



## wwPDB EM Validation Summary Report ⓘ

Dec 18, 2022 – 05:45 am GMT

PDB ID : 7A01  
EMDB ID : EMD-11590  
Title : The Halastavi arva virus intergenic region IRES promotes translation by the simplest possible initiation mechanism  
Authors : Abaeva, I.; Vicens, Q.; Bochler, A.; Soufari, H.; Simonetti, A.; Pestova, T.V.; Hashem, Y.; Hellen, C.U.T.  
Deposited on : 2020-08-05  
Resolution : 3.60 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](mailto: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>.

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

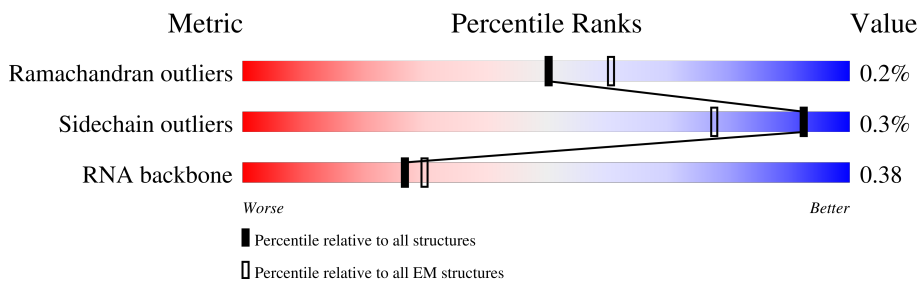
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 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 3.60 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.



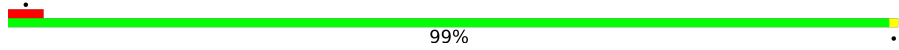
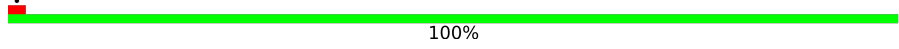
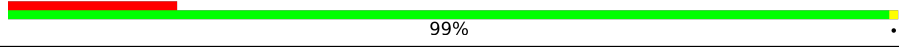
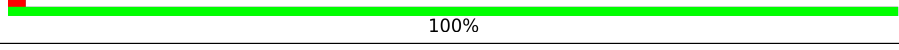
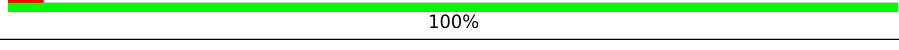
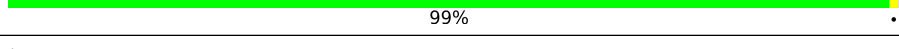
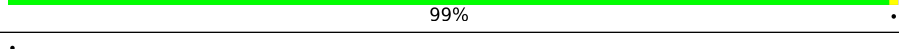
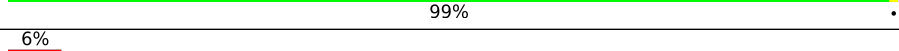
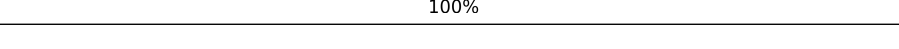
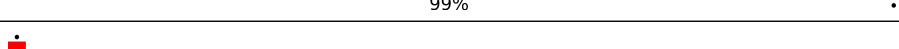
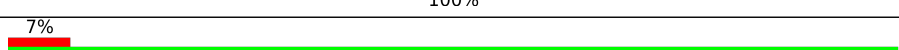
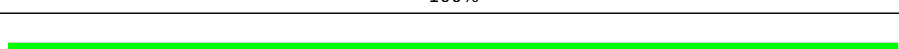
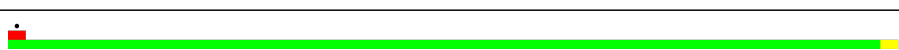
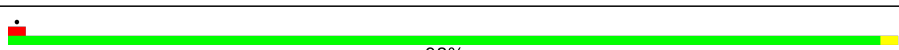
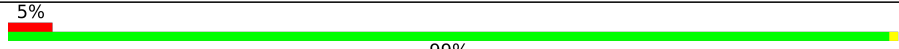
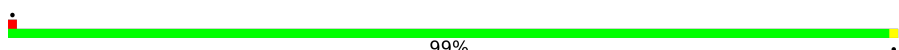
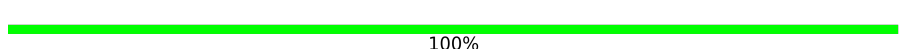
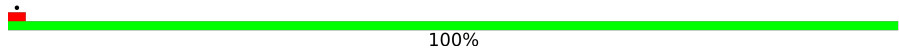
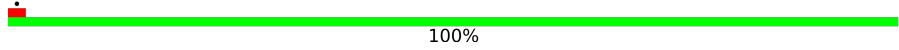
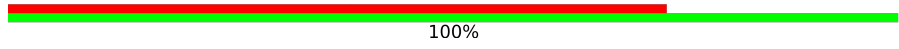
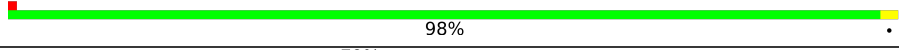
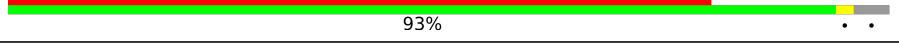
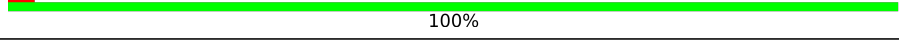
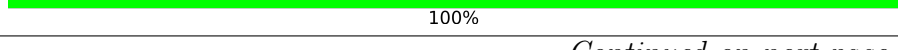

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	E1	153	
2	e2	3825	
3	h2	156	
4	d2	120	
5	p2	69	
6	k2	131	
7	l2	63	
8	m2	119	

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Mol	Chain	Length	Quality of chain
9	o2	134	 99%
10	q2	147	 100%
11	r2	75	 19% 99%
12	t2	362	 100%
13	u2	107	 100%
14	v2	128	 99%
15	w2	199	 99%
16	x2	109	 99%
17	y2	114	 6% 100%
18	g2	244	 99%
19	A2	122	 100%
20	B2	102	 7% 100%
21	C2	86	 100%
22	D2	50	 98%
23	E2	52	 98%
24	F2	104	 5% 99%
25	G2	292	 99%
26	H2	153	 100%
27	I2	91	 100%
28	J2	125	 100%
29	K2	198	 74% 100%
30	L2	102	 98%
31	M2	163	 79% 93%
32	R2	35	 100%
33	S2	187	 100%

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Mol	Chain	Length	Quality of chain
34	T2	201	9% 99%
35	U2	225	99%
36	V2	241	9% 100%
37	W2	190	98%
38	X2	102	100%
39	Y2	169	100%
40	02	138	99%
41	12	203	100%
42	22	135	99%
43	32	180	7% 99%
44	42	217	75% 98%
45	52	394	99%
46	62	175	98%
47	72	159	98%
48	82	99	100%
49	K3	1801	22% 55% 43%
50	s3	43	49% 98%
51	13	94	100%
52	Q3	188	23% 32% 66%
53	G3	153	44% 98%
54	G5	137	52% 98%
55	a3	313	76% 100%
56	a5	136	36% 99%
57	A3	127	41% 99%
58	T3	141	41% 99%

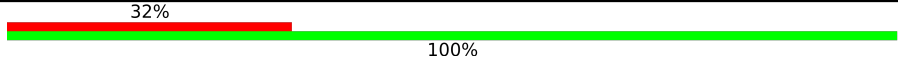
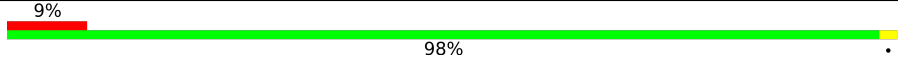
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Mol	Chain	Length	Quality of chain
59	U3	208	52% 100%
60	V3	213	48% 100%
61	W3	218	35% 100%
62	X3	23	. 100%
63	Y3	227	63% 99%
64	j3	262	37% 100%
65	J5	129	42% 98%
66	N3	191	74% 99%
67	b3	237	57% 100%
68	B3	141	70% 99%
69	f3	64	58% 100%
70	F3	150	49% 99%
71	c3	206	46% 100%
72	C3	129	59% 99%
73	d3	185	23% 99%
74	D3	83	49% 99%
75	e3	124	83% 95%
76	E3	98	54% 99%
77	H3	53	30% 100%
78	H5	141	61% 99%
79	P3	189	59% 98%
80	I3	104	48% 97%
81	I5	126	47% 100%
82	L3	83	41% 100%
83	M3	75	81% 100%

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Mol	Chain	Length	Quality of chain
84	O3	98	 32% 100%
85	a7	210	 9% 98%

## 2 Entry composition [i](#)

There are 86 unique types of molecules in this entry. The entry contains 224880 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 INTERNAL RIBOSOME ENTRY SITE.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	E1	153	3208	1443	529	1083	153	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	3825	81951	36501	14984	26650	3816	0	0

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

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

- Molecule 4 is a RNA chain called 5S RIBOSOMAL RNA.

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

- Molecule 5 is a protein called Uncharacterized protein.

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 eL14.

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

- Molecule 7 is a protein called Ribosomal protein L24.

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

- Molecule 8 is a protein called Uncharacterized protein.

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

- Molecule 9 is a protein called Ribosomal protein L26.

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

- Molecule 10 is a protein called uL15.

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

- Molecule 11 is a protein called 60S ribosomal protein L29.

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

- Molecule 12 is a protein called uL4.

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

- Molecule 13 is a protein called eL31.

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

- Molecule 14 is a protein called eL32.



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

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN UL13.

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

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 16 is a protein called eL33.

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

- Molecule 17 is a protein called eL34.

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

- Molecule 18 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	92	244	Total	C	N	O	S	0	0
			1869	1171	382	310	6		

- Molecule 19 is a protein called uL29.

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

- Molecule 20 is a protein called 60S ribosomal protein L36.

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

- Molecule 21 is a protein called Ribosomal protein L37.

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

- Molecule 22 is a protein called ribosomal protein eL39.

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

- Molecule 23 is a protein called 60S RIBOSOMAL PROTEIN EL40.

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

- Molecule 24 is a protein called eL42.

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

- Molecule 25 is a protein called 60S ribosomal protein L5.

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

- Molecule 26 is a protein called uL22.

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

- Molecule 27 is a protein called ribosomal protein eL43.

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

- Molecule 28 is a protein called Uncharacterized protein.

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

- Molecule 29 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 30 is a protein called Ribosomal protein L10 (Predicted).

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

- Molecule 31 is a protein called Uncharacterized protein.

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

- Molecule 32 is a protein called Ribosomal\_L6e\_N domain-containing protein.

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

- Molecule 33 is a protein called 60S RIBOSOMAL PROTEIN EL18.

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

- Molecule 34 is a protein called 60S ribosomal protein L6.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T2	224	GLN	LYS	variant	UNP G1SKF7
T2	231	LYS	GLN	variant	UNP G1SKF7

- Molecule 35 is a protein called uL30.

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

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN EL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	V2	241	1932	1231	371	326	4	0	0

- Molecule 37 is a protein called Uncharacterized protein.

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

- Molecule 38 is a protein called Ribosomal protein L10 (Predicted).

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

- Molecule 39 is a protein called Ribosomal protein L11.

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

- Molecule 40 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	02	138	Total	C	N	O	S	0	0
			1138	727	221	183	7		

- Molecule 41 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	12	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 42 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	22	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN EL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	32	180	Total	C	N	O	S	0	0
			1509	933	328	239	9		

- Molecule 44 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	42	217	Total	C	N	O	S	0	0
			1744	1114	314	307	9		

- Molecule 45 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	52	394	Total	C	N	O	S	0	0
			3173	2020	597	543	13		

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN EL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	62	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 47 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	72	159	1298	823	252	217	6	0	0

- Molecule 48 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	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	variant	UNP G1TSG1
82	36	ALA	GLU	variant	UNP G1TSG1
82	39	PHE	SER	variant	UNP G1TSG1
82	54	GLY	ARG	variant	UNP G1TSG1
82	60	VAL	ALA	variant	UNP G1TSG1
82	97	ARG	HIS	variant	UNP G1TSG1

- Molecule 49 is a RNA chain called 18S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
49	K3	1801	38409	17147	6888	12577	1797	0	0

- Molecule 50 is a protein called 40S RIBOSOMAL PROTEIN ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	s3	43	351	215	80	55	1	0	0

- Molecule 51 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	13	94	733	464	130	133	6	0	0

- Molecule 52 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	Q3	63	527	336	99	86	6	0	0

- Molecule 53 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	G3	153	1248	793	234	215	6	0	0

- Molecule 54 is a protein called ribosomal protein uS13.

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

- Molecule 55 is a protein called ribosomal protein RACK1.

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

- Molecule 56 is a protein called Uncharacterized protein.

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

- Molecule 57 is a protein called ribosomal protein uS19.

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

- Molecule 58 is a protein called Ribosomal protein S23.

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

- Molecule 59 is a protein called 40S\_SA\_C domain-containing protein.

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

- Molecule 60 is a protein called 40S ribosomal protein S3a.

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

- Molecule 61 is a protein called S5 DRBM domain-containing protein.

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

- Molecule 62 is a protein called 60s ribosomal protein l41.

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

- Molecule 63 is a protein called Ribosomal protein S3.

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

- Molecule 64 is a protein called 40S ribosomal protein S4,40S ribosomal protein S4.

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

- Molecule 65 is a protein called Ribosomal protein S15a.

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

- Molecule 66 is a protein called Ribosomal protein S5.

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

- Molecule 67 is a protein called 40S ribosomal protein S6.



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

- Molecule 68 is a protein called Uncharacterized protein.

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

- Molecule 69 is a protein called ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	f3	64	507	308	102	95	2	0	0

- Molecule 70 is a protein called ribosomal protein uS15.

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

- Molecule 71 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	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	variant	UNP G1TJW1

- Molecule 72 is a protein called Uncharacterized protein.

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

- Molecule 73 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 74 is a protein called 40S RIBOSOMAL PROTEIN ES21.

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

There are 5 discrepancies between the modelled and reference sequences:

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

- Molecule 75 is a protein called 40S ribosomal protein S12.

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

- Molecule 76 is a protein called S10\_ plectin domain-containing protein.

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

- Molecule 77 is a protein called ribosomal protein uS14.

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

- Molecule 78 is a protein called Uncharacterized protein.

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

- Molecule 79 is a protein called 40S RIBOSOMAL PROTEIN ES7.

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

- Molecule 80 is a protein called Ribosomal\_S10 domain-containing protein.

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

- Molecule 81 is a protein called 40S ribosomal protein S24.

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

- Molecule 82 is a protein called 40S ribosomal protein S27.

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

- Molecule 83 is a protein called ribosomal protein eS25.

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

- Molecule 84 is a protein called 40S RIBOSOMAL PROTEIN ES26.

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

- Molecule 85 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
85	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

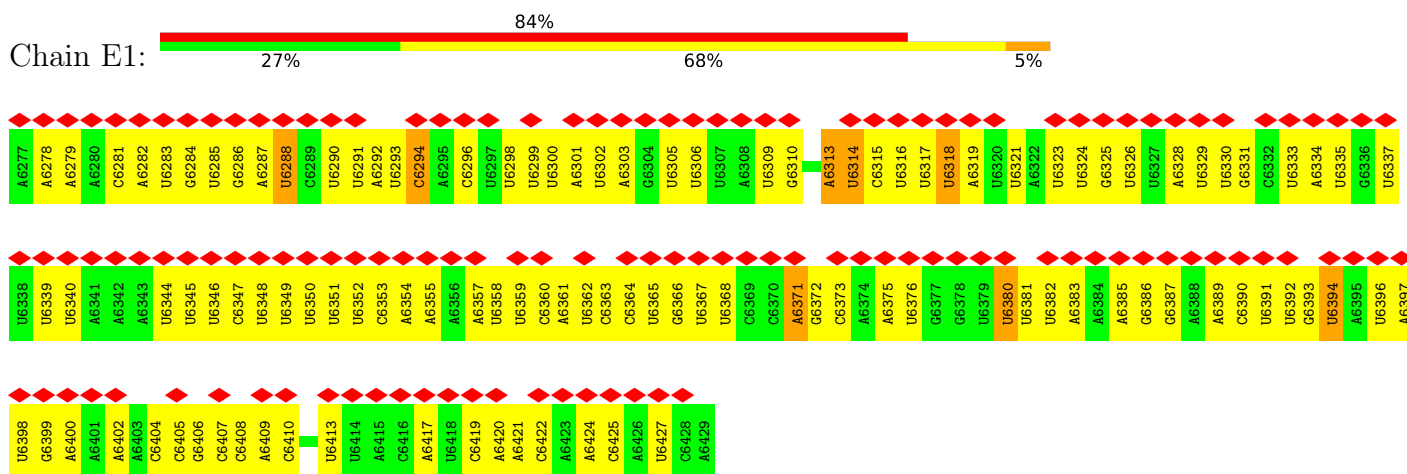
- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

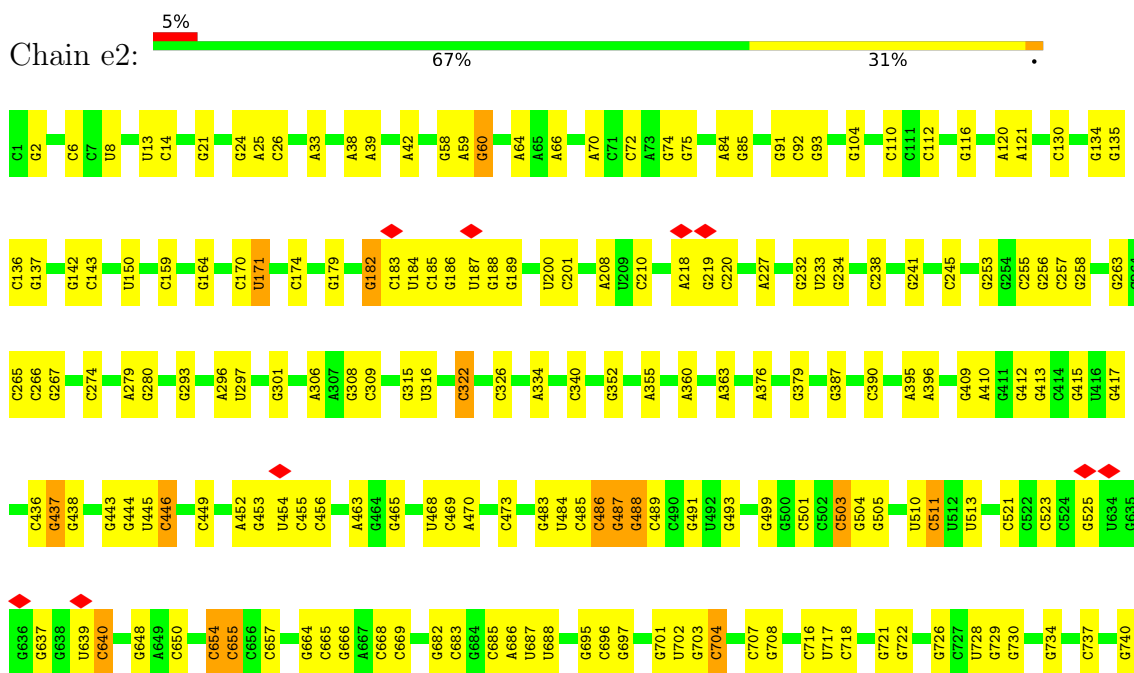
### 3 Residue-property plots

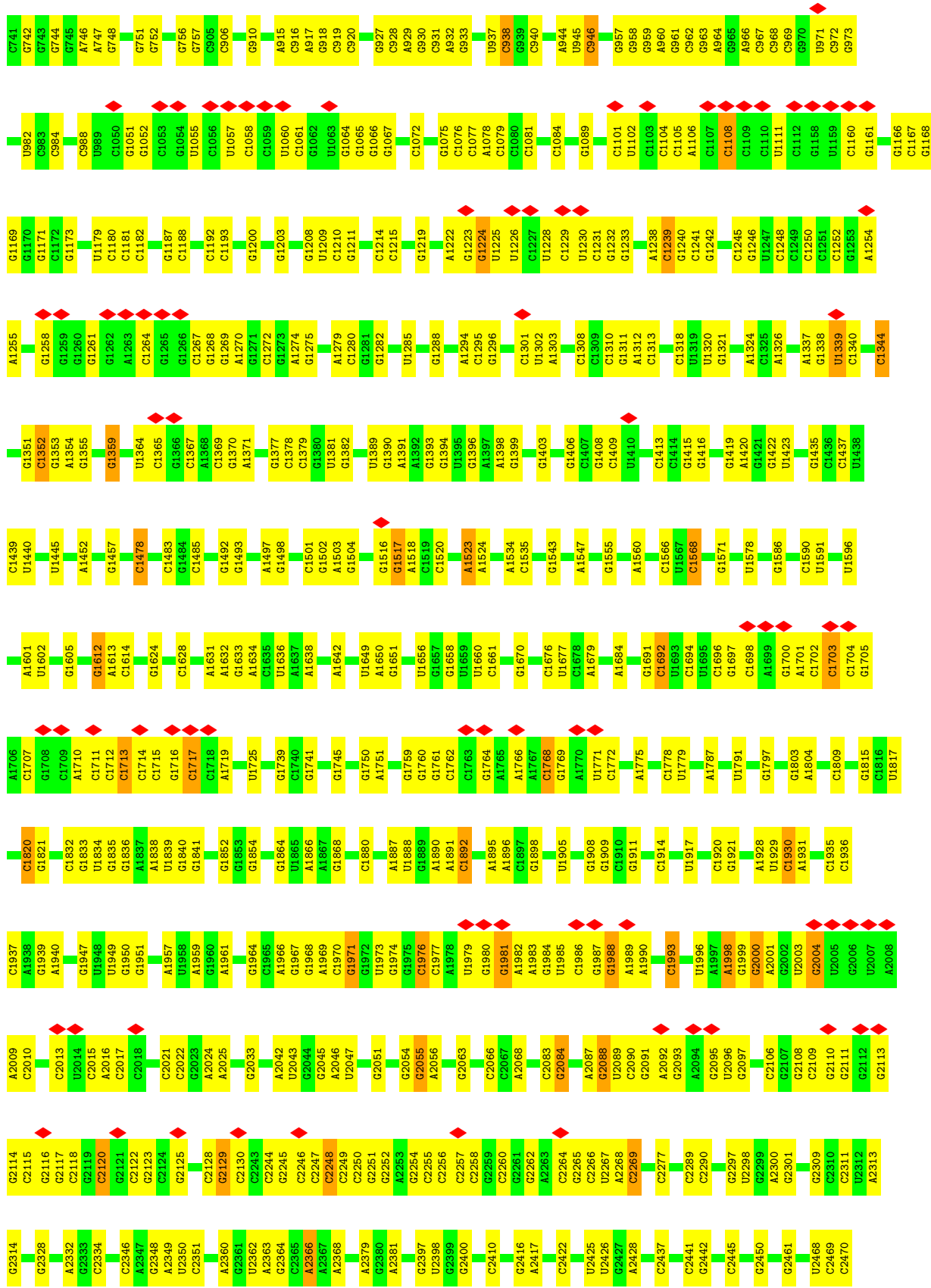
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



#### • Molecule 2: 28S RIBOSOMAL RNA

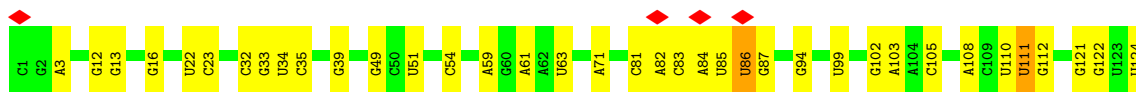




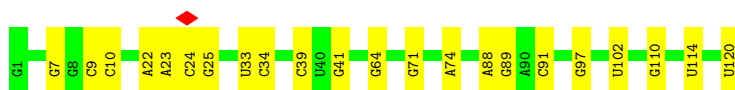
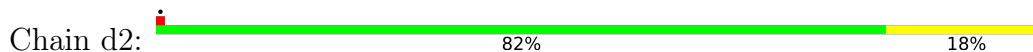
G4868	C4871	C4872	C4873	A4874	C4875	U4876	C4877	C4878	C4883	C4884	U4885	C4886	C4887	A4894	C4895	C4896	C4900	G4901	C4902	C4903	C4904	C4905	C4910	A4911	C4912	C4913	C4914	C4915	C4921	C4926	C4927	C4928	A4934	C4937	A4938	C4939	C4940	G4941	C4942	C4943	C4944	C4945	U4946	U4947	C4948	C4949	U4950	C4951	G4952									
G4545	A4548	C4549	C4550	A4558	U4559	C4560	U4571	U4572	C4573	U4574	G4575	A4584	A4589	A4590	A4599	C4600	U4601	G4604	A4605	C4606	C4617	U4627	U4636	U4637	C4638	C4639	U4642	C4650	A4656	U4657	G4658	U4668	A4669	C4670	C4671	A4672	G4678	A4685	C4686	C4687	C4688	C4689	C4693	C4694	A4701													
G4391	C4392	G4393	U4394	U4395	G4401	C4402	U4406	C4413	U4420	U4421	A4422	A4428	C4429	U4430	U4437	U4438	C4444	C4447	G4448	A4449	U4450	U4451	U4452	A4464	U4465	C4466	U4471	C4476	A4477	U4478	A4479	A4480	U4500	U4512	A4513	A4517	C4518	C4519	C4520	G4527	C4528	C4529																
G4264	U4265	G4266	U4267	C4268	U4270	A4273	U4281	A4282	U4290	C4291	A4304	U4306	A4307	A4313	C4319	A4323	C4326	U4330	C4331	C4337	U4338	A4339	C4349	C4350	C4355	A4366	G4367	U4374	C4375	U4376	C4377	A4378	A4379	A4380	A4381	U4384	A4385	C4386	C4387	A4388																		
G4127	A4128	C4133	C4134	C4140	G4141	C4142	C4143	C4144	C4145	G4151	U4163	C4164	C4165	G4168	G4169	A4170	C4171	A4172	G4183	G4184	G4191	A4192	C4193	G4198	C4199	A4205	C4206	A4212	A4213	A4214	C4215	G4216	G4225	U4229	A4233	A4234	C4241	G4250	A4251	C4252	A4253	G4254																
G4043	U4044	G4045	A4046	A4047	U4048	U4049	A4050	C4051	C4052	A4053	C4054	U4055	U4058	C4059	U4060	C4061	A4062	U4063	C4064	A4073	C4074	U4075	C4076	C4081	C4082	C4088	G4091	G4094	C4095	C4096	C4097	C4100	C4101	C4102	C4103	G4104	A4105	G4108	G4109	C4114	G4115	C4116	U4117	U4118	C4119	U4120	G4121	C4122	C4123	G4124								
G3983	C3984	C3985	C3986	C3987	C3988	C3989	G3990	G3991	G3992	U3993	G3994	U3995	C3996	C3997	C3998	C3999	G4000	C4001	G4002	C4003	G4004	C4005	G4006	C4008	C4009	C4010	G4011	G4012	C4013	G4014	G4015	G4016	G4017	G4018	G4019	U4020	C4021	C4022	C4023	C4024	C4025	G4026	G4027	C4028	C4029	C4030	U4031	G4032	C4033	C4034	G4035	G4036	C4037	C4038	C4039	C4040	C4041	G4042
G3889	A3890	C3891	U3892	G3895	C3896	C3897	G3898	A3901	A3906	C3907	A3908	C3909	U3914	U3915	C3926	G3938	C3939	A3947	C3948	U3950	G3951	A3952	C3953	A3954	G3955	U3957	G3958	U3959	A3960	G3961	A3962	A3963	U3964	A3965	A3966	C3967	U3968	C3969	G3970	C3971	A3972	C3975	C3976	C3977	C3978	C3979	G3980	G3981	C3982									
G3753	G3754	G3755	A3756	G3757	U3758	A3759	A3760	C3761	C3762	G3765	A3766	C3767	U3768	C3769	U3770	C3771	U3772	U3773	A3774	A3775	G3776	G3777	A3784	A3785	C3789	A3795	U3798	U3802	C3810	G3811	U3814	G3815	A3816	A3817	U3818	G3819	U3822	G3839	U3840	C3843	U3844	A3845	A3876	A3877	C3878	C3879												
U3606	G3615	G3616	C3617	C3618	G3619	C3620	G2796	C2797	C2798	C2799	U2803	C2804	C2805	C2814	G2823	C2824	A2825	U2826	C2827	G2830	C2838	G2842	A2845	G2848	U2707	U2708	C2709	C2710	G2711	U2554	G2555	C2556	G2557	C2558	G2559	C2560	C2561	G2562	C2571	G2576	C2579	U2580	G2760	U2761	G2762	U2763	C2768	U2769										
C2770	G2778	U2788	G2638	U2789	U2790	G2796	C2797	C2653	C2491	C2499	C2669	C2670	G2673	A2674	G2675	G2679	C2683	U2687	A2695	A2696	A2697	G2705	G2706	U2707	U2708	C2709	C2710	G2711	G2724	A2725	G2726	A2743	A2744	A2745	G2756	A2757	C2758	G2759	G2760	U2761	G2762	U2763	C2768	U2769														
U3606	G3615	G3616	C3617	C3618	G3619	C3620	G2796	C2797	C2798	C2799	U2803	C2804	C2805	C2814	G2823	C2824	A2825	U2826	C2827	G2830	C2838	G2842	A2845	G2848	U2707	U2708	C2709	C2710	G2711	G2724	A2725	G2726	A2743	A2744	A2745	G2756	A2757	C2758	G2759	G2760	U2761	G2762	U2763	C2768	U2769													
U3606	G3615	G3616	C3617	C3618	G3619	C3620	G2796	C2797	C2798	C2799	U2803	C2804	C2805	C2814	G2823	C2824	A2825	U2826	C2827	G2830	C2838	G2842	A2845	G2848	U2707	U2708	C2709	C2710	G2711	G2724	A2725	G2726	A2743	A2744	A2745	G2756	A2757	C2758	G2759	G2760	U2761	G2762	U2763	C2768	U2769													



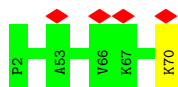
• Molecule 3: 5.8S RIBOSOMAL RNA



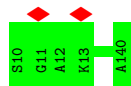
• Molecule 4: 5S RIBOSOMAL RNA



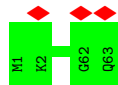
• Molecule 5: Uncharacterized protein



• Molecule 6: eL14



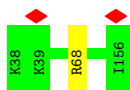
• Molecule 7: Ribosomal protein L24



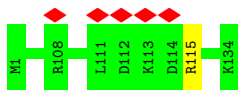
• Molecule 8: Uncharacterized protein







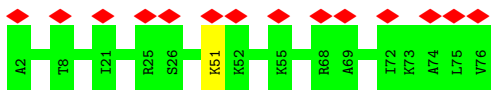
- Molecule 9: Ribosomal protein L26



- Molecule 10: uL15



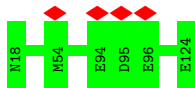
- Molecule 11: 60S ribosomal protein L29



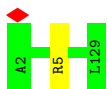
- Molecule 12: uL4



- Molecule 13: eL31

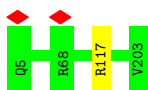


- Molecule 14: eL32



- Molecule 15: 60S RIBOSOMAL PROTEIN UL13

Chain w2:  99%



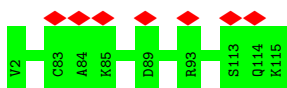
- Molecule 16: eL33

Chain x2:  99%



- Molecule 17: eL34

Chain y2:  6%  100%



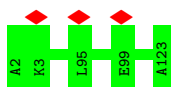
- Molecule 18: Uncharacterized protein

Chain 92:  99%



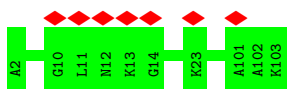
- Molecule 19: uL29

Chain A2:  100%



- Molecule 20: 60S ribosomal protein L36

Chain B2:  7%  100%



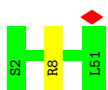
- Molecule 21: Ribosomal protein L37

Chain C2:  100%

There are no outlier residues recorded for this chain.

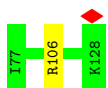
- Molecule 22: ribosomal protein eL39

Chain D2:  98%



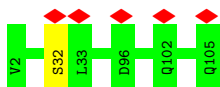
- Molecule 23: 60S RIBOSOMAL PROTEIN EL40

Chain E2:  98%



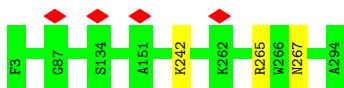
- Molecule 24: eL42

Chain F2:  99%



- Molecule 25: 60S ribosomal protein L5

Chain G2:  99%



- Molecule 26: uL22

Chain H2:  100%

There are no outlier residues recorded for this chain.

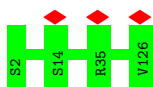
- Molecule 27: ribosomal protein eL43

Chain I2:  100%

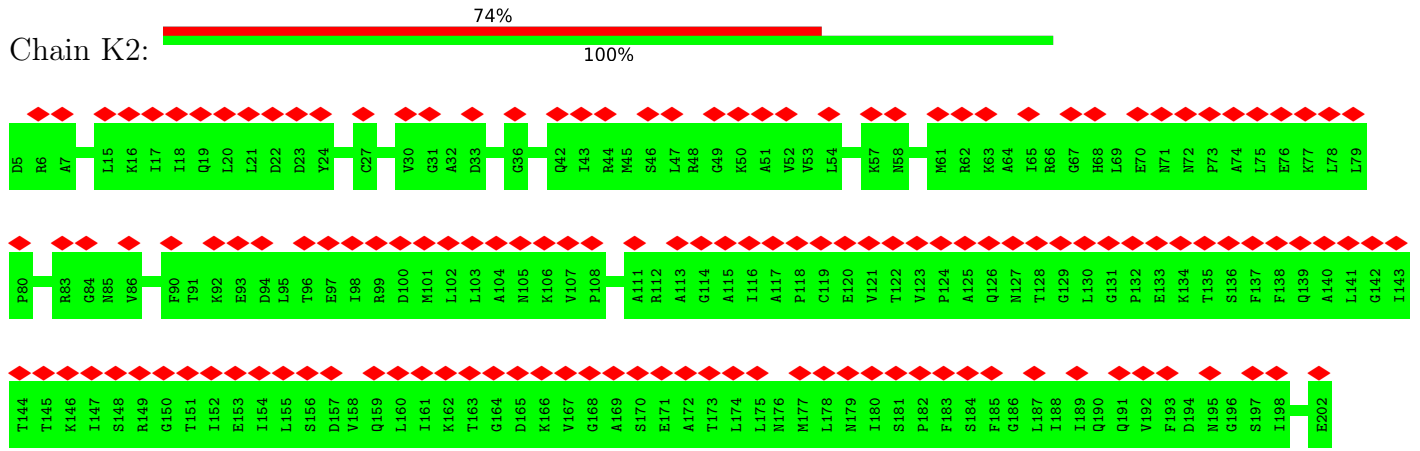


- Molecule 28: Uncharacterized protein

Chain J2:  100%



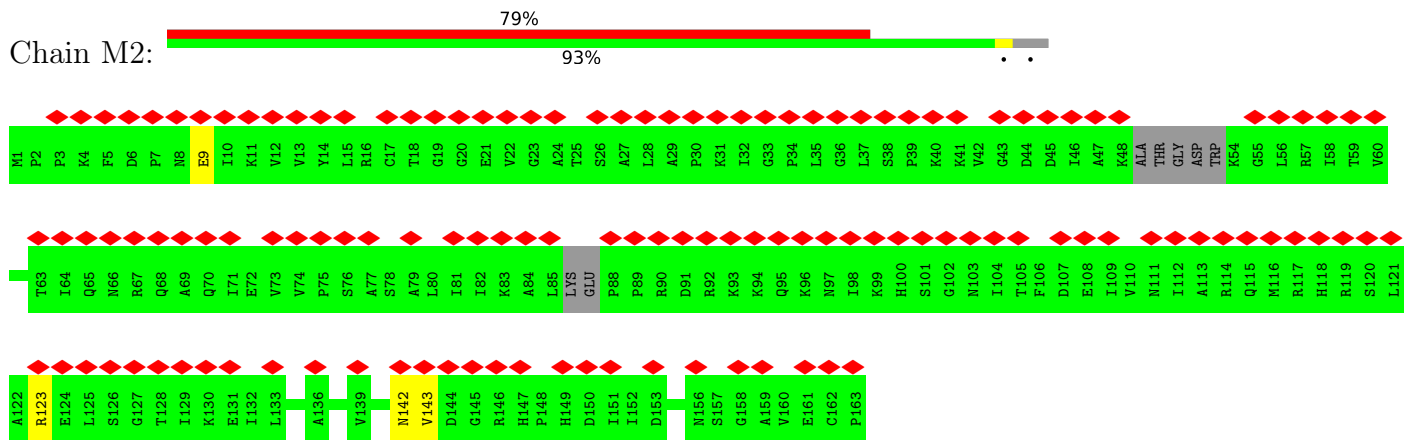
- Molecule 29: 60S acidic ribosomal protein P0



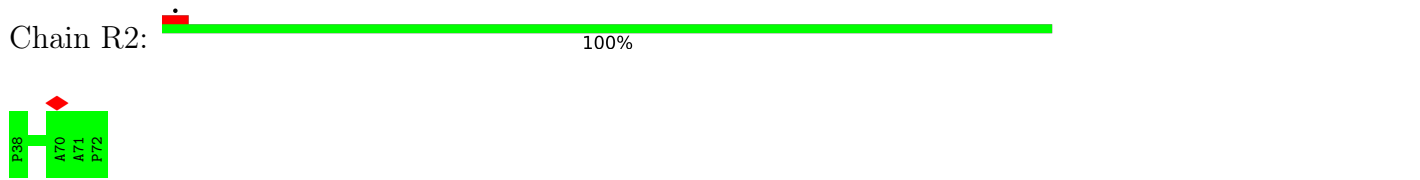
• Molecule 30: Ribosomal protein L10 (Predicted)



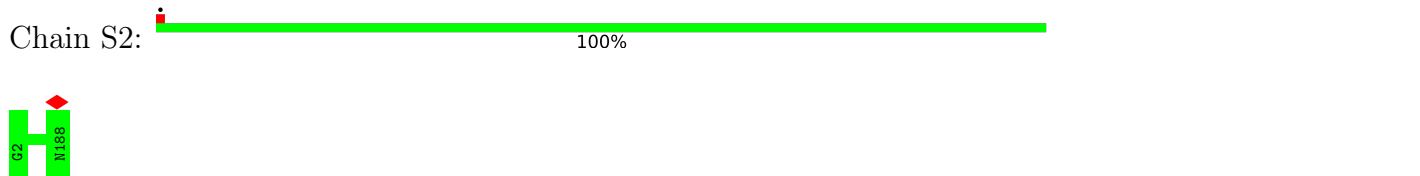
• Molecule 31: Uncharacterized protein



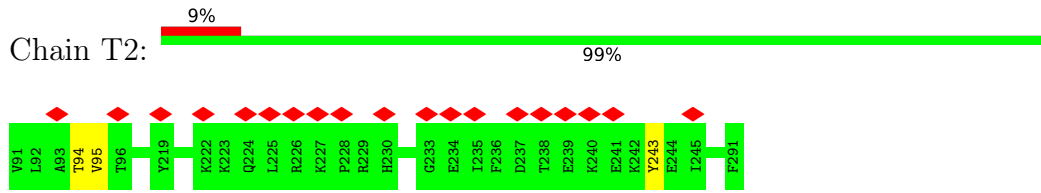
• Molecule 32: Ribosomal\_L6e\_N domain-containing protein



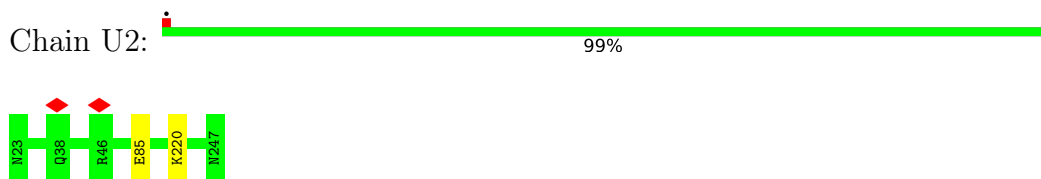
• Molecule 33: 60S RIBOSOMAL PROTEIN EL18



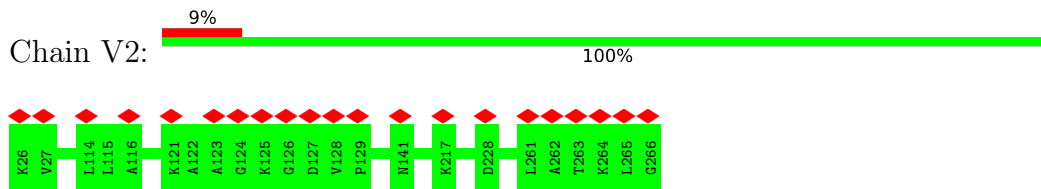
- Molecule 34: 60S ribosomal protein L6



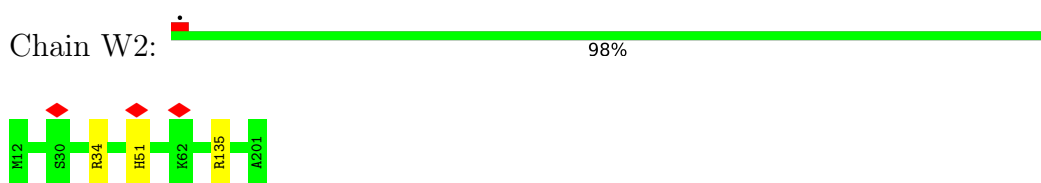
- Molecule 35: uL30



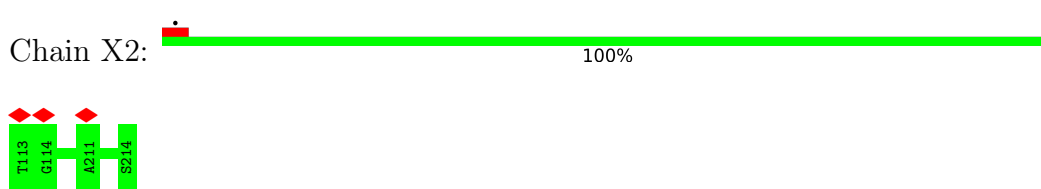
- Molecule 36: 60S RIBOSOMAL PROTEIN EL8



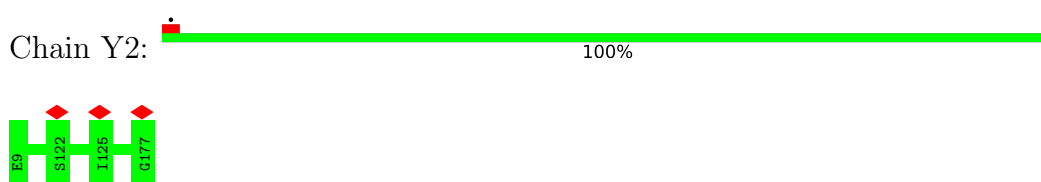
- Molecule 37: Uncharacterized protein



- Molecule 38: Ribosomal protein L10 (Predicted)

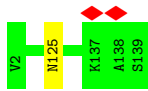


- Molecule 39: Ribosomal protein L11

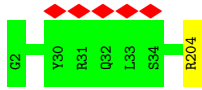


- Molecule 40: Ribosomal protein L14

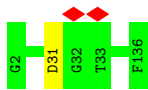




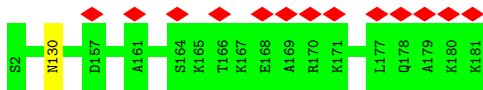
- Molecule 41: Ribosomal protein L15



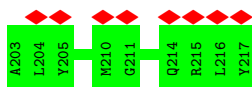
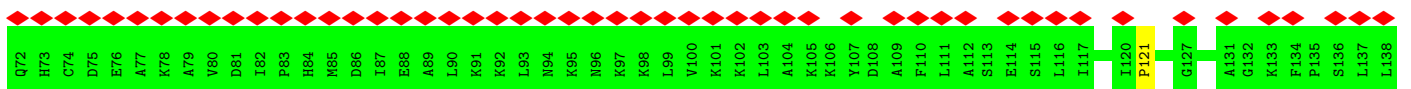
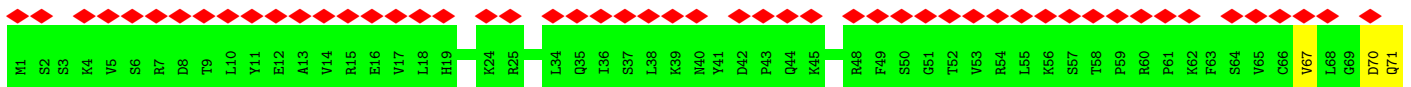
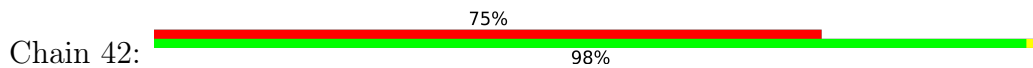
- Molecule 42: 60S ribosomal protein L27



- Molecule 43: 60S RIBOSOMAL PROTEIN EL19



- Molecule 44: Ribosomal protein

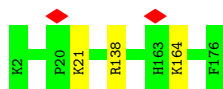


- Molecule 45: uL3

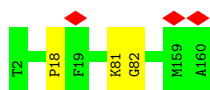




• Molecule 46: 60S RIBOSOMAL PROTEIN EL20



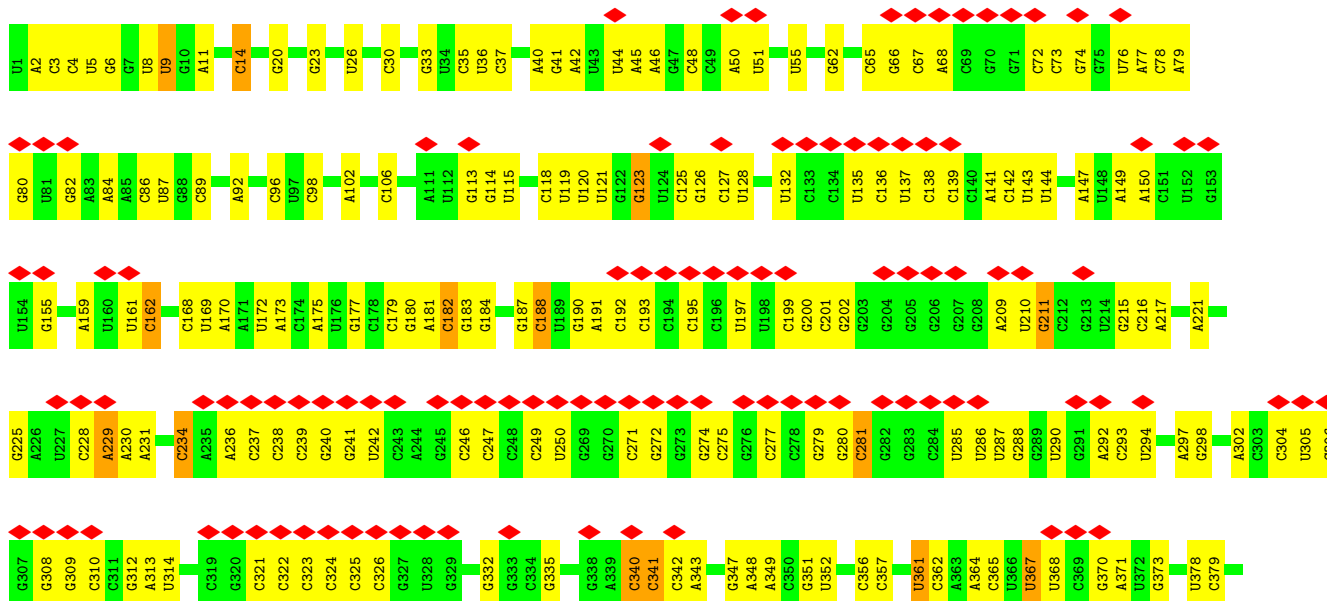
• Molecule 47: eL21

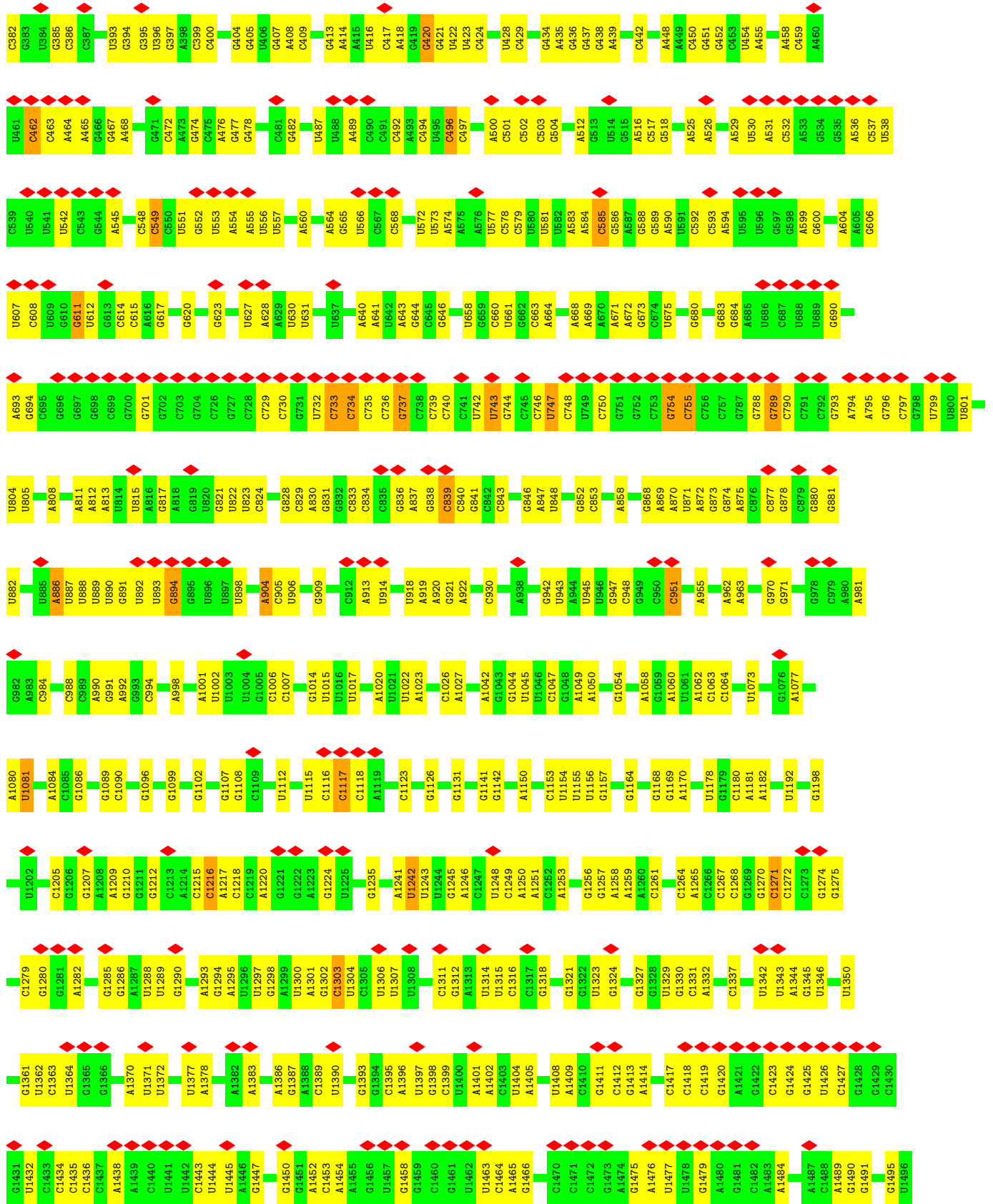


• Molecule 48: Ribosomal protein L22

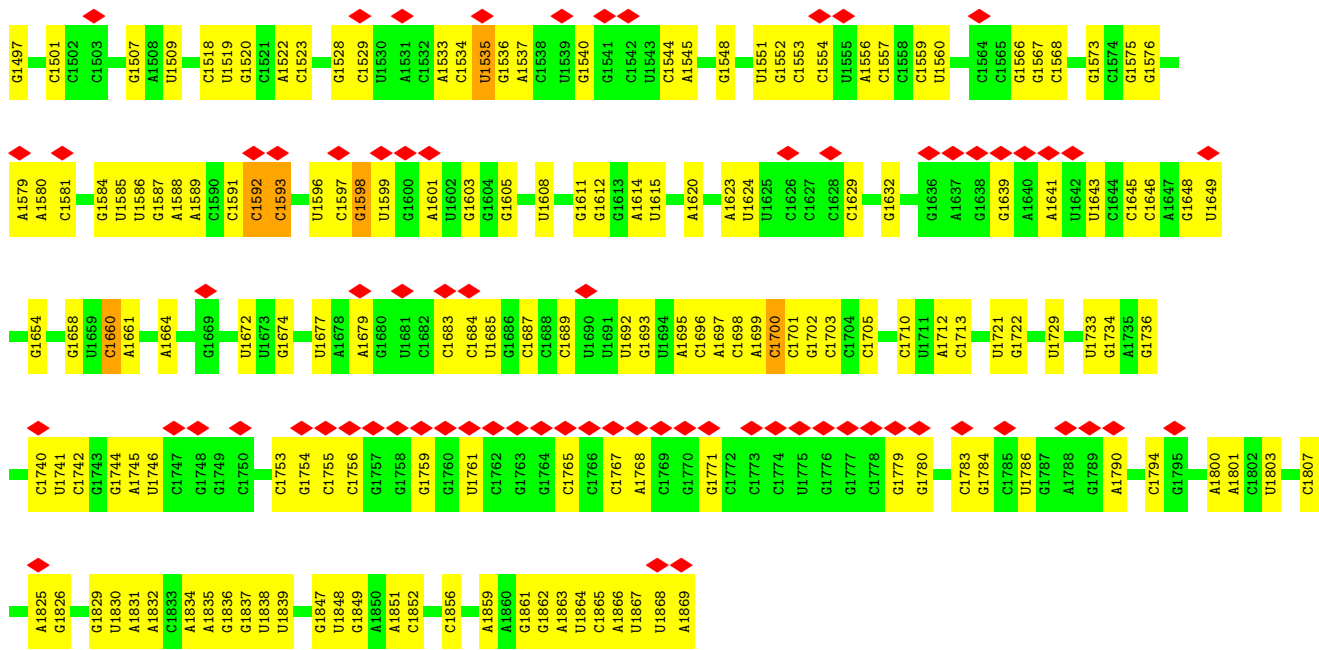


• Molecule 49: 18S RIBOSOMAL RNA

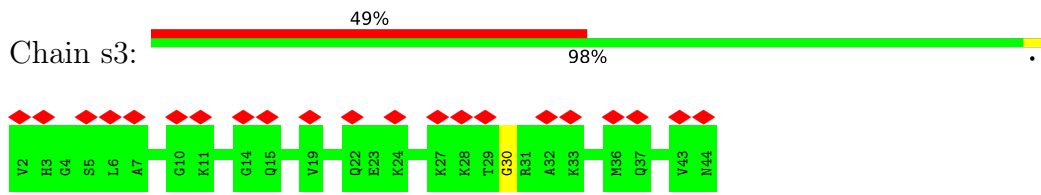




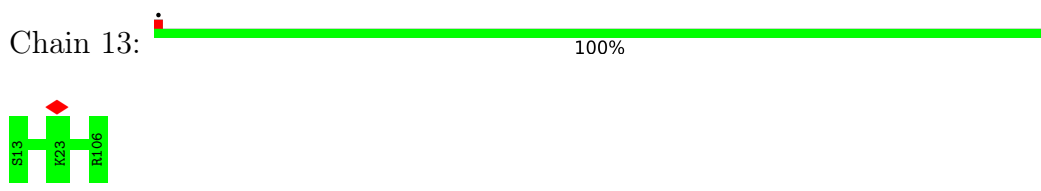




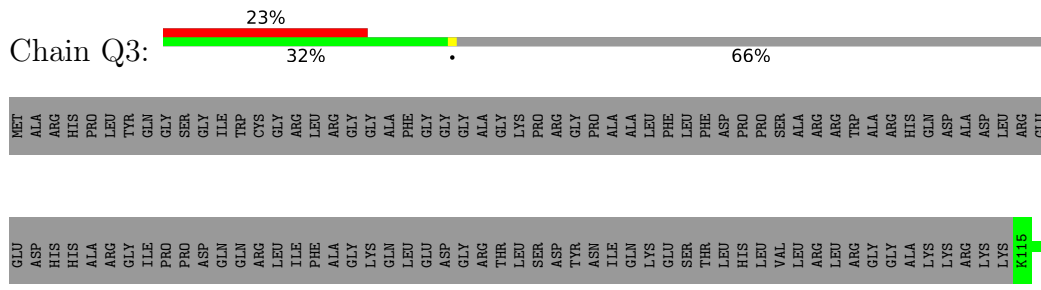
• Molecule 50: 40S RIBOSOMAL PROTEIN ES30



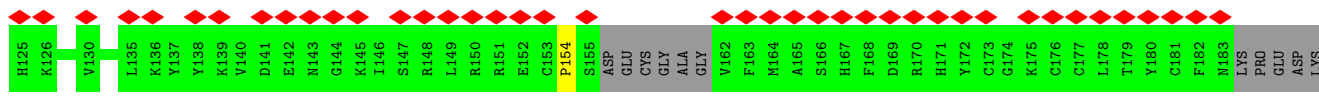
• Molecule 51: Ribosomal protein L30

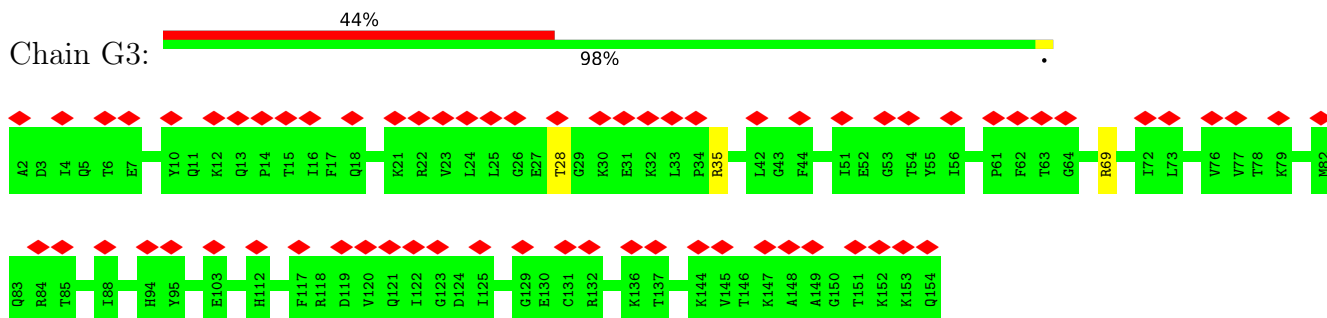


• Molecule 52: 40S ribosomal protein S27a

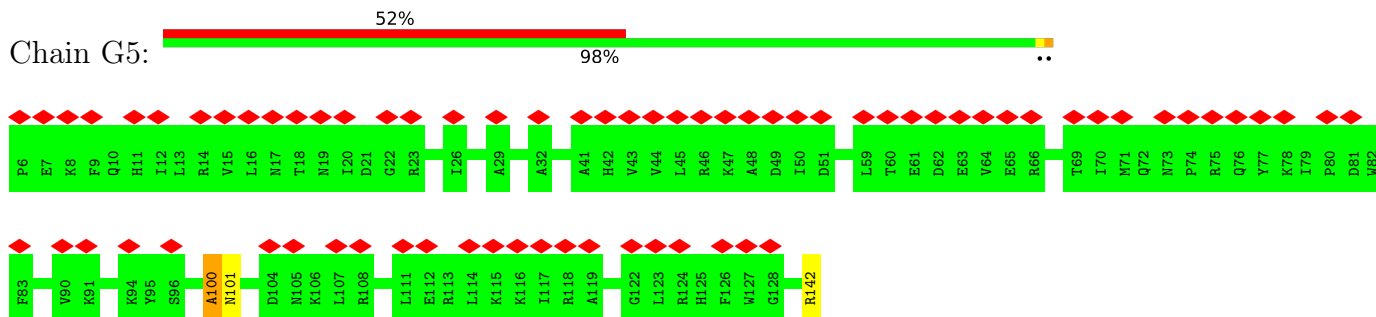


• Molecule 53: Ribosomal protein S11

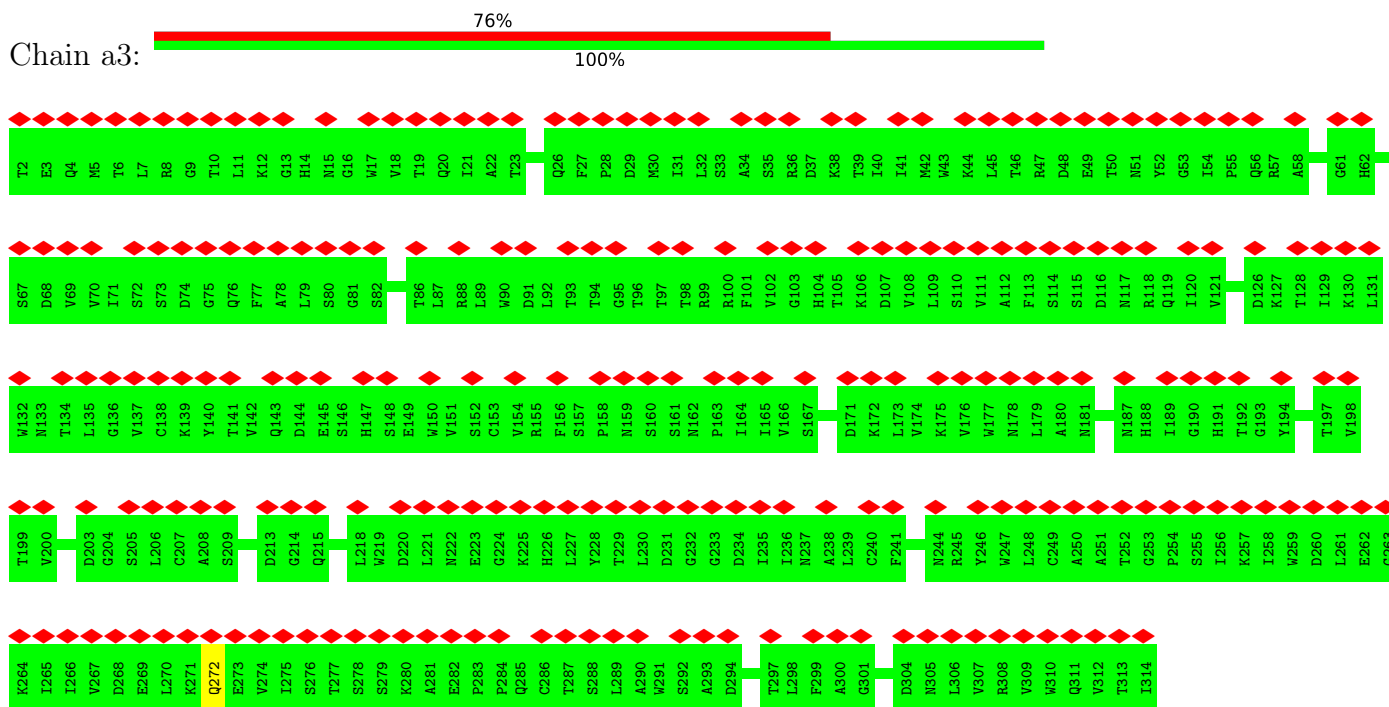




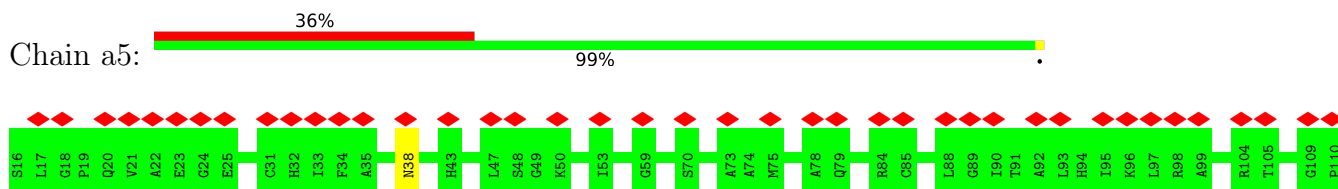
• Molecule 54: ribosomal protein uS13

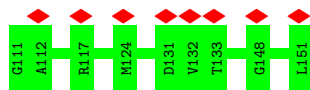


• Molecule 55: ribosomal protein RACK1



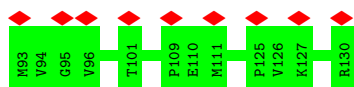
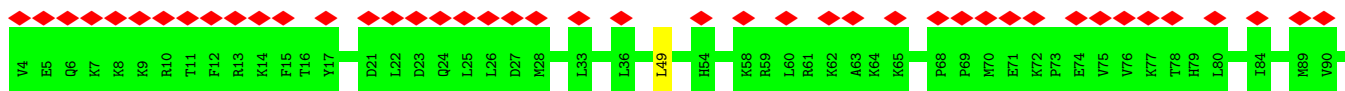
• Molecule 56: Uncharacterized protein





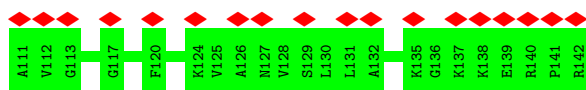
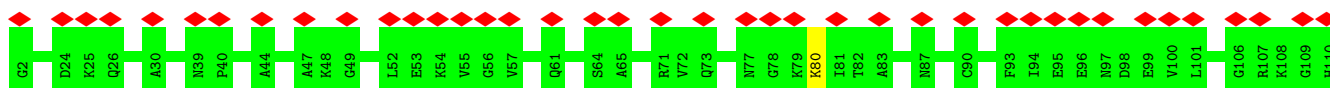
- Molecule 57: ribosomal protein uS19

Chain A3: 41% 99%



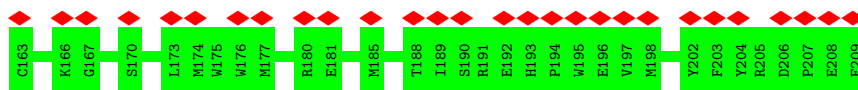
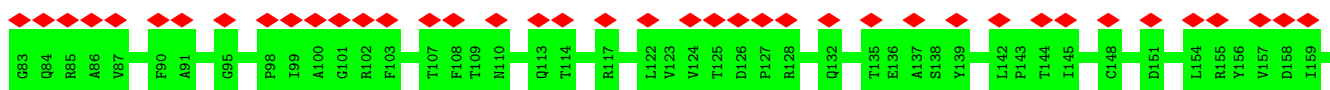
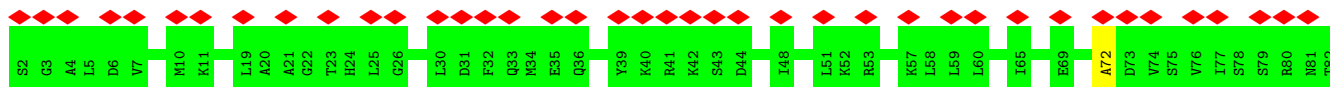
- Molecule 58: Ribosomal protein S23

Chain T3: 41% 99%



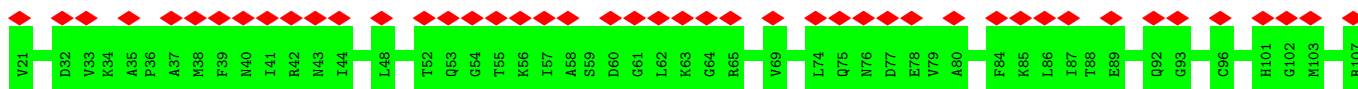
- Molecule 59: 40S\_SA\_C domain-containing protein

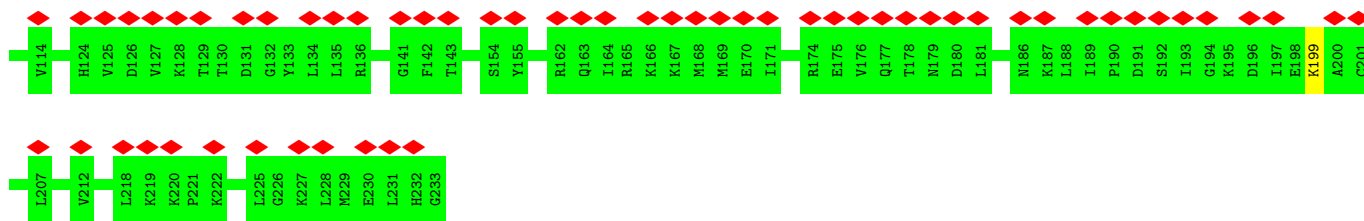
Chain U3: 52% 100%



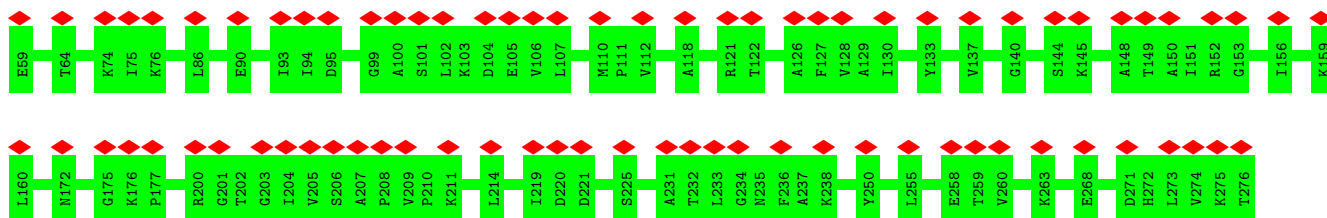
- Molecule 60: 40S ribosomal protein S3a

Chain V3: 48% 100%





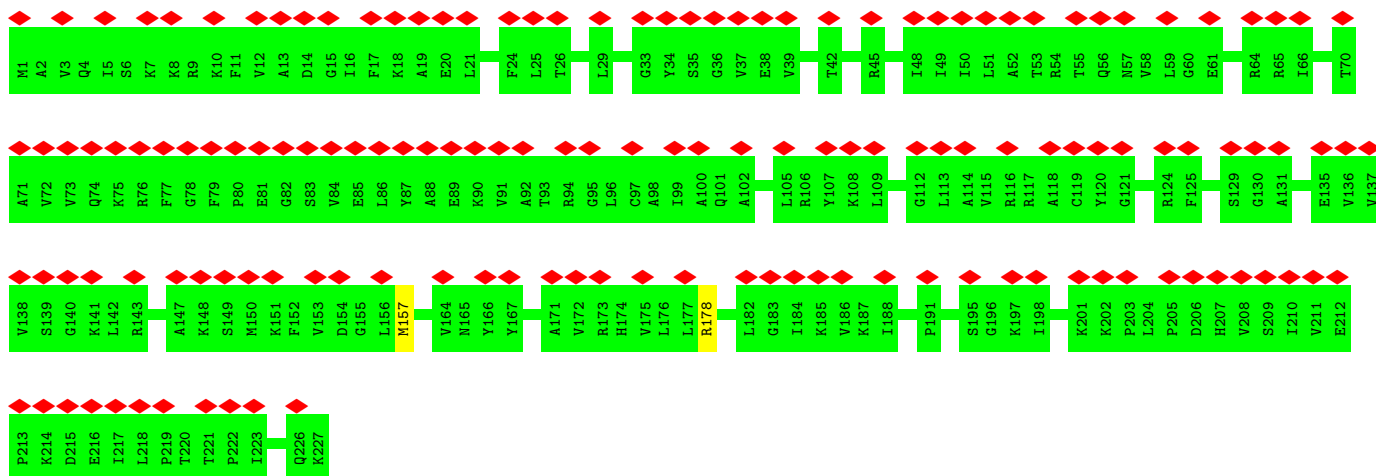
• Molecule 61: S5 DRBM domain-containing protein



• Molecule 62: 60s ribosomal protein l41

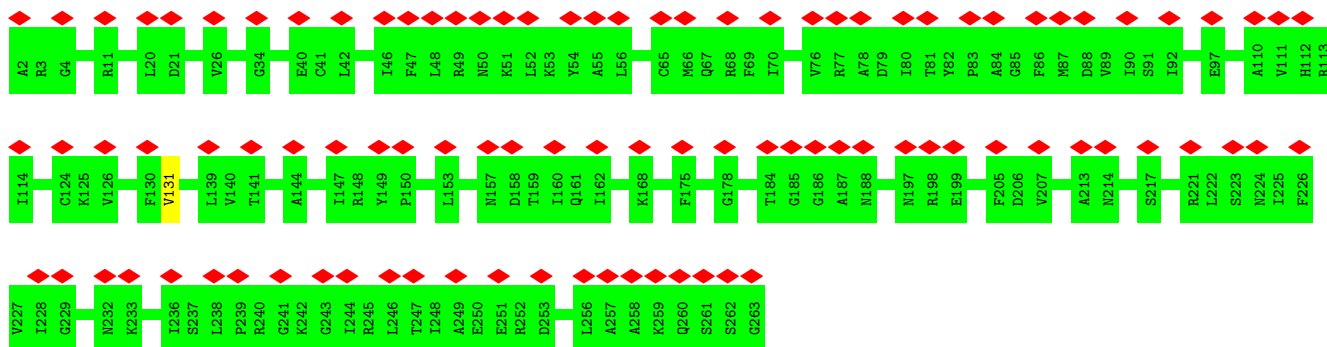


• Molecule 63: Ribosomal protein S3

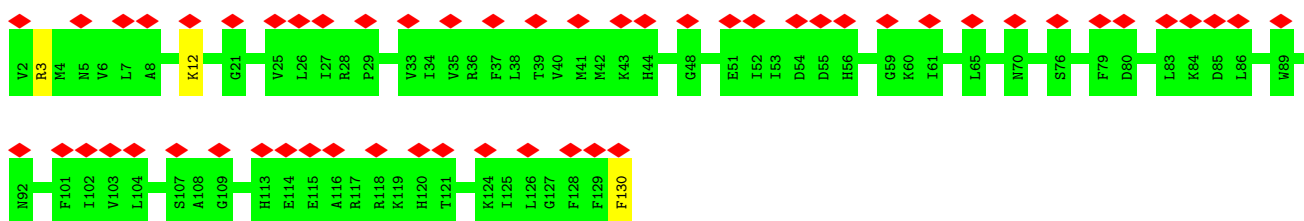
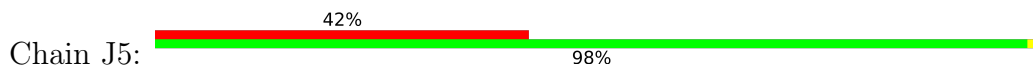


• Molecule 64: 40S ribosomal protein S4,40S ribosomal protein S4

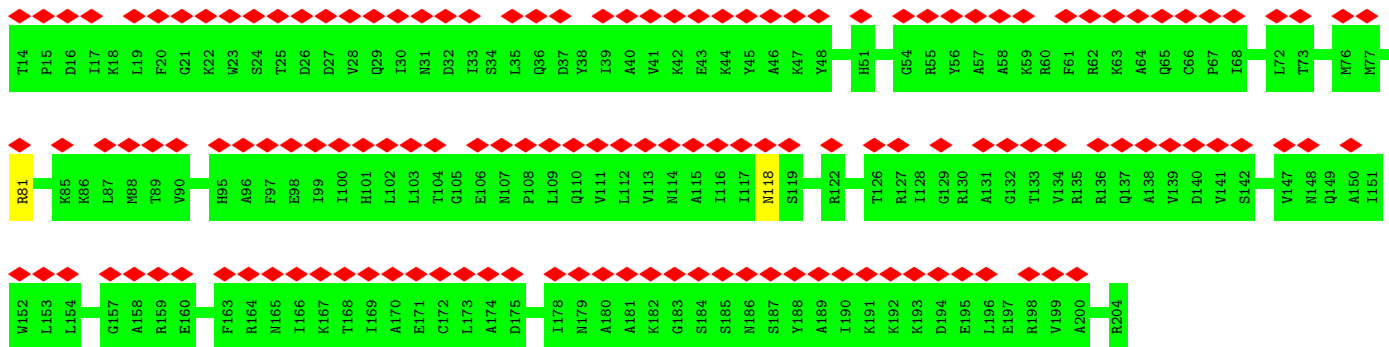
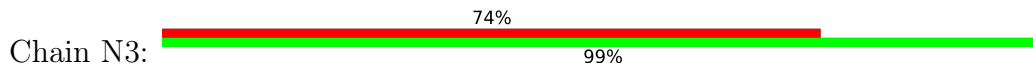




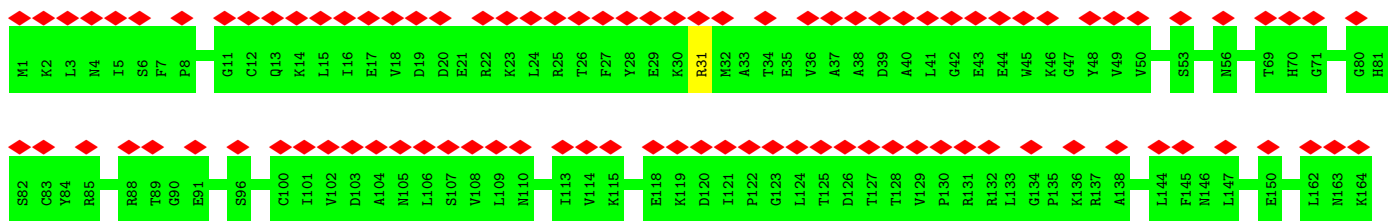
• Molecule 65: Ribosomal protein S15a



• Molecule 66: Ribosomal protein S5

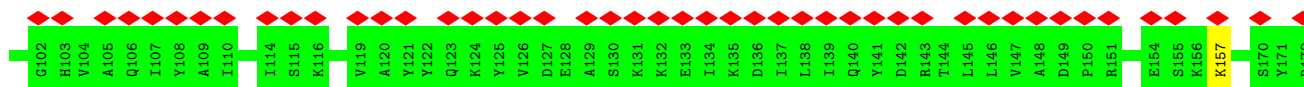
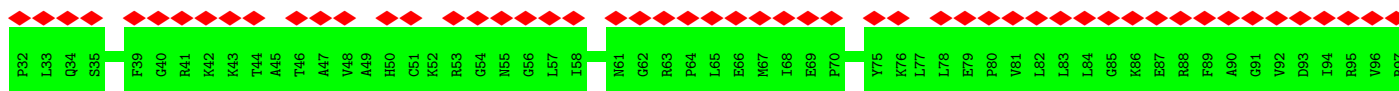
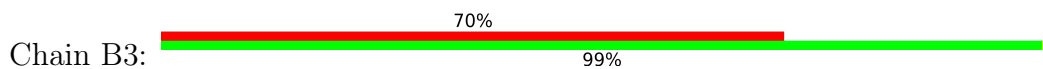


• Molecule 67: 40S ribosomal protein S6

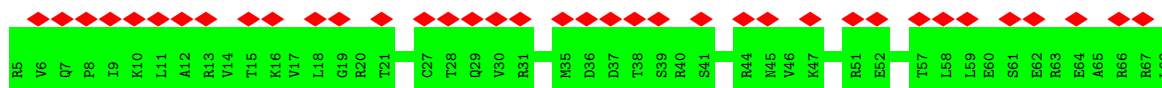




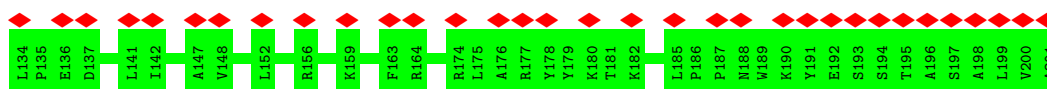
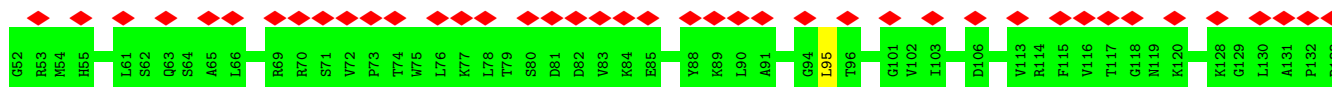
- Molecule 68: Uncharacterized protein



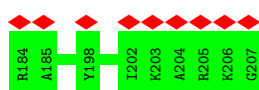
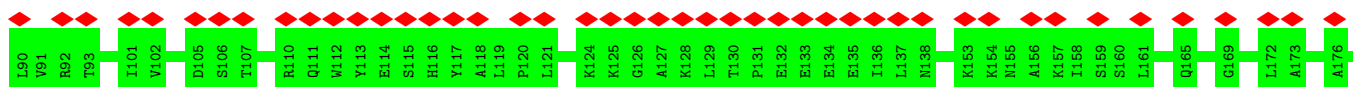
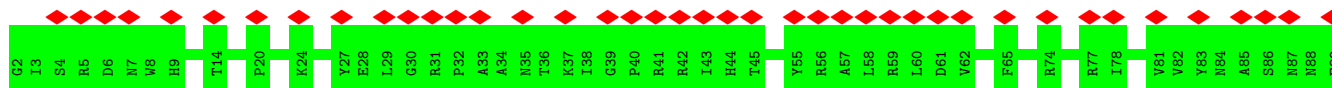
- Molecule 69: ribosomal protein eS28



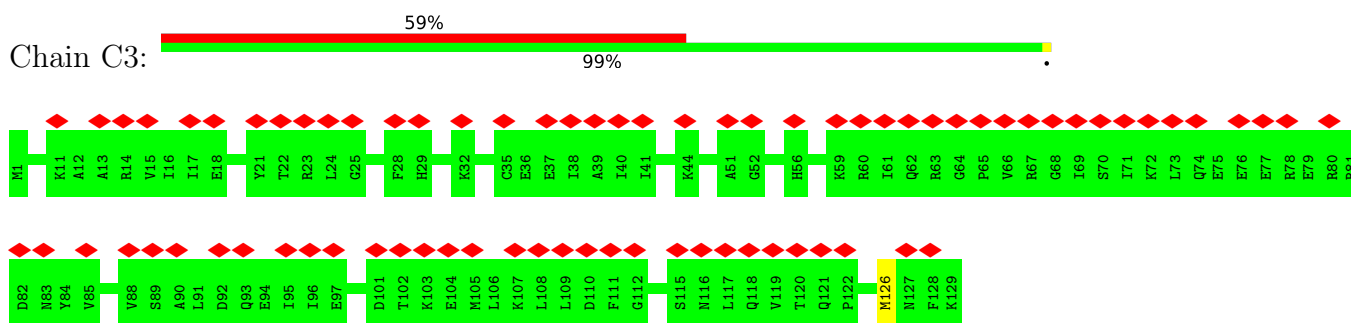
- Molecule 70: ribosomal protein uS15



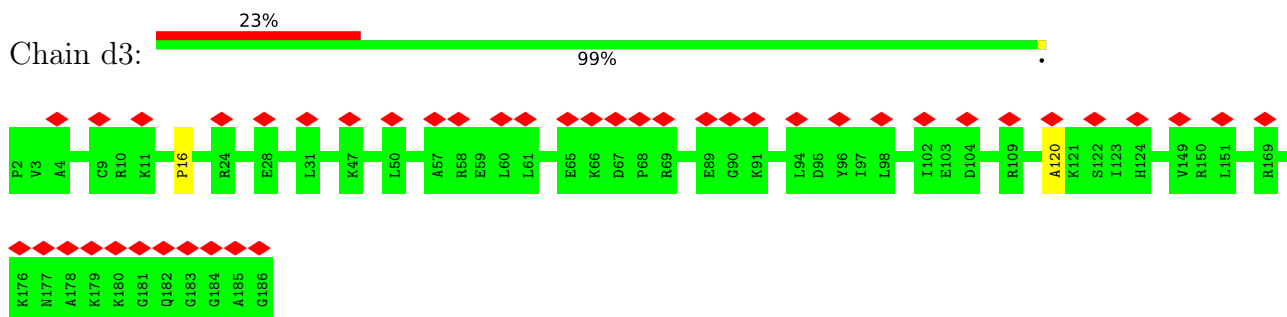
- Molecule 71: 40S ribosomal protein S8



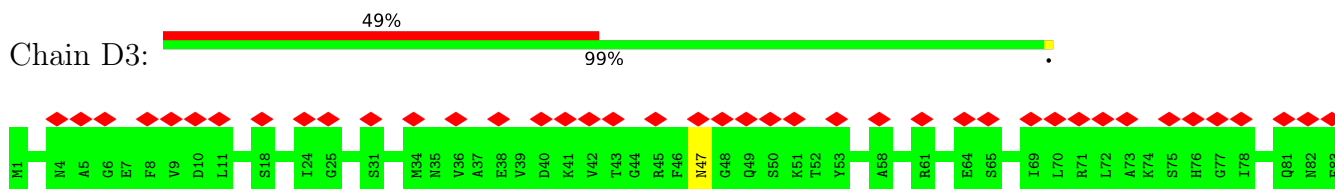
- Molecule 72: Uncharacterized protein



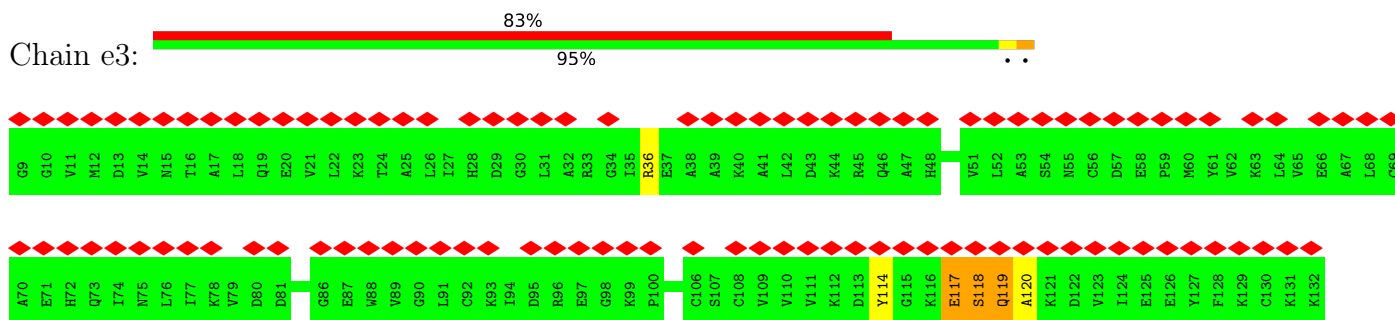
- Molecule 73: Ribosomal protein S9 (Predicted)



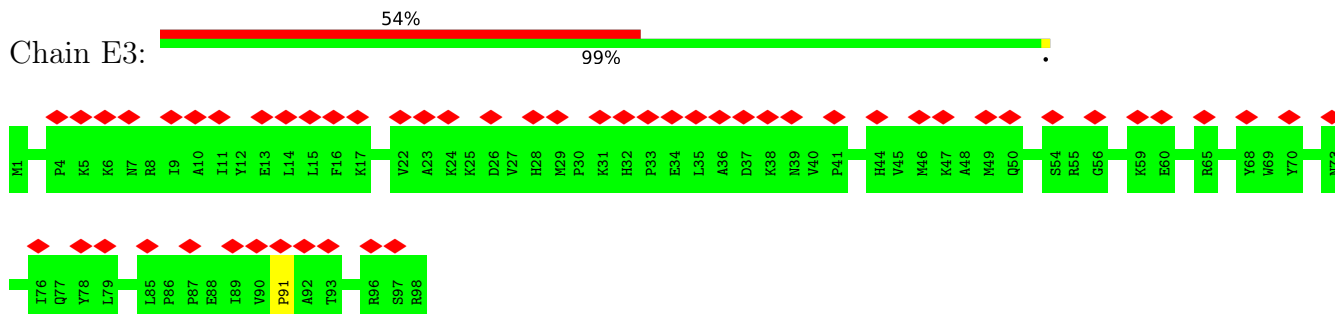
- Molecule 74: 40S RIBOSOMAL PROTEIN ES21



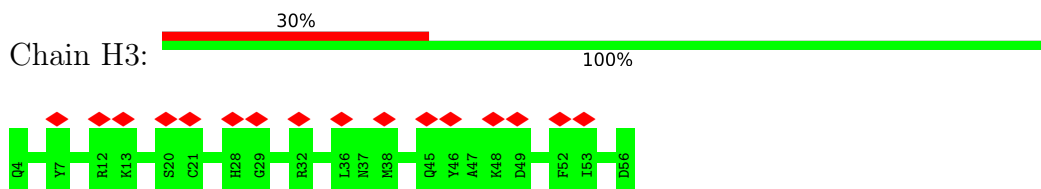
- Molecule 75: 40S ribosomal protein S12



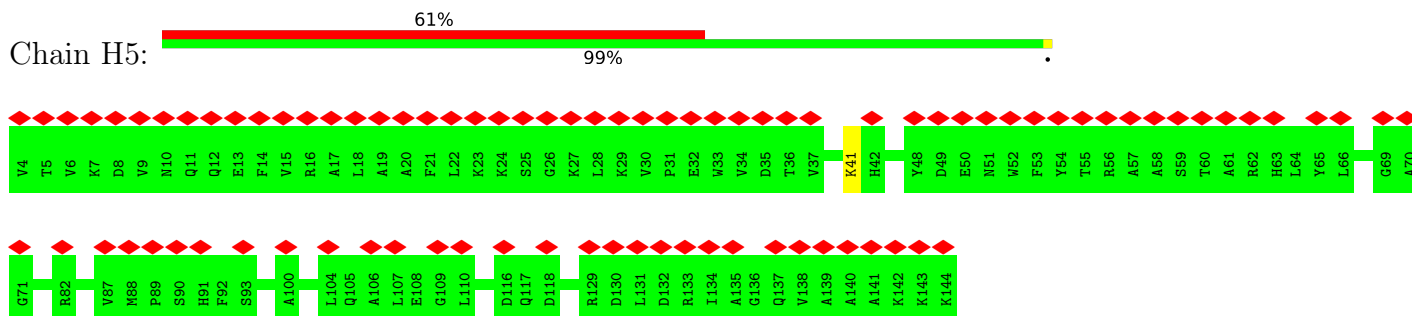
- Molecule 76: S10\_ plectin domain-containing protein



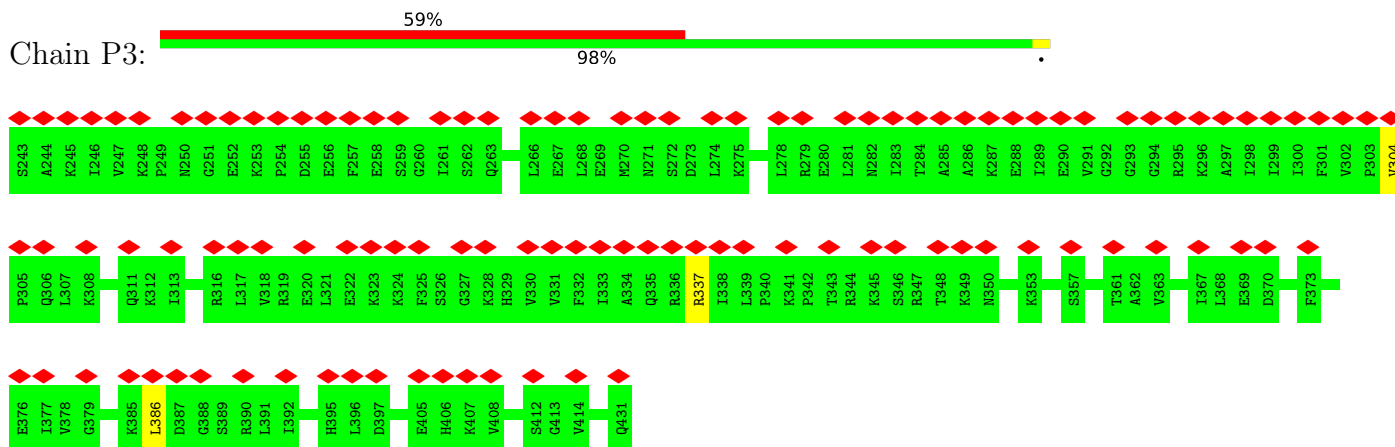
- Molecule 77: ribosomal protein uS14



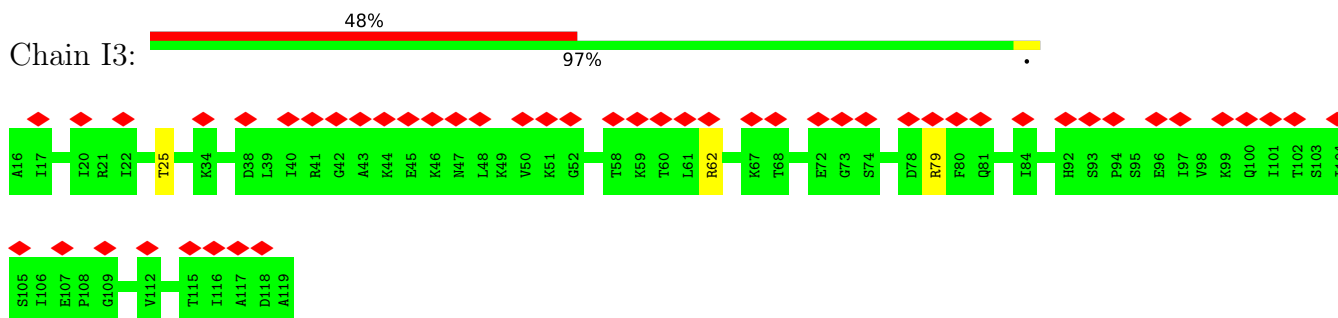
- Molecule 78: Uncharacterized protein



- Molecule 79: 40S RIBOSOMAL PROTEIN ES7



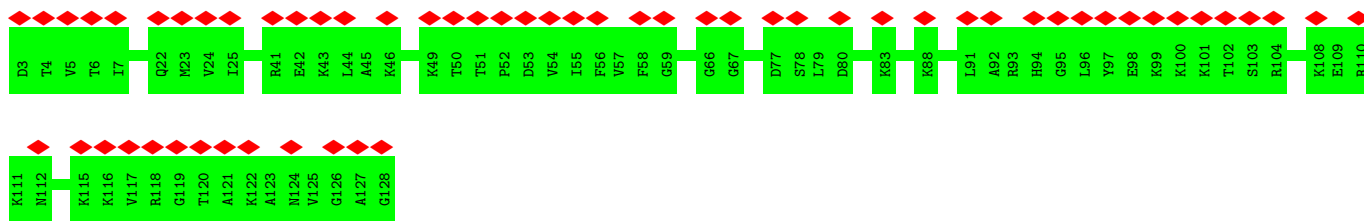
- Molecule 80: Ribosomal\_S10 domain-containing protein



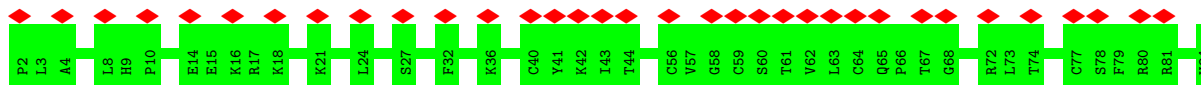
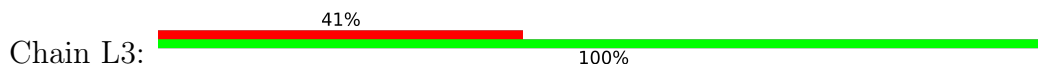
- Molecule 81: 40S ribosomal protein S24



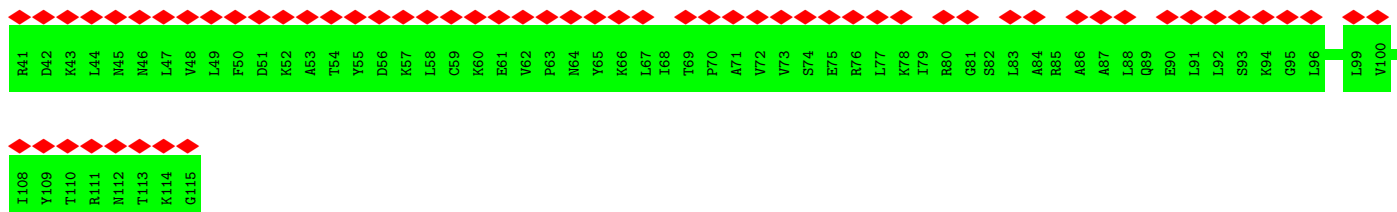
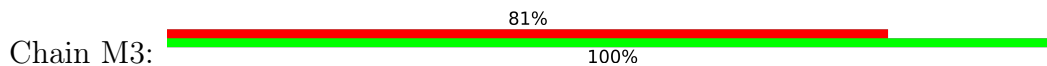




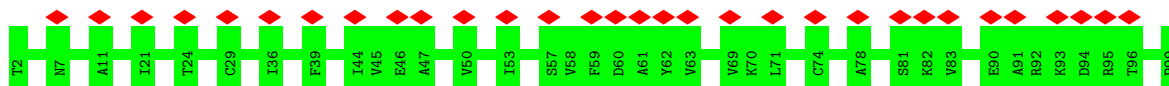
- Molecule 82: 40S ribosomal protein S27



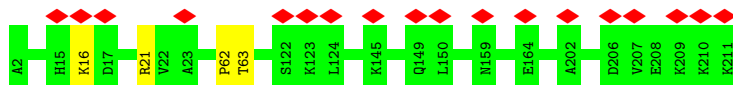
- Molecule 83: ribosomal protein eS25



- Molecule 84: 40S RIBOSOMAL PROTEIN ES26



- Molecule 85: 60S ribosomal protein L13



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42135	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	0.123	Depositor
Minimum map value	-0.073	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	396.0, 396.0, 396.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	E1	0.38	0/3579	1.07	19/5560 (0.3%)
2	e2	0.77	2/91668 (0.0%)	1.07	279/143010 (0.2%)
3	h2	0.78	0/3701	1.03	8/5766 (0.1%)
4	d2	0.69	0/2858	0.95	2/4455 (0.0%)
5	p2	0.41	0/574	0.55	0/761
6	k2	0.44	0/993	0.60	0/1332
7	l2	0.39	0/542	0.55	0/720
8	m2	0.37	0/993	0.51	0/1334
9	o2	0.41	0/1133	0.54	0/1504
10	q2	0.50	0/1191	0.59	0/1590
11	r2	0.35	0/620	0.55	0/818
12	t2	0.43	0/2938	0.56	0/3946
13	u2	0.43	0/904	0.56	0/1216
14	v2	0.45	0/1072	0.55	0/1429
15	w2	0.46	0/1662	0.56	0/2222
16	x2	0.49	0/895	0.63	1/1198 (0.1%)
17	y2	0.49	0/917	0.60	0/1220
18	92	0.46	0/1907	0.58	0/2556
19	A2	0.37	0/1021	0.51	0/1348
20	B2	0.36	0/842	0.51	0/1112
21	C2	0.51	0/721	0.57	0/952
22	D2	0.42	0/454	0.58	0/599
23	E2	0.39	0/435	0.52	0/575
24	F2	0.43	0/865	0.60	0/1140
25	G2	0.41	0/2433	0.53	0/3257
26	H2	0.50	0/1269	0.58	0/1700
27	I2	0.45	0/718	0.57	0/953
28	J2	0.42	0/1018	0.55	0/1364
29	K2	0.30	0/1548	0.57	0/2088
30	L2	0.50	0/853	0.54	0/1137
31	M2	0.28	0/1198	0.59	0/1611
32	R2	0.38	0/292	0.51	0/388

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	S2	0.47	0/1537	0.60	0/2052
34	T2	0.37	0/1646	0.60	0/2213
35	U2	0.49	0/1911	0.59	0/2549
36	V2	0.36	0/1965	0.52	0/2644
37	W2	0.40	0/1536	0.55	0/2063
38	X2	0.43	0/841	0.55	0/1123
39	Y2	0.35	0/1377	0.55	0/1841
40	O2	0.39	0/1159	0.55	0/1547
41	12	0.49	0/1746	0.57	0/2338
42	22	0.40	0/1130	0.54	0/1507
43	32	0.38	0/1525	0.54	0/2013
44	42	0.30	0/1772	0.62	1/2375 (0.0%)
45	52	0.46	0/3241	0.57	1/4339 (0.0%)
46	62	0.44	0/1493	0.57	1/2003 (0.0%)
47	72	0.46	0/1326	0.59	0/1770
48	82	0.36	0/823	0.54	0/1103
49	K3	0.44	0/42945	1.09	188/66942 (0.3%)
50	s3	0.28	0/354	0.55	0/462
51	13	0.38	0/743	0.56	0/995
52	Q3	0.32	0/538	0.65	1/713 (0.1%)
53	G3	0.31	0/1269	0.57	0/1696
54	G5	0.30	0/1158	0.58	0/1548
55	a3	0.30	0/2494	0.55	0/3394
56	a5	0.30	0/1029	0.55	0/1380
57	A3	0.33	0/1080	0.58	1/1437 (0.1%)
58	T3	0.32	0/1117	0.54	0/1490
59	U3	0.30	0/1682	0.52	0/2286
60	V3	0.33	0/1757	0.58	0/2350
61	W3	0.32	0/1727	0.55	0/2332
62	X3	0.32	0/224	0.48	0/284
63	Y3	0.31	0/1793	0.57	0/2412
64	j3	0.29	0/2117	0.54	0/2846
65	J5	1.97	6/1051 (0.6%)	1.69	8/1406 (0.6%)
66	N3	0.29	0/1531	0.56	0/2059
67	b3	0.28	0/1947	0.54	0/2590
68	B3	0.29	0/1142	0.56	0/1528
69	f3	0.29	0/509	0.58	0/680
70	F3	0.31	0/1232	0.56	1/1656 (0.1%)
71	c3	0.31	0/1716	0.56	0/2287
72	C3	0.33	0/1061	0.61	0/1421
73	d3	0.47	1/1551 (0.1%)	0.72	3/2069 (0.1%)
74	D3	0.31	0/639	0.51	0/855
75	e3	0.28	0/968	0.56	0/1296

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	E3	0.29	0/852	0.52	0/1147
77	H3	0.30	0/455	0.51	0/603
78	H5	0.28	0/1133	0.49	0/1517
79	P3	0.30	0/1545	0.59	0/2068
80	I3	0.28	0/832	0.58	0/1117
81	I5	0.28	0/1041	0.54	0/1382
82	L3	0.28	0/665	0.51	0/891
83	M3	0.28	0/605	0.54	0/810
84	O3	0.35	0/795	0.56	0/1065
85	a7	0.38	0/1733	0.55	0/2316
All	All	0.59	9/241872 (0.0%)	0.93	514/355671 (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
9	o2	0	1
11	r2	0	1
24	F2	0	1
25	G2	0	2
30	L2	0	1
31	M2	0	2
34	T2	0	2
35	U2	0	2
37	W2	0	1
42	22	0	1
44	42	0	2
45	52	0	2
46	62	0	1
47	72	0	2
50	s3	0	1
52	Q3	0	1
53	G3	0	1
54	G5	0	1
56	a5	0	1
59	U3	0	1
72	C3	0	1
73	d3	0	1
74	D3	0	1
75	e3	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
79	P3	0	3
80	I3	0	1
85	a7	0	2
All	All	0	40

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	J5	130	PHE	CD2-CE2	36.12	2.11	1.39
65	J5	130	PHE	CD1-CE1	35.40	2.10	1.39
65	J5	130	PHE	CE2-CZ	-22.43	0.94	1.37
65	J5	130	PHE	CE1-CZ	-22.30	0.94	1.37
65	J5	130	PHE	CG-CD1	-14.61	1.16	1.38

The worst 5 of 514 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	J5	130	PHE	CE1-CZ-CE2	-28.57	68.58	120.00
65	J5	130	PHE	CD1-CG-CD2	-23.15	88.21	118.30
65	J5	130	PHE	CG-CD2-CE2	-22.61	95.93	120.80
65	J5	130	PHE	CB-CG-CD2	22.19	136.33	120.80
65	J5	130	PHE	CG-CD1-CE1	-22.03	96.57	120.80

There are no chirality outliers.

5 of 40 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
24	F2	32	SER	Peptide
25	G2	265	ARG	Peptide
25	G2	267	ASN	Peptide
9	o2	115	ARG	Peptide
11	r2	51	LYS	Peptide

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	p2	67/69 (97%)	59 (88%)	8 (12%)	0	100	100
6	k2	129/131 (98%)	111 (86%)	18 (14%)	0	100	100
7	l2	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
8	m2	117/119 (98%)	105 (90%)	12 (10%)	0	100	100
9	o2	132/134 (98%)	112 (85%)	20 (15%)	0	100	100
10	q2	145/147 (99%)	119 (82%)	26 (18%)	0	100	100
11	r2	73/75 (97%)	57 (78%)	16 (22%)	0	100	100
12	t2	360/362 (99%)	299 (83%)	60 (17%)	1 (0%)	41	75
13	u2	105/107 (98%)	89 (85%)	16 (15%)	0	100	100
14	v2	126/128 (98%)	105 (83%)	21 (17%)	0	100	100
15	w2	197/199 (99%)	177 (90%)	20 (10%)	0	100	100
16	x2	107/109 (98%)	89 (83%)	18 (17%)	0	100	100
17	y2	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
18	92	242/244 (99%)	210 (87%)	31 (13%)	1 (0%)	34	71
19	A2	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
20	B2	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
21	C2	84/86 (98%)	69 (82%)	15 (18%)	0	100	100
22	D2	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
23	E2	50/52 (96%)	45 (90%)	5 (10%)	0	100	100
24	F2	102/104 (98%)	91 (89%)	11 (11%)	0	100	100
25	G2	290/292 (99%)	250 (86%)	40 (14%)	0	100	100
26	H2	151/153 (99%)	130 (86%)	21 (14%)	0	100	100
27	I2	89/91 (98%)	81 (91%)	8 (9%)	0	100	100
28	J2	123/125 (98%)	106 (86%)	17 (14%)	0	100	100
29	K2	196/198 (99%)	157 (80%)	39 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	L2	100/102 (98%)	87 (87%)	13 (13%)	0	100	100
31	M2	150/163 (92%)	106 (71%)	43 (29%)	1 (1%)	22	61
32	R2	33/35 (94%)	25 (76%)	8 (24%)	0	100	100
33	S2	185/187 (99%)	153 (83%)	32 (17%)	0	100	100
34	T2	199/201 (99%)	155 (78%)	43 (22%)	1 (0%)	29	68
35	U2	223/225 (99%)	203 (91%)	20 (9%)	0	100	100
36	V2	239/241 (99%)	225 (94%)	14 (6%)	0	100	100
37	W2	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
38	X2	100/102 (98%)	80 (80%)	20 (20%)	0	100	100
39	Y2	167/169 (99%)	147 (88%)	20 (12%)	0	100	100
40	O2	136/138 (99%)	120 (88%)	16 (12%)	0	100	100
41	I2	201/203 (99%)	175 (87%)	26 (13%)	0	100	100
42	J2	133/135 (98%)	112 (84%)	21 (16%)	0	100	100
43	K2	178/180 (99%)	172 (97%)	6 (3%)	0	100	100
44	L2	215/217 (99%)	152 (71%)	62 (29%)	1 (0%)	29	68
45	M2	392/394 (100%)	338 (86%)	53 (14%)	1 (0%)	41	75
46	N2	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
47	O2	157/159 (99%)	127 (81%)	29 (18%)	1 (1%)	25	64
48	P2	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
50	s3	41/43 (95%)	30 (73%)	11 (27%)	0	100	100
51	t3	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
52	Q3	59/188 (31%)	48 (81%)	11 (19%)	0	100	100
53	G3	151/153 (99%)	116 (77%)	35 (23%)	0	100	100
54	G5	135/137 (98%)	114 (84%)	19 (14%)	2 (2%)	10	47
55	a3	311/313 (99%)	255 (82%)	56 (18%)	0	100	100
56	a5	134/136 (98%)	109 (81%)	25 (19%)	0	100	100
57	A3	125/127 (98%)	107 (86%)	18 (14%)	0	100	100
58	T3	139/141 (99%)	115 (83%)	24 (17%)	0	100	100
59	U3	206/208 (99%)	185 (90%)	21 (10%)	0	100	100
60	V3	211/213 (99%)	179 (85%)	32 (15%)	0	100	100
61	W3	216/218 (99%)	187 (87%)	29 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	X3	21/23 (91%)	21 (100%)	0	0	100	100
63	Y3	225/227 (99%)	195 (87%)	30 (13%)	0	100	100
64	j3	260/262 (99%)	215 (83%)	44 (17%)	1 (0%)	34	71
65	J5	127/129 (98%)	113 (89%)	14 (11%)	0	100	100
66	N3	189/191 (99%)	165 (87%)	24 (13%)	0	100	100
67	b3	235/237 (99%)	195 (83%)	40 (17%)	0	100	100
68	B3	139/141 (99%)	122 (88%)	17 (12%)	0	100	100
69	f3	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
70	F3	148/150 (99%)	123 (83%)	25 (17%)	0	100	100
71	c3	204/206 (99%)	176 (86%)	28 (14%)	0	100	100
72	C3	127/129 (98%)	102 (80%)	25 (20%)	0	100	100
73	d3	183/185 (99%)	154 (84%)	29 (16%)	0	100	100
74	D3	81/83 (98%)	72 (89%)	9 (11%)	0	100	100
75	e3	122/124 (98%)	95 (78%)	23 (19%)	4 (3%)	4	31
76	E3	96/98 (98%)	80 (83%)	15 (16%)	1 (1%)	15	55
77	H3	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
78	H5	139/141 (99%)	122 (88%)	16 (12%)	1 (1%)	22	61
79	P3	187/189 (99%)	158 (84%)	29 (16%)	0	100	100
80	I3	102/104 (98%)	81 (79%)	21 (21%)	0	100	100
81	I5	124/126 (98%)	111 (90%)	13 (10%)	0	100	100
82	L3	81/83 (98%)	67 (83%)	14 (17%)	0	100	100
83	M3	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
84	O3	96/98 (98%)	78 (81%)	18 (19%)	0	100	100
85	a7	208/210 (99%)	179 (86%)	27 (13%)	2 (1%)	15	55
All	All	11692/11990 (98%)	9975 (85%)	1699 (14%)	18 (0%)	50	79

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	92	15	VAL
45	52	246	ARG
54	G5	101	ASN
64	j3	131	VAL
75	e3	117	GLU

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	p2	64/64 (100%)	63 (98%)	1 (2%)	62	83
6	k2	101/101 (100%)	101 (100%)	0	100	100
7	l2	55/55 (100%)	55 (100%)	0	100	100
8	m2	107/107 (100%)	106 (99%)	1 (1%)	78	90
9	o2	124/124 (100%)	124 (100%)	0	100	100
10	q2	119/119 (100%)	119 (100%)	0	100	100
11	r2	62/62 (100%)	62 (100%)	0	100	100
12	t2	302/302 (100%)	302 (100%)	0	100	100
13	u2	98/98 (100%)	98 (100%)	0	100	100
14	v2	114/114 (100%)	113 (99%)	1 (1%)	78	90
15	w2	171/171 (100%)	170 (99%)	1 (1%)	86	94
16	x2	88/88 (100%)	88 (100%)	0	100	100
17	y2	98/98 (100%)	98 (100%)	0	100	100
18	92	187/187 (100%)	186 (100%)	1 (0%)	88	95
19	A2	109/109 (100%)	109 (100%)	0	100	100
20	B2	86/86 (100%)	86 (100%)	0	100	100
21	C2	73/73 (100%)	73 (100%)	0	100	100
22	D2	47/47 (100%)	46 (98%)	1 (2%)	53	78
23	E2	48/48 (100%)	47 (98%)	1 (2%)	53	78
24	F2	92/92 (100%)	92 (100%)	0	100	100
25	G2	247/247 (100%)	246 (100%)	1 (0%)	91	97
26	H2	134/134 (100%)	134 (100%)	0	100	100
27	I2	74/74 (100%)	74 (100%)	0	100	100
28	J2	109/109 (100%)	109 (100%)	0	100	100
29	K2	166/166 (100%)	166 (100%)	0	100	100
30	L2	89/89 (100%)	88 (99%)	1 (1%)	73	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	M2	131/136 (96%)	130 (99%)	1 (1%)	81	91
32	R2	29/29 (100%)	29 (100%)	0	100	100
33	S2	164/164 (100%)	164 (100%)	0	100	100
34	T2	180/180 (100%)	180 (100%)	0	100	100
35	U2	196/196 (100%)	196 (100%)	0	100	100
36	V2	205/205 (100%)	205 (100%)	0	100	100
37	W2	169/169 (100%)	167 (99%)	2 (1%)	71	87
38	X2	85/85 (100%)	85 (100%)	0	100	100
39	Y2	142/142 (100%)	142 (100%)	0	100	100
40	02	117/117 (100%)	116 (99%)	1 (1%)	78	90
41	12	171/171 (100%)	170 (99%)	1 (1%)	86	94
42	22	117/117 (100%)	117 (100%)	0	100	100
43	32	159/159 (100%)	158 (99%)	1 (1%)	86	94
44	42	196/196 (100%)	196 (100%)	0	100	100
45	52	342/342 (100%)	340 (99%)	2 (1%)	86	94
46	62	156/156 (100%)	155 (99%)	1 (1%)	86	94
47	72	139/139 (100%)	139 (100%)	0	100	100
48	82	89/89 (100%)	89 (100%)	0	100	100
50	s3	35/35 (100%)	35 (100%)	0	100	100
51	13	80/80 (100%)	80 (100%)	0	100	100
52	Q3	59/154 (38%)	59 (100%)	0	100	100
53	G3	137/137 (100%)	135 (98%)	2 (2%)	65	84
54	G5	119/119 (100%)	118 (99%)	1 (1%)	81	91
55	a3	272/272 (100%)	271 (100%)	1 (0%)	91	97
56	a5	106/106 (100%)	106 (100%)	0	100	100
57	A3	116/116 (100%)	116 (100%)	0	100	100
58	T3	113/113 (100%)	112 (99%)	1 (1%)	78	90
59	U3	175/175 (100%)	175 (100%)	0	100	100
60	V3	194/194 (100%)	193 (100%)	1 (0%)	88	95
61	W3	184/184 (100%)	184 (100%)	0	100	100
62	X3	22/22 (100%)	22 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	Y3	190/190 (100%)	188 (99%)	2 (1%)	73	88
64	j3	224/224 (100%)	224 (100%)	0	100	100
65	J5	112/112 (100%)	110 (98%)	2 (2%)	59	81
66	N3	161/161 (100%)	159 (99%)	2 (1%)	71	87
67	b3	207/207 (100%)	206 (100%)	1 (0%)	88	95
68	B3	117/117 (100%)	116 (99%)	1 (1%)	78	90
69	f3	57/57 (100%)	57 (100%)	0	100	100
70	F3	130/130 (100%)	130 (100%)	0	100	100
71	c3	178/178 (100%)	178 (100%)	0	100	100
72	C3	117/117 (100%)	117 (100%)	0	100	100
73	d3	161/161 (100%)	161 (100%)	0	100	100
74	D3	68/68 (100%)	68 (100%)	0	100	100
75	e3	104/104 (100%)	103 (99%)	1 (1%)	76	88
76	E3	89/89 (100%)	89 (100%)	0	100	100
77	H3	47/47 (100%)	47 (100%)	0	100	100
78	H5	113/113 (100%)	113 (100%)	0	100	100
79	P3	169/169 (100%)	169 (100%)	0	100	100
80	I3	94/94 (100%)	92 (98%)	2 (2%)	53	78
81	I5	108/108 (100%)	108 (100%)	0	100	100
82	L3	75/75 (100%)	75 (100%)	0	100	100
83	M3	66/66 (100%)	66 (100%)	0	100	100
84	O3	85/85 (100%)	85 (100%)	0	100	100
85	a7	175/175 (100%)	175 (100%)	0	100	100
All	All	10210/10310 (99%)	10175 (100%)	35 (0%)	92	97

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
66	N3	81	ARG
66	N3	118	ASN
75	e3	36	ARG
40	O2	125	ASN
37	W2	135	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
46	62	77	ASN
80	I3	92	HIS
53	G3	112	HIS
79	P3	314	GLN
70	F3	86	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E1	152/153 (99%)	107 (70%)	13 (8%)
2	e2	3816/3825 (99%)	1178 (30%)	0
3	h2	155/156 (99%)	46 (29%)	0
4	d2	119/120 (99%)	21 (17%)	0
49	K3	1797/1801 (99%)	767 (42%)	24 (1%)
All	All	6039/6055 (99%)	2119 (35%)	37 (0%)

5 of 2119 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	E1	6278	A
1	E1	6279	A
1	E1	6281	C
1	E1	6282	A
1	E1	6283	U

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	K3	919	A
49	K3	1579	A
49	K3	1248	U
49	K3	1344	A
1	E1	6393	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.

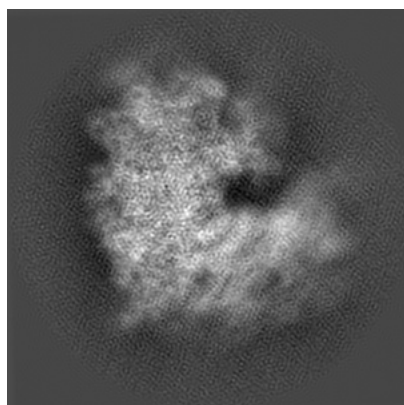
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11590. These allow visual inspection of the internal detail of the map and identification of artifacts.

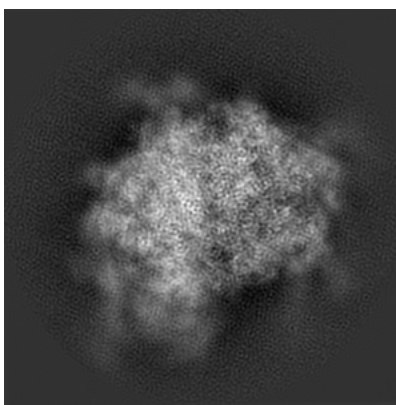
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

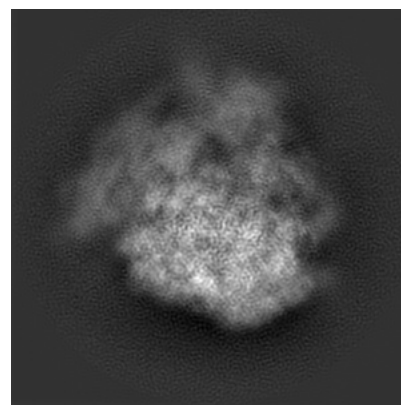
#### 6.1.1 Primary map



X



Y

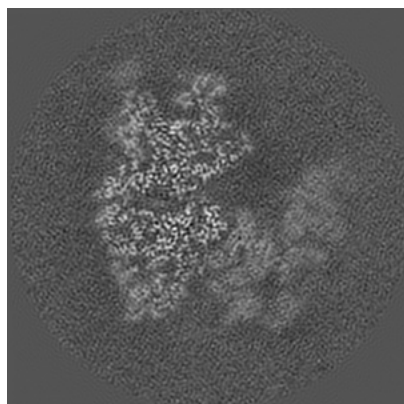


Z

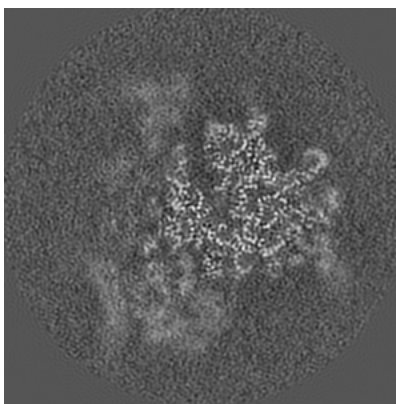
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

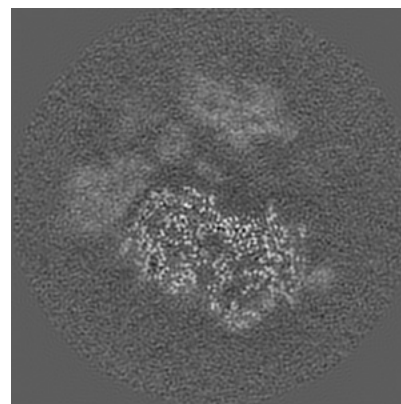
#### 6.2.1 Primary map



X Index: 180



Y Index: 180

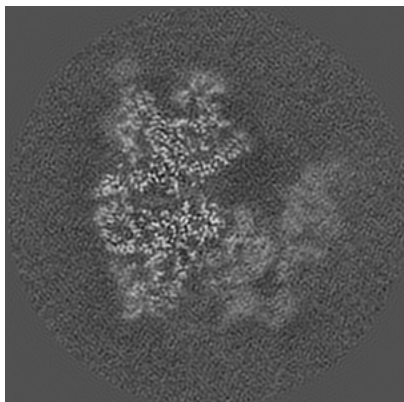


Z Index: 180

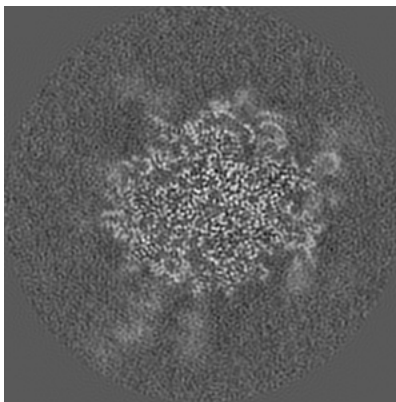
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

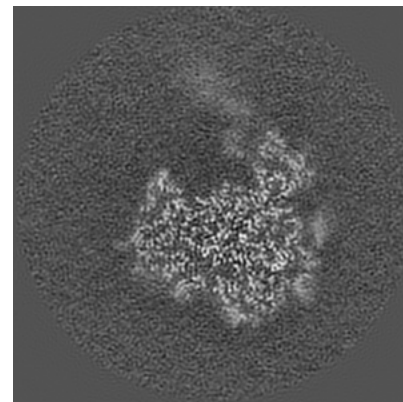
### 6.3.1 Primary map



X Index: 179



Y Index: 158

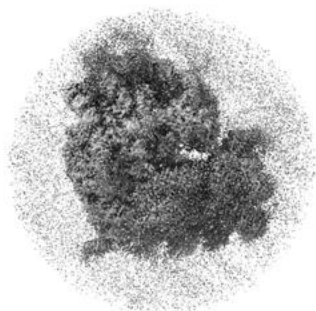


Z Index: 212

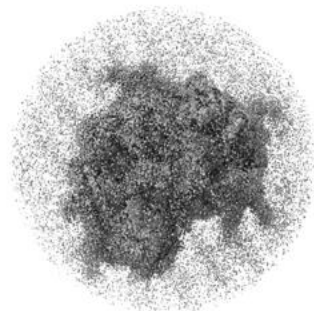
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

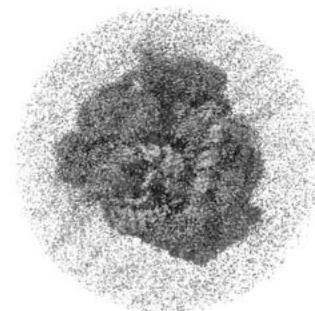
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



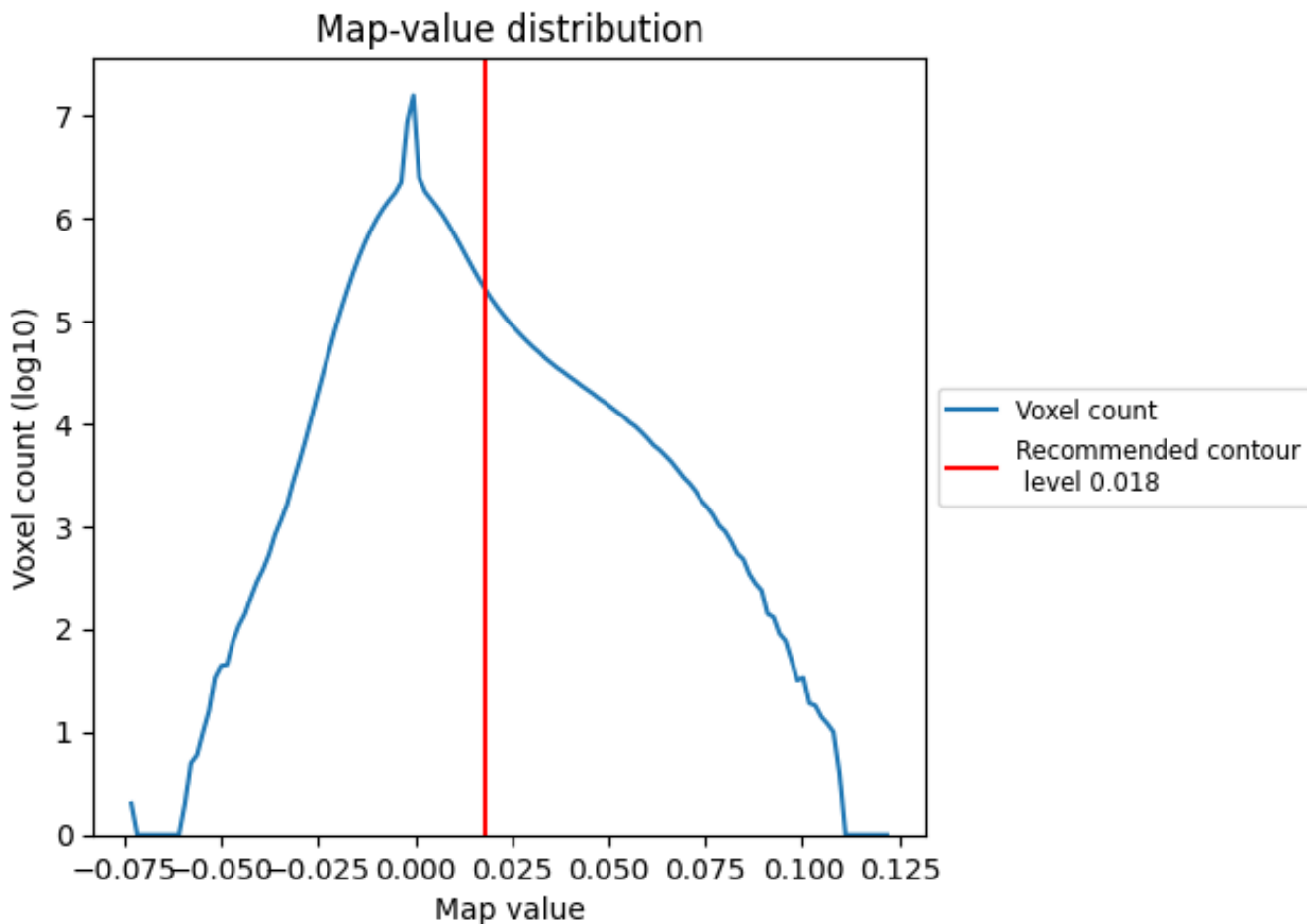
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

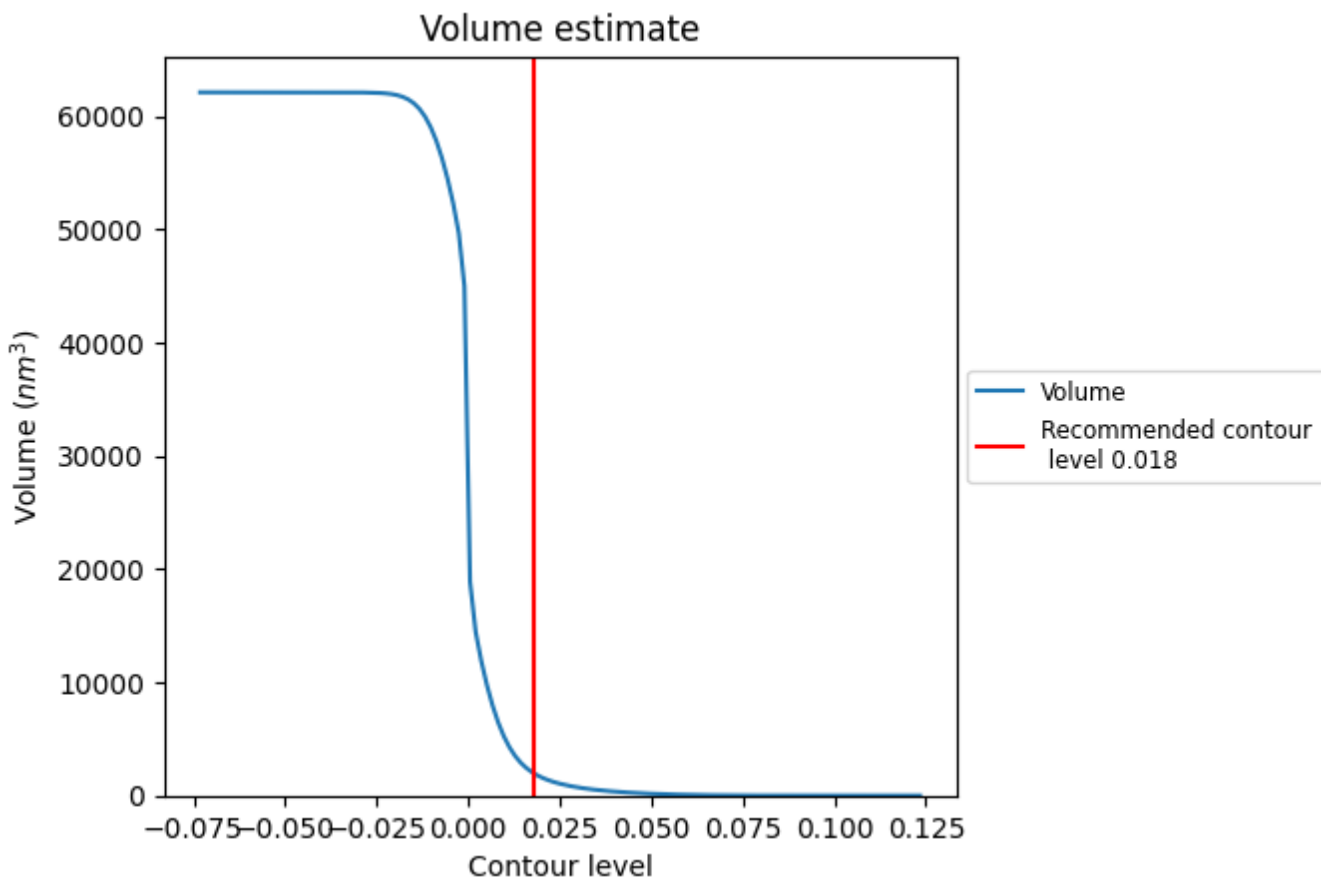
This section contains the results of statistical analysis of the map.

### 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.

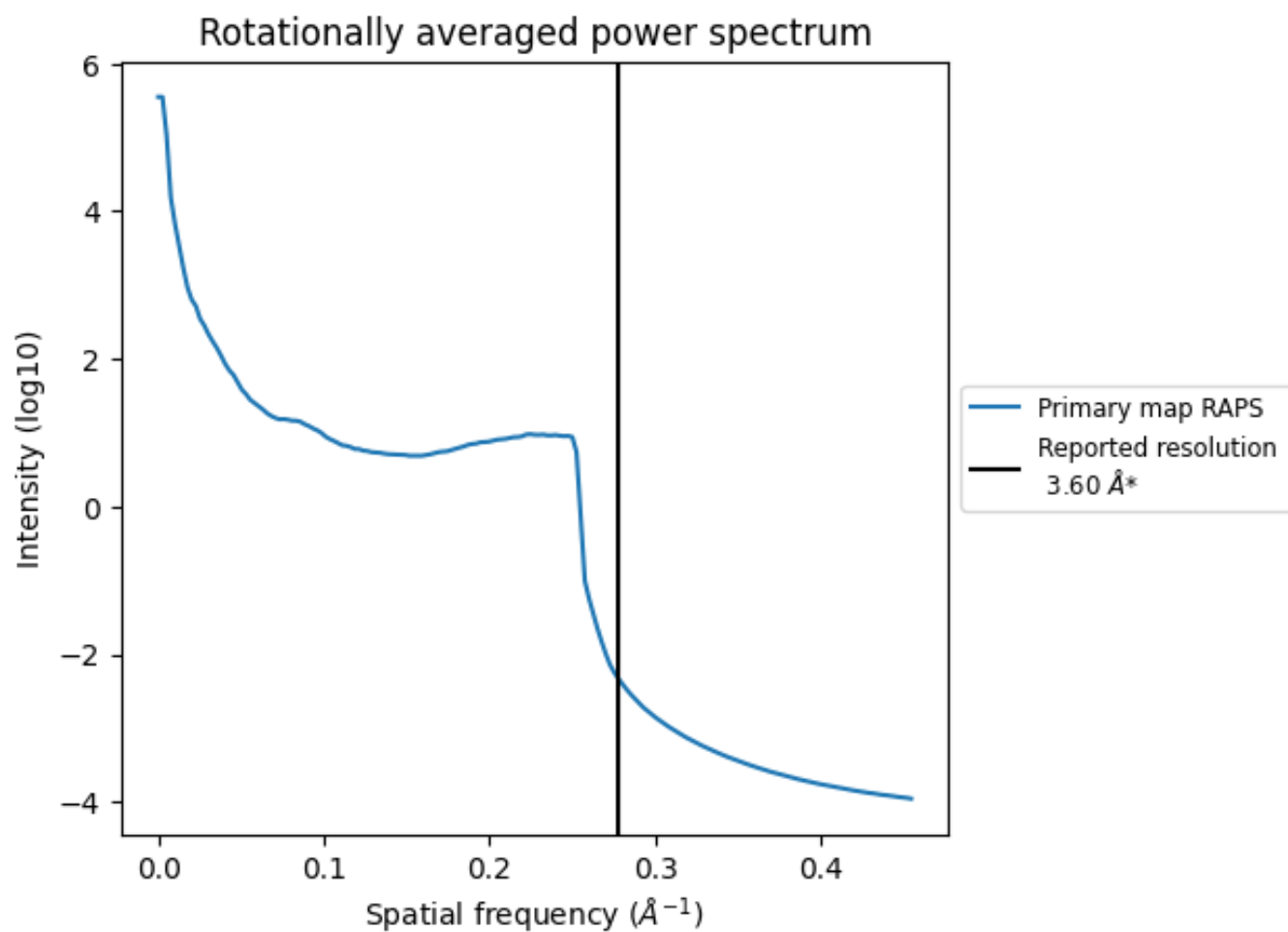
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1960 nm<sup>3</sup>; this corresponds to an approximate mass of 1770 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 0.278 Å<sup>-1</sup>

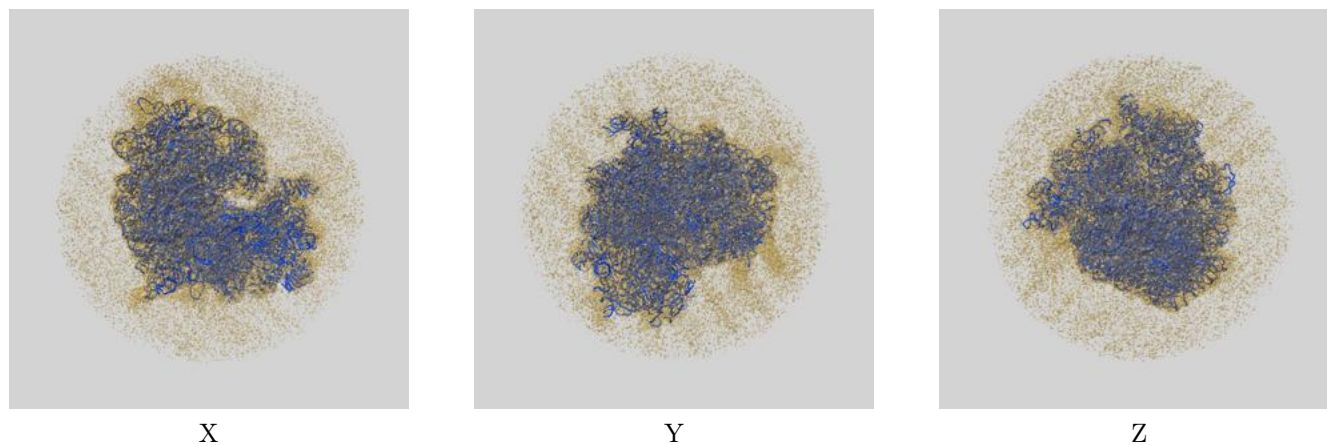
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

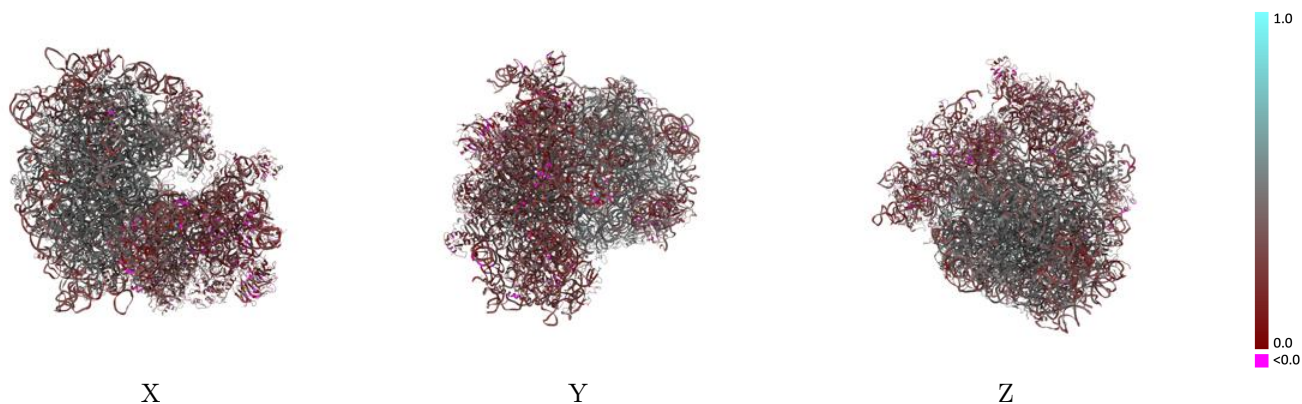
This section contains information regarding the fit between EMDB map EMD-11590 and PDB model 7A01. Per-residue inclusion information can be found in section 3 on page 21.

### 9.1 Map-model overlay [i](#)



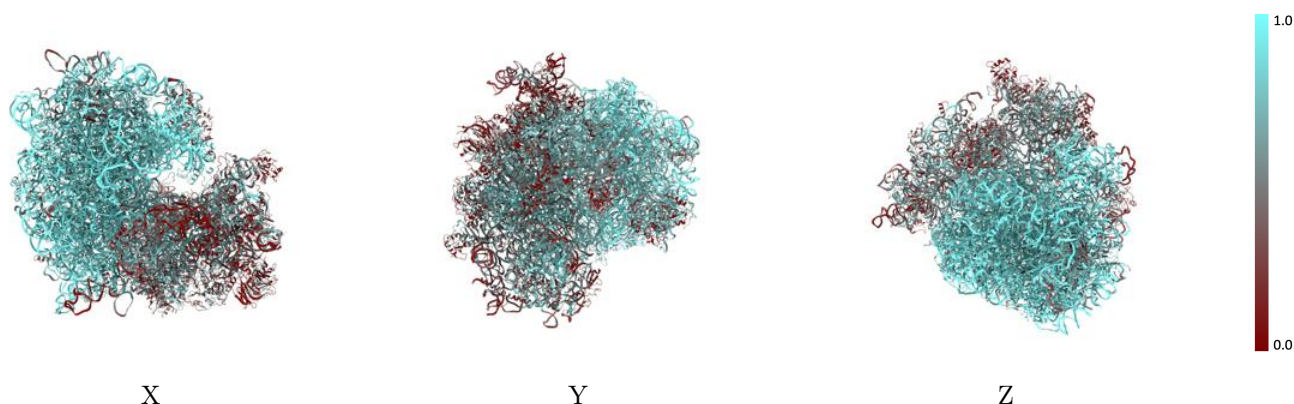
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



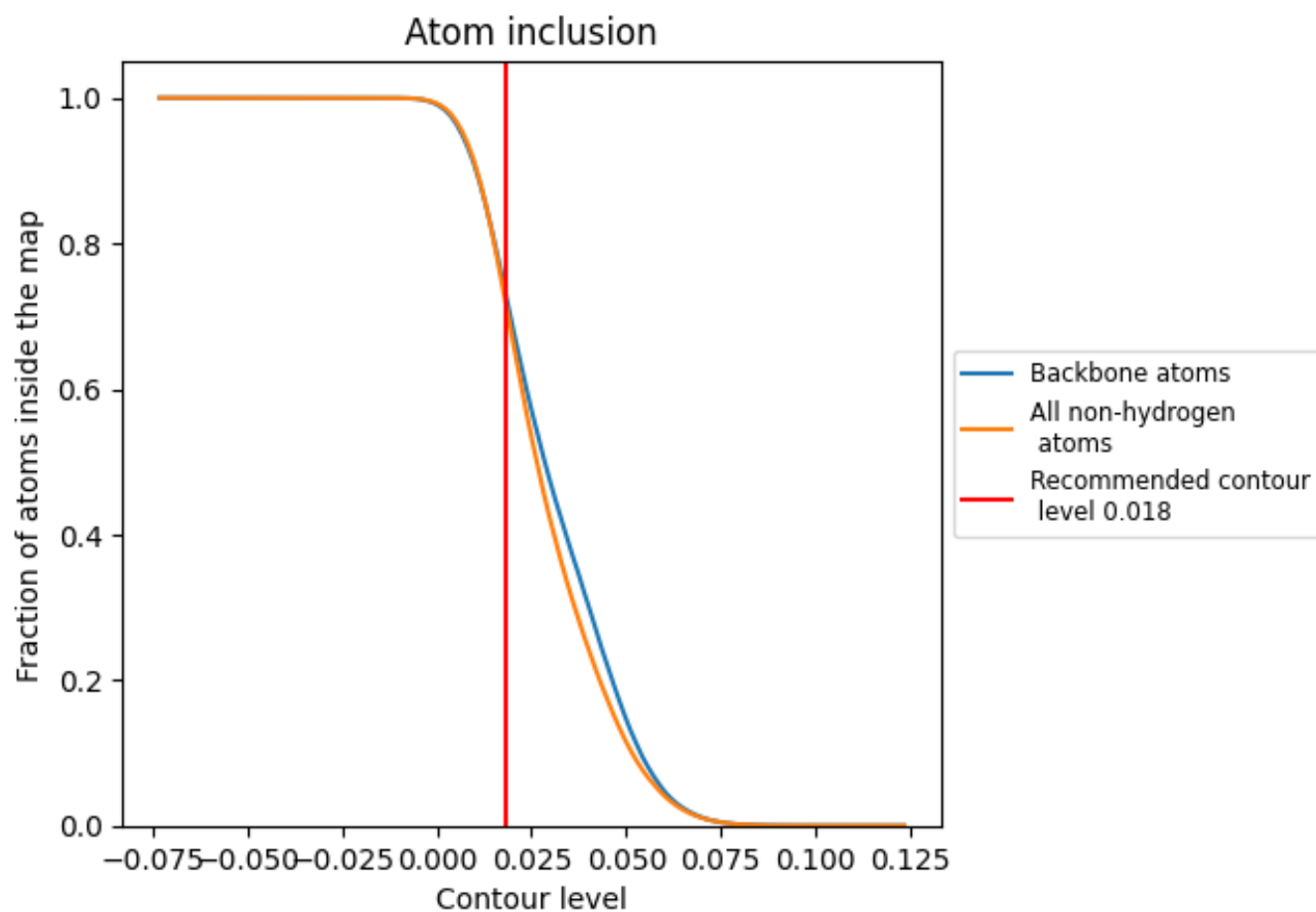
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).

## 9.4 Atom inclusion [i](#)









































































At the recommended contour level, 73% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.



## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7227	 0.3700
02	 0.8764	 0.4520
12	 0.8605	 0.4890
13	 0.8366	 0.4510
22	 0.8583	 0.4430
32	 0.7982	 0.4470
42	 0.2700	 0.2610
52	 0.8666	 0.4770
62	 0.8601	 0.4850
72	 0.8187	 0.4820
82	 0.8407	 0.4270
92	 0.8562	 0.5050
A2	 0.8284	 0.4600
A3	 0.4625	 0.2890
B2	 0.8181	 0.4510
B3	 0.2904	 0.2470
C2	 0.9050	 0.5190
C3	 0.3529	 0.2680
D2	 0.8818	 0.4960
D3	 0.4473	 0.3090
E1	 0.2154	 0.2500
E2	 0.8317	 0.4760
E3	 0.3809	 0.2650
F2	 0.8041	 0.4810
F3	 0.4420	 0.3290
G2	 0.8540	 0.4180
G3	 0.4798	 0.3360
G5	 0.4011	 0.2980
H2	 0.8641	 0.4860
H3	 0.5444	 0.2900
H5	 0.3420	 0.2630
I2	 0.8244	 0.4900
I3	 0.4582	 0.2810
I5	 0.4588	 0.2680
J2	 0.8580	 0.4580





















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Chain	Atom inclusion	Q-score
J5	0.4634	0.3290
K2	0.2517	0.2480
K3	0.6095	0.2730
L2	0.8211	0.4950
L3	0.4867	0.3230
M2	0.2263	0.2640
M3	0.1747	0.2390
N3	0.2595	0.2620
O3	0.5438	0.3390
P3	0.3530	0.3040
Q3	0.3086	0.2570
R2	0.8439	0.3710
S2	0.8557	0.4930
T2	0.7760	0.4050
T3	0.4776	0.3350
U2	0.8462	0.4680
U3	0.4052	0.2990
V2	0.7806	0.4220
V3	0.4365	0.3070
W2	0.8350	0.4590
W3	0.5154	0.3250
X2	0.8177	0.4550
X3	0.7178	0.4630
Y2	0.8218	0.4250
Y3	0.3287	0.2580
a3	0.2559	0.2500
a5	0.5056	0.3330
a7	0.8054	0.4340
b3	0.3702	0.2770
c3	0.4459	0.2780
d2	0.9590	0.4240
d3	0.5907	0.2760
e2	0.8797	0.4000
e3	0.2267	0.2400
f3	0.3511	0.2880
h2	0.9267	0.4260
j3	0.5163	0.3020
k2	0.8036	0.5040
l2	0.8137	0.4730
m2	0.8567	0.4910
o2	0.8526	0.4650
p2	0.7788	0.4250

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Chain	Atom inclusion	Q-score
q2	 0.8812	 0.4850
r2	 0.7205	 0.3830
s3	 0.3780	 0.2870
t2	 0.8456	 0.4820
u2	 0.8357	 0.4700
v2	 0.8576	 0.5080
w2	 0.8668	 0.4780
x2	 0.8717	 0.5050
y2	 0.7966	 0.4570