



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2026 – 05:48 pm BST

PDB ID : 9QOH / pdb_00009qoh
EMDB ID : EMD-53262
Title : Mouse Ribosome POST translocation state
Authors : Santo, P.E.; Astier, A.; Plisson-Chastang, C.
Deposited on : 2025-03-26
Resolution : 2.78 Å(reported)
Based on initial model : 7LS1

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

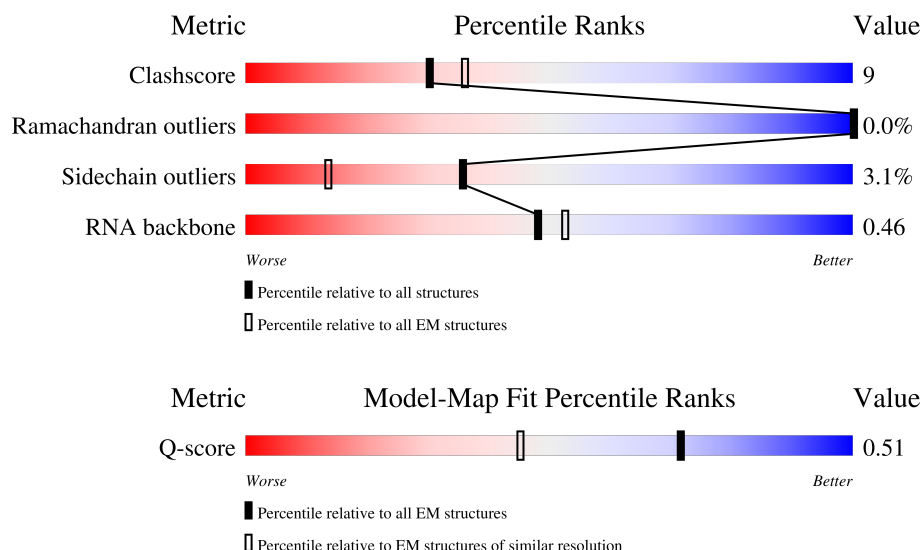
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal 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 2.78 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	10754 (2.28 - 3.28)

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	A1	270	5% 59% 23% 18%
2	A2	3615	19% 53% 39% 7%
3	A3	152	69% 56% 34% 8%

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Mol	Chain	Length	Quality of chain
4	B1	266	
5	B2	121	
6	B3	145	
7	Bv	76	
7	n2	76	
8	Bx	10	
9	C1	192	
10	C2	156	
11	C3	119	
12	D1	214	
13	D2	257	
14	D3	83	
15	E1	178	
16	E2	403	
17	E3	143	
18	F1	203	
19	F2	419	
20	F3	115	
21	G1	217	
22	G2	297	
23	G3	69	
24	H1	204	
25	H2	296	
26	H3	56	
27	I2	203	

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Mol	Chain	Length	Quality of chain
28	I3	317	
29	J2	184	
30	J3	293	
31	K2	188	
32	K3	249	
33	L1	217	
34	L2	196	
35	L3	194	
36	M2	176	
37	M3	132	
38	N2	160	
39	N3	151	
40	O2	128	
41	O3	151	
42	P2	140	
43	P3	130	
44	Q2	157	
45	Q3	133	
46	R2	156	
47	R3	125	
48	S2	145	
49	S3	84	
50	T2	136	
51	T3	133	
52	U2	148	

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Mol	Chain	Length	Quality of chain
53	U3	156	
54	V2	160	
55	W2	115	
56	X2	125	
57	Y2	135	
58	Z2	110	
59	a2	117	
60	b2	123	
61	c2	105	
62	d2	97	
63	e2	70	
64	f2	51	
65	g2	128	
66	h2	25	
67	i2	106	
68	j2	92	
69	k2	137	
70	m2	1635	
71	o2	295	
72	p2	264	
73	q2	243	
74	r2	263	
75	s2	204	
76	t2	194	
77	u2	208	

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Mol	Chain	Length	Quality of chain
78	v2	165	
79	w2	158	
80	x2	145	
81	y2	146	
82	z2	135	
83	A	22	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 213902 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	222	Total	C	N	O	S	1	0
			1851	1190	356	297	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A2	3615	Total	C	N	O	P	0	0
			77547	34568	14148	25217	3614		

- Molecule 3 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A3	140	Total	C	N	O	S	0	0
			1157	728	231	197	1		

- Molecule 4 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B1	223	Total	C	N	O	S	1	0
			1812	1156	351	301	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B2	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 6 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B3	141	Total	C	N	O	S	0	0
			1104	691	215	196	2		

- Molecule 7 is a RNA chain called transfer RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Bv	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		
7	n2	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 8 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Bx	10	Total	C	N	O	P	0	0
			200	90	20	80	10		

- Molecule 9 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C1	190	Total	C	N	O	S	0	0
			1519	956	284	273	6		

- Molecule 10 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C2	156	Total	C	N	O	P	0	0
			3315	1481	585	1094	155		

- Molecule 11 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C3	102	Total	C	N	O	S	0	0
			808	507	154	143	4		

- Molecule 12 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D1	204	Total	C	N	O	S	0	0
			1656	1052	319	272	13		

- Molecule 13 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D2	251	Total	C	N	O	S	0	0
			1921	1204	393	318	6		

- Molecule 14 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D3	83	Total	C	N	O	S	0	0
			638	392	119	122	5		

- Molecule 15 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E1	174	Total	C	N	O	S	0	0
			1397	880	260	251	6		

- Molecule 16 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	E2	402	Total	C	N	O	S	0	0
			3238	2060	609	555	14		

- Molecule 17 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	E3	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 18 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	F1	203	Total	C	N	O	S	0	0
			1643	1029	339	271	4		

- Molecule 19 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	F2	359	Total	C	N	O	S	0	0
			2867	1803	573	476	15		

- Molecule 20 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	F3	98	Total	C	N	O	S	1	0
			789	491	164	129	5		

- Molecule 21 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	G1	139	Total	C	N	O	S	0	0
			1143	732	221	183	7		

- Molecule 22 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	G2	293	Total	C	N	O	S	0	0
			2389	1509	441	425	14		

- Molecule 23 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	G3	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 24 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	H1	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 25 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	H2	221	Total	C	N	O	S	0	0
			1789	1145	342	298	4		

- Molecule 26 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	H3	54	Total	C	N	O	S	0	0
			454	284	93	72	5		

- Molecule 27 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	I2	201	Total	C	N	O	S	0	0
			1640	1055	320	259	6		

- Molecule 28 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	I3	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 29 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	J2	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 30 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	J3	219	Total	C	N	O	S	0	0
			1700	1101	292	298	9		

- Molecule 31 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	K2	186	Total	C	N	O	S	0	0
			1511	946	313	248	4		

- Molecule 32 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	K3	227	Total	C	N	O	S	0	0
			1840	1149	367	317	7		

- Molecule 33 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L1	161	Total	C	N	O	S	0	0
			1300	833	230	231	6		

- Molecule 34 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L2	179	Total	C	N	O	S	0	0
			1499	927	326	237	9		

- Molecule 35 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L3	184	Total	C	N	O	S	0	0
			1518	964	305	247	2		

- Molecule 36 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	M2	175	Total	C	N	O	S	0	0
			1450	924	283	233	10		

- Molecule 37 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	M3	122	Total	C	N	O	S	0	0
			952	599	168	177	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M3	69	LEU	CYS	variant	UNP P63323

- Molecule 38 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	N2	159	Total	C	N	O	S	0	0
			1299	824	252	217	6		

- Molecule 39 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	N3	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 40 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	O2	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 41 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	O3	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 42 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	P2	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 43 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	P3	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 44 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Q2	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 45 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Q3	122	Total	C	N	O	S	0	0
			1002	635	196	166	5		

- Molecule 46 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	R2	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 47 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	R3	85	Total	C	N	O	S	0	0
			683	439	128	115	1		

- Molecule 48 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S2	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 49 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S3	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 50 is a protein called Large ribosomal subunit protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	T2	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 51 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	T3	55	Total	C	N	O	S	0	0
			438	271	95	71	1		

- Molecule 52 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	U2	147	Total	C	N	O	S	0	0
			1164	736	239	185	4		

- Molecule 53 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	U3	52	Total	C	N	O	S	0	0
			415	260	74	74	7		

- Molecule 54 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	V2	117	Total	C	N	O	S	0	0
			945	596	198	146	5		

- Molecule 55 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	W2	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 56 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X2	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 57 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Y2	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 58 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Z2	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 59 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	a2	114	Total	C	N	O	S	0	0
			906	565	187	148	6		

- Molecule 60 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	b2	120	Total	C	N	O	S	0	0
			1001	634	201	165	1		

- Molecule 61 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	c2	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 62 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	d2	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 63 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	e2	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

- Molecule 64 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	f2	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 65 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	g2	52	Total	C	N	O	S	0	0
			428	266	90	66	6		

- Molecule 66 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	h2	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 67 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	i2	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 68 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	j2	89	Total	C	N	O	S	0	0
			693	436	133	117	7		

- Molecule 69 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	k2	125	Total	C	N	O	S	0	0
			1001	621	207	168	5		

- Molecule 70 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	m2	1635	Total	C	N	O	P	0	0
			34939	15614	6270	11420	1635		

- Molecule 71 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	o2	214	Total	C	N	O	S	0	0
			1694	1077	297	312	8		

- Molecule 72 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	p2	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 73 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	q2	220	Total	C	N	O	S	0	0
			1711	1092	308	304	7		

- Molecule 74 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	r2	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 75 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	s2	183	Total	C	N	O	S	0	0
			1457	912	275	263	7		

- Molecule 76 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	t2	183	Total	C	N	O	0	0
			1278	822	243	213		

- Molecule 77 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	u2	206	Total	C	N	O	S	0	0
			1633	1025	322	281	5		

- Molecule 78 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	v2	95	Total	C	N	O	S	0	0
			800	522	142	131	5		

- Molecule 79 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	w2	150	Total	C	N	O	S	0	0
			1220	776	228	210	6		

- Molecule 80 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	x2	123	Total	C	N	O	S	0	0
			1005	638	188	172	7		

- Molecule 81 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	y2	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 82 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	z2	134	Total	C	N	O	S	0	0
			1080	678	201	197	4		

- Molecule 83 is a protein called Nascent protein chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	A	22	Total	C	N	O	0	0
			110	66	22	22		

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

Mol	Chain	Residues	Atoms		AltConf
84	A2	82	Total	Mg	0
			82	82	
84	Bv	2	Total	Mg	0
			2	2	
84	H1	1	Total	Mg	0
			1	1	
84	J2	1	Total	Mg	0
			1	1	
84	P2	1	Total	Mg	0
			1	1	
84	d2	1	Total	Mg	0
			1	1	
84	m2	34	Total	Mg	0
			34	34	

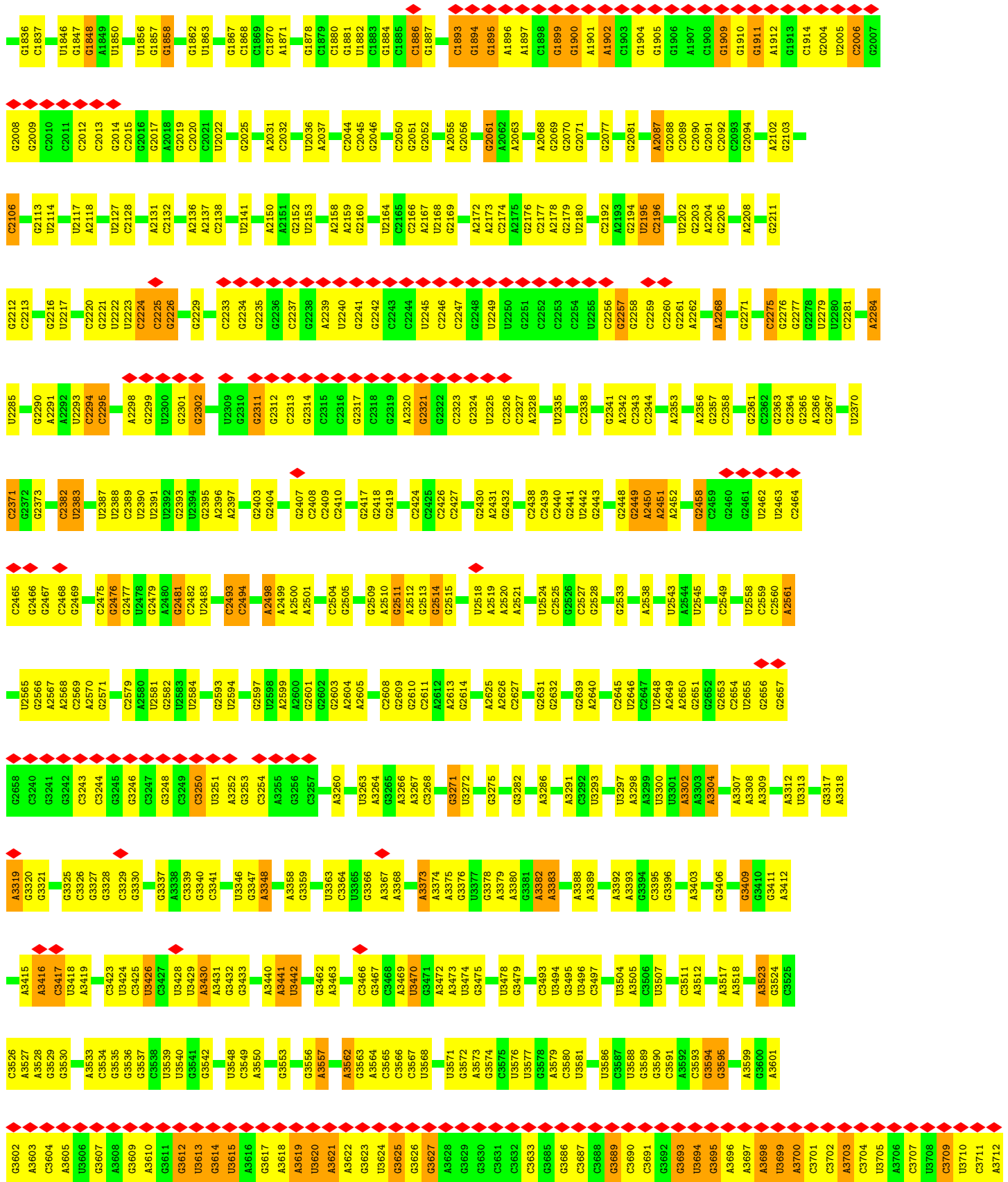
- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

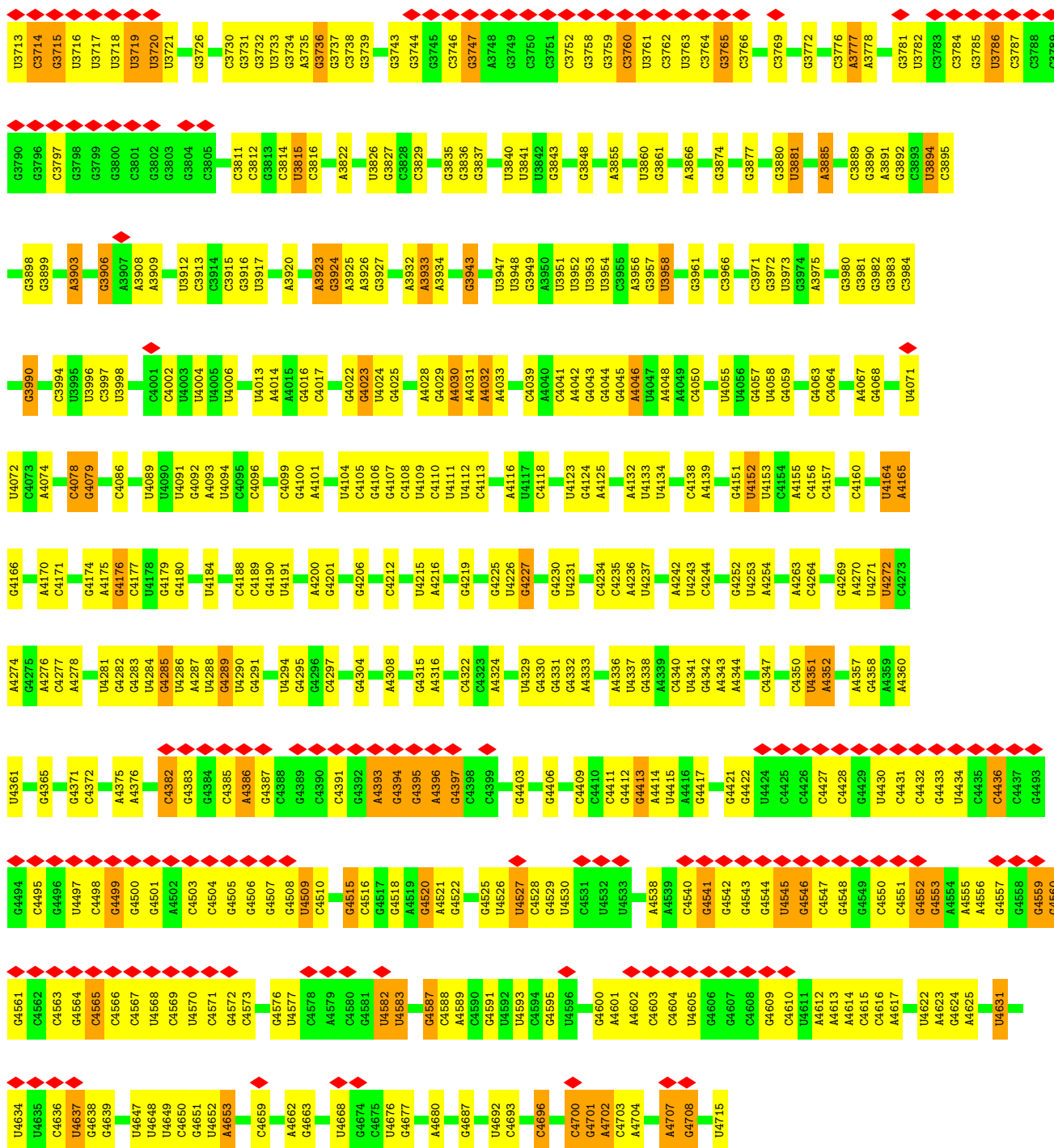
Mol	Chain	Residues	Atoms		AltConf
85	F3	1	Total	Zn	0
			1	1	
85	H3	1	Total	Zn	0
			1	1	
85	d2	1	Total	Zn	0
			1	1	
85	g2	1	Total	Zn	0
			1	1	
85	i2	1	Total	Zn	0
			1	1	
85	j2	1	Total	Zn	0
			1	1	

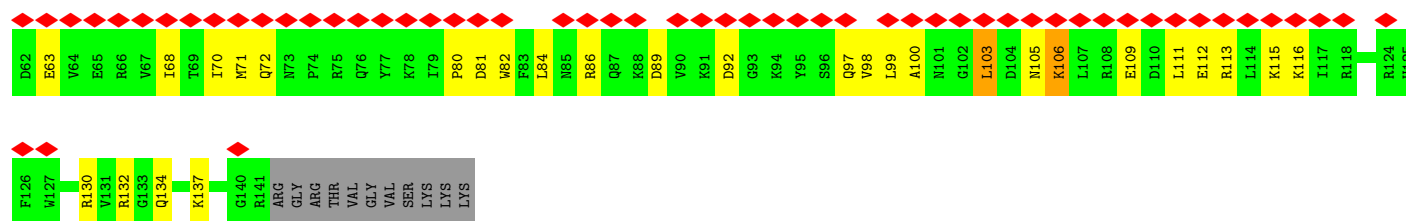
- Molecule 86 is water.

Mol	Chain	Residues	Atoms		AltConf
86	B1	1	Total	O	0
			1	1	



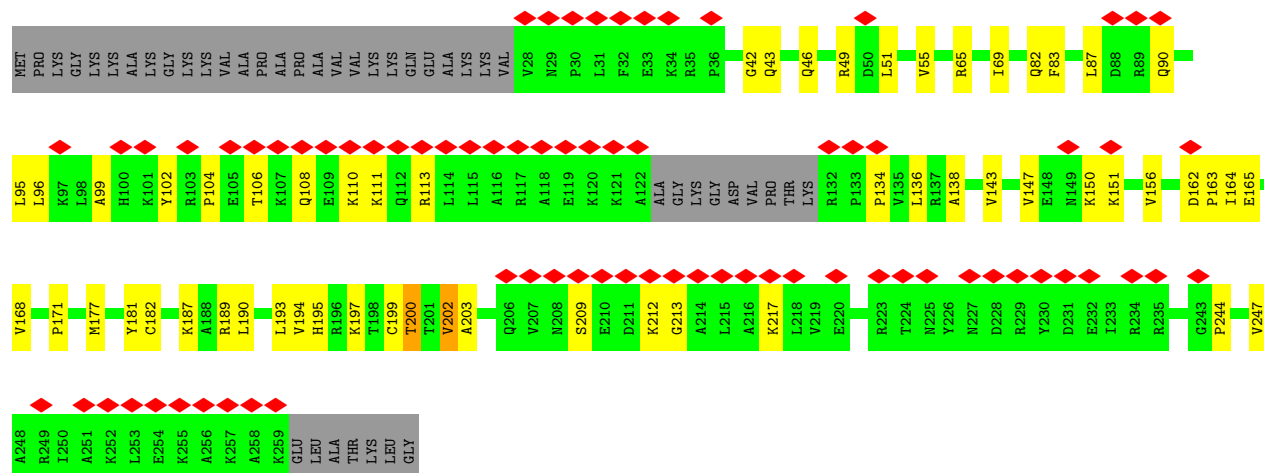






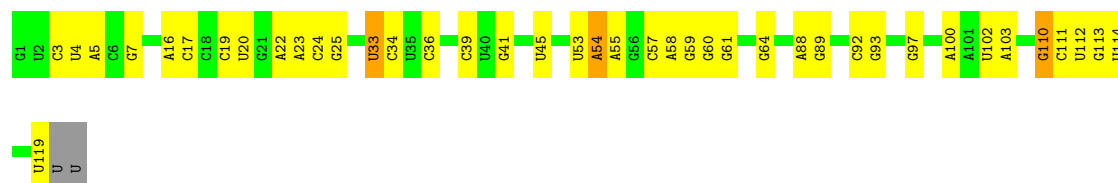
• Molecule 4: Large ribosomal subunit protein eL8

Chain B1: 29% 63% 20% 16%



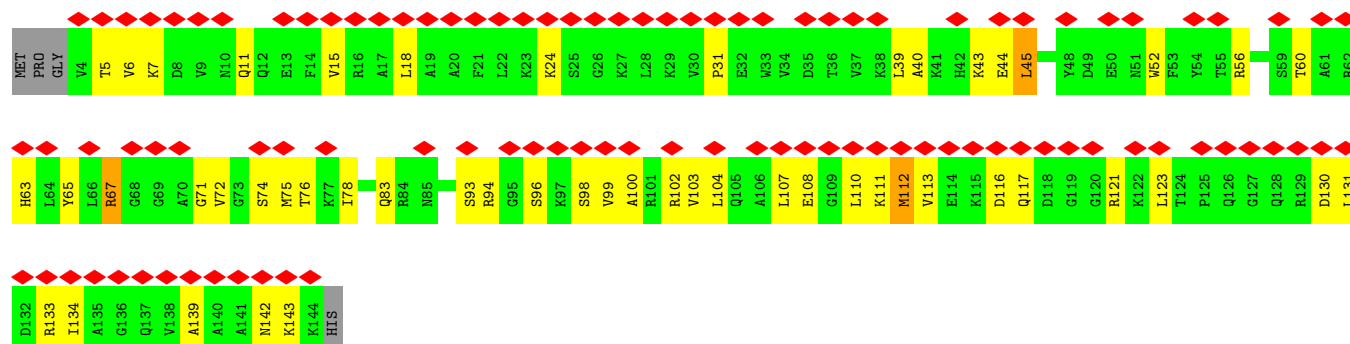
• Molecule 5: 5S ribosomal RNA

Chain B2: 64% 31%

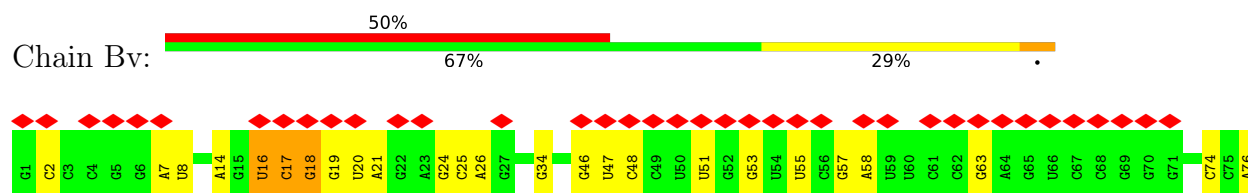


• Molecule 6: Small ribosomal subunit protein eS19

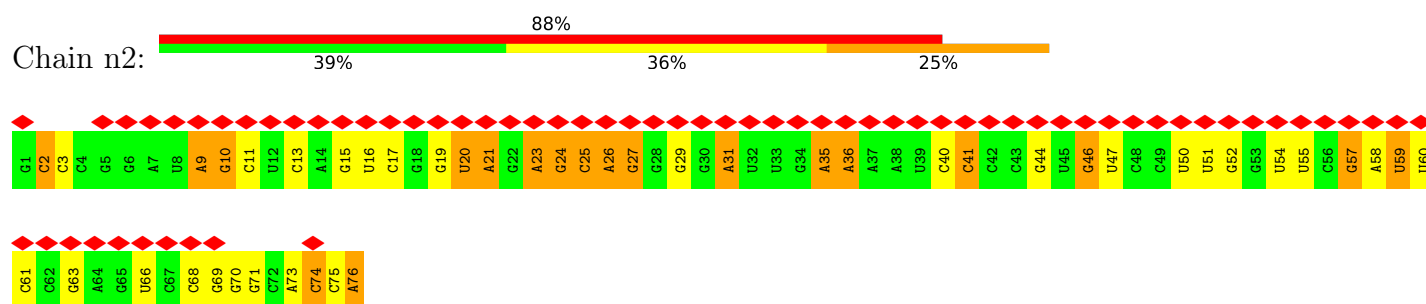
Chain B3: 68% 61% 34%



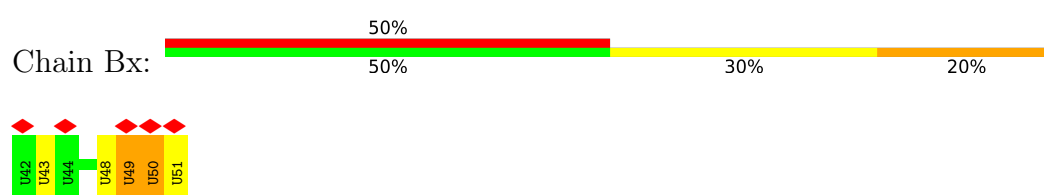
- Molecule 7: transfer RNA



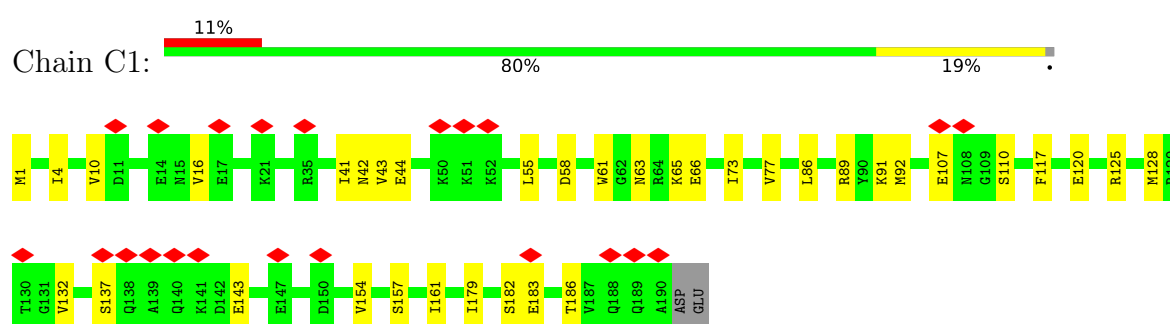
- Molecule 7: transfer RNA



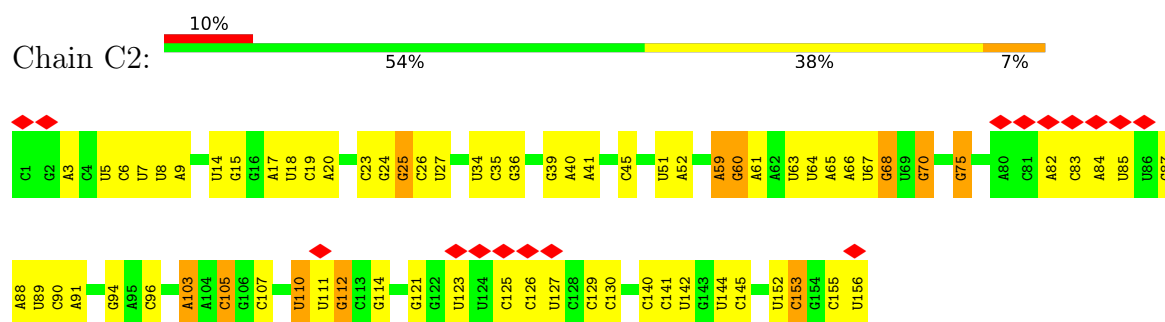
- Molecule 8: messenger RNA



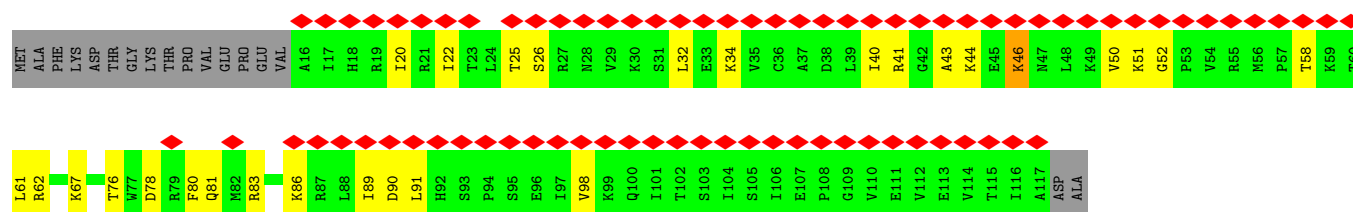
- Molecule 9: Large ribosomal subunit protein uL6



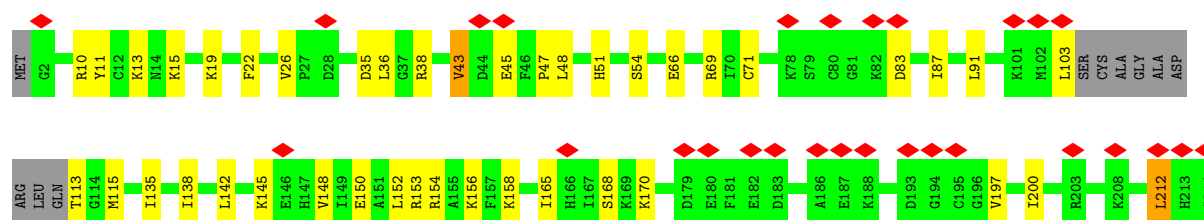
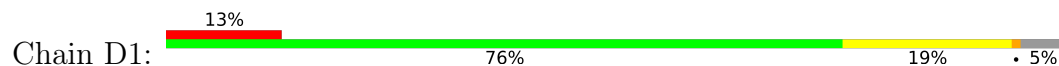
- Molecule 10: 5.8S ribosomal RNA



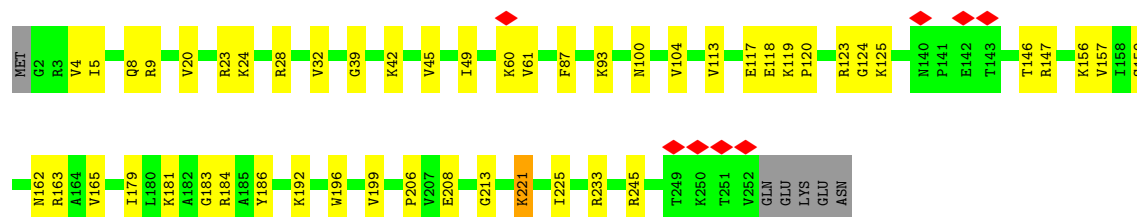
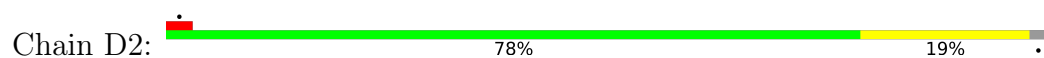
- Molecule 11: Small ribosomal subunit protein uS10



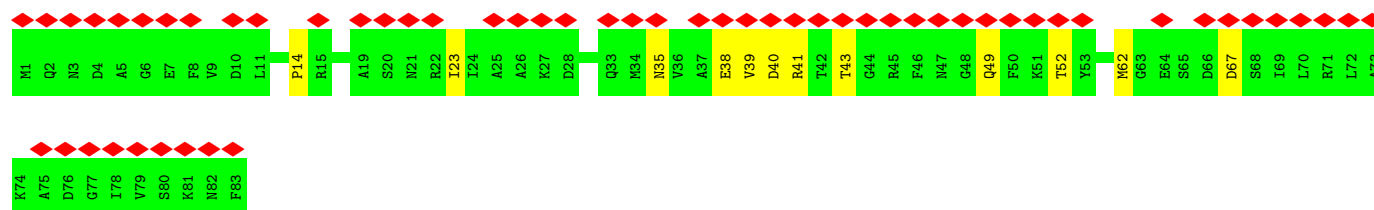
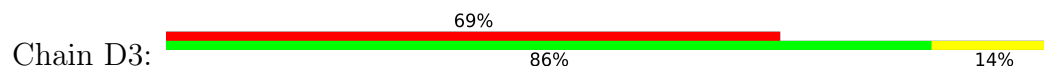
• Molecule 12: Large ribosomal subunit protein uL16



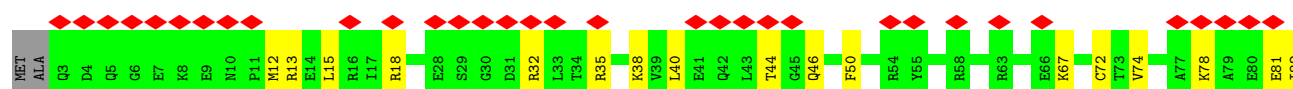
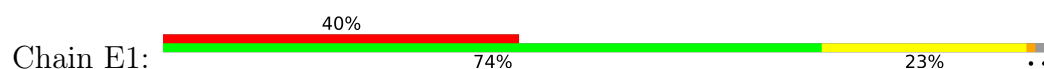
• Molecule 13: Large ribosomal subunit protein uL2

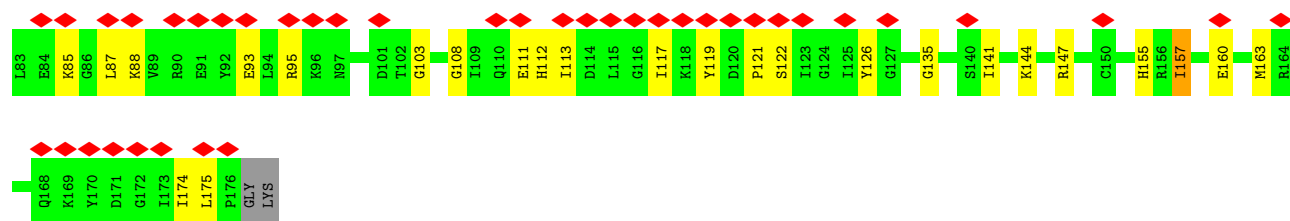


• Molecule 14: Small ribosomal subunit protein eS21

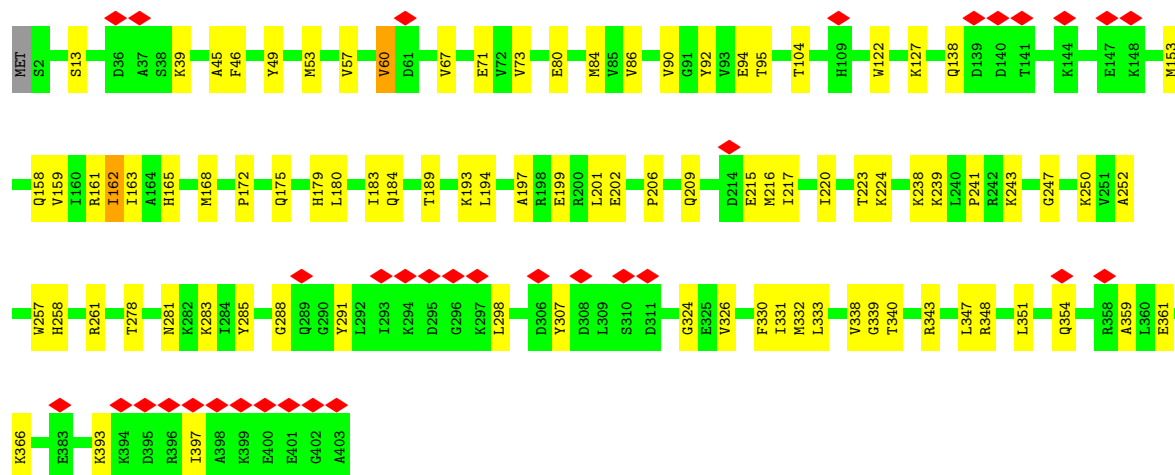
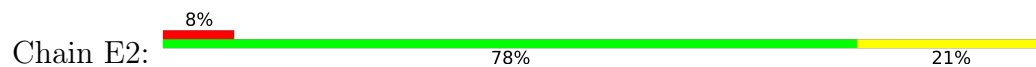


• Molecule 15: Large ribosomal subunit protein uL5

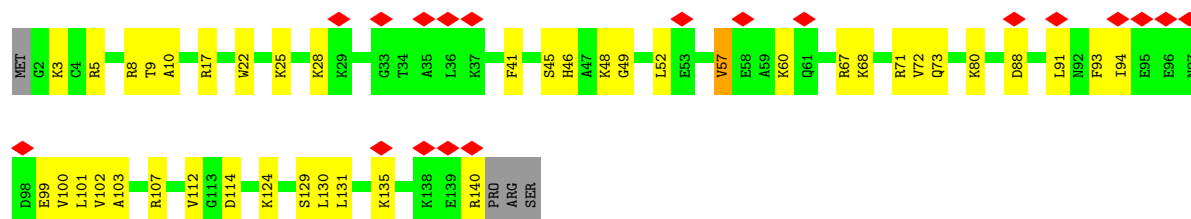




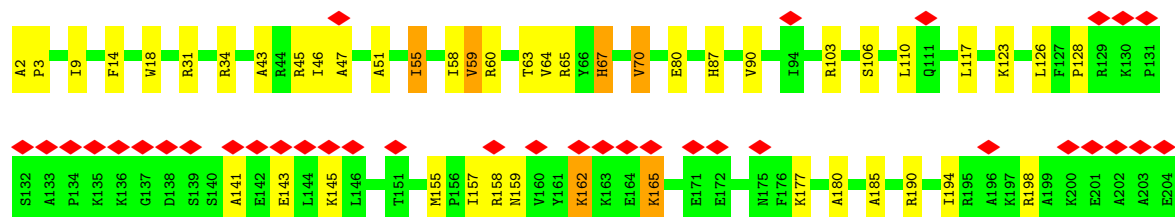
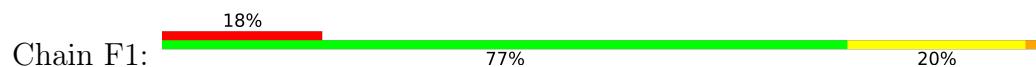
- Molecule 16: Large ribosomal subunit protein uL3



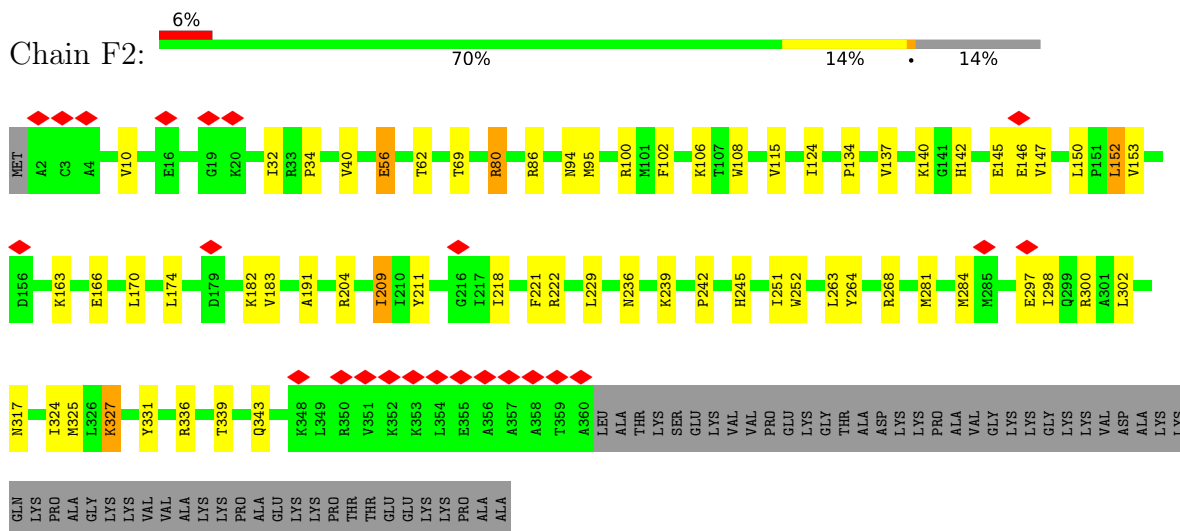
- Molecule 17: Small ribosomal subunit protein uS12



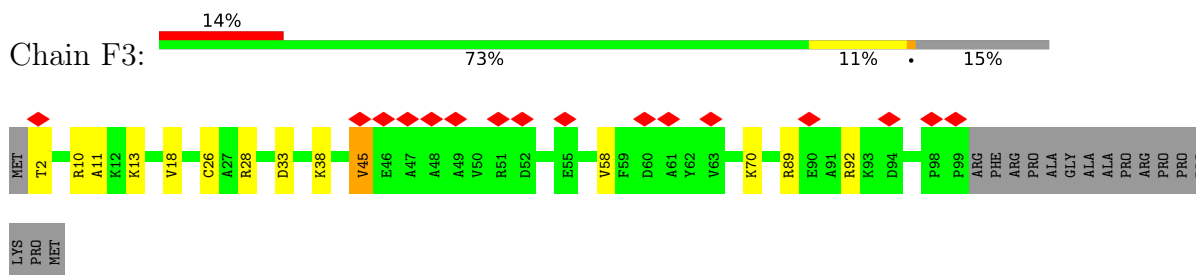
- Molecule 18: Large ribosomal subunit protein eL13



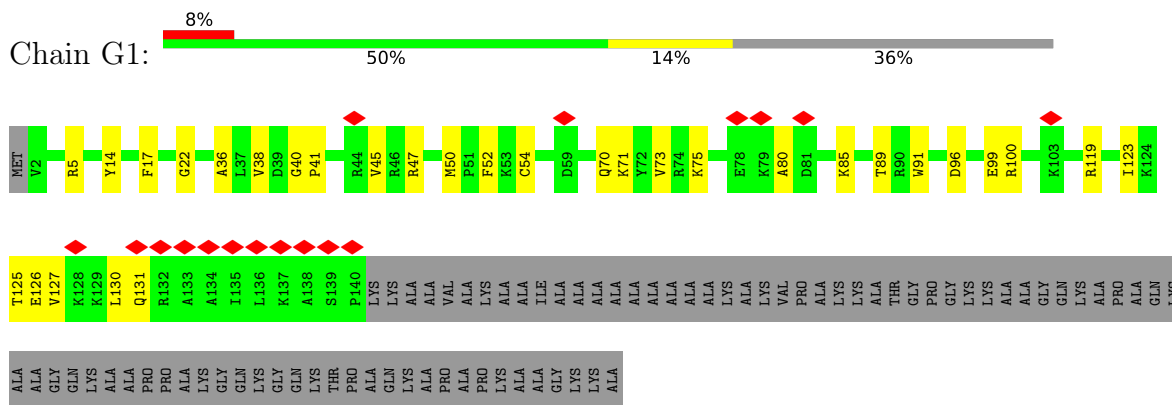
- Molecule 19: Large ribosomal subunit protein uL4



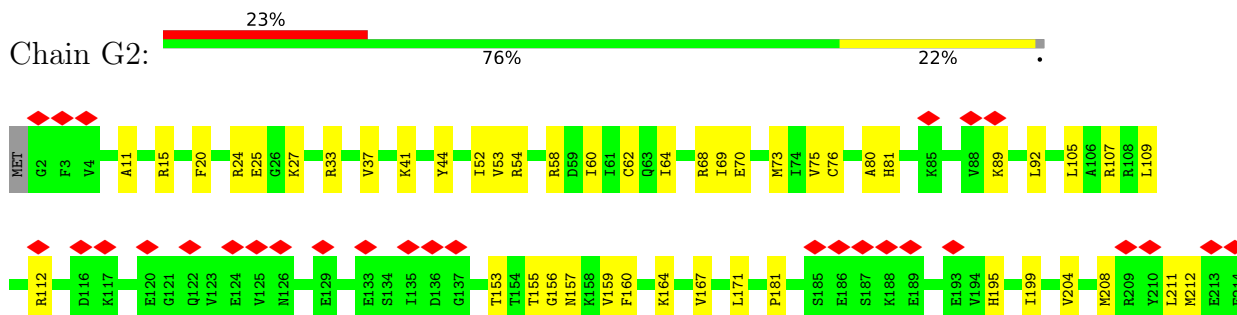
- Molecule 20: Small ribosomal subunit protein eS26



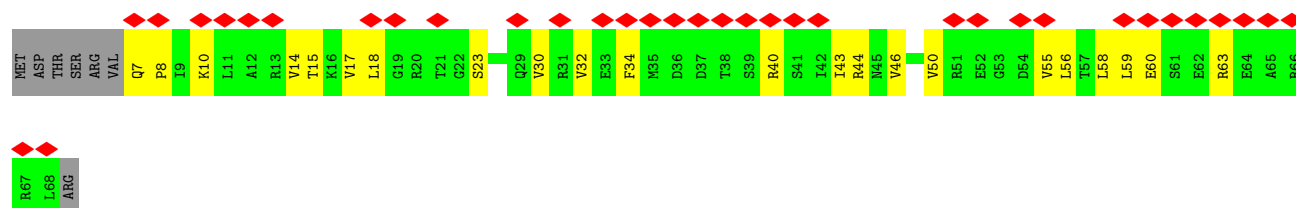
- Molecule 21: Large ribosomal subunit protein eL14



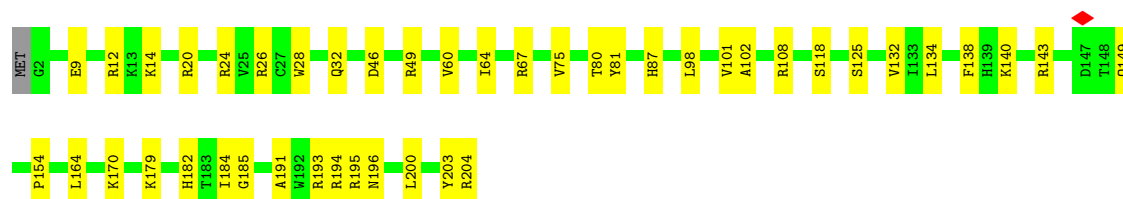
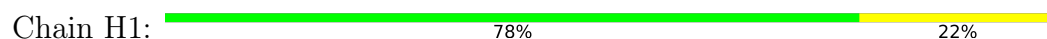
- Molecule 22: Large ribosomal subunit protein uL18



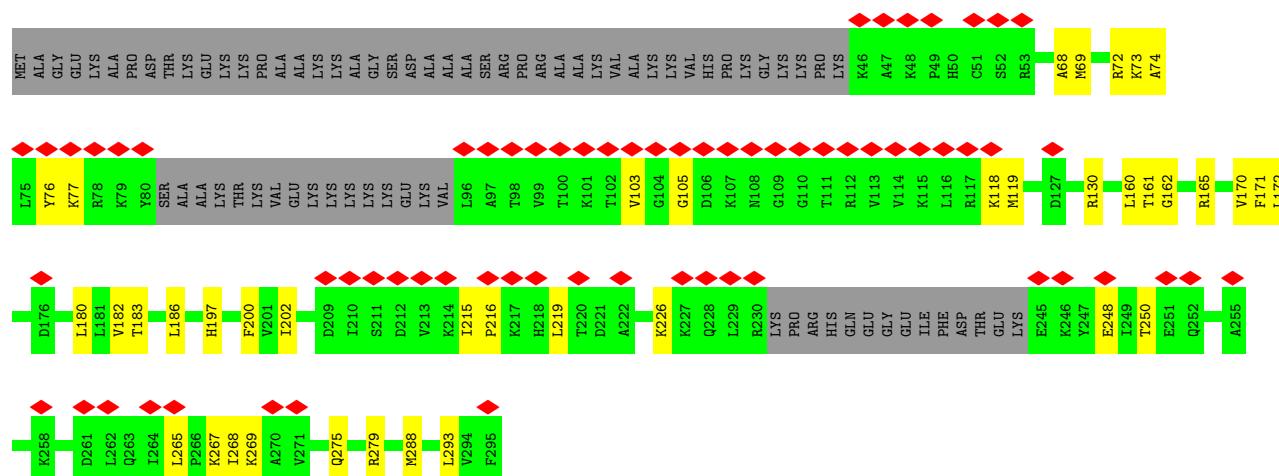
- Molecule 23: Small ribosomal subunit protein eS28



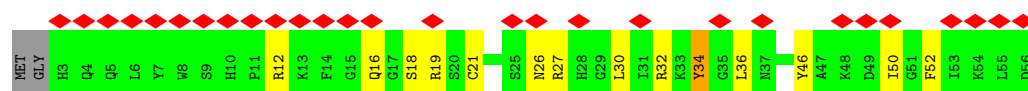
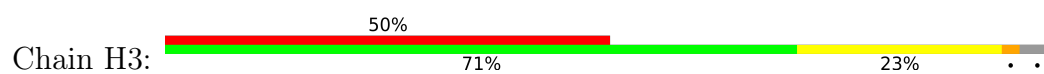
- Molecule 24: Large ribosomal subunit protein eL15



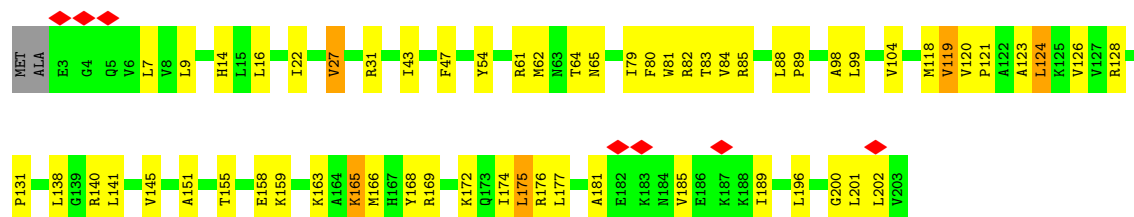
- Molecule 25: Large ribosomal subunit protein eL6



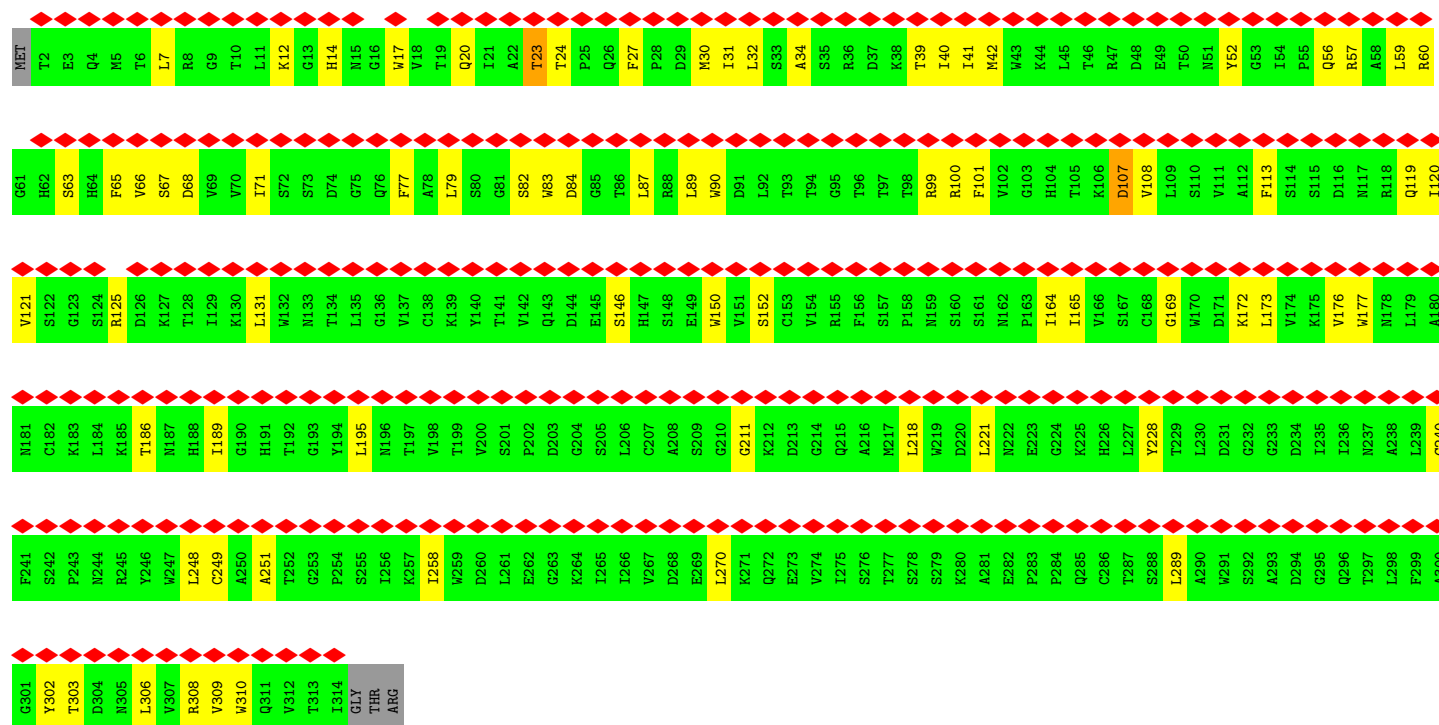
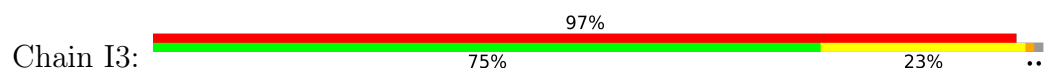
- Molecule 26: Small ribosomal subunit protein uS14



• Molecule 27: Large ribosomal subunit protein uL13



• Molecule 28: Small ribosomal subunit protein RACK1

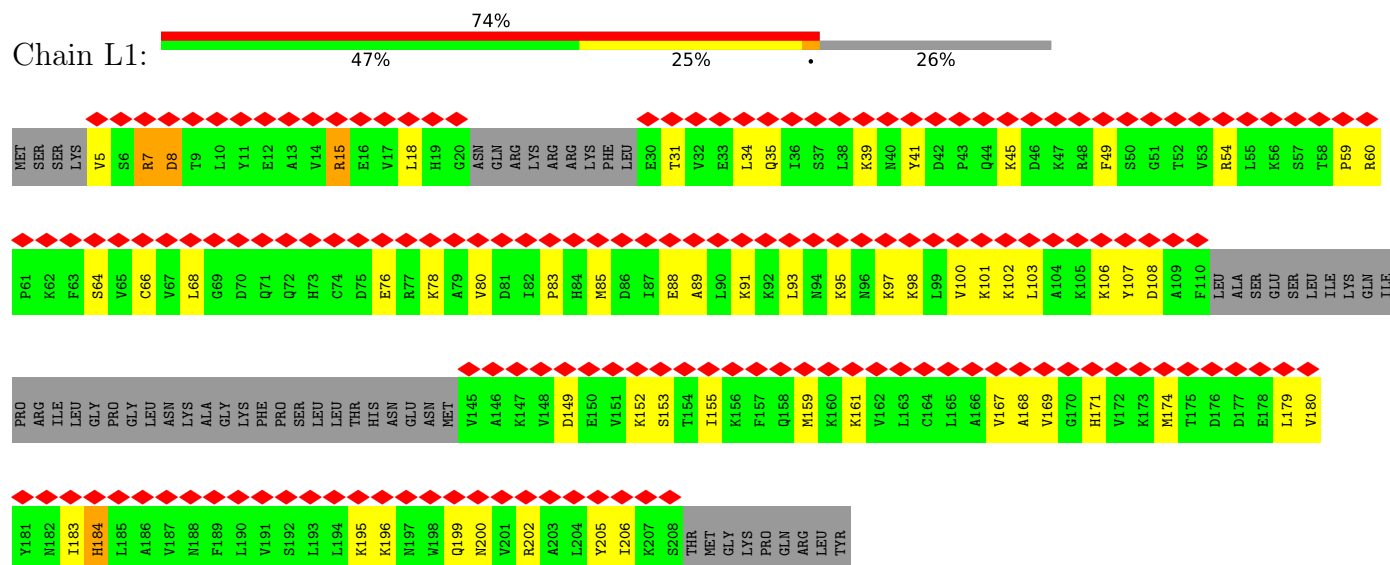


• Molecule 29: Large ribosomal subunit protein uL22



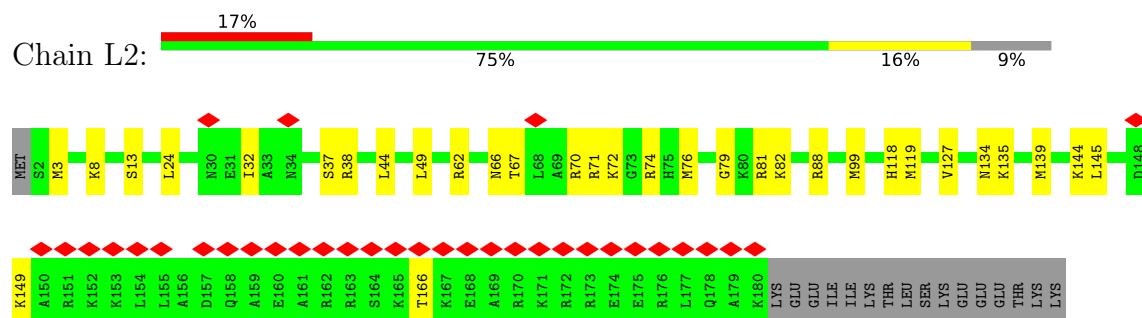
- Molecule 33: Large ribosomal subunit protein uL1

Chain L1:



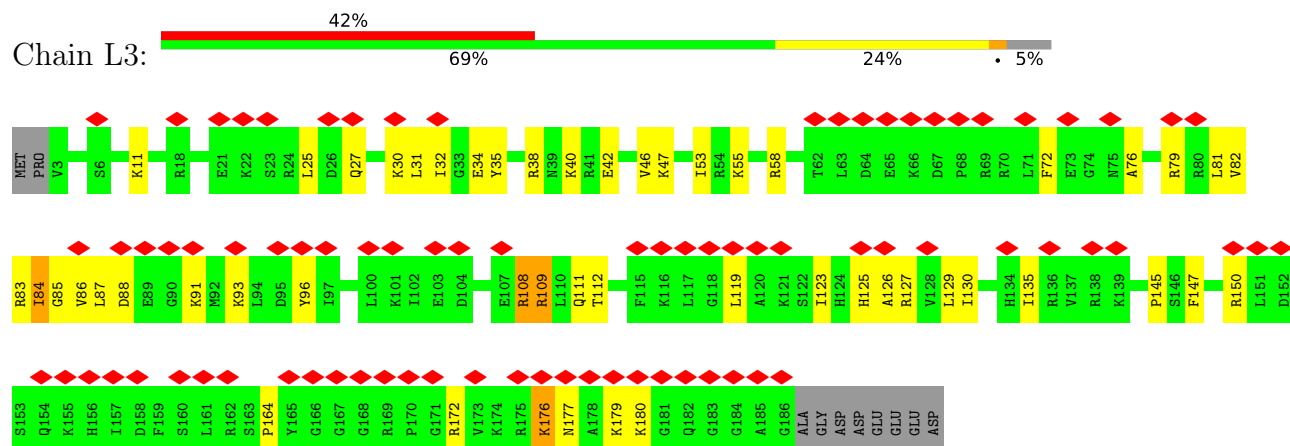
- Molecule 34: Large ribosomal subunit protein eL19

Chain L2:



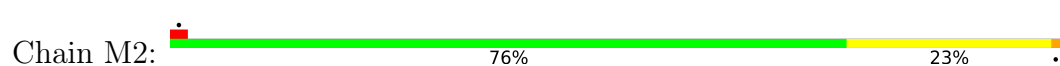
- Molecule 35: Small ribosomal subunit protein uS4

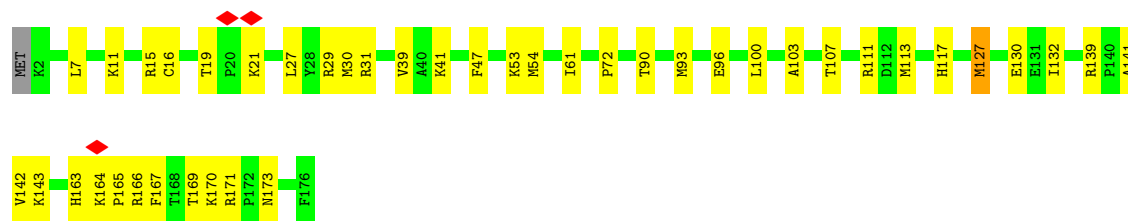
Chain L3:



- Molecule 36: Large ribosomal subunit protein eL20

Chain M2:

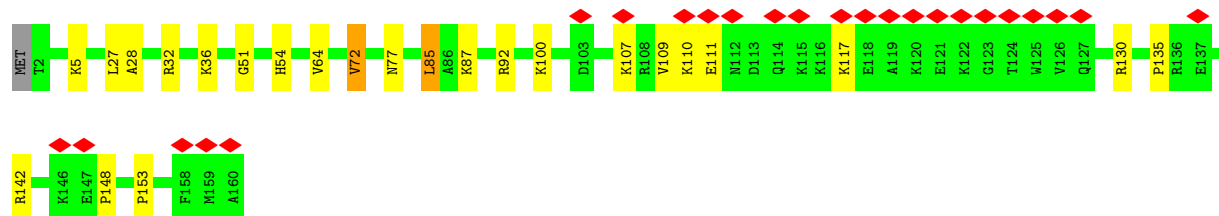
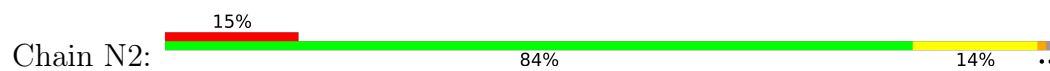




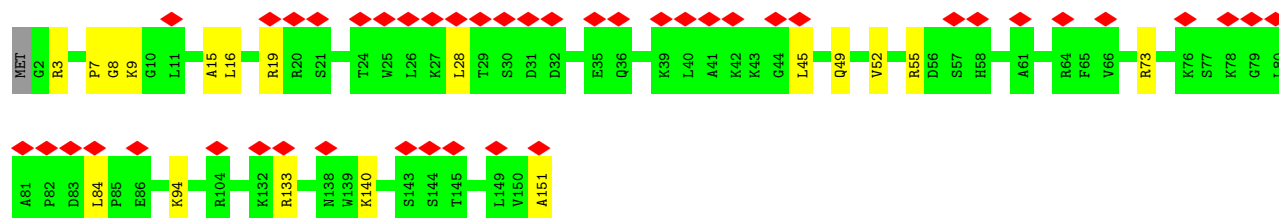
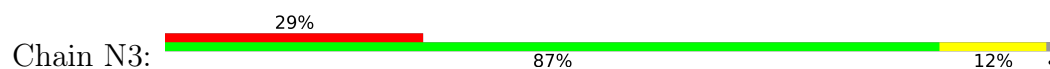
- Molecule 37: Small ribosomal subunit protein eS12



- Molecule 38: Large ribosomal subunit protein eL21

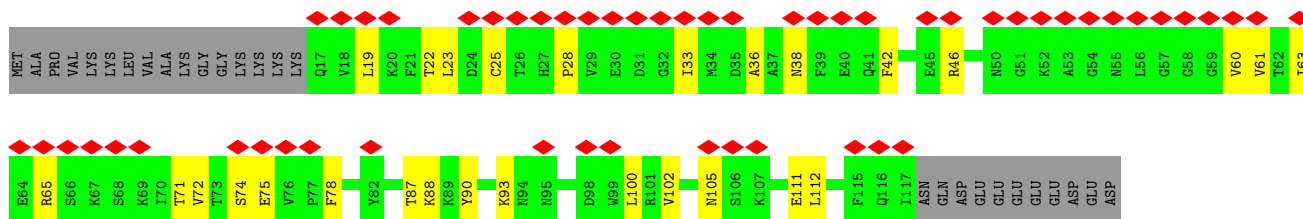


- Molecule 39: Small ribosomal subunit protein uS15

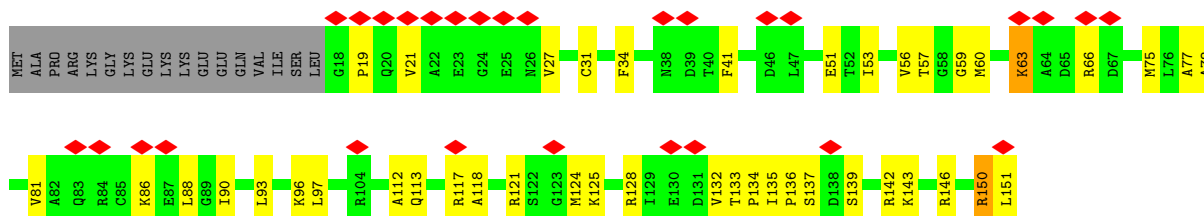


- Molecule 40: Large ribosomal subunit protein eL22

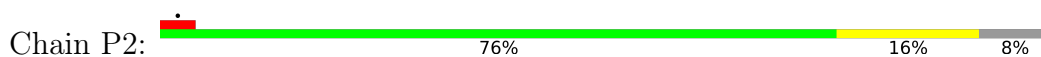




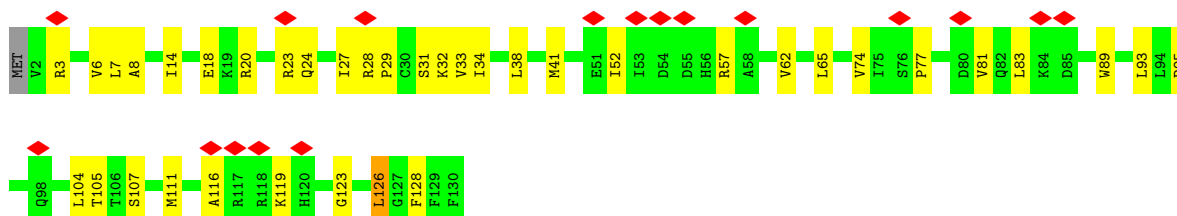
- Molecule 41: Small ribosomal subunit protein uS11



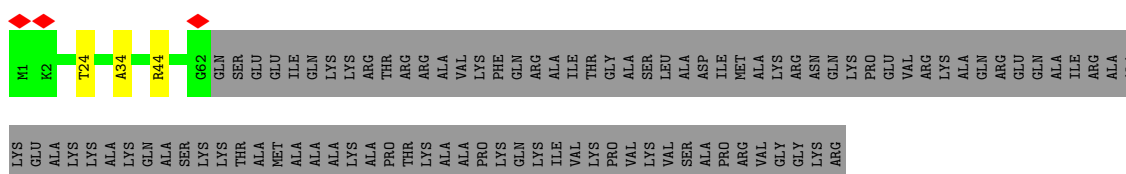
- Molecule 42: Large ribosomal subunit protein uL14



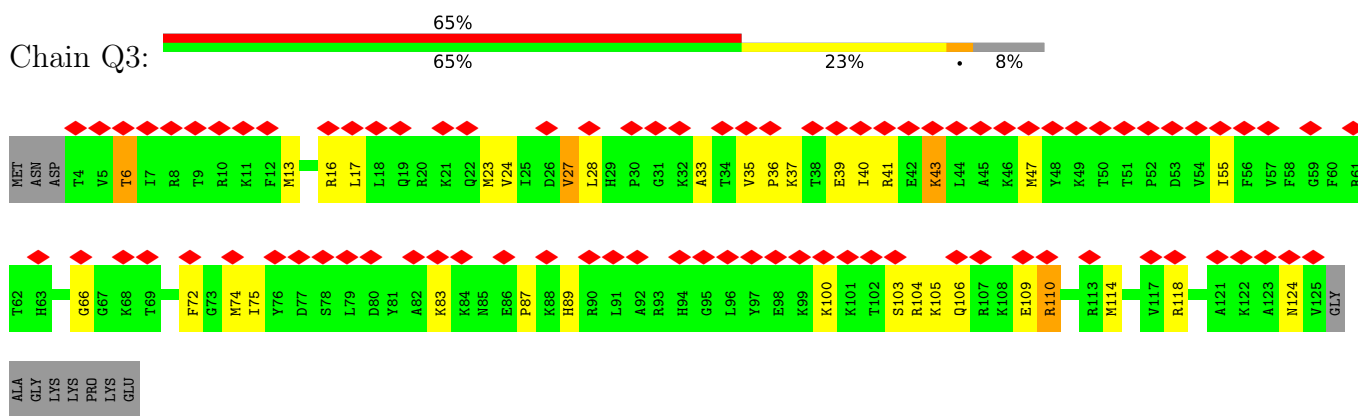
- Molecule 43: Small ribosomal subunit protein uS8



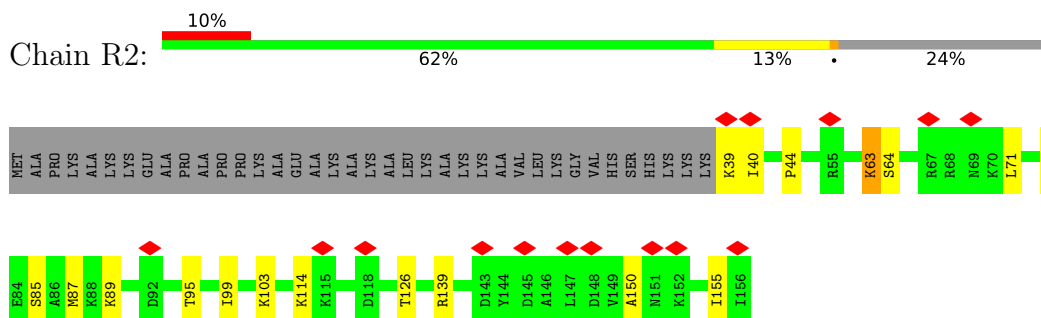
- Molecule 44: Large ribosomal subunit protein eL24



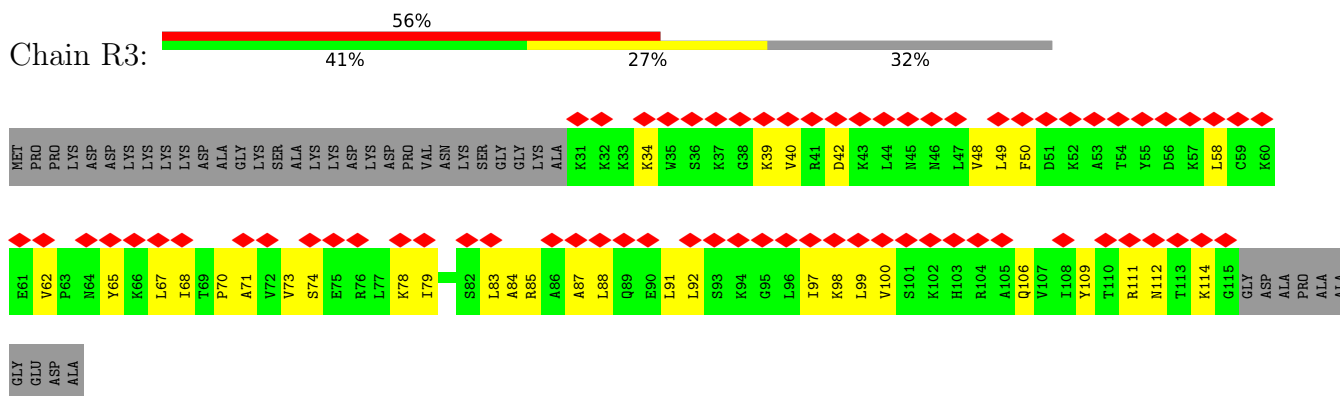
- Molecule 45: Small ribosomal subunit protein eS24



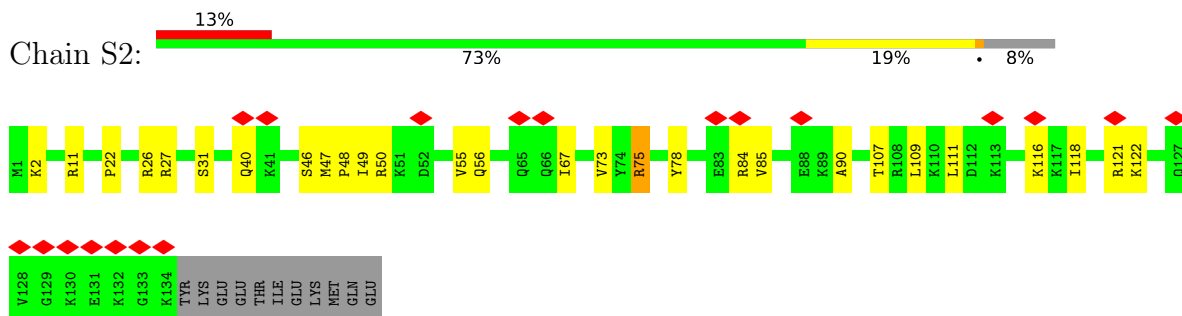
- Molecule 46: Large ribosomal subunit protein uL23



- Molecule 47: Small ribosomal subunit protein eS25

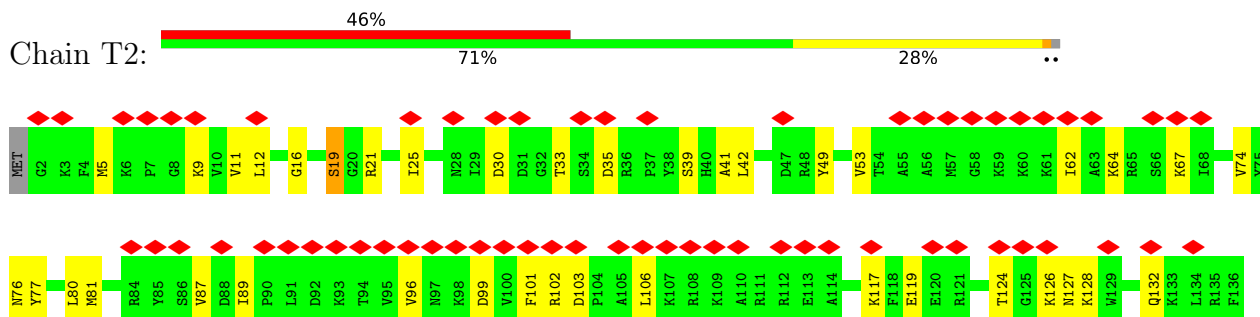


- Molecule 48: Large ribosomal subunit protein uL24

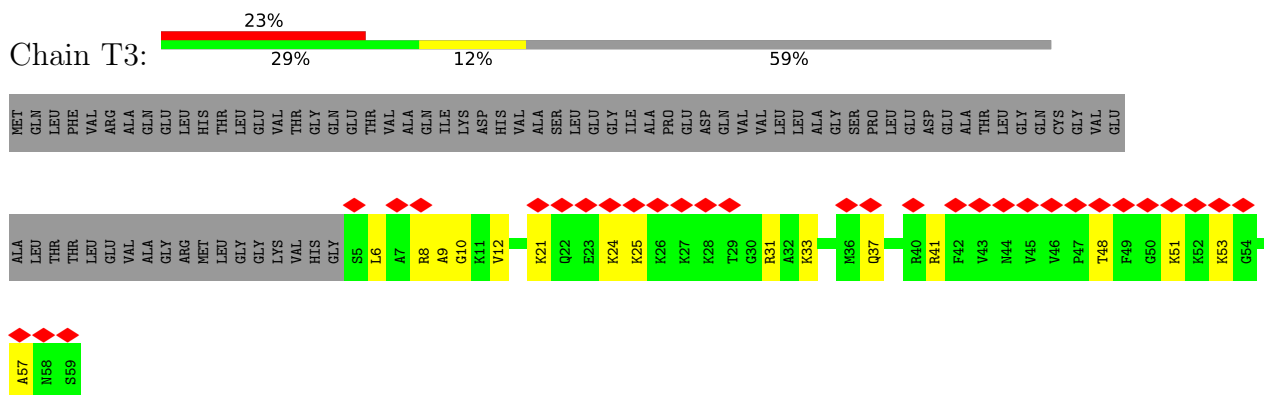


- Molecule 49: Small ribosomal subunit protein eS27

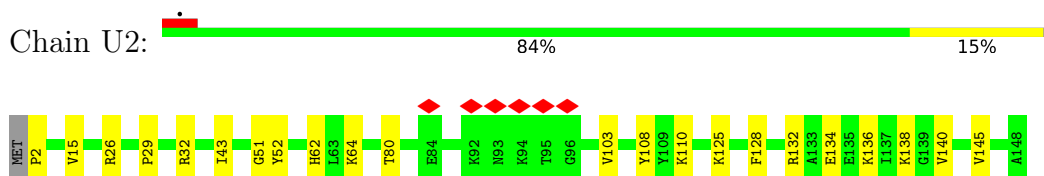
- Molecule 50: Large ribosomal subunit protein eL27



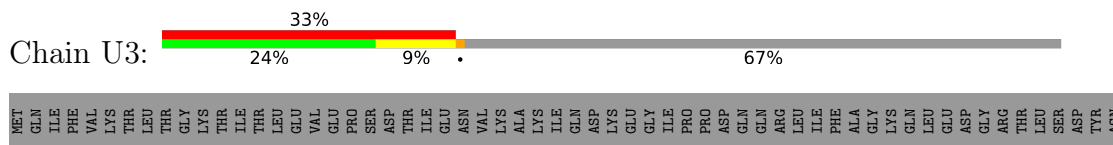
- Molecule 51: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

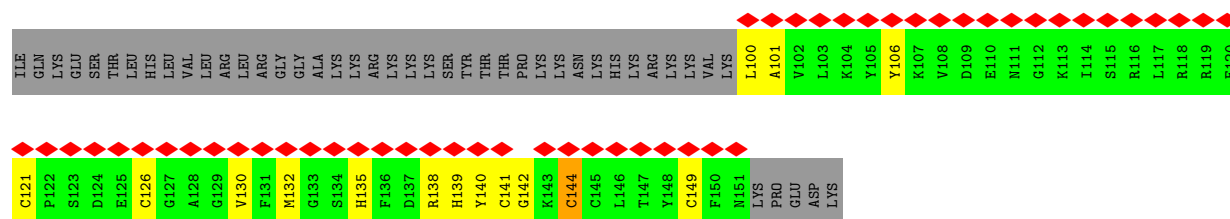


- Molecule 52: Large ribosomal subunit protein uL15

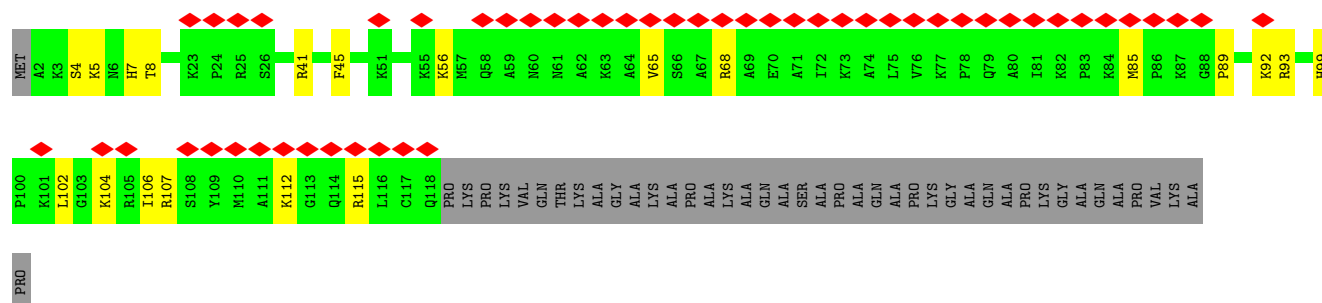


- Molecule 53: Ubiquitin-ribosomal protein eS31 fusion protein

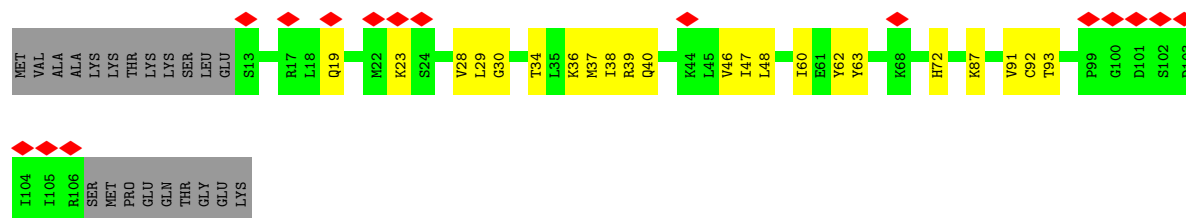




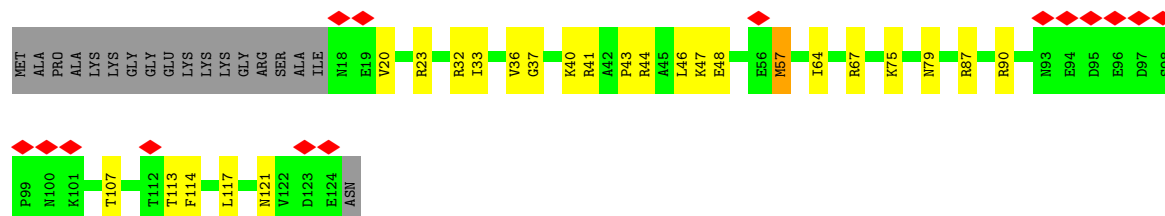
- Molecule 54: Large ribosomal subunit protein eL29



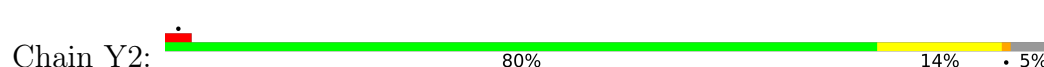
- Molecule 55: Large ribosomal subunit protein eL30



- Molecule 56: Large ribosomal subunit protein eL31

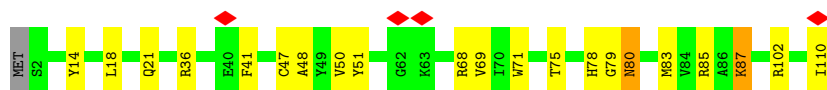


- Molecule 57: Large ribosomal subunit protein eL32



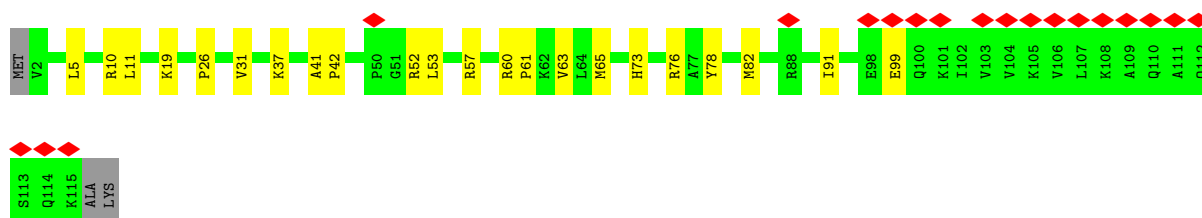
- Molecule 58: Large ribosomal subunit protein eL33

Chain Z2:  80% 17% ..



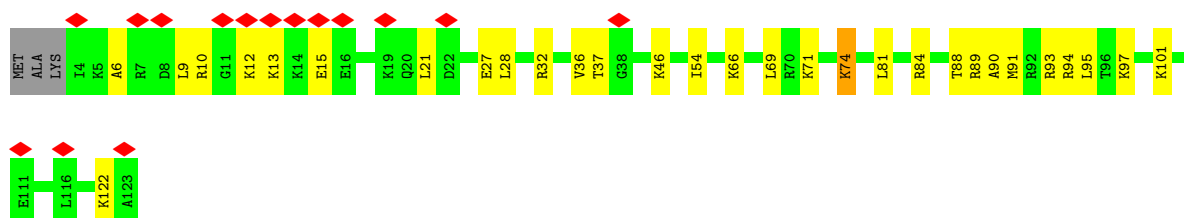
- Molecule 59: Large ribosomal subunit protein eL34

Chain a2:  16% 79% 19% .



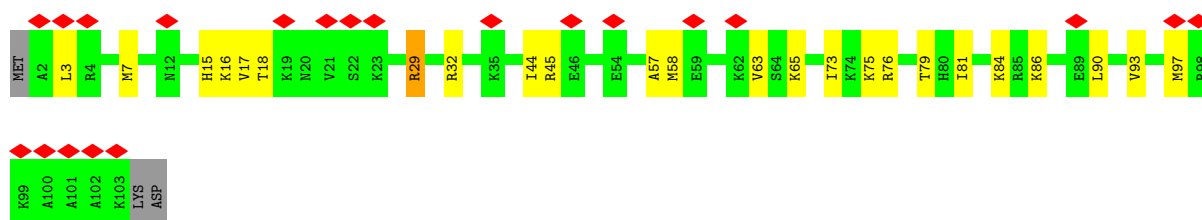
- Molecule 60: Large ribosomal subunit protein uL29

Chain b2:  12% 73% 24% ..



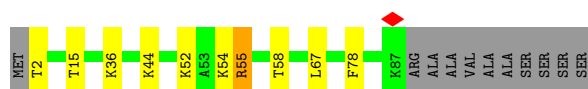
- Molecule 61: Large ribosomal subunit protein eL36

Chain c2:  20% 74% 22% ..

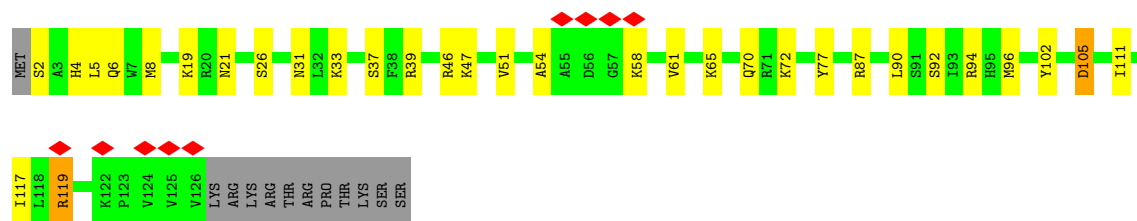


- Molecule 62: Large ribosomal subunit protein eL37

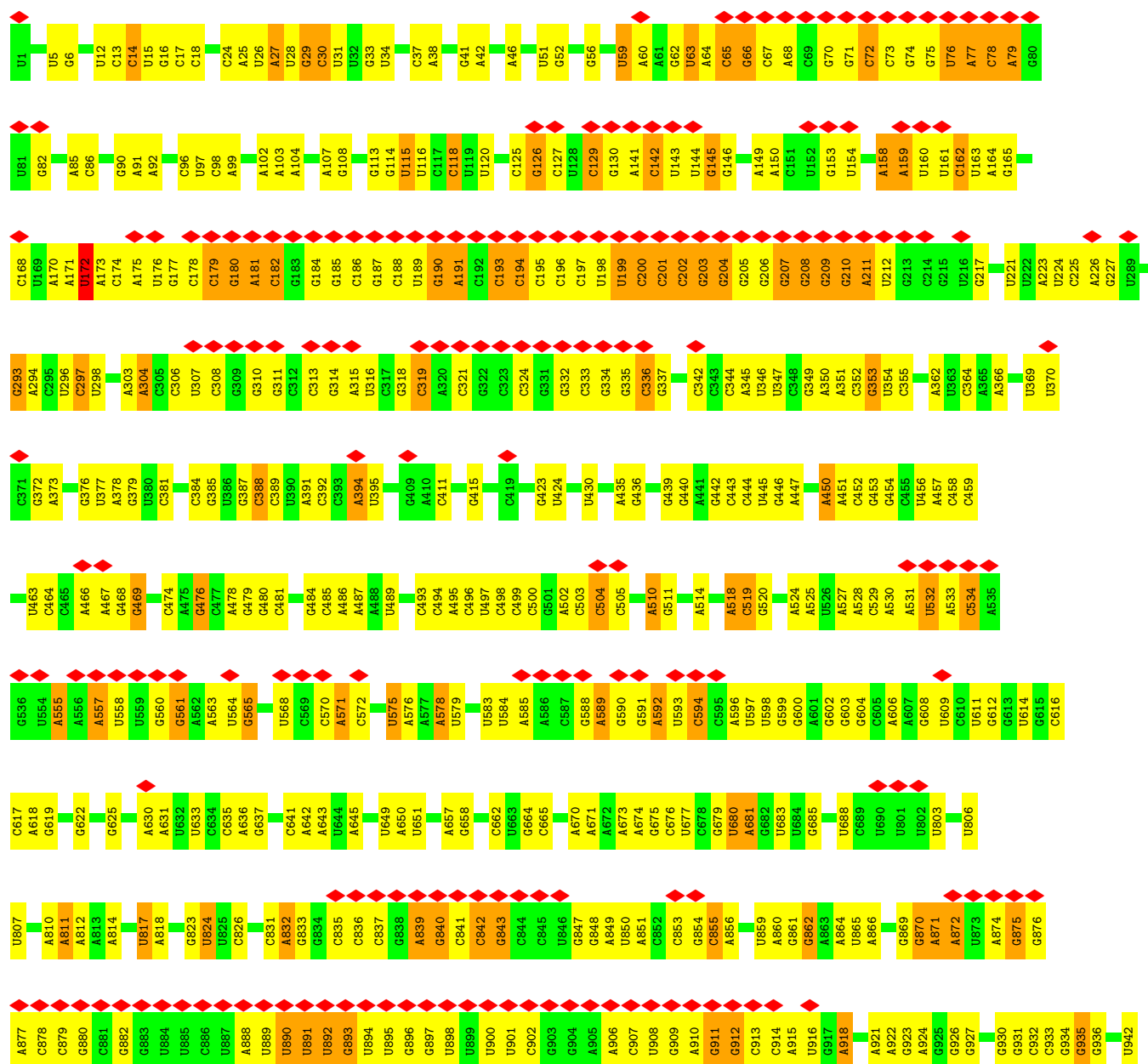
Chain d2:  78% 9% 11%

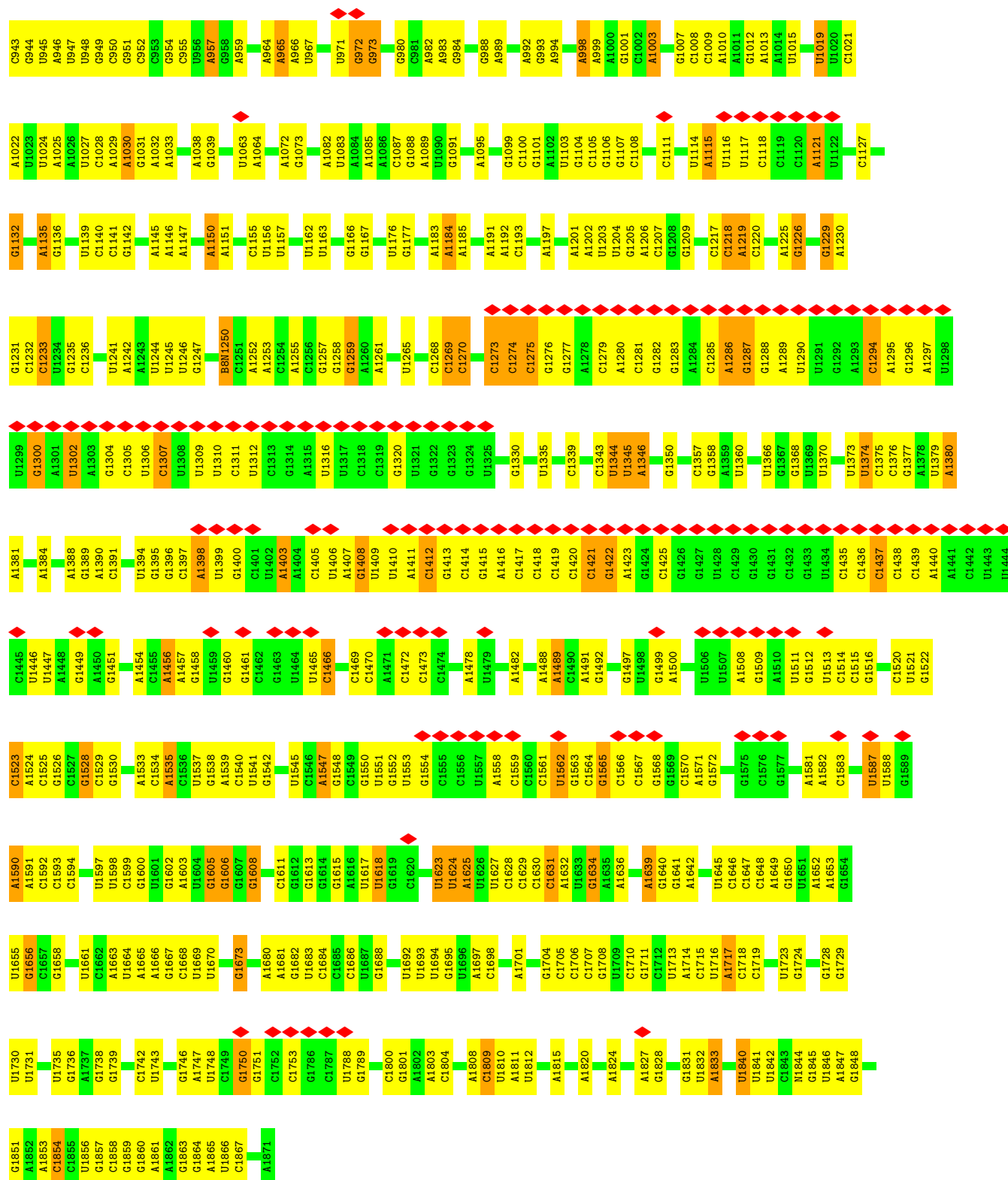


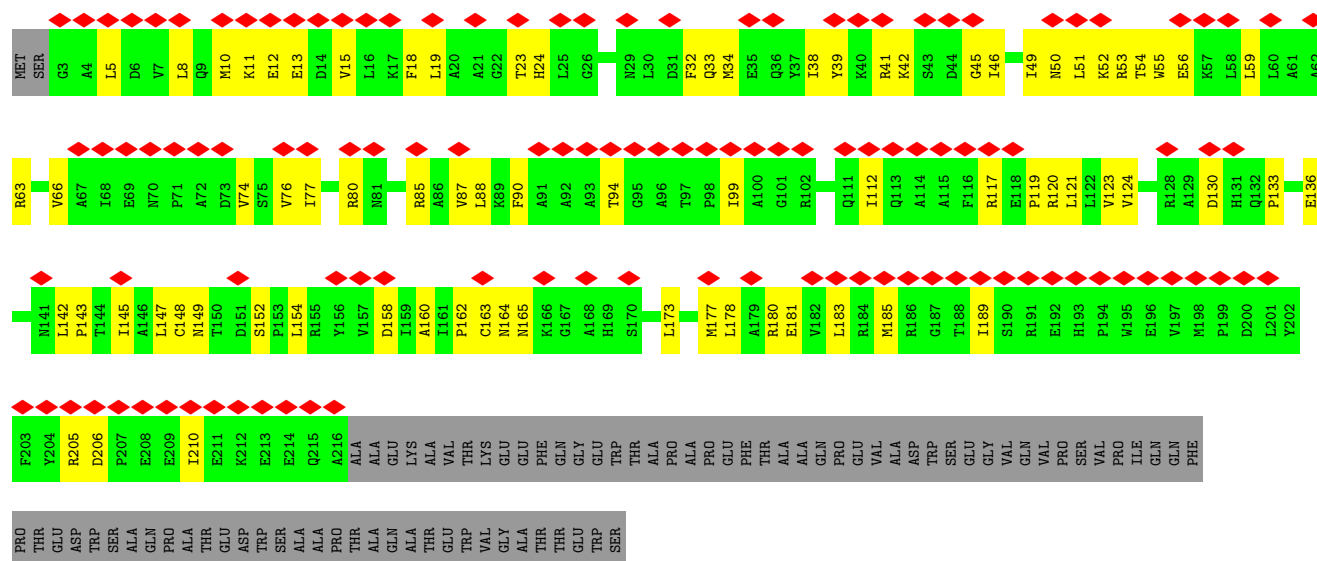
- Molecule 63: Large ribosomal subunit protein eL38



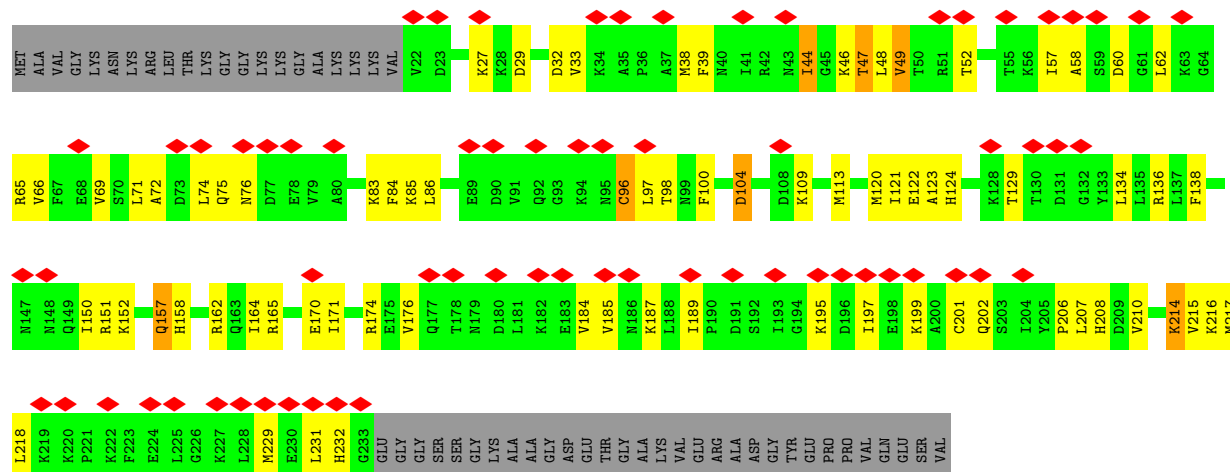
• Molecule 70: 18S ribosomal RNA



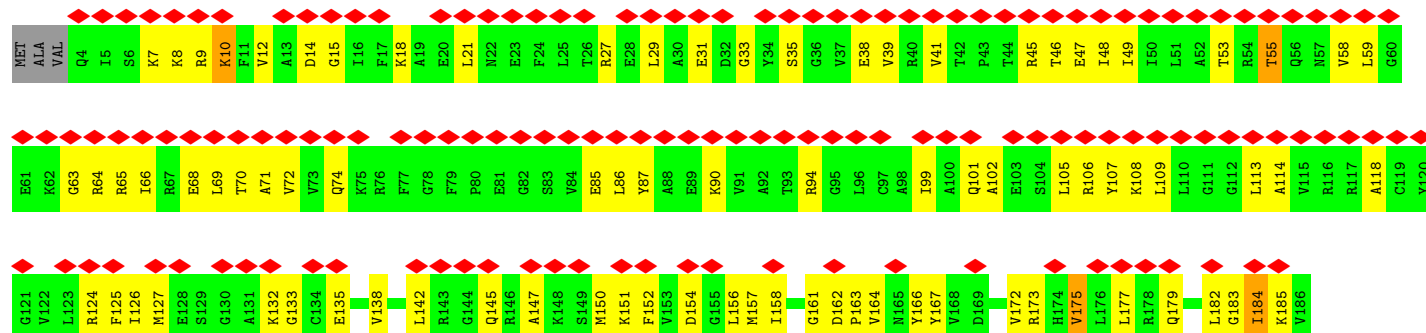
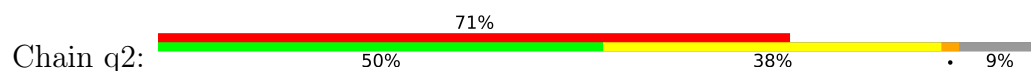




• Molecule 72: 40S ribosomal protein S3a

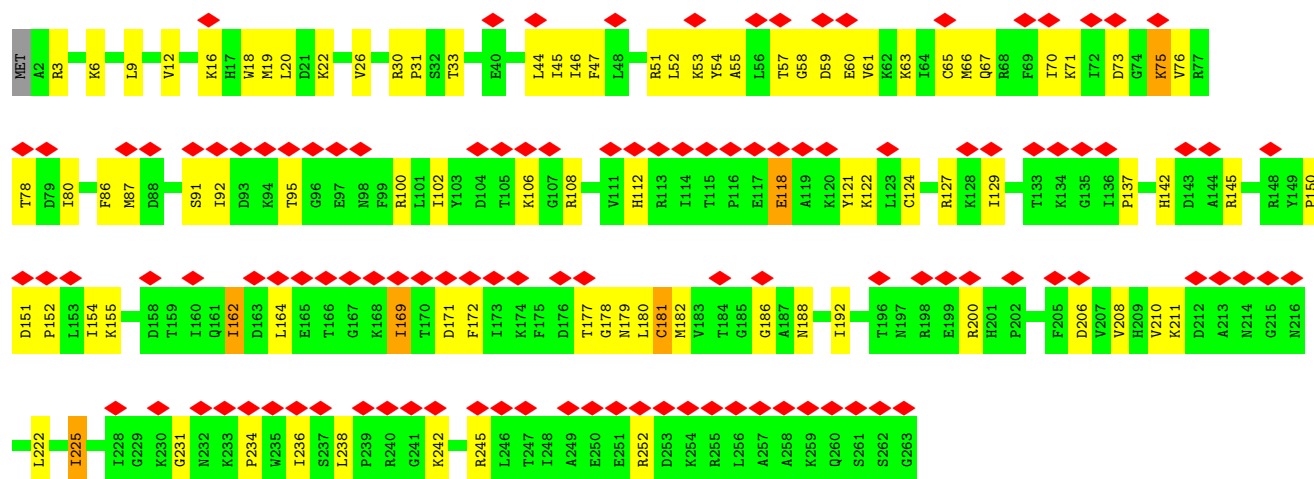


• Molecule 73: Small ribosomal subunit protein uS3

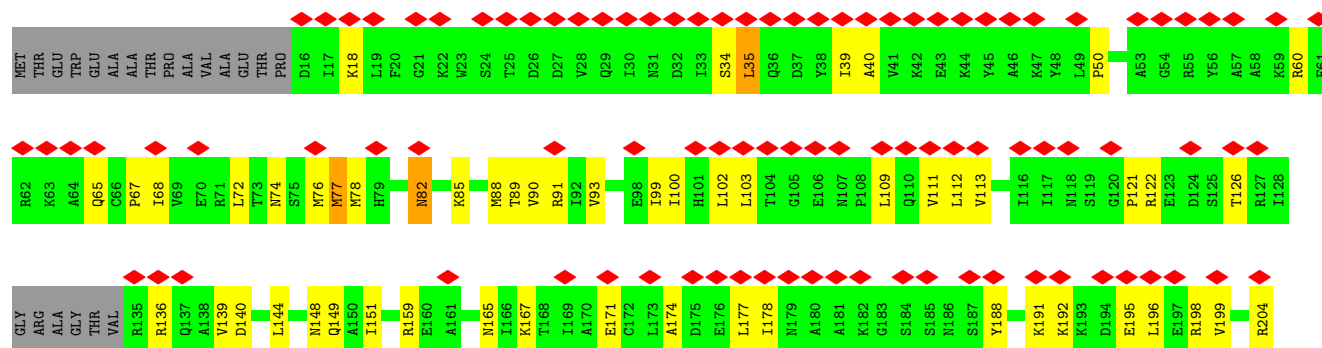




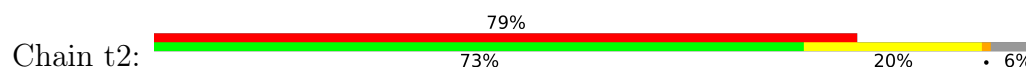
• Molecule 74: Small ribosomal subunit protein eS4

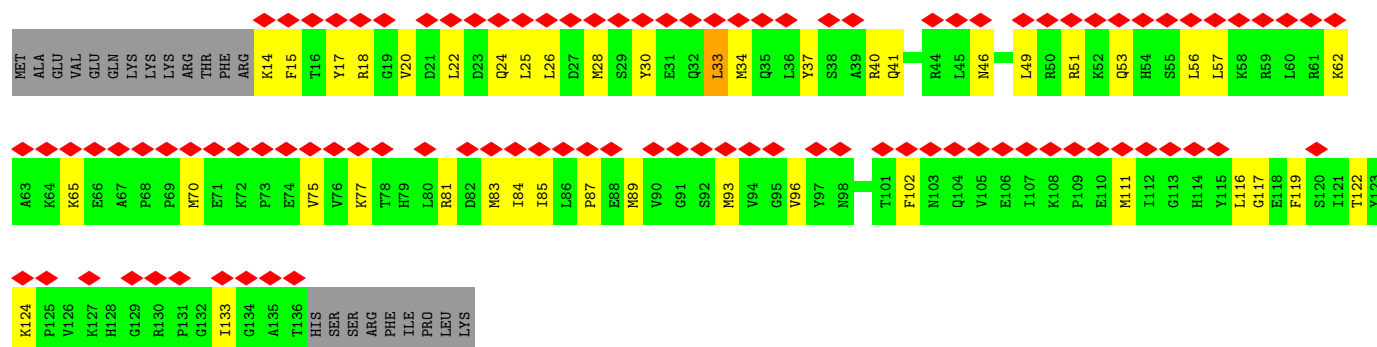


• Molecule 75: Small ribosomal subunit protein uS7

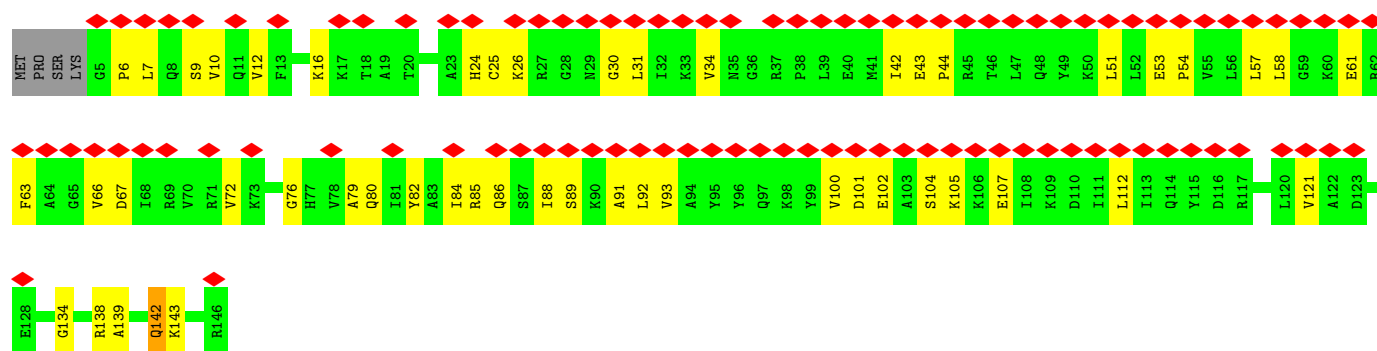


• Molecule 76: Small ribosomal subunit protein eS7

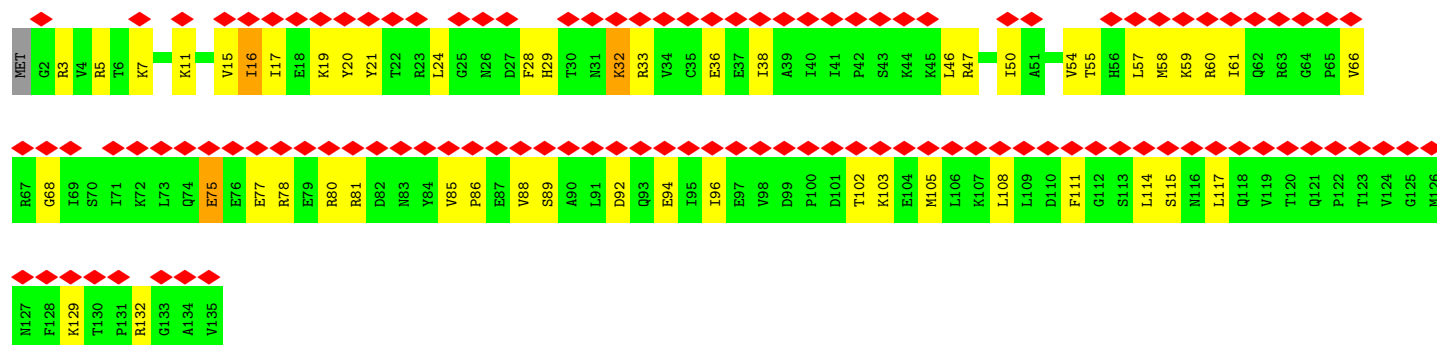
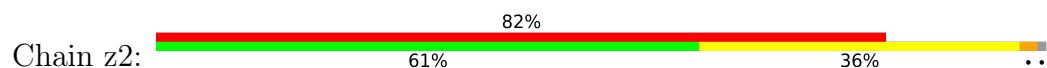




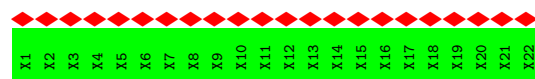
- Molecule 81: Small ribosomal subunit protein uS9



- Molecule 82: Small ribosomal subunit protein eS17



- Molecule 83: Nascent protein chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	221320	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2900	Depositor
Magnification	100000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.403	Depositor
Minimum map value	-0.217	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.0422	Depositor
Map size (Å)	315.12, 315.12, 315.12	wwPDB
Map dimensions	312, 312, 312	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.01, 1.01, 1.01	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: B8N, B8T, 1MA, OMG, 5MC, 2MG, A2M, UR3, ZN, PSU, MG, OMU, OMC, 4AC

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	A1	0.21	0/1888	0.38	0/2516
2	A2	0.20	0/84889	0.30	0/132400
3	A3	0.18	0/1175	0.46	0/1575
4	B1	0.18	0/1847	0.39	0/2486
5	B2	0.18	0/2836	0.27	0/4421
6	B3	0.26	0/1122	0.49	0/1503
7	Bv	0.13	0/1813	0.29	0/2823
7	n2	0.12	0/1813	0.29	0/2823
8	Bx	0.13	0/219	0.31	0/336
9	C1	0.18	0/1537	0.38	0/2065
10	C2	0.19	0/3675	0.29	0/5725
11	C3	0.17	0/818	0.41	0/1099
12	D1	0.17	0/1694	0.33	0/2261
13	D2	0.22	0/1959	0.38	0/2627
14	D3	0.18	0/645	0.36	0/863
15	E1	0.18	0/1420	0.45	0/1899
16	E2	0.21	0/3305	0.42	0/4422
17	E3	0.18	0/1097	0.40	0/1464
18	F1	0.18	0/1674	0.38	0/2241
19	F2	0.20	0/2921	0.37	0/3921
20	F3	0.19	0/805	0.42	0/1079
21	G1	0.19	0/1165	0.37	0/1558
22	G2	0.17	0/2435	0.32	0/3260
23	G3	0.17	0/490	0.44	0/656
24	H1	0.22	0/1746	0.37	0/2338
25	H2	0.16	0/1822	0.35	0/2443
26	H3	0.18	0/465	0.44	0/618
27	I2	0.21	0/1670	0.39	0/2232
28	I3	0.15	0/2493	0.42	0/3394
29	J2	0.19	0/1268	0.37	0/1700
30	J3	0.21	0/1737	0.48	0/2348
31	K2	0.20	0/1535	0.36	0/2048

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	K3	0.17	0/1863	0.42	0/2481
33	L1	0.15	0/1318	0.46	1/1767 (0.1%)
34	L2	0.18	0/1515	0.29	0/2002
35	L3	0.19	0/1542	0.41	0/2058
36	M2	0.22	0/1490	0.39	0/2000
37	M3	0.13	0/962	0.34	0/1289
38	N2	0.19	0/1327	0.32	0/1771
39	N3	0.17	0/1232	0.37	0/1656
40	O2	0.15	0/839	0.36	0/1126
41	O3	0.21	0/1015	0.41	0/1361
42	P2	0.20	0/983	0.44	1/1319 (0.1%)
43	P3	0.21	0/1051	0.43	0/1406
44	Q2	0.18	0/532	0.33	0/708
45	Q3	0.20	0/1019	0.49	0/1354
46	R2	0.18	0/984	0.36	0/1323
47	R3	0.17	0/691	0.44	0/922
48	S2	0.17	0/1132	0.31	0/1504
49	S3	0.17	0/665	0.44	0/891
50	T2	0.21	0/1130	0.49	0/1507
51	T3	0.15	0/443	0.34	0/582
52	U2	0.21	0/1193	0.39	0/1593
53	U3	0.22	0/424	0.47	0/566
54	V2	0.15	0/963	0.32	0/1275
55	W2	0.20	0/742	0.41	0/996
56	X2	0.19	0/903	0.37	0/1216
57	Y2	0.19	0/1071	0.36	0/1429
58	Z2	0.27	0/895	0.49	2/1198 (0.2%)
59	a2	0.22	0/916	0.38	0/1221
60	b2	0.16	0/1009	0.36	0/1332
61	c2	0.16	0/843	0.32	0/1115
62	d2	0.21	0/720	0.44	0/952
63	e2	0.18	0/574	0.41	0/760
64	f2	0.23	0/454	0.32	0/599
65	g2	0.16	0/434	0.44	1/575 (0.2%)
66	h2	0.18	0/231	0.31	0/294
67	i2	0.19	0/855	0.42	0/1128
68	j2	0.23	0/703	0.45	0/935
69	k2	0.20	0/1016	0.39	0/1363
70	m2	0.20	0/38274	0.31	0/59646
71	o2	0.19	0/1731	0.44	1/2352 (0.0%)
72	p2	0.24	0/1749	0.55	0/2340
73	q2	0.20	0/1739	0.51	0/2342
74	r2	0.21	0/2118	0.49	0/2849

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	s2	0.21	0/1477	0.41	0/1983
76	t2	0.18	0/1299	0.47	1/1767 (0.1%)
77	u2	0.20	0/1662	0.46	0/2228
78	v2	0.16	0/824	0.36	0/1112
79	w2	0.23	0/1241	0.46	0/1662
80	x2	0.16	0/1024	0.41	0/1369
81	y2	0.20	0/1146	0.44	0/1534
82	z2	0.16	0/1094	0.48	0/1469
All	All	0.20	0/227035	0.35	7/333371 (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
82	z2	0	1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	P2	92	ASP	N-CA-C	-5.68	104.56	113.02
71	o2	112	ILE	N-CA-C	-5.46	107.06	111.91
33	L1	108	ASP	CB-CA-C	-5.44	109.83	117.23
65	g2	108	VAL	N-CA-C	-5.40	107.59	112.12
76	t2	75	ILE	CA-CB-CG1	5.29	119.40	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
82	z2	115	SER	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	A1	1851	0	1988	53	0
2	A2	77547	0	39263	1013	0
3	A3	1157	0	1213	42	0
4	B1	1812	0	1947	46	0
5	B2	2538	0	1286	26	0
6	B3	1104	0	1139	39	0
7	Bv	1623	0	821	10	0
7	n2	1623	0	821	23	0
8	Bx	200	0	101	3	0
9	C1	1519	0	1603	27	0
10	C2	3315	0	1685	46	0
11	C3	808	0	878	21	0
12	D1	1656	0	1706	30	0
13	D2	1921	0	2022	33	0
14	D3	638	0	635	8	0
15	E1	1397	0	1425	33	0
16	E2	3238	0	3380	55	0
17	E3	1080	0	1147	31	0
18	F1	1643	0	1750	32	0
19	F2	2867	0	3040	43	0
20	F3	789	0	841	10	0
21	G1	1143	0	1219	24	0
22	G2	2389	0	2420	47	0
23	G3	488	0	514	14	0
24	H1	1701	0	1749	34	0
25	H2	1789	0	1932	25	0
26	H3	454	0	445	15	0
27	I2	1640	0	1792	40	0
28	I3	2436	0	2393	49	0
29	J2	1242	0	1274	16	0
30	J3	1700	0	1786	31	0
31	K2	1511	0	1636	25	0
32	K3	1840	0	1989	45	0
33	L1	1300	0	1375	43	0
34	L2	1499	0	1651	24	0
35	L3	1518	0	1632	37	0
36	M2	1450	0	1488	26	0
37	M3	952	0	993	19	0
38	N2	1299	0	1368	20	0
39	N3	1208	0	1294	18	0
40	O2	825	0	850	15	0
41	O3	1002	0	1023	34	0
42	P2	969	0	1031	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	P3	1034	0	1080	29	0
44	Q2	519	0	533	3	0
45	Q3	1002	0	1075	24	0
46	R2	967	0	1040	14	0
47	R3	683	0	761	28	0
48	S2	1115	0	1205	21	0
49	S3	651	0	672	15	0
50	T2	1107	0	1182	27	0
51	T3	438	0	484	11	0
52	U2	1164	0	1213	18	0
53	U3	415	0	393	12	0
54	V2	945	0	1037	16	0
55	W2	732	0	769	14	0
56	X2	888	0	930	15	0
57	Y2	1053	0	1147	18	0
58	Z2	876	0	912	15	0
59	a2	906	0	997	17	0
60	b2	1001	0	1138	27	0
61	c2	832	0	917	18	0
62	d2	705	0	737	9	0
63	e2	568	0	635	17	0
64	f2	444	0	483	6	0
65	g2	428	0	465	6	0
66	h2	230	0	276	8	0
67	i2	842	0	912	15	0
68	j2	693	0	738	10	0
69	k2	1001	0	1066	24	0
70	m2	34939	0	17651	562	0
71	o2	1694	0	1696	57	0
72	p2	1722	0	1794	51	0
73	q2	1711	0	1805	69	0
74	r2	2076	0	2177	65	0
75	s2	1457	0	1508	46	0
76	t2	1278	0	1207	33	0
77	u2	1633	0	1666	45	0
78	v2	800	0	818	21	0
79	w2	1220	0	1289	38	0
80	x2	1005	0	1053	28	0
81	y2	1128	0	1195	38	0
82	z2	1080	0	1135	38	0
83	A	110	0	32	0	0
84	A2	82	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	Bv	2	0	0	0	0
84	H1	1	0	0	0	0
84	J2	1	0	0	0	0
84	P2	1	0	0	0	0
84	d2	1	0	0	0	0
84	m2	34	0	0	0	0
85	F3	1	0	0	0	0
85	H3	1	0	0	0	0
85	d2	1	0	0	0	0
85	g2	1	0	0	0	0
85	i2	1	0	0	0	0
85	j2	1	0	0	0	0
86	B1	1	0	0	0	0
All	All	213902	0	158368	3337	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 9.

The worst 5 of 3337 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)
22:G2:76:CYS:HB2	22:G2:112:ARG:HH22	1.26	1.01
2:A2:740:A:H62	2:A2:828:G:H21	1.01	0.96
22:G2:68:ARG:HG3	22:G2:73:MET:HE1	1.44	0.95
2:A2:1374:G:N2	2:A2:1379:C:O2	2.00	0.94
70:m2:70:G:H21	70:m2:79:A:H62	0.99	0.93

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	221/270 (82%)	216 (98%)	5 (2%)	0	100	100
3	A3	138/152 (91%)	132 (96%)	6 (4%)	0	100	100
4	B1	220/266 (83%)	217 (99%)	3 (1%)	0	100	100
6	B3	139/145 (96%)	135 (97%)	4 (3%)	0	100	100
9	C1	188/192 (98%)	185 (98%)	3 (2%)	0	100	100
11	C3	100/119 (84%)	97 (97%)	3 (3%)	0	100	100
12	D1	200/214 (94%)	197 (98%)	3 (2%)	0	100	100
13	D2	249/257 (97%)	238 (96%)	11 (4%)	0	100	100
14	D3	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
15	E1	172/178 (97%)	165 (96%)	7 (4%)	0	100	100
16	E2	400/403 (99%)	388 (97%)	12 (3%)	0	100	100
17	E3	137/143 (96%)	132 (96%)	5 (4%)	0	100	100
18	F1	201/203 (99%)	190 (94%)	11 (6%)	0	100	100
19	F2	357/419 (85%)	346 (97%)	11 (3%)	0	100	100
20	F3	97/115 (84%)	94 (97%)	3 (3%)	0	100	100
21	G1	137/217 (63%)	135 (98%)	2 (2%)	0	100	100
22	G2	291/297 (98%)	287 (99%)	4 (1%)	0	100	100
23	G3	60/69 (87%)	58 (97%)	2 (3%)	0	100	100
24	H1	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
25	H2	215/296 (73%)	212 (99%)	3 (1%)	0	100	100
26	H3	52/56 (93%)	49 (94%)	3 (6%)	0	100	100
27	I2	199/203 (98%)	195 (98%)	4 (2%)	0	100	100
28	I3	311/317 (98%)	299 (96%)	12 (4%)	0	100	100
29	J2	151/184 (82%)	148 (98%)	3 (2%)	0	100	100
30	J3	217/293 (74%)	211 (97%)	6 (3%)	0	100	100
31	K2	184/188 (98%)	180 (98%)	4 (2%)	0	100	100
32	K3	225/249 (90%)	221 (98%)	4 (2%)	0	100	100
33	L1	155/217 (71%)	149 (96%)	6 (4%)	0	100	100
34	L2	177/196 (90%)	176 (99%)	1 (1%)	0	100	100
35	L3	182/194 (94%)	176 (97%)	6 (3%)	0	100	100
36	M2	173/176 (98%)	164 (95%)	9 (5%)	0	100	100
37	M3	120/132 (91%)	120 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	N2	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
39	N3	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
40	O2	99/128 (77%)	98 (99%)	1 (1%)	0	100	100
41	O3	132/151 (87%)	126 (96%)	6 (4%)	0	100	100
42	P2	127/140 (91%)	119 (94%)	8 (6%)	0	100	100
43	P3	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
44	Q2	60/157 (38%)	57 (95%)	3 (5%)	0	100	100
45	Q3	120/133 (90%)	119 (99%)	1 (1%)	0	100	100
46	R2	116/156 (74%)	113 (97%)	3 (3%)	0	100	100
47	R3	83/125 (66%)	77 (93%)	6 (7%)	0	100	100
48	S2	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
49	S3	81/84 (96%)	75 (93%)	6 (7%)	0	100	100
50	T2	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
51	T3	53/133 (40%)	52 (98%)	1 (2%)	0	100	100
52	U2	145/148 (98%)	140 (97%)	5 (3%)	0	100	100
53	U3	50/156 (32%)	49 (98%)	1 (2%)	0	100	100
54	V2	115/160 (72%)	111 (96%)	4 (4%)	0	100	100
55	W2	92/115 (80%)	90 (98%)	2 (2%)	0	100	100
56	X2	105/125 (84%)	105 (100%)	0	0	100	100
57	Y2	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
58	Z2	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
59	a2	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
60	b2	118/123 (96%)	117 (99%)	1 (1%)	0	100	100
61	c2	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
62	d2	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
63	e2	67/70 (96%)	67 (100%)	0	0	100	100
64	f2	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
65	g2	50/128 (39%)	50 (100%)	0	0	100	100
66	h2	22/25 (88%)	22 (100%)	0	0	100	100
67	i2	101/106 (95%)	96 (95%)	5 (5%)	0	100	100
68	j2	87/92 (95%)	82 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	k2	123/137 (90%)	121 (98%)	2 (2%)	0	100	100
71	o2	212/295 (72%)	206 (97%)	6 (3%)	0	100	100
72	p2	210/264 (80%)	192 (91%)	18 (9%)	0	100	100
73	q2	218/243 (90%)	212 (97%)	6 (3%)	0	100	100
74	r2	260/263 (99%)	249 (96%)	11 (4%)	0	100	100
75	s2	179/204 (88%)	174 (97%)	5 (3%)	0	100	100
76	t2	179/194 (92%)	166 (93%)	13 (7%)	0	100	100
77	u2	204/208 (98%)	192 (94%)	12 (6%)	0	100	100
78	v2	93/165 (56%)	92 (99%)	1 (1%)	0	100	100
79	w2	148/158 (94%)	138 (93%)	9 (6%)	1 (1%)	18	44
80	x2	121/145 (83%)	115 (95%)	6 (5%)	0	100	100
81	y2	140/146 (96%)	133 (95%)	7 (5%)	0	100	100
82	z2	132/135 (98%)	119 (90%)	13 (10%)	0	100	100
All	All	11266/12996 (87%)	10908 (97%)	357 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
79	w2	25	LEU

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	
1	A1	194/234 (83%)	192 (99%)	2 (1%)	68	86
3	A3	122/132 (92%)	117 (96%)	5 (4%)	27	59
4	B1	193/223 (86%)	191 (99%)	2 (1%)	68	86
6	B3	112/115 (97%)	103 (92%)	9 (8%)	11	31
9	C1	169/171 (99%)	167 (99%)	2 (1%)	63	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	C3	93/107 (87%)	90 (97%)	3 (3%)	34	67
12	D1	174/181 (96%)	170 (98%)	4 (2%)	44	75
13	D2	193/199 (97%)	188 (97%)	5 (3%)	40	72
14	D3	67/67 (100%)	66 (98%)	1 (2%)	57	81
15	E1	147/149 (99%)	144 (98%)	3 (2%)	48	77
16	E2	347/348 (100%)	340 (98%)	7 (2%)	48	77
17	E3	111/115 (96%)	109 (98%)	2 (2%)	51	79
18	F1	170/170 (100%)	162 (95%)	8 (5%)	23	54
19	F2	301/348 (86%)	293 (97%)	8 (3%)	39	71
20	F3	86/98 (88%)	83 (96%)	3 (4%)	32	64
21	G1	118/157 (75%)	118 (100%)	0	100	100
22	G2	246/249 (99%)	242 (98%)	4 (2%)	55	81
23	G3	55/62 (89%)	52 (94%)	3 (6%)	19	47
24	H1	171/172 (99%)	169 (99%)	2 (1%)	63	84
25	H2	198/256 (77%)	194 (98%)	4 (2%)	48	77
26	H3	48/49 (98%)	46 (96%)	2 (4%)	26	58
27	I2	172/173 (99%)	164 (95%)	8 (5%)	23	54
28	I3	272/275 (99%)	270 (99%)	2 (1%)	76	90
29	J2	134/163 (82%)	130 (97%)	4 (3%)	36	69
30	J3	185/224 (83%)	180 (97%)	5 (3%)	39	71
31	K2	164/165 (99%)	160 (98%)	4 (2%)	43	74
32	K3	198/218 (91%)	191 (96%)	7 (4%)	32	64
33	L1	147/197 (75%)	140 (95%)	7 (5%)	23	53
34	L2	158/175 (90%)	155 (98%)	3 (2%)	50	78
35	L3	160/168 (95%)	152 (95%)	8 (5%)	22	51
36	M2	155/156 (99%)	150 (97%)	5 (3%)	34	67
37	M3	104/108 (96%)	101 (97%)	3 (3%)	37	70
38	N2	139/140 (99%)	136 (98%)	3 (2%)	45	75
39	N3	130/131 (99%)	128 (98%)	2 (2%)	57	81
40	O2	91/114 (80%)	89 (98%)	2 (2%)	45	75
41	O3	104/119 (87%)	100 (96%)	4 (4%)	29	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	P2	100/107 (94%)	100 (100%)	0	100	100
43	P3	112/113 (99%)	109 (97%)	3 (3%)	39	71
44	Q2	54/126 (43%)	54 (100%)	0	100	100
45	Q3	107/115 (93%)	98 (92%)	9 (8%)	10	29
46	R2	106/133 (80%)	104 (98%)	2 (2%)	50	78
47	R3	75/103 (73%)	73 (97%)	2 (3%)	39	71
48	S2	124/135 (92%)	119 (96%)	5 (4%)	28	60
49	S3	75/76 (99%)	71 (95%)	4 (5%)	20	49
50	T2	117/118 (99%)	115 (98%)	2 (2%)	53	80
51	T3	45/106 (42%)	42 (93%)	3 (7%)	15	39
52	U2	120/121 (99%)	120 (100%)	0	100	100
53	U3	45/140 (32%)	44 (98%)	1 (2%)	45	75
54	V2	98/124 (79%)	98 (100%)	0	100	100
55	W2	79/97 (81%)	77 (98%)	2 (2%)	42	73
56	X2	98/110 (89%)	96 (98%)	2 (2%)	48	77
57	Y2	114/121 (94%)	112 (98%)	2 (2%)	51	79
58	Z2	88/89 (99%)	85 (97%)	3 (3%)	32	65
59	a2	98/100 (98%)	96 (98%)	2 (2%)	48	77
60	b2	108/110 (98%)	107 (99%)	1 (1%)	70	87
61	c2	86/89 (97%)	83 (96%)	3 (4%)	32	64
62	d2	73/80 (91%)	72 (99%)	1 (1%)	59	82
63	e2	64/65 (98%)	63 (98%)	1 (2%)	55	81
64	f2	47/48 (98%)	46 (98%)	1 (2%)	47	76
65	g2	48/116 (41%)	48 (100%)	0	100	100
66	h2	23/24 (96%)	22 (96%)	1 (4%)	26	57
67	i2	91/94 (97%)	88 (97%)	3 (3%)	33	66
68	j2	73/75 (97%)	70 (96%)	3 (4%)	27	59
69	k2	109/121 (90%)	104 (95%)	5 (5%)	24	55
71	o2	179/242 (74%)	173 (97%)	6 (3%)	32	65
72	p2	193/229 (84%)	176 (91%)	17 (9%)	9	27
73	q2	184/202 (91%)	168 (91%)	16 (9%)	9	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
74	r2	224/225 (100%)	211 (94%)	13 (6%)	18	45
75	s2	156/170 (92%)	151 (97%)	5 (3%)	34	67
76	t2	110/174 (63%)	106 (96%)	4 (4%)	31	63
77	u2	165/180 (92%)	157 (95%)	8 (5%)	23	53
78	v2	86/136 (63%)	84 (98%)	2 (2%)	44	75
79	w2	134/142 (94%)	127 (95%)	7 (5%)	21	50
80	x2	109/130 (84%)	102 (94%)	7 (6%)	16	41
81	y2	117/121 (97%)	115 (98%)	2 (2%)	53	80
82	z2	120/121 (99%)	111 (92%)	9 (8%)	12	34
All	All	9782/11056 (88%)	9479 (97%)	303 (3%)	36	68

5 of 303 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
73	q2	27	ARG
80	x2	26	LEU
73	q2	124	ARG
75	s2	65	GLN
82	z2	94	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 114 such sidechains are listed below:

Mol	Chain	Res	Type
36	M2	77	ASN
81	y2	86	GLN
51	T3	44	ASN
81	y2	80	GLN
73	q2	165	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	C2	155/156 (99%)	31 (20%)	1 (0%)
2	A2	3593/3615 (99%)	751 (20%)	12 (0%)
5	B2	118/121 (97%)	11 (9%)	0
7	Bv	75/76 (98%)	16 (21%)	0
7	n2	75/76 (98%)	37 (49%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
70	m2	1628/1635 (99%)	441 (27%)	0
8	Bx	9/10 (90%)	4 (44%)	0
All	All	5653/5689 (99%)	1291 (22%)	13 (0%)

5 of 1291 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A2	2	G
2	A2	13	U
2	A2	21	G
2	A2	25	A
2	A2	39	A

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A2	2430	G
2	A2	2463	U
10	C2	59	A
2	A2	4351	U
2	A2	4582	U

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

108 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	5MC	A2	4099	2	18,22,23	0.33	0	26,32,35	0.63	0
70	PSU	m2	825	70	18,21,22	0.54	0	22,30,33	0.56	0
70	A2M	m2	1680	70	22,25,26	0.10	0	31,36,39	0.20	0
70	B8T	m2	1339	70	19,22,23	0.42	0	26,31,34	0.47	0
2	OMU	A2	3958	2	19,22,23	0.30	0	26,31,34	0.45	0
70	A2M	m2	514	70	22,25,26	0.11	0	31,36,39	0.48	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A2M	A2	398	2	22,25,26	0.09	0	31,36,39	0.30	0
70	OMG	m2	1330	70	23,26,27	0.33	0	33,38,41	0.42	0
70	PSU	m2	614	70	18,21,22	0.55	0	22,30,33	0.60	1 (4%)
2	OMC	A2	2616	2	19,22,23	0.28	0	26,31,34	0.37	0
2	OMU	A2	3474	2	19,22,23	0.33	0	26,31,34	0.45	0
70	OMU	m2	172	70	19,22,23	0.27	0	26,31,34	0.67	1 (3%)
2	OMG	A2	3880	2	23,26,27	0.30	0	33,38,41	0.53	0
70	OMU	m2	121	70	19,22,23	0.32	0	26,31,34	0.52	0
2	PSU	A2	2263	2	18,21,22	0.48	0	22,30,33	0.61	0
2	PSU	A2	3420	2	18,21,22	0.60	0	22,30,33	0.37	0
70	UR3	m2	1832	70	19,22,23	0.31	0	26,32,35	0.42	0
2	OMG	A2	4022	2	23,26,27	0.33	0	33,38,41	0.38	0
2	OMC	A2	3525	2	19,22,23	0.29	0	26,31,34	0.39	0
2	OMC	A2	1683	2,84	19,22,23	0.30	0	26,31,34	0.55	0
2	OMC	A2	3357	2	19,22,23	0.27	0	26,31,34	0.46	0
2	A2M	A2	1337	2	22,25,26	0.14	0	31,36,39	0.38	0
70	PSU	m2	1245	70	18,21,22	0.51	0	22,30,33	0.59	0
2	OMC	A2	2579	2	19,22,23	0.30	0	26,31,34	0.40	0
2	OMG	A2	4151	2	23,26,27	0.34	0	33,38,41	0.50	0
2	A2M	A2	2118	2,84	22,25,26	0.09	0	31,36,39	0.21	0
70	B8N	m2	1250	70	24,29,30	0.59	0	29,42,45	0.64	1 (3%)
2	A2M	A2	1347	2,84	22,25,26	0.10	0	31,36,39	0.50	0
2	OMG	A2	4044	2	23,26,27	0.29	0	33,38,41	0.35	0
2	PSU	A2	1496	2	18,21,22	0.54	0	22,30,33	0.58	0
2	OMG	A2	3283	2	23,26,27	0.31	0	33,38,41	0.53	0
2	OMG	A2	4146	2	23,26,27	0.31	0	33,38,41	0.39	0
2	A2M	A2	4175	2,84	22,25,26	0.11	0	31,36,39	0.38	0
70	OMU	m2	116	70	19,22,23	0.30	0	26,31,34	0.49	0
2	OMC	A2	4108	2	19,22,23	0.31	0	26,31,34	0.36	0
2	A2M	A2	4270	2	22,25,26	0.09	0	31,36,39	0.36	0
2	PSU	A2	4288	2	18,21,22	0.50	0	22,30,33	0.61	0
70	OMC	m2	519	70	19,22,23	0.28	0	26,31,34	0.49	0
2	5MC	A2	3438	2,84	18,22,23	0.31	0	26,32,35	0.43	0
2	OMG	A2	3448	2	23,26,27	0.31	0	33,38,41	0.34	0
2	OMG	A2	2119	2,84	23,26,27	0.30	0	33,38,41	0.39	0
2	A2M	A2	1137	2	22,25,26	0.11	0	31,36,39	0.22	0
2	PSU	A2	4183	2	18,21,22	0.54	0	22,30,33	0.41	0
2	OMU	A2	4150	2	19,22,23	0.28	0	26,31,34	0.46	0
2	PSU	A2	1490	2	18,21,22	0.91	1 (5%)	22,30,33	0.59	0
70	A2M	m2	1033	70	22,25,26	0.10	0	31,36,39	0.26	0
2	OMG	A2	1335	2	23,26,27	0.35	0	33,38,41	0.44	0
70	A2M	m2	670	70,84	22,25,26	0.13	0	31,36,39	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A2M	A2	2570	2	22,25,26	0.08	0	31,36,39	0.19	0
2	PSU	A2	3945	2	18,21,22	0.51	0	22,30,33	0.55	0
2	A2M	A2	3481	2	22,25,26	0.09	0	31,36,39	0.24	0
2	A2M	A2	3486	2	22,25,26	0.07	0	31,36,39	0.33	0
10	OMG	C2	75	10	23,26,27	0.30	0	33,38,41	0.37	0
2	OMC	A2	2177	2,84	19,22,23	0.30	0	26,31,34	0.40	0
2	A2M	A2	3441	2	22,25,26	0.10	0	31,36,39	0.31	0
2	A2M	A2	3380	2	22,25,26	0.10	0	31,36,39	0.38	0
2	A2M	A2	1673	2	22,25,26	0.10	0	31,36,39	0.43	0
70	PSU	m2	824	70	18,21,22	0.69	1 (5%)	22,30,33	0.66	0
2	OMU	A2	2592	2	19,22,23	0.32	0	26,31,34	0.60	0
70	OMG	m2	511	70,84	23,26,27	0.33	0	33,38,41	0.41	0
2	OMC	A2	2106	2	19,22,23	0.32	0	26,31,34	0.35	0
2	PSU	A2	4055	2	18,21,22	0.55	0	22,30,33	0.61	1 (4%)
70	OMC	m2	355	70	19,22,23	0.29	0	26,31,34	0.38	0
2	1MA	A2	4067	2	21,25,26	0.31	0	31,37,40	0.46	0
2	PSU	A2	4152	2	18,21,22	0.55	0	22,30,33	0.63	0
2	OMG	A2	4289	2	23,26,27	0.35	0	33,38,41	0.40	0
2	A2M	A2	4223	2	22,25,26	0.09	0	31,36,39	0.18	0
70	OMG	m2	646	70	23,26,27	0.32	0	33,38,41	0.39	0
2	OMC	A2	3464	2	19,22,23	0.30	0	26,31,34	0.36	0
70	A2M	m2	27	70	22,25,26	0.13	0	31,36,39	0.34	0
2	PSU	A2	4280	2	18,21,22	0.54	0	22,30,33	0.57	0
2	PSU	A2	1395	2	18,21,22	0.56	0	22,30,33	0.53	0
2	OMC	A2	2559	2	19,22,23	0.31	0	26,31,34	0.36	0
2	A2M	A2	2542	2	22,25,26	0.08	0	31,36,39	0.30	0
70	OMG	m2	685	70	23,26,27	0.31	0	33,38,41	0.51	0
70	PSU	m2	1083	70	18,21,22	0.61	1 (5%)	22,30,33	0.66	0
2	PSU	A2	3371	2	18,21,22	0.54	0	22,30,33	0.57	0
2	OMC	A2	3497	2	19,22,23	0.26	0	26,31,34	0.43	0
2	OMG	A2	1130	2	23,26,27	0.34	0	33,38,41	0.48	0
2	OMC	A2	3543	2	19,22,23	0.33	0	26,31,34	0.43	0
2	A2M	A2	1140	2	22,25,26	0.08	0	31,36,39	0.19	0
2	A2M	A2	2156	2	22,25,26	0.10	0	31,36,39	0.21	0
70	A2M	m2	486	70	22,25,26	0.08	0	31,36,39	0.25	0
2	OMC	A2	2120	2	19,22,23	0.31	0	26,31,34	0.47	0
70	A2M	m2	578	70	22,25,26	0.08	0	31,36,39	0.20	0
70	4AC	m2	1844	70	21,24,25	0.31	0	29,34,37	0.30	0
2	OMC	A2	1154	2	19,22,23	0.29	0	26,31,34	0.39	0
2	OMG	A2	4275	2	23,26,27	0.33	0	33,38,41	0.49	0
2	OMG	A2	3555	2,84	23,26,27	0.33	0	33,38,41	0.51	0
2	PSU	A2	3385	2	18,21,22	0.53	0	22,30,33	0.55	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMG	A2	1438	2	23,26,27	0.30	0	33,38,41	0.39	0
2	PSU	A2	4102	2,84	18,21,22	0.50	0	22,30,33	0.43	0
70	OMC	m2	174	70	19,22,23	0.34	0	26,31,34	0.56	0
2	OMC	A2	4188	2	19,22,23	0.32	0	26,31,34	0.48	0
2	OMU	A2	3581	2	19,22,23	0.31	0	26,31,34	0.53	0
2	2MG	A2	1330	2	23,26,27	0.33	0	32,38,41	0.38	0
70	OMC	m2	1705	70	19,22,23	0.29	0	26,31,34	0.43	0
2	OMU	A2	4272	2	19,22,23	0.39	0	26,31,34	0.62	0
2	OMG	A2	2179	2	23,26,27	0.29	0	33,38,41	0.34	0
70	OMG	m2	603	70	23,26,27	0.31	0	33,38,41	0.34	0
2	OMG	A2	3848	7,2	23,26,27	0.31	0	33,38,41	0.38	0
70	OMU	m2	430	70	19,22,23	0.26	0	26,31,34	0.45	0
2	A2M	A2	3374	2	22,25,26	0.09	0	31,36,39	0.26	0
2	PSU	A2	4094	2	18,21,22	0.52	0	22,30,33	0.62	1 (4%)
70	OMG	m2	438	70	23,26,27	0.34	0	33,38,41	0.47	0
70	OMG	m2	869	70	23,26,27	0.29	0	33,38,41	0.34	0
70	A2M	m2	99	70,84	22,25,26	0.10	0	31,36,39	0.34	0
2	OMG	A2	3400	2	23,26,27	0.29	0	33,38,41	0.38	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	5MC	A2	4099	2	-	3/7/25/26	0/2/2/2
70	PSU	m2	825	70	-	0/7/25/26	0/2/2/2
70	A2M	m2	1680	70	-	1/9/27/28	0/3/3/3
70	B8T	m2	1339	70	-	2/7/27/28	0/2/2/2
2	OMU	A2	3958	2	-	0/9/27/28	0/2/2/2
70	A2M	m2	514	70	-	3/9/27/28	0/3/3/3
2	A2M	A2	398	2	-	0/9/27/28	0/3/3/3
70	OMG	m2	1330	70	-	2/9/27/28	0/3/3/3
70	PSU	m2	614	70	-	0/7/25/26	0/2/2/2
2	OMC	A2	2616	2	-	0/9/27/28	0/2/2/2
2	OMU	A2	3474	2	-	1/9/27/28	0/2/2/2
70	OMU	m2	172	70	-	3/9/27/28	0/2/2/2
2	OMG	A2	3880	2	-	0/9/27/28	0/3/3/3
70	OMU	m2	121	70	-	0/9/27/28	0/2/2/2
2	PSU	A2	2263	2	-	0/7/25/26	0/2/2/2
2	PSU	A2	3420	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
70	UR3	m2	1832	70	-	2/7/25/26	0/2/2/2
2	OMG	A2	4022	2	-	0/9/27/28	0/3/3/3
2	OMC	A2	3525	2	-	0/9/27/28	0/2/2/2
2	OMC	A2	1683	2,84	-	0/9/27/28	0/2/2/2
2	OMC	A2	3357	2	-	4/9/27/28	0/2/2/2
2	A2M	A2	1337	2	-	1/9/27/28	0/3/3/3
70	PSU	m2	1245	70	-	2/7/25/26	0/2/2/2
2	OMC	A2	2579	2	-	1/9/27/28	0/2/2/2
2	OMG	A2	4151	2	-	0/9/27/28	0/3/3/3
2	A2M	A2	2118	2,84	-	0/9/27/28	0/3/3/3
70	B8N	m2	1250	70	-	5/16/34/35	0/2/2/2
2	A2M	A2	1347	2,84	-	3/9/27/28	0/3/3/3
2	OMG	A2	4044	2	-	0/9/27/28	0/3/3/3
2	PSU	A2	1496	2	-	0/7/25/26	0/2/2/2
2	OMG	A2	3283	2	-	0/9/27/28	0/3/3/3
2	OMG	A2	4146	2	-	0/9/27/28	0/3/3/3
2	A2M	A2	4175	2,84	-	1/9/27/28	0/3/3/3
70	OMU	m2	116	70	-	0/9/27/28	0/2/2/2
2	OMC	A2	4108	2	-	0/9/27/28	0/2/2/2
2	A2M	A2	4270	2	-	0/9/27/28	0/3/3/3
2	PSU	A2	4288	2	-	5/7/25/26	0/2/2/2
70	OMC	m2	519	70	-	2/9/27/28	0/2/2/2
2	5MC	A2	3438	2,84	-	0/7/25/26	0/2/2/2
2	OMG	A2	3448	2	-	0/9/27/28	0/3/3/3
2	OMG	A2	2119	2,84	-	2/9/27/28	0/3/3/3
2	A2M	A2	1137	2	-	2/9/27/28	0/3/3/3
2	PSU	A2	4183	2	-	2/7/25/26	0/2/2/2
2	OMU	A2	4150	2	-	1/9/27/28	0/2/2/2
2	PSU	A2	1490	2	-	1/7/25/26	0/2/2/2
70	A2M	m2	1033	70	-	0/9/27/28	0/3/3/3
2	OMG	A2	1335	2	-	0/9/27/28	0/3/3/3
70	A2M	m2	670	70,84	-	2/9/27/28	0/3/3/3
2	A2M	A2	2570	2	-	0/9/27/28	0/3/3/3
2	PSU	A2	3945	2	-	0/7/25/26	0/2/2/2
2	A2M	A2	3481	2	-	0/9/27/28	0/3/3/3
2	A2M	A2	3486	2	-	0/9/27/28	0/3/3/3
10	OMG	C2	75	10	-	2/9/27/28	0/3/3/3
2	OMC	A2	2177	2,84	-	1/9/27/28	0/2/2/2
2	A2M	A2	3441	2	-	4/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A2M	A2	3380	2	-	0/9/27/28	0/3/3/3
2	A2M	A2	1673	2	-	0/9/27/28	0/3/3/3
70	PSU	m2	824	70	-	0/7/25/26	0/2/2/2
2	OMU	A2	2592	2	-	0/9/27/28	0/2/2/2
70	OMG	m2	511	70,84	-	0/9/27/28	0/3/3/3
2	OMC	A2	2106	2	-	4/9/27/28	0/2/2/2
2	PSU	A2	4055	2	-	0/7/25/26	0/2/2/2
70	OMC	m2	355	70	-	1/9/27/28	0/2/2/2
2	1MA	A2	4067	2	-	2/7/25/26	0/3/3/3
2	PSU	A2	4152	2	-	1/7/25/26	0/2/2/2
2	OMG	A2	4289	2	-	3/9/27/28	0/3/3/3
2	A2M	A2	4223	2	-	0/9/27/28	0/3/3/3
70	OMG	m2	646	70	-	3/9/27/28	0/3/3/3
2	OMC	A2	3464	2	-	0/9/27/28	0/2/2/2
70	A2M	m2	27	70	-	3/9/27/28	0/3/3/3
2	PSU	A2	4280	2	-	0/7/25/26	0/2/2/2
2	PSU	A2	1395	2	-	1/7/25/26	0/2/2/2
2	OMC	A2	2559	2	-	1/9/27/28	0/2/2/2
2	A2M	A2	2542	2	-	3/9/27/28	0/3/3/3
70	OMG	m2	685	70	-	3/9/27/28	0/3/3/3
70	PSU	m2	1083	70	-	1/7/25/26	0/2/2/2
2	PSU	A2	3371	2	-	0/7/25/26	0/2/2/2
2	OMC	A2	3497	2	-	0/9/27/28	0/2/2/2
2	OMG	A2	1130	2	-	1/9/27/28	0/3/3/3
2	OMC	A2	3543	2	-	1/9/27/28	0/2/2/2
2	A2M	A2	1140	2	-	4/9/27/28	0/3/3/3
2	A2M	A2	2156	2	-	0/9/27/28	0/3/3/3
70	A2M	m2	486	70	-	0/9/27/28	0/3/3/3
2	OMC	A2	2120	2	-	0/9/27/28	0/2/2/2
70	A2M	m2	578	70	-	1/9/27/28	0/3/3/3
70	4AC	m2	1844	70	-	0/11/29/30	0/2/2/2
2	OMC	A2	1154	2	-	0/9/27/28	0/2/2/2
2	OMG	A2	4275	2	-	0/9/27/28	0/3/3/3
2	OMG	A2	3555	2,84	-	0/9/27/28	0/3/3/3
2	PSU	A2	3385	2	-	0/7/25/26	0/2/2/2
2	OMG	A2	1438	2	-	3/9/27/28	0/3/3/3
2	PSU	A2	4102	2,84	-	3/7/25/26	0/2/2/2
70	OMC	m2	174	70	-	2/9/27/28	0/2/2/2
2	OMC	A2	4188	2	-	0/9/27/28	0/2/2/2
2	OMU	A2	3581	2	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2MG	A2	1330	2	-	0/9/27/28	0/3/3/3
70	OMC	m2	1705	70	-	0/9/27/28	0/2/2/2
2	OMU	A2	4272	2	-	3/9/27/28	0/2/2/2
2	OMG	A2	2179	2	-	1/9/27/28	0/3/3/3
70	OMG	m2	603	70	-	1/9/27/28	0/3/3/3
2	OMG	A2	3848	7,2	-	1/9/27/28	0/3/3/3
70	OMU	m2	430	70	-	6/9/27/28	0/2/2/2
2	A2M	A2	3374	2	-	1/9/27/28	0/3/3/3
2	PSU	A2	4094	2	-	0/7/25/26	0/2/2/2
70	OMG	m2	438	70	-	0/9/27/28	0/3/3/3
70	OMG	m2	869	70	-	1/9/27/28	0/3/3/3
70	A2M	m2	99	70,84	-	1/9/27/28	0/3/3/3
2	OMG	A2	3400	2	-	0/9/27/28	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A2	1490	PSU	O4'-C1'	-3.33	1.39	1.43
70	m2	824	PSU	O4'-C1'	-2.54	1.40	1.43
70	m2	1083	PSU	O4'-C1'	-2.18	1.40	1.43

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
70	m2	172	OMU	O2'-C2'-C1'	2.47	113.89	109.08
70	m2	514	A2M	C2'-C3'-C4'	-2.19	97.23	101.99
2	A2	4055	PSU	O4'-C1'-C2'	2.13	108.14	105.14
70	m2	614	PSU	O4'-C1'-C2'	2.09	108.09	105.14
2	A2	4094	PSU	O4'-C1'-C2'	2.06	108.05	105.14

There are no chirality outliers.

5 of 114 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	C2	75	OMG	O4'-C4'-C5'-O5'
10	C2	75	OMG	C3'-C4'-C5'-O5'
2	A2	1140	A2M	O4'-C4'-C5'-O5'
2	A2	1140	A2M	C3'-C4'-C5'-O5'
2	A2	1140	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

54 monomers are involved in 80 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A2	4099	5MC	2	0
70	m2	1680	A2M	1	0
2	A2	3958	OMU	1	0
2	A2	3474	OMU	2	0
70	m2	172	OMU	1	0
2	A2	3880	OMG	1	0
70	m2	1832	UR3	1	0
2	A2	4022	OMG	1	0
2	A2	2579	OMC	1	0
2	A2	2118	A2M	1	0
2	A2	1347	A2M	2	0
2	A2	4044	OMG	2	0
2	A2	1496	PSU	2	0
2	A2	4175	A2M	1	0
70	m2	116	OMU	1	0
2	A2	4108	OMC	1	0
2	A2	4270	A2M	2	0
70	m2	519	OMC	1	0
70	m2	1033	A2M	1	0
2	A2	2570	A2M	2	0
10	C2	75	OMG	1	0
2	A2	3441	A2M	1	0
2	A2	3380	A2M	1	0
2	A2	1673	A2M	1	0
70	m2	511	OMG	3	0
2	A2	2106	OMC	2	0
70	m2	355	OMC	1	0
2	A2	4067	1MA	1	0
2	A2	4152	PSU	1	0
2	A2	4289	OMG	1	0
70	m2	27	A2M	1	0
2	A2	2559	OMC	3	0
70	m2	685	OMG	1	0
2	A2	3497	OMC	1	0
2	A2	1130	OMG	2	0
2	A2	1140	A2M	2	0
70	m2	486	A2M	2	0
70	m2	578	A2M	2	0
70	m2	1844	4AC	2	0
2	A2	1154	OMC	2	0
2	A2	1438	OMG	2	0
70	m2	174	OMC	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A2	4188	OMC	1	0
2	A2	3581	OMU	1	0
2	A2	1330	2MG	1	0
70	m2	1705	OMC	2	0
2	A2	4272	OMU	4	0
2	A2	2179	OMG	1	0
70	m2	603	OMG	1	0
2	A2	3848	OMG	1	0
70	m2	430	OMU	1	0
2	A2	3374	A2M	4	0
70	m2	869	OMG	1	0
70	m2	99	A2M	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 128 ligands modelled in this entry, 128 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	A2	21

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Mol	Chain	Number of breaks
70	m2	6

The worst 5 of 27 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	m2	130:G	O3'	141:A	P	25.23
1	A2	1512:U	O3'	1521:A	P	24.40
1	A2	2658:G	O3'	3240:C	P	19.11
1	A2	891:C	O3'	917:G	P	17.99
1	m2	690:U	O3'	801:U	P	17.79

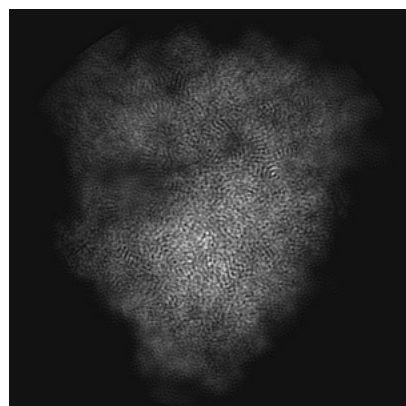
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53262. These allow visual inspection of the internal detail of the map and identification of artifacts.

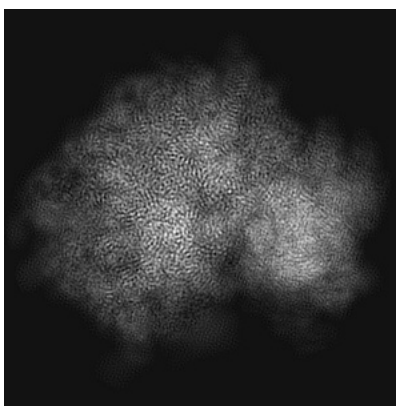
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

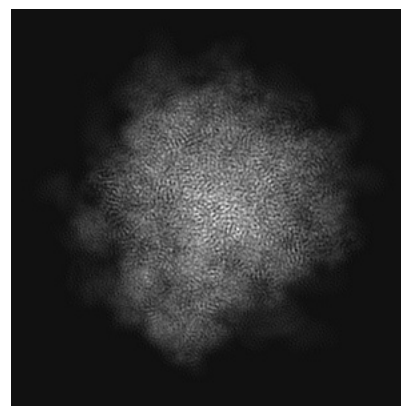
6.1.1 Primary map



X

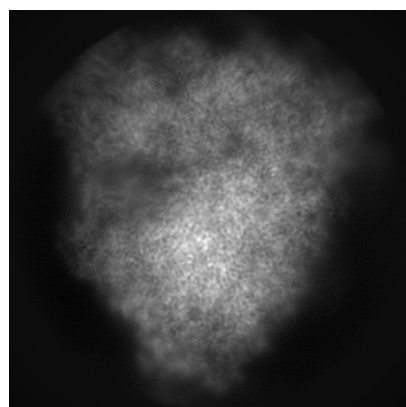


Y

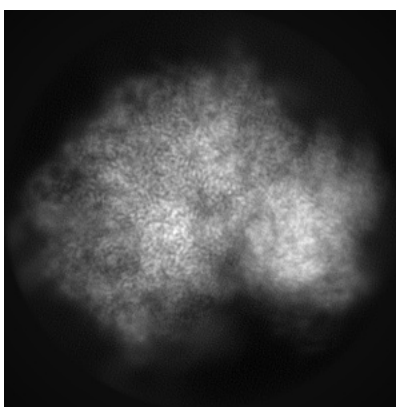


Z

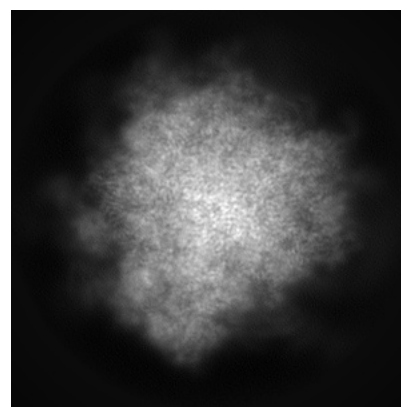
6.1.2 Raw map



X



Y

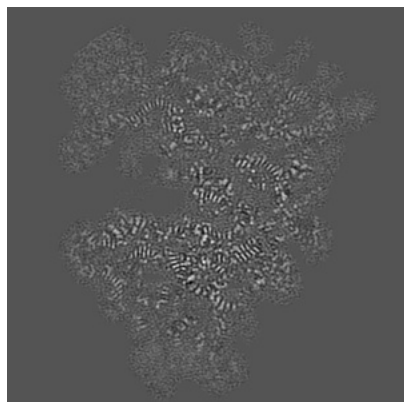


Z

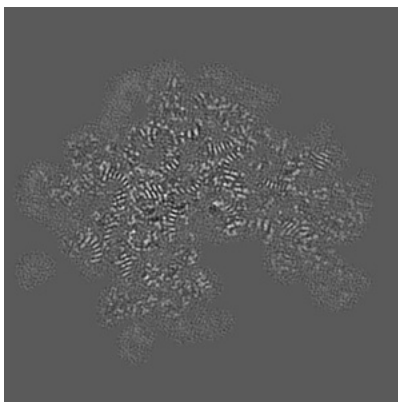
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

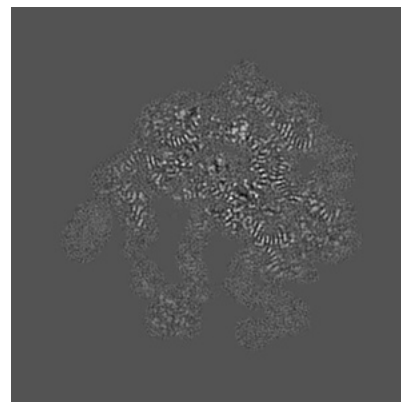
6.2.1 Primary map



X Index: 156

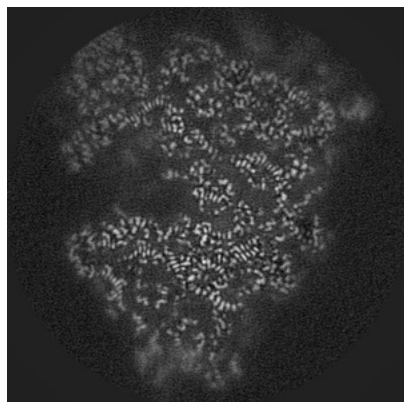


Y Index: 156

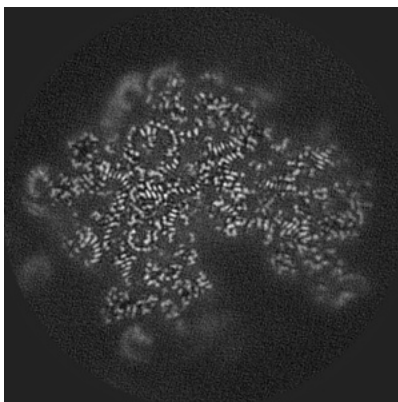


Z Index: 156

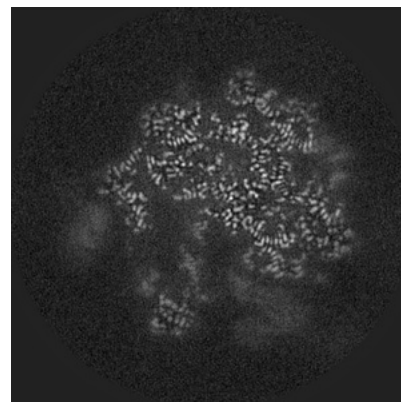
6.2.2 Raw map



X Index: 156



Y Index: 156

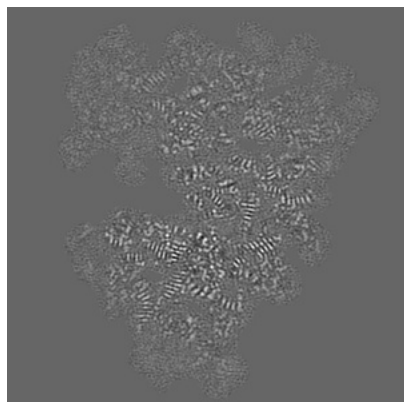


Z Index: 156

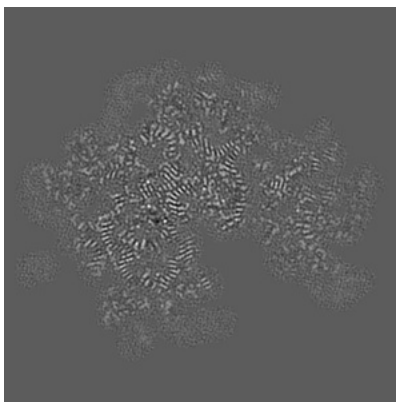
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

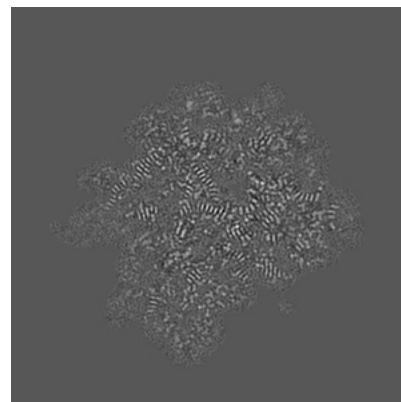
6.3.1 Primary map



X Index: 161

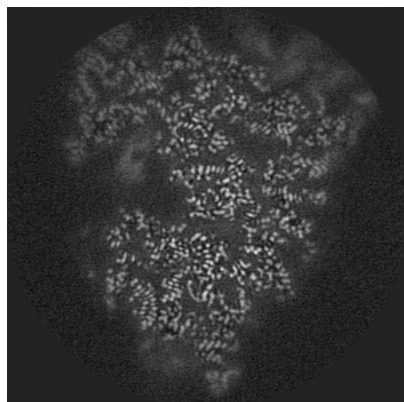


Y Index: 153

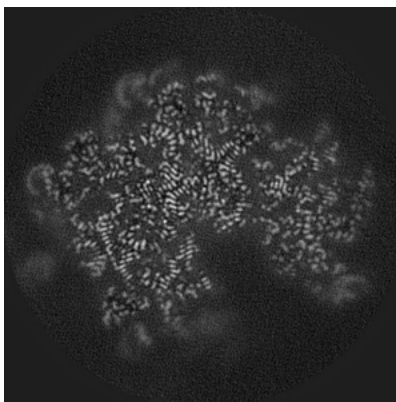


Z Index: 132

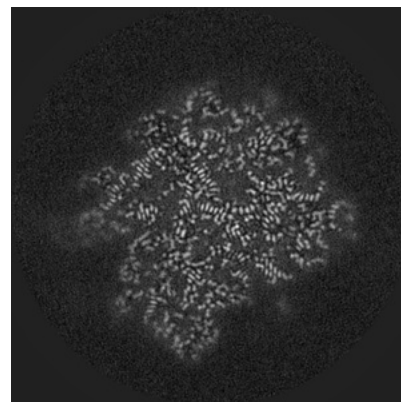
6.3.2 Raw map



X Index: 164



Y Index: 153

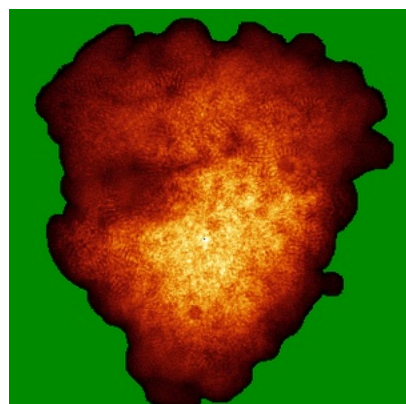


Z Index: 132

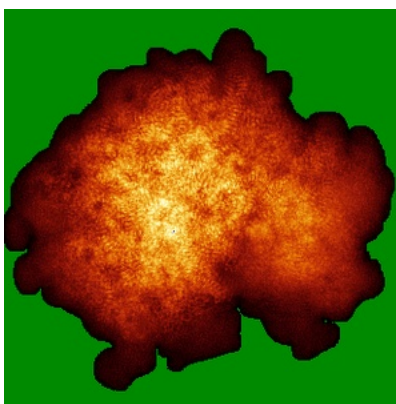
The images above show the largest variance slices of the map in three orthogonal directions.

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

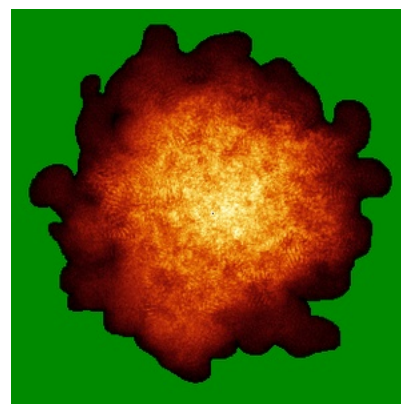
6.4.1 Primary map



X

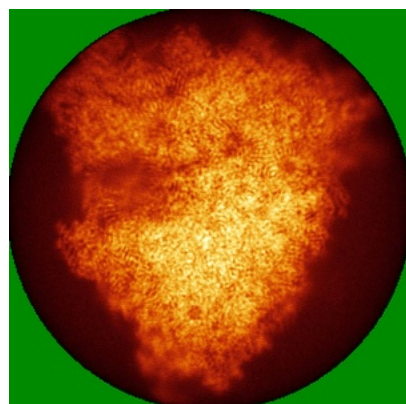


Y

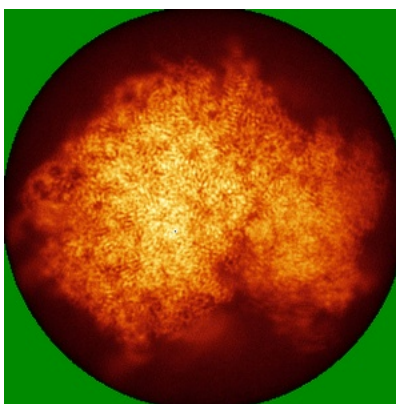


Z

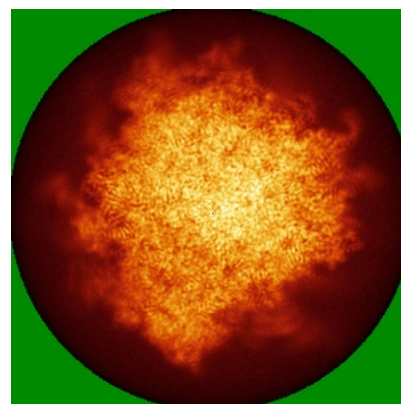
6.4.2 Raw map



X



Y

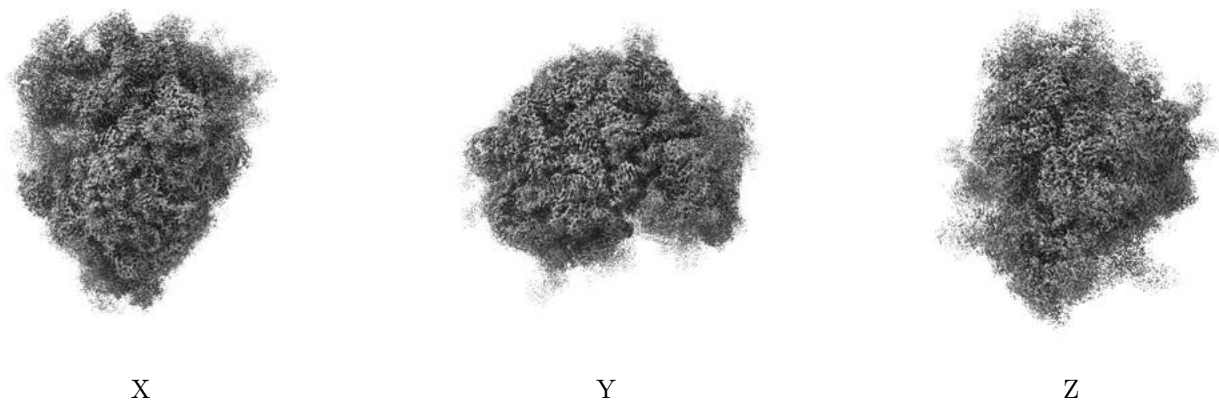


Z

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

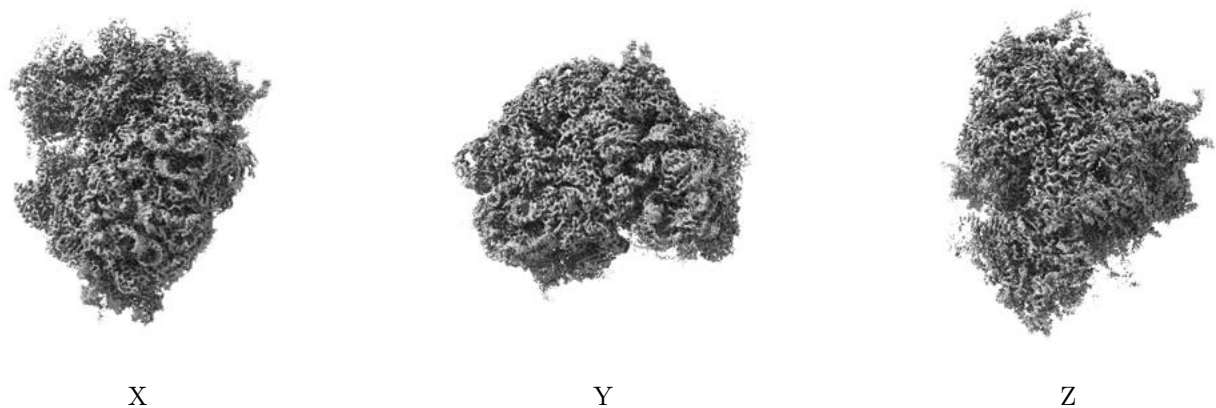
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0422. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

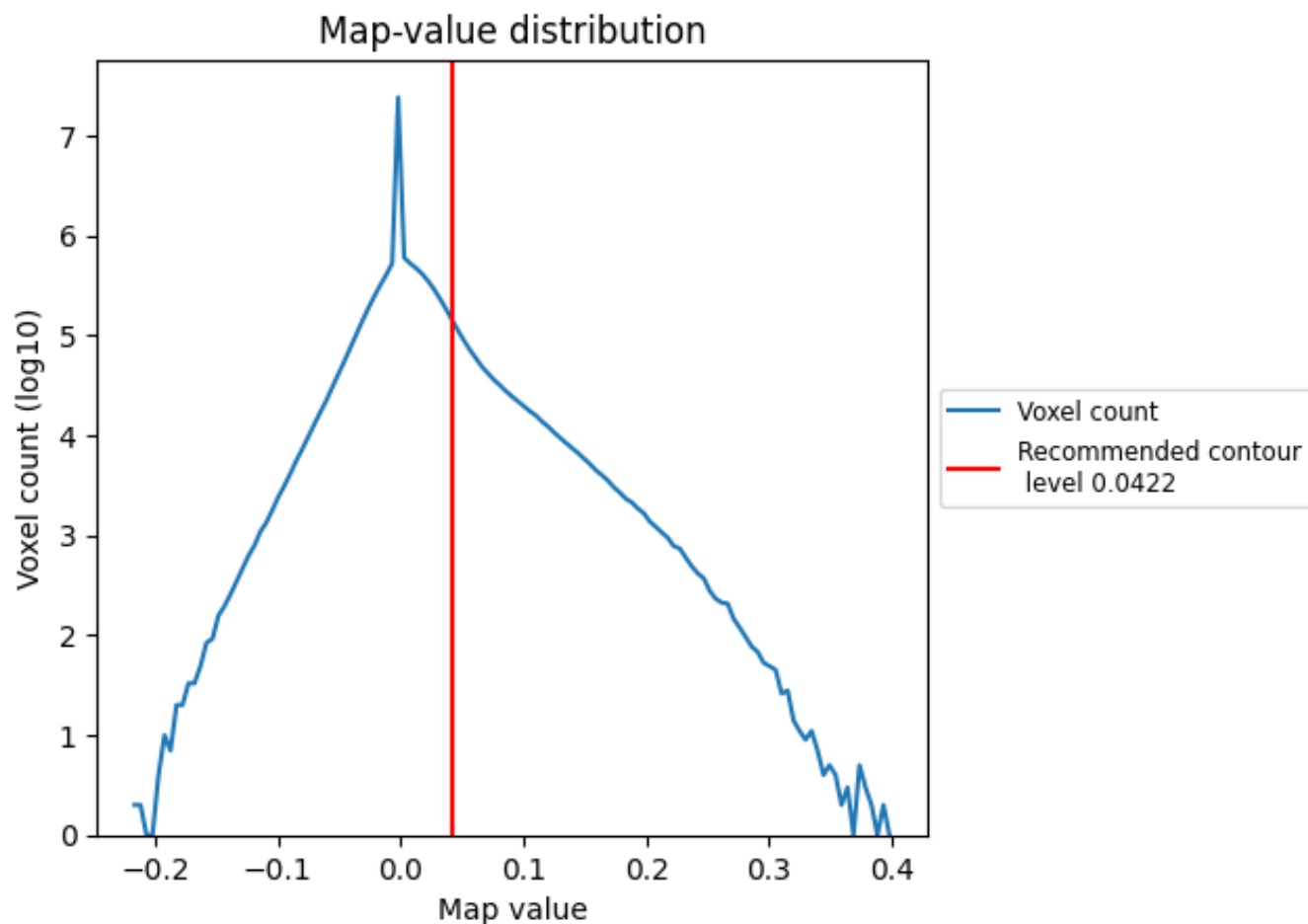
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

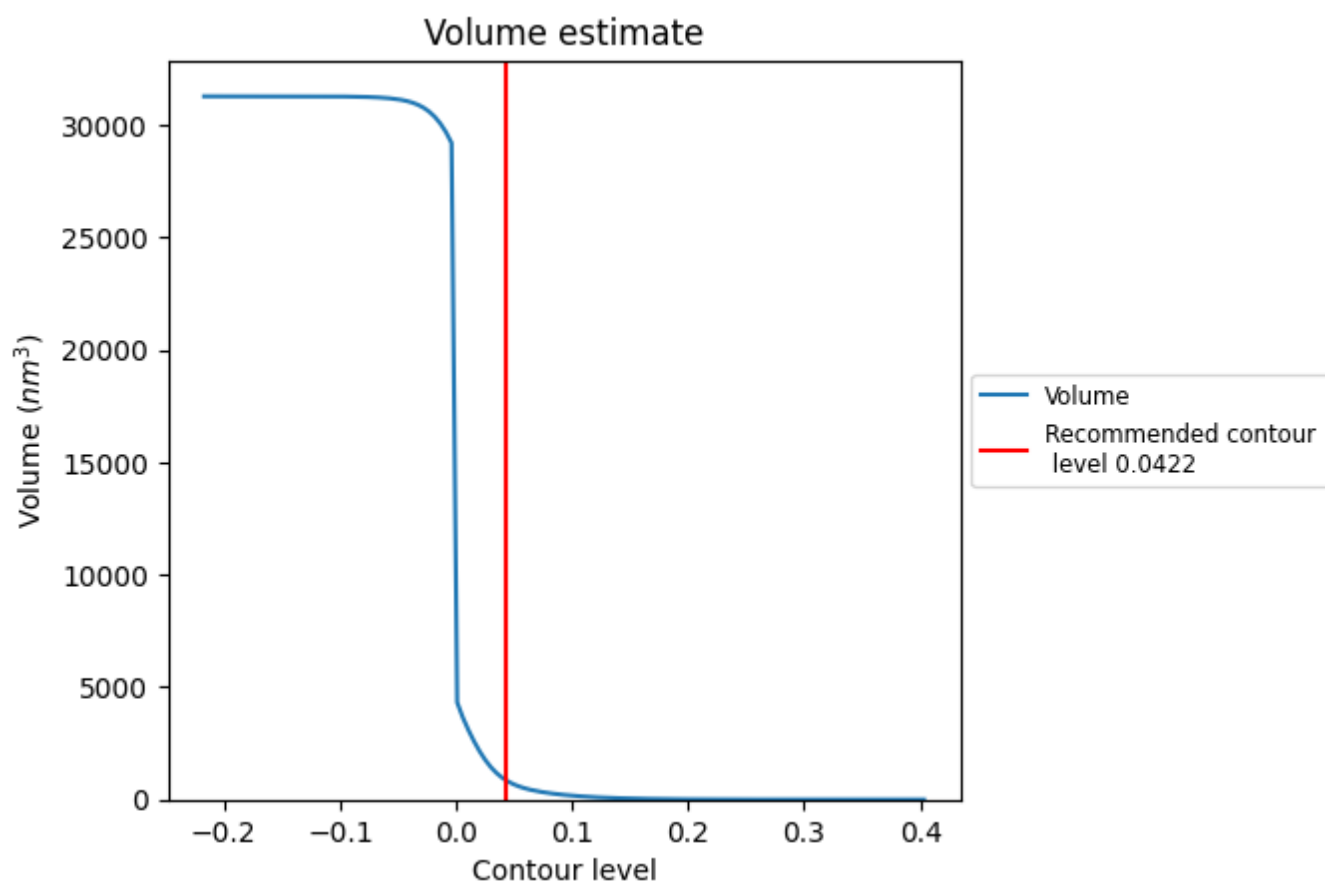
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

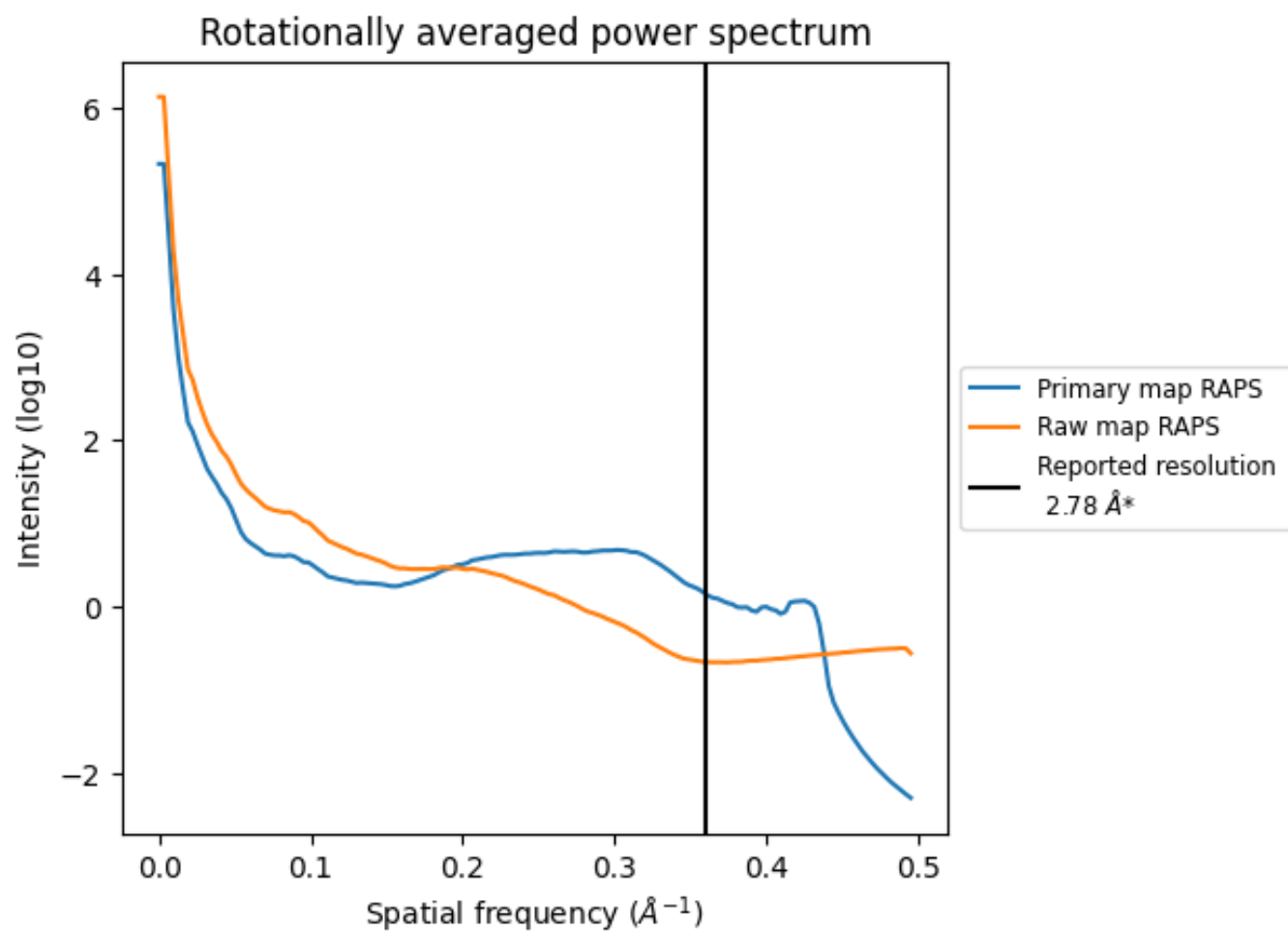
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 893 nm³; this corresponds to an approximate mass of 807 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 ⓘ

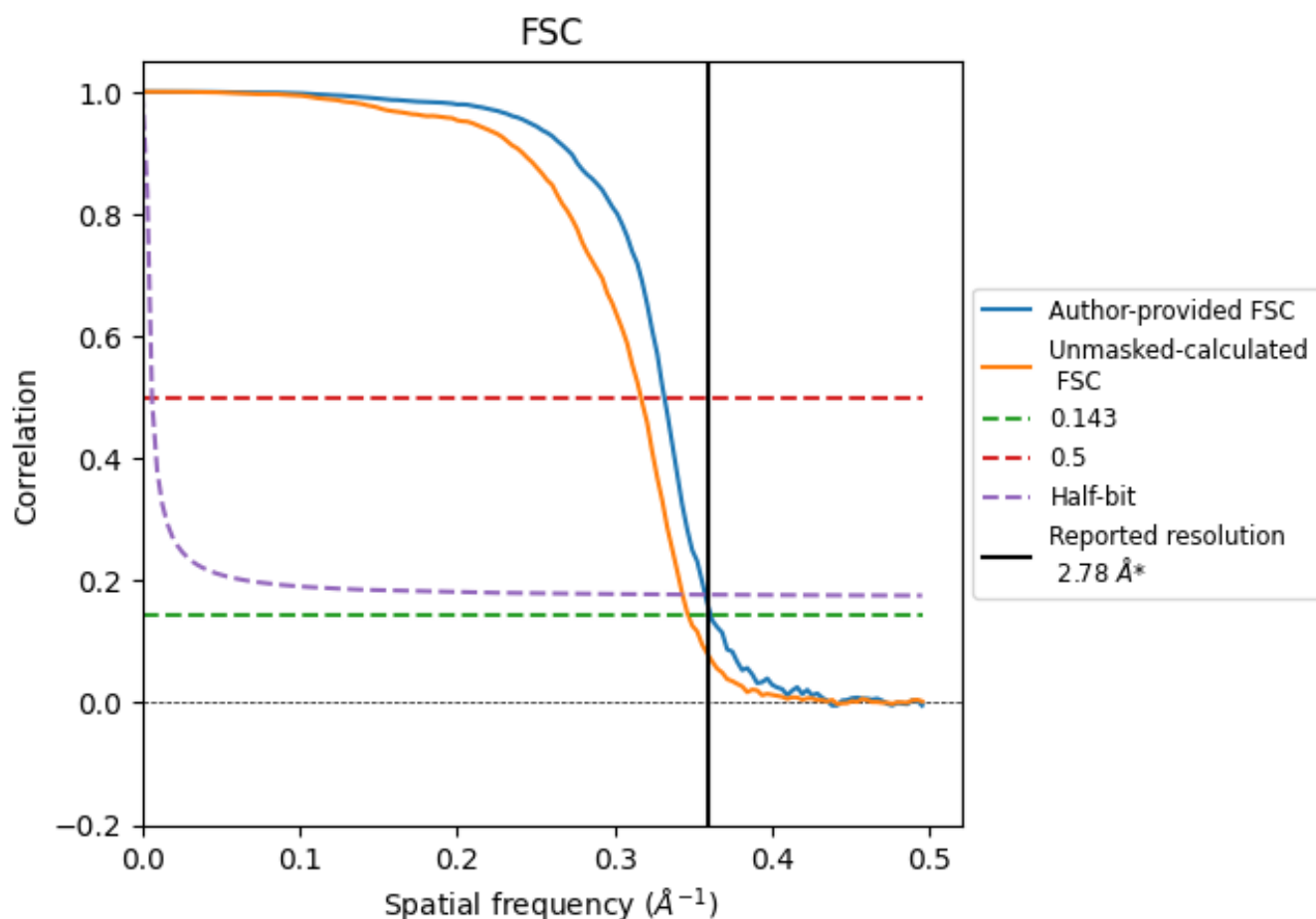


*Reported resolution corresponds to spatial frequency of 0.360 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.360 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

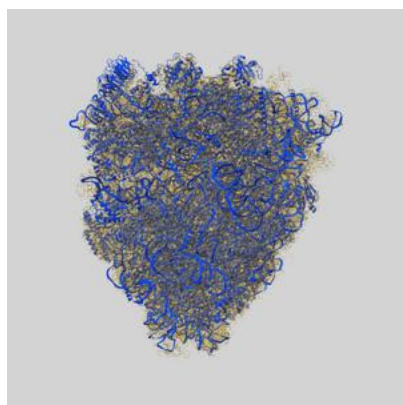
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.78	-	-
Author-provided FSC curve	2.77	3.02	2.80
Unmasked-calculated*	2.89	3.16	2.92

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

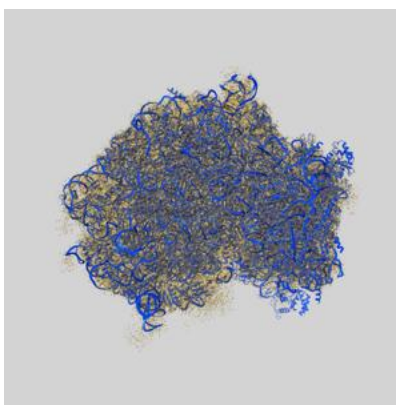
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53262 and PDB model 9QOH. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

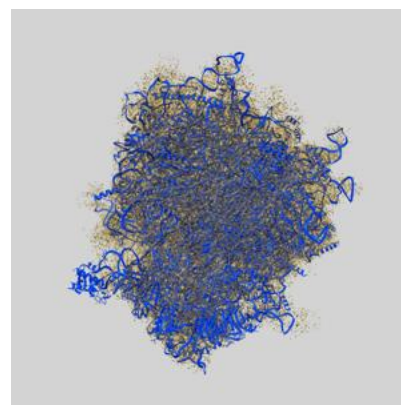
9.1 Map-model overlay [i](#)



X



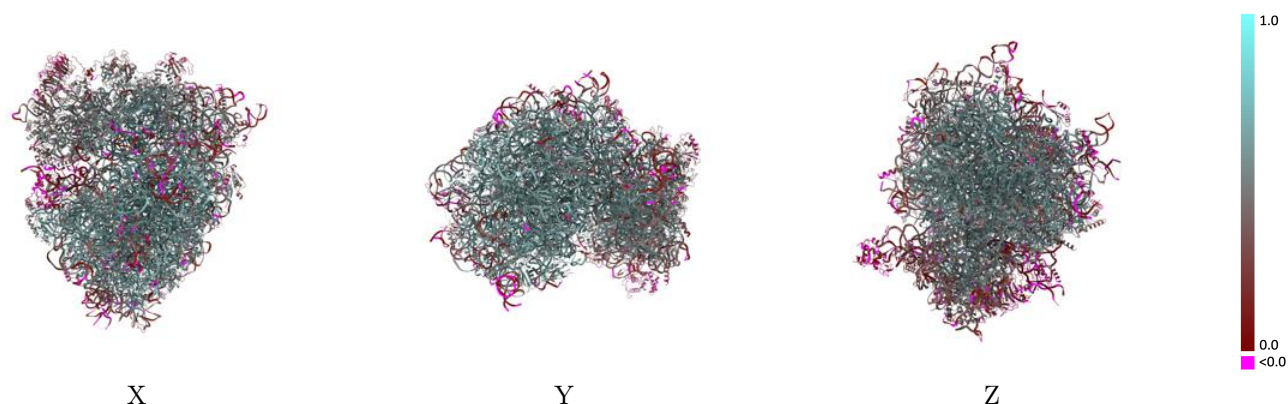
Y



Z

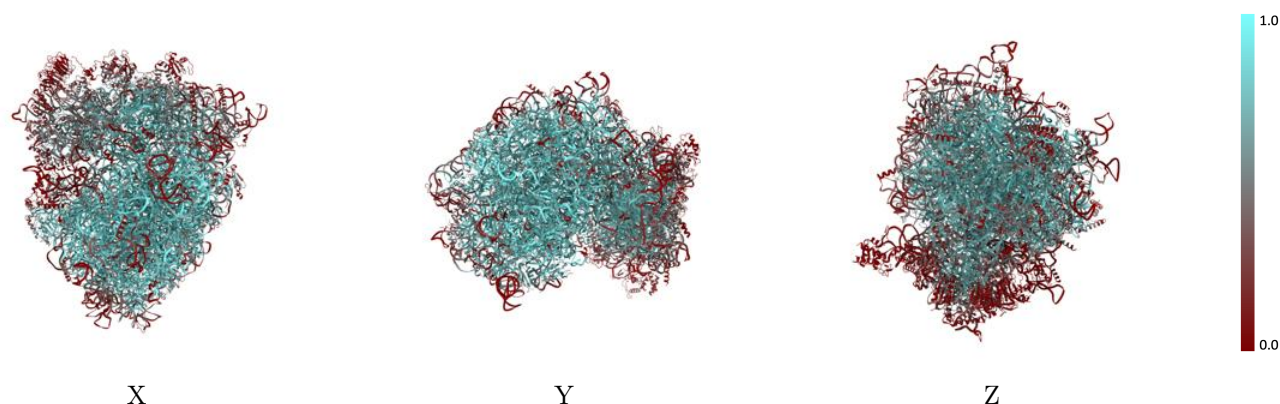
The images above show the 3D surface view of the map at the recommended contour level 0.0422 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



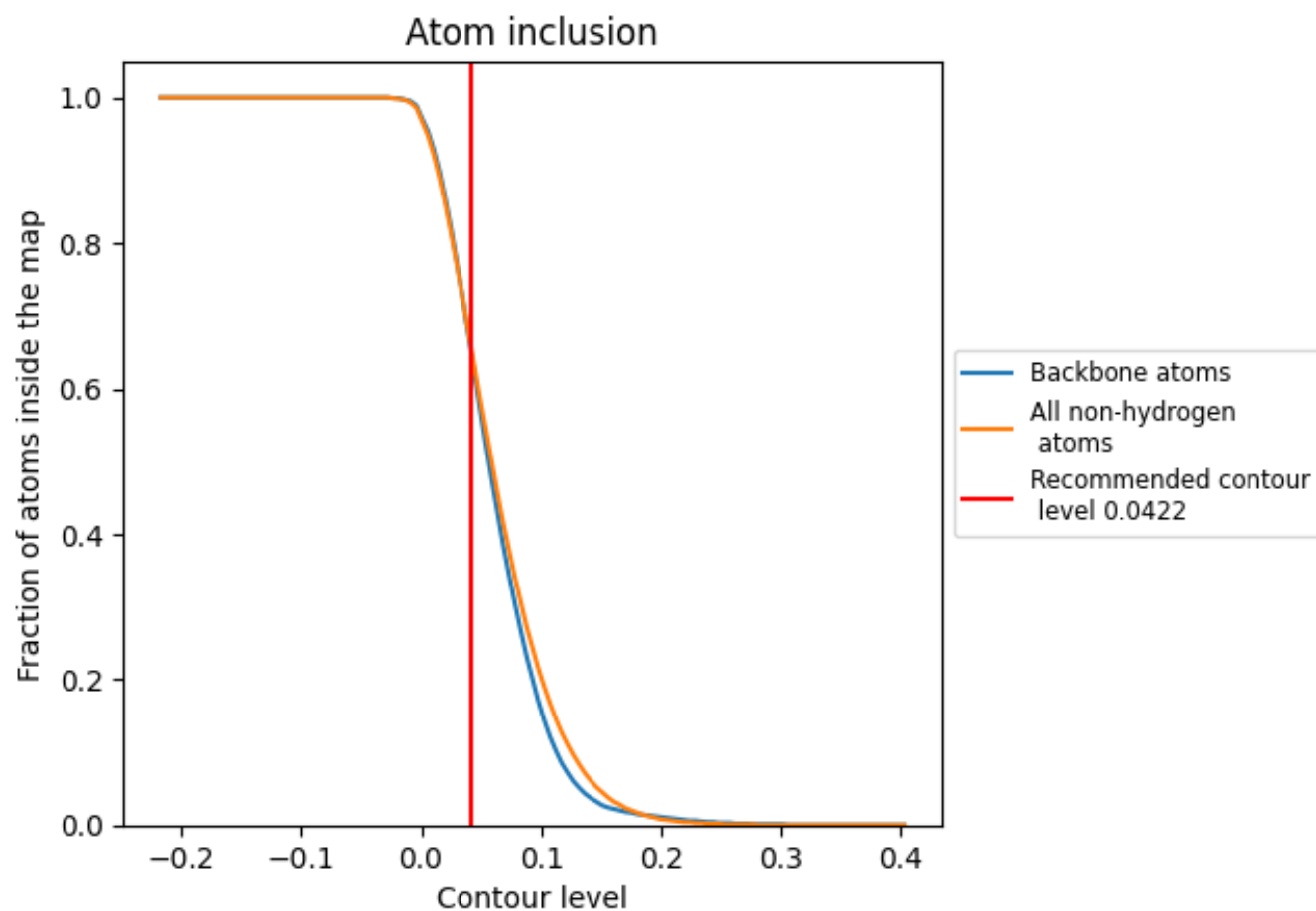
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0422).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 66% 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 (0.0422) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6550	 0.5100
A	 0.0450	 0.0970
A1	 0.8240	 0.5970
A2	 0.7510	 0.5360
A3	 0.2880	 0.3720
B1	 0.5570	 0.4380
B2	 0.8690	 0.6190
B3	 0.2950	 0.4020
Bv	 0.4190	 0.4260
Bx	 0.4050	 0.3650
C1	 0.7090	 0.5720
C2	 0.8270	 0.5690
C3	 0.2350	 0.3360
D1	 0.7460	 0.5640
D2	 0.8670	 0.6170
D3	 0.3340	 0.4330
E1	 0.4890	 0.4480
E2	 0.7880	 0.5900
E3	 0.7060	 0.5520
F1	 0.7000	 0.5510
F2	 0.8220	 0.5990
F3	 0.6800	 0.5490
G1	 0.7190	 0.5750
G2	 0.6370	 0.5220
G3	 0.3530	 0.3950
H1	 0.9150	 0.6440
H2	 0.5750	 0.5000
H3	 0.4160	 0.4310
I2	 0.8410	 0.6180
I3	 0.0660	 0.2100
J2	 0.8380	 0.6160
J3	 0.5440	 0.5140
K2	 0.8560	 0.6200
K3	 0.2610	 0.3260
L1	 0.0140	 0.0600



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Chain	Atom inclusion	Q-score
L2	 0.7080	 0.5320
L3	 0.4640	 0.4630
M2	 0.8480	 0.6190
M3	 0.0030	 0.0680
N2	 0.7630	 0.5720
N3	 0.6010	 0.5260
O2	 0.4290	 0.4240
O3	 0.6210	 0.5000
P2	 0.8170	 0.6000
P3	 0.6430	 0.5290
Q2	 0.7600	 0.5700
Q3	 0.3060	 0.3900
R2	 0.7270	 0.5400
R3	 0.1900	 0.3010
S2	 0.7200	 0.5490
S3	 0.4210	 0.4440
T2	 0.4610	 0.3080
T3	 0.3690	 0.3770
U2	 0.8600	 0.6230
U3	 0.0150	 0.0680
V2	 0.5090	 0.4330
W2	 0.6660	 0.5010
X2	 0.7330	 0.5610
Y2	 0.8590	 0.6230
Z2	 0.8840	 0.6310
a2	 0.7320	 0.5340
b2	 0.6850	 0.5330
c2	 0.6350	 0.5180
d2	 0.8830	 0.6220
e2	 0.3850	 0.3210
f2	 0.8370	 0.6040
g2	 0.7660	 0.5890
h2	 0.8130	 0.5690
i2	 0.7660	 0.5720
j2	 0.7910	 0.5850
k2	 0.7870	 0.5850
m2	 0.6680	 0.5170
n2	 0.1510	 0.1700
o2	 0.3610	 0.4540
p2	 0.5470	 0.5070
q2	 0.2550	 0.3660
r2	 0.4570	 0.4870

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Chain	Atom inclusion	Q-score
s2	 0.4090	 0.4390
t2	 0.2090	 0.3540
u2	 0.5810	 0.4880
v2	 0.1100	 0.2630
w2	 0.6530	 0.5280
x2	 0.2230	 0.3480
y2	 0.3220	 0.4170
z2	 0.2120	 0.3300