



wwPDB EM Validation Summary Report ⓘ

Apr 6, 2026 – 03:52 AM UTC

PDB ID : 9Q7Q / pdb_00009q7q
EMDB ID : EMD-72314
Title : ABCE1-eRF1-RNC-AMD1C
Authors : Maldosevic, E.; Jomaa, A.
Deposited on : 2025-08-25
Resolution : 2.86 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

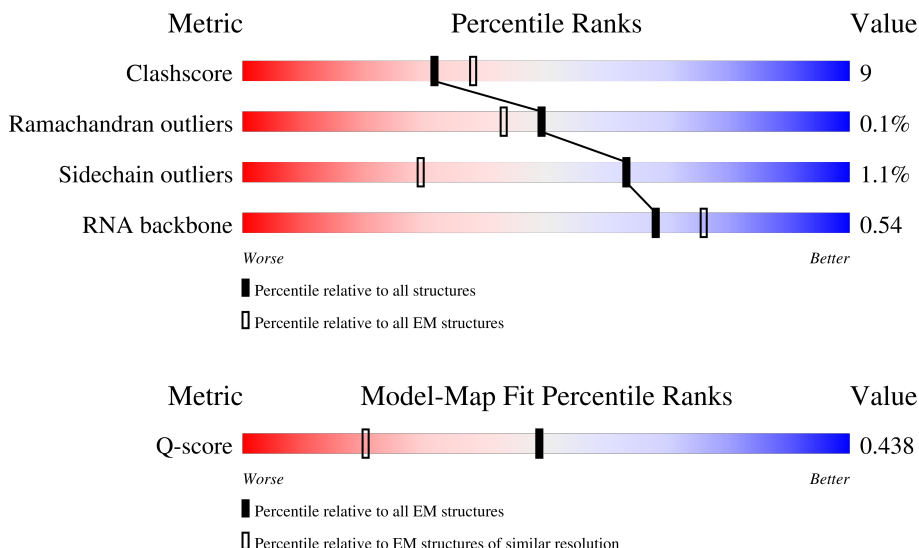
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.86 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.



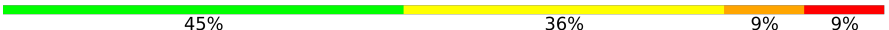



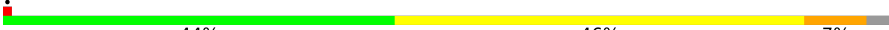





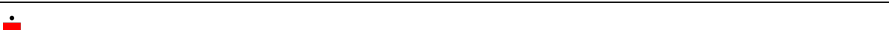

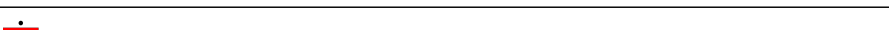
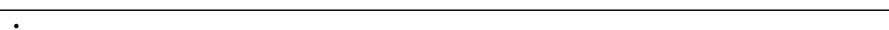











Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12017 (2.36 - 3.36)

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	0	156	
2	1	32	
3	2	76	







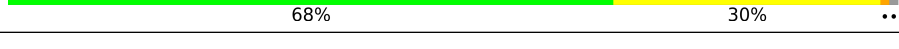
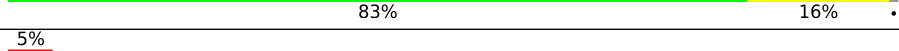
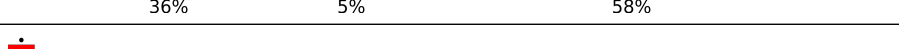
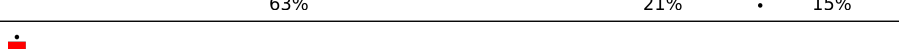
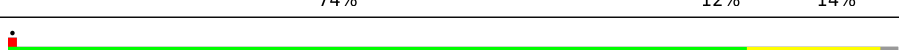

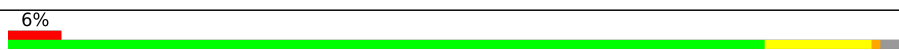

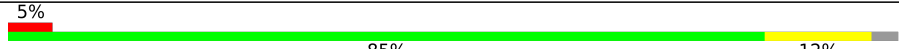





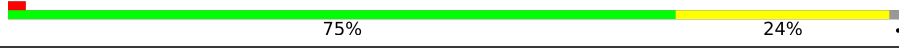
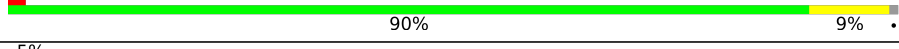



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Mol	Chain	Length	Quality of chain
4	4	11	
5	5	7224	
6	6	317	
7	7	120	
8	8	156	
9	9	56	
10	A	257	
11	B	403	
12	C	413	
13	D	297	
14	E	291	
15	F	249	
16	G	319	
17	H	192	
18	I	214	
19	J	178	
20	K	4592	
21	L	211	
22	M	139	
23	N	203	
24	O	203	
25	P	183	
26	Q	187	
27	R	181	
28	S	176	

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Mol	Chain	Length	Quality of chain
29	T	160	
30	U	99	
31	V	140	
32	W	157	
33	X	156	
34	Y	145	
35	Z	136	
36	a	148	
37	b	245	
38	c	115	
39	d	125	
40	e	130	
41	f	110	
42	g	117	
43	h	123	
44	i	105	
45	j	97	
46	k	69	
47	l	51	
48	m	128	
49	n	25	
50	o	106	
51	p	92	
52	q	222	
53	r	137	

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Mol	Chain	Length	Quality of chain
54	s	318	
55	t	165	
56	u	264	
57	v	278	
58	w	243	
59	x	263	
60	y	204	
61	z	249	
62	AA	133	
63	BB	194	
64	CC	208	
65	DD	194	
66	EE	158	
67	FF	69	
68	GG	119	
69	HH	83	
70	II	152	
71	JJ	84	
72	KK	134	
73	LL	115	
74	MM	151	
75	NN	133	
76	OO	124	
77	PP	145	
78	QQ	151	

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Mol	Chain	Length	Quality of chain
79	RF	437	
80	RR	132	
81	SS	165	
82	TT	130	
83	UU	146	
84	VV	143	
85	WW	145	
86	AB	599	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 218503 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 2 is a protein called AMD1 C-tail.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	32	Total	C	N	O	0	0
			225	143	45	37		

- Molecule 3 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	76	Total	C	N	O	P	0	0
			1622	723	286	537	76		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	11	Total	C	N	O	P	0	0
			230	103	37	79	11		

- Molecule 5 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	3444	Total	C	N	O	P	0	0
			73867	32899	13535	23989	3444		

- Molecule 6 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 7 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 8 is a RNA chain called 5.8S rRNA.

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

- Molecule 9 is a protein called eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	44	Total	C	N	O	S	0	0
			359	222	73	59	5		

- Molecule 10 is a protein called Ribosomal protein L8.

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

- Molecule 11 is a protein called Ribosomal protein L3.

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

- Molecule 12 is a protein called 60S ribosomal protein L4.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	290	Total	C	N	O	S	0	0
			2364	1492	434	424	14		

- Molecule 14 is a protein called 60S ribosomal protein L6.

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

- Molecule 15 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 16 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	228	Total	C	N	O	S	0	0
			1845	1178	355	308	4		

- Molecule 17 is a protein called 60S ribosomal protein L9.

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

- Molecule 18 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	I	213	Total	C	N	O	S	0	0
			1717	1086	332	285	14		

- Molecule 19 is a protein called Ribosomal protein L11.

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

- Molecule 20 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	K	1662	Total	C	N	O	P	0	0
			35481	15839	6373	11608	1661		

- Molecule 21 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 22 is a protein called Large ribosomal subunit protein eL14.

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

- Molecule 23 is a protein called 60S ribosomal protein L15.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 25 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 26 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 27 is a protein called Large ribosomal subunit protein eL19.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	176	Total	C	N	O	S	0	0
			1457	924	288	234	11		

- Molecule 29 is a protein called eL21.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	98	Total	C	N	O	S	0	0
			795	507	140	146	2		

- Molecule 31 is a protein called Ribosomal protein L23.

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

- Molecule 32 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 33 is a protein called eL23.

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

- Molecule 34 is a protein called uL24.

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

- Molecule 35 is a protein called 60S ribosomal protein L27.

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

- Molecule 36 is a protein called 60S ribosomal protein L27a.

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

- Molecule 37 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	b	102	Total	C	N	O	S	0	0
			833	516	187	127	3		

- Molecule 38 is a protein called eL30.

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

- Molecule 39 is a protein called eL31.

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

- Molecule 40 is a protein called 60S ribosomal protein L32.

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

- Molecule 41 is a protein called eL33.

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

- Molecule 42 is a protein called 60S ribosomal protein L34.

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

- Molecule 43 is a protein called eL35.

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

- Molecule 44 is a protein called Large ribosomal subunit protein eL36.

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

- Molecule 45 is a protein called Ribosomal protein L37.

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

- Molecule 46 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 47 is a protein called eL39.

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

- Molecule 48 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

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

- Molecule 49 is a protein called eL41.

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

- Molecule 50 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 51 is a protein called eL43.

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

- Molecule 52 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	q	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 53 is a protein called eL28.

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

- Molecule 54 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 55 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	t	137	Total	C	N	O	S	0	0
			1022	640	187	191	4		

- Molecule 56 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	u	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 57 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	v	221	Total	C	N	O	S	0	0
			1715	1111	295	300	9		

- Molecule 58 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	w	211	Total	C	N	O	S	0	0
			1642	1047	299	289	7		

- Molecule 59 is a protein called Small ribosomal subunit protein eS4.

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

- Molecule 60 is a protein called Ribosomal protein S5.

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

- Molecule 61 is a protein called 40S ribosomal protein S6.

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

- Molecule 62 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AA	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 63 is a protein called 40S ribosomal protein S7.

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

- Molecule 64 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	CC	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 65 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
65	DD	181	Total	C	N	O	S	0	0
			1495	950	299	244	2		

- Molecule 66 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	EE	139	Total	C	N	O	S	0	0
			1140	728	214	192	6		

- Molecule 67 is a protein called Ribosomal protein S28.

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

- Molecule 68 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	GG	99	Total	C	N	O	S	0	0
			785	492	149	140	4		

- Molecule 69 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	HH	83	Total	C	N	O	S	0	0
			637	392	117	123	5		

- Molecule 70 is a protein called uS13.

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

- Molecule 71 is a protein called 40S ribosomal protein S27.

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

- Molecule 72 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	KK	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 73 is a protein called eS26.

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

- Molecule 74 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	MM	135	Total	C	N	O	S	0	0
			1004	614	196	188	6		

- Molecule 75 is a protein called Small ribosomal subunit protein eS24.

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

- Molecule 76 is a protein called eS25.

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

- Molecule 77 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	PP	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 78 is a protein called Ribosomal protein S13.

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

- Molecule 79 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	RF	414	Total	C	N	O	S	0	0
			3268	2080	557	620	11		

- Molecule 80 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	RR	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 81 is a protein called S10_ plectin domain-containing protein.

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

- Molecule 82 is a protein called Ribosomal protein S15a.

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

- Molecule 83 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	UU	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 84 is a protein called uS12.

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

- Molecule 85 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	WW	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 86 is a protein called ATP binding cassette subfamily E member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	AB	576	Total	C	N	O	S	0	0
			4543	2904	779	829	31		

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
87	4	1	Total	Mg	0
			1	1	
87	5	195	Total	Mg	0
			195	195	
87	7	7	Total	Mg	0
			7	7	
87	8	5	Total	Mg	0
			5	5	
87	A	1	Total	Mg	0
			1	1	
87	K	75	Total	Mg	0
			75	75	
87	P	1	Total	Mg	0
			1	1	
87	V	1	Total	Mg	0
			1	1	
87	a	1	Total	Mg	0
			1	1	
87	g	1	Total	Mg	0
			1	1	
87	j	2	Total	Mg	0
			2	2	
87	PP	1	Total	Mg	0
			1	1	

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
88	g	1	Total 1	Zn 1	0
88	j	1	Total 1	Zn 1	0
88	m	1	Total 1	Zn 1	0
88	o	1	Total 1	Zn 1	0
88	p	1	Total 1	Zn 1	0
88	LL	1	Total 1	Zn 1	0

Frequency	Percentage
Often	25%
Sometimes	19%
Never	52%

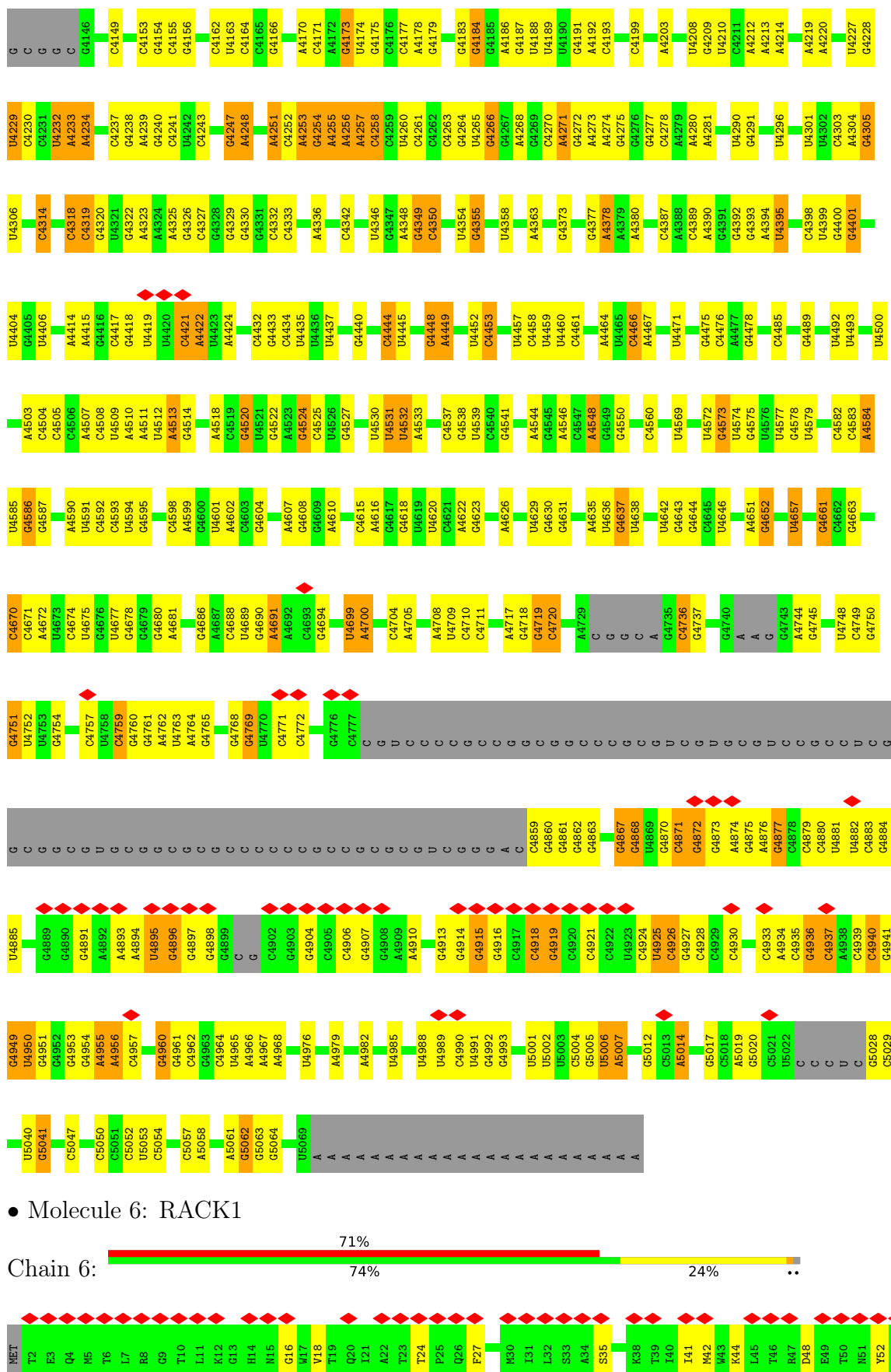


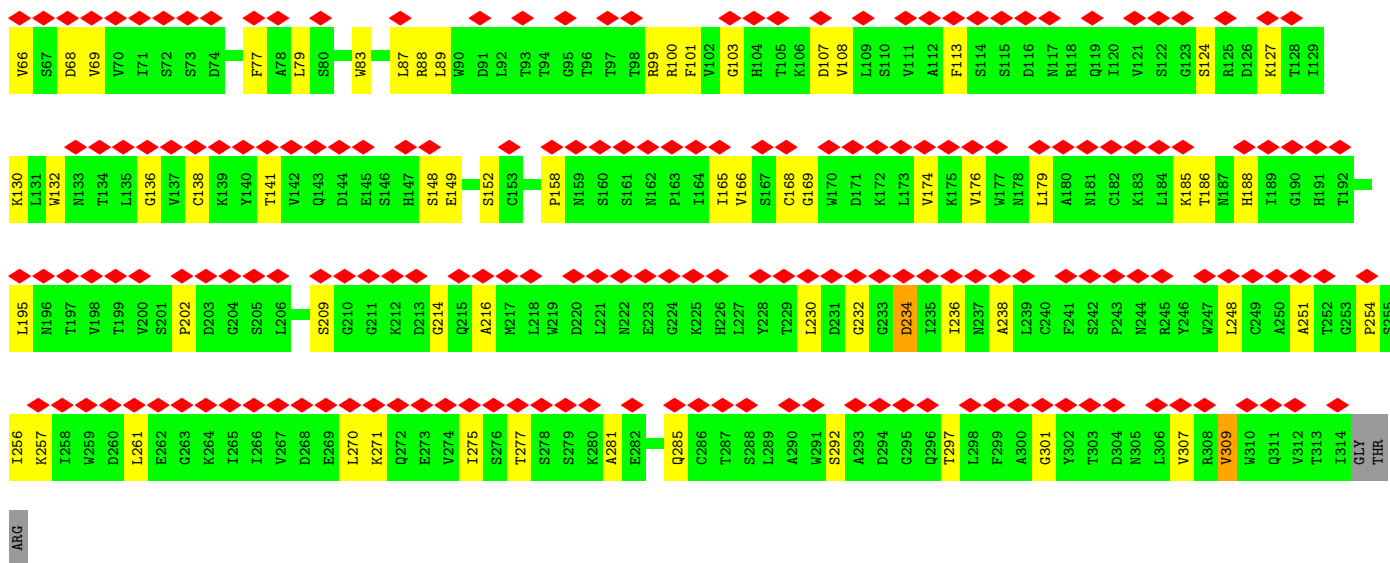




G1502	G1603	U1725	A1794	C1875	G1955	C2019	G2100	G2345	G2452	C2540	C2634	G2722
A1503	G1604	U1726	A1795	C1879	A1956	U2020	A2101	G2348	A2453	G2541	U2635	U2723
C1505	G1605	U1727	G1799	U1882	U1957	C2021	G2102	G2351	U2454	G2546	U2636	U2724
A1508	A1612	U1728	A1802	U1883	U1959	C2022	A2103	G2352	G2455	G2547	U2637	A2725
U1511	G1613	U1730	A1803	C1884	A1960	A2025	A2104	U2362	G2456	A2553	G2640	G2726
G1512	G1617	G1734	G1803	C1885	G1961	A2026	A2105	A2363	C2457	U2554	A2641	U2734
U1513	G1624	U1735	A1804	G1886	U1962	U2027	G2106	A2365	C2458	U2555	C2655	U2735
G1514	G1625	U1736	G1805	G1887	C1963	C2028	A2107	U2370	G2459	G2556	A2647	U2736
A1515	G1626	C1740	G1806	A1887	A1964	A2029	A2108	A2371	C2462	G2557	C2654	C2737
G1516	U1741	U1741	C1807	G1888	G1965	A2030	A2109	A2374	U2463	C2558	C2655	C2738
A1517	U1742	A1742	G1808	A1889	U1966	C2031	G2110	A2375	G2464	G2559	U2658	U2739
G1517	U1743	A1743	C1809	A1890	A1967	U2032	G2111	G2378	C2465	C2560	U2659	U2740
A1518	A1631	U1744	G1810	A1891	G1968	A2033	A	A2381	G2466	C2561	G2662	U2741
C1519	G1632	U1745	G1811	A1892	U1970	G2039	C	U2382	A2471	G2562	G2663	A2742
C1520	A1633	U1746	G1815	A1893	A1971	A2040	G	G2383	G2472	C2563	U2666	A2743
A1523	A1634	U1748	G1818	C1898	G1972	A2041	G	U2384	G2473	U2564	U2667	A2744
A1524	A1638	A1749	G1819	A1907	G1973	G2045	A	U2385	G2474	G2565	C2668	A2745
G1525	U1639	G1750	C1820	A1908	U1974	G2046	C	U2386	A2475	A2566	G2669	U2746
G1526	C1640	A1751	G1821	G1909	U1975	A2047	C	G2387	G2476	G2567	C2670	U2747
A1534	U1646	G1752	U1822	G1910	G1976	U2048	G	A2388	G2477	U2568	U2671	C2748
C1541	A1655	U1753	U1823	C1914	U1980	G2049	C	G2389	U2478	C2569	C2672	G2753
G1545	A1656	U1754	G1824	G1915	G1981	G2050	G	A2390	C2479	U2570	G2675	U2754
C1546	G1651	U1755	A1825	G1916	U1982	C2051	G	A2391	U2480	U2571	U2755	A2757
A1547	G1654	U1756	C1828	U1917	A1983	G2052	C	G2392	G2403	C2572	A2676	U2758
G1548	C1655	G1757	G1829	U1918	A1984	G2053	A	U2393	U2404	G2573	U2677	U2759
C1551	U1661	U1759	U1836	G1919	U1985	G2054	C	G2394	G2405	A2574	U2678	U2760
G1552	C1662	G1760	A1837	C1920	G1988	A2057	C	A2395	C2406	U2575	U2679	U2761
A1553	C1663	U1762	G1840	G1921	U1989	C2062	C	G2396	G2407	U2576	C2580	U2762
G1555	A1669	C1763	U1841	G1922	A1991	G2063	C	U2397	U2408	U2577	A2581	U2763
G1562	U1676	A1765	G1842	U1926	U1992	G2064	C	A2404	G2409	U2578	C2582	U2764
A1563	U1677	U1766	C1847	U1927	G1993	C2067	C	G2398	U2410	U2579	G2583	A2765
A1564	G1685	A1767	U1848	U1930	G1994	G2075	G	A2399	C2411	U2580	U2686	U2766
U1565	U1686	U1768	U1849	C1931	U1995	G2076	G	G2400	A2412	A2581	C2689	U2767
C1566	C1686	G1769	A1850	A1932	U1996	C2077	C	U2401	U2413	A2582	U2690	U2768
U1567	U1691	U1770	G1851	G1933	A1997	G2078	G	G2402	G2414	G2583	A2583	C2770
C1568	U1691	A1771	U1852	A1934	U1999	G2079	C	U2403	U2415	U2584	U2691	C2771
G1574	C1694	C1772	G1855	A1939	G2000	U2080	U	A2404	G2416	C2585	U2692	U2772
U1577	U1695	U1773	C1856	G1940	A2001	C2081	C	G2405	A2420	C2586	C2693	U2773
C1579	C1696	C1774	C1857	A1941	G2003	U2084	C	G2406	G2421	U2587	U2694	U2774
G1580	G	A1775	A1858	A1942	U2004	G2085	C	U2407	C2422	C2588	U2695	U2775
A1581	C	U1776	C1859	A1943	G2006	G2086	G	U2408	U2425	A2589	U2696	U2776
U1591	A	C1777	G1865	G1944	U2007	U2089	C	G2409	A2428	C2590	U2697	U2777
G1592	C	U1778	A1867	G1945	U2008	U2090	A	G2410	G2433	U2591	G2607	U2778
A1593	U1782	A1780	G1868	U1946	A2009	G2093	C	U2411	U2434	G2592	G2608	U2779
U1596	G1721	U1781	C1869	G1947	A2010	C2094	C	G2412	G2435	U2593	U2609	U2780
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	A1723	U1783	A1871	U1949	A2012	A2097	C	G2414	G2437	U2595	U2611	U2782
	U1786	G1785	A1872	U1950	U2015	G2098	C	U2415	U2438	U2596	U2612	U2783
	A1787	A1786	A1873	G1951	C2016	C2099	C	U2416	G2439	U2597	U2613	U2784
	U1954	U1954	A1874	U1952	A2017		C	U2417	U2440	U2598	U2614	U2785
				U1954	C2018		C	U2418	U2441	U2599	U2615	U2786
							C	U2419	U2442	U2600	U2616	U2787
							C	U2420	U2443	U2601	U2617	U2788
							C	U2421	U2444	U2602	U2618	U2789
							C	U2422	U2445	U2603	U2619	U2790
							C	U2423	U2446	U2604	U2620	U2791
							C	U2424	U2447	U2605	U2621	U2792
							C	U2425	U2448	U2606	U2622	U2793
							C	U2426	U2449	U2607	U2623	U2794
							C	U2427	U2450	U2608	U2624	U2795
							C	U2428	U2451	U2609	U2625	U2796
							C	U2429	U2452	U2610	U2626	U2797
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							C	U2431	U2454	U2612	U2628	U2799
							C	U2432	U2455	U2613	U2629	U2800
							C	U2433	U2456	U2614	U2630	U2801
							C	U2434	U2457	U2615	U2631	U2802
							C	U2435	U2458	U2616	U2632	U2803
							C	U2436	U2459	U2617	U2633	U2804
							C	U2437	U2460	U2618	U2634	U2805
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							C	U2442	U2465	U2623	U2639	U2810
							C	U2443	U2466	U2624	U2640	U2811
							C	U2444	U2467	U2625	U2641	U2812
							C	U2445	U2468	U2626	U2642	U2813
							C	U2446	U2469	U2627	U2643	U2814
							C	U2447	U2470	U2628	U2644	U2815
							C	U2448	U2471	U2629	U2645	U2816
							C	U2449	U2472	U2630	U2646	U2817
							C	U2450	U2473	U2631	U2647	U2818
							C	U2451	U2474	U2632	U2648	U2819
							C	U2452	U2475	U2633	U2649	U2820
							C	U2453	U2476	U2634	U2650	U2821
							C	U2454	U2477	U2635	U2651	U2822
							C	U2455	U2478	U2636	U2652	U2823
							C	U2456	U2479	U2637	U2653	U2824
							C	U2457	U2480	U2638	U2654	U2825
							C	U2458	U2481	U2639	U2655	U2826
							C	U2459	U2482	U2640	U2656	U2827
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							C	U2461	U2484	U2642	U2658	U2829
							C	U2462	U2485	U2643	U2659	U2830
							C	U2463	U2486	U2644	U2660	U2831
							C	U2464	U2487	U2645	U2661	U2832
							C	U2465	U2488	U2646	U2662	U2833
							C	U2466	U2489	U2647	U2663	U2834
							C	U2467	U2490	U2648	U2664	U2835
							C	U2468	U2491	U2649	U2665	U2836
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							C	U2470	U2493	U2651	U2667	U2838
							C	U2471	U2494	U2652	U2668	U2839
							C	U2472	U2495	U2653	U2669	U2840
							C	U2473	U2496	U2654	U2670	U2841
							C	U2474	U2497	U2655	U2671	U2842
							C	U2475	U2498	U2656	U2672	U2843
							C	U2476	U2499	U2657	U2673	U2844
							C	U2477	U2500	U2658	U2674	U2845
							C	U2478	U2501	U2659	U2675	U2846
							C	U2479	U2502	U2660	U2676	U2847
							C	U2480	U2503	U2661	U2677	U2848
							C	U2481	U2504	U2662	U2678	U2849
							C	U2482	U2505	U2663	U2679	U2850
							C	U2483	U2506	U2664	U2680	U2851
							C	U2484	U2507	U2665	U2681	U2852
							C	U2485	U2508	U2666	U2682	U2853
							C	U2486	U2509	U2667	U2683	U2854
							C	U2487	U2510	U2668	U2684	U2855
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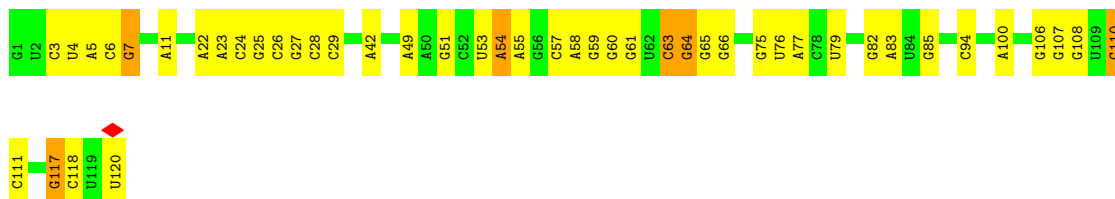






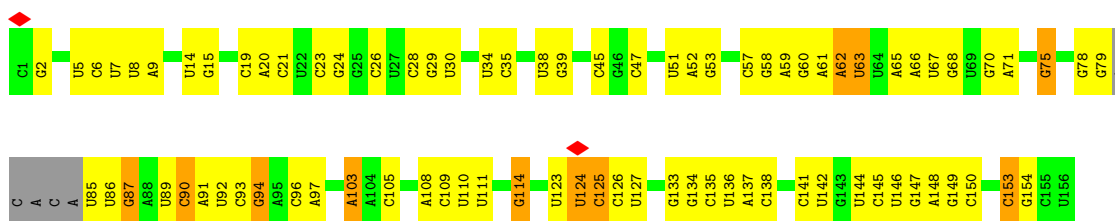
- Molecule 7: 5S rRNA

Chain 7: 62% 33% 5%



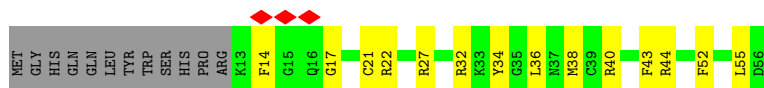
- Molecule 8: 5.8S rRNA

Chain 8: 44% 46% 7%



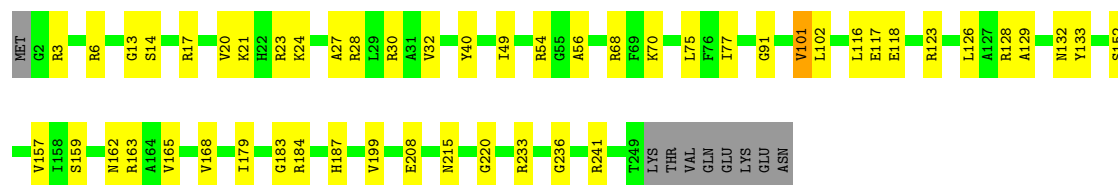
- Molecule 9: eS29

Chain 9: 5% 54% 25% 21%



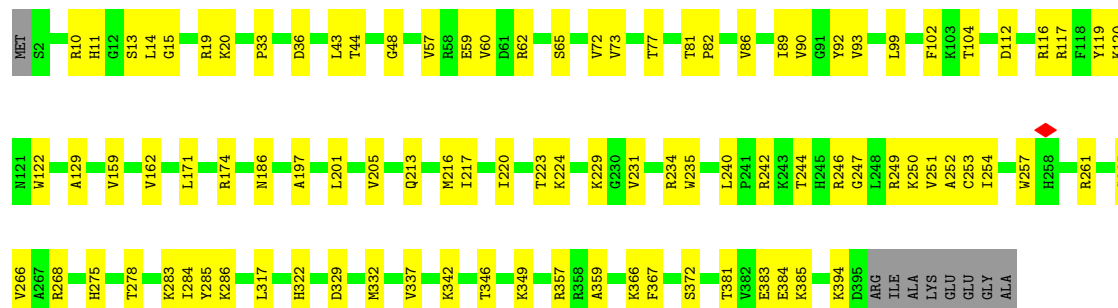
- Molecule 10: Ribosomal protein L8

Chain A: 77% 19%



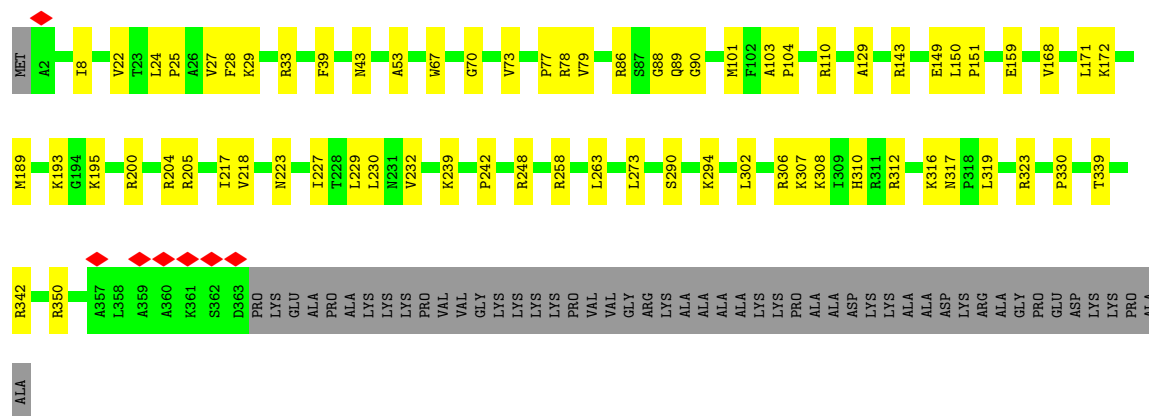
• Molecule 11: Ribosomal protein L3

Chain B: 74% 24%



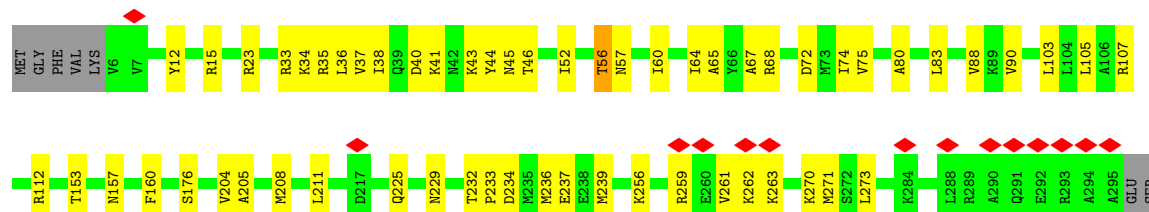
• Molecule 12: 60S ribosomal protein L4

Chain C: 71% 17% 12%



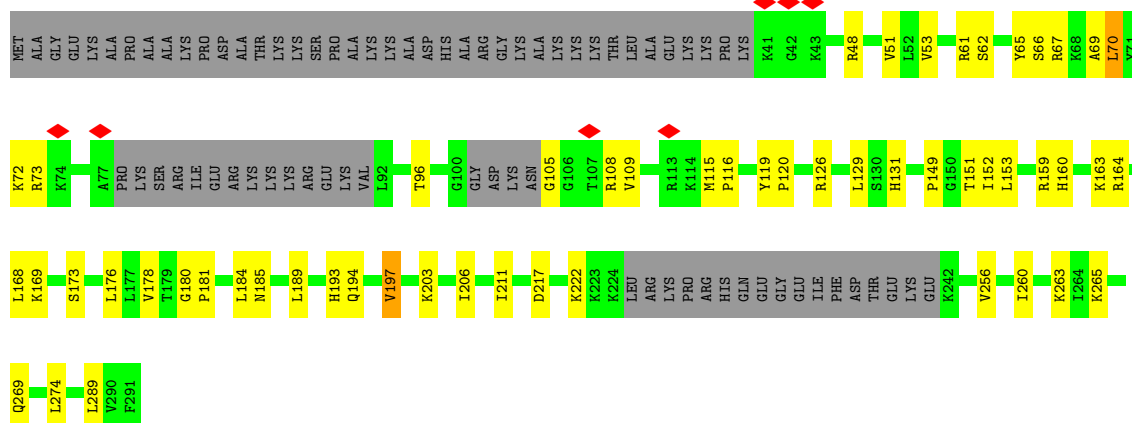
• Molecule 13: Large ribosomal subunit protein uL18

Chain D: 5% 78% 19%



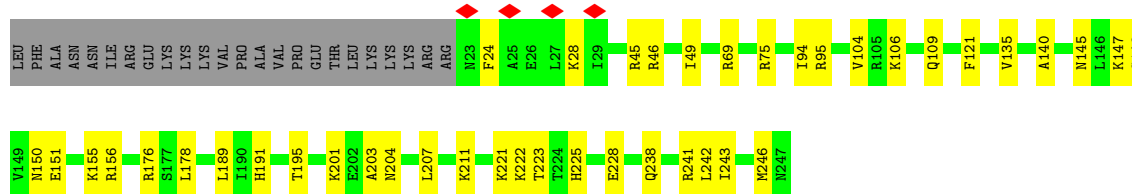
• Molecule 14: 60S ribosomal protein L6

Chain E: 



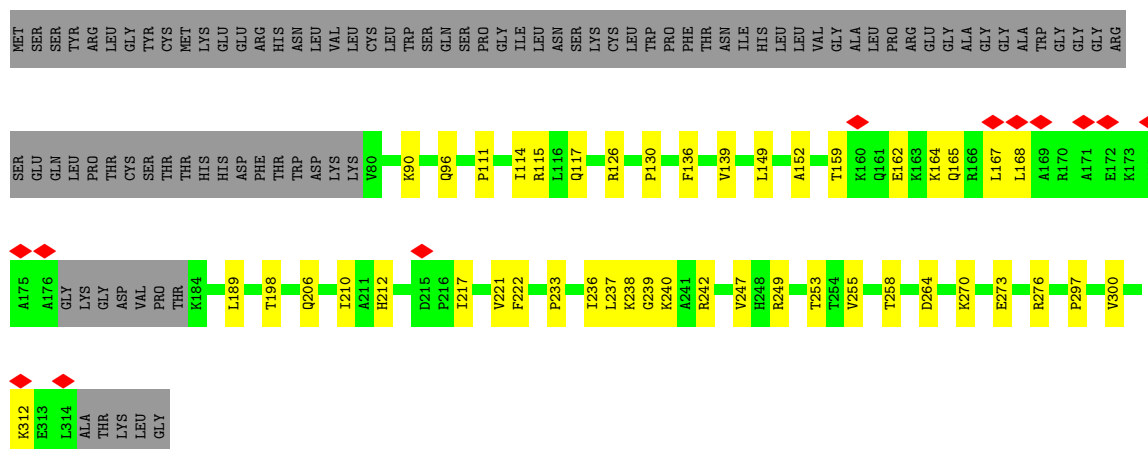
- Molecule 15: Large ribosomal subunit protein uL30

Chain F: 




- Molecule 16: 60S ribosomal protein L7a

Chain G: 



- Molecule 17: 60S ribosomal protein L9

Chain H: 



G C C C D G G G G G A G C G D D C C C D C G G G G D C C G G G D G C D D C C G G G C A D G G A G A D C C G G A D G

G D D G G A D G G G C G G G A G A D G G C C G G A G G G C C G D C C G G D G D G C C G D D G G G G A D D C G

G G D G G A G G C C C C D G G C C G G G G G C C D C D D C G G D G D C C G D G G C A G A A G A C D D G G G A G G D C G

G C A G A G G G G G C D C C G G D D C C C A G G G G D C A C G G G A C G C C C D G G D G D G G G G D G G G A

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A G D C C C C D C C D D G G G D G G G D D D G G D D G C C C D G D D G G C A C C G C C G D C C C A C C G A A

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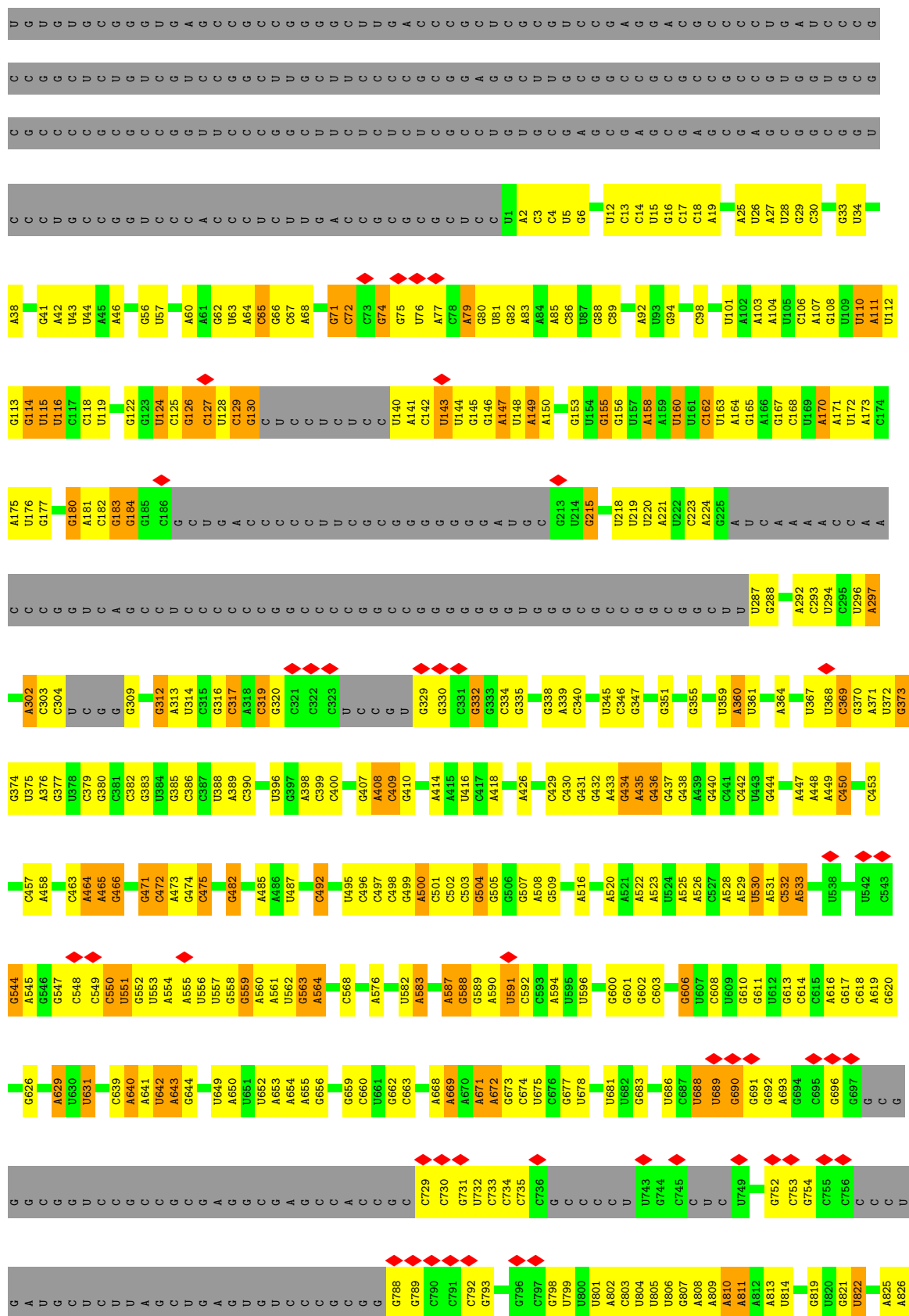
C D C G A G C C D D G C C C G D G G G G G C C C D D G G A C A C G A G G D C C A C G A C G D A A C G A

C C G G C D G G G C C C D D C C C C C G G C D D G G A C A C G A G G D C C A C G A C G D A A C G G

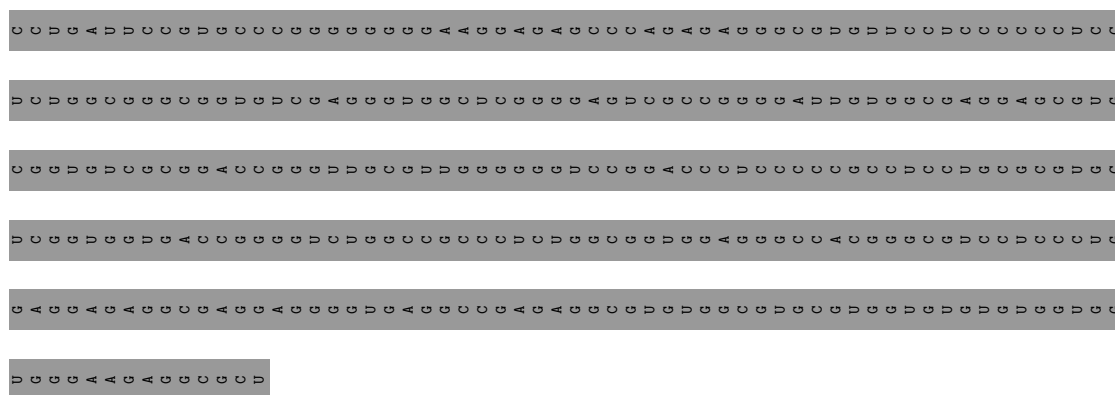
G D C G G G D C C C C D D G G G G G G G D D G G D D G G D D G G G G G G G G G G A G C C C C G G G D

G D C G G G D C C C C D D G G G G G G G D D G G D D G G D D G G G G G G G G G G A G C C C C G G G D

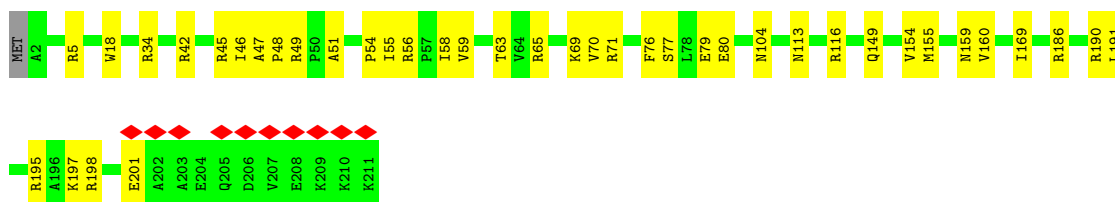
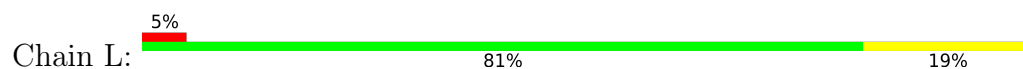
G C C C D C C C G A D C C C D D C C C C C C C D D G G C C C C C C C D C C D G G G G



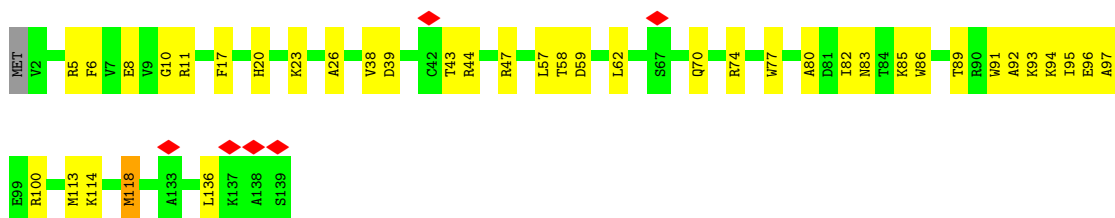




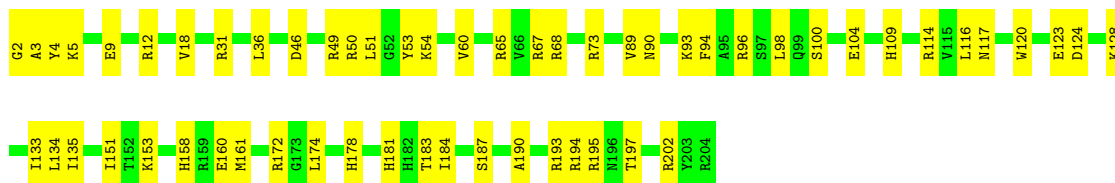
- Molecule 21: Large ribosomal subunit protein eL13



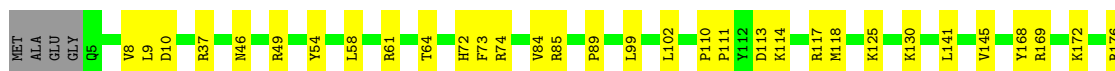
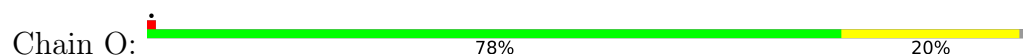
- Molecule 22: Large ribosomal subunit protein eL14



- Molecule 23: 60S ribosomal protein L15



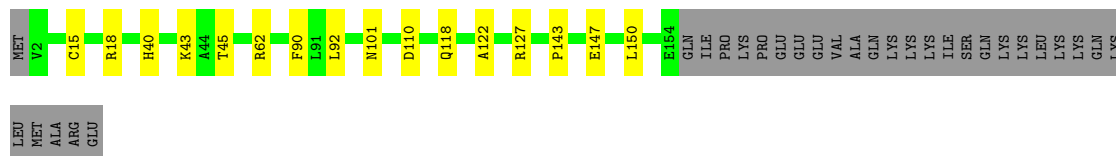
- Molecule 24: Large ribosomal subunit protein uL13





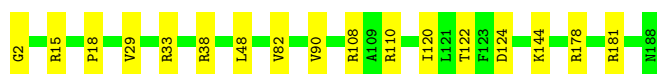
- Molecule 25: Large ribosomal subunit protein uL22

Chain P: 75% 9% 16%



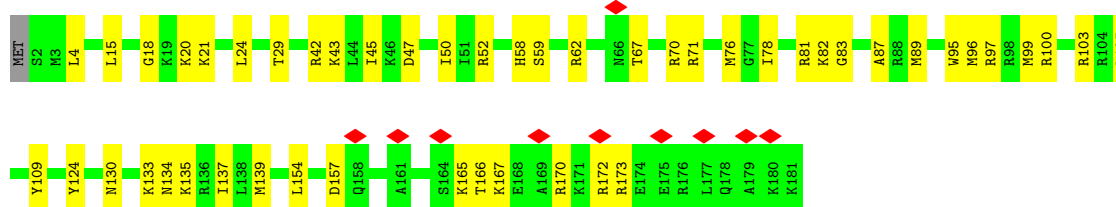
- Molecule 26: Large ribosomal subunit protein eL18

Chain Q: 91% 9%



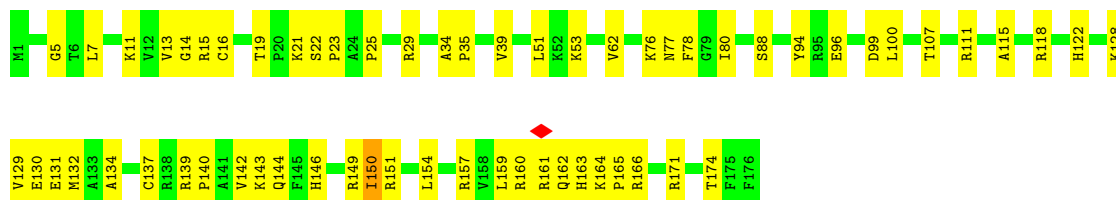
- Molecule 27: Large ribosomal subunit protein eL19

Chain R: 6% 72% 27%



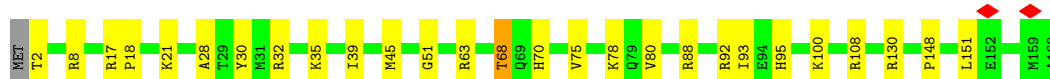
- Molecule 28: Large ribosomal subunit protein eL20

Chain S: 65% 34%

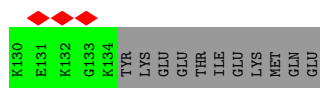


- Molecule 29: eL21

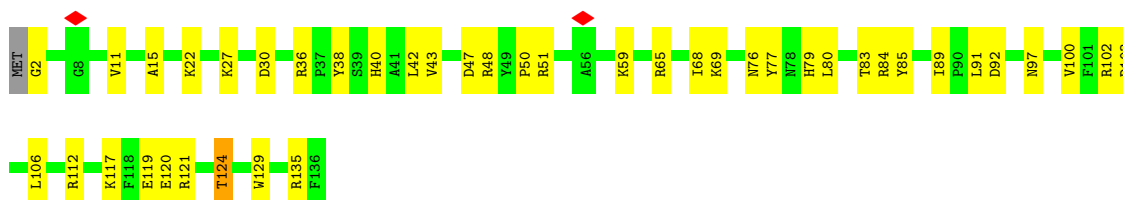
Chain T: 82% 16%



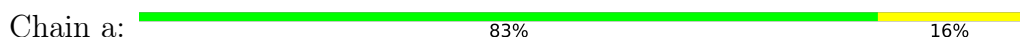
- Molecule 30: Large ribosomal subunit protein eL22



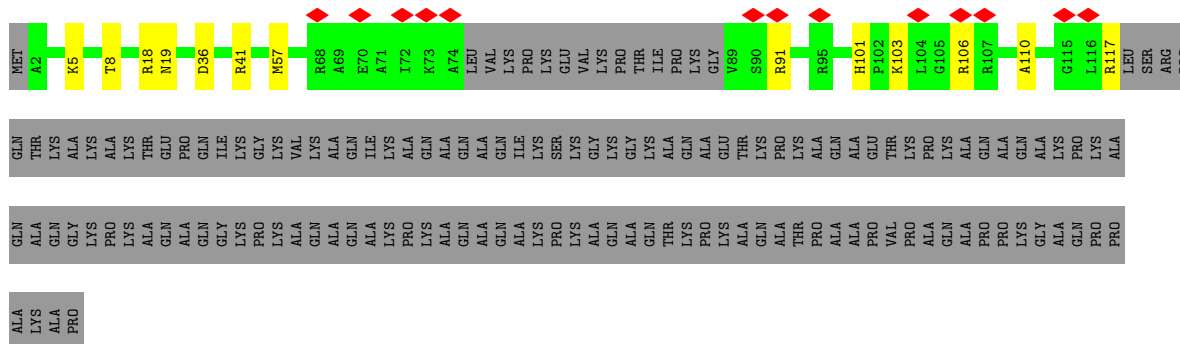
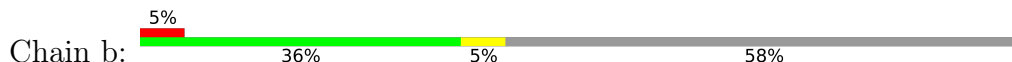
• Molecule 35: 60S ribosomal protein L27



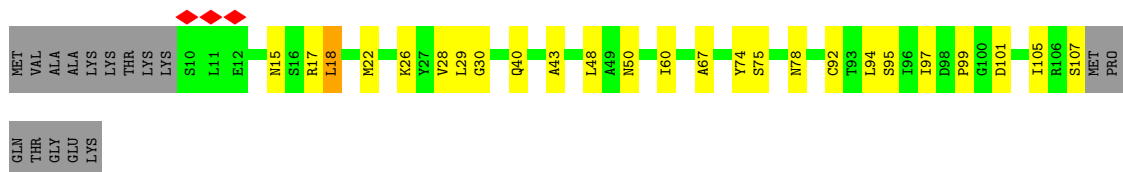
• Molecule 36: 60S ribosomal protein L27a



• Molecule 37: Large ribosomal subunit protein eL29

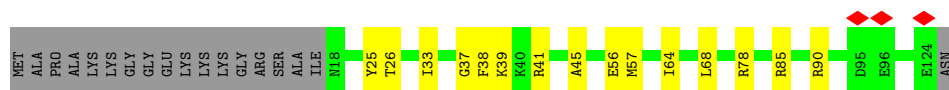


• Molecule 38: eL30



• Molecule 39: eL31





- Molecule 40: 60S ribosomal protein L32

Chain e: 83% 15%



- Molecule 41: eL33

Chain f: 84% 14%



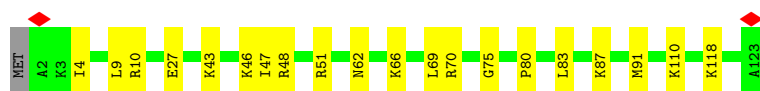
- Molecule 42: 60S ribosomal protein L34

Chain g: 6% 85% 12%



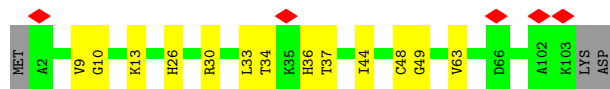
- Molecule 43: eL35

Chain h: 83% 16%



- Molecule 44: Large ribosomal subunit protein eL36

Chain i: 5% 85% 12%



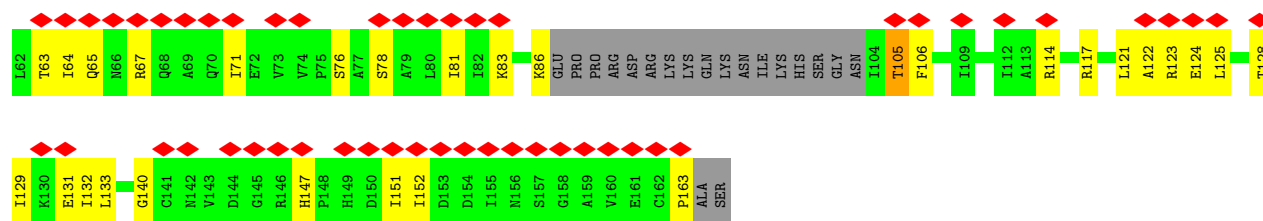
- Molecule 45: Ribosomal protein L37

Chain j: 73% 14% 11%

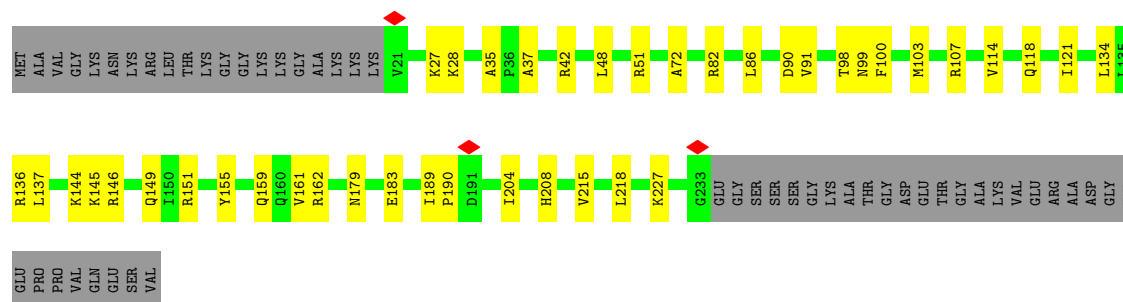


- Molecule 46: Large ribosomal subunit protein eL38

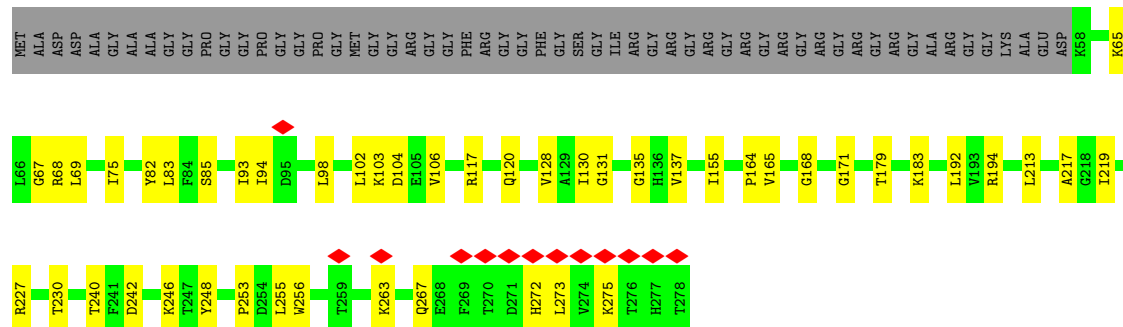




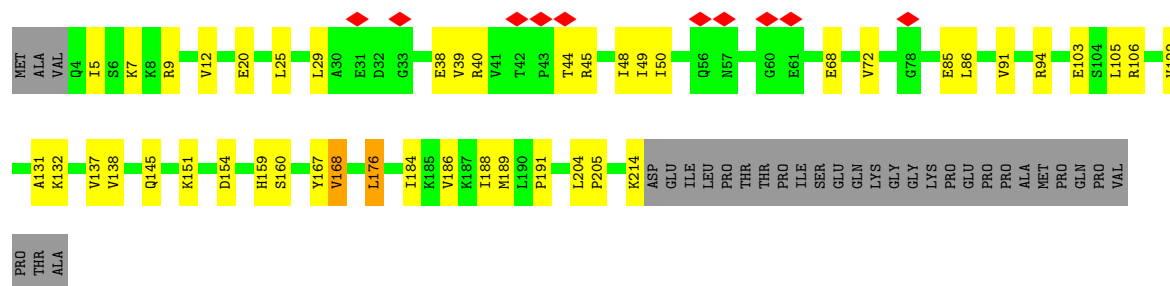
• Molecule 56: 40S ribosomal protein S3a



• Molecule 57: Small ribosomal subunit protein uS5

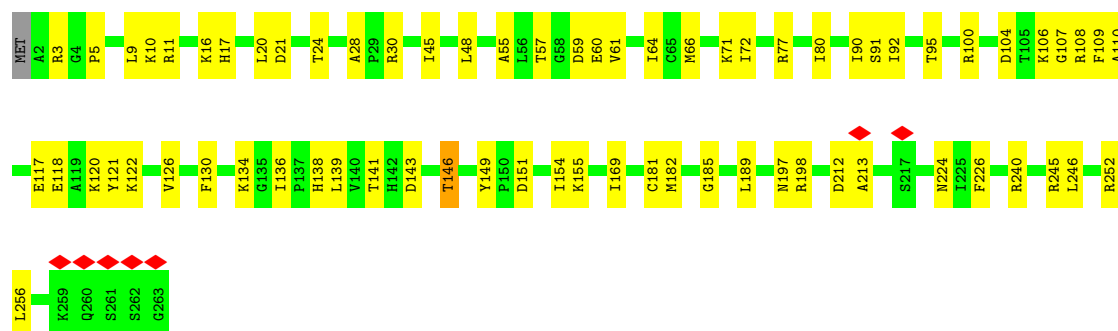


• Molecule 58: Ribosomal protein S3



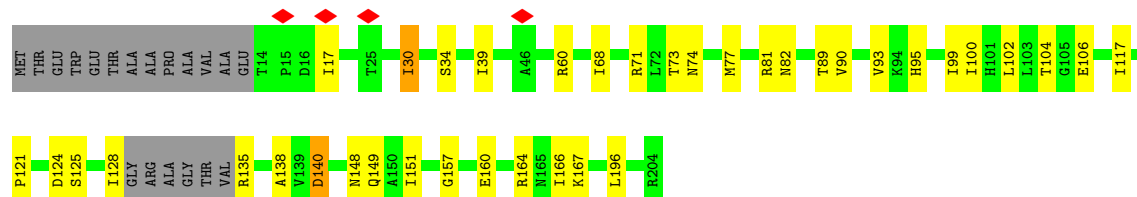
• Molecule 59: Small ribosomal subunit protein eS4

Chain x:  73% 26%



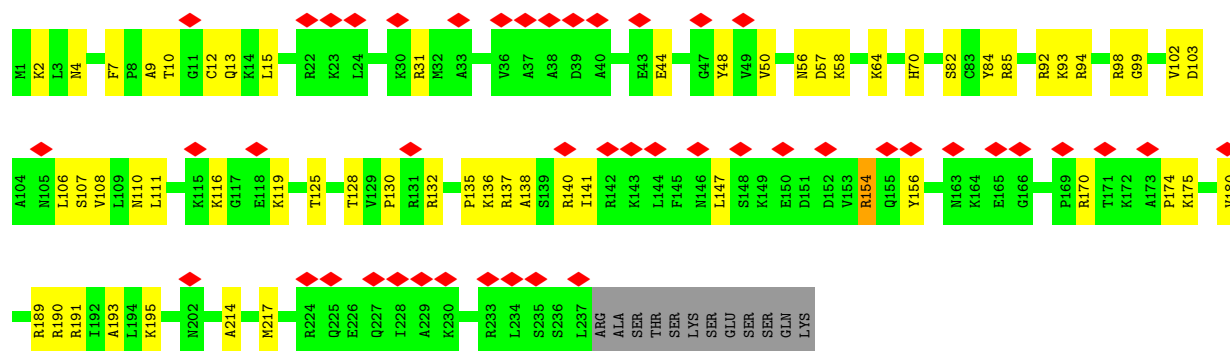
- Molecule 60: Ribosomal protein S5

Chain y:  72% 18% 9%

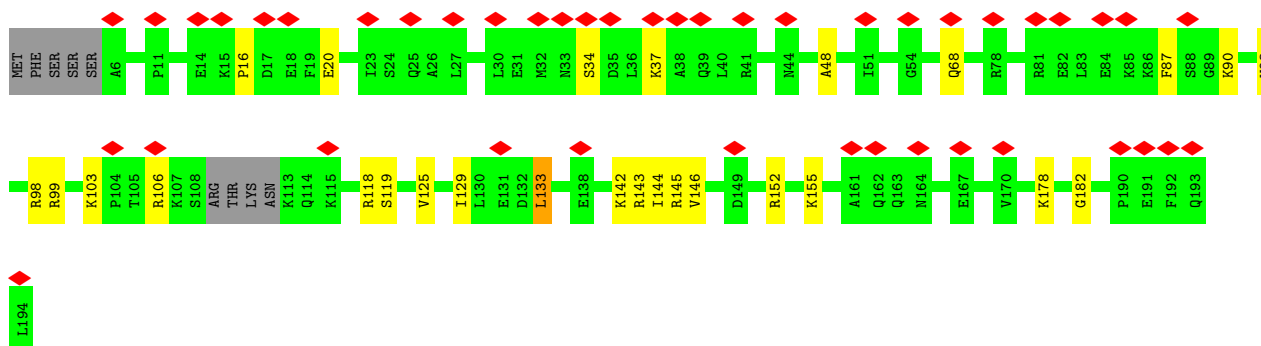


- Molecule 61: 40S ribosomal protein S6

Chain z:  18% 72% 23% 5%

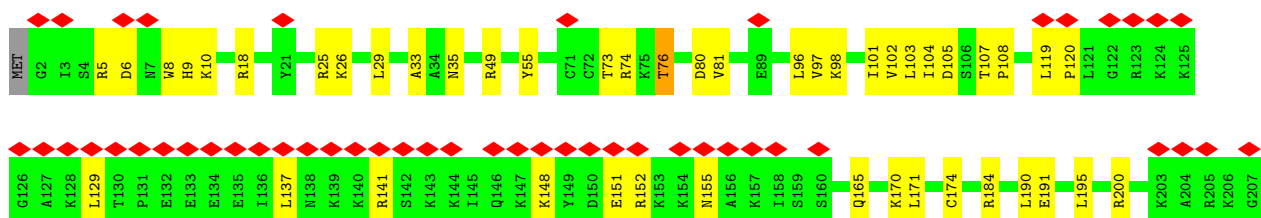


Chain BB: 23% 81% 13% 5%



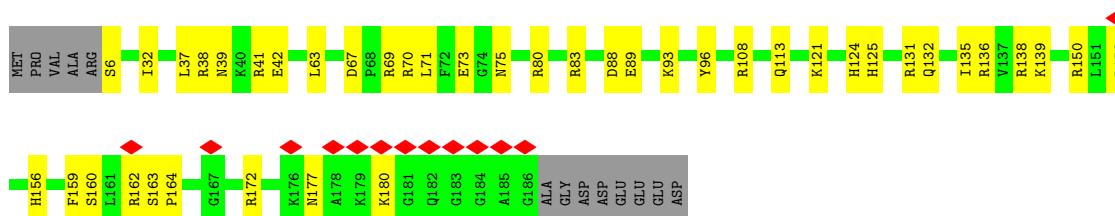
- Molecule 64: eS8

Chain CC: 24% 77% 22%



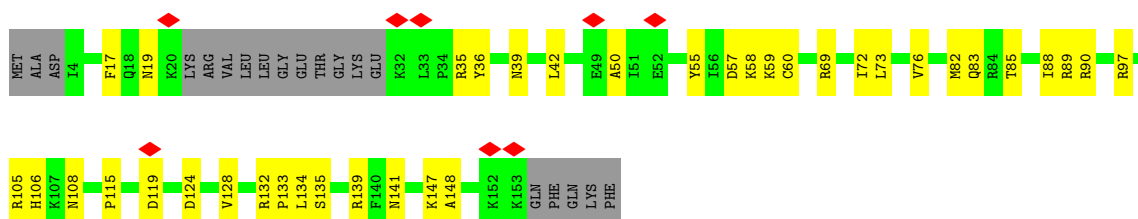
- Molecule 65: Ribosomal protein S9 (Predicted)

Chain DD: 7% 72% 22% 7%



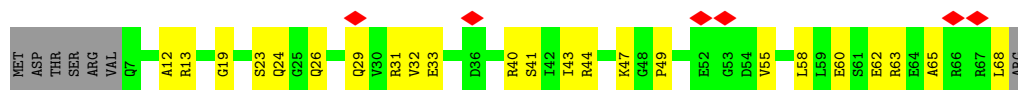
- Molecule 66: Ribosomal protein S11

Chain EE: 5% 64% 24% 12%



- Molecule 67: Ribosomal protein S28

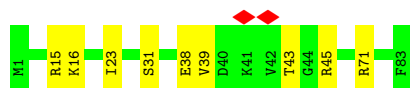
Chain FF: 9% 57% 33% 10%



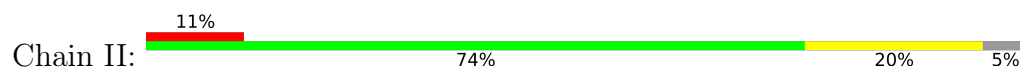
- Molecule 68: uS10



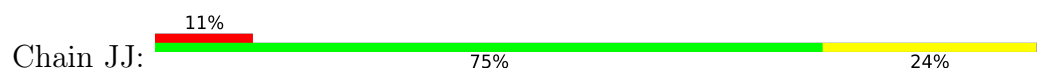
- Molecule 69: Small ribosomal subunit protein eS21



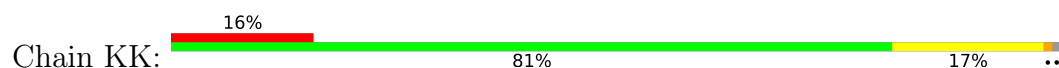
- Molecule 70: uS13

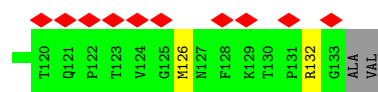


- Molecule 71: 40S ribosomal protein S27

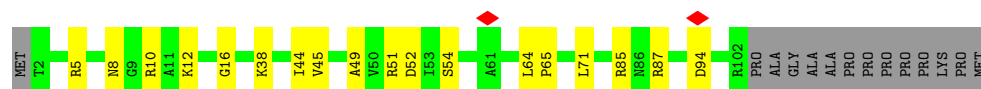


- Molecule 72: Small ribosomal subunit protein eS17

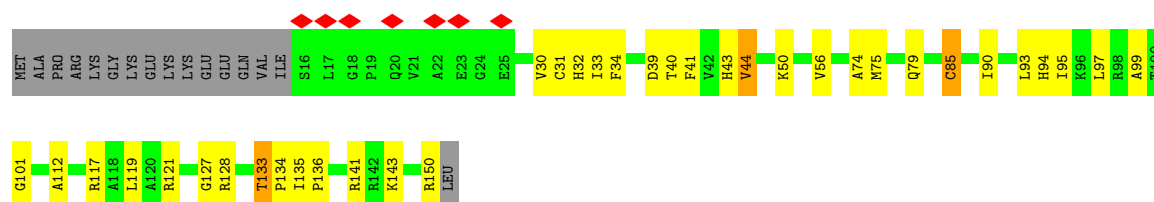




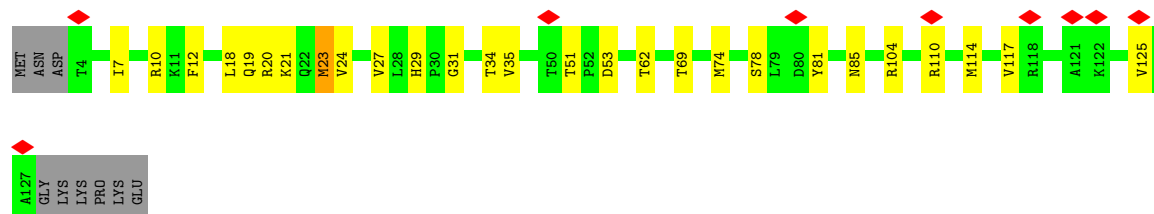
- Molecule 73: eS26



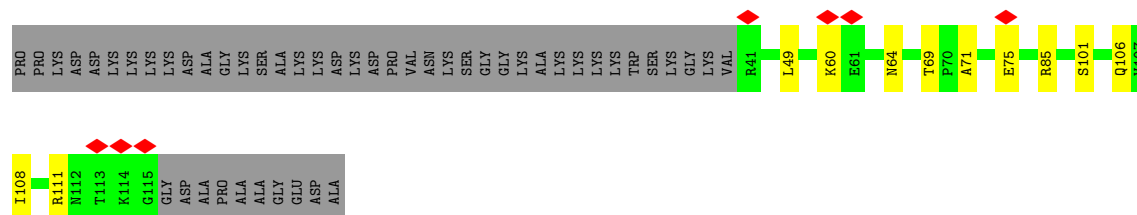
- Molecule 74: Small ribosomal subunit protein uS11



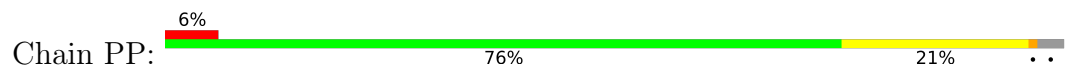
- Molecule 75: Small ribosomal subunit protein eS24



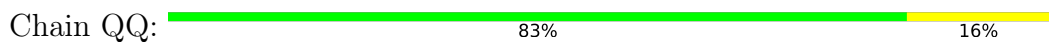
- Molecule 76: eS25



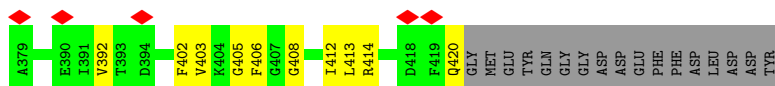
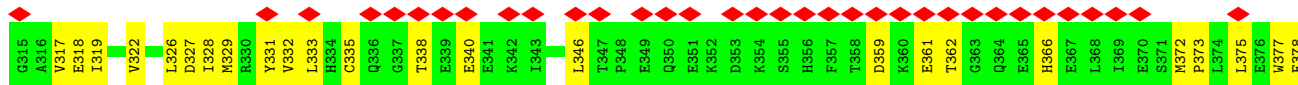
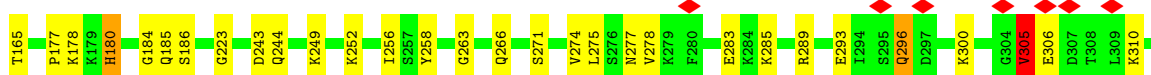
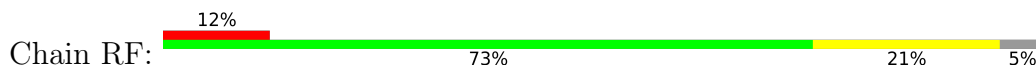
- Molecule 77: eS19



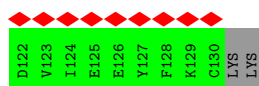
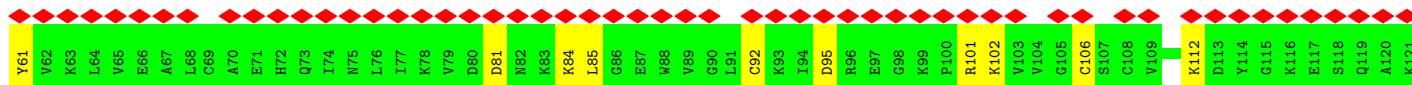
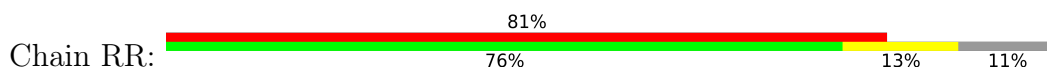
- Molecule 78: Ribosomal protein S13



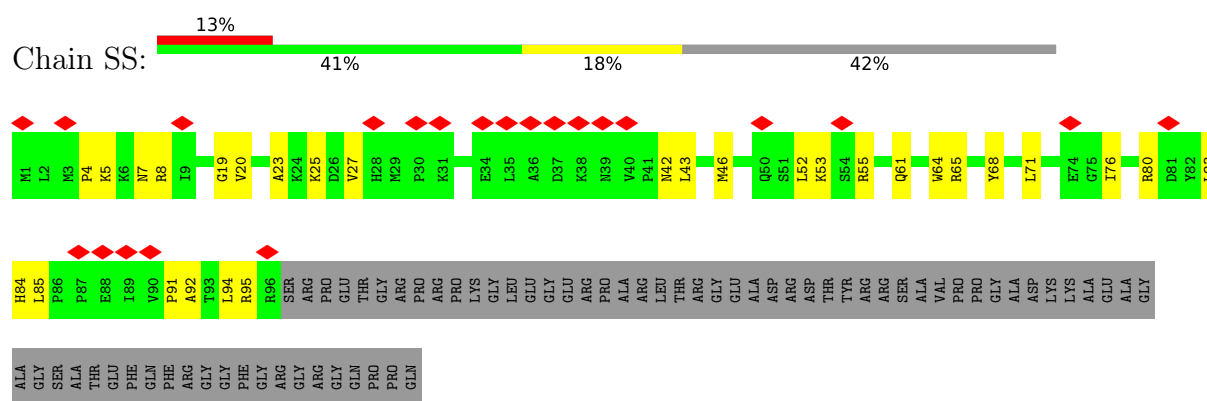
- Molecule 79: Eukaryotic peptide chain release factor subunit 1



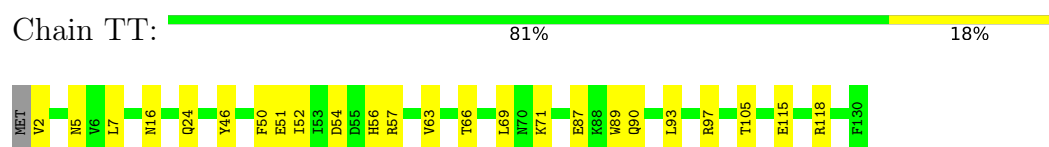
- Molecule 80: 40S ribosomal protein S12



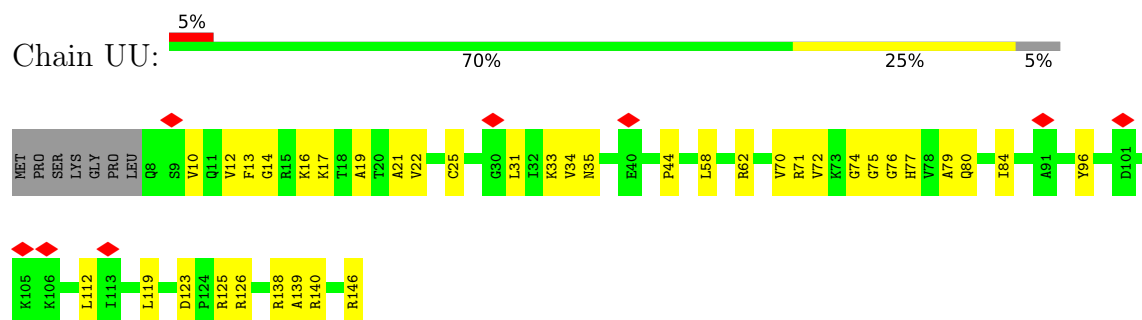
- Molecule 81: S10_pectin domain-containing protein



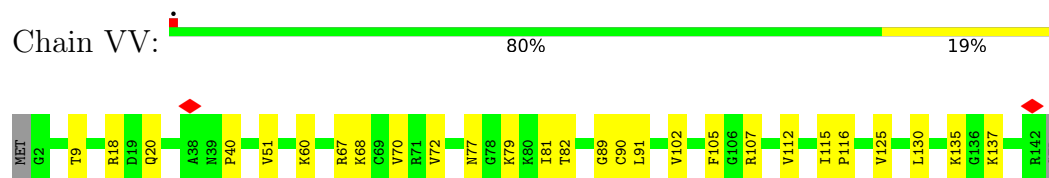
- Molecule 82: Ribosomal protein S15a



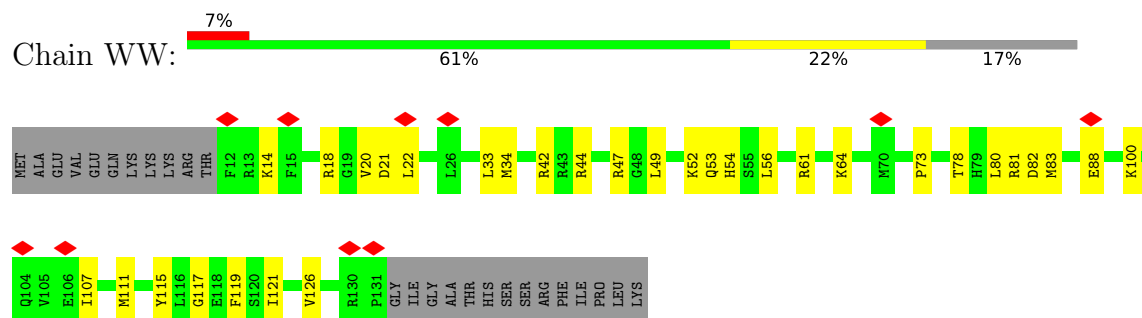
- Molecule 83: uS9




- Molecule 84: uS12

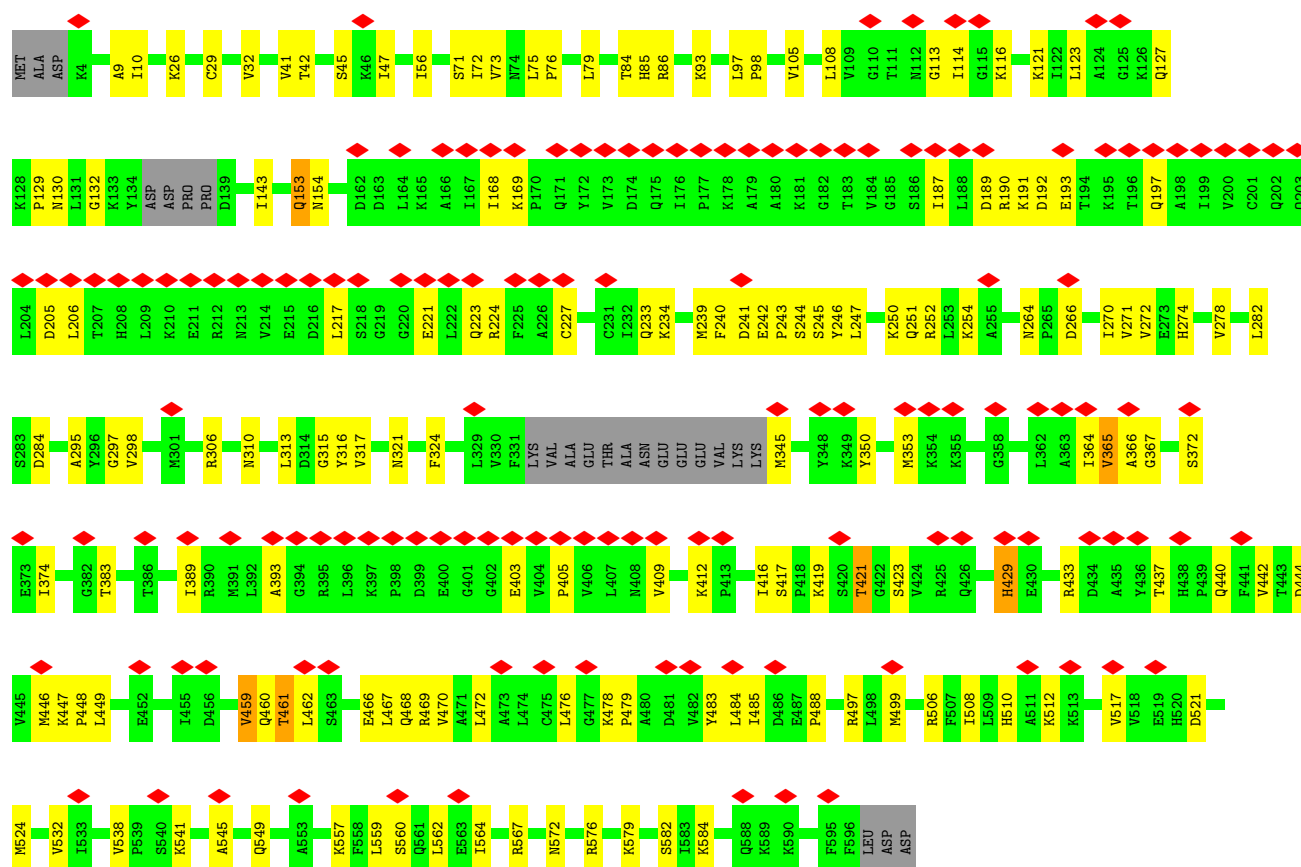


- Molecule 85: uS19



- Molecule 86: ATP binding cassette subfamily E member 1

Chain AB:  24% 69% 26%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15310	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.485	Depositor
Minimum map value	-0.206	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.044	Depositor
Map size (\AA)	385.12, 385.12, 385.12	wwPDB
Map dimensions	464, 464, 464	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.06	0/567	0.19	0/753
2	1	0.40	0/170	0.58	0/228
3	2	0.16	0/1812	0.28	0/2823
4	4	0.32	0/255	0.60	1/394 (0.3%)
5	5	0.10	0/82626	0.24	5/128845 (0.0%)
6	6	0.08	0/2493	0.22	0/3394
7	7	0.07	0/2858	0.19	0/4455
8	8	0.08	0/3581	0.21	0/5577
9	9	0.07	0/364	0.21	0/478
10	A	0.07	0/1936	0.23	0/2596
11	B	0.07	0/3240	0.20	0/4339
12	C	0.07	0/2937	0.20	0/3946
13	D	0.07	0/2409	0.19	0/3227
14	E	0.07	0/1762	0.21	0/2362
15	F	0.07	0/1911	0.20	0/2549
16	G	0.08	0/1876	0.21	0/2525
17	H	0.06	0/1535	0.20	0/2063
18	I	0.06	0/1756	0.20	0/2346
19	J	0.07	0/1385	0.21	0/1852
20	K	0.11	0/39671	0.26	12/61813 (0.0%)
21	L	0.08	0/1733	0.20	0/2316
22	M	0.09	0/1158	0.23	0/1547
23	N	0.07	0/1746	0.19	0/2338
24	O	0.08	0/1662	0.21	0/2222
25	P	0.07	0/1268	0.21	0/1700
26	Q	0.07	0/1539	0.21	0/2054
27	R	0.07	0/1524	0.19	0/2013
28	S	0.37	0/1497	0.44	0/2008
29	T	0.07	0/1326	0.20	0/1770
30	U	0.09	0/808	0.25	0/1084
31	V	0.07	0/993	0.20	0/1332
32	W	0.08	0/541	0.23	0/720

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	X	0.06	0/984	0.20	0/1323
34	Y	0.07	0/1132	0.20	0/1504
35	Z	0.07	0/1130	0.21	0/1507
36	a	0.06	0/1191	0.19	0/1590
37	b	0.06	0/846	0.17	0/1117
38	c	0.06	0/771	0.17	0/1034
39	d	0.08	0/903	0.22	0/1216
40	e	0.06	0/1071	0.20	0/1429
41	f	0.07	0/895	0.20	0/1198
42	g	0.07	0/916	0.21	0/1220
43	h	0.07	0/1021	0.18	0/1348
44	i	0.08	0/841	0.21	0/1112
45	j	0.07	0/720	0.20	0/952
46	k	0.07	0/575	0.22	0/761
47	l	0.07	0/459	0.20	0/608
48	m	0.06	0/435	0.23	0/575
49	n	0.07	0/240	0.15	0/305
50	o	0.06	0/864	0.19	0/1140
51	p	0.07	0/718	0.20	0/953
52	q	0.07	0/1747	0.20	0/2374
53	r	0.07	0/1010	0.24	0/1354
54	s	0.07	0/1530	0.20	0/2064
55	t	0.12	0/1033	0.37	0/1395
56	u	0.07	0/1756	0.20	0/2350
57	v	0.15	0/1752	0.27	0/2368
58	w	0.08	0/1668	0.25	0/2242
59	x	0.07	0/2118	0.22	0/2849
60	y	0.08	0/1492	0.24	0/2005
61	z	0.08	0/1946	0.26	1/2590 (0.0%)
62	AA	0.06	0/447	0.18	0/587
63	BB	0.07	0/1510	0.20	0/2022
64	CC	0.08	0/1715	0.22	0/2287
65	DD	0.07	0/1519	0.20	0/2027
66	EE	0.07	0/1160	0.20	0/1551
67	FF	0.07	0/490	0.22	0/656
68	GG	0.06	0/794	0.19	0/1066
69	HH	0.06	0/644	0.19	0/862
70	II	0.07	0/1208	0.22	0/1618
71	JJ	0.06	0/665	0.20	0/891
72	KK	0.06	0/1082	0.18	0/1452
73	LL	0.07	0/828	0.21	0/1109
74	MM	0.07	0/1017	0.23	0/1365
75	NN	0.09	0/1028	0.25	0/1366

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	OO	0.07	0/604	0.20	0/810
77	PP	0.07	0/1115	0.21	0/1493
78	QQ	0.06	0/1226	0.20	0/1649
79	RF	0.09	0/3321	0.22	0/4466
80	RR	0.07	0/918	0.20	0/1233
81	SS	0.07	0/834	0.23	0/1125
82	TT	0.06	0/1051	0.20	0/1406
83	UU	0.07	0/1126	0.20	0/1506
84	VV	0.07	0/1116	0.20	0/1490
85	WW	0.07	0/1017	0.23	0/1358
86	AB	0.08	0/4626	0.24	0/6241
All	All	0.10	0/233764	0.24	19/341788 (0.0%)

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	K	1623	A	P-O3'-C3'	-10.12	105.02	120.20
20	K	1698	C	P-O3'-C3'	-8.48	107.49	120.20
5	5	4133	C	P-O3'-C3'	-8.37	107.65	120.20
20	K	1624	U	P-O3'-C3'	-8.13	108.00	120.20
5	5	3692	A	P-O3'-C3'	-7.97	108.24	120.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	555	0	567	10	0
2	1	225	0	184	8	0
3	2	1622	0	816	22	0
4	4	230	0	118	7	0
5	5	73867	0	37311	1114	0
6	6	2436	0	2393	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	7	2558	0	1296	41	0
8	8	3208	0	1629	54	0
9	9	359	0	364	12	0
10	A	1898	0	1993	39	0
11	B	3172	0	3310	68	0
12	C	2883	0	3053	50	0
13	D	2364	0	2393	49	0
14	E	1729	0	1887	36	0
15	F	1875	0	1995	31	0
16	G	1845	0	1986	30	0
17	H	1516	0	1597	24	0
18	I	1717	0	1764	33	0
19	J	1362	0	1399	22	0
20	K	35481	0	17923	667	0
21	L	1702	0	1820	26	0
22	M	1137	0	1211	28	0
23	N	1701	0	1749	47	0
24	O	1630	0	1778	29	0
25	P	1242	0	1274	12	0
26	Q	1515	0	1634	13	0
27	R	1508	0	1664	37	0
28	S	1457	0	1492	55	0
29	T	1298	0	1366	23	0
30	U	795	0	818	16	0
31	V	979	0	1039	22	0
32	W	528	0	541	10	0
33	X	967	0	1040	12	0
34	Y	1115	0	1205	23	0
35	Z	1107	0	1182	29	0
36	a	1162	0	1209	20	0
37	b	833	0	900	12	0
38	c	761	0	794	15	0
39	d	888	0	930	9	0
40	e	1053	0	1147	17	0
41	f	876	0	912	13	0
42	g	906	0	998	12	0
43	h	1013	0	1147	18	0
44	i	830	0	914	11	0
45	j	705	0	737	12	0
46	k	569	0	637	9	0
47	l	447	0	480	13	0
48	m	429	0	465	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	n	239	0	289	4	0
50	o	851	0	920	18	0
51	p	708	0	757	6	0
52	q	1710	0	1711	28	0
53	r	994	0	1051	20	0
54	s	1507	0	1564	35	0
55	t	1022	0	1075	30	0
56	u	1729	0	1803	28	0
57	v	1715	0	1806	31	0
58	w	1642	0	1734	29	0
59	x	2076	0	2177	46	0
60	y	1471	0	1522	27	0
61	z	1923	0	2089	47	0
62	AA	443	0	492	14	0
63	BB	1488	0	1582	19	0
64	CC	1686	0	1772	37	0
65	DD	1495	0	1605	32	0
66	EE	1140	0	1210	26	0
67	FF	488	0	514	15	0
68	GG	785	0	855	19	0
69	HH	637	0	632	10	0
70	II	1190	0	1249	22	0
71	JJ	651	0	672	15	0
72	KK	1068	0	1121	19	0
73	LL	814	0	860	13	0
74	MM	1004	0	1021	25	0
75	NN	1011	0	1083	18	0
76	OO	598	0	656	8	0
77	PP	1097	0	1130	25	0
78	QQ	1202	0	1289	18	0
79	RF	3268	0	3314	59	0
80	RR	908	0	939	11	0
81	SS	810	0	836	20	0
82	TT	1034	0	1080	19	0
83	UU	1109	0	1174	29	0
84	VV	1098	0	1167	19	0
85	WW	997	0	1045	27	0
86	AB	4543	0	4681	107	0
87	4	1	0	0	0	0
87	5	195	0	0	0	0
87	7	7	0	0	0	0
87	8	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	A	1	0	0	0	0
87	K	75	0	0	0	0
87	P	1	0	0	0	0
87	PP	1	0	0	0	0
87	V	1	0	0	0	0
87	a	1	0	0	0	0
87	g	1	0	0	0	0
87	j	2	0	0	0	0
88	LL	1	0	0	0	0
88	g	1	0	0	0	0
88	j	1	0	0	0	0
88	m	1	0	0	0	0
88	o	1	0	0	0	0
88	p	1	0	0	0	0
All	All	218503	0	165538	3262	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 3262 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)
30:U:62:THR:OG1	30:U:73:THR:HB	1.60	1.01
5:5:4421:C:H42	5:5:4475:G:N2	1.73	0.87
5:5:1199:U:H2'	5:5:1200:G:H8	1.40	0.85
3:2:50:U:H3	3:2:64:G:H1	1.25	0.81
5:5:4135:G:H2'	5:5:4136:G:H8	1.47	0.80

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	
1	0	66/156 (42%)	63 (96%)	3 (4%)	0	100	100
2	1	19/32 (59%)	15 (79%)	4 (21%)	0	100	100
6	6	311/317 (98%)	304 (98%)	7 (2%)	0	100	100
9	9	42/56 (75%)	42 (100%)	0	0	100	100
10	A	246/257 (96%)	235 (96%)	11 (4%)	0	100	100
11	B	392/403 (97%)	379 (97%)	13 (3%)	0	100	100
12	C	360/413 (87%)	353 (98%)	7 (2%)	0	100	100
13	D	288/297 (97%)	283 (98%)	5 (2%)	0	100	100
14	E	208/291 (72%)	200 (96%)	8 (4%)	0	100	100
15	F	223/249 (90%)	217 (97%)	6 (3%)	0	100	100
16	G	224/319 (70%)	222 (99%)	2 (1%)	0	100	100
17	H	188/192 (98%)	186 (99%)	2 (1%)	0	100	100
18	I	211/214 (99%)	205 (97%)	6 (3%)	0	100	100
19	J	168/178 (94%)	164 (98%)	4 (2%)	0	100	100
21	L	208/211 (99%)	200 (96%)	8 (4%)	0	100	100
22	M	136/139 (98%)	132 (97%)	4 (3%)	0	100	100
23	N	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
24	O	197/203 (97%)	195 (99%)	2 (1%)	0	100	100
25	P	151/183 (82%)	147 (97%)	4 (3%)	0	100	100
26	Q	185/187 (99%)	181 (98%)	4 (2%)	0	100	100
27	R	178/181 (98%)	174 (98%)	4 (2%)	0	100	100
28	S	174/176 (99%)	166 (95%)	7 (4%)	1 (1%)	21	38
29	T	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
30	U	96/99 (97%)	94 (98%)	2 (2%)	0	100	100
31	V	129/140 (92%)	127 (98%)	2 (2%)	0	100	100
32	W	61/157 (39%)	58 (95%)	3 (5%)	0	100	100
33	X	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
34	Y	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
35	Z	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
36	a	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
37	b	98/245 (40%)	94 (96%)	4 (4%)	0	100	100
38	c	96/115 (84%)	95 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	d	105/125 (84%)	101 (96%)	4 (4%)	0	100	100
40	e	126/130 (97%)	124 (98%)	2 (2%)	0	100	100
41	f	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
42	g	112/117 (96%)	112 (100%)	0	0	100	100
43	h	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
44	i	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
45	j	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
46	k	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
47	l	48/51 (94%)	48 (100%)	0	0	100	100
48	m	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
49	n	23/25 (92%)	23 (100%)	0	0	100	100
50	o	102/106 (96%)	99 (97%)	3 (3%)	0	100	100
51	p	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
52	q	215/222 (97%)	209 (97%)	6 (3%)	0	100	100
53	r	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
54	s	194/318 (61%)	192 (99%)	2 (1%)	0	100	100
55	t	133/165 (81%)	113 (85%)	17 (13%)	3 (2%)	5	11
56	u	211/264 (80%)	204 (97%)	7 (3%)	0	100	100
57	v	219/278 (79%)	217 (99%)	2 (1%)	0	100	100
58	w	209/243 (86%)	205 (98%)	4 (2%)	0	100	100
59	x	260/263 (99%)	250 (96%)	10 (4%)	0	100	100
60	y	181/204 (89%)	173 (96%)	8 (4%)	0	100	100
61	z	235/249 (94%)	228 (97%)	7 (3%)	0	100	100
62	AA	53/133 (40%)	53 (100%)	0	0	100	100
63	BB	181/194 (93%)	179 (99%)	2 (1%)	0	100	100
64	CC	204/208 (98%)	197 (97%)	7 (3%)	0	100	100
65	DD	179/194 (92%)	177 (99%)	2 (1%)	0	100	100
66	EE	135/158 (85%)	129 (96%)	6 (4%)	0	100	100
67	FF	60/69 (87%)	58 (97%)	2 (3%)	0	100	100
68	GG	97/119 (82%)	95 (98%)	2 (2%)	0	100	100
69	HH	81/83 (98%)	81 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	II	142/152 (93%)	138 (97%)	4 (3%)	0	100	100
71	JJ	81/84 (96%)	77 (95%)	4 (5%)	0	100	100
72	KK	130/134 (97%)	130 (100%)	0	0	100	100
73	LL	99/115 (86%)	94 (95%)	5 (5%)	0	100	100
74	MM	133/151 (88%)	124 (93%)	9 (7%)	0	100	100
75	NN	122/133 (92%)	118 (97%)	4 (3%)	0	100	100
76	OO	73/124 (59%)	72 (99%)	1 (1%)	0	100	100
77	PP	139/145 (96%)	132 (95%)	7 (5%)	0	100	100
78	QQ	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
79	RF	412/437 (94%)	396 (96%)	13 (3%)	3 (1%)	18	35
80	RR	115/132 (87%)	110 (96%)	5 (4%)	0	100	100
81	SS	94/165 (57%)	91 (97%)	3 (3%)	0	100	100
82	TT	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
83	UU	137/146 (94%)	135 (98%)	2 (2%)	0	100	100
84	VV	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
85	WW	118/145 (81%)	110 (93%)	8 (7%)	0	100	100
86	AB	570/599 (95%)	537 (94%)	30 (5%)	3 (0%)	24	42
All	All	12419/14223 (87%)	12056 (97%)	353 (3%)	10 (0%)	49	68

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	S	150	ILE
55	t	30	PRO
79	RF	305	VAL
86	AB	417	SER
79	RF	317	VAL

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	0	61/140 (44%)	61 (100%)	0	100	100
2	1	19/19 (100%)	19 (100%)	0	100	100
6	6	272/275 (99%)	269 (99%)	3 (1%)	65	81
9	9	38/49 (78%)	37 (97%)	1 (3%)	40	65
10	A	190/199 (96%)	186 (98%)	4 (2%)	47	70
11	B	342/348 (98%)	341 (100%)	1 (0%)	86	93
12	C	302/337 (90%)	300 (99%)	2 (1%)	76	87
13	D	244/250 (98%)	242 (99%)	2 (1%)	73	86
14	E	190/251 (76%)	185 (97%)	5 (3%)	40	65
15	F	196/218 (90%)	196 (100%)	0	100	100
16	G	197/273 (72%)	196 (100%)	1 (0%)	81	90
17	H	169/171 (99%)	168 (99%)	1 (1%)	78	89
18	I	180/181 (99%)	178 (99%)	2 (1%)	65	81
19	J	143/149 (96%)	141 (99%)	2 (1%)	59	78
21	L	175/176 (99%)	173 (99%)	2 (1%)	65	81
22	M	117/118 (99%)	112 (96%)	5 (4%)	26	50
23	N	171/171 (100%)	171 (100%)	0	100	100
24	O	171/173 (99%)	170 (99%)	1 (1%)	78	89
25	P	134/162 (83%)	134 (100%)	0	100	100
26	Q	164/164 (100%)	163 (99%)	1 (1%)	78	89
27	R	159/160 (99%)	157 (99%)	2 (1%)	61	79
28	S	154/154 (100%)	153 (99%)	1 (1%)	78	89
29	T	139/140 (99%)	138 (99%)	1 (1%)	76	87
30	U	87/88 (99%)	87 (100%)	0	100	100
31	V	101/107 (94%)	101 (100%)	0	100	100
32	W	55/126 (44%)	55 (100%)	0	100	100
33	X	106/134 (79%)	106 (100%)	0	100	100
34	Y	124/135 (92%)	122 (98%)	2 (2%)	55	76
35	Z	117/118 (99%)	115 (98%)	2 (2%)	53	75
36	a	119/120 (99%)	119 (100%)	0	100	100
37	b	82/184 (45%)	82 (100%)	0	100	100
38	c	84/98 (86%)	83 (99%)	1 (1%)	63	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	d	98/110 (89%)	98 (100%)	0	100	100
40	e	114/116 (98%)	114 (100%)	0	100	100
41	f	88/89 (99%)	86 (98%)	2 (2%)	44	68
42	g	98/100 (98%)	97 (99%)	1 (1%)	68	83
43	h	109/110 (99%)	109 (100%)	0	100	100
44	i	86/90 (96%)	85 (99%)	1 (1%)	63	80
45	j	73/80 (91%)	72 (99%)	1 (1%)	59	78
46	k	64/64 (100%)	64 (100%)	0	100	100
47	l	47/48 (98%)	47 (100%)	0	100	100
48	m	48/116 (41%)	48 (100%)	0	100	100
49	n	24/24 (100%)	24 (100%)	0	100	100
50	o	92/94 (98%)	91 (99%)	1 (1%)	65	81
51	p	74/75 (99%)	74 (100%)	0	100	100
52	q	180/184 (98%)	178 (99%)	2 (1%)	65	81
53	r	108/121 (89%)	103 (95%)	5 (5%)	24	48
54	s	164/258 (64%)	162 (99%)	2 (1%)	63	80
55	t	111/137 (81%)	109 (98%)	2 (2%)	51	73
56	u	194/231 (84%)	193 (100%)	1 (0%)	81	90
57	v	186/211 (88%)	185 (100%)	1 (0%)	81	90
58	w	175/202 (87%)	168 (96%)	7 (4%)	28	53
59	x	224/225 (100%)	221 (99%)	3 (1%)	61	79
60	y	158/170 (93%)	155 (98%)	3 (2%)	50	72
61	z	207/218 (95%)	204 (99%)	3 (1%)	59	78
62	AA	46/106 (43%)	46 (100%)	0	100	100
63	BB	165/174 (95%)	164 (99%)	1 (1%)	78	89
64	CC	178/180 (99%)	176 (99%)	2 (1%)	65	81
65	DD	158/168 (94%)	157 (99%)	1 (1%)	78	89
66	EE	126/142 (89%)	126 (100%)	0	100	100
67	FF	55/62 (89%)	54 (98%)	1 (2%)	51	73
68	GG	91/107 (85%)	89 (98%)	2 (2%)	45	69
69	HH	68/68 (100%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	II	125/132 (95%)	125 (100%)	0	100	100
71	JJ	75/76 (99%)	74 (99%)	1 (1%)	61	79
72	KK	119/120 (99%)	117 (98%)	2 (2%)	53	75
73	LL	88/99 (89%)	88 (100%)	0	100	100
74	MM	104/119 (87%)	100 (96%)	4 (4%)	29	54
75	NN	107/115 (93%)	105 (98%)	2 (2%)	50	72
76	OO	66/102 (65%)	65 (98%)	1 (2%)	57	77
77	PP	111/116 (96%)	108 (97%)	3 (3%)	39	63
78	QQ	130/131 (99%)	130 (100%)	0	100	100
79	RF	357/376 (95%)	352 (99%)	5 (1%)	59	78
80	RR	99/108 (92%)	99 (100%)	0	100	100
81	SS	87/136 (64%)	86 (99%)	1 (1%)	65	81
82	TT	112/113 (99%)	111 (99%)	1 (1%)	70	84
83	UU	115/121 (95%)	115 (100%)	0	100	100
84	VV	113/115 (98%)	110 (97%)	3 (3%)	39	63
85	WW	109/130 (84%)	107 (98%)	2 (2%)	51	73
86	AB	506/526 (96%)	497 (98%)	9 (2%)	51	73
All	All	10834/12103 (90%)	10716 (99%)	118 (1%)	63	81

5 of 118 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	t	22	VAL
86	AB	298	VAL
60	y	30	ILE
86	AB	153	GLN
79	RF	296	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 203 such sidechains are listed below:

Mol	Chain	Res	Type
56	u	147	ASN
66	EE	83	GLN
86	AB	321	ASN
57	v	115	GLN

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Mol	Chain	Res	Type
61	z	197	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	K	1648/4592 (35%)	350 (21%)	15 (0%)
3	2	75/76 (98%)	15 (20%)	1 (1%)
4	4	10/11 (90%)	4 (40%)	1 (10%)
5	5	3415/7224 (47%)	679 (19%)	48 (1%)
7	7	119/120 (99%)	10 (8%)	0
8	8	149/156 (95%)	27 (18%)	1 (0%)
All	All	5416/12179 (44%)	1085 (20%)	66 (1%)

5 of 1085 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	2	10	G
3	2	11	G
3	2	12	C
3	2	14	U
3	2	15	A

5 of 66 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	K	642	U
20	K	752	G
20	K	1679	A
5	5	1633	G
5	5	1455	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 297 ligands modelled in this entry, 297 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

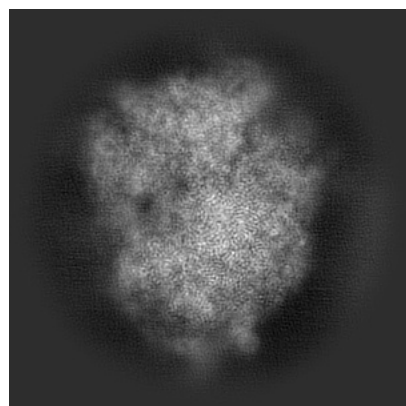
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72314. These allow visual inspection of the internal detail of the map and identification of artifacts.

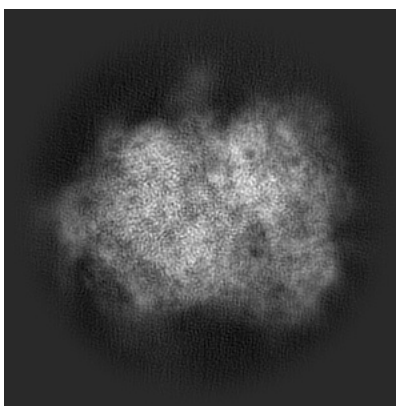
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

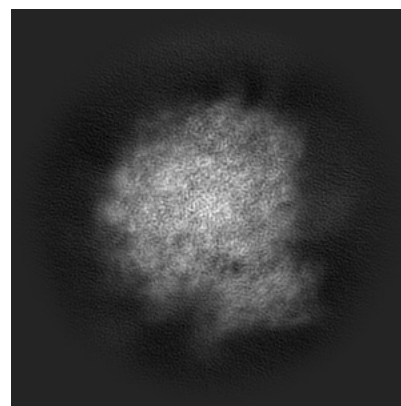
6.1.1 Primary map



X

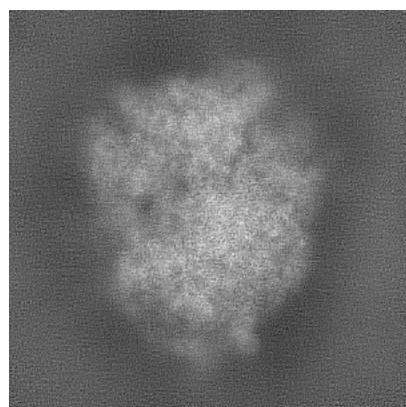


Y

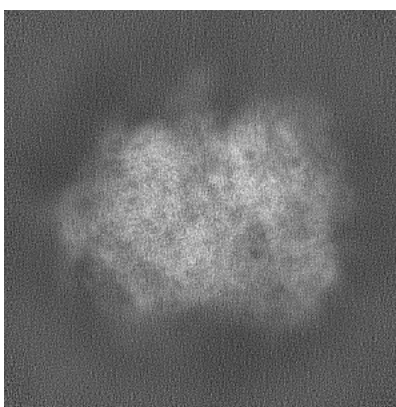


Z

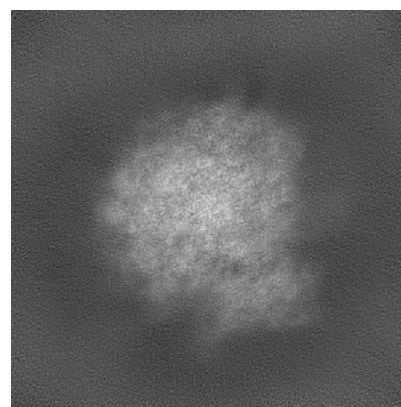
6.1.2 Raw map



X



Y

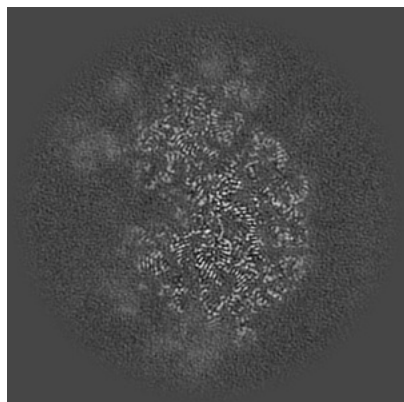


Z

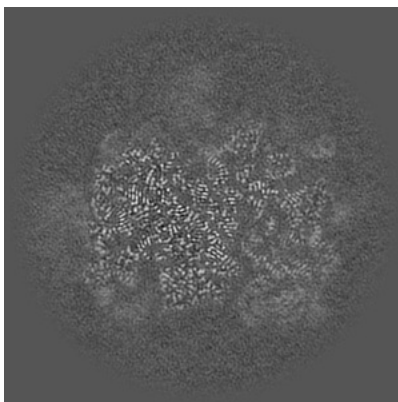
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

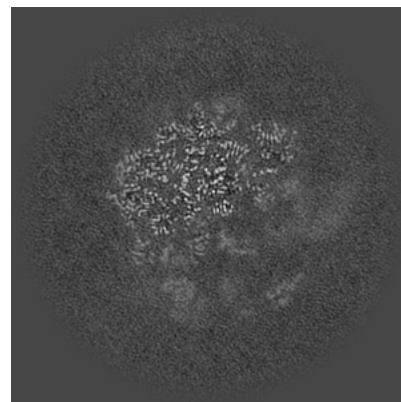
6.2.1 Primary map



X Index: 232

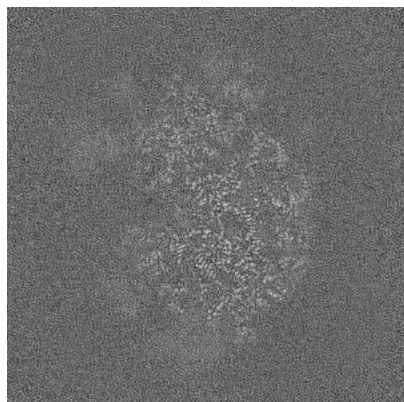


Y Index: 232

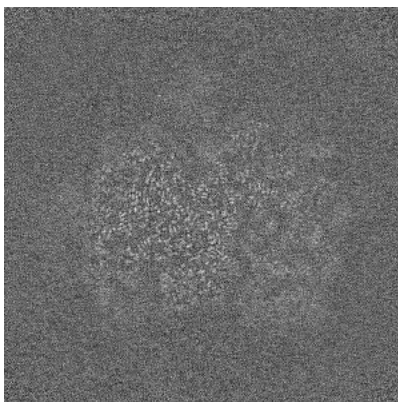


Z Index: 232

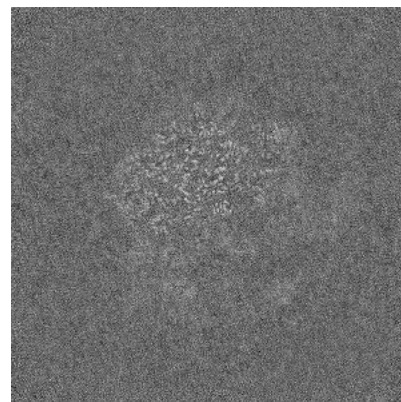
6.2.2 Raw map



X Index: 232



Y Index: 232

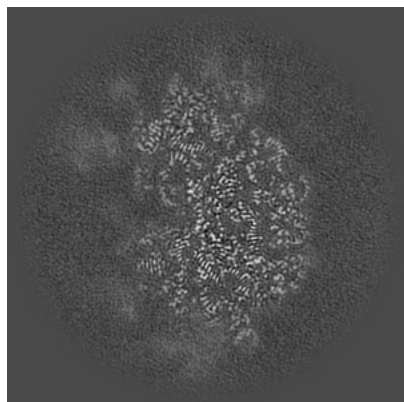


Z Index: 232

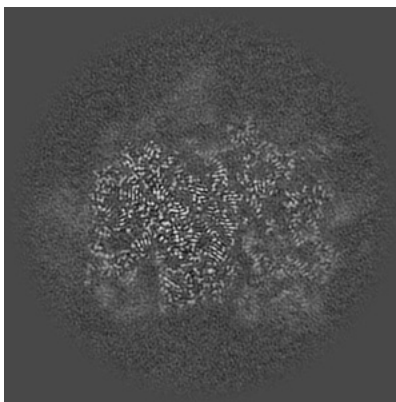
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

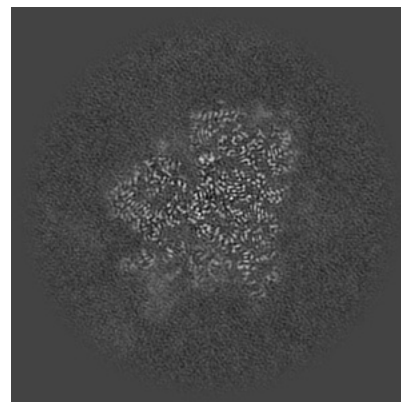
6.3.1 Primary map



X Index: 230

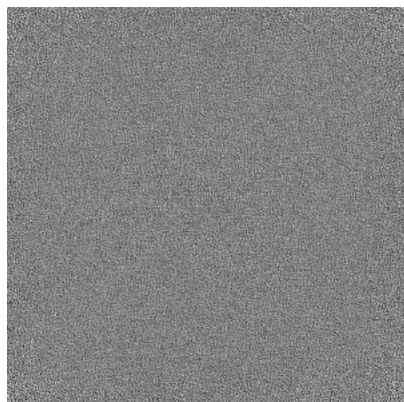


Y Index: 234

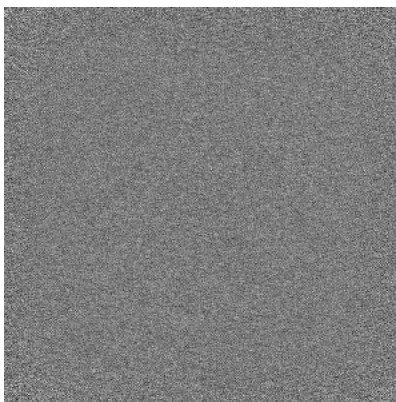


Z Index: 191

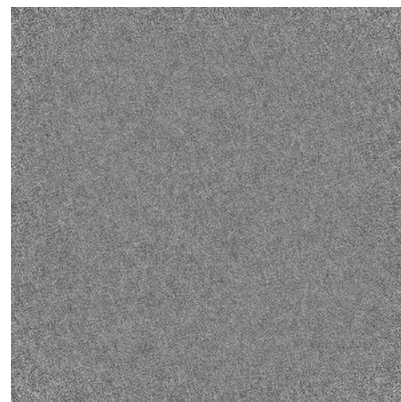
6.3.2 Raw map



X Index: 0



Y Index: 0

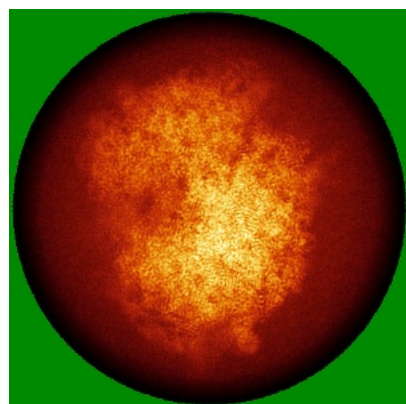


Z Index: 0

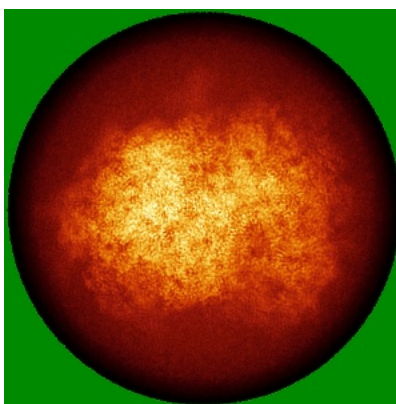
The images above show the largest variance slices of the map in three orthogonal directions.

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

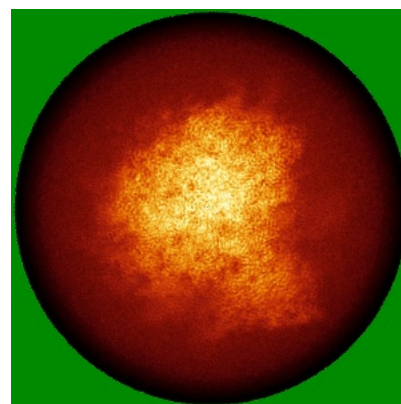
6.4.1 Primary map



X

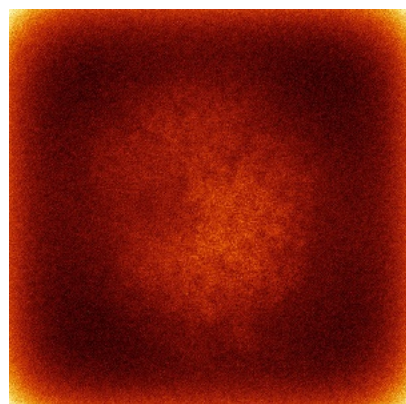


Y

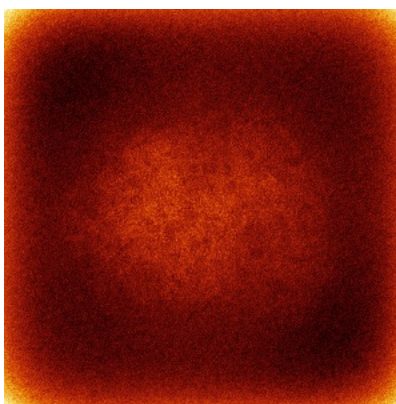


Z

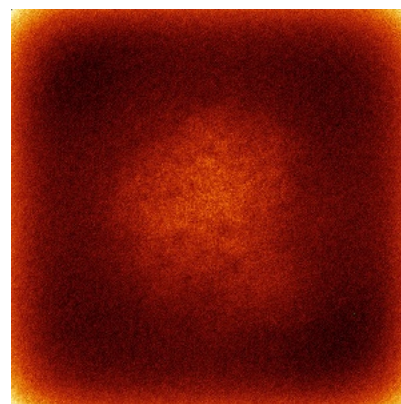
6.4.2 Raw map



X



Y

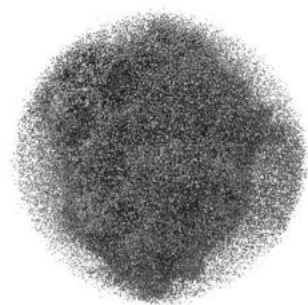


Z

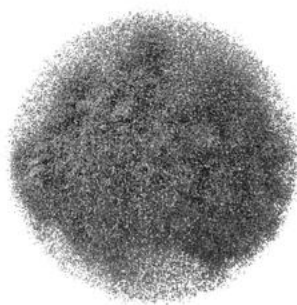
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

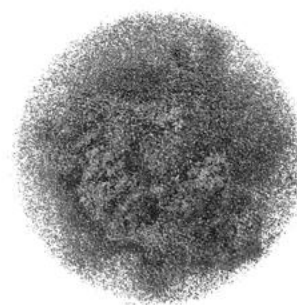
6.5.1 Primary map



X



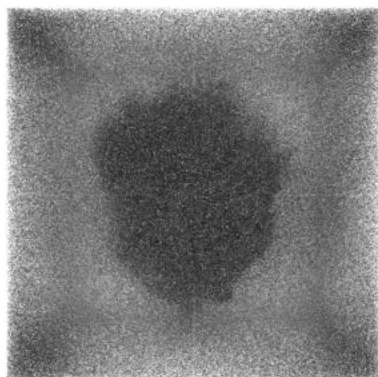
Y



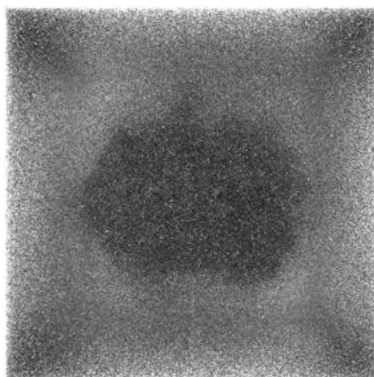
Z

The images above show the 3D surface view of the map at the recommended contour level 0.044. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

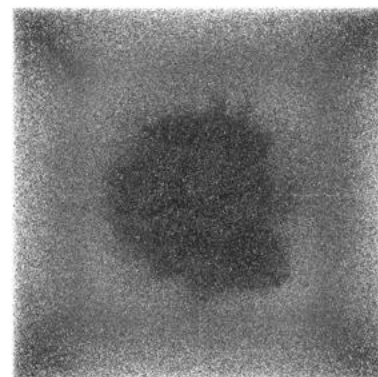
6.5.2 Raw map



X



Y



Z

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.

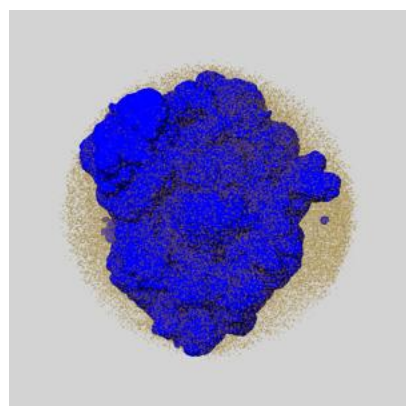
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

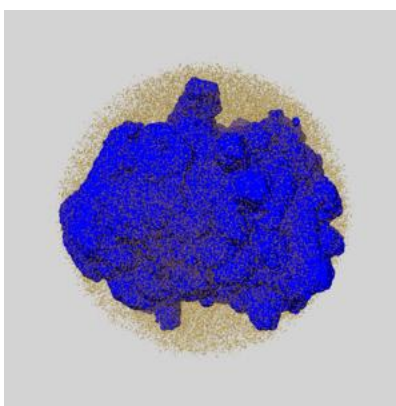
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

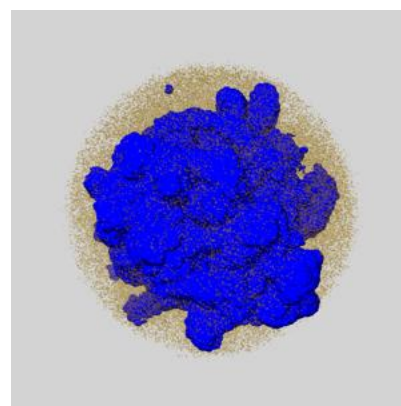
6.6.1 emd_72314_msk_1.map [i](#)



X



Y

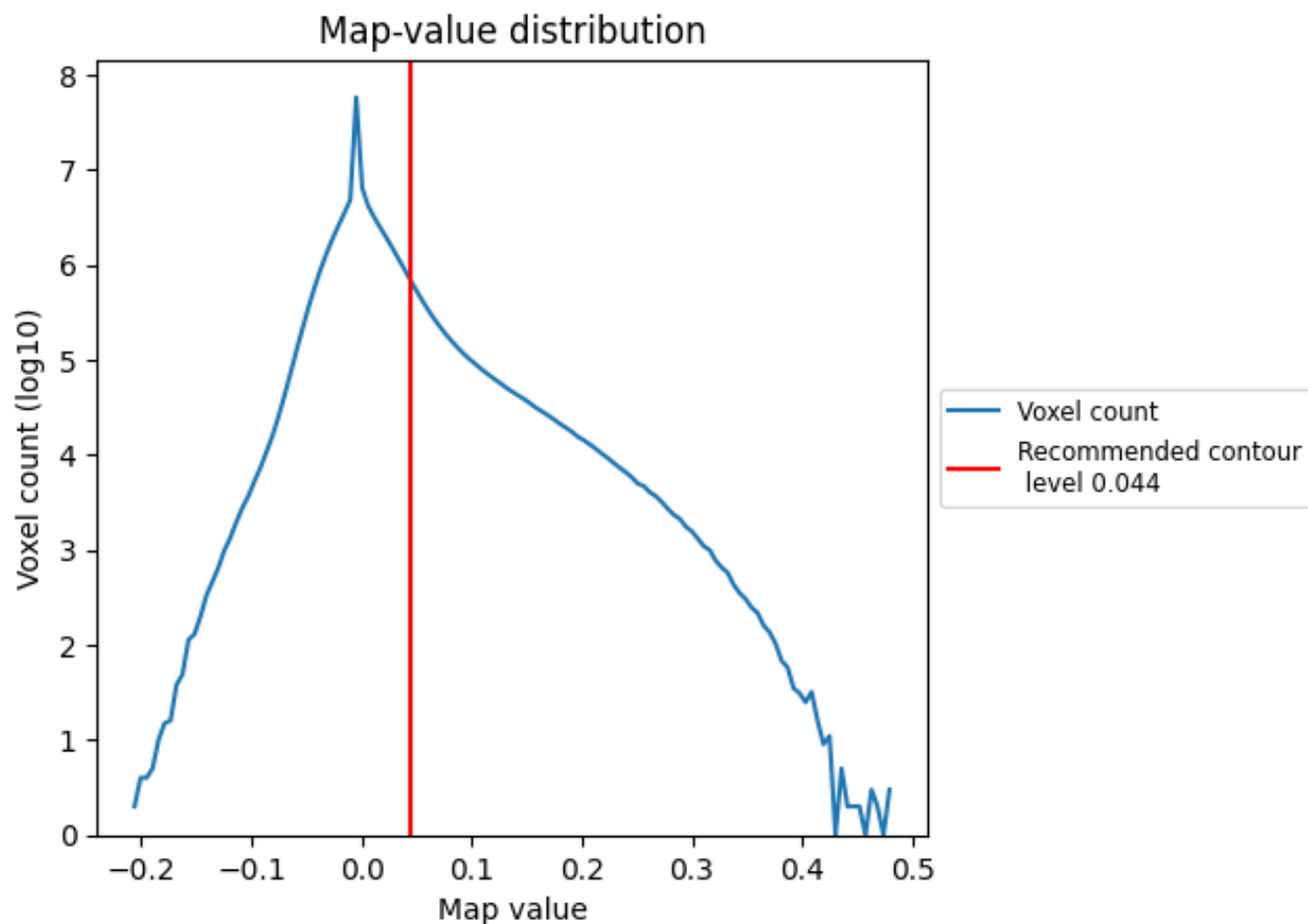


Z

7 Map analysis [i](#)

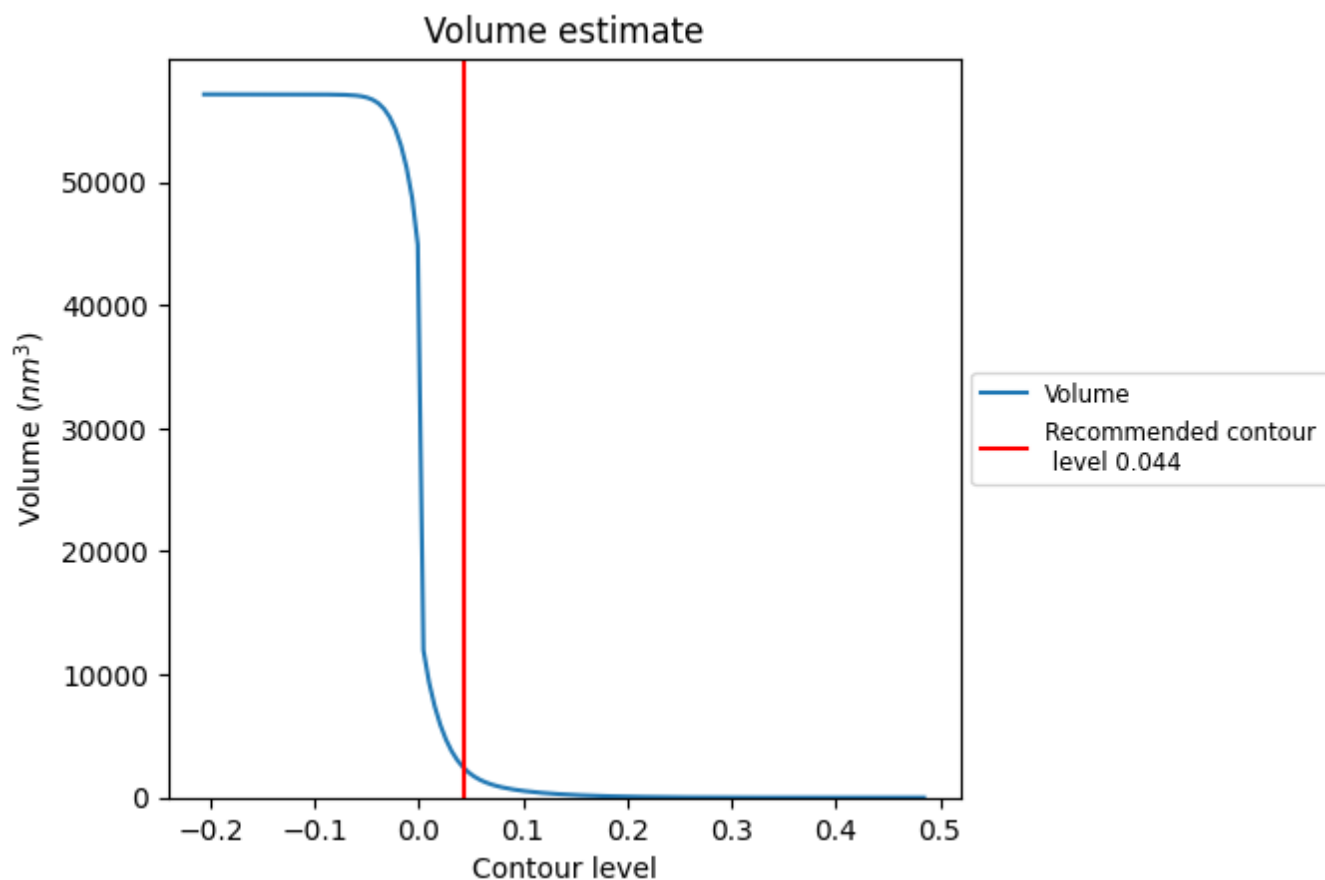
This section contains the results of statistical analysis of the map.

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.

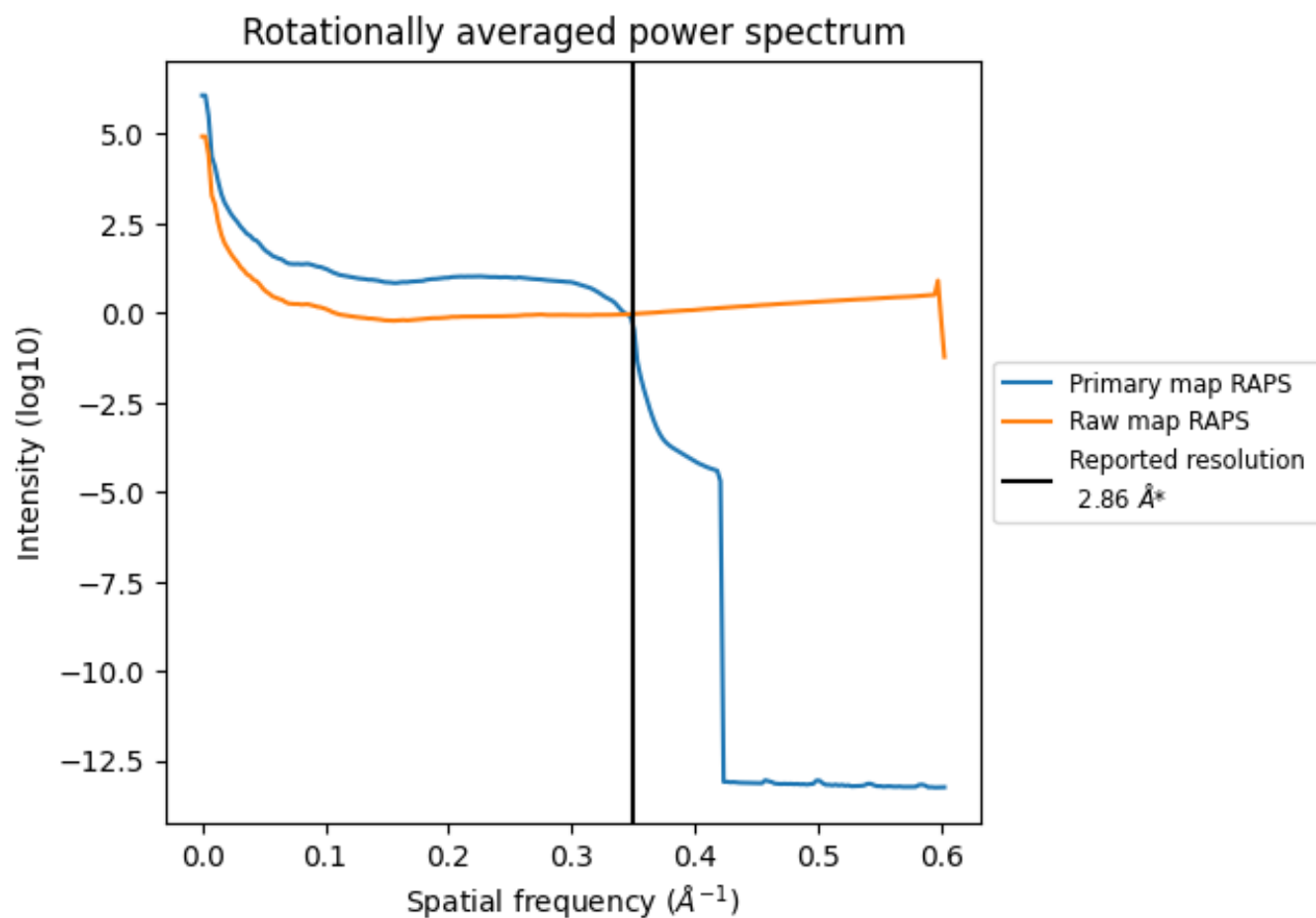
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2354 nm³; this corresponds to an approximate mass of 2126 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 ⓘ

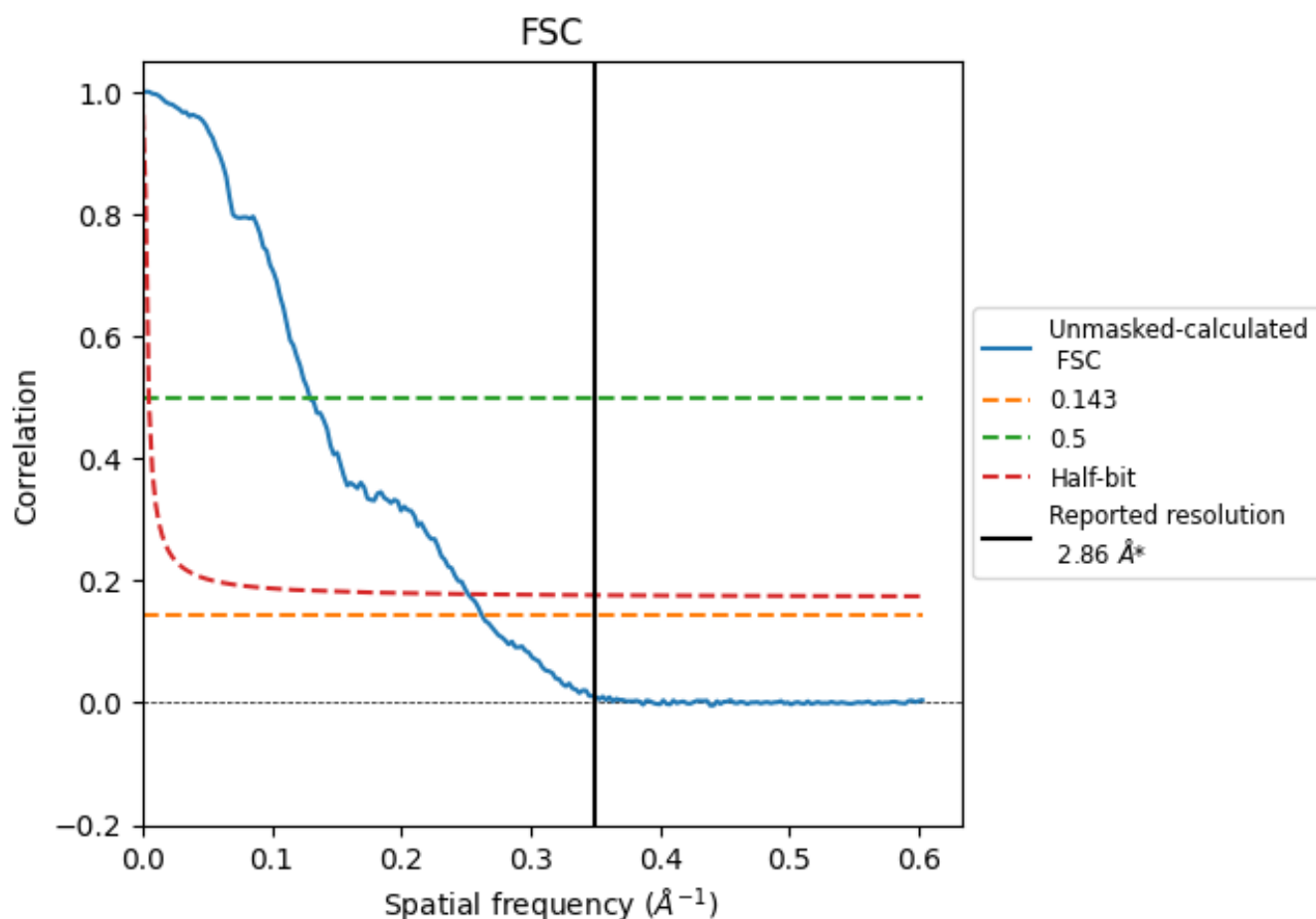


*Reported resolution corresponds to spatial frequency of 0.350 \AA^{-1}

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 0.350 Å⁻¹

8.2 Resolution estimates [i](#)

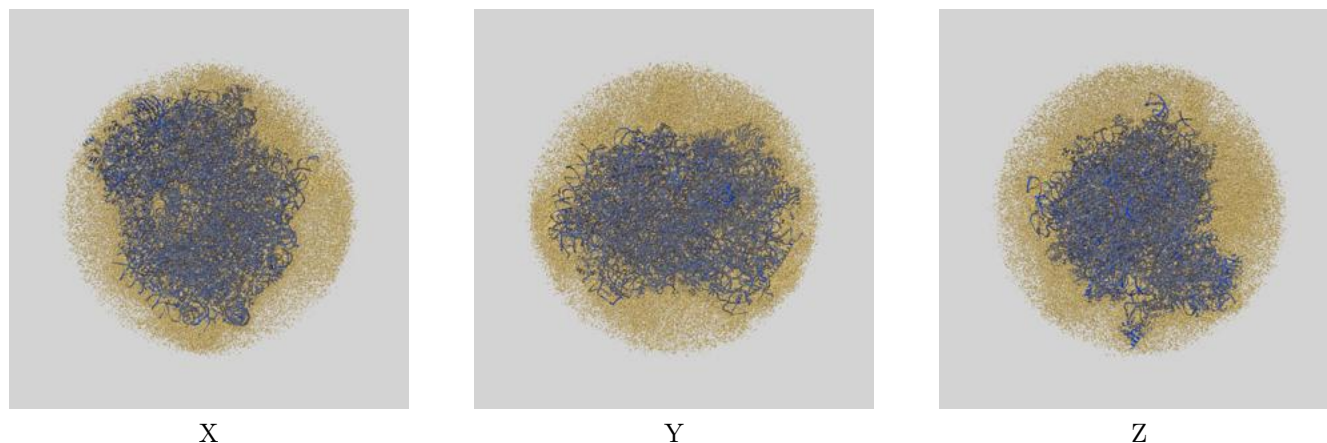
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.81	7.73	3.97

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.81 differs from the reported value 2.86 by more than 10 %

9 Map-model fit [i](#)

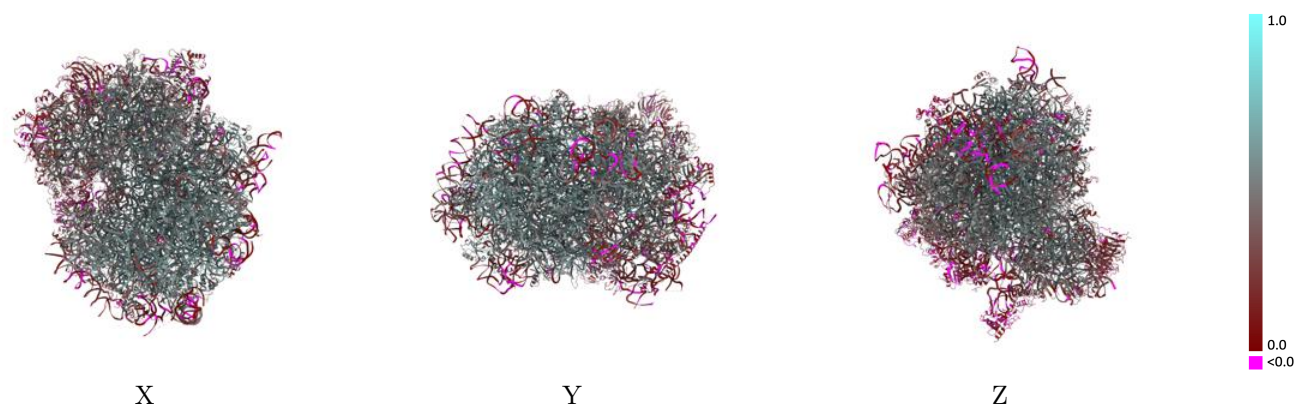
This section contains information regarding the fit between EMDB map EMD-72314 and PDB model 9Q7Q. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



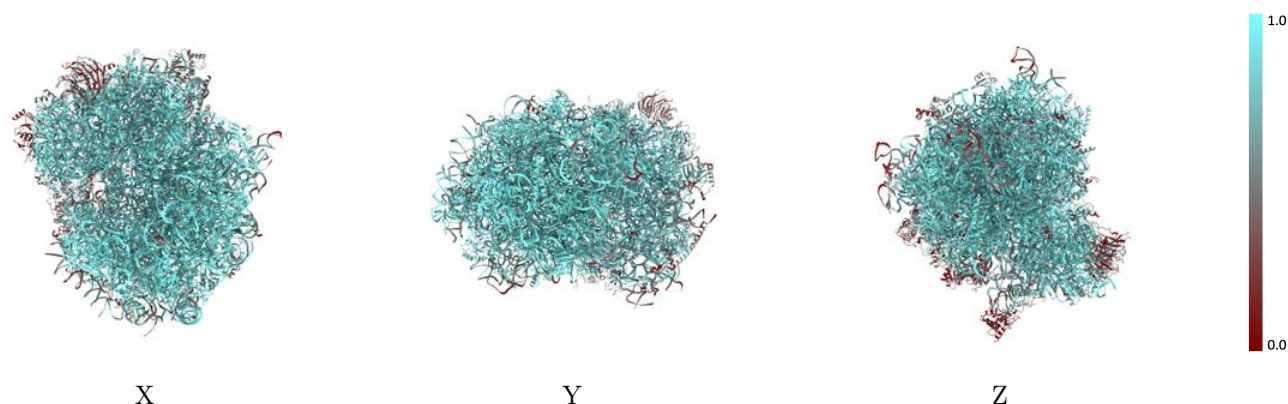
The images above show the 3D surface view of the map at the recommended contour level 0.044 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



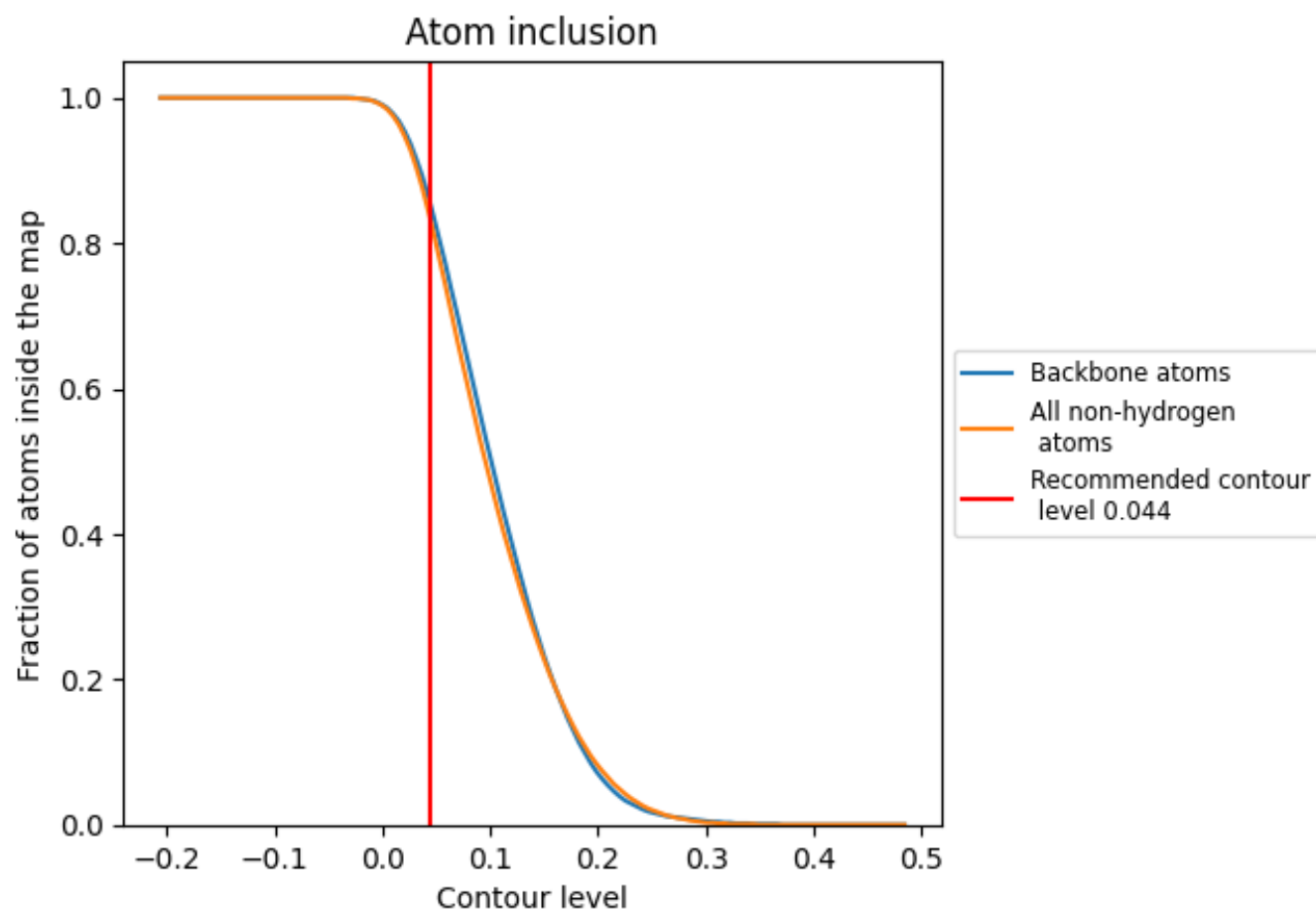
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.044).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 84% 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 (0.044) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8360	 0.4380
0	 0.1000	 0.0630
1	 0.8330	 0.4650
2	 0.9020	 0.4520
4	 0.9350	 0.5260
5	 0.8850	 0.4550
6	 0.3070	 0.2020
7	 0.9520	 0.5160
8	 0.9330	 0.5060
9	 0.8090	 0.4340
A	 0.9520	 0.5810
AA	 0.7250	 0.3680
AB	 0.5930	 0.2650
B	 0.9220	 0.5400
BB	 0.6170	 0.2820
C	 0.9260	 0.5500
CC	 0.6300	 0.3150
D	 0.8470	 0.4570
DD	 0.7890	 0.4100
E	 0.8220	 0.4500
EE	 0.8290	 0.4620
F	 0.9130	 0.5390
FF	 0.7190	 0.3620
G	 0.8400	 0.4620
GG	 0.7330	 0.3650
H	 0.7990	 0.4180
HH	 0.7880	 0.4400
I	 0.8040	 0.4640
II	 0.7200	 0.3470
J	 0.8130	 0.4200
JJ	 0.7370	 0.3560
K	 0.8690	 0.4190
KK	 0.6940	 0.3670
L	 0.8650	 0.5020
LL	 0.8430	 0.4470























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Chain	Atom inclusion	Q-score
M	 0.8600	 0.4560
MM	 0.8440	 0.4640
N	 0.9650	 0.5850
NN	 0.7550	 0.3580
O	 0.9020	 0.5360
OO	 0.6830	 0.3360
P	 0.9380	 0.5590
PP	 0.7950	 0.3790
Q	 0.9410	 0.5740
QQ	 0.8470	 0.4950
R	 0.8320	 0.4590
RF	 0.7120	 0.3900
RR	 0.1390	 0.0790
S	 0.8910	 0.5140
SS	 0.6060	 0.2250
T	 0.8780	 0.5180
TT	 0.9080	 0.5200
U	 0.5400	 0.1490
UU	 0.7610	 0.3860
V	 0.9220	 0.5650
VV	 0.8560	 0.5010
W	 0.8760	 0.5160
WW	 0.7230	 0.3340
X	 0.9120	 0.5320
Y	 0.8980	 0.5290
Z	 0.8950	 0.4960
a	 0.9420	 0.5630
b	 0.7720	 0.3970
c	 0.8640	 0.4980
d	 0.8940	 0.5140
e	 0.9370	 0.5700
f	 0.9310	 0.5610
g	 0.8770	 0.4990
h	 0.8920	 0.5070
i	 0.8510	 0.4660
j	 0.9380	 0.5580
k	 0.6890	 0.3990
l	 0.8780	 0.5050
m	 0.2430	 0.1390
n	 0.9400	 0.5480
o	 0.8830	 0.5040
p	 0.9060	 0.5540

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Chain	Atom inclusion	Q-score
q	 0.7920	 0.4280
r	 0.9340	 0.5470
s	 0.2710	 0.0880
t	 0.3270	 0.1030
u	 0.8490	 0.4640
v	 0.8150	 0.4730
w	 0.7520	 0.3780
x	 0.8370	 0.4230
y	 0.7720	 0.4140
z	 0.6330	 0.2610