



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:01 PM UTC

PDB ID : 7A01 / pdb_00007a01
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

A user guide is available at

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

The types of validation reports are described at

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

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

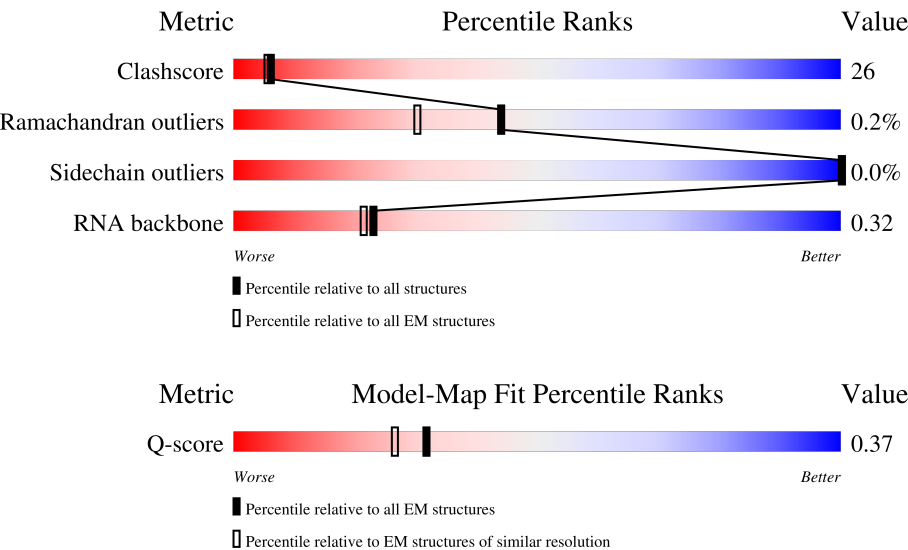
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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.



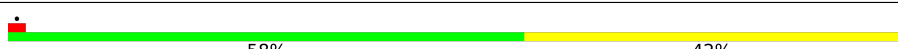
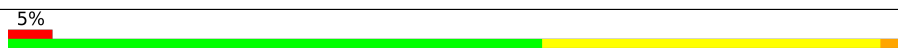
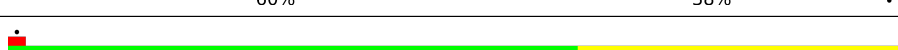
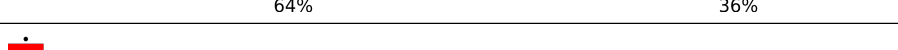
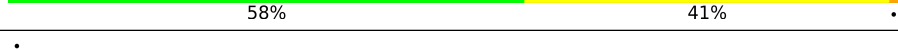
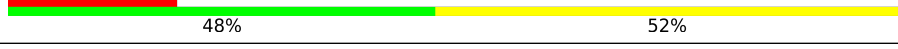
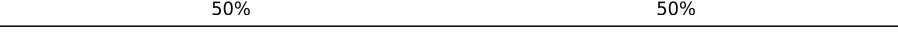
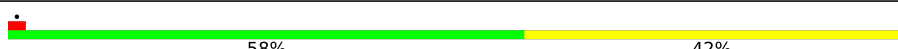
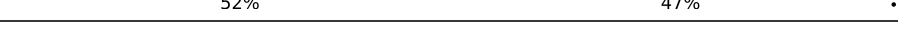
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	E1	153	 84% 15% 39% 46%
2	e2	3825	 5% 23% 54% 23%
3	h2	156	 18% 61% 21%

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Mol	Chain	Length	Quality of chain
4	d2	120	
5	p2	69	
6	k2	131	
7	l2	63	
8	m2	119	
9	o2	134	
10	q2	147	
11	r2	75	
12	t2	362	
13	u2	107	
14	v2	128	
15	w2	199	
16	x2	109	
17	y2	114	
18	92	244	
19	A2	122	
20	B2	102	
21	C2	86	
22	D2	50	
23	E2	52	
24	F2	104	
25	G2	292	
26	H2	153	
27	I2	91	
28	J2	125	

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Mol	Chain	Length	Quality of chain
29	K2	198	
30	L2	102	
31	M2	163	
32	R2	35	
33	S2	187	
34	T2	201	
35	U2	225	
36	V2	241	
37	W2	190	
38	X2	102	
39	Y2	169	
40	O2	138	
41	I2	203	
42	J2	135	
43	K3	180	
44	L3	217	
45	M3	394	
46	N3	175	
47	O3	159	
48	P3	99	
49	K3	1801	
50	s3	43	
51	I3	94	
52	Q3	188	
53	G3	153	

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Mol	Chain	Length	Quality of chain
54	G5	137	
55	a3	313	
56	a5	136	
57	A3	127	
58	T3	141	
59	U3	208	
60	V3	213	
61	W3	218	
62	X3	23	
63	Y3	227	
64	j3	262	
65	J5	129	
66	N3	191	
67	b3	237	
68	B3	141	
69	f3	64	
70	F3	150	
71	c3	206	
72	C3	129	
73	d3	185	
74	D3	83	
75	e3	124	
76	E3	98	
77	H3	53	
78	H5	141	

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Mol	Chain	Length	Quality of chain
79	P3	189	
80	I3	104	
81	I5	126	
82	L3	83	
83	M3	75	
84	O3	98	
85	a7	210	

2 Entry composition

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
1	E1	153	Total	C	N	O	P	0	0
			3208	1443	529	1083	153		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	e2	3825	Total	C	N	O	P	0	0
			81951	36501	14984	26650	3816		

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

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

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

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

- Molecule 5 is a protein called Uncharacterized protein.

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

- Molecule 6 is a protein called eL14.

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

- Molecule 7 is a protein called Ribosomal protein L24.

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

- Molecule 8 is a protein called Uncharacterized protein.

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

- Molecule 9 is a protein called Ribosomal protein L26.

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

- Molecule 10 is a protein called uL15.

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

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

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

- Molecule 12 is a protein called uL4.

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

- Molecule 13 is a protein called eL31.

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

- 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
34	T2	201	Total	C	N	O	S	0	0
			1614	1039	301	273	1		

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
35	U2	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

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

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

- Molecule 37 is a protein called Uncharacterized protein.

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

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

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

- Molecule 39 is a protein called Ribosomal protein L11.

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

- 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
47	72	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 48 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	82	99	Total	C	N	O	S	0	0
			809	518	141	148	2		

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
49	K3	1801	Total	C	N	O	P	0	0
			38409	17147	6888	12577	1797		

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

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

- Molecule 51 is a protein called Ribosomal protein L30.

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

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

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

- 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
			1248	793	234	215	6		

- Molecule 54 is a protein called ribosomal protein uS13.

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

- Molecule 55 is a protein called ribosomal protein RACK1.

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

- Molecule 56 is a protein called Uncharacterized protein.

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

- Molecule 57 is a protein called ribosomal protein uS19.

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

- Molecule 58 is a protein called Ribosomal protein S23.

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

- Molecule 59 is a protein called 40S_SA_C domain-containing protein.

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

- 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
67	b3	237	Total	C	N	O	S	0	0
			1924	1200	387	330	7		

- Molecule 68 is a protein called Uncharacterized protein.

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

- Molecule 69 is a protein called ribosomal protein eS28.

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

- Molecule 70 is a protein called ribosomal protein uS15.

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

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

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

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
72	C3	129	Total	C	N	O	S	0	0
			1048	658	193	192	5		

- 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_pectin 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
79	P3	189	Total	C	N	O	S	0	0
			1522	969	280	272	1		

- Molecule 80 is a protein called Ribosomal_S10 domain-containing protein.

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

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

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

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

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

- Molecule 83 is a protein called ribosomal protein eS25.

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

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

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

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

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

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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

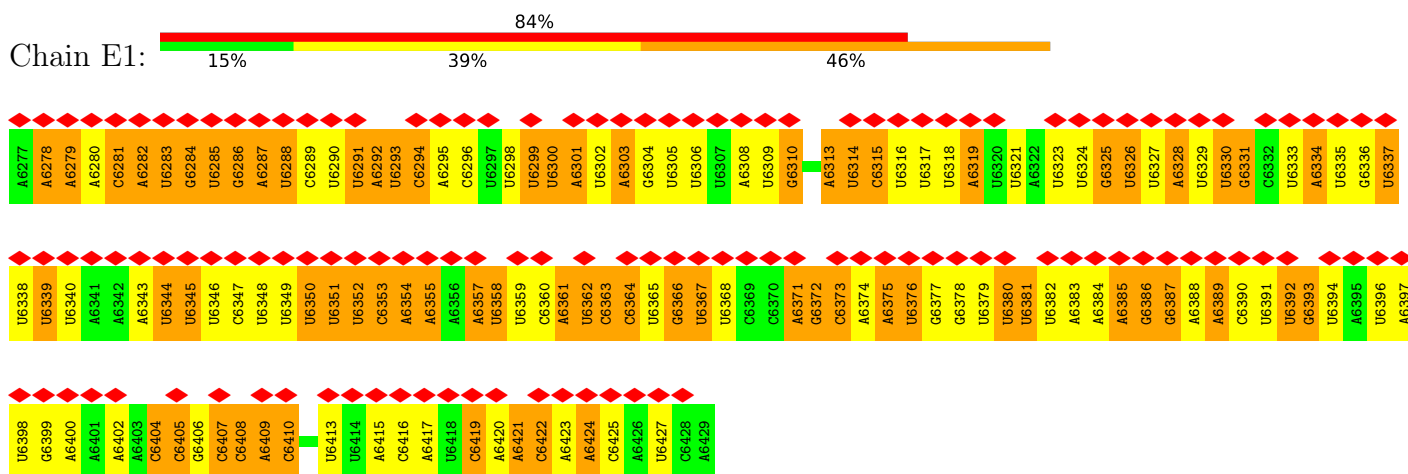
- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

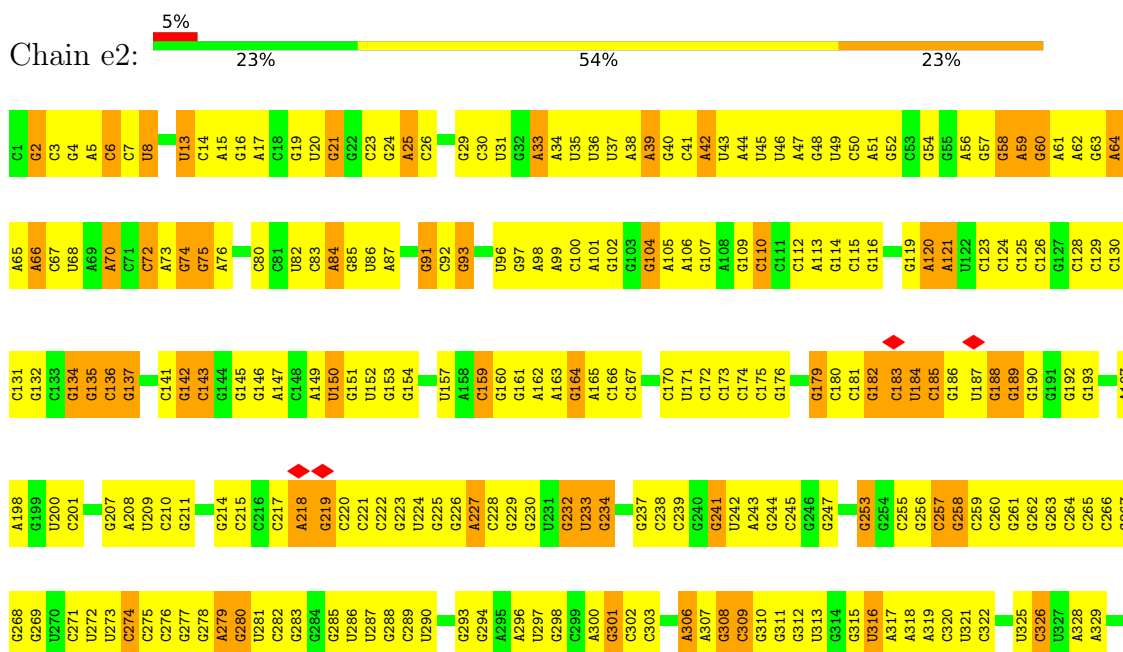
3 Residue-property plots

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



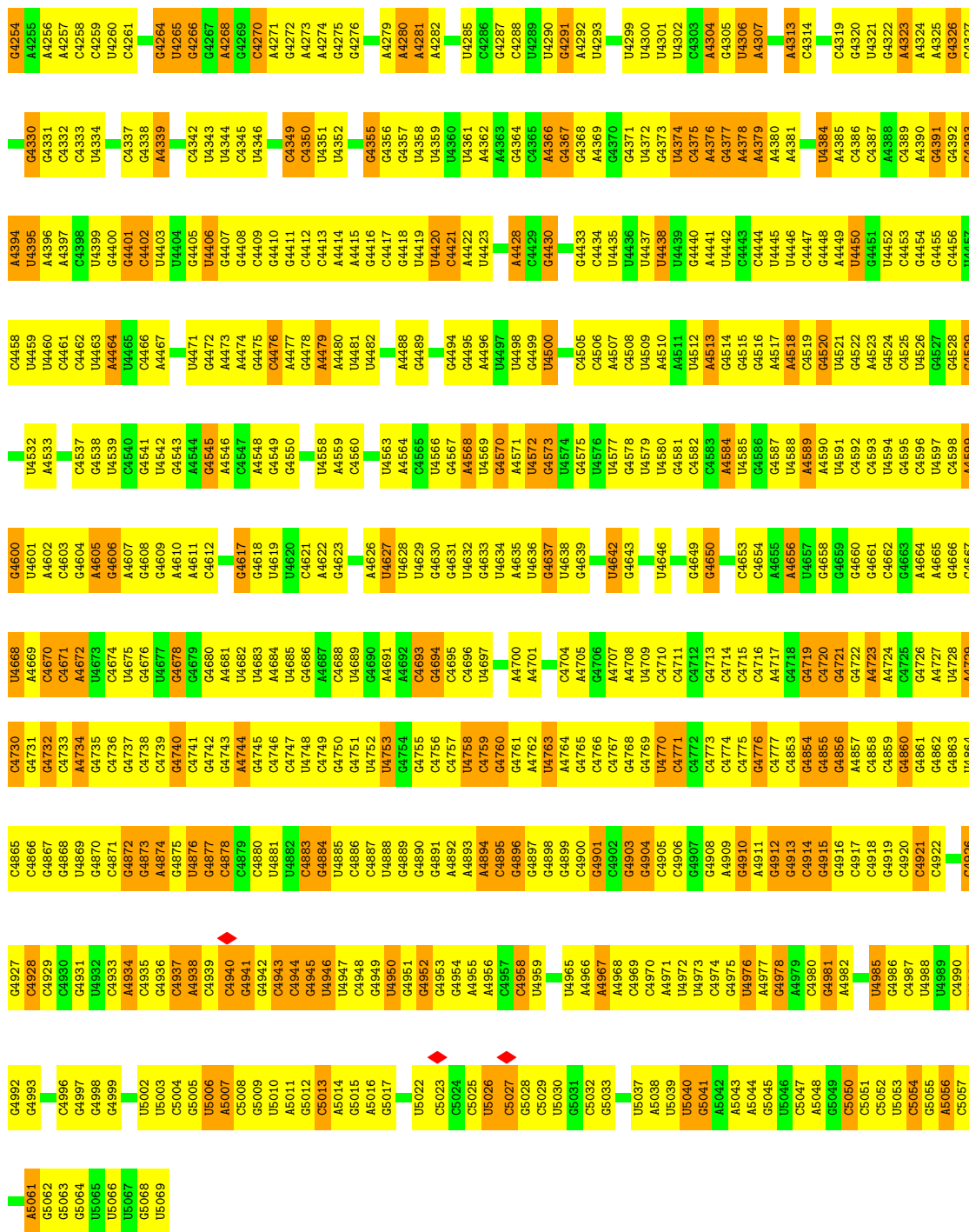
• Molecule 2: 28S RIBOSOMAL RNA





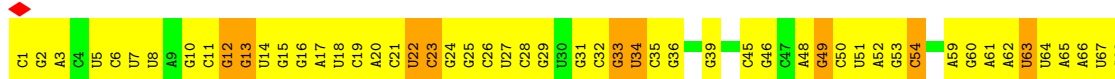


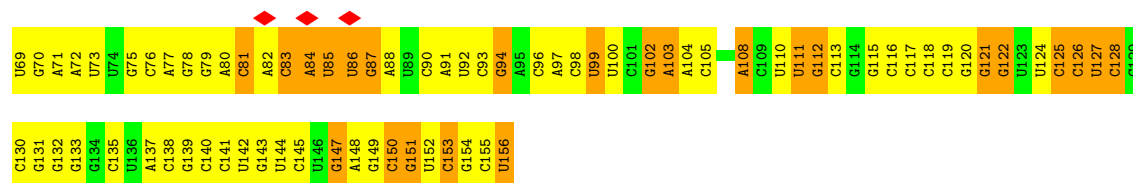
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U4118	C4119	U4120	C4121	U4122	C4123	U4124	C4125	U4126	C4127	U4128	C4129	U4130	C4131	U4132	C4133	U4134	C4135	U4136	C4137	U4138	C4139	U4140	C4141	U4142	C4143	U4144	C4145	U4146	C4147	U4148	C4149	U4150	C4151	U4152	C4153	U4154	C4155	U4156	C4157	U4158	U4159	C4160	U4161	C4162	U4163	C4164	U4165	C4166	U4167	C4168	U4169	C4170	U4171	C4172	U4173	C4174	U4175	C4176	U4177	C4178	U4179	C4180	U4181	C4182	U4183	C4184																																																																																																																																																																																																																																																																																																																																																																																																
U4055	A4056	C4057	U4058	C4059	U4060	C4061	A4062	U4063	C4064	A4065	U4066	C4067	U4068	A4069	U4070	C4071	U4072	A4073	U4074	C4075	U4076	A4077	C4078	U4079	A4080	C4081	U4082	A4083	U4084	C4085	U4086	A4087	C4088	U4089	A4090	C4091	U4092	A4093	C4094	U4095	A4096	C4097	U4098	C4099	U4100	C4101	U4102	C4103	U4104	A4105	C4106	U4107	C4108	U4109	C4110	U4111	C4112	U4113	C4114	U4115	A4116	U4117	C4118	U4119	C4120	U4121	C4122	U4123	C4124	U4125	C4126	U4127	C4128	U4129	C4130	U4131	C4132	U4133	C4134	U4135	C4136	U4137	C4138	U4139	C4140	U4141	C4142	U4143	C4144	U4145	C4146	U4147	C4148	U4149	C4150	U4151	C4152	U4153	C4154	U4155	C4156	U4157	C4158	U4159	C4160	U4161	C4162	U4163	C4164	U4165	C4166	U4167	C4168	U4169	C4170	U4171	C4172	U4173	C4174	U4175	C4176	U4177	C4178	U4179	C4180	U4181	C4182	U4183	C4184	U4185	C4186	U4187	C4188	U4189	C4190	U4191	C4192	U4193	C4194	U4195	C4196	U4197	C4198	U4199	C4200	U4201	C4202	U4203	C4204	U4205	C4206	U4207	C4208	U4209	C4209	U4210	C4211	U4212	C4213	U4214	C4215	U4216	C4217	U4218	C4219	U4220	C4221	U4222	C4223	U4224	C4225	U4226	C4227	U4228	C4229	U4230	C4231	U4232	C4233	U4234	C4235	U4236	C4237	U4238	C4239	U4240	C4241	U4242	C4243	U4244	C4245	U4246	C4247	U4248	C4249	U4250	C4251	U4252	C4253																																																																																																																																																																																																																																																											
U3995	C3996	C3997	C3998	C3999	C4000	C4001	C4002	C4003	C4004	C4005	C4006	C4007	C4008	C4009	C4010	C4011	C4012	C4013	C4014	C4015	C4016	C4017	C4018	C4019	C4020	C4021	C4022	C4023	C4024	C4025	C4026	C4027	C4028	C4029	C4030	C4031	C4032	C4033	C4034	C4035	C4036	C4037	C4038	C4039	C4040	C4041	C4042	C4043	C4044	C4045	C4046	C4047	C4048	C4049	C4050	C4051	C4052	C4053	C4054	C4055	C4056	C4057	C4058	C4059	C4060	C4061	C4062	C4063	C4064	C4065	C4066	C4067	C4068	C4069	C4070	C4071	C4072	C4073	C4074	C4075	C4076	C4077	C4078	C4079	C4080	C4081	C4082	C4083	C4084	C4085	C4086	C4087	C4088	C4089	C4090	C4091	C4092	C4093	C4094	C4095	C4096	C4097	C4098	C4099	C4100	C4101	C4102	C4103	C4104	C4105	C4106	C4107	C4108	C4109	C4110	C4111	C4112	C4113	C4114	C4115	C4116	C4117	C4118	C4119	C4120	C4121	C4122	C4123	C4124	C4125	C4126	C4127	C4128	C4129	C4130	C4131	C4132	C4133	C4134	C4135	C4136	C4137	C4138	C4139	C4140	C4141	C4142	C4143	C4144	C4145	C4146	C4147	C4148	C4149	C4150	C4151	C4152	C4153	C4154	C4155	C4156	C4157	C4158	C4159	C4160	C4161	C4162	C4163	C4164	C4165	C4166	C4167	C4168	C4169	C4170	C4171	C4172	C4173	C4174	C4175	C4176	C4177	C4178	C4179	C4180	C4181	C4182	C4183	C4184	C4185	C4186	C4187	C4188	C4189	C4190	C4191	C4192	C4193	C4194	C4195	C4196	C4197	C4198	C4199	C4200	C4201	C4202	C4203	C4204	C4205	C4206	C4207	C4208	C4209	C4210	C4211	C4212	C4213	C4214	C4215	C4216	C4217	C4218	C4219	C4220	C4221	C4222	C4223	C4224	C4225	C4226	C4227	C4228	C4229	C4230	C4231	C4232	C4233	C4234	C4235	C4236	C4237	C4238	C4239	C4240	C4241	C4242	C4243	C4244	C4245	C4246	C4247	C4248	C4249	C4250	C4251	C4252	C4253																																																																																																																																																																																																
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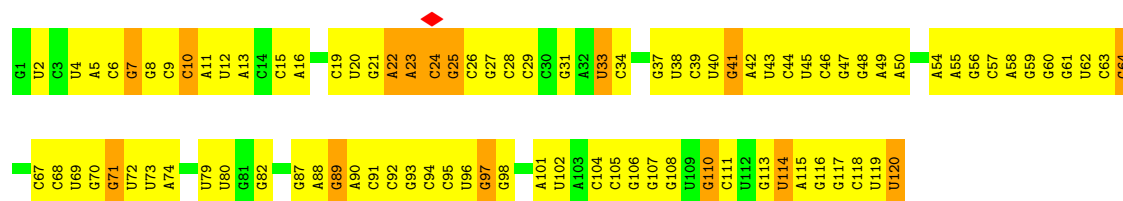
• Molecule 3: 5.8S RIBOSOMAL RNA

Chain h2: 18% 61% 21%

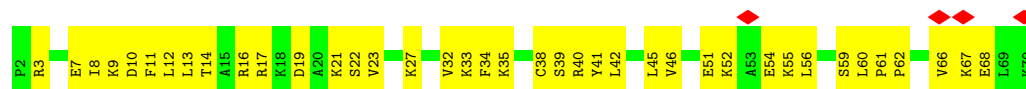
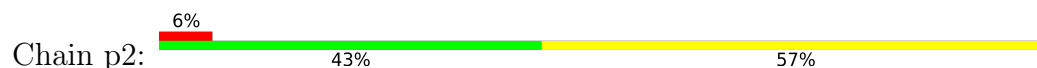




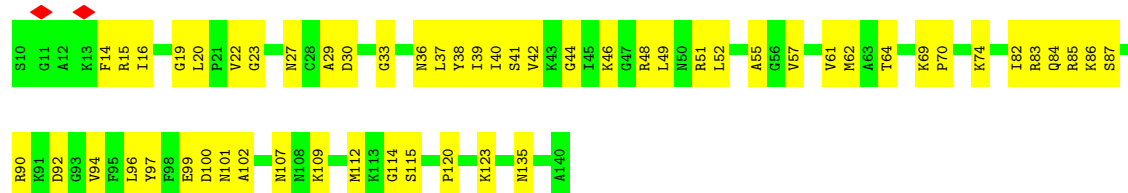
- Molecule 4: 5S RIBOSOMAL RNA



- Molecule 5: Uncharacterized protein



- Molecule 6: eL14



- Molecule 7: Ribosomal protein L24



- Molecule 8: Uncharacterized protein

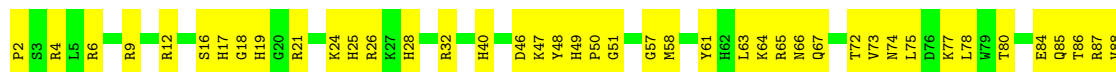




• Molecule 9: Ribosomal protein L26



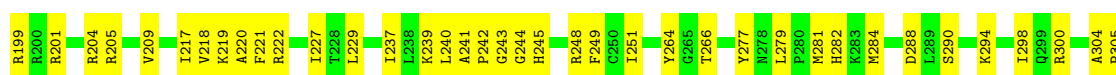
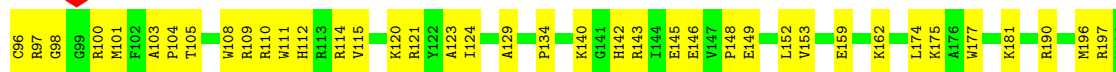
• Molecule 10: uL15



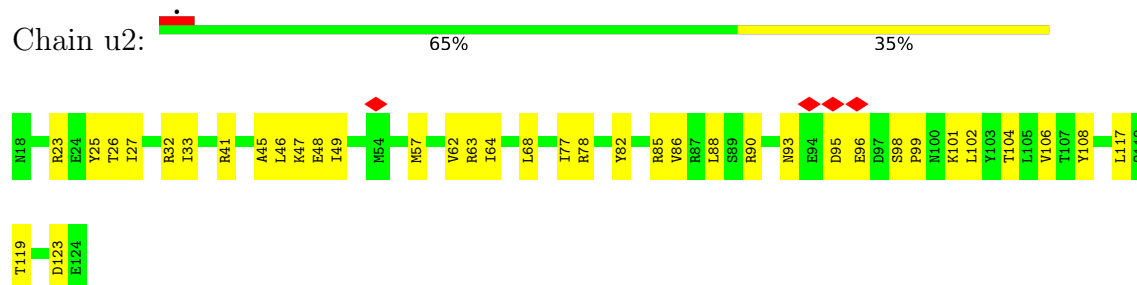
• Molecule 11: 60S ribosomal protein L29



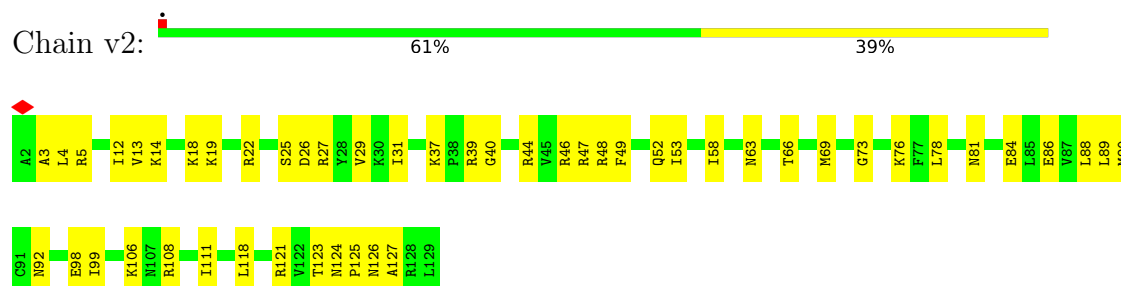
• Molecule 12: uL4



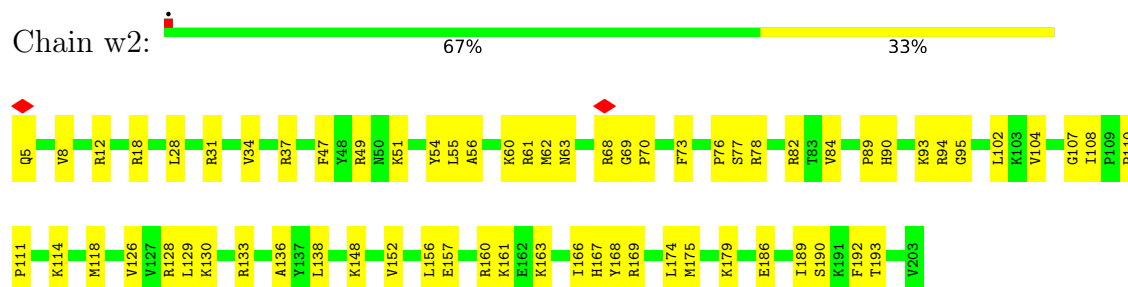
- Molecule 13: eL31



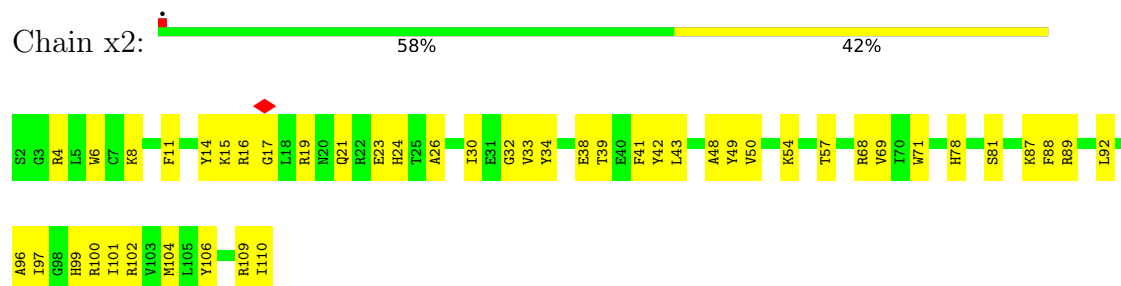
- Molecule 14: eL32



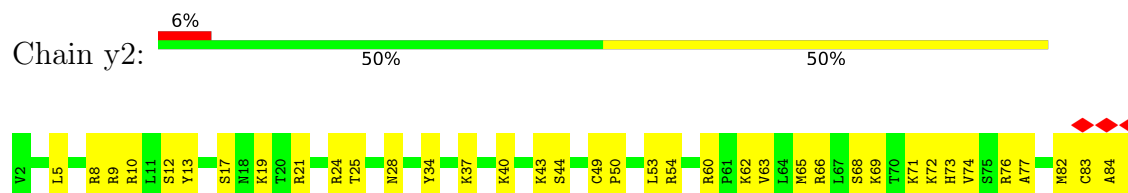
- Molecule 15: 60S RIBOSOMAL PROTEIN UL13

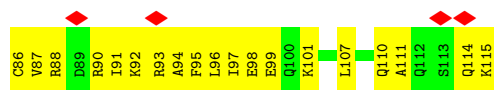


- Molecule 16: eL33



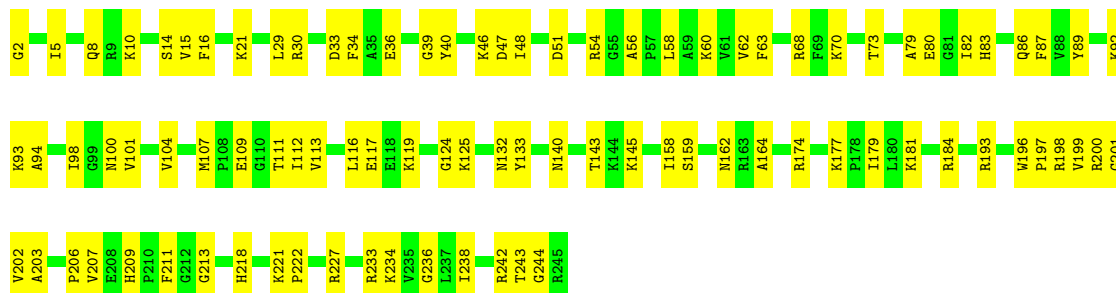
- Molecule 17: eL34





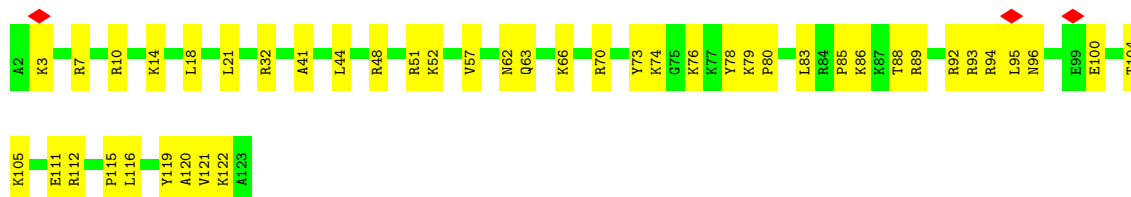
• Molecule 18: Uncharacterized protein

Chain 92: 63% 37%



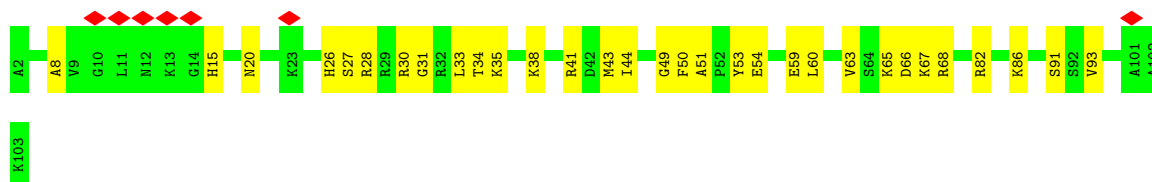
• Molecule 19: uL29

Chain A2: 64% 36%



• Molecule 20: 60S ribosomal protein L36

Chain B2: 7% 70% 30%



• Molecule 21: Ribosomal protein L37

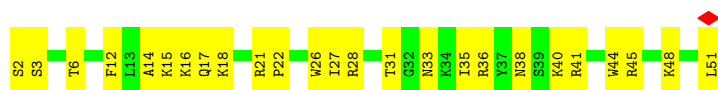
Chain C2: 63% 37%



• Molecule 22: ribosomal protein eL39

Chain D2: 50% 50%

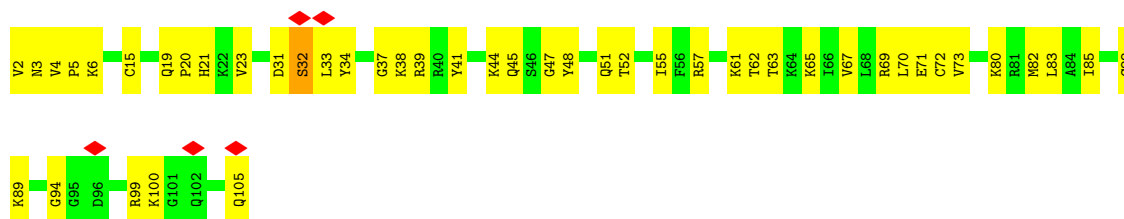




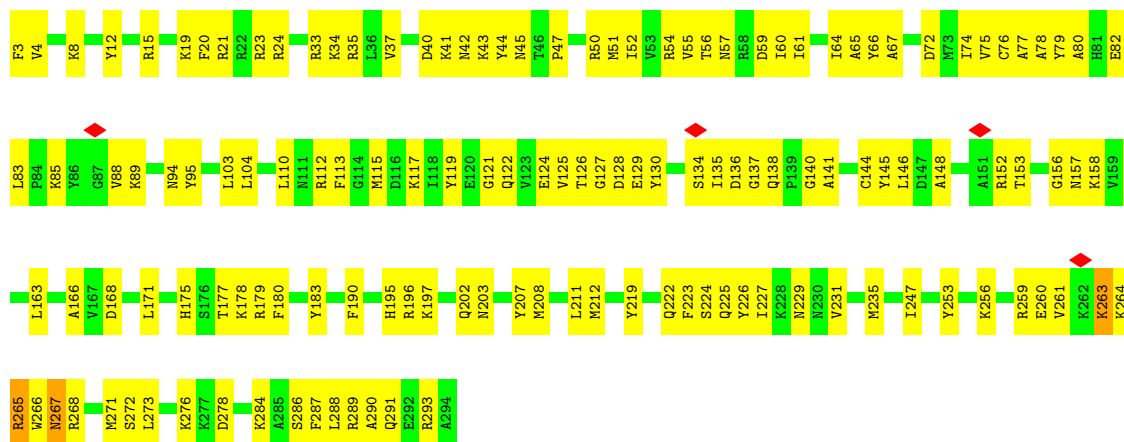
• Molecule 23: 60S RIBOSOMAL PROTEIN EL40



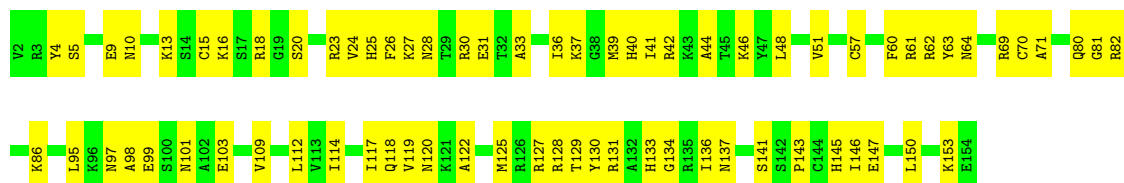
• Molecule 24: eL42



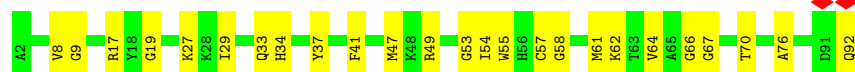
• Molecule 25: 60S ribosomal protein L5



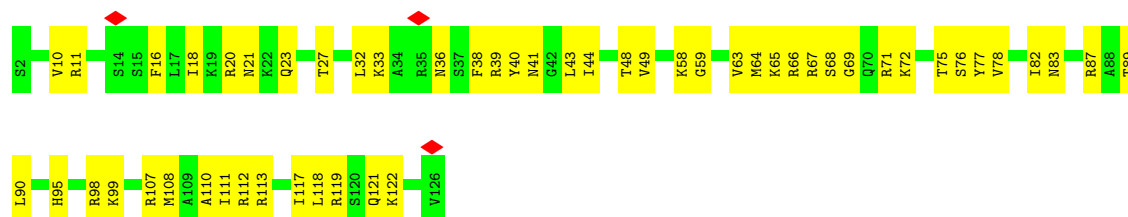
• Molecule 26: uL22



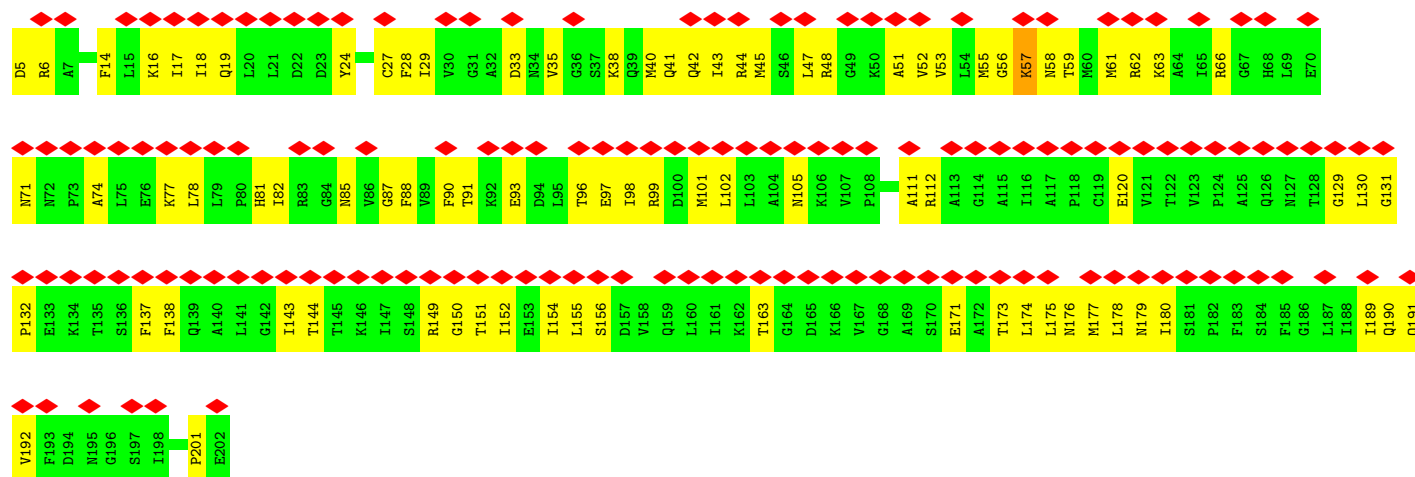
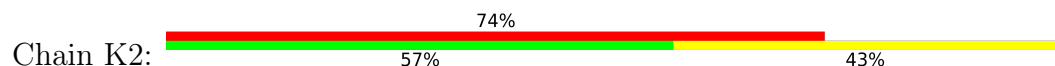
• Molecule 27: ribosomal protein eL43



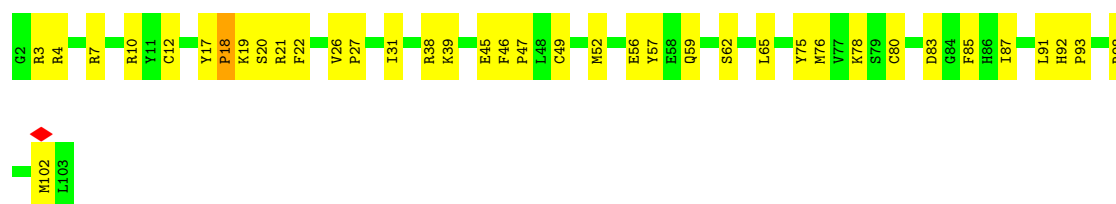
- Molecule 28: Uncharacterized protein



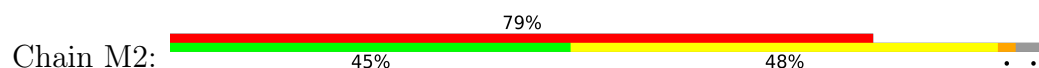
- Molecule 29: 60S acidic ribosomal protein P0

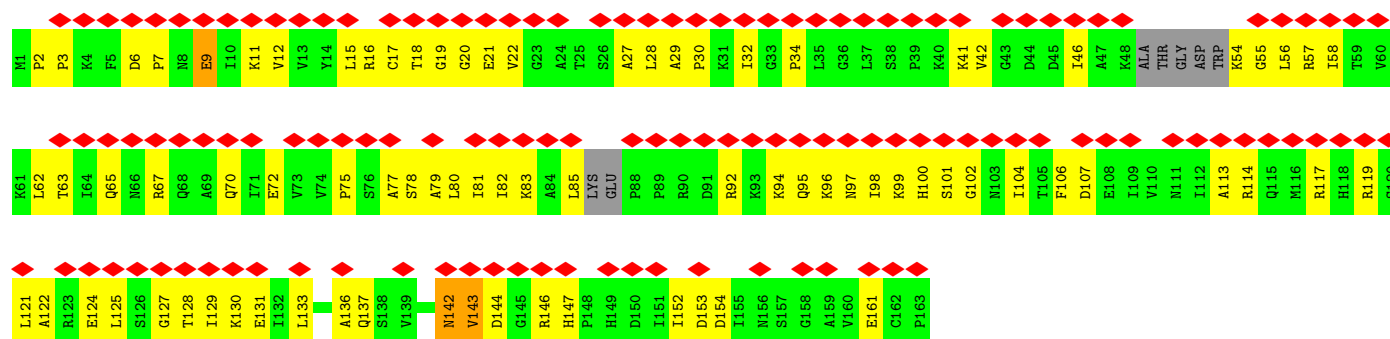


- Molecule 30: Ribosomal protein L10 (Predicted)



- Molecule 31: Uncharacterized protein

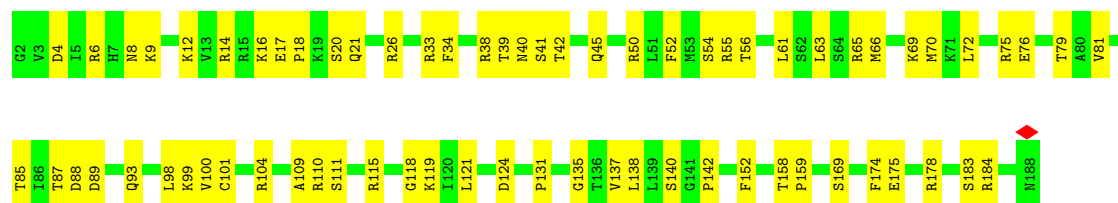




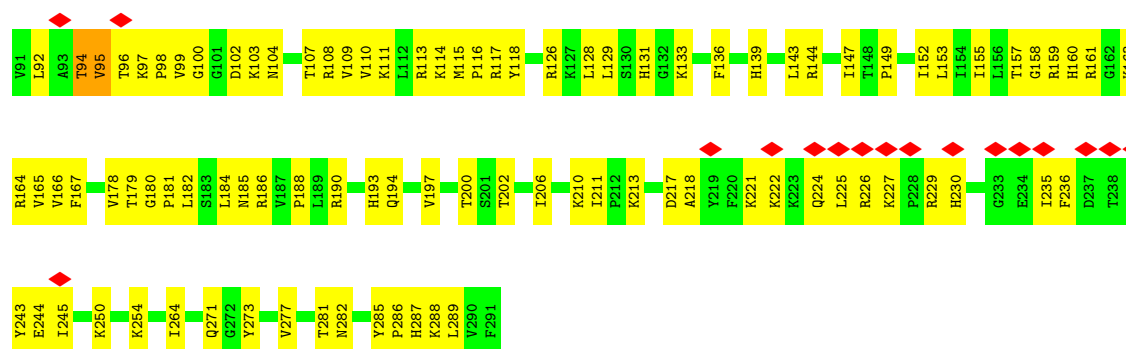
• Molecule 32: Ribosomal_L6e_N domain-containing protein



• Molecule 33: 60S RIBOSOMAL PROTEIN EL18

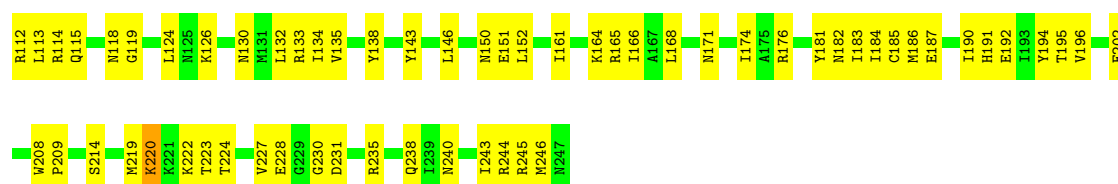


• Molecule 34: 60S ribosomal protein L6

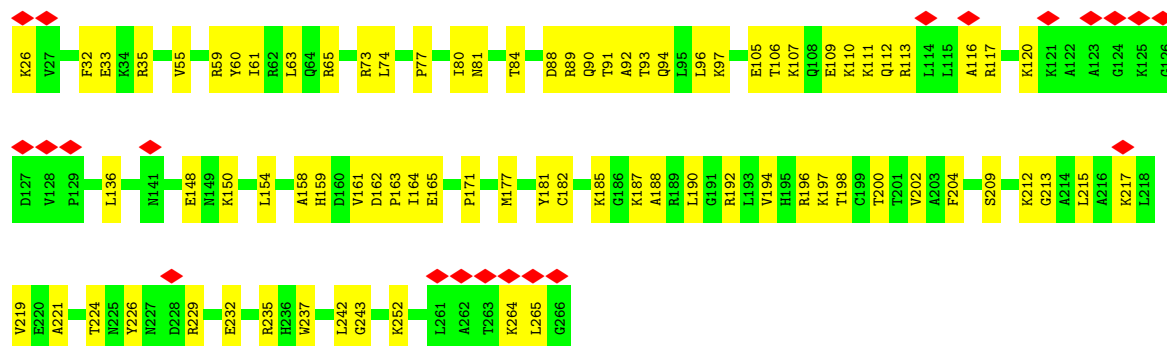


• Molecule 35: uL30

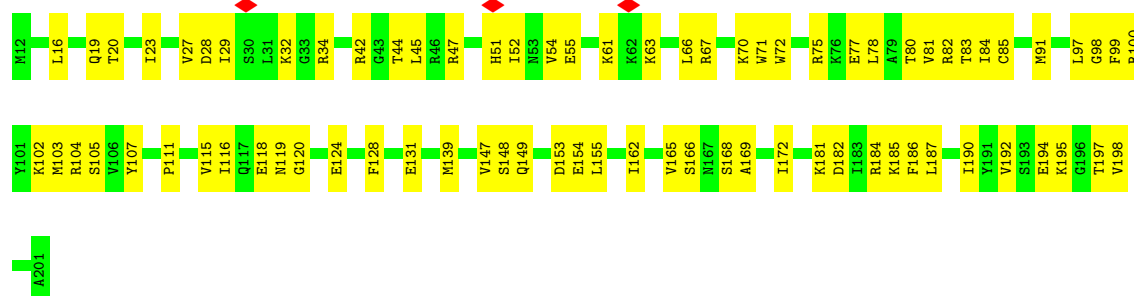




• Molecule 36: 60S RIBOSOMAL PROTEIN EL8



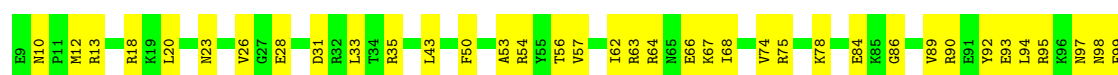
• Molecule 37: Uncharacterized protein

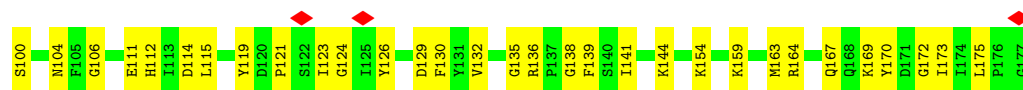


• Molecule 38: Ribosomal protein L10 (Predicted)

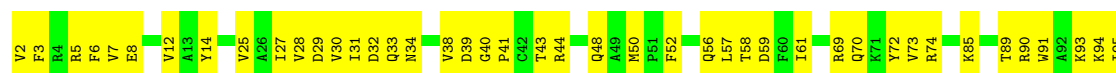


• Molecule 39: Ribosomal protein L11





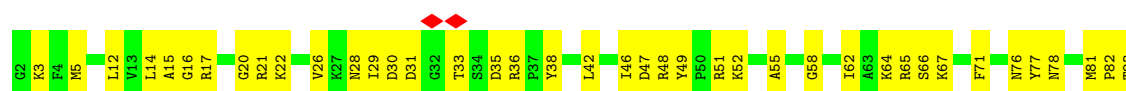
- Molecule 40: Ribosomal protein L14



- Molecule 41: Ribosomal protein L15



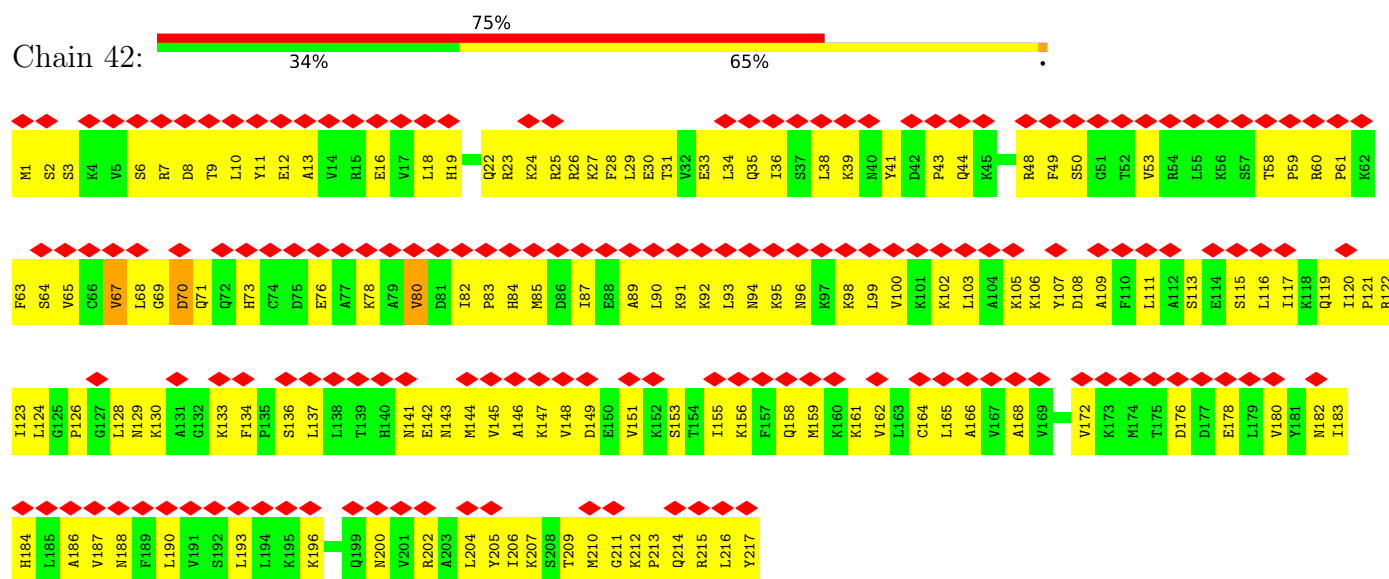
- Molecule 42: 60S ribosomal protein L27



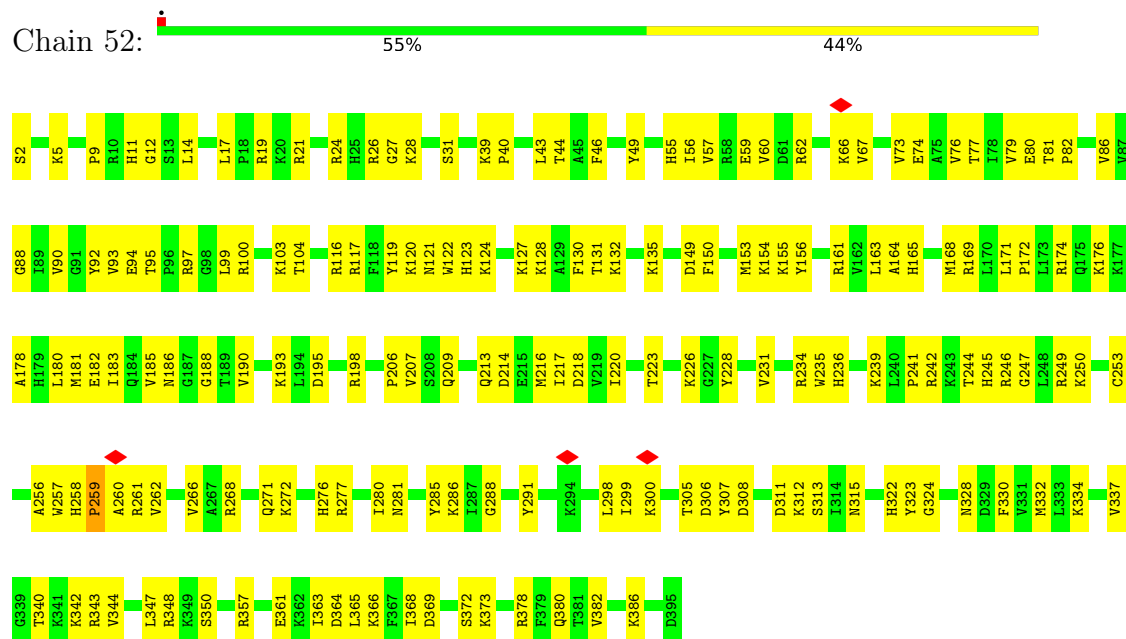
- Molecule 43: 60S RIBOSOMAL PROTEIN EL19



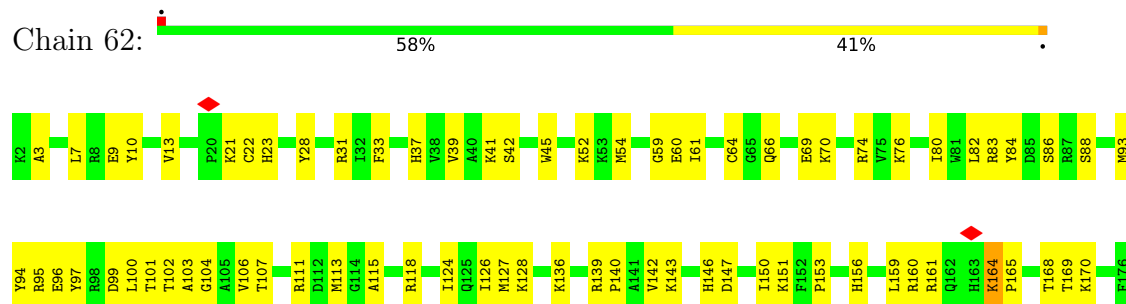
- Molecule 44: Ribosomal protein



• Molecule 45: uL3

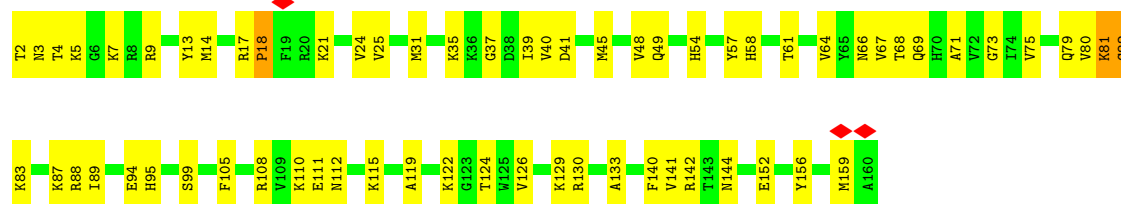


• Molecule 46: 60S RIBOSOMAL PROTEIN EL20



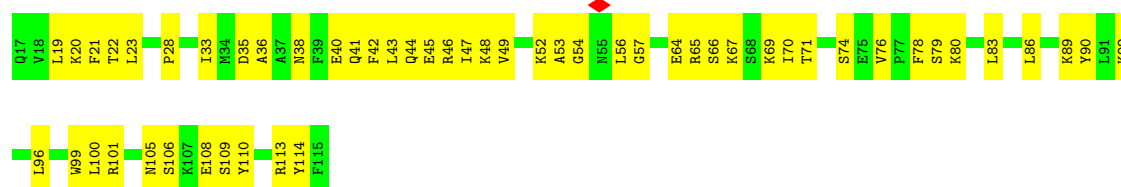
• Molecule 47: eL21

Chain 72:  59% 39%

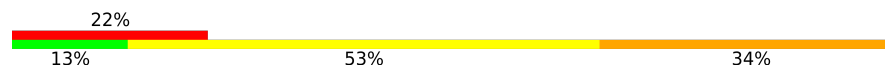


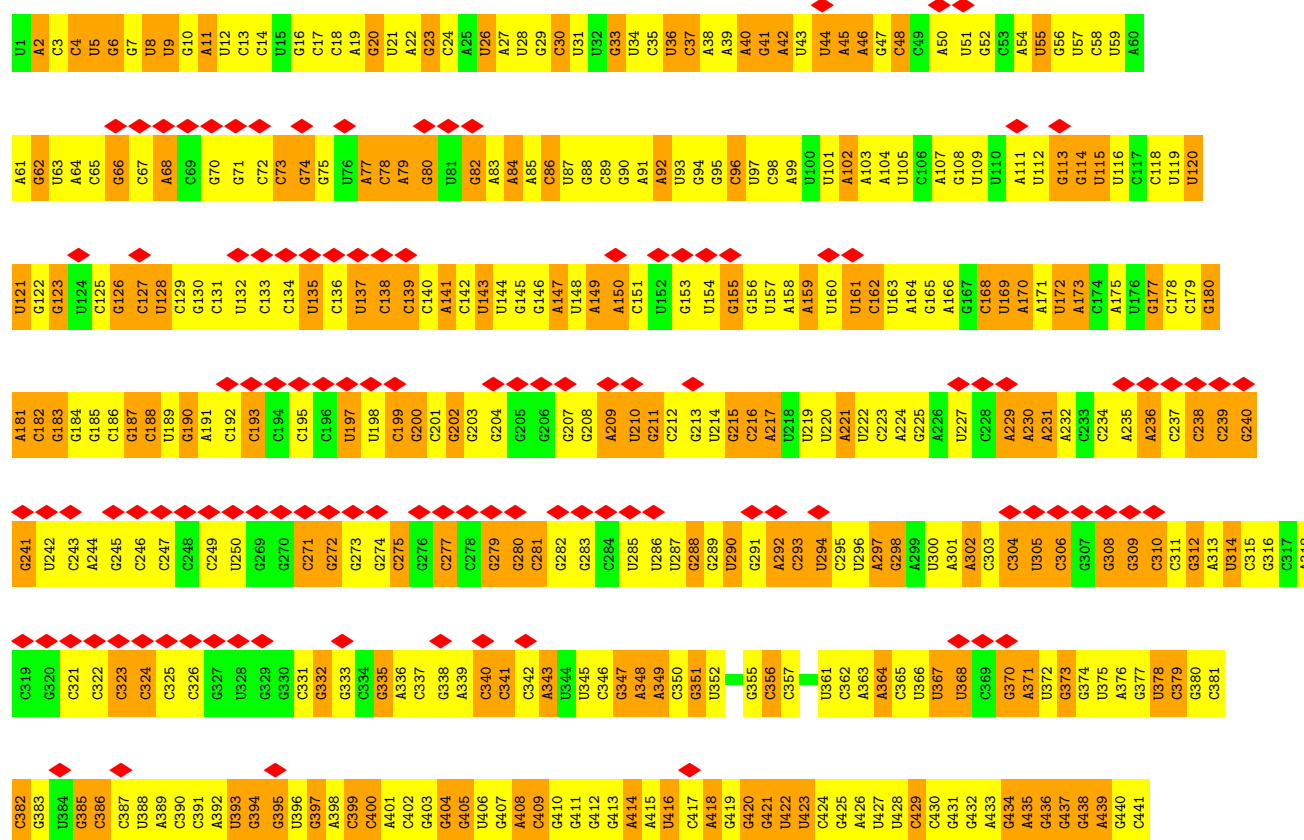
• Molecule 48: Ribosomal protein L22

Chain 82:  46% 54%

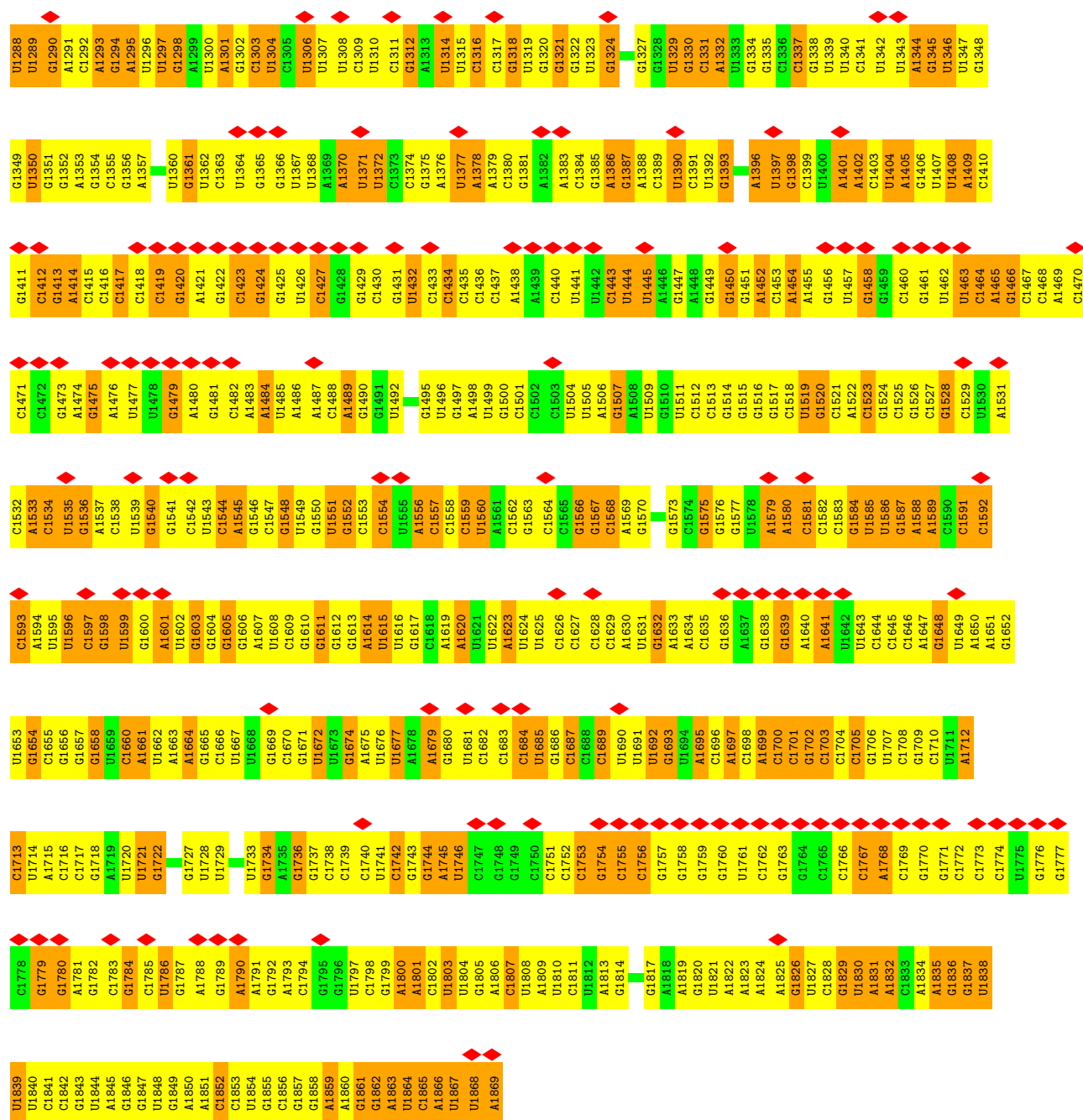


• Molecule 49: 18S RIBOSOMAL RNA

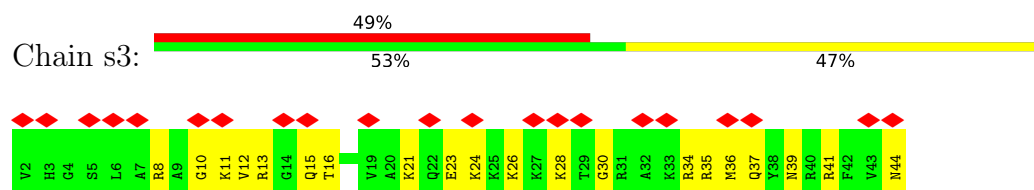
Chain K3:  13% 53% 34%



A1228	G1166	G1105	G1043	G982	G793	U882	C622	U562	C502	C442
G1229	G1167	C1106	G1044	A983	A794	G883	G823	G563	C503	U443
C1230	G1168	G1107	U1045	G859	A795	G884	C524	A564	G504	U444
C1231	G1169	G1108	G984	G859	A795	G885	G825	G565	G505	A445
U1232	A1170	C1109	G1046	A861	G796	U886	G826	U566	G506	G446
G1233	G1173	G1110	G1047	A862	G797	G887	G827	G567	G507	A447
C1234	A1173	G1111	G1048	U863	G798	G888	G828	C568	U448	A448
G1235	U1174	A1050	A1049	U864	G799	U889	A829	A569	A508	A449
U1236	A1175	A1113	A1051	A865	U799	G890	A830	G570	G510	C450
C1237	G1176	A1052	A1052	U866	U800	G891	U831	U511	G451	G451
U1238	G1177	G929	C1053	U867	U801	G892	C632	U512	U512	C452
U1178	U1178	C930	G1054	G868	U804	A693	C633	U572	C453	C453
A1240	A1179	C931	A1055	A869	U805	G694	C634	U573	U573	A554
A1241	C1180	G932	U1056	A870	U805	G695	A634	A574	A455	A455
U1242	A1181	G933	C1057	U871	A808	G696	G635	A575	C456	C456
U1243	A1182	G934	A1058	A872	A809	G697	U637	U577	C457	A458
U1244	A1183	G935	G1059	G873	A810	G698	C638	C578	C459	C459
G1245	G1184	G936	U1060	G874	A811	G699	C639	C579	A460	A460
A1185	C1185	G937	U1061	A875	A812	G700	A640	U580	U461	U461
A1246	U1186	A1122	U1062	C876	A813	G701	A641	U581	C462	C462
G1247	G1187	U1120	A1063	G877	U814	G702	U642	U582	C463	C463
U1248	A1188	G1121	C1064	G878	U815	G703	A643	A584	A464	A464
A1249	A1189	C1127	G1065	C879	U816	G704	G644	C585	A465	A465
A1250	A1190	G1128	U1066	G880	A817	G705	G645	U587	G466	G466
A1251	C1191	G1129	G1067	G881	A818	G706	G646	A588	G467	G467
C1252	U1192	G1130	U1068	U882	U819	G707	U647	U589	A468	A468
A1253	U1193	G1131	U1069	U883	U820	G708	G648	A590	G470	G470
G1254	A1194	U946	U1070	U884	U821	G709	U649	U591	C471	C471
C1255	G1197	G947	C1071	U885	U822	G710	U650	C592	C472	C472
G1256	G1198	C948	G1072	U886	U823	G711	U651	C593	A473	A473
G1257	A1199	G949	G1073	U887	C924	G712	U652	C594	G474	G474
A1258	A1200	U1136	U1074	U888	A825	G713	A653	G595	C475	C475
A1259	A1201	U1137	G1075	U889	A826	G714	A654	G596	A476	A476
C1260	C1261	G1138	C1076	U890	A827	G715	A655	U597	G477	G477
C1262	U1202	U1015	C1077	G891	A828	G716	G656	G598	C478	C478
U1263	G1203	U1016	C1078	U892	G829	G717	U657	G599	G480	G480
C1264	A1204	U1017	A1080	U893	A830	G718	U658	G600	C481	C481
A1265	C1205	C1018	U1081	G894	G831	G719	U659	G601	G482	G482
C1266	G1206	U1019	A1082	G895	G832	G720	C660	G602	C483	C483
C1267	A1143	A1020	A1083	G896	G833	G721	U661	C603	A484	A484
A1268	G1207	U1028	G1084	U897	C834	G722	G662	A604	A485	A485
G1269	A1208	G1029	G1085	U898	C835	G723	G663	G605	U486	U486
A1209	U1209	U1152	U1086	U899	G836	G724	U664	G606	U487	U487
G1270	G1210	C1147	A1087	G900	G837	G725	G665	U607	U488	U488
C1271	A1148	U1148	U1088	G901	G838	G726	U666	C608	A489	A489
A1211	A1149	A1027	G1089	U902	C839	G727	U667	G609	C490	C490
G1212	G1212	A1028	A1090	U903	C840	G728	G668	G610	C491	C491
C1213	C1213	G1091	C1091	U904	G841	G729	U669	G611	C492	C492
A1214	A1214	G1092	A1092	U905	G842	G730	G670	G612	A493	A493
C1215	C1215	A1093	A1093	G906	G843	G731	A671	G613	C494	C494
A1216	A1216	C1094	C1094	U907	C942	G732	U672	G614	U495	U495
C1217	A1217	U1155	U1095	G908	C943	G733	G673	G615	C496	C496
A1218	C1218	U1156	G1096	U909	C944	G734	G674	G616	C497	C497
C1219	C1219	G1157	G1097	G910	U944	G735	U675	G617	A555	A555
A1220	A1220	U1158	C1098	G911	G845	G736	G676	G618	U556	U556
G1221	G1221	G1159	G1099	C911	G846	G737	U677	G619	G557	G557
G1222	G1222	U1160	U1037	C912	A847	G738	G678	G620	A560	A560
A1223	A1223	U1161	U1038	A913	C851	G739	G679	G621	A561	A561
G1224	G1224	C1162	C1039	U914	G852	G740	U680	G622		
U1225	U1225	C1163	G1040	G915	C853	G741	G681	G623		
G1226	G1226	G1164	G1104	A916	A854	G742	G682	G624		
A1267	G1227	G1165	A1042	U917	G855	G743	U683	G625		
				U918	C856	G744				
						G745				
						G746				
						U747				
						G748				
						U749				
						G750				
						U751				
						G752				
						C753				
						G754				
						U755				
						C756				
						U757				
						G787				
						G788				
						G789				
						C790				
						U791				
						C792				



• Molecule 50: 40S RIBOSOMAL PROTEIN ES30

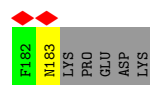
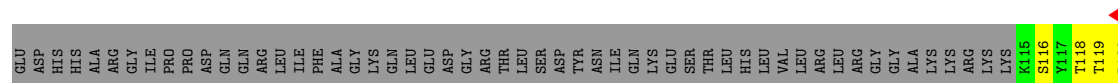
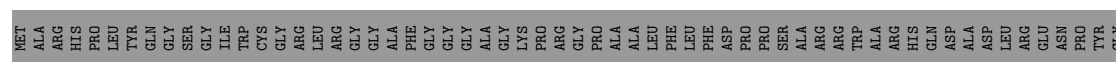


• Molecule 51: Ribosomal protein L30

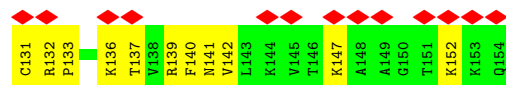
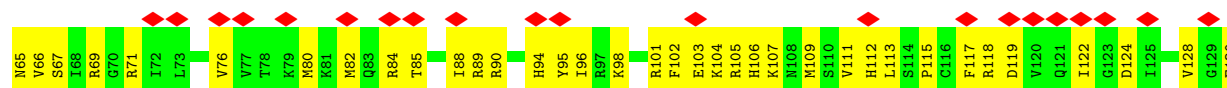
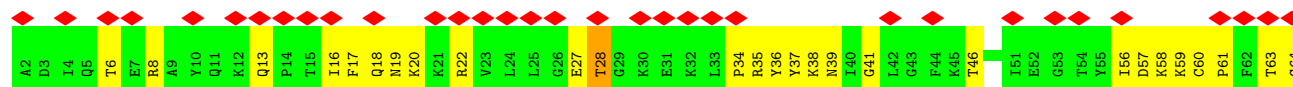




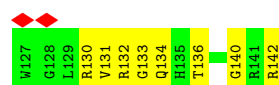
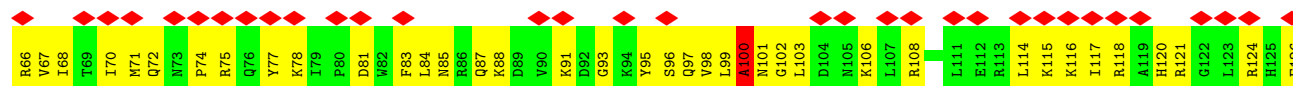
• Molecule 52: 40S ribosomal protein S27a



• Molecule 53: Ribosomal protein S11



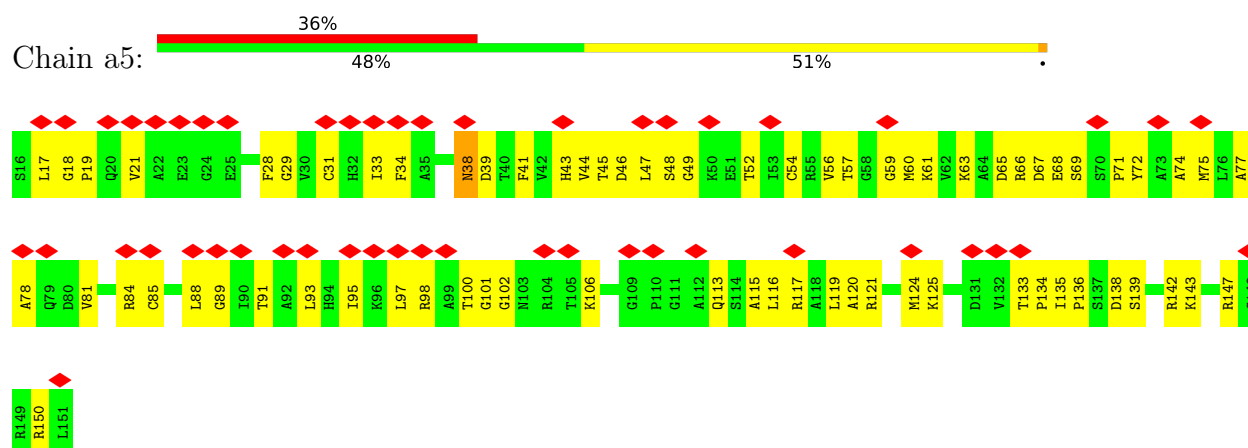
• Molecule 54: ribosomal protein uS13



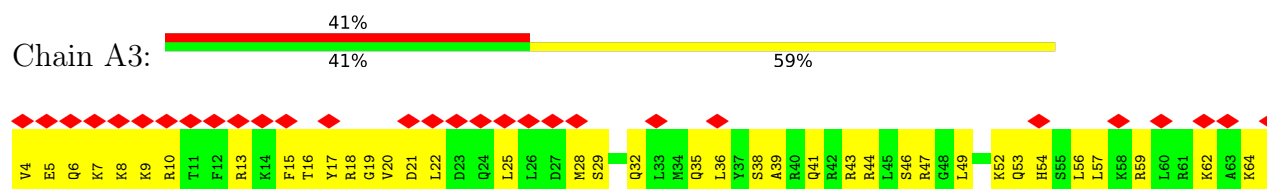
- Molecule 55: ribosomal protein RACK1

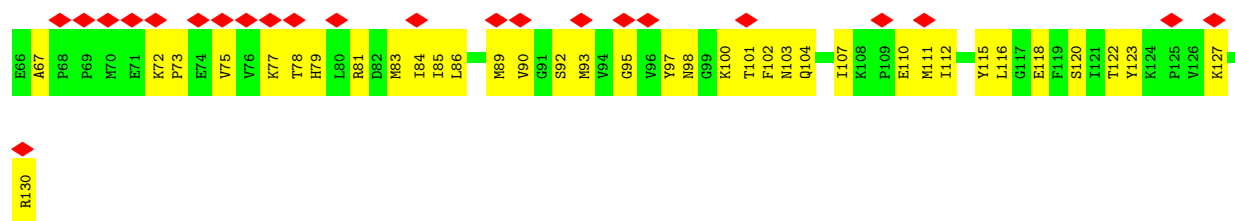


- Molecule 56: Uncharacterized protein

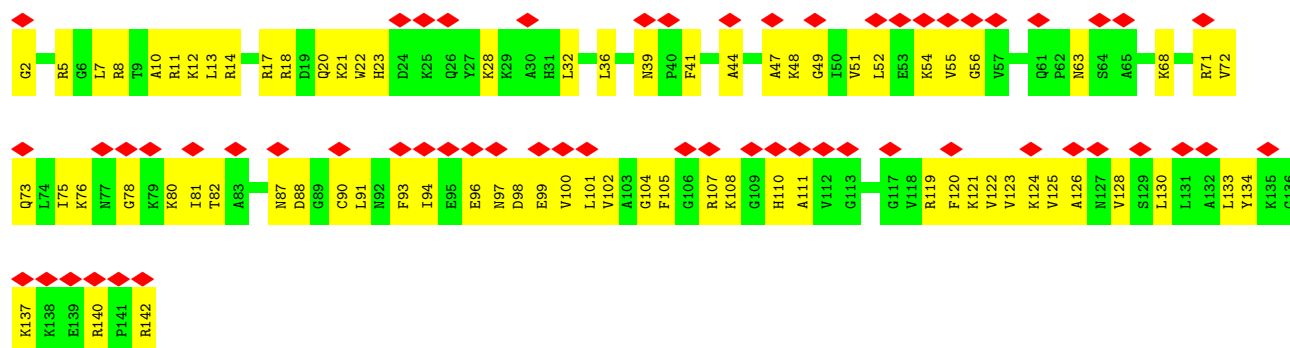
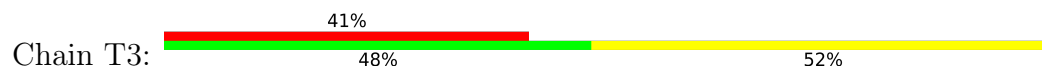


- Molecule 57: ribosomal protein uS19





• Molecule 58: Ribosomal protein S23

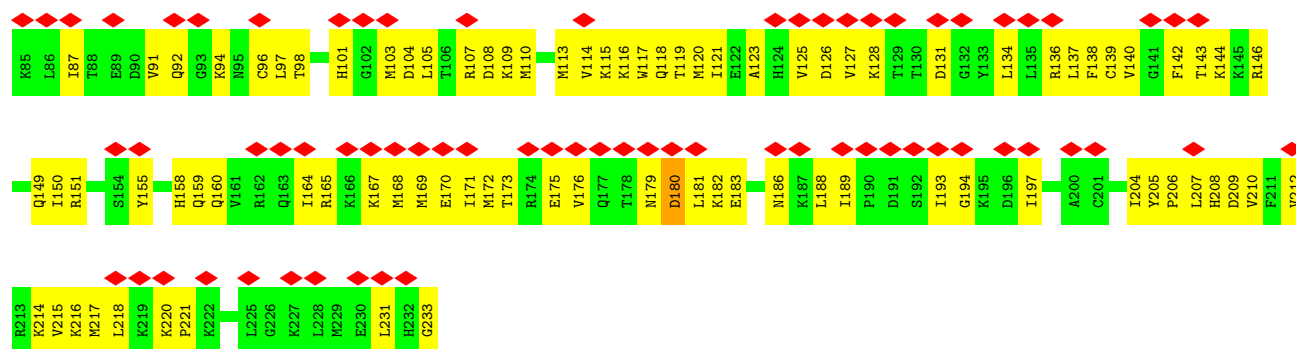


• Molecule 59: 40S_SA_C domain-containing protein

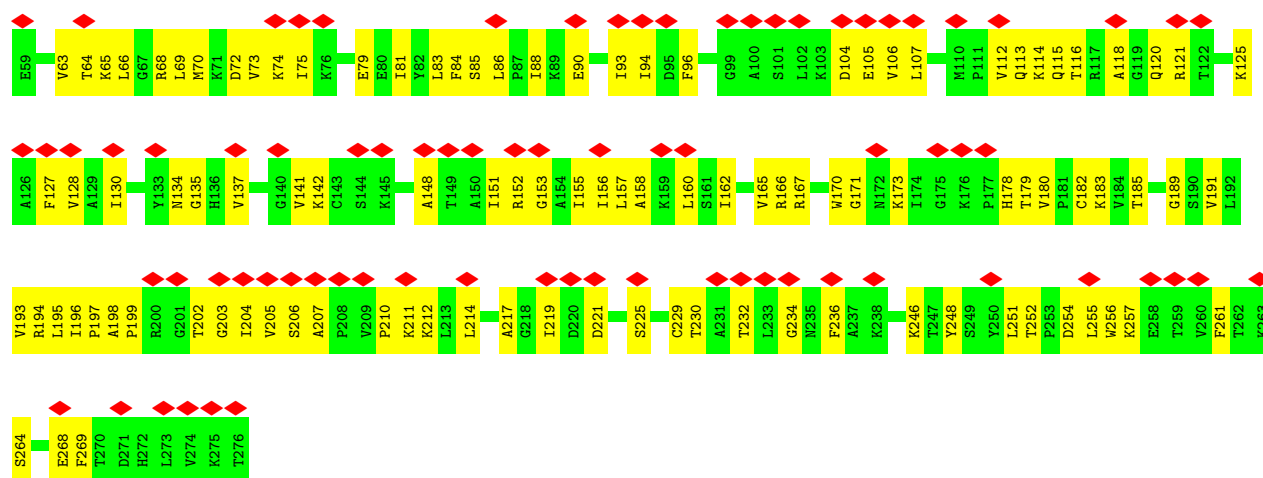


• Molecule 60: 40S ribosomal protein S3a

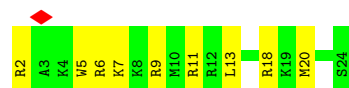




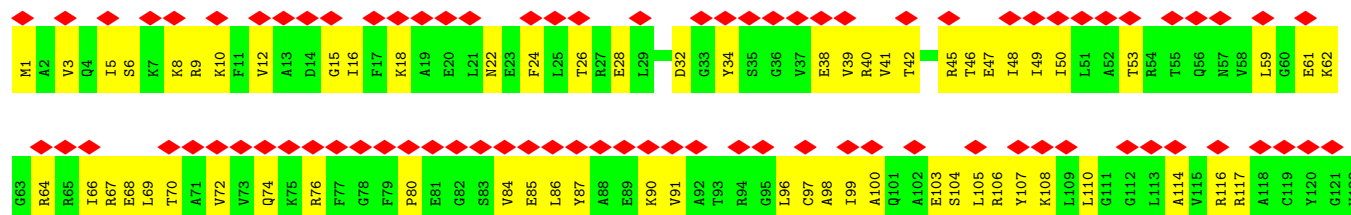
• Molecule 61: S5 DRBM domain-containing protein

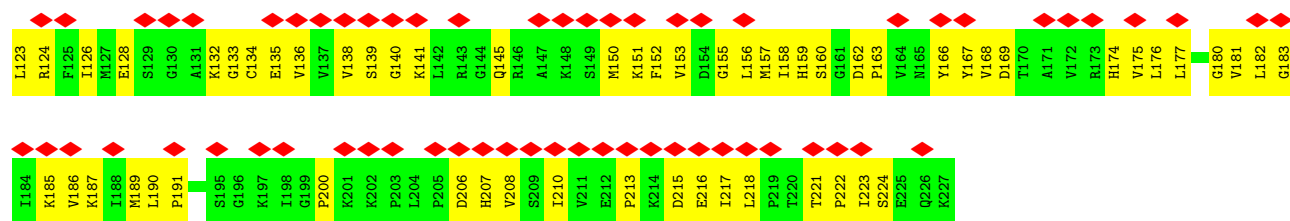


• Molecule 62: 60s ribosomal protein 141

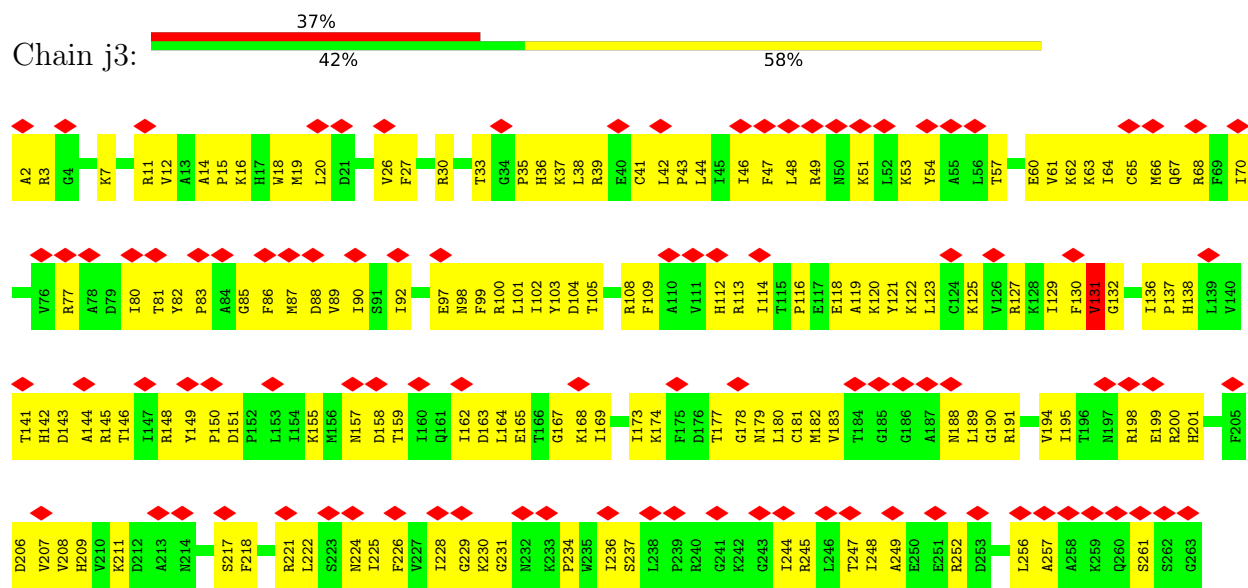


• Molecule 63: Ribosomal protein S3

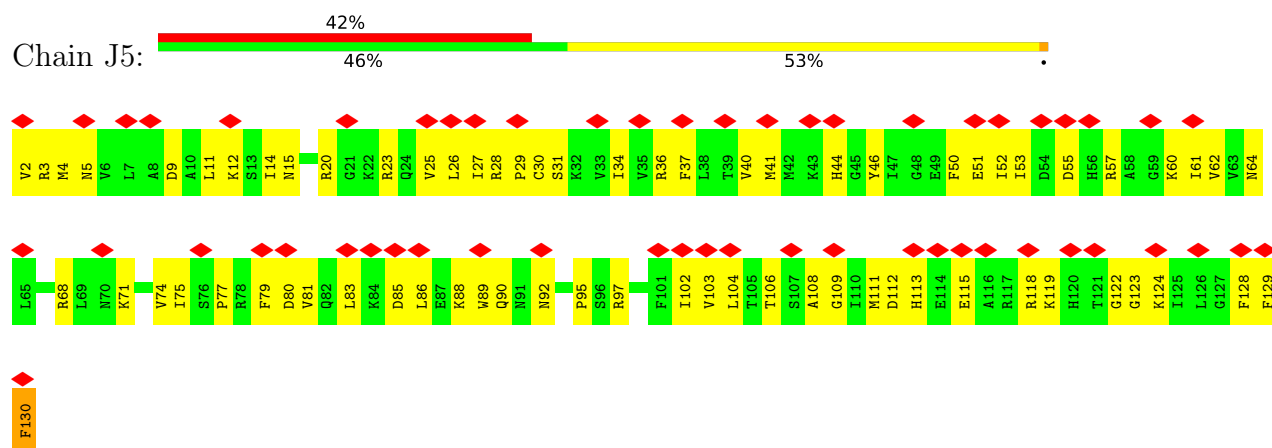




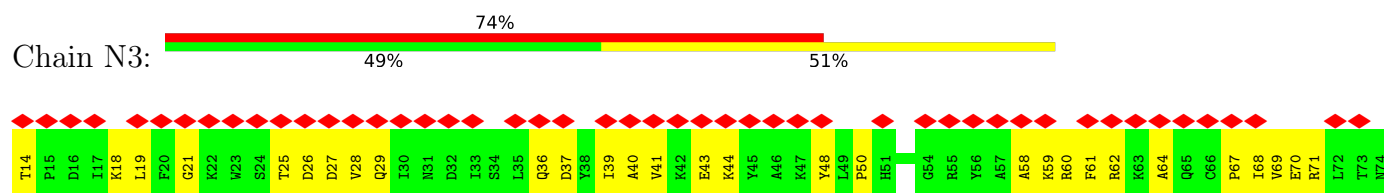
• Molecule 64: 40S ribosomal protein S4, 40S ribosomal protein S4

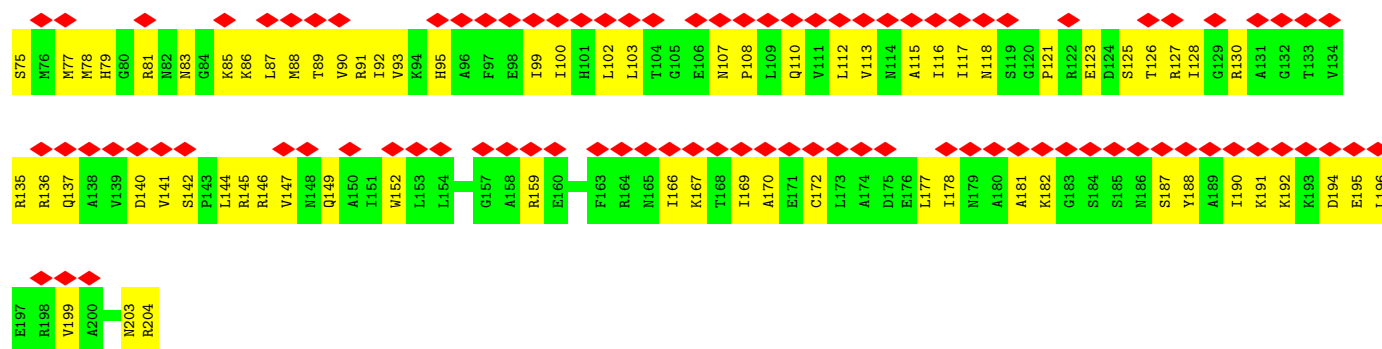


• Molecule 65: Ribosomal protein S15a

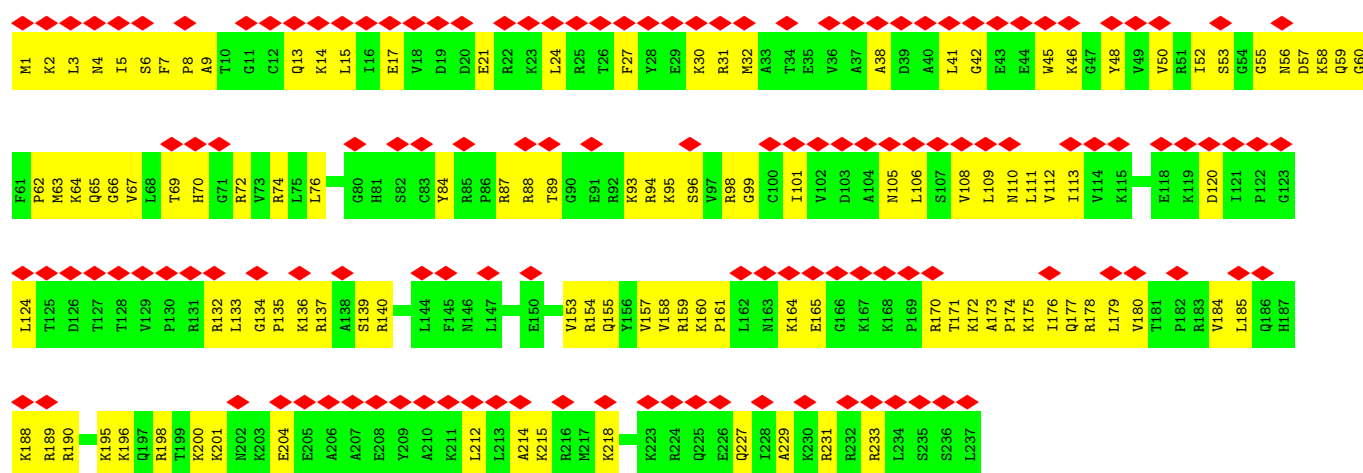


• Molecule 66: Ribosomal protein S5

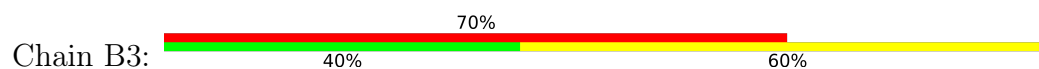




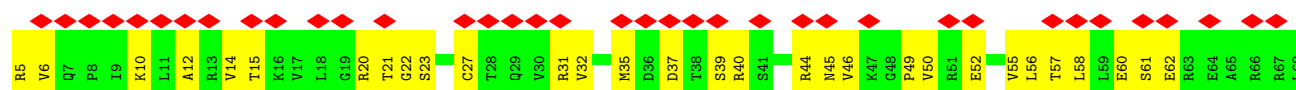
• Molecule 67: 40S ribosomal protein S6



• Molecule 68: Uncharacterized protein

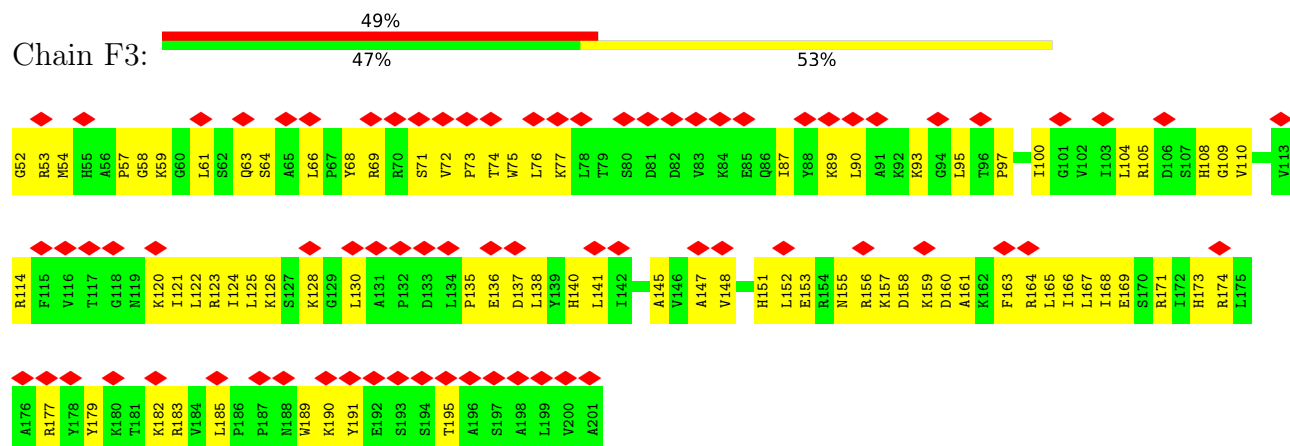


• Molecule 69: ribosomal protein eS28



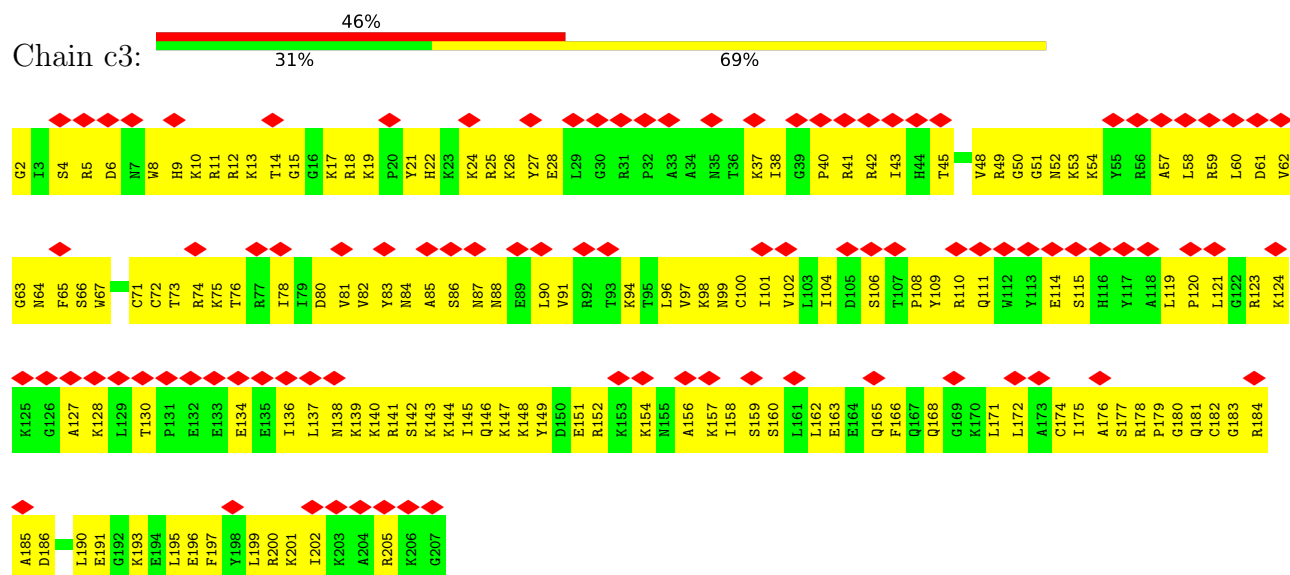
• Molecule 70: ribosomal protein uS15

Chain F3:



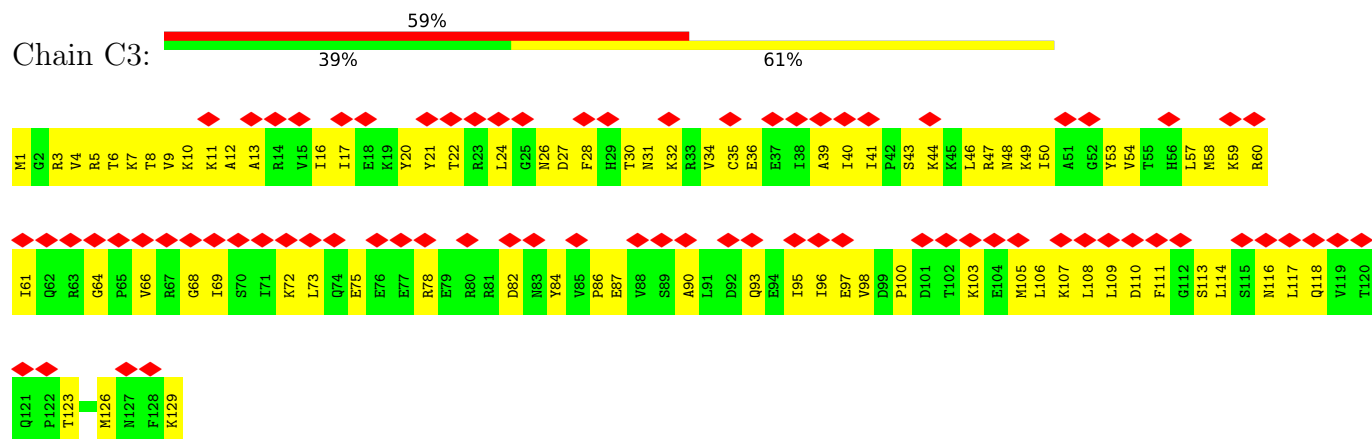
• Molecule 71: 40S ribosomal protein S8

Chain c3:

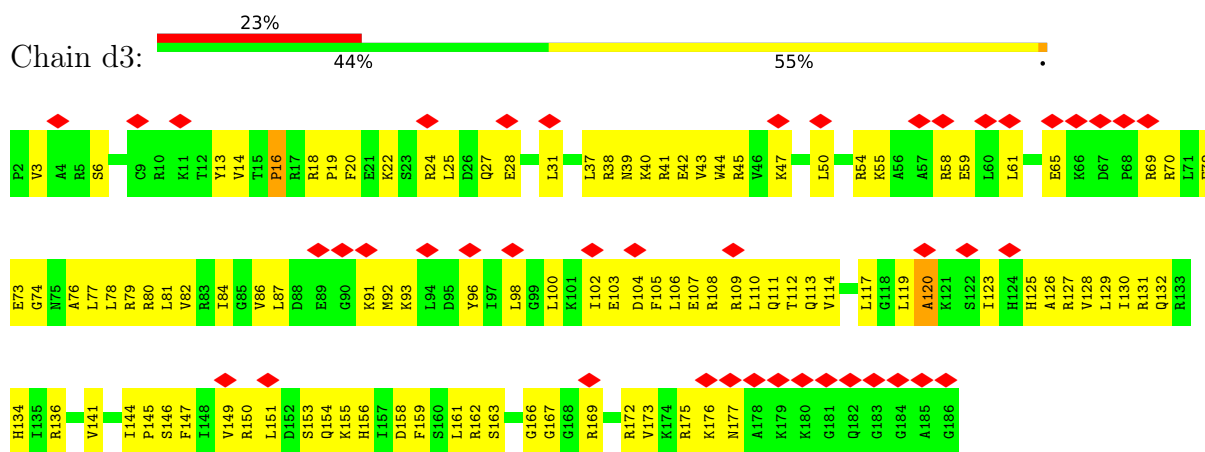


• Molecule 72: Uncharacterized protein

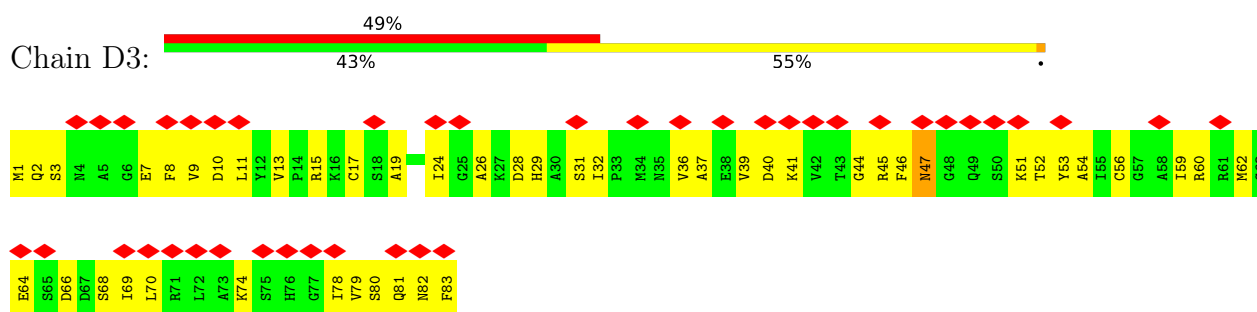
Chain C3:



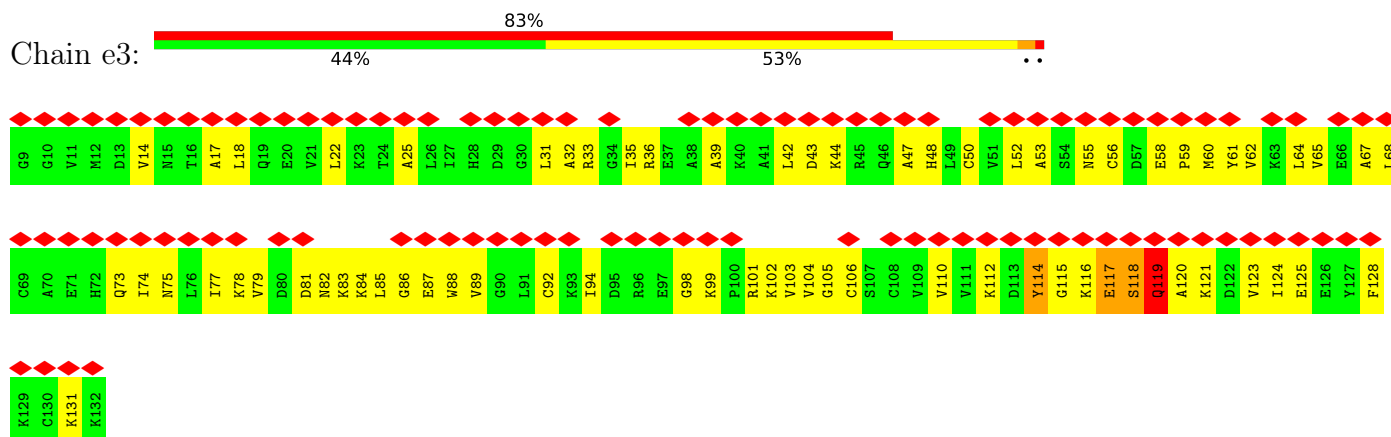
• Molecule 73: Ribosomal protein S9 (Predicted)



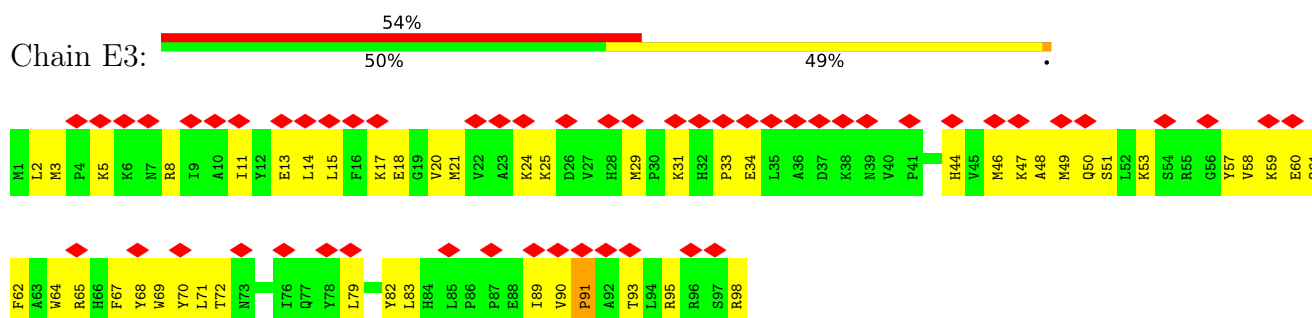
• Molecule 74: 40S RIBOSOMAL PROTEIN ES21



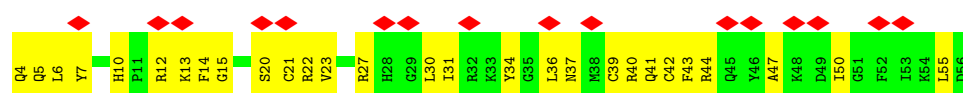
• Molecule 75: 40S ribosomal protein S12



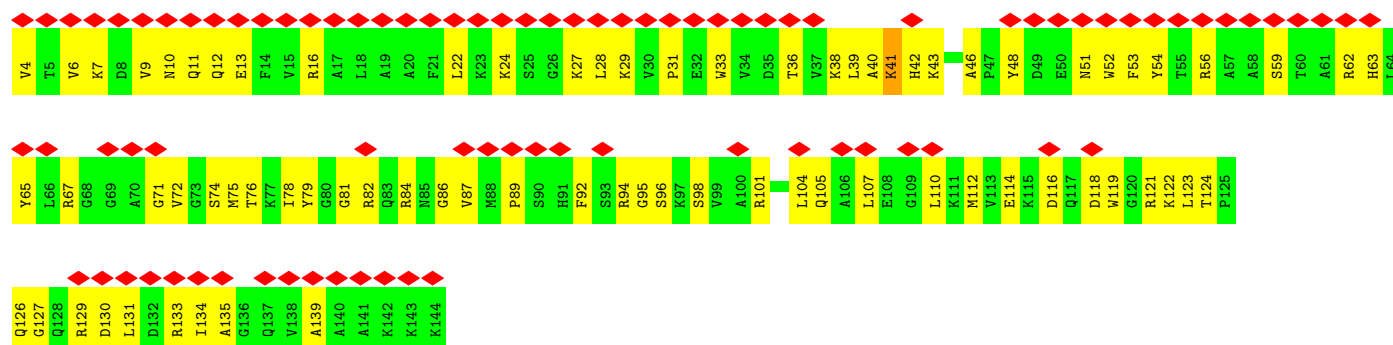
• Molecule 76: S10_pectin domain-containing protein



• Molecule 77: ribosomal protein uS14



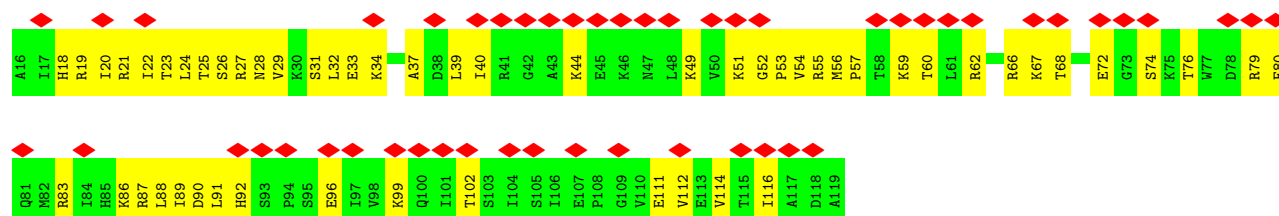
• Molecule 78: Uncharacterized protein



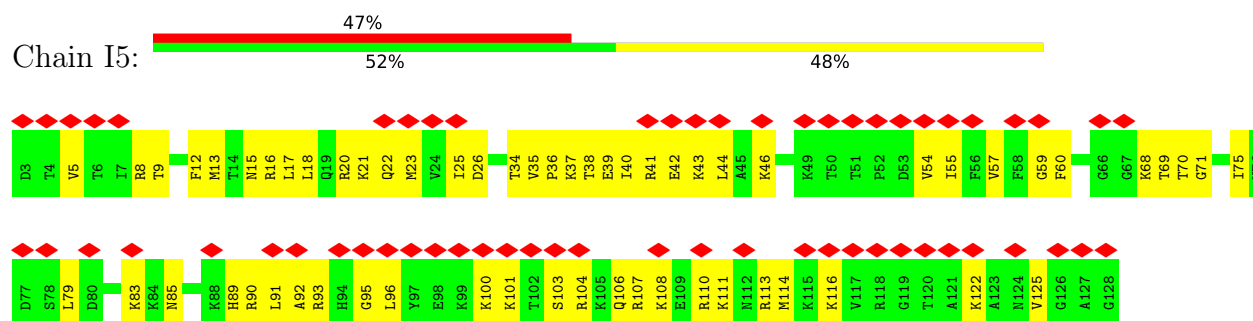
• Molecule 79: 40S RIBOSOMAL PROTEIN ES7



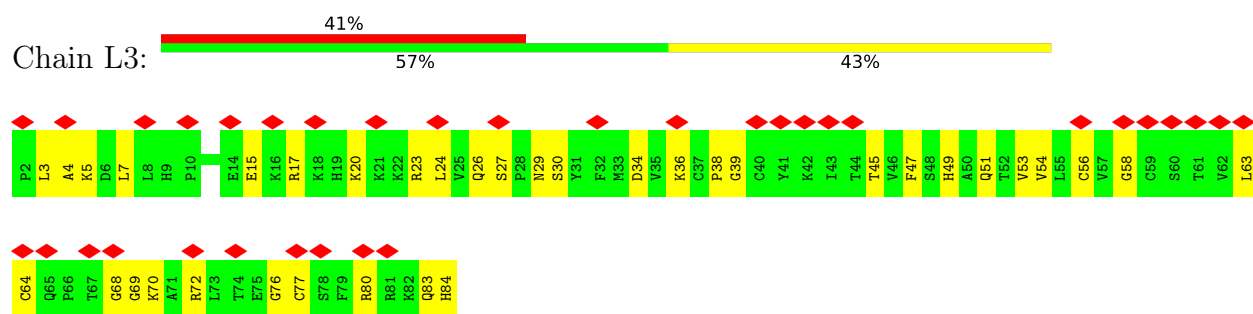
• Molecule 80: Ribosomal_S10 domain-containing protein



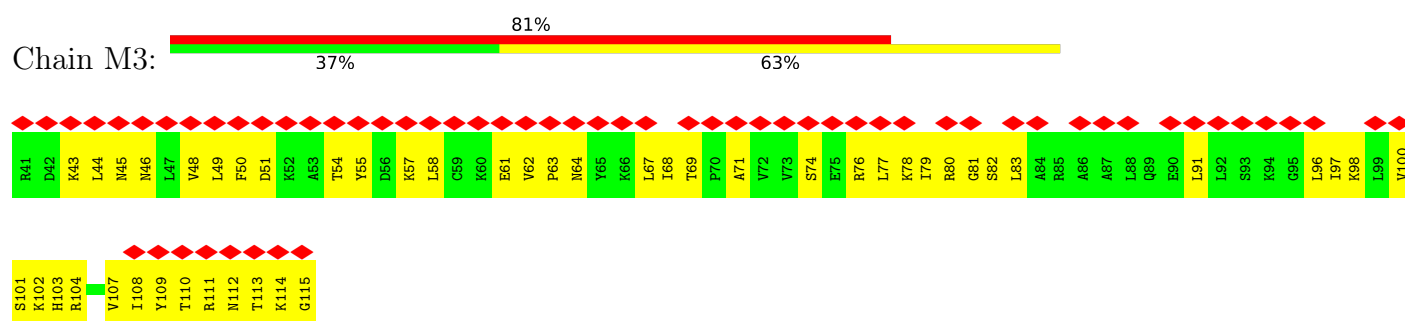
- Molecule 81: 40S ribosomal protein S24



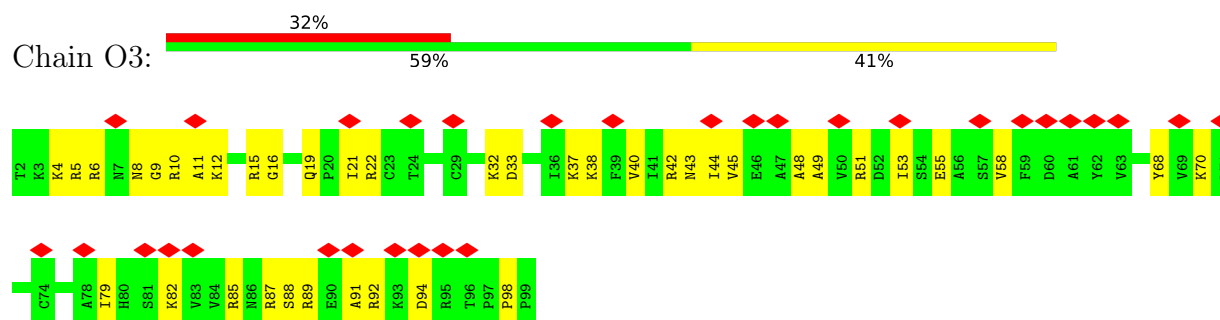
- Molecule 82: 40S ribosomal protein S27



- Molecule 83: ribosomal protein eS25

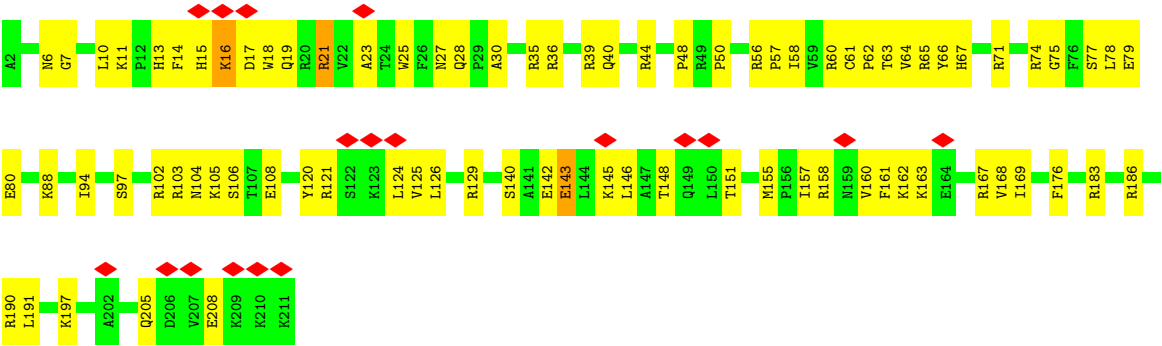


- Molecule 84: 40S RIBOSOMAL PROTEIN ES26



- 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

5.1 Standard geometry

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	0.21	0/3579	0.48	0/5560
2	e2	0.36	0/91668	0.44	0/143010
3	h2	0.37	0/3701	0.43	0/5766
4	d2	0.32	0/2858	0.37	0/4455
5	p2	0.35	0/574	0.59	0/761
6	k2	0.37	0/993	0.60	0/1332
7	l2	0.32	0/542	0.70	1/720 (0.1%)
8	m2	0.31	0/993	0.54	0/1334
9	o2	0.35	0/1133	0.55	0/1504
10	q2	0.45	0/1191	0.62	0/1590
11	r2	0.31	0/620	0.61	0/818
12	t2	0.38	0/2938	0.58	0/3946
13	u2	0.38	0/904	0.56	0/1216
14	v2	0.42	0/1072	0.56	0/1429
15	w2	0.41	0/1662	0.57	0/2222
16	x2	0.43	0/895	0.64	0/1198
17	y2	0.39	0/917	0.63	0/1220
18	92	0.41	0/1907	0.60	0/2556
19	A2	0.31	0/1021	0.48	0/1348
20	B2	0.30	0/842	0.55	0/1112
21	C2	0.43	0/721	0.61	0/952
22	D2	0.39	0/454	0.62	0/599
23	E2	0.33	0/435	0.59	0/575
24	F2	0.36	0/865	0.64	0/1140
25	G2	0.31	0/2433	0.58	2/3257 (0.1%)
26	H2	0.43	0/1269	0.59	0/1700
27	I2	0.38	0/718	0.58	0/953
28	J2	0.38	0/1018	0.55	0/1364
29	K2	0.25	0/1548	0.62	1/2088 (0.0%)
30	L2	0.42	0/853	0.56	0/1137
31	M2	0.23	0/1198	0.69	0/1611
32	R2	0.32	0/292	0.56	0/388

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	S2	0.41	0/1537	0.61	0/2052
34	T2	0.32	0/1646	0.64	0/2213
35	U2	0.43	0/1911	0.60	0/2549
36	V2	0.29	0/1965	0.51	0/2644
37	W2	0.35	0/1536	0.53	0/2063
38	X2	0.37	0/841	0.54	0/1123
39	Y2	0.29	0/1377	0.54	0/1841
40	O2	0.33	0/1159	0.62	0/1547
41	12	0.44	0/1746	0.68	1/2338 (0.0%)
42	22	0.32	0/1130	0.54	0/1507
43	32	0.34	0/1525	0.56	0/2013
44	42	0.25	0/1772	0.69	2/2375 (0.1%)
45	52	0.39	0/3241	0.58	0/4339
46	62	0.38	0/1493	0.59	0/2003
47	72	0.39	0/1326	0.64	2/1770 (0.1%)
48	82	0.29	0/823	0.54	0/1103
49	K3	0.22	0/42945	0.44	0/66942
50	s3	0.22	0/354	0.54	0/462
51	13	0.31	0/743	0.50	0/995
52	Q3	0.26	0/538	0.65	1/713 (0.1%)
53	G3	0.25	0/1269	0.57	0/1696
54	G5	0.25	0/1158	0.64	0/1548
55	a3	0.23	0/2494	0.56	0/3394
56	a5	0.24	0/1029	0.56	0/1380
57	A3	0.24	0/1080	0.55	0/1437
58	T3	0.26	0/1117	0.55	0/1490
59	U3	0.24	0/1682	0.53	0/2286
60	V3	0.26	0/1757	0.66	1/2350 (0.0%)
61	W3	0.25	0/1727	0.58	0/2332
62	X3	0.27	0/224	0.59	0/284
63	Y3	0.25	0/1793	0.57	0/2412
64	j3	0.25	0/2117	0.58	0/2846
65	J5	1.33	6/1051 (0.6%)	1.30	8/1406 (0.6%)
66	N3	0.24	0/1531	0.57	0/2059
67	b3	0.24	0/1947	0.54	0/2590
68	B3	0.20	0/1142	0.59	0/1528
69	f3	0.24	0/509	0.60	0/680
70	F3	0.26	0/1232	0.60	2/1656 (0.1%)
71	c3	0.25	0/1716	0.57	0/2287
72	C3	0.27	0/1061	0.65	0/1421
73	d3	0.43	1/1551 (0.1%)	0.78	3/2069 (0.1%)
74	D3	0.24	0/639	0.52	0/855
75	e3	0.22	0/968	0.63	0/1296

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	E3	0.24	0/852	0.55	1/1147 (0.1%)
77	H3	0.23	0/455	0.59	0/603
78	H5	0.21	0/1133	0.52	0/1517
79	P3	0.23	0/1545	0.65	0/2068
80	I3	0.26	0/832	0.60	0/1117
81	I5	0.22	0/1041	0.54	0/1382
82	L3	0.21	0/665	0.52	0/891
83	M3	0.25	0/605	0.52	0/810
84	O3	0.25	0/795	0.58	0/1065
85	a7	0.34	0/1733	0.65	1/2316 (0.0%)
All	All	0.34	7/241872 (0.0%)	0.51	26/355671 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
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 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	J5	130	PHE	CD2-CE2	24.28	2.11	1.38
65	J5	130	PHE	CD1-CE1	23.80	2.10	1.38
65	J5	130	PHE	CE2-CZ	-14.64	0.94	1.38
65	J5	130	PHE	CE1-CZ	-14.56	0.94	1.38
73	d3	16	PRO	CG-CD	-12.13	1.09	1.50

The worst 5 of 26 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	-20.26	88.21	118.60
73	d3	16	PRO	N-CD-CG	-14.70	81.15	103.20
65	J5	130	PHE	CG-CD2-CE2	-14.57	95.93	120.70
65	J5	130	PHE	CG-CD1-CE1	-14.19	96.57	120.70

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E1	3208	0	1622	92	0
2	e2	81951	0	41450	3399	0
3	h2	3314	0	1683	153	0
4	d2	2558	0	1296	107	0
5	p2	568	0	630	39	0
6	k2	979	0	1039	46	0
7	l2	529	0	541	30	0
8	m2	976	0	1053	44	0
9	o2	1116	0	1205	66	0
10	q2	1162	0	1209	69	0
11	r2	610	0	650	36	0
12	t2	2884	0	3053	145	0
13	u2	889	0	930	33	0
14	v2	1054	0	1147	41	0
15	w2	1630	0	1778	71	0
16	x2	876	0	912	47	0
17	y2	907	0	1002	75	0
18	92	1869	0	1959	84	0
19	A2	1013	0	1147	46	0
20	B2	831	0	916	27	0
21	C2	706	0	737	35	0
22	D2	444	0	483	29	0
23	E2	429	0	465	20	0
24	F2	852	0	920	45	0
25	G2	2387	0	2419	150	0
26	H2	1243	0	1274	66	0
27	I2	708	0	756	20	0
28	J2	1002	0	1060	52	0
29	K2	1524	0	1577	114	0
30	L2	834	0	855	42	0
31	M2	1183	0	1246	87	0
32	R2	285	0	298	27	0
33	S2	1513	0	1628	67	0
34	T2	1614	0	1748	116	0
35	U2	1875	0	1995	105	0
36	V2	1932	0	2083	76	0
37	W2	1517	0	1594	62	0
38	X2	822	0	849	42	0
39	Y2	1354	0	1386	63	0
40	O2	1138	0	1211	59	0
41	12	1701	0	1749	89	0
42	22	1107	0	1182	63	0
43	32	1509	0	1664	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	42	1744	0	1859	145	0
45	52	3173	0	3310	176	0
46	62	1453	0	1490	72	0
47	72	1298	0	1366	66	0
48	82	809	0	831	43	0
49	K3	38409	0	19428	2181	0
50	s3	351	0	388	21	0
51	l3	733	0	767	32	0
52	Q3	527	0	546	39	0
53	G3	1248	0	1323	90	0
54	G5	1140	0	1191	94	0
55	a3	2437	0	2393	161	0
56	a5	1016	0	1039	68	0
57	A3	1061	0	1120	88	0
58	T3	1099	0	1167	83	0
59	U3	1645	0	1648	105	0
60	V3	1730	0	1803	121	0
61	W3	1691	0	1777	113	0
62	X3	223	0	264	10	0
63	Y3	1765	0	1863	119	0
64	j3	2075	0	2177	157	0
65	J5	1034	0	1080	82	0
66	N3	1509	0	1563	97	0
67	b3	1924	0	2089	139	0
68	B3	1124	0	1193	76	0
69	f3	507	0	536	29	0
70	F3	1208	0	1294	85	0
71	c3	1687	0	1772	175	0
72	C3	1048	0	1103	89	0
73	d3	1526	0	1640	132	0
74	D3	631	0	631	55	0
75	e3	958	0	993	61	0
76	E3	828	0	854	58	0
77	H3	445	0	438	31	0
78	H5	1113	0	1149	89	0
79	P3	1522	0	1616	107	0
80	I3	822	0	887	64	0
81	I5	1024	0	1090	62	0
82	L3	651	0	672	36	0
83	M3	599	0	656	52	0
84	O3	782	0	828	50	0
85	a7	1702	0	1820	102	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	C2	1	0	0	0	0
86	E2	1	0	0	0	0
86	F2	1	0	0	0	0
86	H3	1	0	0	0	0
86	I2	1	0	0	0	0
86	O3	1	0	0	0	0
All	All	224880	0	166055	10018	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 26.

The worst 5 of 10018 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:K3:1709:G:H1	49:K3:1824:A:N6	1.35	1.22
49:K3:1743:G:N2	49:K3:1791:A:H62	1.41	1.19
49:K3:1605:G:C2	49:K3:1634:A:N6	2.13	1.17
49:K3:1743:G:H21	49:K3:1791:A:N6	1.43	1.16
2:e2:1968:G:C2	2:e2:2016:A:N6	2.14	1.14

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	36	65
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%)	30	61
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
30	L2	100/102 (98%)	87 (87%)	13 (13%)	0	100	100
31	M2	150/163 (92%)	106 (71%)	43 (29%)	1 (1%)	18	51
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%)	24	57
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	12	201/203 (99%)	175 (87%)	26 (13%)	0	100	100
42	22	133/135 (98%)	112 (84%)	21 (16%)	0	100	100
43	32	178/180 (99%)	172 (97%)	6 (3%)	0	100	100
44	42	215/217 (99%)	152 (71%)	62 (29%)	1 (0%)	24	57
45	52	392/394 (100%)	338 (86%)	53 (14%)	1 (0%)	36	65
46	62	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
47	72	157/159 (99%)	127 (81%)	29 (18%)	1 (1%)	21	54
48	82	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
50	s3	41/43 (95%)	30 (73%)	11 (27%)	0	100	100
51	13	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%)	8	37
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
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%)	30	61
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	3	24
76	E3	96/98 (98%)	80 (83%)	15 (16%)	1 (1%)	12	45
77	H3	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
78	H5	139/141 (99%)	122 (88%)	16 (12%)	1 (1%)	18	51
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%)	12	45
All	All	11692/11990 (98%)	9975 (85%)	1699 (14%)	18 (0%)	44	72

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 ⓘ

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%)	64 (100%)	0	100	100
6	k2	101/101 (100%)	101 (100%)	0	100	100
7	l2	55/55 (100%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	m2	107/107 (100%)	107 (100%)	0	100	100
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%)	114 (100%)	0	100	100
15	w2	171/171 (100%)	171 (100%)	0	100	100
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%)	187 (100%)	0	100	100
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%)	47 (100%)	0	100	100
23	E2	48/48 (100%)	48 (100%)	0	100	100
24	F2	92/92 (100%)	92 (100%)	0	100	100
25	G2	247/247 (100%)	247 (100%)	0	100	100
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%)	89 (100%)	0	100	100
31	M2	131/136 (96%)	131 (100%)	0	100	100
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%)	169 (100%)	0	100	100
38	X2	85/85 (100%)	85 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Y2	142/142 (100%)	142 (100%)	0	100	100
40	02	117/117 (100%)	117 (100%)	0	100	100
41	12	171/171 (100%)	171 (100%)	0	100	100
42	22	117/117 (100%)	117 (100%)	0	100	100
43	32	159/159 (100%)	158 (99%)	1 (1%)	78	79
44	42	196/196 (100%)	196 (100%)	0	100	100
45	52	342/342 (100%)	342 (100%)	0	100	100
46	62	156/156 (100%)	156 (100%)	0	100	100
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%)	137 (100%)	0	100	100
54	G5	119/119 (100%)	119 (100%)	0	100	100
55	a3	272/272 (100%)	271 (100%)	1 (0%)	84	81
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%)	113 (100%)	0	100	100
59	U3	175/175 (100%)	175 (100%)	0	100	100
60	V3	194/194 (100%)	194 (100%)	0	100	100
61	W3	184/184 (100%)	184 (100%)	0	100	100
62	X3	22/22 (100%)	22 (100%)	0	100	100
63	Y3	190/190 (100%)	190 (100%)	0	100	100
64	j3	224/224 (100%)	223 (100%)	1 (0%)	84	81
65	J5	112/112 (100%)	112 (100%)	0	100	100
66	N3	161/161 (100%)	160 (99%)	1 (1%)	78	79
67	b3	207/207 (100%)	207 (100%)	0	100	100
68	B3	117/117 (100%)	117 (100%)	0	100	100
69	f3	57/57 (100%)	57 (100%)	0	100	100
70	F3	130/130 (100%)	130 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	104 (100%)	0	100	100
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%)	94 (100%)	0	100	100
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%)	10206 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	32	130	ASN
55	a3	272	GLN
64	j3	131	VAL
66	N3	118	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 109 such sidechains are listed below:

Mol	Chain	Res	Type
44	42	199	GLN
58	T3	110	HIS
76	E3	32	HIS
46	62	77	ASN
53	G3	112	HIS

5.3.3 RNA ⓘ

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 oligosaccharides 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.

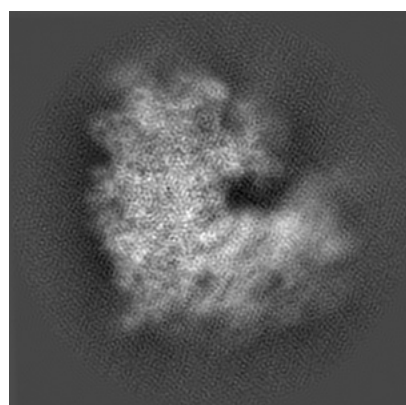
6 Map visualisation [i](#)

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.

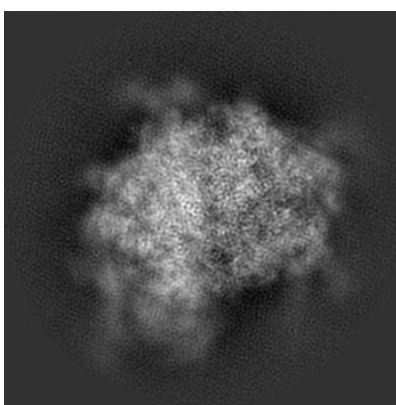
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

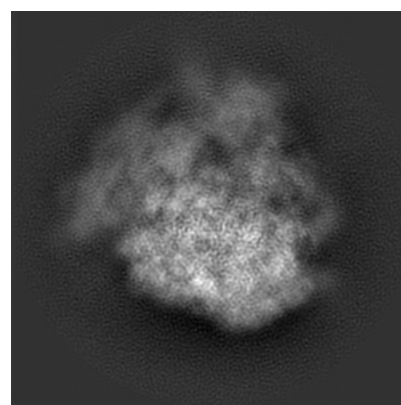
6.1.1 Primary map



X



Y

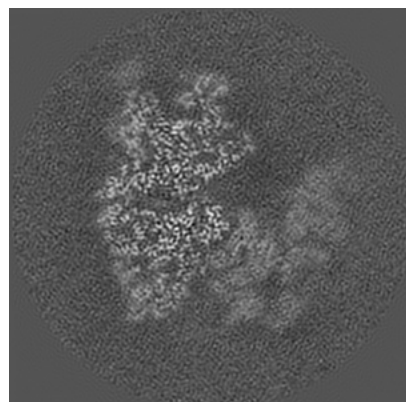


Z

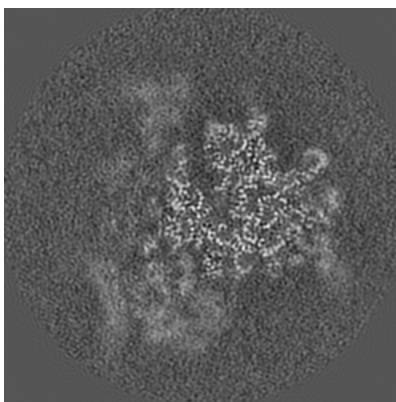
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

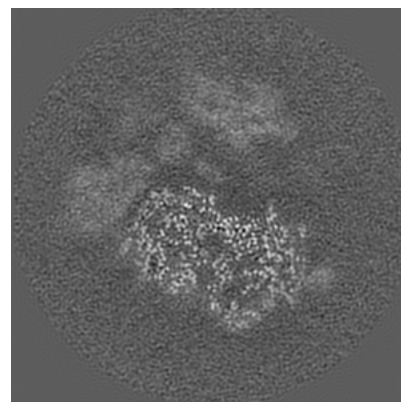
6.2.1 Primary map



X Index: 180



Y Index: 180

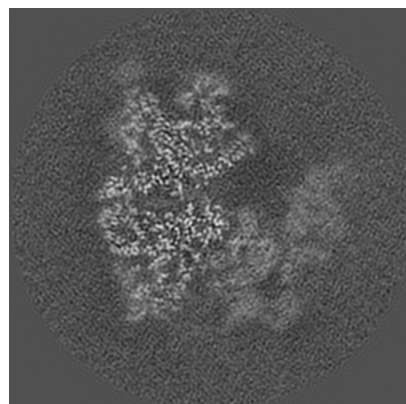


Z Index: 180

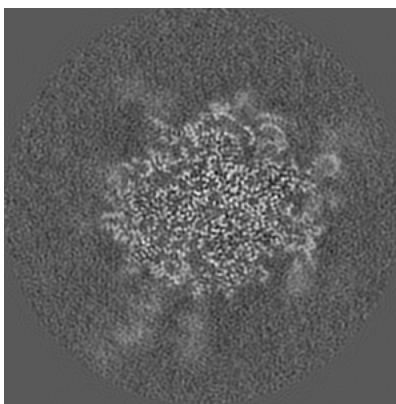
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

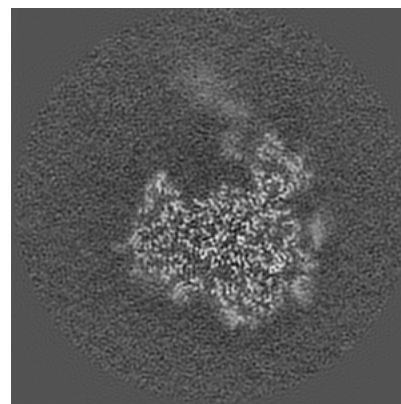
6.3.1 Primary map



X Index: 179



Y Index: 158

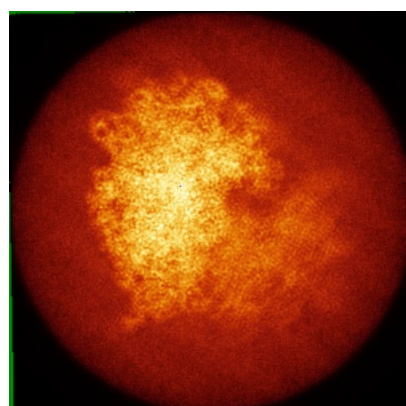


Z Index: 212

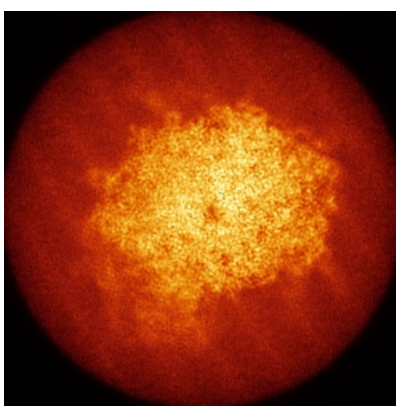
The images above show the largest variance slices of the map in three orthogonal directions.

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

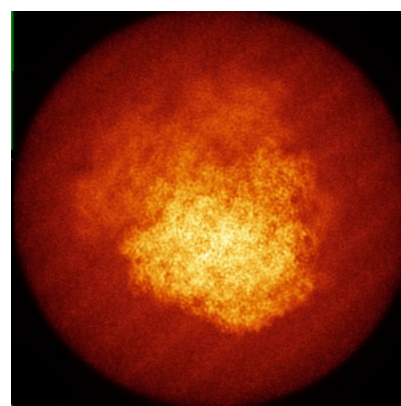
6.4.1 Primary map



X



Y

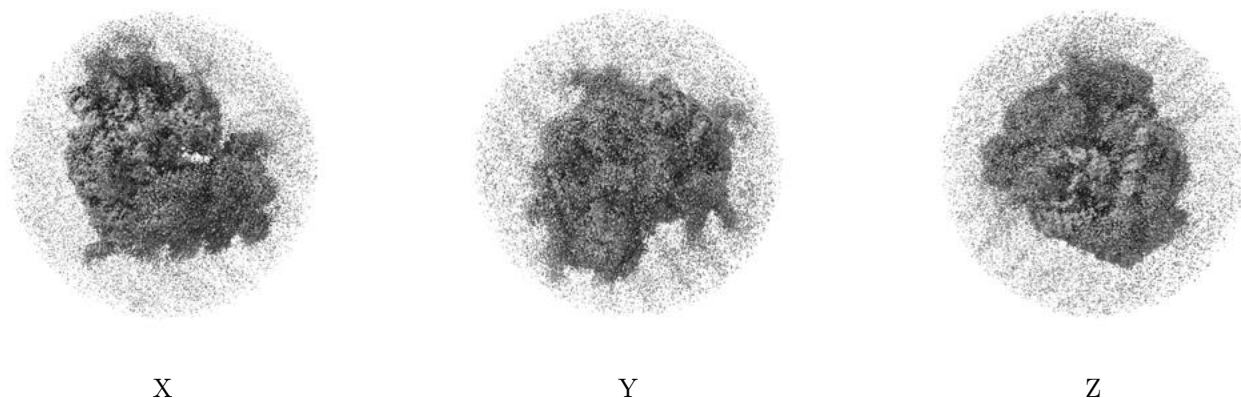


Z

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 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

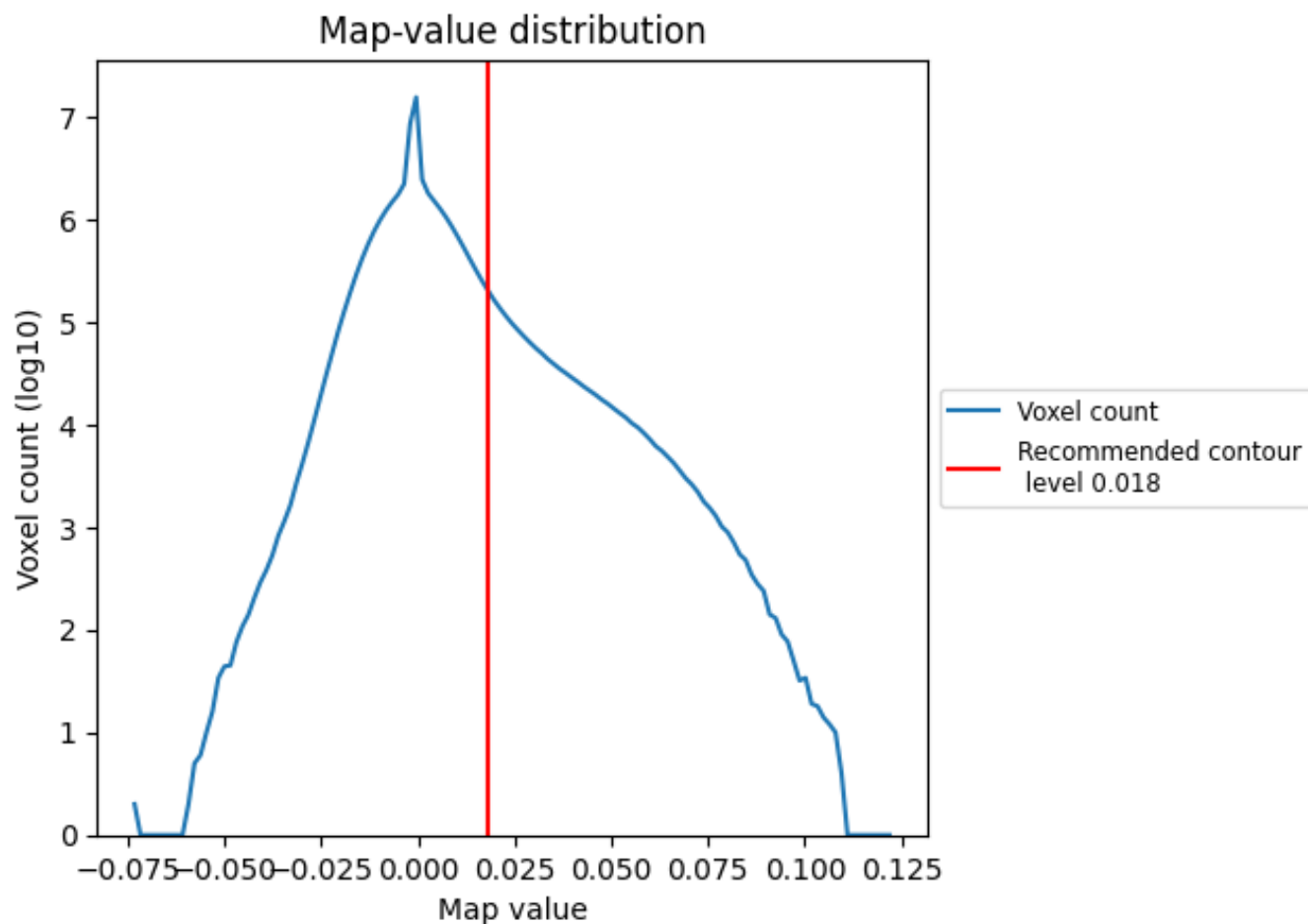
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

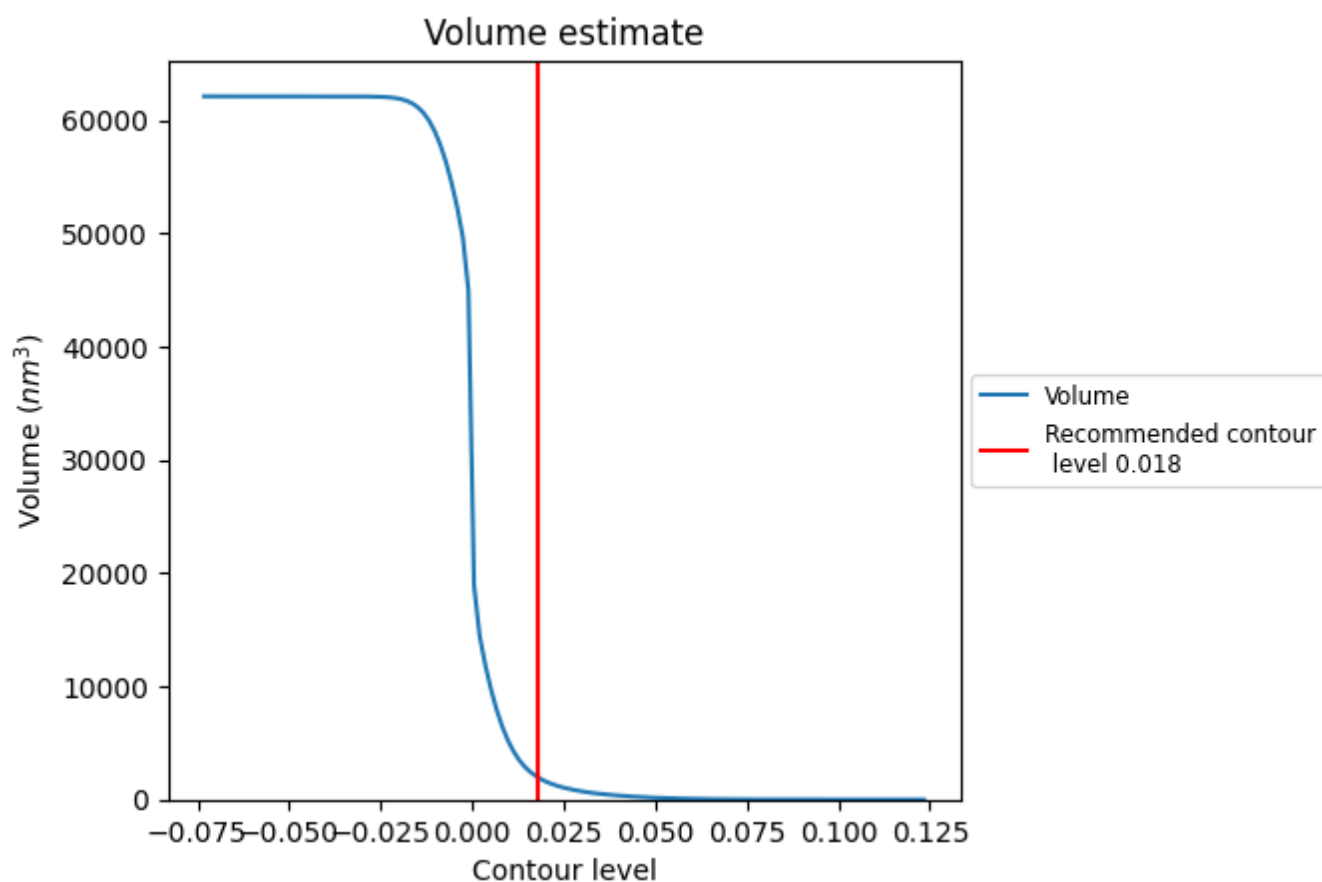
This section contains the results of statistical analysis of the map.

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.

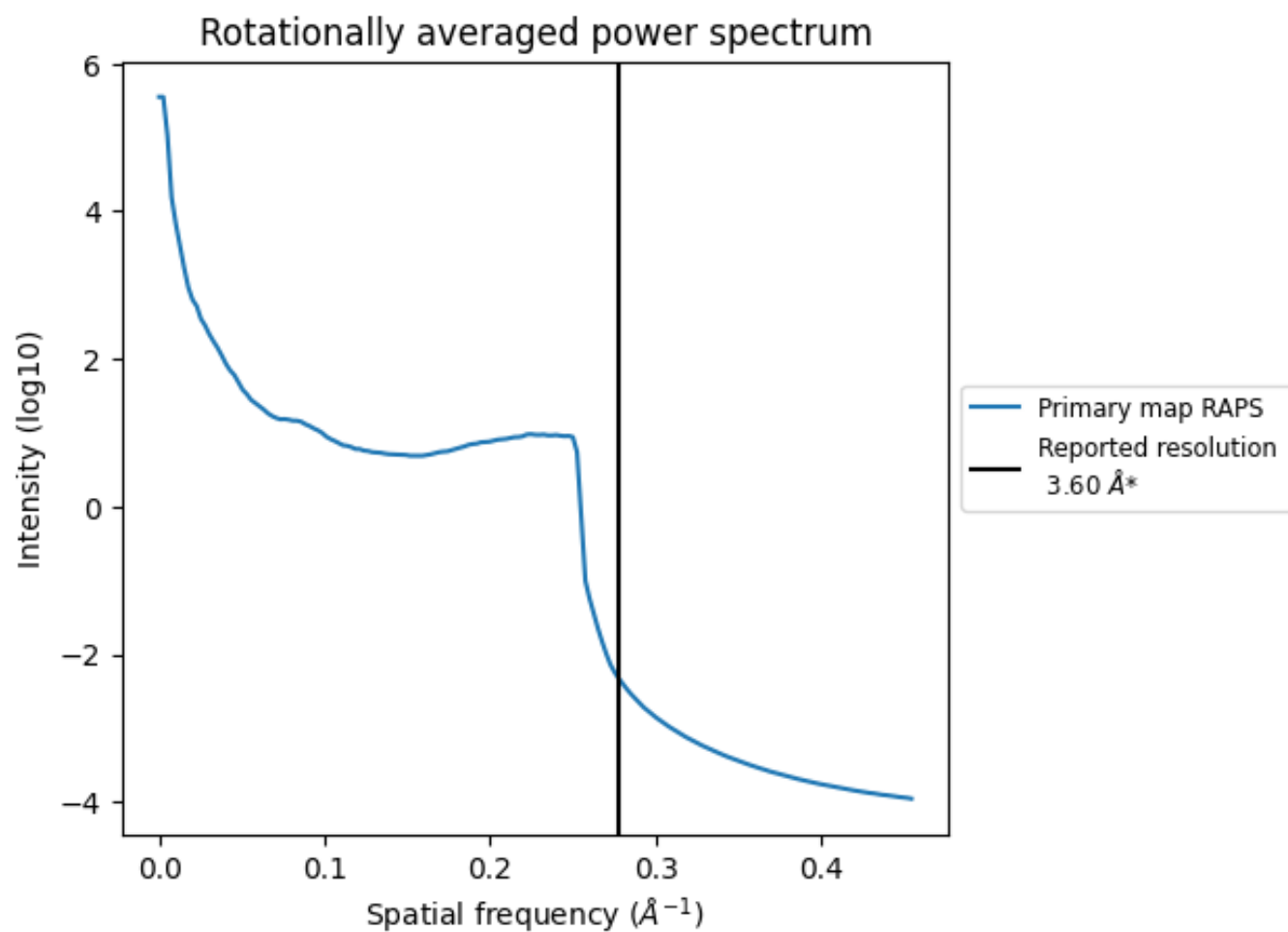
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1960 nm³; 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

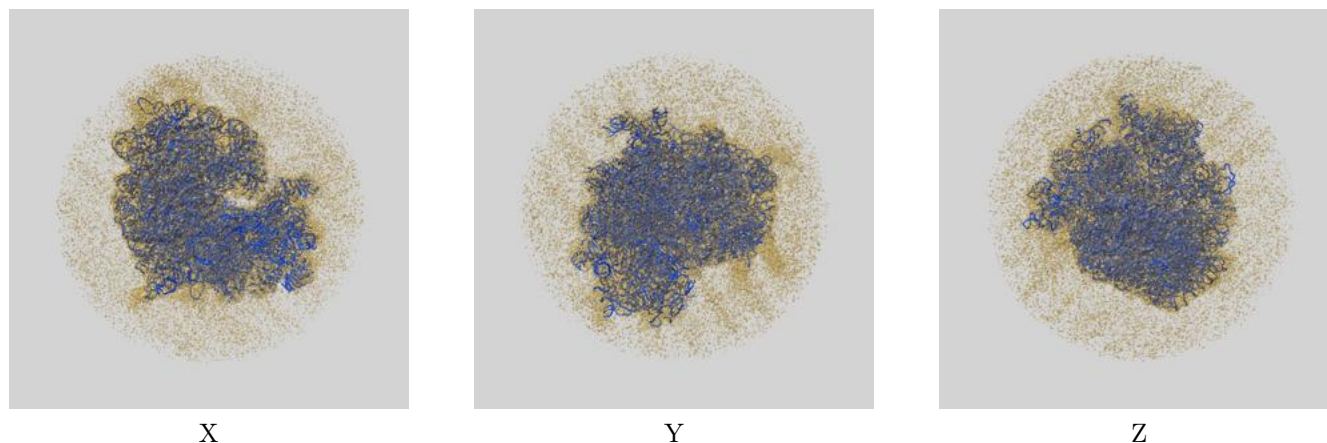
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

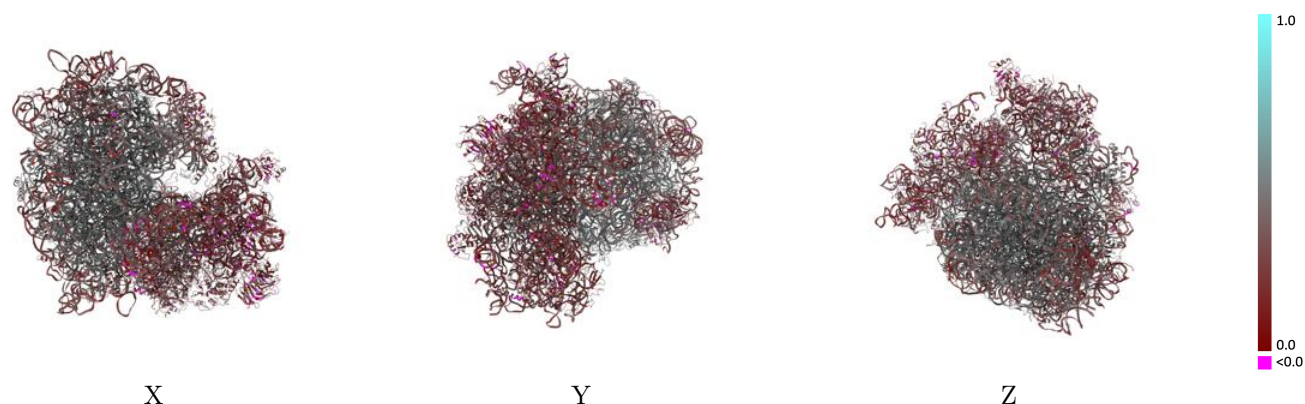
This section contains information regarding the fit between EMDB map EMD-11590 and PDB model 7A01. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



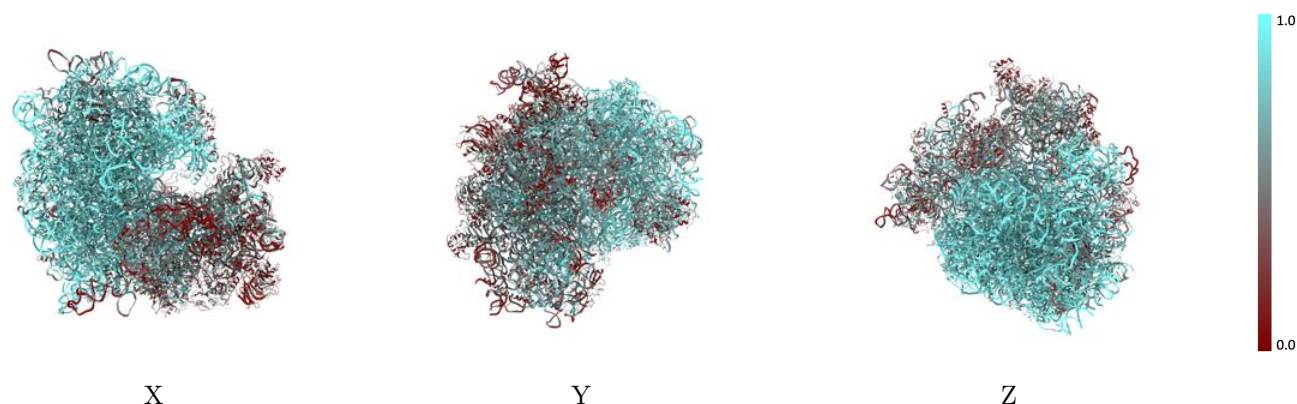
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



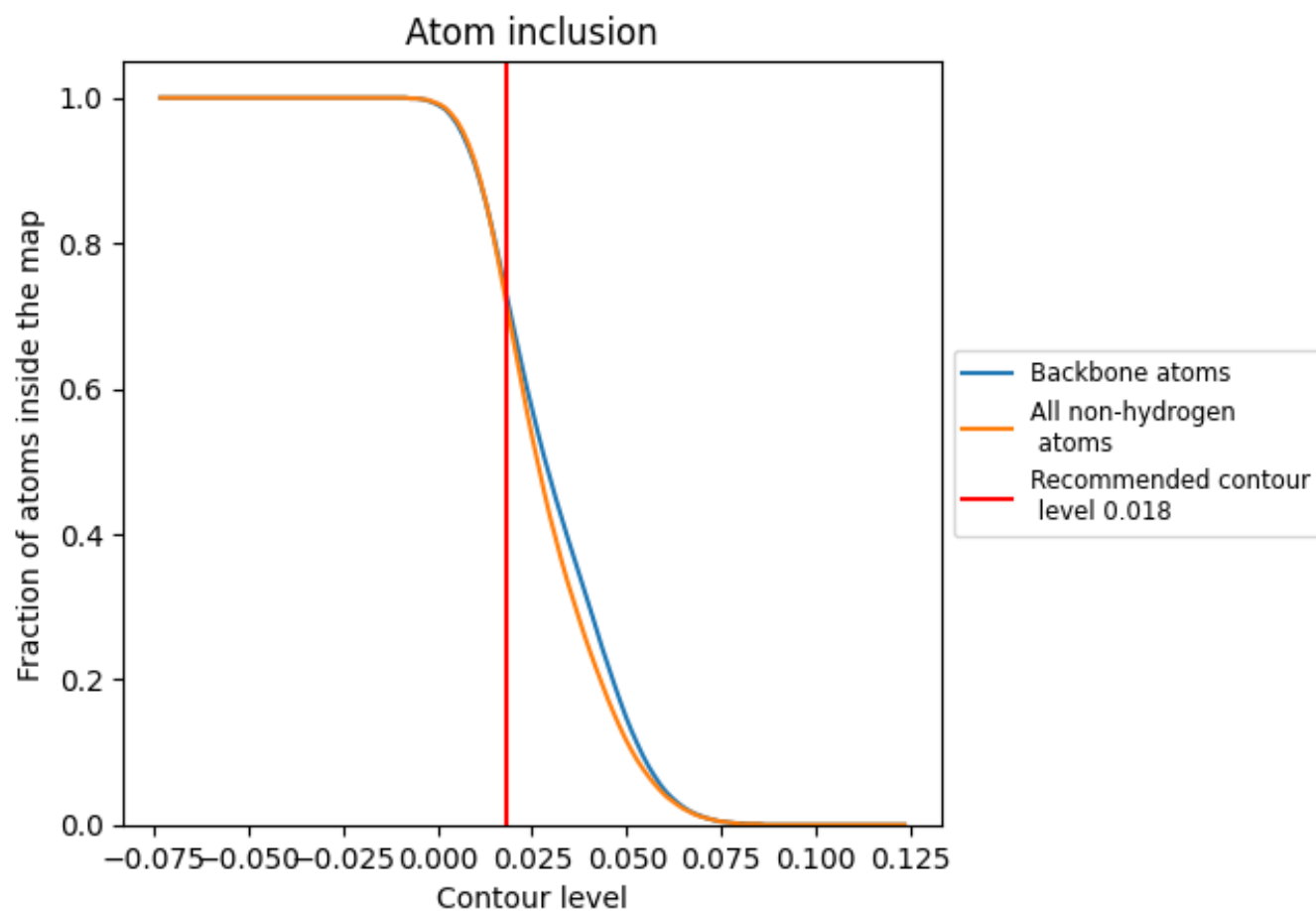
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.7230	 0.3700
02	 0.8760	 0.4520
12	 0.8610	 0.4890
13	 0.8370	 0.4510
22	 0.8580	 0.4430
32	 0.7980	 0.4470
42	 0.2700	 0.2610
52	 0.8670	 0.4770
62	 0.8600	 0.4850
72	 0.8190	 0.4820
82	 0.8410	 0.4270
92	 0.8560	 0.5050
A2	 0.8280	 0.4600
A3	 0.4630	 0.2890
B2	 0.8180	 0.4510
B3	 0.2900	 0.2470
C2	 0.9050	 0.5190
C3	 0.3530	 0.2680
D2	 0.8820	 0.4960
D3	 0.4470	 0.3090
E1	 0.2150	 0.2500
E2	 0.8320	 0.4760
E3	 0.3810	 0.2650
F2	 0.8040	 0.4810
F3	 0.4420	 0.3290
G2	 0.8540	 0.4170
G3	 0.4800	 0.3360
G5	 0.4010	 0.2980
H2	 0.8640	 0.4860
H3	 0.5440	 0.2900
H5	 0.3420	 0.2630
I2	 0.8240	 0.4900
I3	 0.4580	 0.2810
I5	 0.4590	 0.2680
J2	 0.8580	 0.4580



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Chain	Atom inclusion	Q-score
J5	 0.4630	 0.3290
K2	 0.2520	 0.2480
K3	 0.6100	 0.2730
L2	 0.8210	 0.4950
L3	 0.4870	 0.3230
M2	 0.2260	 0.2640
M3	 0.1750	 0.2390
N3	 0.2600	 0.2620
O3	 0.5440	 0.3390
P3	 0.3530	 0.3040
Q3	 0.3090	 0.2570
R2	 0.8440	 0.3710
S2	 0.8560	 0.4930
T2	 0.7760	 0.4050
T3	 0.4780	 0.3350
U2	 0.8460	 0.4680
U3	 0.4050	 0.2990
V2	 0.7810	 0.4220
V3	 0.4360	 0.3070
W2	 0.8350	 0.4590
W3	 0.5150	 0.3250
X2	 0.8180	 0.4550
X3	 0.7180	 0.4630
Y2	 0.8220	 0.4250
Y3	 0.3290	 0.2580
a3	 0.2560	 0.2500
a5	 0.5060	 0.3330
a7	 0.8050	 0.4340
b3	 0.3700	 0.2770
c3	 0.4460	 0.2780
d2	 0.9590	 0.4240
d3	 0.5910	 0.2760
e2	 0.8800	 0.4000
e3	 0.2270	 0.2400
f3	 0.3510	 0.2880
h2	 0.9270	 0.4260
j3	 0.5160	 0.3020
k2	 0.8040	 0.5040
l2	 0.8140	 0.4730
m2	 0.8570	 0.4910
o2	 0.8530	 0.4650
p2	 0.7790	 0.4250

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Chain	Atom inclusion	Q-score
q2	 0.8810	 0.4850
r2	 0.7210	 0.3830
s3	 0.3780	 0.2870
t2	 0.8460	 0.4820
u2	 0.8360	 0.4700
v2	 0.8580	 0.5080
w2	 0.8670	 0.4780
x2	 0.8720	 0.5050
y2	 0.7970	 0.4570