	L3	75/75 (100%)	75 (100%)	0	100	100
67	M3	66/66 (100%)	66 (100%)	0	100	100
68	O3	85/85 (100%)	83 (98%)	2 (2%)	49	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Q3	59/62 (95%)	59 (100%)	0	100	100
70	a3	272/272 (100%)	272 (100%)	0	100	100
71	T3	113/113 (100%)	112 (99%)	1 (1%)	78	90
72	U3	175/175 (100%)	172 (98%)	3 (2%)	60	82
73	V3	194/194 (100%)	194 (100%)	0	100	100
74	W3	184/184 (100%)	175 (95%)	9 (5%)	25	59
75	X3	22/22 (100%)	22 (100%)	0	100	100
76	Y3	190/190 (100%)	190 (100%)	0	100	100
77	j3	224/224 (100%)	220 (98%)	4 (2%)	59	81
78	N3	161/161 (100%)	161 (100%)	0	100	100
79	b3	207/207 (100%)	204 (99%)	3 (1%)	67	85
80	c3	178/178 (100%)	176 (99%)	2 (1%)	73	88
81	d3	161/161 (100%)	161 (100%)	0	100	100
82	e3	104/104 (100%)	104 (100%)	0	100	100
83	F3	130/130 (100%)	130 (100%)	0	100	100
84	E3	89/89 (100%)	89 (100%)	0	100	100
85	H3	47/47 (100%)	47 (100%)	0	100	100
All	All	10204/10218 (100%)	10124 (99%)	80 (1%)	82	91

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
68	O3	77	CYS
77	j3	26	VAL
72	U3	113	GLN
74	W3	120	GLN
79	b3	98	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
65	I5	19	GLN
80	c3	9	HIS
66	L3	26	GLN
77	j3	50	ASN

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Mol	Chain	Res	Type
84	E3	66	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	e2	3910/3920 (99%)	1126 (28%)	0
3	d2	119/120 (99%)	20 (16%)	0
4	h2	155/156 (99%)	38 (24%)	0
50	E1	152/153 (99%)	96 (63%)	9 (5%)
55	K3	1868/1869 (99%)	494 (26%)	30 (1%)
All	All	6204/6218 (99%)	1774 (28%)	39 (0%)

5 of 1774 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	e2	2	G
2	e2	12	A
2	e2	13	U
2	e2	21	G
2	e2	25	A

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	K3	1394	G
55	K3	1489	A
55	K3	1395	C
55	K3	1432	U
55	K3	1575	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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](#)

There are no chain breaks in this entry.

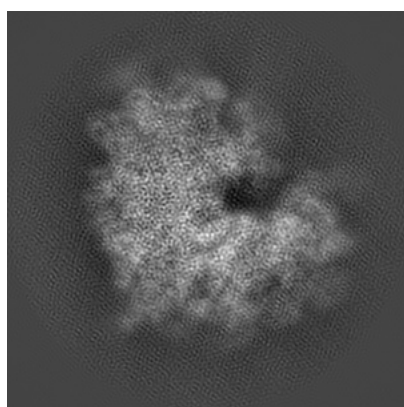
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11459. These allow visual inspection of the internal detail of the map and identification of artifacts.

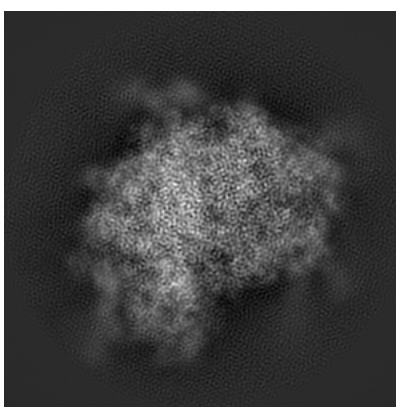
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

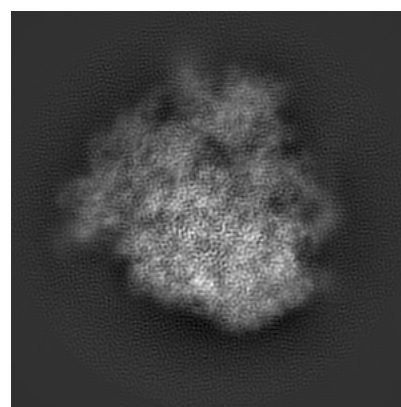
6.1.1 Primary map



X



Y

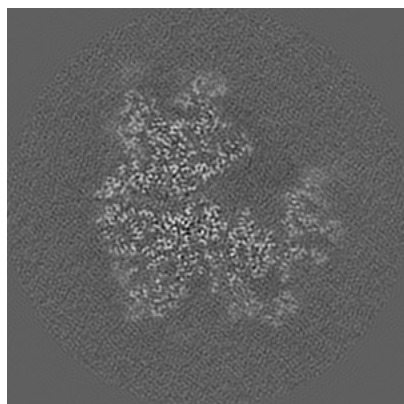


Z

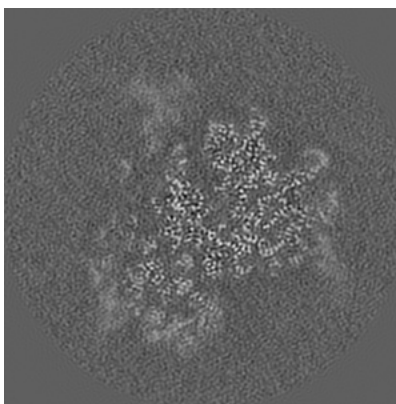
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

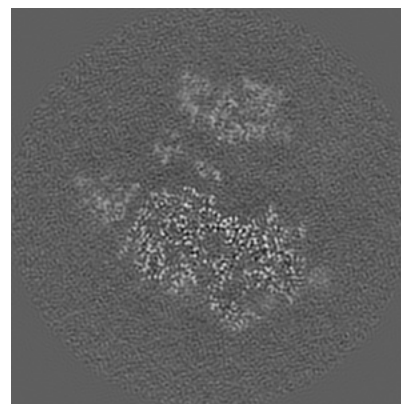
6.2.1 Primary map



X Index: 180



Y Index: 180

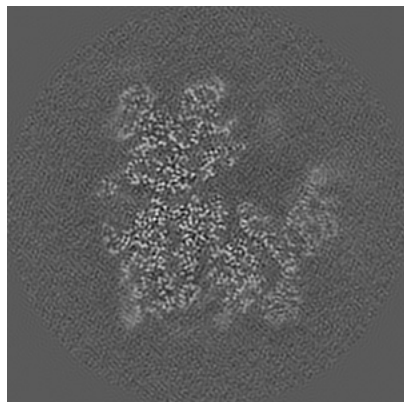


Z Index: 180

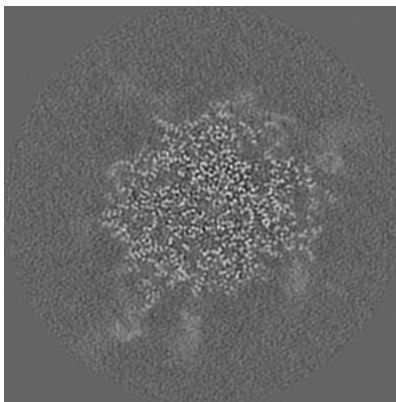
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

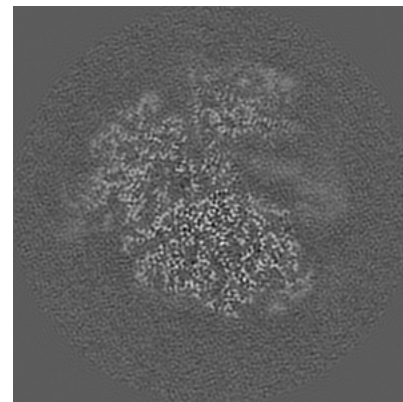
6.3.1 Primary map



X Index: 172



Y Index: 156

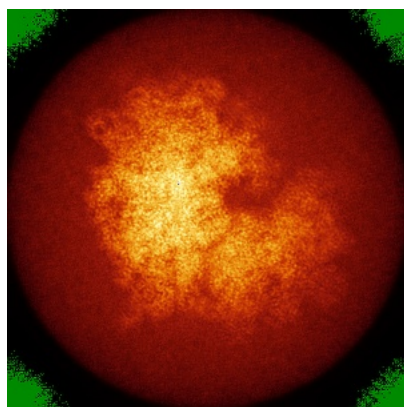


Z Index: 157

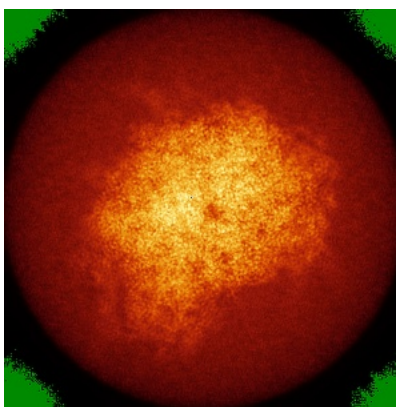
The images above show the largest variance slices of the map in three orthogonal directions.

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

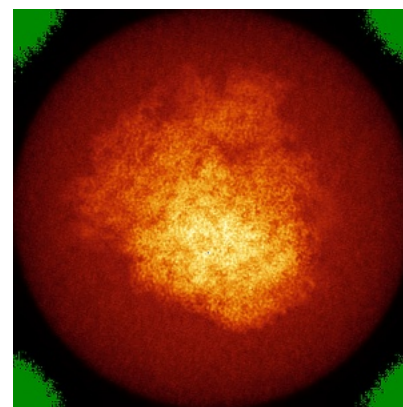
6.4.1 Primary map



X



Y

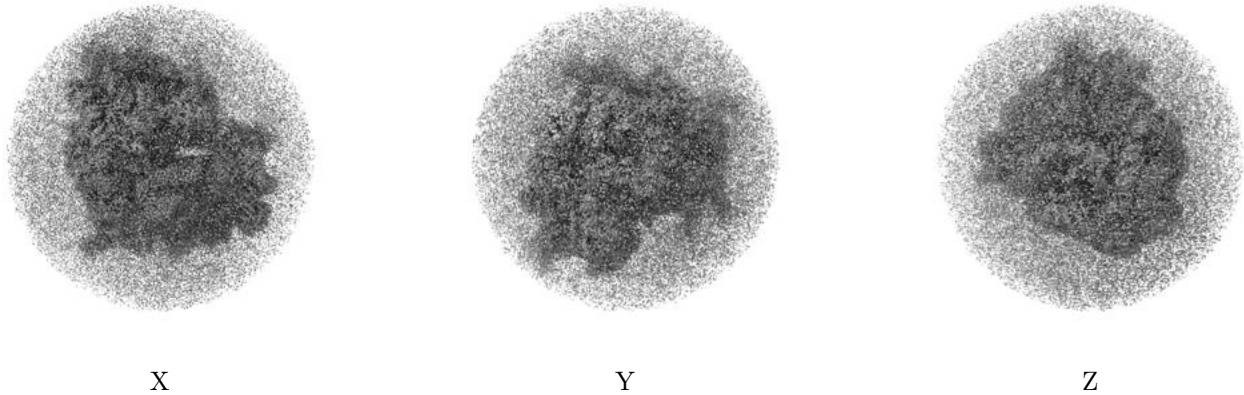


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.027. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

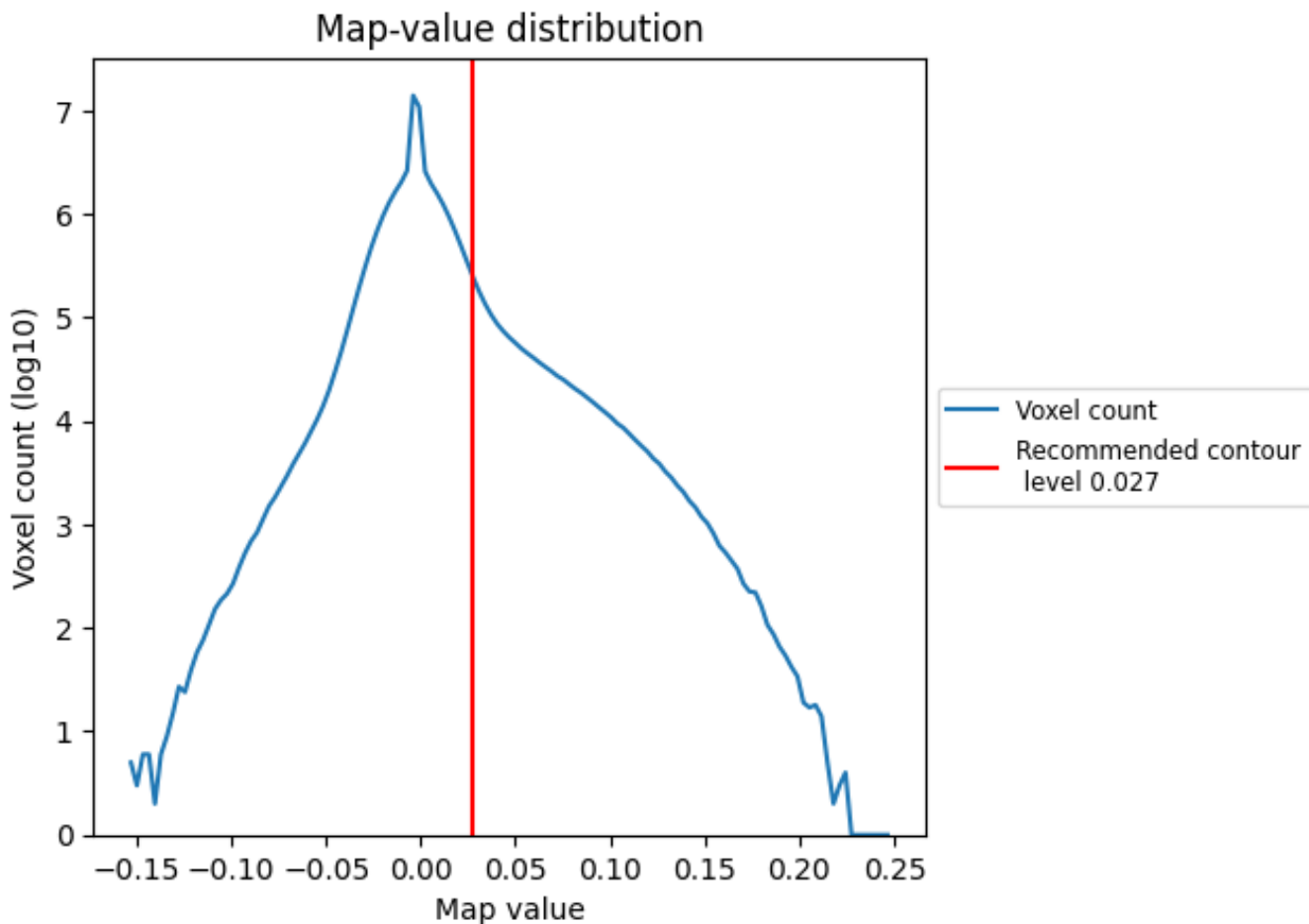
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

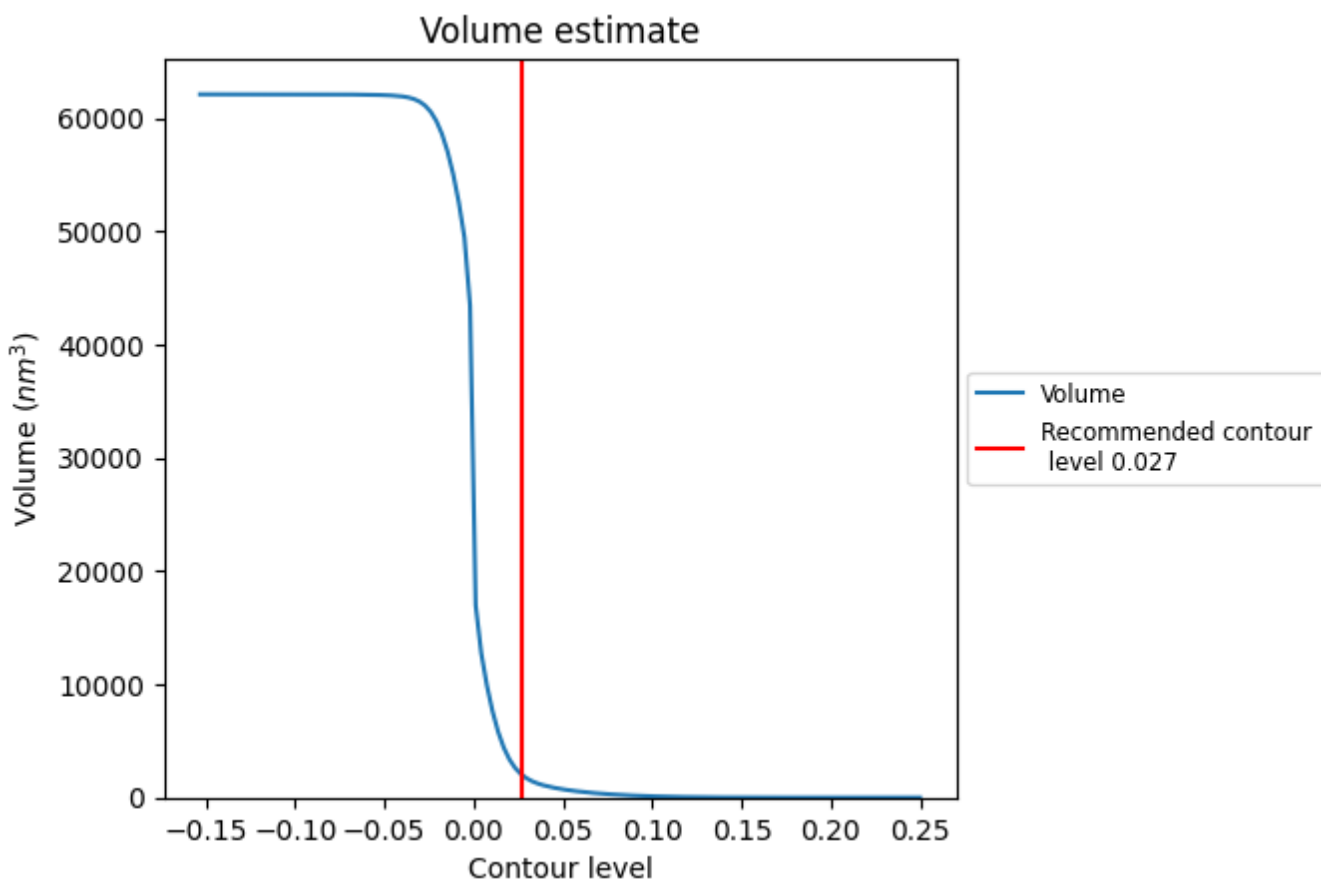
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

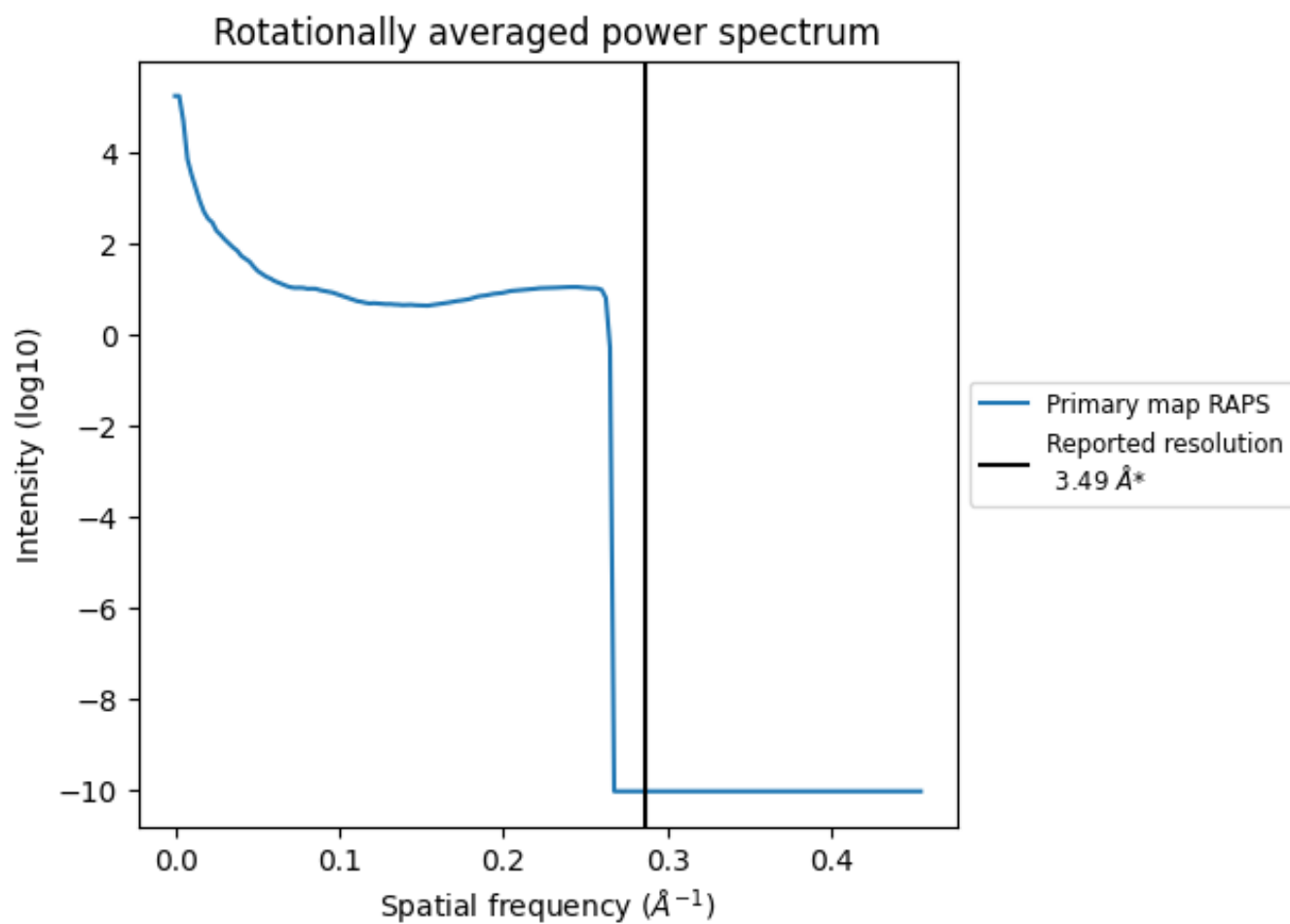
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2019 nm^3 ; this corresponds to an approximate mass of 1823 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.287\AA^{-1}

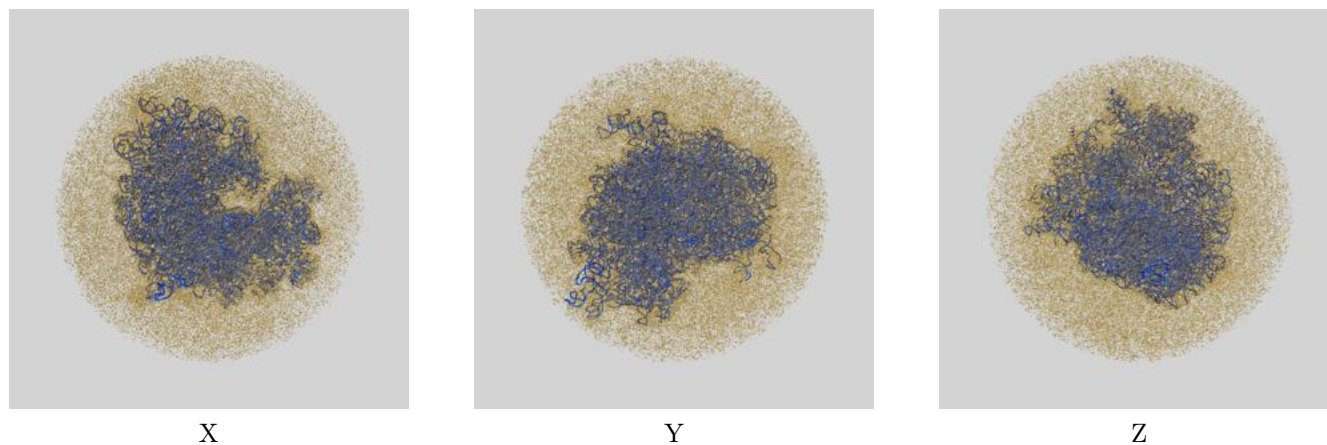
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

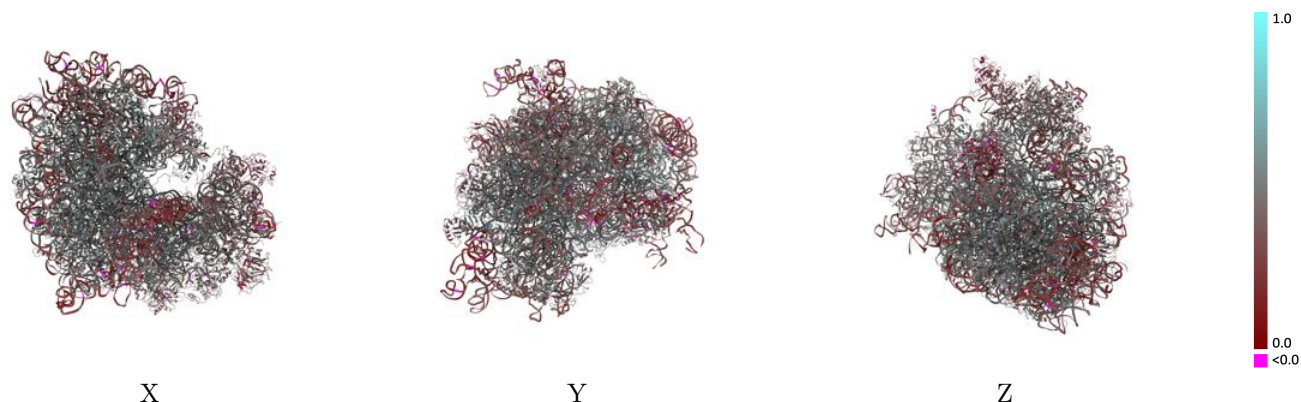
This section contains information regarding the fit between EMDB map EMD-11459 and PDB model 6ZVK. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



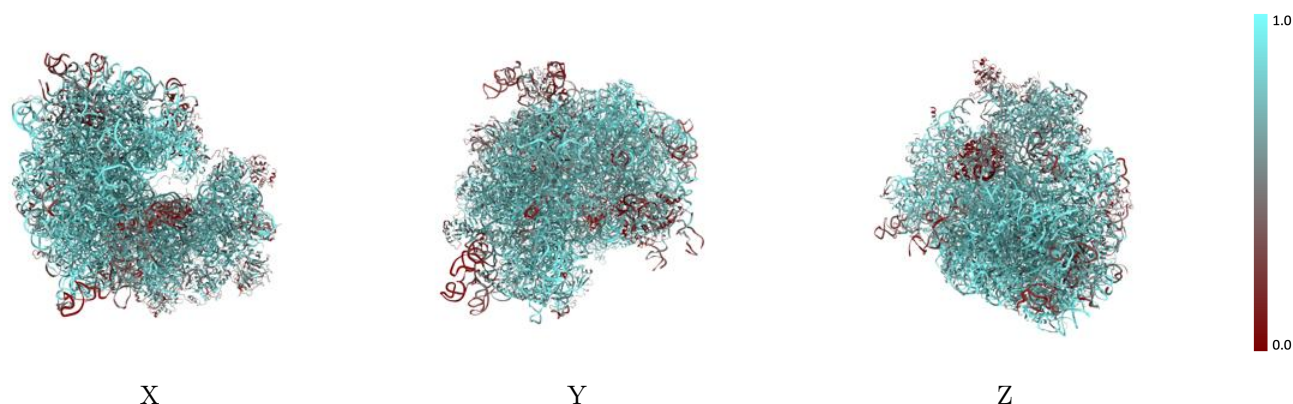
The images above show the 3D surface view of the map at the recommended contour level 0.027 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



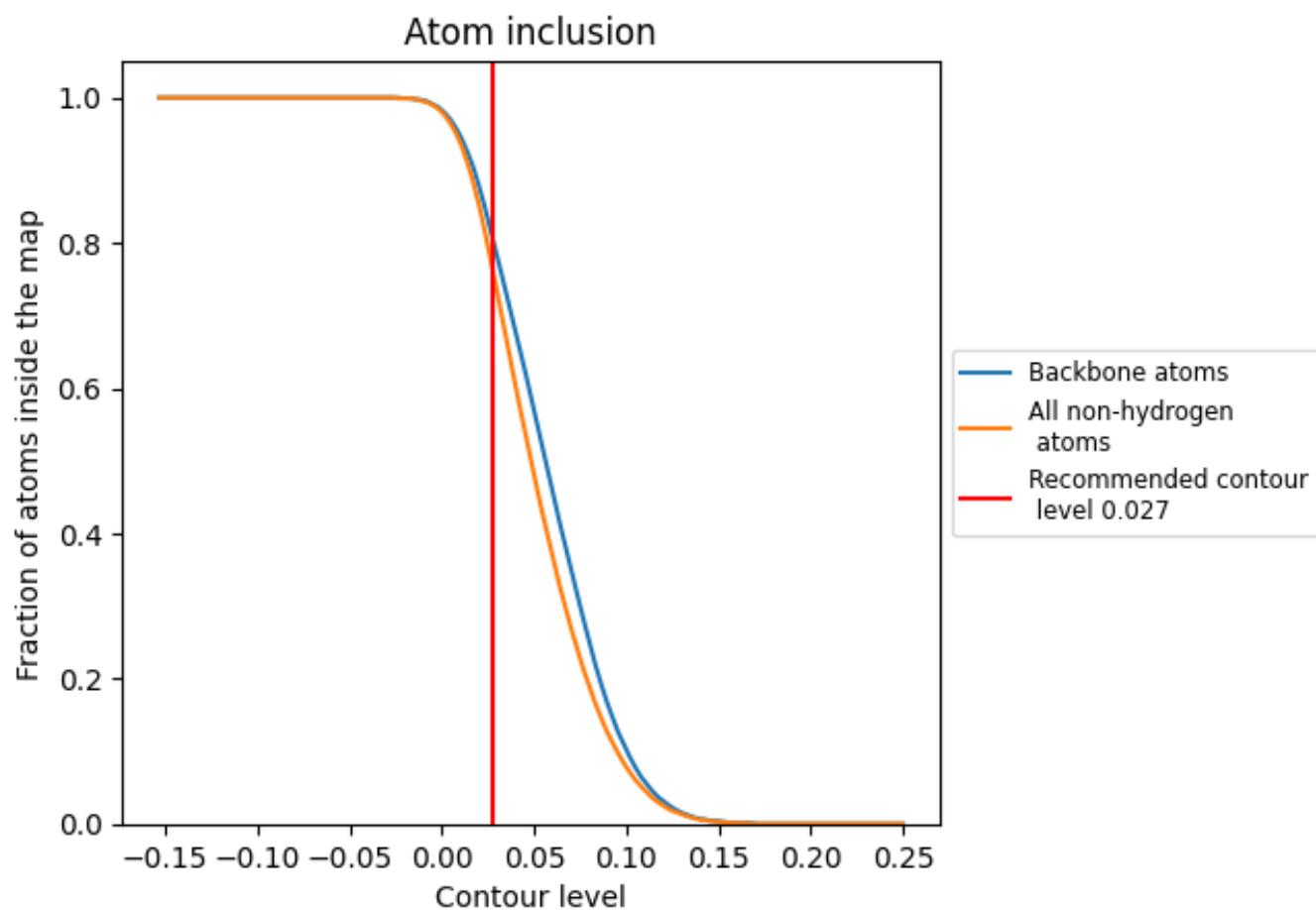
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.027).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 77% 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 (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7700	 0.4210
12	 0.8610	 0.5110
13	 0.8380	 0.5090
22	 0.8430	 0.4990
32	 0.8010	 0.4890
42	 0.2820	 0.2550
52	 0.8590	 0.5130
62	 0.8370	 0.5040
72	 0.8230	 0.5000
82	 0.8140	 0.4540
92	 0.8670	 0.5300
A2	 0.8350	 0.5050
A3	 0.6300	 0.3780
B2	 0.7820	 0.4710
B3	 0.7190	 0.4240
C2	 0.9120	 0.5470
C3	 0.6380	 0.3970
D2	 0.8790	 0.5140
D3	 0.7080	 0.4280
E1	 0.3000	 0.2390
E2	 0.8440	 0.5000
E3	 0.6170	 0.3510
F2	 0.8250	 0.5080
F3	 0.8030	 0.4960
G2	 0.8010	 0.4480
G3	 0.7010	 0.4430
G5	 0.6940	 0.4010
H2	 0.8630	 0.5260
H3	 0.7450	 0.4530
H5	 0.7020	 0.4030
I2	 0.8270	 0.5250
I3	 0.6070	 0.3920
I5	 0.7540	 0.4260
J2	 0.8400	 0.4970
J5	 0.8280	 0.5020





















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Chain	Atom inclusion	Q-score
K2	0.1920	0.2260
K3	0.7830	0.3910
L2	0.8150	0.5100
L3	0.7280	0.4320
M2	0.1860	0.2130
M3	0.6080	0.3530
N3	0.7060	0.4320
O3	0.8410	0.5010
P3	0.5880	0.3830
Q3	0.2440	0.2300
R2	0.7140	0.4100
S2	0.8410	0.5070
T2	0.7030	0.4090
T3	0.8060	0.5040
U2	0.8410	0.4960
U3	0.7290	0.4460
V2	0.7700	0.4720
V3	0.7930	0.4770
W2	0.8000	0.4880
W3	0.7900	0.4720
X2	0.8100	0.4740
X3	0.8560	0.5030
Y2	0.8130	0.4680
Y3	0.6460	0.4120
Z2	0.8460	0.4970
a3	0.5530	0.3430
a5	0.7970	0.4820
a7	0.7550	0.4420
b3	0.7060	0.4130
c3	0.7490	0.4540
d2	0.9130	0.4440
d3	0.7950	0.4670
e2	0.8030	0.4050
e3	0.2450	0.2300
f3	0.6360	0.4080
h2	0.8750	0.4400
j3	0.7620	0.4610
k2	0.8390	0.5300
l2	0.8550	0.5160
m2	0.8260	0.5000
o2	0.8350	0.5000
p2	0.7540	0.4600

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Chain	Atom inclusion	Q-score
q2	 0.8480	 0.5090
r2	 0.6830	 0.4040
s3	 0.7670	 0.4640
t2	 0.8510	 0.5040
u2	 0.8050	 0.4920
v2	 0.8440	 0.5110
w2	 0.8360	 0.5010
x2	 0.8600	 0.5210
y2	 0.8200	 0.4820