



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 03:12 PM UTC

PDB ID : 9BDP / pdb_00009bdp
EMDB ID : EMD-44464
Title : 80S ribosome bound with angiogenin and complex of eEF1A and Ala-tRNAAla
Authors : Loveland, A.B.; Korostelev, A.A.
Deposited on : 2024-04-12
Resolution : 3.70 Å (reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

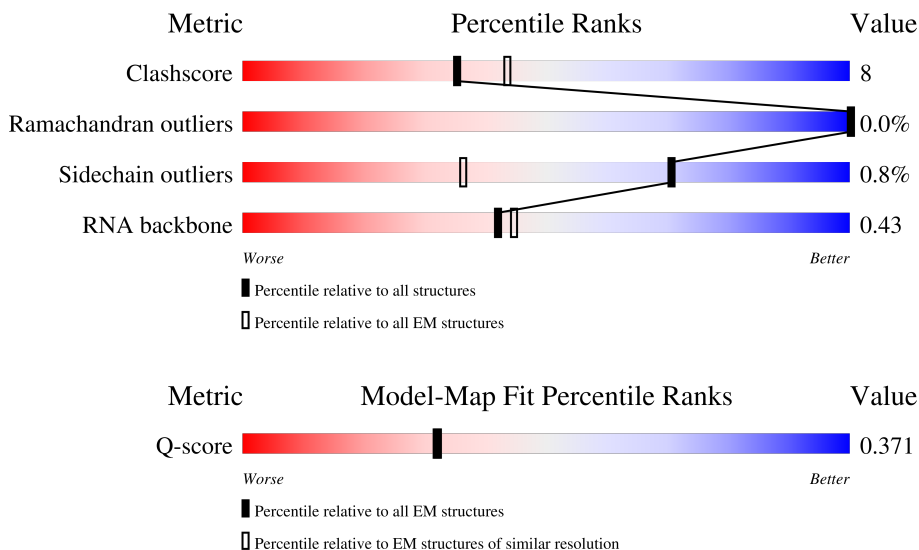
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	A18S	1869	
2	A28S	3601	
3	A58S	156	

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Mol	Chain	Length	Quality of chain
4	A5S	120	72% 28%
5	AL02	248	100%
6	AL03	394	8% 99%
7	AL04	362	7% 99%
8	AL05	293	11% 100%
9	AL06	251	18% 86% 14%
10	AL07	225	8% 99%
11	AL08	240	36% 96%
12	AL09	190	15% 100%
13	AL10	213	8% 96%
14	AL11	170	16% 100%
15	AL12	153	92% 98%
16	AL13	210	18% 99%
17	AL14	138	9% 100%
18	AL15	203	100%
19	AL16	199	8% 99%
20	AL17	153	7% 100%
21	AL18	187	8% 99%
22	AL19	180	17% 100%
23	AL20	176	10% 100%
24	AL21	159	11% 97%
25	AL22	99	26% 99%
26	AL23	131	8% 99%
27	AL24	121	10% 52% 48%
28	AL25	118	10% 99%

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Mol	Chain	Length	Quality of chain
29	AL26	134	9% 99%
30	AL27	135	14% 100%
31	AL28	147	5% 97%
32	AL29	245	16% 42% 58%
33	AL30	98	15% 100%
34	AL31	107	9% 100%
35	AL32	128	• 99%
36	AL33	109	7% 100%
37	AL34	114	12% 96%
38	AL35	122	13% 99%
39	AL36	102	17% 98%
40	AL37	86	• 100%
41	AL38	69	30% 100%
42	AL39	50	12% 98%
43	AL40	52	10% 100%
44	AL41	25	40% 100%
45	AL42	104	9% 99%
46	AL43	91	7% 99%
47	ALNW	124	6% 99%
48	ALP0	196	96% 99%
49	ANG	147	29% 62% 19% 18%
50	ARAC	313	75% 100%
51	AS00	217	38% 99%
52	AS01	213	21% 99%
53	AS02	221	25% 99%

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Mol	Chain	Length	Quality of chain
54	AS03	228	49% 99%
55	AS04	262	30% 99%
56	AS05	191	29% 96%
57	AS06	237	40% 100%
58	AS07	189	56% 97%
59	AS08	206	25% 100%
60	AS09	185	23% 99%
61	AS10	96	60% 98%
62	AS11	151	15% 94% 5%
63	AS12	117	82% 85% 15%
64	AS13	149	17% 99%
65	AS14	135	19% 100%
66	AS15	120	42% 99%
67	AS16	142	41% 99%
68	AS17	132	50% 100%
69	AS18	144	33% 100%
70	AS19	141	38% 98%
71	AS20	100	62% 100%
72	AS21	83	51% 100%
73	AS22	129	26% 98%
74	AS23	141	15% 99%
75	AS24	124	41% 100%
76	AS25	254	9% 29% 70%
77	AS26	101	17% 98%
78	AS27	83	33% 98%

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Mol	Chain	Length	Quality of chain
79	AS28	62	<p>24% 100%</p>
80	AS29	55	<p>35% 100%</p>
81	AS30	55	<p>42% 98%</p>
82	EF1A	458	<p>92% 91% 6%</p>
83	ETRN	77	<p>21% 77% 23%</p>
83	PTRN	77	<p>5% 79% 21%</p>
84	MRNA	28	<p>21% 14% 64%</p>
85	TIRN	76	<p>34% 71% 21%</p>

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 220396 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A18S	1691	36103	16115	6485	11813	1690	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A28S	3557	76286	33976	13979	24774	3557	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	A58S	151	3208	1432	564	1062	150	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	A5S	120	2558	1141	456	842	119	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A5S	2	U	N	conflict	GB X06789.1
A5S	36	C	N	conflict	GB X06789.1
A5S	102	U	N	conflict	GB X06789.1
A5S	112	U	N	conflict	GB X06789.1
A5S	114	U	N	conflict	GB X06789.1
A5S	119	U	C	conflict	GB X06789.1
A5S	120	U	N	conflict	GB X06789.1

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AL02	248	1898	1189	389	314	6	0	0

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AL03	394	3172	2020	597	542	13	0	0

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	AL04	362	2883	1812	577	480	14	0	0

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AL05	293	2391	1512	438	427	14	0	0

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	AL06	216	1729	1115	329	282	3	0	0

- Molecule 10 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	AL07	225	1875	1205	358	303	9	0	0

- Molecule 11 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AL08	233	1879	1199	361	315	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL08	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	AL09	190	1516	954	284	272	6	0	0

- Molecule 13 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AL10	205	1664	1056	321	274	13	0	0

- Molecule 14 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	AL11	170	1361	861	254	240	6	0	0

- Molecule 15 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	AL12	153	1160	722	218	217	3	0	0

- Molecule 16 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	AL13	210	1702	1065	354	279	4	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL13	74	ARG	HIS	conflict	UNP G1TKB3
AL13	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 17 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	AL14	138	1137	727	221	182	7	0	0

- Molecule 18 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	AL15	203	1701	1072	359	266	4	0	0

- Molecule 19 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	AL16	199	1630	1051	319	255	5	0	0

- Molecule 20 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	AL17	153	1242	777	241	215	9	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	AL18	187	1515	946	315	250	4	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL18	4	ASP	ASN	conflict	UNP G1TFE0
AL18	14	ARG	TRP	conflict	UNP G1TFE0
AL18	53	MET	LEU	conflict	UNP G1TFE0
AL18	58	ARG	TRP	conflict	UNP G1TFE0
AL18	75	ARG	GLN	conflict	UNP G1TFE0
AL18	80	ALA	PRO	conflict	UNP G1TFE0
AL18	86	VAL	ILE	conflict	UNP G1TFE0
AL18	104	ARG	HIS	conflict	UNP G1TFE0
AL18	110	ARG	CYS	conflict	UNP G1TFE0
AL18	137	VAL	GLY	conflict	UNP G1TFE0
AL18	157	GLY	ARG	conflict	UNP G1TFE0
AL18	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 22 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	AL19	180	1508	933	328	238	9	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL19	38	ARG	HIS	conflict	UNP G1TYL6
AL19	151	ARG	HIS	conflict	UNP G1TYL6

- Molecule 23 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	AL20	176	1462	930	285	236	11	0	0

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL20	1	MET	THR	conflict	UNP G1TTY7
AL20	18	PRO	-	insertion	UNP G1TTY7
AL20	19	THR	-	insertion	UNP G1TTY7
AL20	20	PRO	SER	conflict	UNP G1TTY7
AL20	22	CYS	SER	conflict	UNP G1TTY7
AL20	23	ARG	PRO	conflict	UNP G1TTY7
AL20	24	THR	ALA	conflict	UNP G1TTY7
AL20	49	SER	LEU	conflict	UNP G1TTY7
AL20	50	GLN	GLU	conflict	UNP G1TTY7
AL20	95	ARG	HIS	conflict	UNP G1TTY7
AL20	101	THR	ILE	conflict	UNP G1TTY7
AL20	102	THR	MET	conflict	UNP G1TTY7
AL20	104	GLY	SER	conflict	UNP G1TTY7
AL20	126	ILE	VAL	conflict	UNP G1TTY7
AL20	132	ILE	MET	conflict	UNP G1TTY7
AL20	135	SER	ALA	conflict	UNP G1TTY7
AL20	136	LYS	ARG	conflict	UNP G1TTY7
AL20	138	ARG	PRO	conflict	UNP G1TTY7
AL20	149	LYS	ARG	conflict	UNP G1TTY7
AL20	151	LYS	ARG	conflict	UNP G1TTY7
AL20	168	THR	TYR	conflict	UNP G1TTY7
AL20	169	THR	ALA	conflict	UNP G1TTY7
AL20	176	PHE	-	insertion	UNP G1TTY7

- Molecule 24 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	AL21	159	1298	823	252	217	6	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	AL22	99	809	519	141	147	2	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL22	18	LEU	VAL	conflict	UNP G1TSG1
AL22	32	GLY	ARG	conflict	UNP G1TSG1
AL22	36	ALA	GLU	conflict	UNP G1TSG1
AL22	39	PHE	SER	conflict	UNP G1TSG1
AL22	54	GLY	ARG	conflict	UNP G1TSG1
AL22	60	VAL	ALA	conflict	UNP G1TSG1
AL22	62	SER	THR	conflict	UNP G1TSG1
AL22	63	LEU	ILE	conflict	UNP G1TSG1
AL22	97	ARG	HIS	conflict	UNP G1TSG1
AL22	106	THR	SER	conflict	UNP G1TSG1

- Molecule 26 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	AL23	131	979	618	184	172	5	0	0

- Molecule 27 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	AL24	63	528	337	103	85	3	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	AL25	118	967	618	181	167	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	AL26	134	1115	700	226	186	3	0	0

- Molecule 30 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	AL27	135	1107	714	208	182	3	0	0

- Molecule 31 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	AL28	147	1162	734	239	185	4	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	AL29	104	848	527	189	129	3	0	0

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	AL30	98	761	481	134	140	6	0	0

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	AL31	107	888	560	171	155	2	0	0

- Molecule 35 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	AL32	128	1053	667	216	165	5	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL32	3	ALA	SER	conflict	UNP G1TUN8
AL32	13	VAL	ILE	conflict	UNP G1TUN8
AL32	16	ARG	TRP	conflict	UNP G1TUN8
AL32	81	ASN	SER	conflict	UNP G1TUN8
AL32	98	GLU	LYS	conflict	UNP G1TUN8
AL32	108	ARG	CYS	conflict	UNP G1TUN8
AL32	115	ALA	VAL	conflict	UNP G1TUN8

- Molecule 36 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	AL33	109	876	555	174	143	4	0	0

- Molecule 37 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	AL34	114	906	566	187	147	6	0	0

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	AL35	122	1013	640	204	168	1	0	0

- Molecule 39 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	AL36	102	830	520	176	129	5	0	0

- Molecule 40 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	AL37	86	705	434	155	111	5	0	0

- Molecule 41 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	AL38	69	569	366	103	99	1	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL38	24	LYS	ASN	conflict	UNP G1U001

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	AL39	50	447	286	96	64	1	0	0

- Molecule 43 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	AL40	52	429	266	90	67	6	0	0

- Molecule 44 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	AL41	25	239	145	64	27	3	0	0

- Molecule 45 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	AL42	104	851	533	174	138	6	0	0

- Molecule 46 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	AL43	91	708	445	136	120	7	0	0

- Molecule 47 is a protein called 60S ribosomal protein L28.

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

- Molecule 48 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	ALP0	196	1507	959	263	276	9	0	0

- Molecule 49 is a protein called Angiogenin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	ANG	120	955	591	186	171	7	0	0

- Molecule 50 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 51 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	AS00	217	1710	1086	300	316	8	0	0

- Molecule 52 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	AS01	213	1729	1098	309	308	14	0	0

- Molecule 53 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	AS02	221	1716	1111	295	301	9	0	0

- Molecule 54 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AS03	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 55 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AS04	262	Total	C	N	O	S	0	0
			2075	1323	386	358	8		

- Molecule 56 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AS05	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 57 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AS06	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 58 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AS07	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 59 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS08	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS08	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 60 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	AS09	185	1525	969	306	248	2	0	0

- Molecule 61 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	AS10	96	810	530	143	131	6	0	0

- Molecule 62 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	AS11	143	1175	749	222	198	6	0	0

- Molecule 63 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	AS12	99	758	475	139	137	7	0	0

- Molecule 64 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	AS13	149	1202	770	228	203	1	0	0

- Molecule 65 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	AS14	135	1004	614	196	188	6	0	0

- Molecule 66 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	AS15	120	997	635	187	168	7	0	0

- Molecule 67 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	AS16	142	1128	717	213	195	3	0	0

- Molecule 68 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	AS17	132	1068	670	199	195	4	0	0

- Molecule 69 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	AS18	144	1190	746	241	202	1	0	0

- Molecule 70 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	AS19	141	1097	688	211	195	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS19	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 71 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	AS20	100	795	498	152	141	4	0	0

- Molecule 72 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	AS21	83	636	393	117	121	5	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS21	3	ASN	SER	conflict	UNP G1TM82

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Chain	Residue	Modelled	Actual	Comment	Reference
AS21	4	ASP	ASN	conflict	UNP G1TM82
AS21	33	GLN	PRO	conflict	UNP G1TM82
AS21	50	PHE	SER	conflict	UNP G1TM82
AS21	75	ALA	SER	conflict	UNP G1TM82
AS21	76	ASP	HIS	conflict	UNP G1TM82
AS21	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 73 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	AS22	129	1034	659	193	176	6	0	0

- Molecule 74 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	AS23	141	1098	693	219	183	3	0	0

- Molecule 75 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	AS24	124	1011	640	198	168	5	0	0

- Molecule 76 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	AS25	75	598	382	111	104	1	0	0

- Molecule 77 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	AS26	101	814	507	170	132	5	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS26	28	ARG	CYS	conflict	UNP G1TFE8

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Chain	Residue	Modelled	Actual	Comment	Reference
AS26	56	ALA	VAL	conflict	UNP G1TFE8

- Molecule 78 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	AS27	83	651	408	121	115	7	0	0

- Molecule 79 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	AS28	62	488	297	97	92	2	0	0

- Molecule 80 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	AS29	55	459	286	94	74	5	0	0

- Molecule 81 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
81	AS30	55	443	274	97	71	1	0	0

- Molecule 82 is a protein called Elongation factor 1-alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
82	EF1A	430	3311	2105	579	613	14	0	0

- Molecule 83 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
83	ETRN	77	1640	732	297	535	76	0	0
83	PTRN	77	1640	732	297	535	76	0	0

- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
84	MRNA	10	207	93	33	71	10	0	0

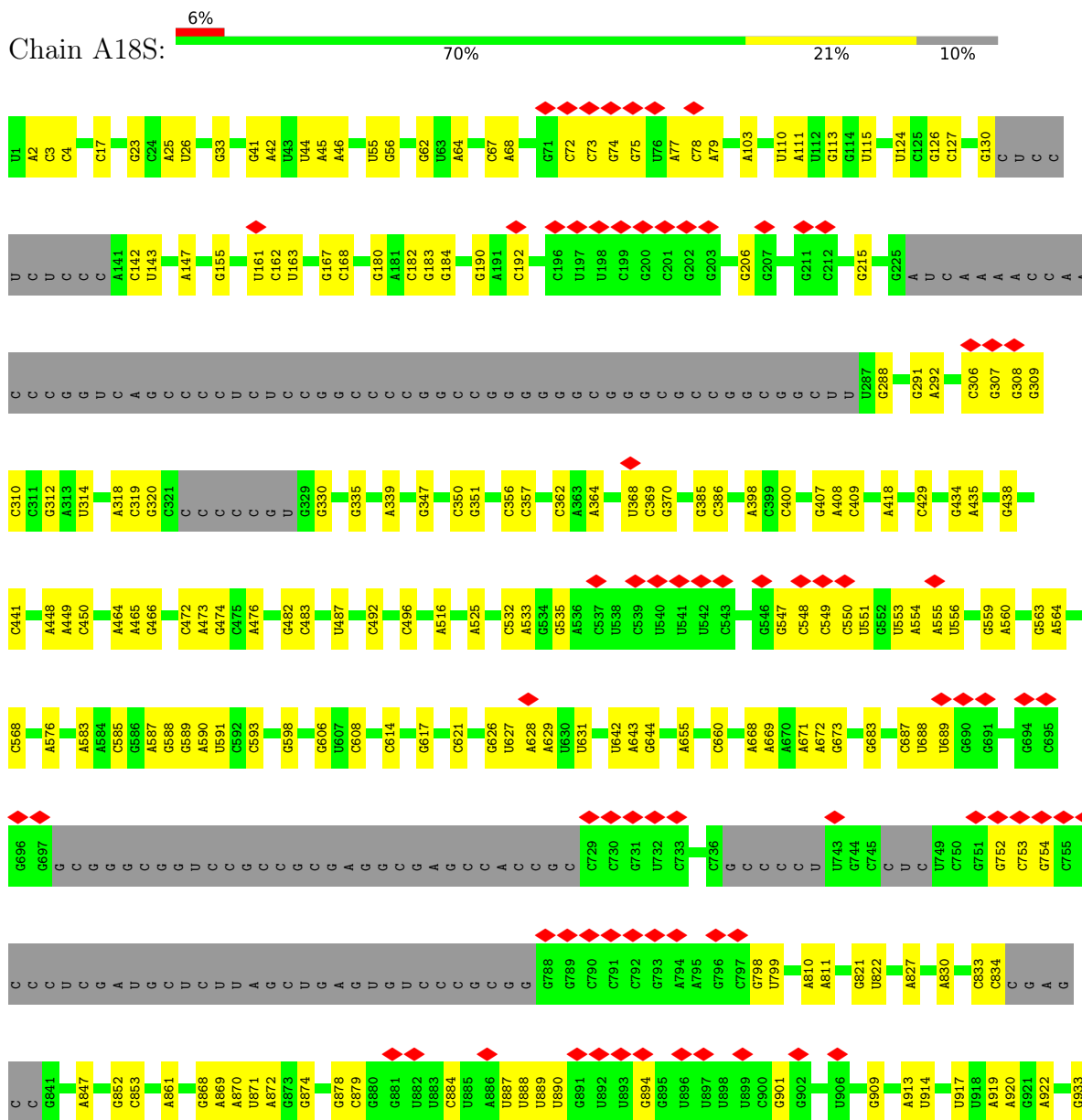
- Molecule 85 is a RNA chain called tRNAAla.

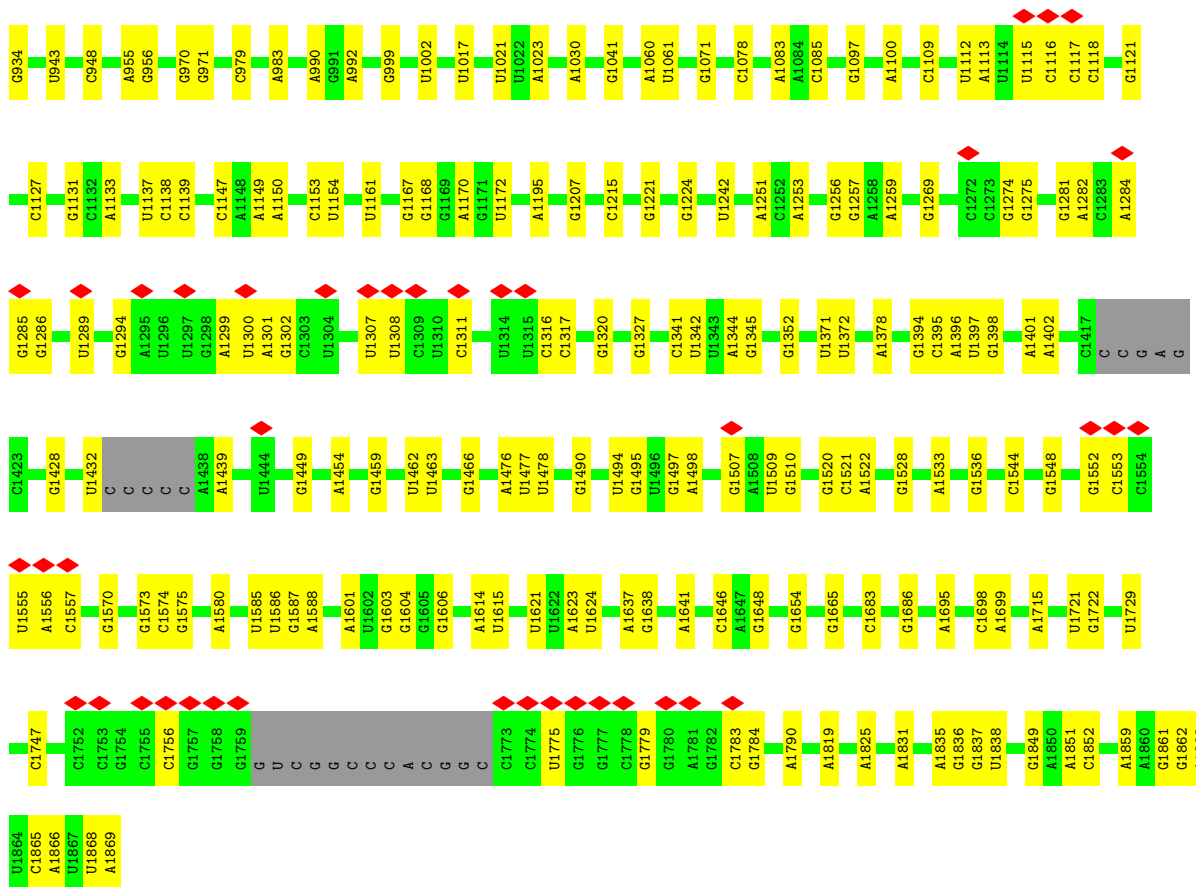
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
85	TIRN	70	1491	664	263	495	69	0	0

3 Residue-property plots i

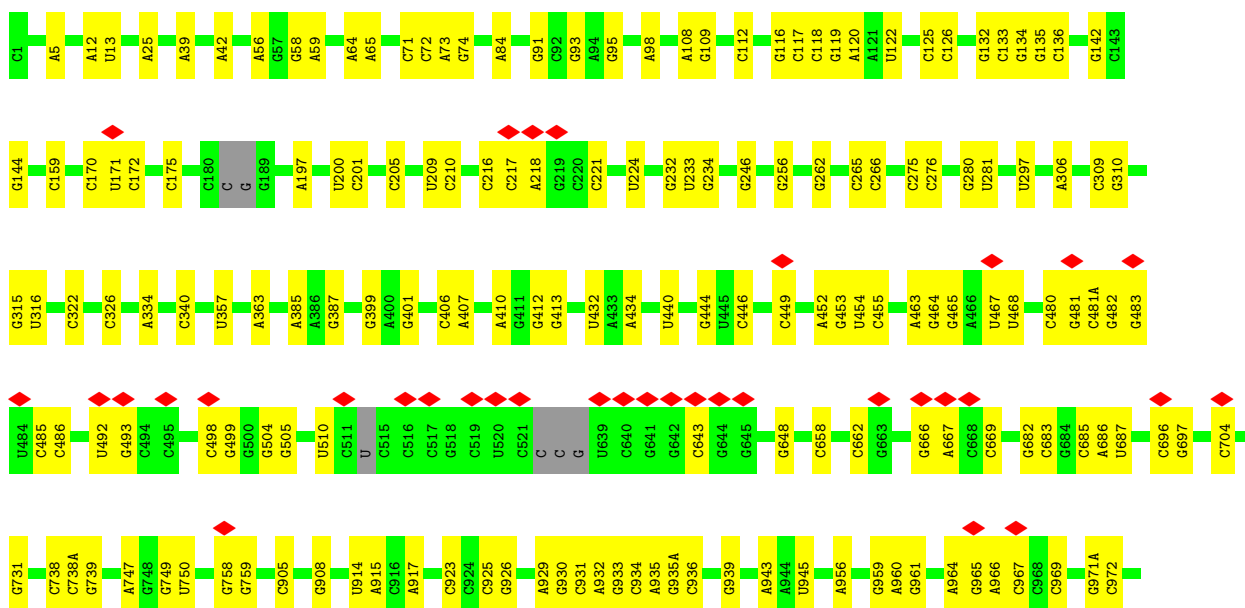
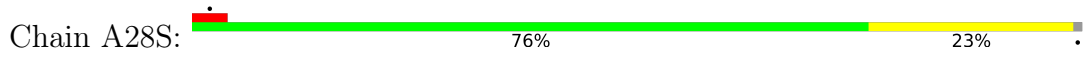
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

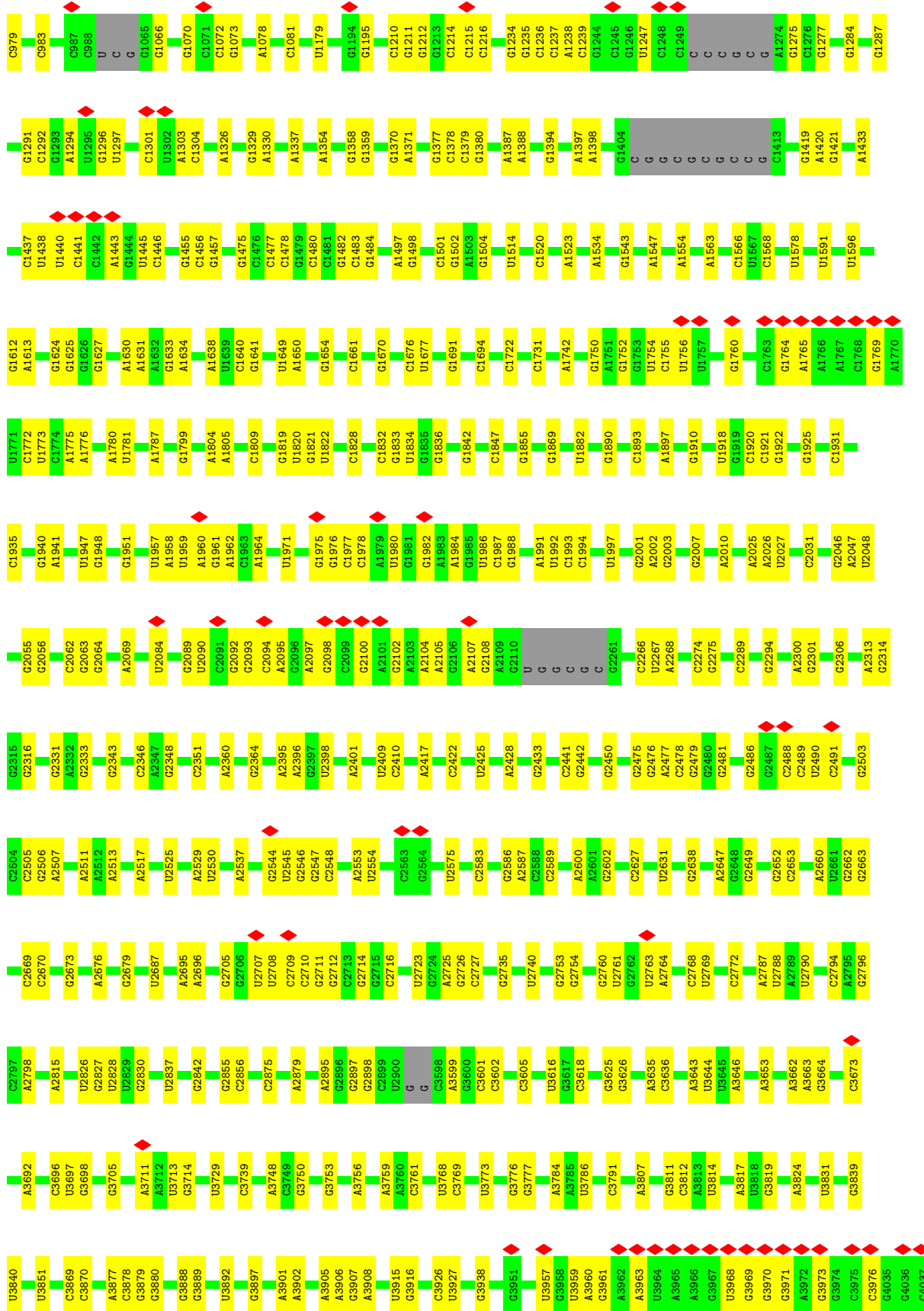
- Molecule 1: 18S rRNA

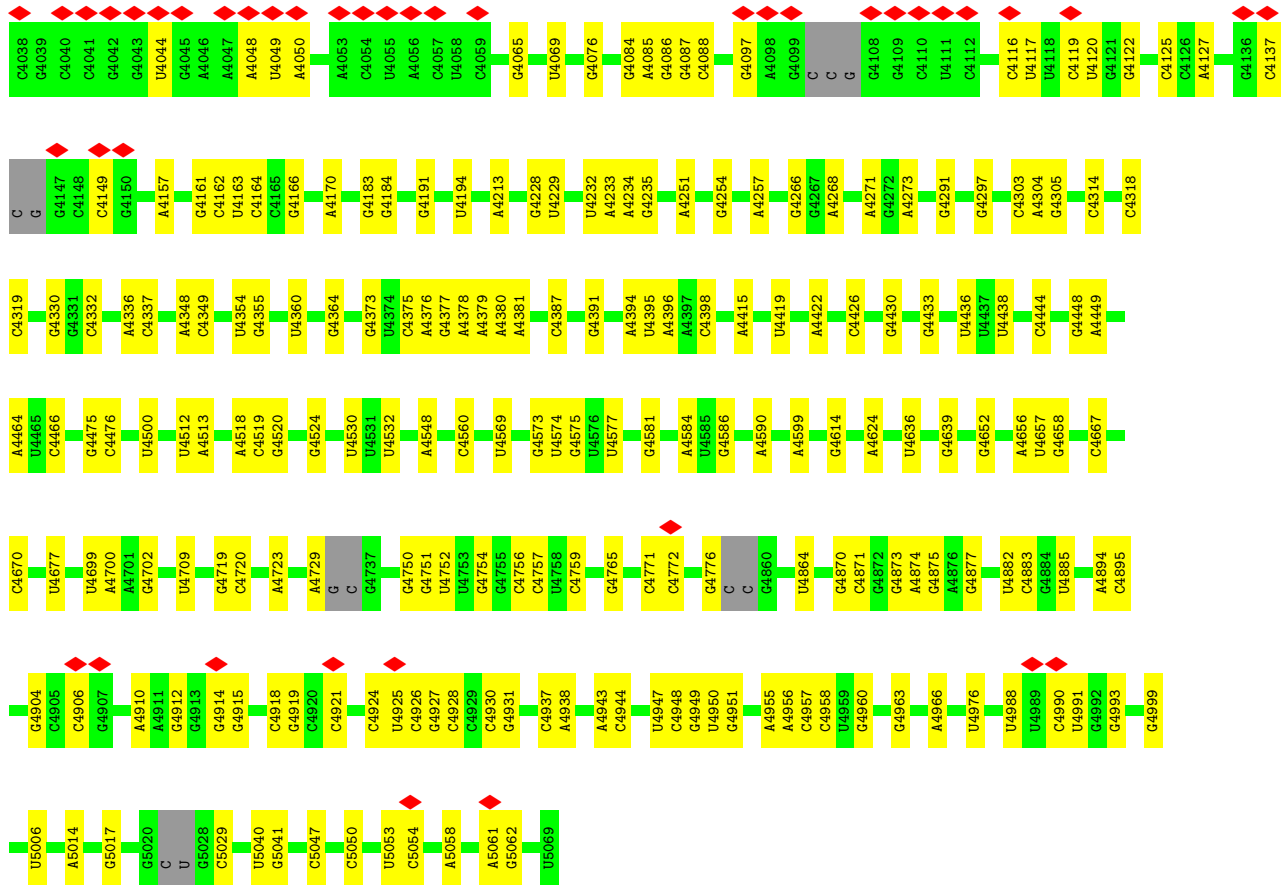




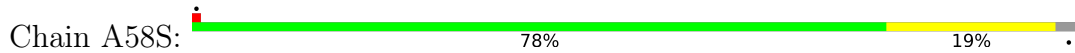
• Molecule 2: 28S rRNA



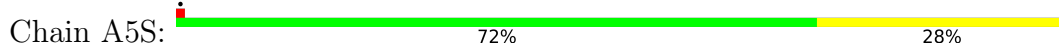




• Molecule 3: 5.8S rRNA



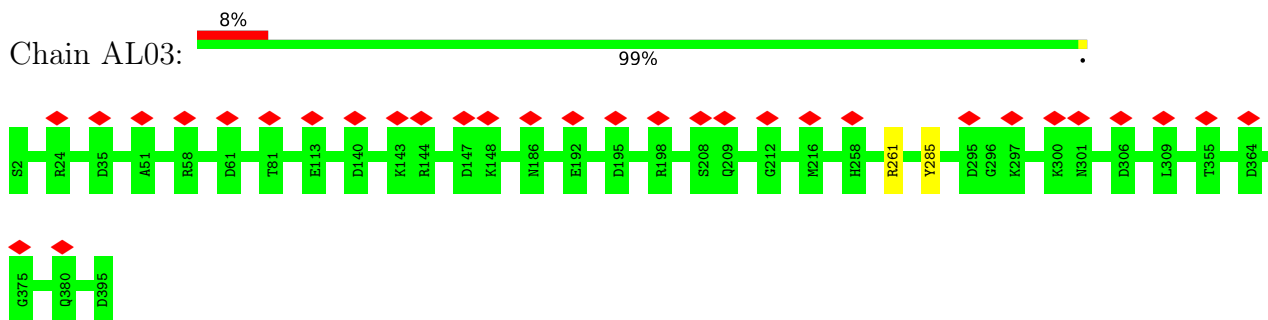
• Molecule 4: 5S rRNA



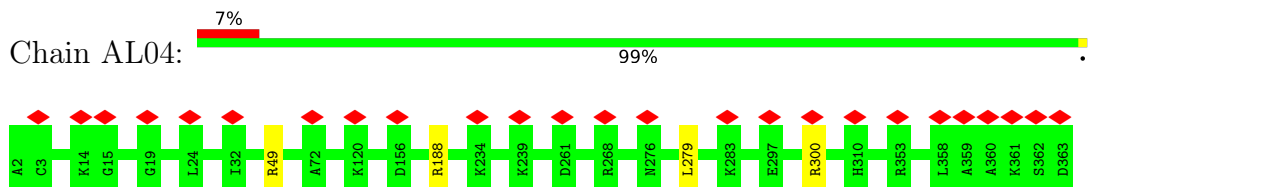
• Molecule 5: 60S ribosomal protein L8



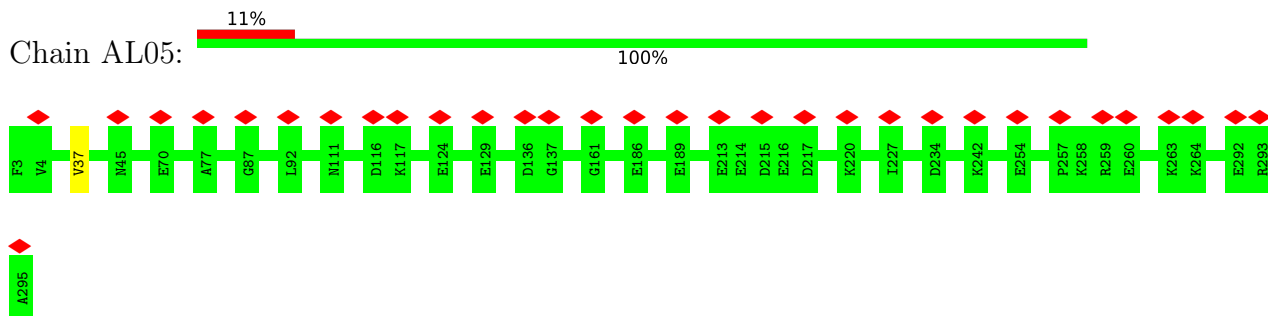
• Molecule 6: 60S ribosomal protein L3



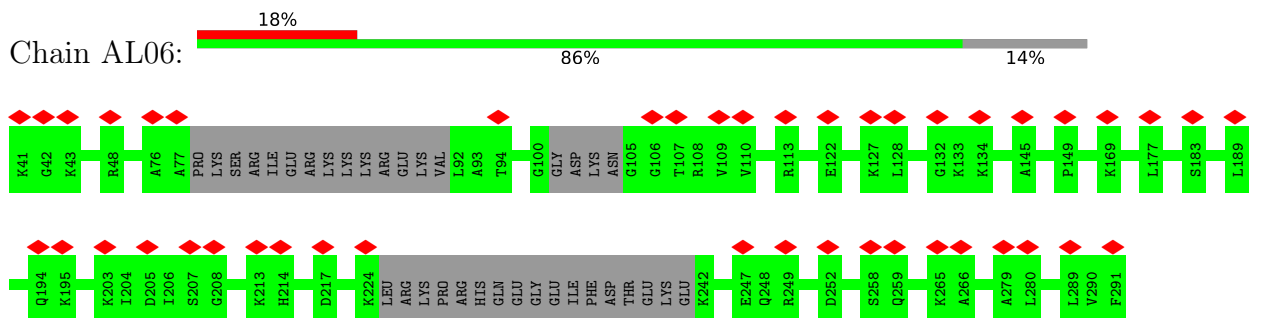
- Molecule 7: 60S ribosomal protein L4



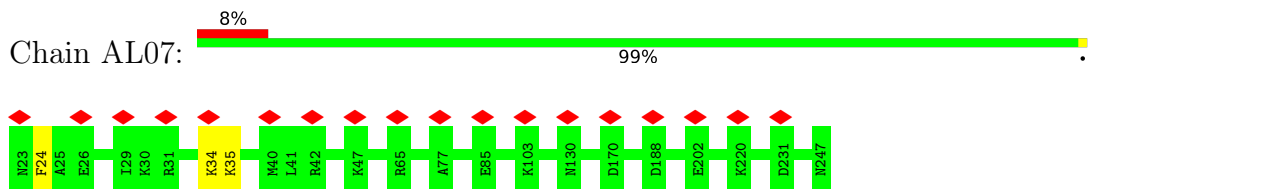
- Molecule 8: 60S ribosomal protein L5



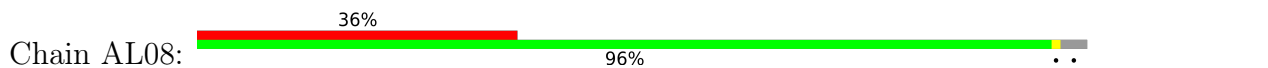
- Molecule 9: 60S ribosomal protein L6

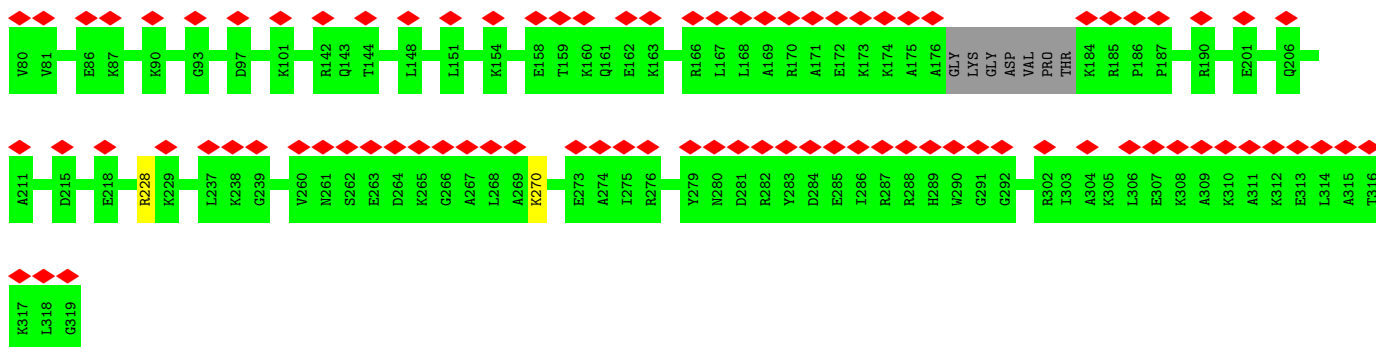


- Molecule 10: 60S ribosomal protein L7

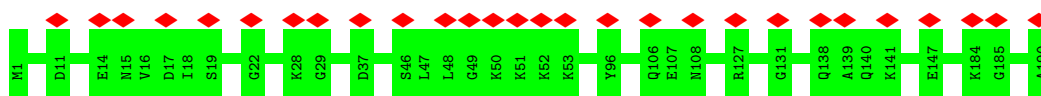


- Molecule 11: Large ribosomal subunit protein eL8

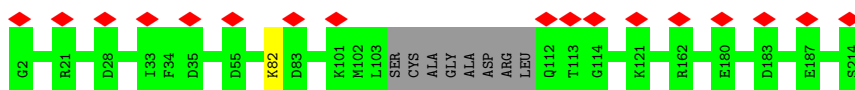




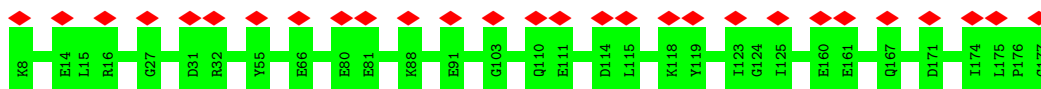
- Molecule 12: 60S ribosomal protein L9



- Molecule 13: Ribosomal protein L10



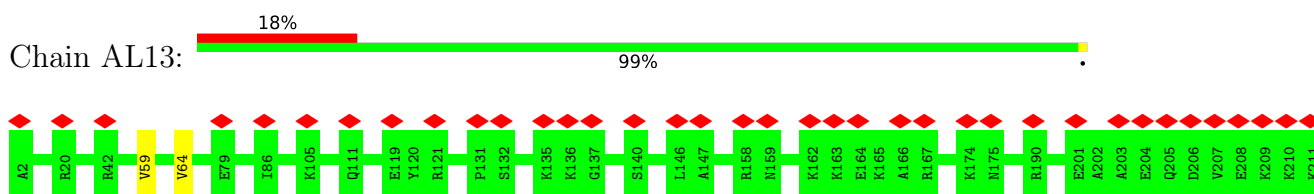
- Molecule 14: 60S ribosomal protein L11



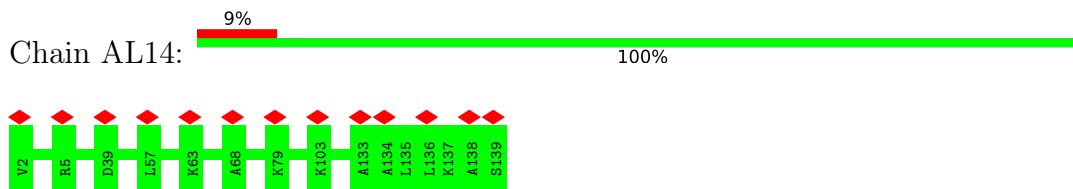
- Molecule 15: uL11



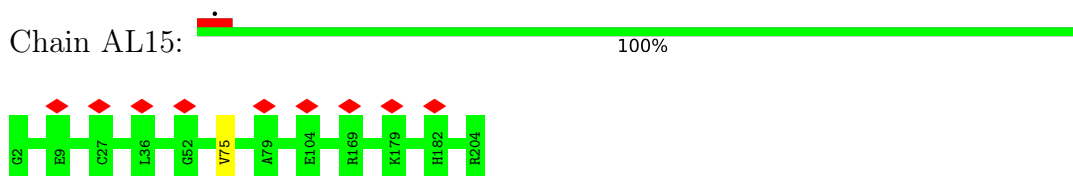
- Molecule 16: Large ribosomal subunit protein eL13



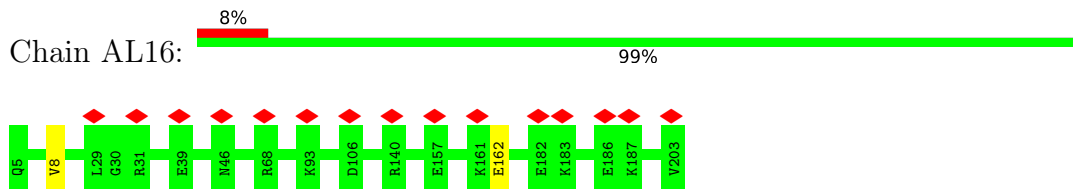
- Molecule 17: 60S ribosomal protein L14



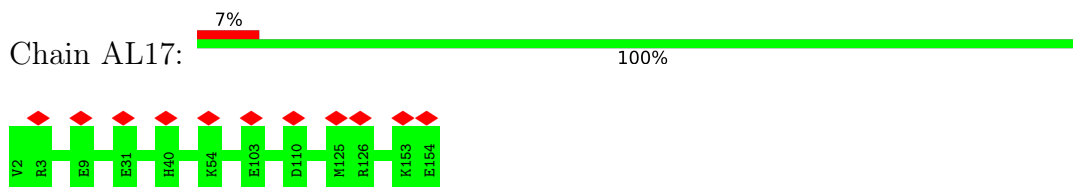
- Molecule 18: 60S ribosomal protein L15



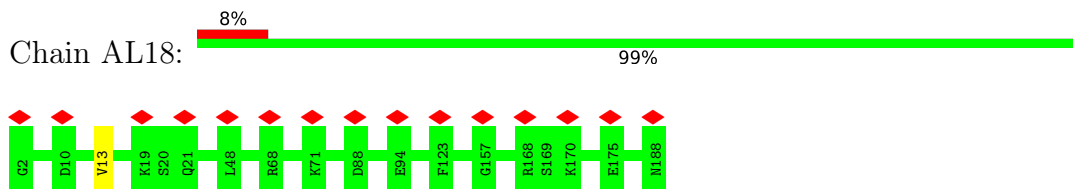
- Molecule 19: Large ribosomal subunit protein uL13



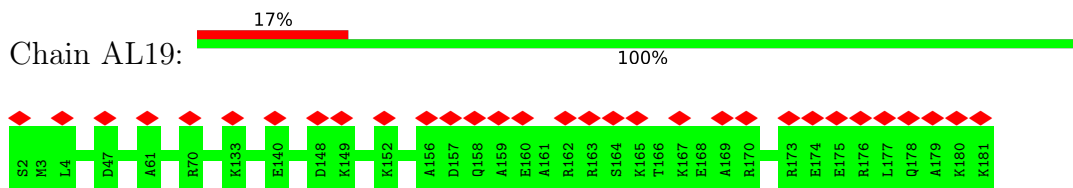
- Molecule 20: 60S ribosomal protein L17



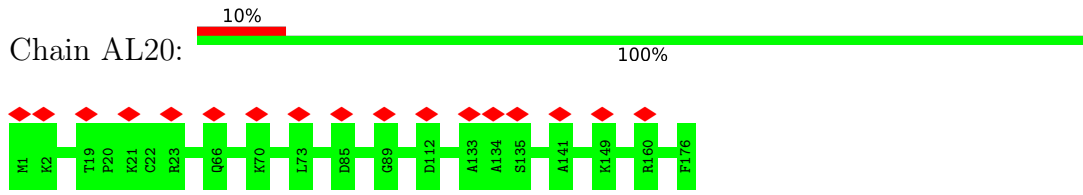
- Molecule 21: Large ribosomal subunit protein eL18



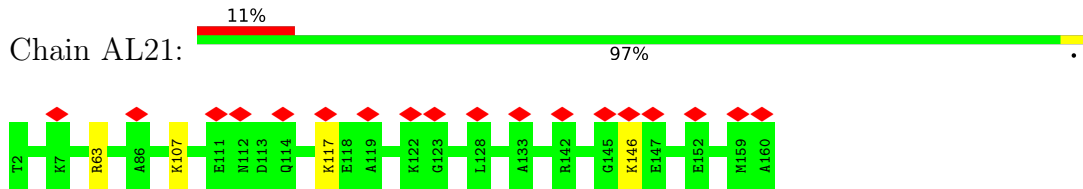
- Molecule 22: 60S ribosomal protein L19



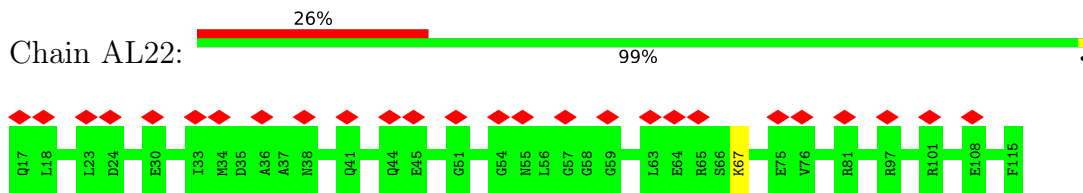
• Molecule 23: 60S ribosomal protein L18a



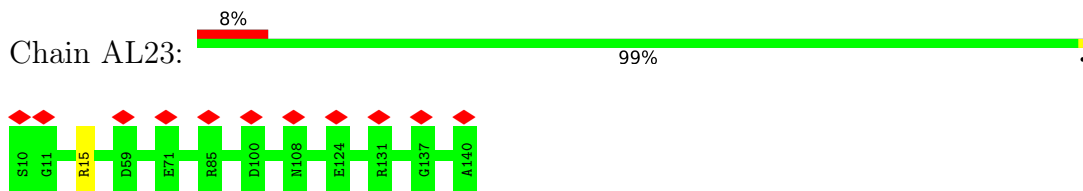
• Molecule 24: 60S ribosomal protein L21



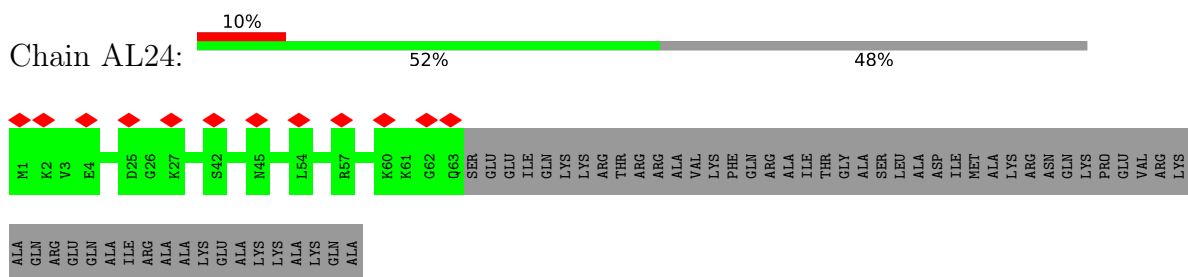
• Molecule 25: Large ribosomal subunit protein eL22



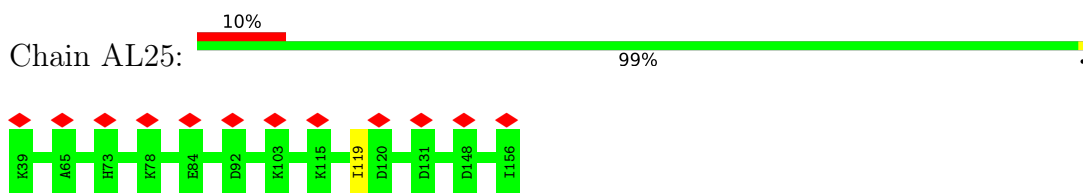
• Molecule 26: 60S ribosomal protein L23



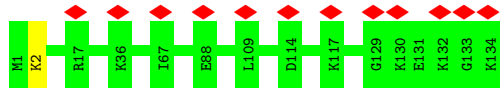
• Molecule 27: Ribosomal protein L24



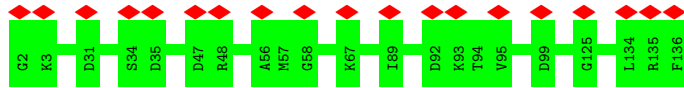
• Molecule 28: Large ribosomal subunit protein uL23



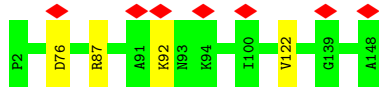
• Molecule 29: 60S ribosomal protein L26



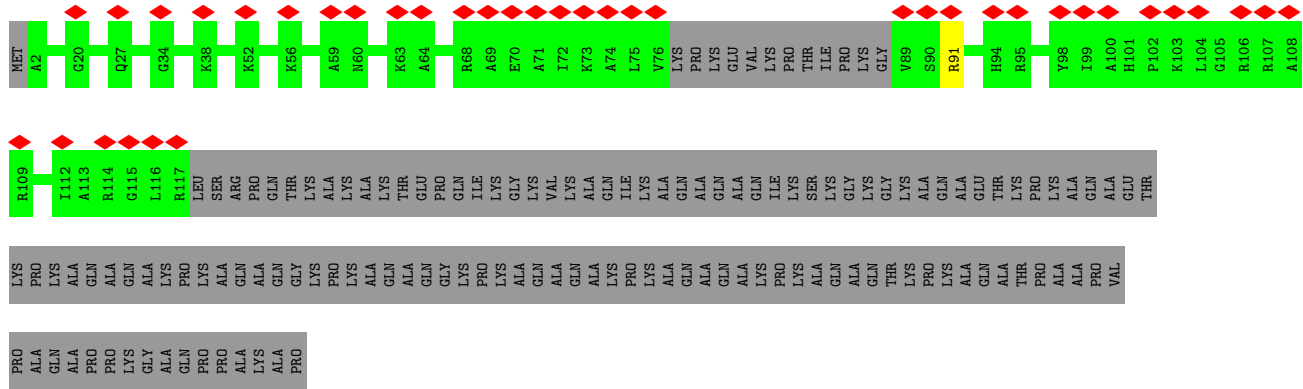
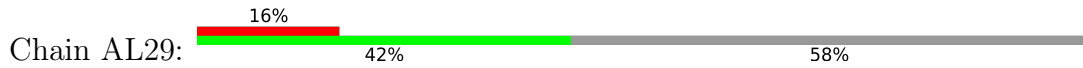
- Molecule 30: 60S ribosomal protein L27



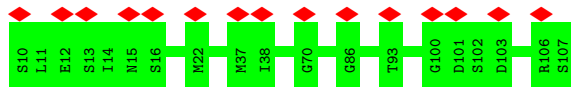
- Molecule 31: 60S ribosomal protein L27a



- Molecule 32: Large ribosomal subunit protein eL29

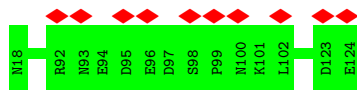


- Molecule 33: 60S ribosomal protein L30



- Molecule 34: 60S ribosomal protein L31

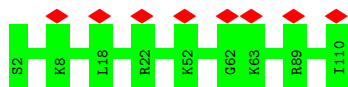




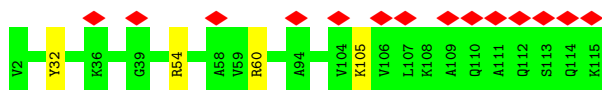
- Molecule 35: Large ribosomal subunit protein eL32



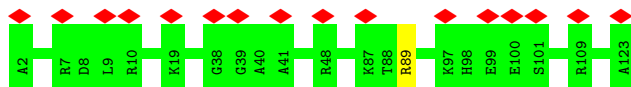
- Molecule 36: 60S ribosomal protein L35a



- Molecule 37: 60S ribosomal protein L34



- Molecule 38: 60S ribosomal protein L35



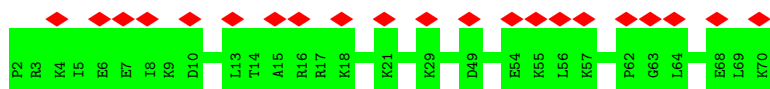
- Molecule 39: 60S ribosomal protein L36



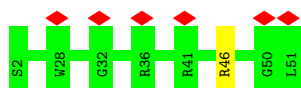
- Molecule 40: 60S ribosomal protein L37



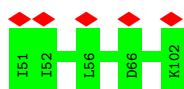
- Molecule 41: Large ribosomal subunit protein eL38



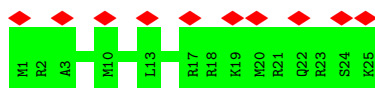
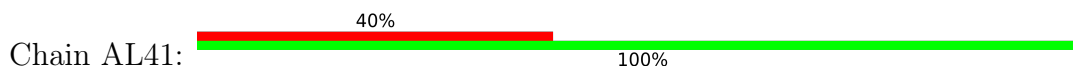
- Molecule 42: 60S ribosomal protein L39



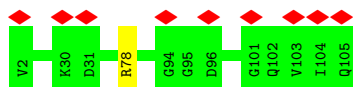
- Molecule 43: Large ribosomal subunit protein eL40



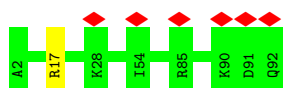
- Molecule 44: eL41



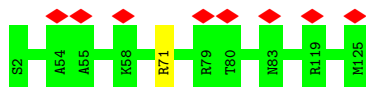
- Molecule 45: eL42



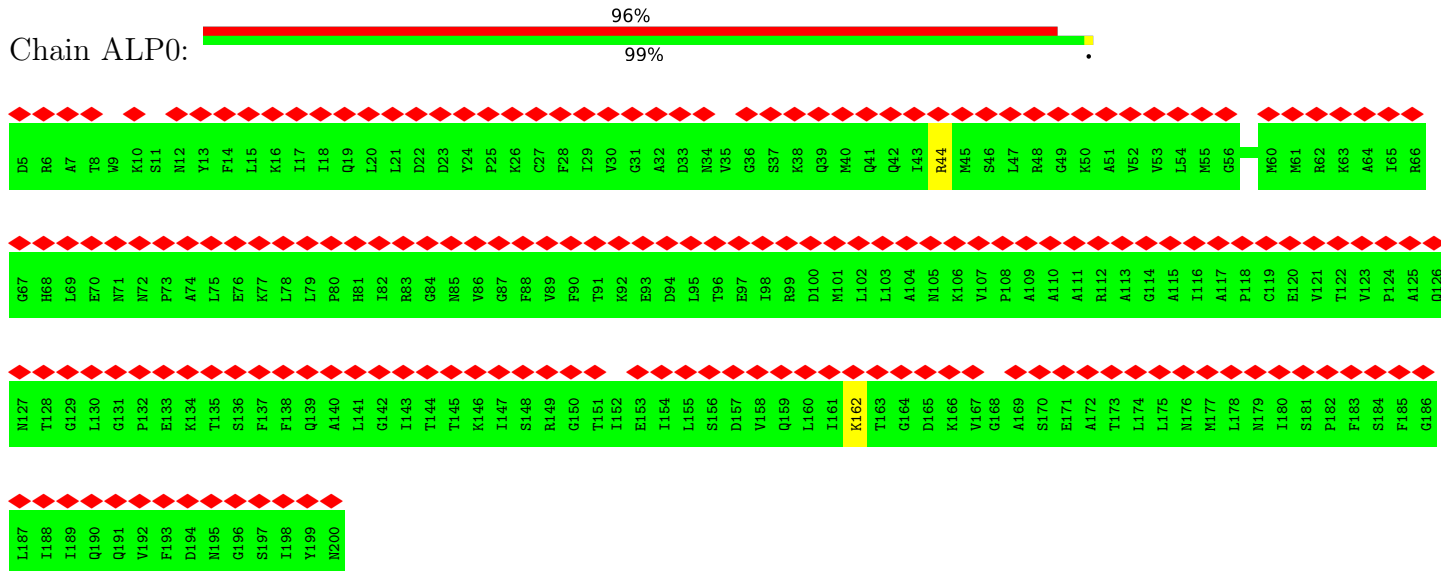
- Molecule 46: 60S ribosomal protein L37a



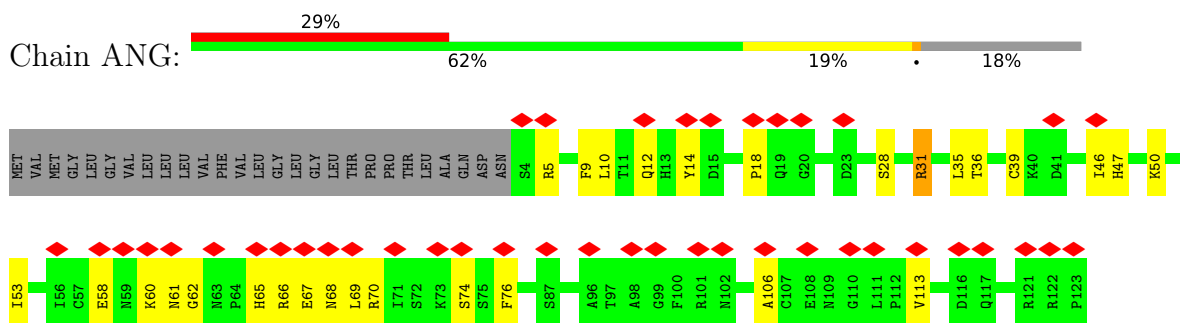
- Molecule 47: 60S ribosomal protein L28



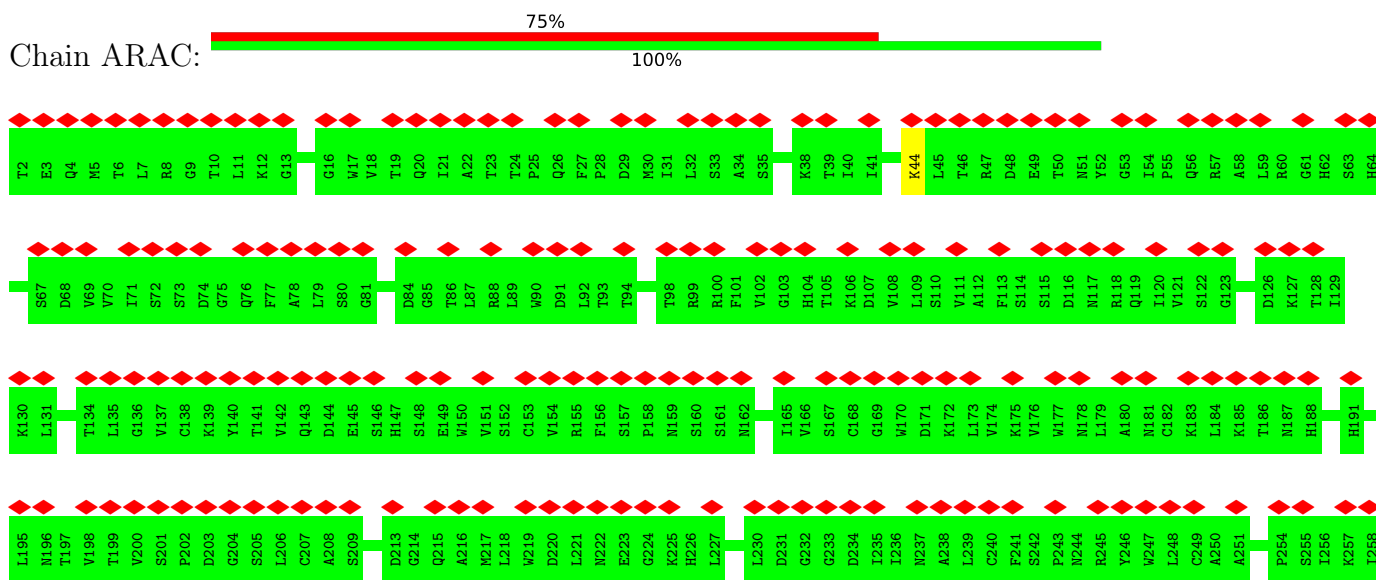
• Molecule 48: 60S acidic ribosomal protein P0

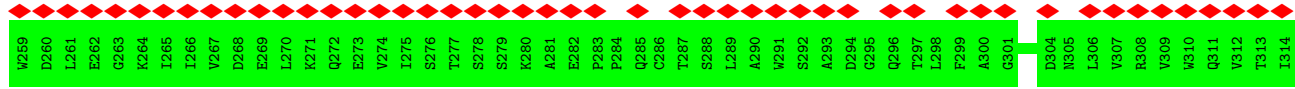


• Molecule 49: Angiogenin

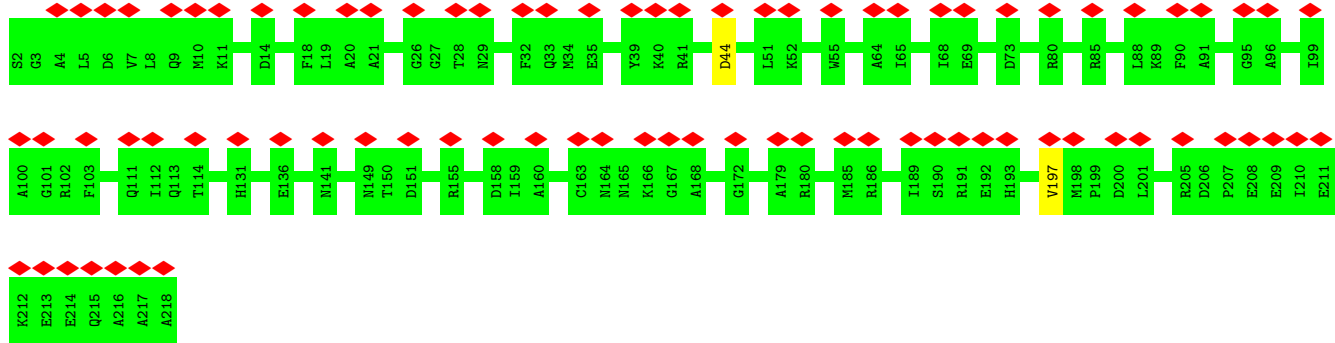


• Molecule 50: Receptor of activated protein C kinase 1

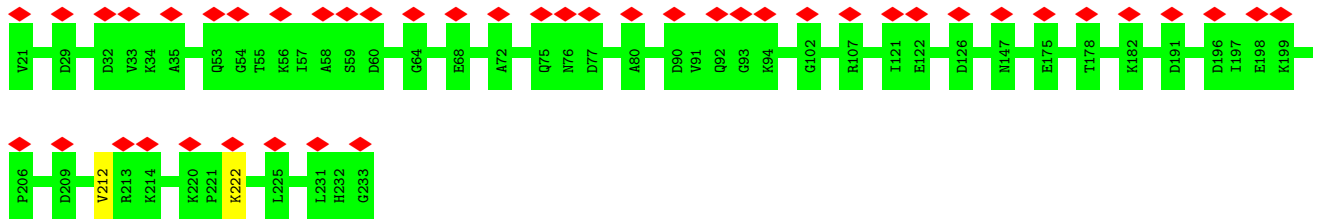




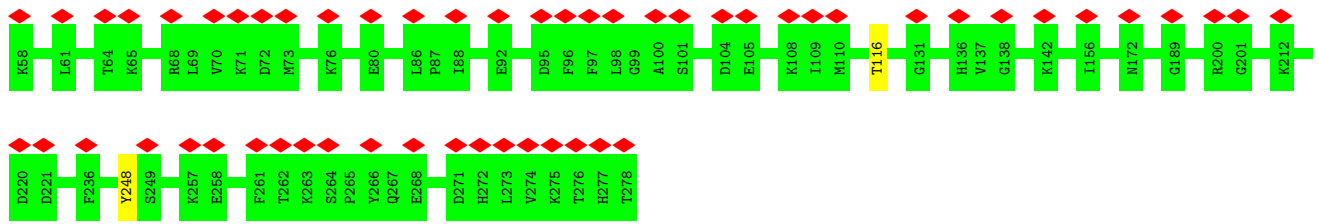
• Molecule 51: 40S_SA_C domain-containing protein



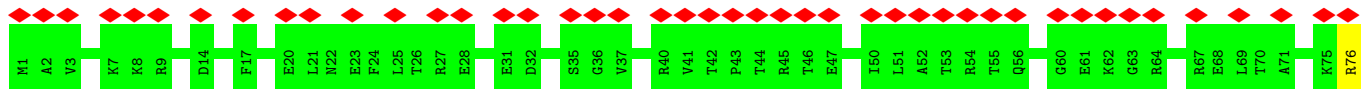
• Molecule 52: 40S ribosomal protein S3a

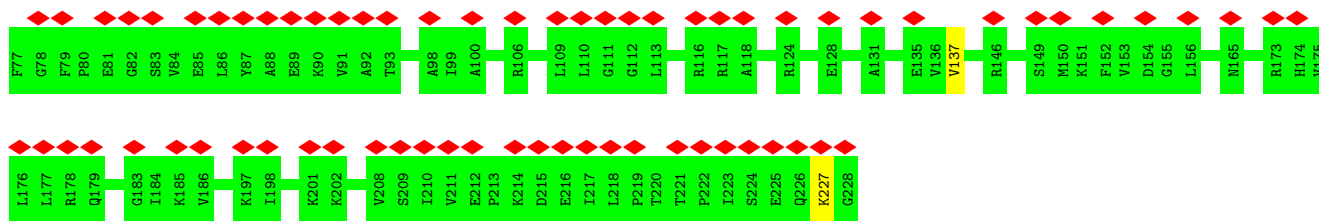


• Molecule 53: 40S ribosomal protein S2

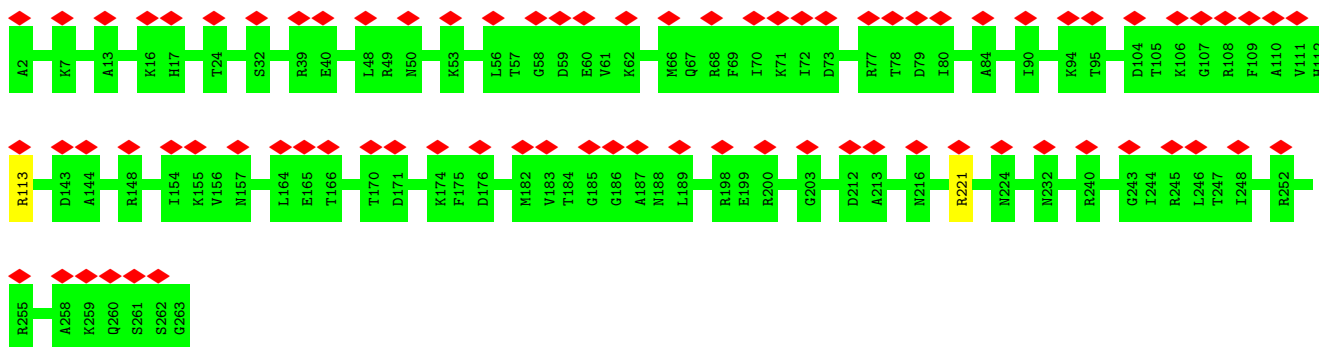


• Molecule 54: 40S ribosomal protein S3

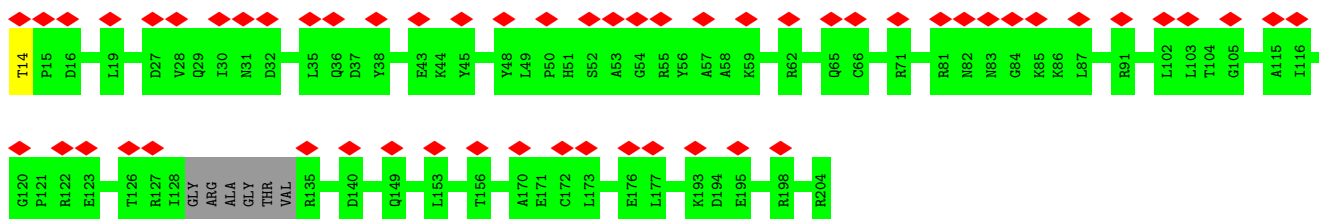




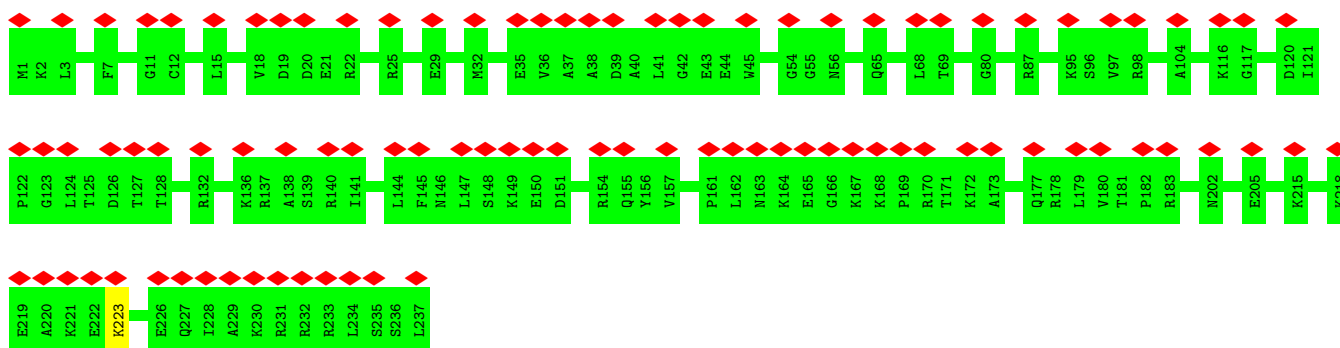
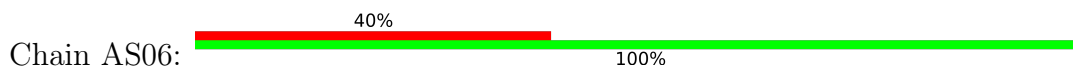
- Molecule 55: 40S ribosomal protein S4



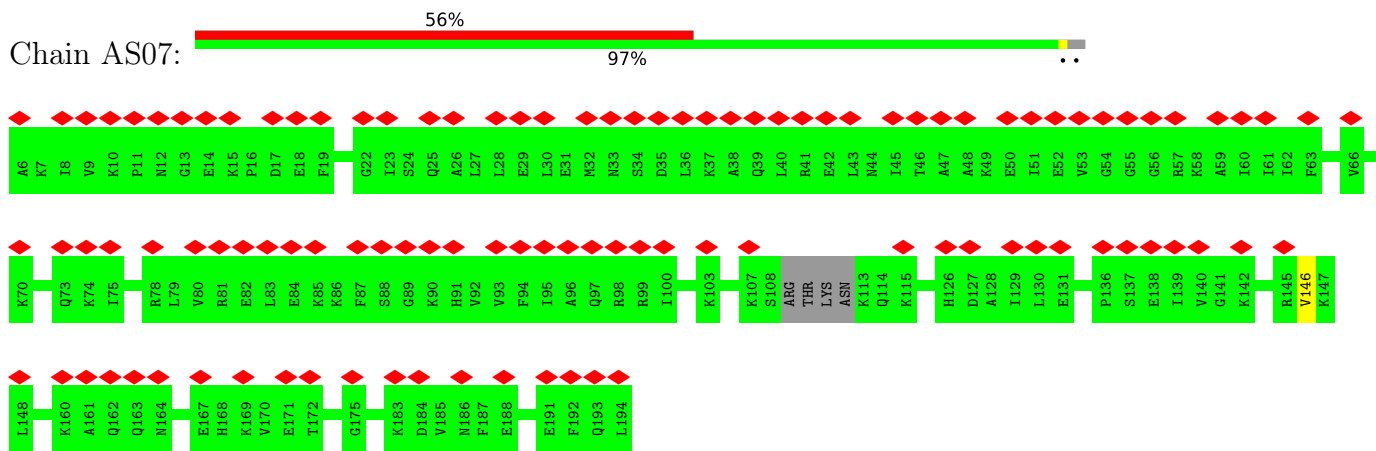
- Molecule 56: Ribosomal protein S5



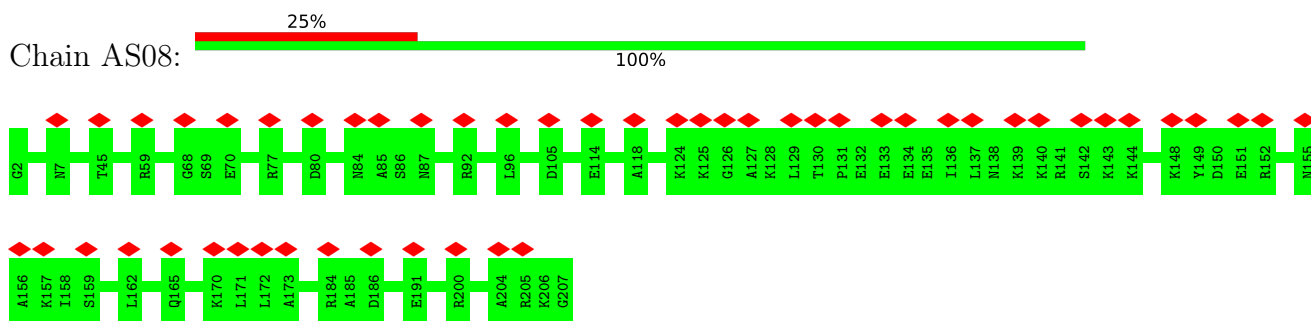
- Molecule 57: 40S ribosomal protein S6



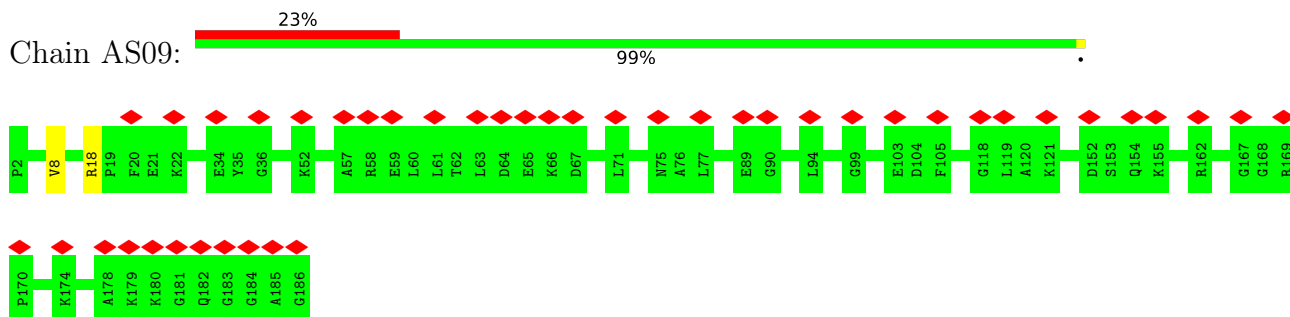
- Molecule 58: Small ribosomal subunit protein eS7



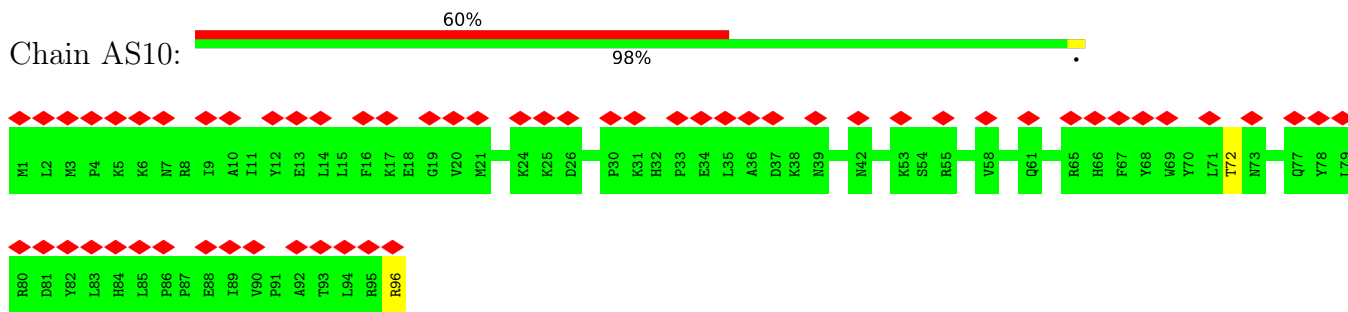
• Molecule 59: 40S ribosomal protein S8



• Molecule 60: 40S ribosomal protein S9

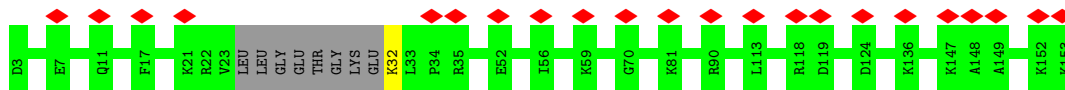


• Molecule 61: 40S ribosomal protein S10

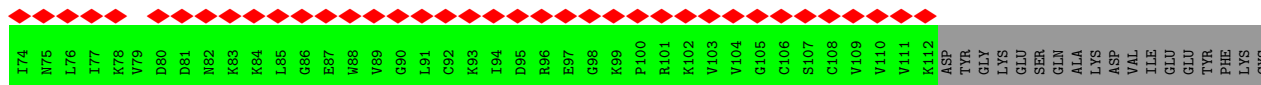
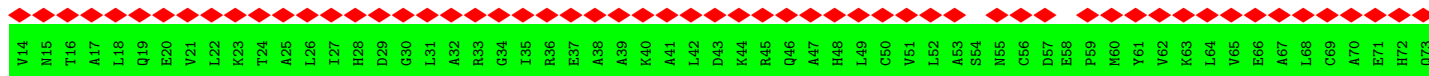
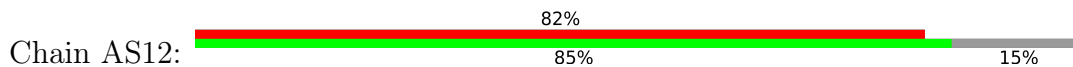


• Molecule 62: 40S ribosomal protein S11

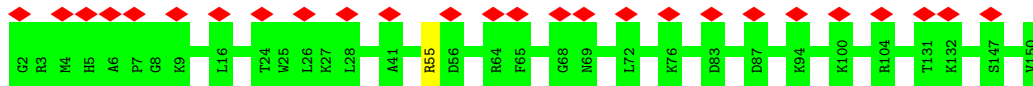




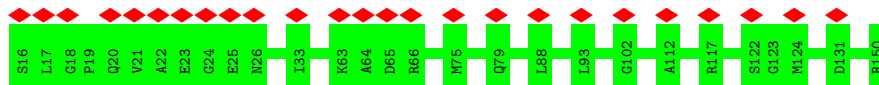
• Molecule 63: 40S ribosomal protein S12



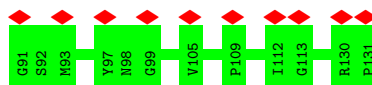
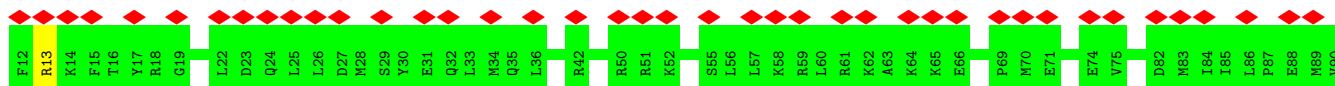
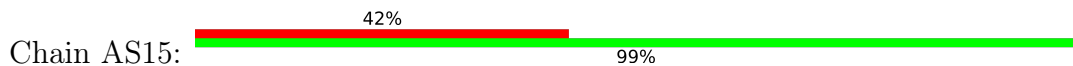
• Molecule 64: 40S ribosomal protein S13



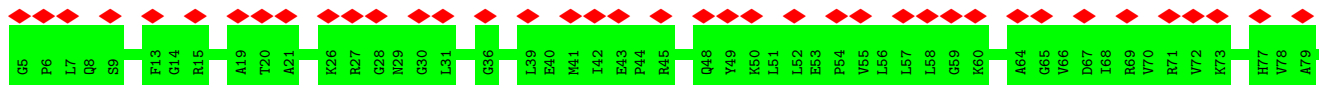
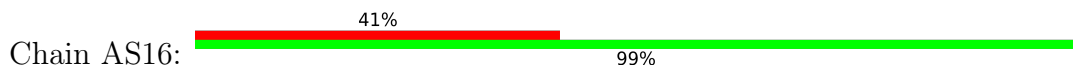
• Molecule 65: Small ribosomal subunit protein uS11

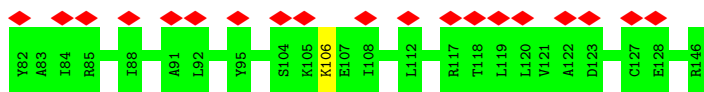


• Molecule 66: 40S ribosomal protein S15

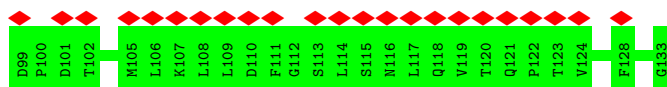
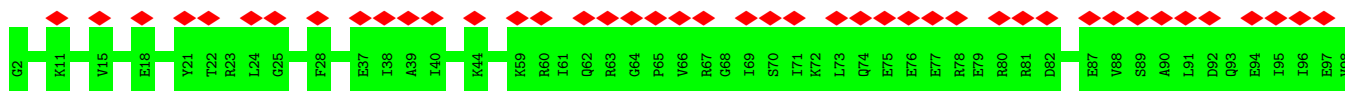


• Molecule 67: Small ribosomal subunit protein uS9

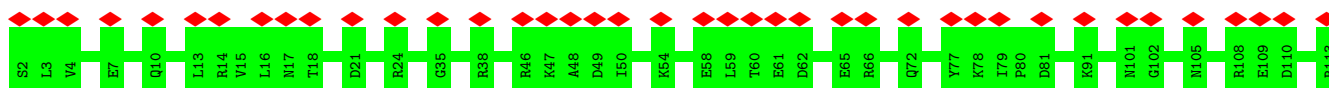




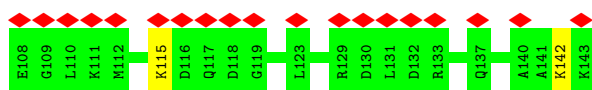
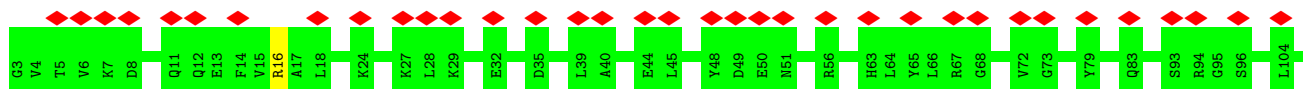
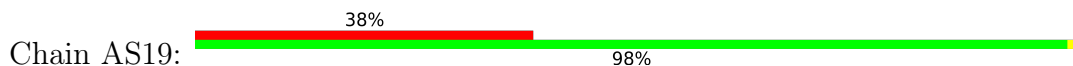
- Molecule 68: 40S ribosomal protein S17



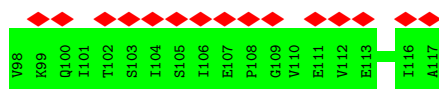
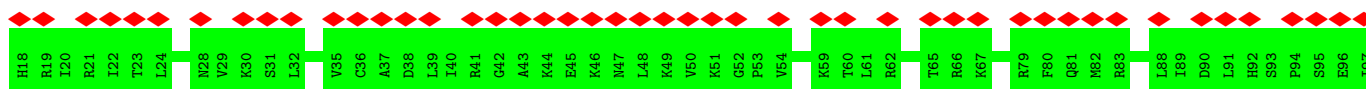
- Molecule 69: 40S ribosomal protein S18



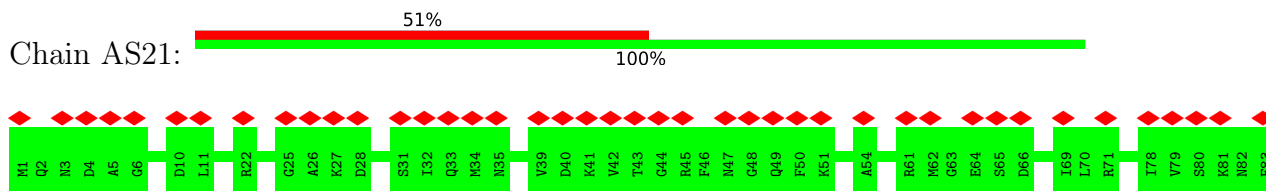
- Molecule 70: Small ribosomal subunit protein eS19



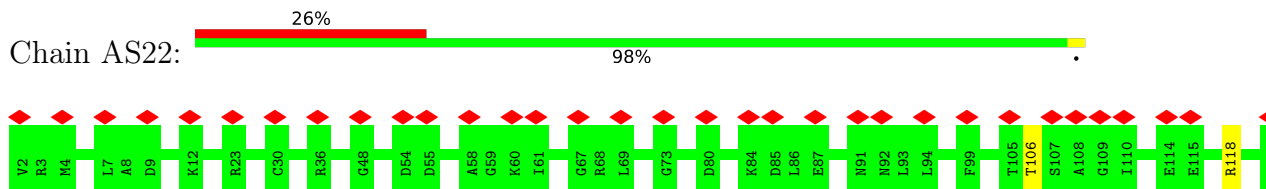
- Molecule 71: 40S ribosomal protein S20



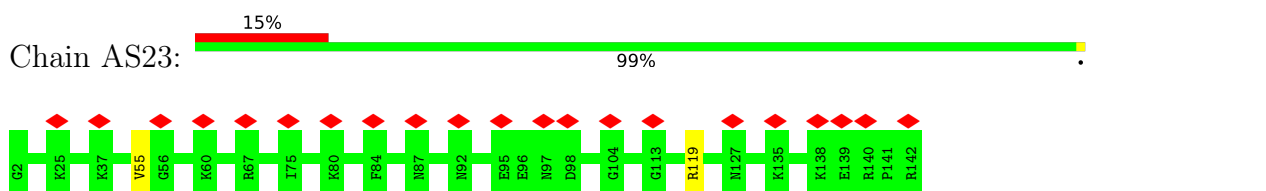
- Molecule 72: eS21



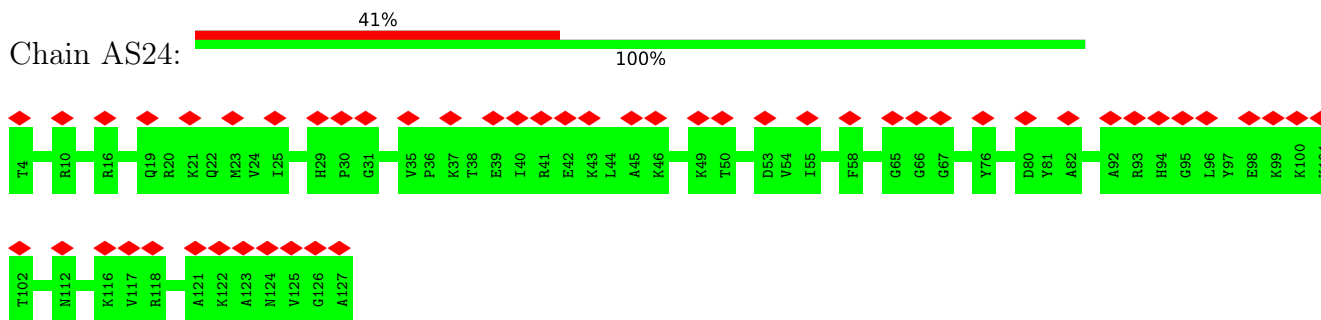
• Molecule 73: 40S ribosomal protein S15a



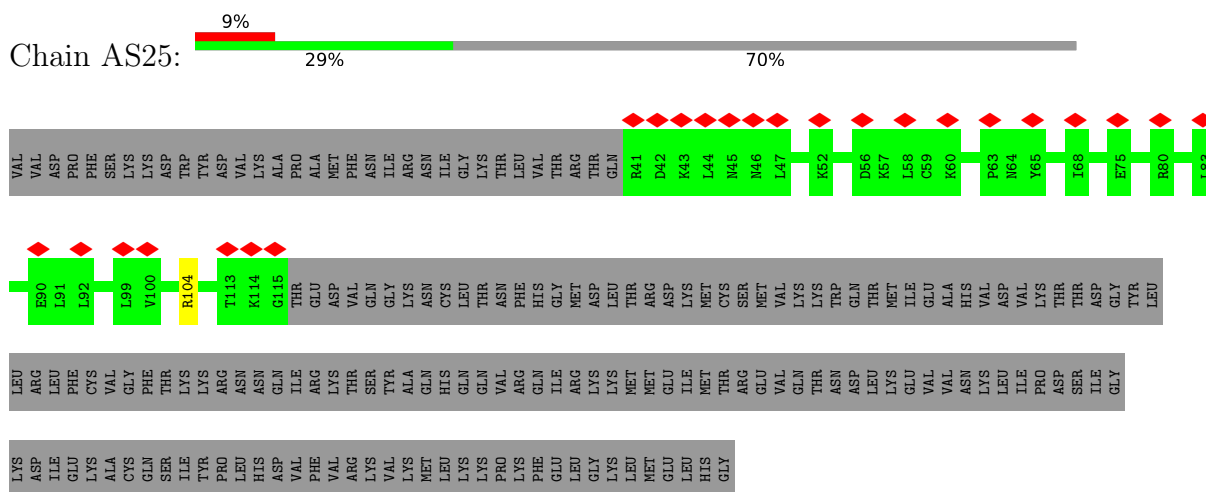
• Molecule 74: 40S ribosomal protein S23



• Molecule 75: 40S ribosomal protein S24



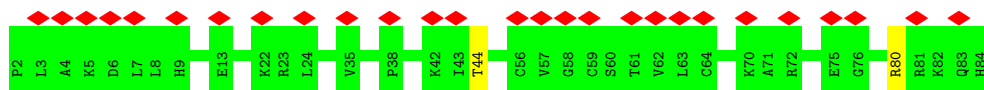
• Molecule 76: 40S ribosomal protein S25



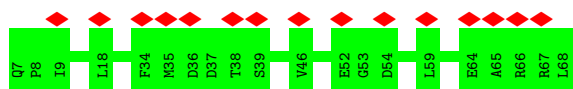
• Molecule 77: eS26



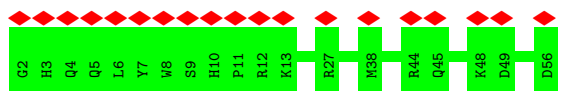
• Molecule 78: 40S ribosomal protein S27



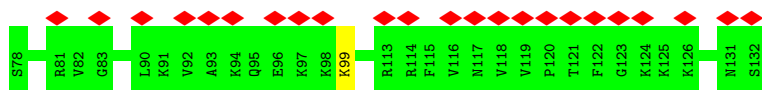
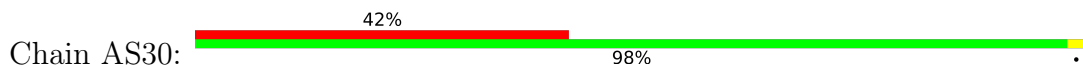
• Molecule 79: 40S ribosomal protein S28



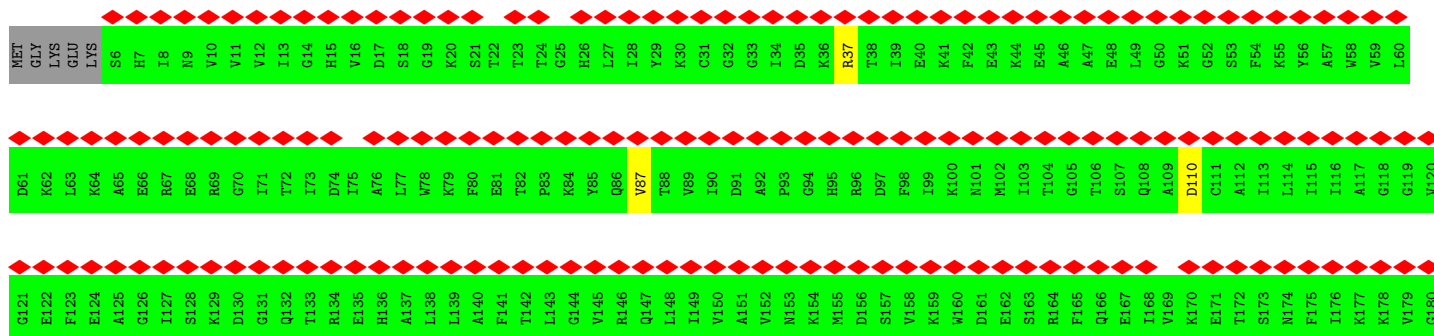
• Molecule 80: 40S ribosomal protein S29



• Molecule 81: 40S ribosomal protein S30



• Molecule 82: Elongation factor 1-alpha



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3604	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	20.347	Depositor
Minimum map value	-9.072	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.110	Depositor
Recommended contour level	4	Depositor
Map size (\AA)	528.96, 528.96, 528.96	wwPDB
Map dimensions	608, 608, 608	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.87000006, 0.87000006, 0.87000006	Depositor

5 Model quality

5.1 Standard geometry

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	A18S	0.20	0/40369	0.31	0/62910
2	A28S	0.23	0/85336	0.31	0/133086
3	A58S	0.23	0/3581	0.29	0/5577
4	A5S	0.20	0/2858	0.26	0/4455
5	AL02	0.27	0/1936	0.55	0/2596
6	AL03	0.26	0/3240	0.51	0/4339
7	AL04	0.25	0/2937	0.50	2/3946 (0.1%)
8	AL05	0.21	0/2437	0.49	0/3264
9	AL06	0.22	0/1762	0.51	0/2362
10	AL07	0.24	0/1911	0.51	0/2549
11	AL08	0.22	0/1910	0.55	0/2569
12	AL09	0.25	0/1535	0.57	0/2063
13	AL10	0.23	0/1702	0.47	0/2272
14	AL11	0.22	0/1384	0.52	0/1850
15	AL12	0.23	0/1174	0.67	2/1582 (0.1%)
16	AL13	0.24	0/1733	0.54	0/2316
17	AL14	0.23	0/1158	0.51	0/1547
18	AL15	0.25	0/1746	0.53	0/2338
19	AL16	0.25	0/1662	0.52	0/2222
20	AL17	0.25	0/1268	0.51	0/1700
21	AL18	0.23	0/1539	0.52	0/2054
22	AL19	0.22	0/1524	0.53	0/2013
23	AL20	0.23	0/1501	0.48	0/2012
24	AL21	0.24	0/1326	0.50	0/1770
25	AL22	0.20	0/823	0.51	0/1104
26	AL23	0.26	0/993	0.54	0/1332
27	AL24	0.28	0/541	0.56	0/720
28	AL25	0.23	0/984	0.47	0/1323
29	AL26	0.24	0/1132	0.53	0/1504
30	AL27	0.21	0/1130	0.50	0/1507
31	AL28	0.25	0/1191	0.49	0/1590
32	AL29	0.21	0/861	0.49	0/1138
33	AL30	0.23	0/771	0.44	0/1034
34	AL31	0.26	0/903	0.57	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AL32	0.25	0/1071	0.52	0/1429
36	AL33	0.28	0/895	0.55	0/1198
37	AL34	0.24	0/916	0.51	0/1220
38	AL35	0.22	0/1021	0.52	0/1348
39	AL36	0.20	0/841	0.54	1/1112 (0.1%)
40	AL37	0.28	0/720	0.50	0/952
41	AL38	0.21	0/575	0.52	0/761
42	AL39	0.24	0/459	0.49	0/608
43	AL40	0.22	0/435	0.50	0/575
44	AL41	0.23	0/240	0.54	0/305
45	AL42	0.24	0/864	0.55	0/1140
46	AL43	0.25	0/718	0.53	0/953
47	ALNW	0.24	0/1010	0.51	0/1354
48	ALP0	0.19	0/1530	0.51	0/2064
49	ANG	0.30	0/979	0.72	2/1322 (0.2%)
50	ARAC	0.24	1/2493 (0.0%)	0.52	0/3394
51	AS00	0.24	0/1747	0.63	2/2374 (0.1%)
52	AS01	0.23	0/1756	0.55	0/2350
53	AS02	0.23	0/1753	0.52	0/2369
54	AS03	0.21	0/1796	0.51	0/2417
55	AS04	0.21	0/2117	0.51	0/2847
56	AS05	0.23	0/1492	0.59	0/2005
57	AS06	0.20	0/1946	0.54	0/2590
58	AS07	0.23	0/1510	0.55	0/2022
59	AS08	0.22	0/1715	0.53	0/2287
60	AS09	0.21	0/1550	0.50	0/2069
61	AS10	0.25	0/834	0.62	0/1125
62	AS11	0.24	0/1195	0.52	0/1597
63	AS12	0.21	0/765	0.60	0/1029
64	AS13	0.20	0/1226	0.51	0/1649
65	AS14	0.24	0/1017	0.56	0/1365
66	AS15	0.22	0/1017	0.56	0/1358
67	AS16	0.21	0/1146	0.54	0/1534
68	AS17	0.23	0/1082	0.52	0/1452
69	AS18	0.23	0/1208	0.61	0/1618
70	AS19	0.22	0/1115	0.53	0/1493
71	AS20	0.22	0/805	0.52	0/1081
72	AS21	0.21	0/643	0.49	0/860
73	AS22	0.25	0/1051	0.53	0/1406
74	AS23	0.23	0/1116	0.53	0/1490
75	AS24	0.20	0/1028	0.52	0/1366
76	AS25	0.27	0/604	0.53	0/810
77	AS26	0.24	0/828	0.50	0/1109

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	AS27	0.22	0/665	0.54	0/891
79	AS28	0.28	0/490	0.56	0/656
80	AS29	0.24	0/470	0.55	0/623
81	AS30	0.19	0/447	0.50	0/587
82	EF1A	0.41	0/3376	0.87	12/4560 (0.3%)
83	ETRN	0.16	0/1832	0.29	0/2855
83	PTRN	0.18	0/1832	0.28	0/2855
84	MRNA	0.19	0/229	0.34	0/353
85	TIRN	0.14	0/1663	0.28	0/2590
All	All	0.23	1/236691 (0.0%)	0.41	21/347237 (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
15	AL12	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	ARAC	44	LYS	CA-CB	6.26	1.61	1.53

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	AS00	197	VAL	CA-C-N	10.99	137.39	120.68
51	AS00	197	VAL	C-N-CA	10.99	137.39	120.68
82	EF1A	347	HIS	CA-C-N	8.63	130.63	119.84
82	EF1A	347	HIS	C-N-CA	8.63	130.63	119.84
82	EF1A	429	GLN	N-CA-C	7.10	117.89	107.88

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	AL12	124	GLU	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	A18S	36103	0	0	0	0
2	A28S	76286	0	0	0	0
3	A58S	3208	0	0	0	0
4	A5S	2558	0	1296	11	0
5	AL02	1898	0	0	0	0
6	AL03	3172	0	0	0	0
7	AL04	2883	0	0	0	0
8	AL05	2391	0	0	0	0
9	AL06	1729	0	0	0	0
10	AL07	1875	0	0	0	0
11	AL08	1879	0	0	0	0
12	AL09	1516	0	0	0	0
13	AL10	1664	0	0	0	0
14	AL11	1361	0	0	0	0
15	AL12	1160	0	0	0	0
16	AL13	1702	0	0	0	0
17	AL14	1137	0	0	0	0
18	AL15	1701	0	0	0	0
19	AL16	1630	0	0	0	0
20	AL17	1242	0	0	0	0
21	AL18	1515	0	0	0	0
22	AL19	1508	0	0	0	0
23	AL20	1462	0	0	0	0
24	AL21	1298	0	0	0	0
25	AL22	809	0	0	0	0
26	AL23	979	0	0	0	0
27	AL24	528	0	0	0	0
28	AL25	967	0	0	0	0
29	AL26	1115	0	0	0	0
30	AL27	1107	0	0	0	0
31	AL28	1162	0	0	0	0
32	AL29	848	0	0	0	0
33	AL30	761	0	0	0	0
34	AL31	888	0	0	0	0
35	AL32	1053	0	0	0	0
36	AL33	876	0	0	0	0
37	AL34	906	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	AL35	1013	0	0	0	0
39	AL36	830	0	0	0	0
40	AL37	705	0	0	0	0
41	AL38	569	0	0	0	0
42	AL39	447	0	0	0	0
43	AL40	429	0	0	0	0
44	AL41	239	0	0	0	0
45	AL42	851	0	0	0	0
46	AL43	708	0	0	0	0
47	ALNW	994	0	0	0	0
48	ALP0	1507	0	0	0	0
49	ANG	955	0	922	14	0
50	ARAC	2436	0	0	0	0
51	AS00	1710	0	0	0	0
52	AS01	1729	0	0	0	0
53	AS02	1716	0	0	0	0
54	AS03	1768	0	0	0	0
55	AS04	2075	0	0	0	0
56	AS05	1471	0	0	0	0
57	AS06	1923	0	0	0	0
58	AS07	1488	0	0	0	0
59	AS08	1686	0	0	0	0
60	AS09	1525	0	0	0	0
61	AS10	810	0	0	0	0
62	AS11	1175	0	0	0	0
63	AS12	758	0	0	0	0
64	AS13	1202	0	0	0	0
65	AS14	1004	0	0	0	0
66	AS15	997	0	0	0	0
67	AS16	1128	0	0	0	0
68	AS17	1068	0	0	0	0
69	AS18	1190	0	0	0	0
70	AS19	1097	0	0	0	0
71	AS20	795	0	0	0	0
72	AS21	636	0	0	0	0
73	AS22	1034	0	0	0	0
74	AS23	1098	0	0	0	0
75	AS24	1011	0	0	0	0
76	AS25	598	0	0	0	0
77	AS26	814	0	0	0	0
78	AS27	651	0	0	0	0
79	AS28	488	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	AS29	459	0	0	0	0
81	AS30	443	0	0	0	0
82	EF1A	3311	0	0	0	0
83	ETRN	1640	0	0	0	0
83	PTRN	1640	0	0	0	0
84	MRNA	207	0	0	0	0
85	TIRN	1491	0	0	0	0
All	All	220396	0	2218	25	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 8.

The worst 5 of 25 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)
4:A5S:38:U:N3	4:A5S:41:G:OP2	2.30	0.60
49:ANG:5:ARG:HE	49:ANG:113:VAL:HG21	1.67	0.59
49:ANG:50:LYS:HA	49:ANG:53:ILE:HD12	1.85	0.59
4:A5S:23:A:N3	4:A5S:118:C:O2'	2.34	0.56
49:ANG:28:SER:O	49:ANG:31:ARG:NH2	2.37	0.56

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AL02	246/248 (99%)	228 (93%)	18 (7%)	0	100	100
6	AL03	392/394 (100%)	375 (96%)	17 (4%)	0	100	100
7	AL04	360/362 (99%)	345 (96%)	15 (4%)	0	100	100
8	AL05	291/293 (99%)	278 (96%)	12 (4%)	1 (0%)	36	65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	AL06	208/251 (83%)	202 (97%)	6 (3%)	0	100	100
10	AL07	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
11	AL08	229/240 (95%)	218 (95%)	11 (5%)	0	100	100
12	AL09	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
13	AL10	201/213 (94%)	190 (94%)	11 (6%)	0	100	100
14	AL11	168/170 (99%)	165 (98%)	3 (2%)	0	100	100
15	AL12	151/153 (99%)	133 (88%)	18 (12%)	0	100	100
16	AL13	208/210 (99%)	199 (96%)	8 (4%)	1 (0%)	24	56
17	AL14	136/138 (99%)	127 (93%)	9 (7%)	0	100	100
18	AL15	201/203 (99%)	189 (94%)	12 (6%)	0	100	100
19	AL16	197/199 (99%)	190 (96%)	7 (4%)	0	100	100
20	AL17	151/153 (99%)	143 (95%)	8 (5%)	0	100	100
21	AL18	185/187 (99%)	173 (94%)	12 (6%)	0	100	100
22	AL19	178/180 (99%)	176 (99%)	2 (1%)	0	100	100
23	AL20	174/176 (99%)	164 (94%)	10 (6%)	0	100	100
24	AL21	157/159 (99%)	152 (97%)	5 (3%)	0	100	100
25	AL22	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
26	AL23	129/131 (98%)	122 (95%)	7 (5%)	0	100	100
27	AL24	61/121 (50%)	58 (95%)	3 (5%)	0	100	100
28	AL25	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
29	AL26	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
30	AL27	133/135 (98%)	126 (95%)	7 (5%)	0	100	100
31	AL28	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
32	AL29	100/245 (41%)	98 (98%)	2 (2%)	0	100	100
33	AL30	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
34	AL31	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
35	AL32	126/128 (98%)	119 (94%)	7 (6%)	0	100	100
36	AL33	107/109 (98%)	101 (94%)	6 (6%)	0	100	100
37	AL34	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
38	AL35	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	16	48
39	AL36	100/102 (98%)	99 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	AL37	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
41	AL38	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
42	AL39	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
43	AL40	50/52 (96%)	50 (100%)	0	0	100	100
44	AL41	23/25 (92%)	23 (100%)	0	0	100	100
45	AL42	102/104 (98%)	96 (94%)	6 (6%)	0	100	100
46	AL43	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
47	ALNW	122/124 (98%)	114 (93%)	8 (7%)	0	100	100
48	ALP0	194/196 (99%)	182 (94%)	12 (6%)	0	100	100
49	ANG	118/147 (80%)	109 (92%)	8 (7%)	1 (1%)	16	48
50	ARAC	311/313 (99%)	290 (93%)	21 (7%)	0	100	100
51	AS00	215/217 (99%)	206 (96%)	9 (4%)	0	100	100
52	AS01	211/213 (99%)	202 (96%)	9 (4%)	0	100	100
53	AS02	219/221 (99%)	212 (97%)	7 (3%)	0	100	100
54	AS03	226/228 (99%)	219 (97%)	7 (3%)	0	100	100
55	AS04	260/262 (99%)	251 (96%)	9 (4%)	0	100	100
56	AS05	181/191 (95%)	161 (89%)	20 (11%)	0	100	100
57	AS06	235/237 (99%)	228 (97%)	7 (3%)	0	100	100
58	AS07	181/189 (96%)	175 (97%)	6 (3%)	0	100	100
59	AS08	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
60	AS09	183/185 (99%)	179 (98%)	4 (2%)	0	100	100
61	AS10	94/96 (98%)	87 (93%)	7 (7%)	0	100	100
62	AS11	139/151 (92%)	136 (98%)	3 (2%)	0	100	100
63	AS12	97/117 (83%)	92 (95%)	5 (5%)	0	100	100
64	AS13	147/149 (99%)	142 (97%)	5 (3%)	0	100	100
65	AS14	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
66	AS15	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
67	AS16	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
68	AS17	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
69	AS18	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
70	AS19	139/141 (99%)	134 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
71	AS20	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
72	AS21	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
73	AS22	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
74	AS23	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
75	AS24	122/124 (98%)	118 (97%)	4 (3%)	0	100	100
76	AS25	73/254 (29%)	69 (94%)	4 (6%)	0	100	100
77	AS26	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
78	AS27	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
79	AS28	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
80	AS29	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
81	AS30	53/55 (96%)	49 (92%)	4 (8%)	0	100	100
82	EF1A	424/458 (93%)	408 (96%)	16 (4%)	0	100	100
All	All	11935/12632 (94%)	11387 (95%)	544 (5%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
49	ANG	66	ARG
8	AL05	37	VAL
16	AL13	64	VAL
38	AL35	89	ARG

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	AL02	190/190 (100%)	189 (100%)	1 (0%)	81	80
6	AL03	342/342 (100%)	340 (99%)	2 (1%)	78	79
7	AL04	302/302 (100%)	299 (99%)	3 (1%)	68	74
8	AL05	247/247 (100%)	247 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	AL06	190/223 (85%)	190 (100%)	0	100	100
10	AL07	196/196 (100%)	193 (98%)	3 (2%)	57	68
11	AL08	200/205 (98%)	198 (99%)	2 (1%)	68	74
12	AL09	169/169 (100%)	169 (100%)	0	100	100
13	AL10	175/180 (97%)	174 (99%)	1 (1%)	78	79
14	AL11	143/143 (100%)	143 (100%)	0	100	100
15	AL12	126/126 (100%)	125 (99%)	1 (1%)	73	76
16	AL13	175/175 (100%)	174 (99%)	1 (1%)	78	79
17	AL14	117/117 (100%)	117 (100%)	0	100	100
18	AL15	171/171 (100%)	170 (99%)	1 (1%)	78	79
19	AL16	171/171 (100%)	169 (99%)	2 (1%)	63	72
20	AL17	134/134 (100%)	134 (100%)	0	100	100
21	AL18	164/164 (100%)	163 (99%)	1 (1%)	78	79
22	AL19	159/159 (100%)	159 (100%)	0	100	100
23	AL20	157/157 (100%)	157 (100%)	0	100	100
24	AL21	139/139 (100%)	135 (97%)	4 (3%)	37	57
25	AL22	89/89 (100%)	88 (99%)	1 (1%)	65	73
26	AL23	101/101 (100%)	100 (99%)	1 (1%)	68	74
27	AL24	55/100 (55%)	55 (100%)	0	100	100
28	AL25	106/106 (100%)	105 (99%)	1 (1%)	70	75
29	AL26	124/124 (100%)	123 (99%)	1 (1%)	73	76
30	AL27	117/117 (100%)	117 (100%)	0	100	100
31	AL28	119/119 (100%)	115 (97%)	4 (3%)	32	55
32	AL29	84/184 (46%)	83 (99%)	1 (1%)	63	72
33	AL30	84/84 (100%)	84 (100%)	0	100	100
34	AL31	98/98 (100%)	98 (100%)	0	100	100
35	AL32	114/114 (100%)	113 (99%)	1 (1%)	70	75
36	AL33	88/88 (100%)	88 (100%)	0	100	100
37	AL34	98/98 (100%)	94 (96%)	4 (4%)	27	52
38	AL35	109/109 (100%)	109 (100%)	0	100	100
39	AL36	86/86 (100%)	85 (99%)	1 (1%)	63	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	AL37	73/73 (100%)	73 (100%)	0	100	100
41	AL38	64/64 (100%)	64 (100%)	0	100	100
42	AL39	47/47 (100%)	46 (98%)	1 (2%)	47	64
43	AL40	48/48 (100%)	48 (100%)	0	100	100
44	AL41	24/24 (100%)	24 (100%)	0	100	100
45	AL42	92/92 (100%)	91 (99%)	1 (1%)	65	73
46	AL43	74/74 (100%)	73 (99%)	1 (1%)	59	70
47	ALNW	108/108 (100%)	107 (99%)	1 (1%)	70	75
48	ALP0	164/164 (100%)	162 (99%)	2 (1%)	63	72
49	ANG	105/129 (81%)	102 (97%)	3 (3%)	37	57
50	ARAC	272/272 (100%)	272 (100%)	0	100	100
51	AS00	180/181 (99%)	179 (99%)	1 (1%)	78	79
52	AS01	194/194 (100%)	192 (99%)	2 (1%)	68	74
53	AS02	187/187 (100%)	185 (99%)	2 (1%)	65	73
54	AS03	190/190 (100%)	187 (98%)	3 (2%)	55	68
55	AS04	224/224 (100%)	222 (99%)	2 (1%)	70	75
56	AS05	158/161 (98%)	157 (99%)	1 (1%)	78	79
57	AS06	207/207 (100%)	206 (100%)	1 (0%)	81	80
58	AS07	165/169 (98%)	164 (99%)	1 (1%)	78	79
59	AS08	178/178 (100%)	178 (100%)	0	100	100
60	AS09	161/161 (100%)	159 (99%)	2 (1%)	63	72
61	AS10	87/87 (100%)	85 (98%)	2 (2%)	44	62
62	AS11	130/136 (96%)	129 (99%)	1 (1%)	73	76
63	AS12	83/99 (84%)	83 (100%)	0	100	100
64	AS13	130/130 (100%)	129 (99%)	1 (1%)	73	76
65	AS14	104/105 (99%)	104 (100%)	0	100	100
66	AS15	109/109 (100%)	108 (99%)	1 (1%)	70	75
67	AS16	117/117 (100%)	116 (99%)	1 (1%)	70	75
68	AS17	119/119 (100%)	119 (100%)	0	100	100
69	AS18	125/125 (100%)	125 (100%)	0	100	100
70	AS19	111/111 (100%)	108 (97%)	3 (3%)	39	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	AS20	92/92 (100%)	92 (100%)	0	100	100
72	AS21	67/67 (100%)	67 (100%)	0	100	100
73	AS22	112/112 (100%)	110 (98%)	2 (2%)	51	67
74	AS23	113/113 (100%)	111 (98%)	2 (2%)	51	67
75	AS24	107/107 (100%)	107 (100%)	0	100	100
76	AS25	66/232 (28%)	65 (98%)	1 (2%)	57	68
77	AS26	88/88 (100%)	86 (98%)	2 (2%)	44	62
78	AS27	75/75 (100%)	73 (97%)	2 (3%)	39	59
79	AS28	55/55 (100%)	55 (100%)	0	100	100
80	AS29	48/48 (100%)	48 (100%)	0	100	100
81	AS30	46/46 (100%)	45 (98%)	1 (2%)	45	63
82	EF1A	358/379 (94%)	355 (99%)	3 (1%)	73	76
All	All	10396/10826 (96%)	10313 (99%)	83 (1%)	70	76

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	AS06	223	LYS
73	AS22	118	ARG
60	AS09	8	VAL
66	AS15	13	ARG
77	AS26	18	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A18S	1679/1869 (89%)	384 (22%)	11 (0%)
2	A28S	3533/3601 (98%)	798 (22%)	41 (1%)
3	A58S	149/156 (95%)	29 (19%)	1 (0%)
4	A5S	119/120 (99%)	14 (11%)	0
83	ETR N	76/77 (98%)	18 (23%)	0
83	PTR N	76/77 (98%)	16 (21%)	0
84	MRNA	9/28 (32%)	4 (44%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
85	TIRN	68/76 (89%)	16 (23%)	0
All	All	5709/6004 (95%)	1279 (22%)	53 (0%)

5 of 1279 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A18S	2	A
1	A18S	3	C
1	A18S	4	C
1	A18S	17	C
1	A18S	23	G

5 of 53 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A28S	1329	G
2	A28S	2046	G
2	A28S	4719	G
2	A28S	1370	G
2	A28S	1455	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	A28S	12

The worst 5 of 12 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A28S	1219:G	O3'	1233:G	P	18.77
1	A28S	3976:C	O3'	4035:G	P	15.23
1	A28S	1696:C	O3'	1720:C	P	14.24
1	A28S	1364:U	O3'	1368:A	P	13.99
1	A28S	1180:C	O3'	1183:C	P	9.81

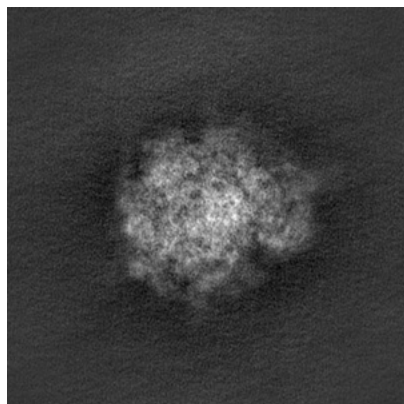
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44464. These allow visual inspection of the internal detail of the map and identification of artifacts.

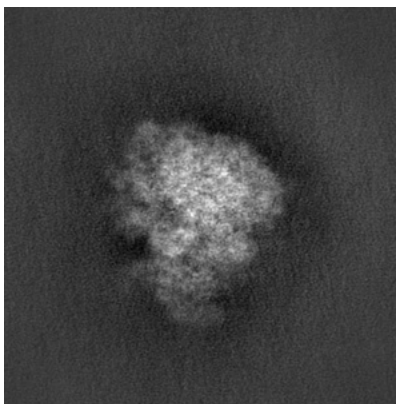
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

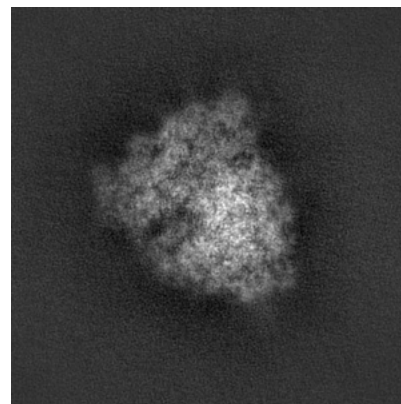
6.1.1 Primary map



X

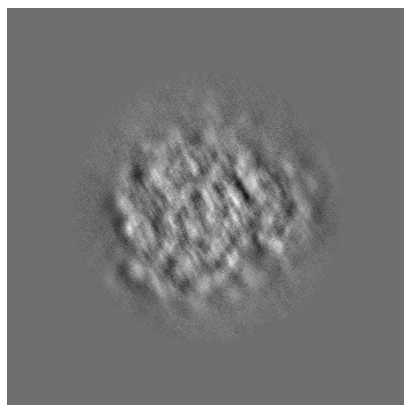


Y

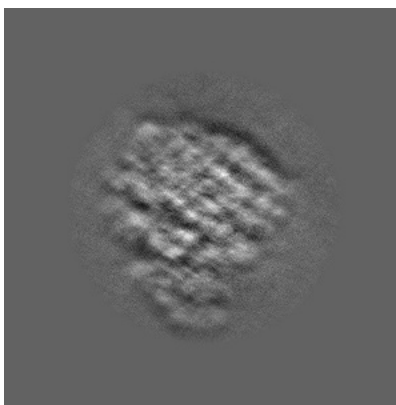


Z

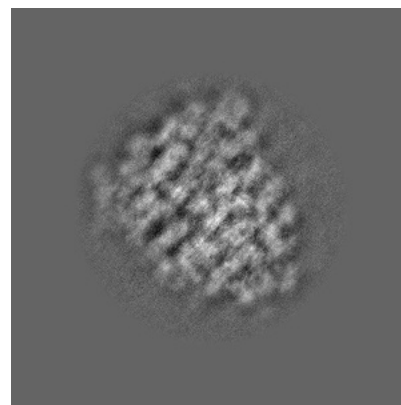
6.1.2 Raw map



X



Y

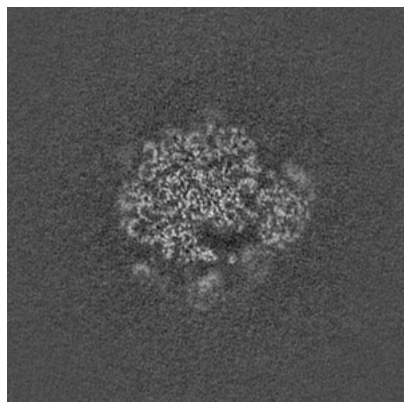


Z

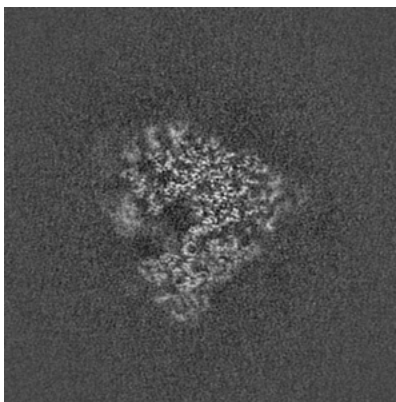
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

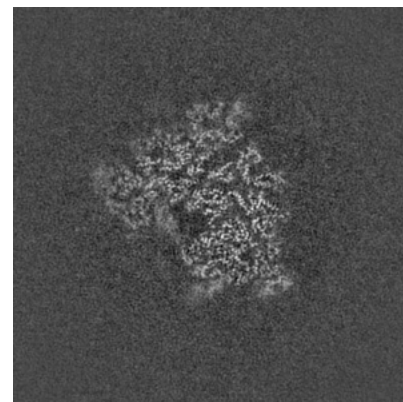
6.2.1 Primary map



X Index: 304

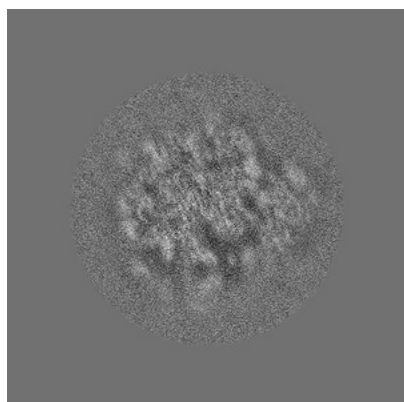


Y Index: 304

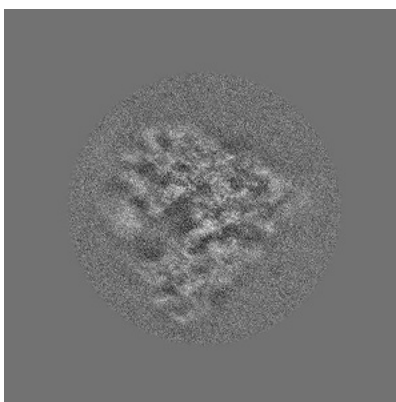


Z Index: 304

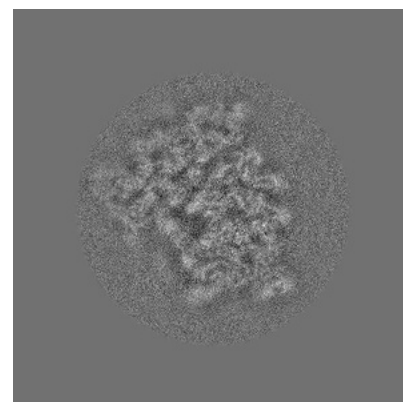
6.2.2 Raw map



X Index: 304



Y Index: 304

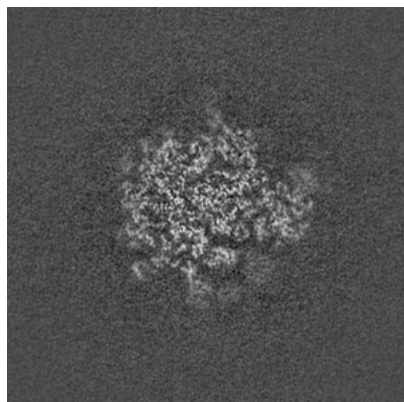


Z Index: 304

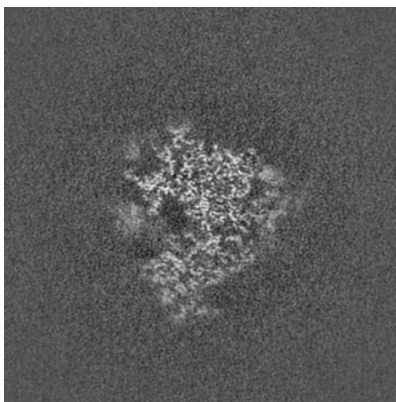
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

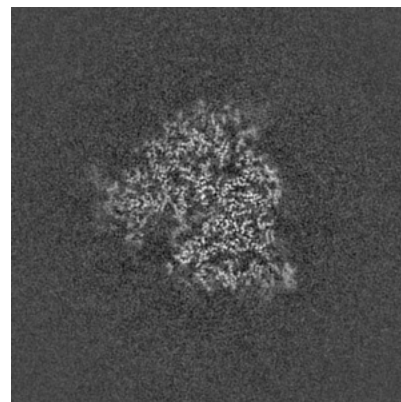
6.3.1 Primary map



X Index: 314

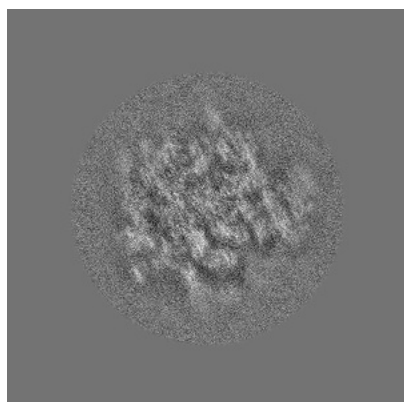


Y Index: 312

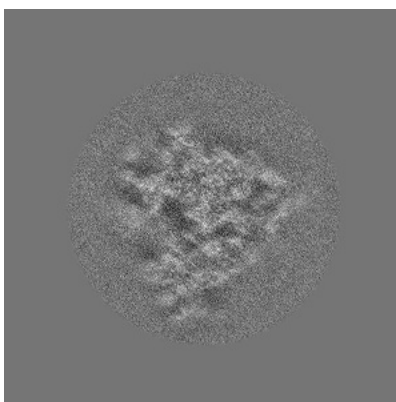


Z Index: 285

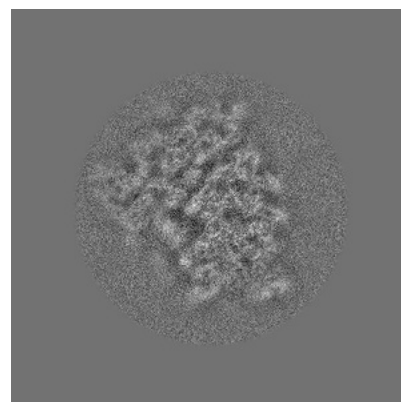
6.3.2 Raw map



X Index: 314



Y Index: 311

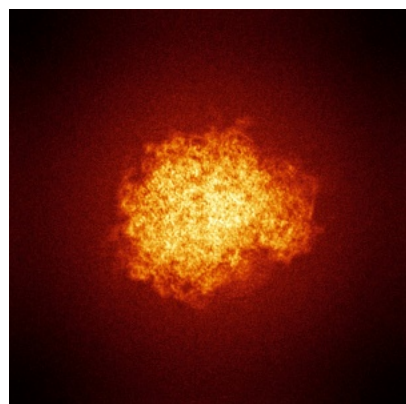


Z Index: 307

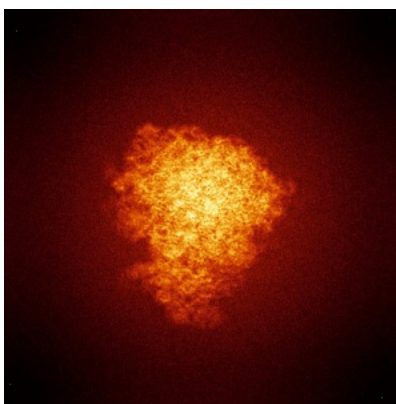
The images above show the largest variance slices of the map in three orthogonal directions.

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

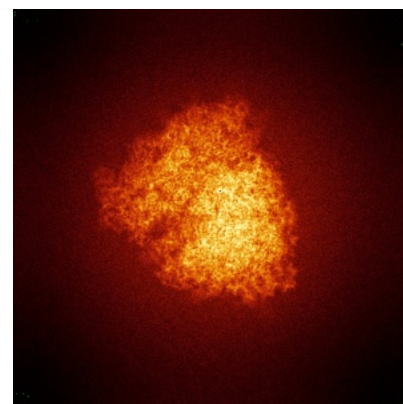
6.4.1 Primary map



X

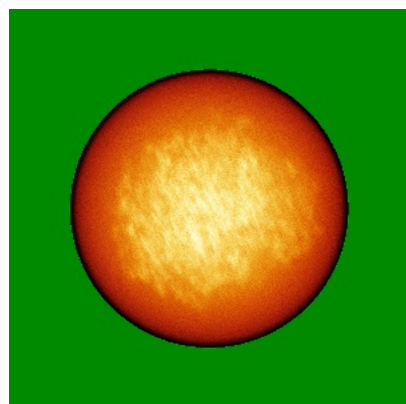


Y

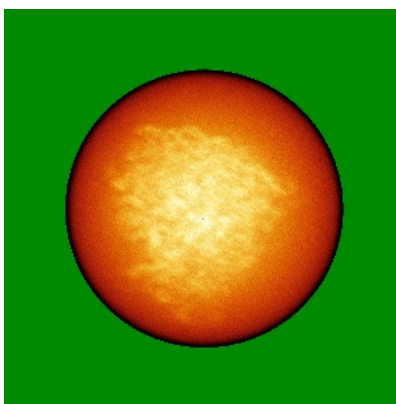


Z

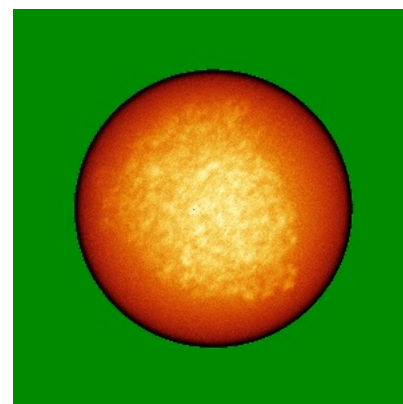
6.4.2 Raw map



X



Y

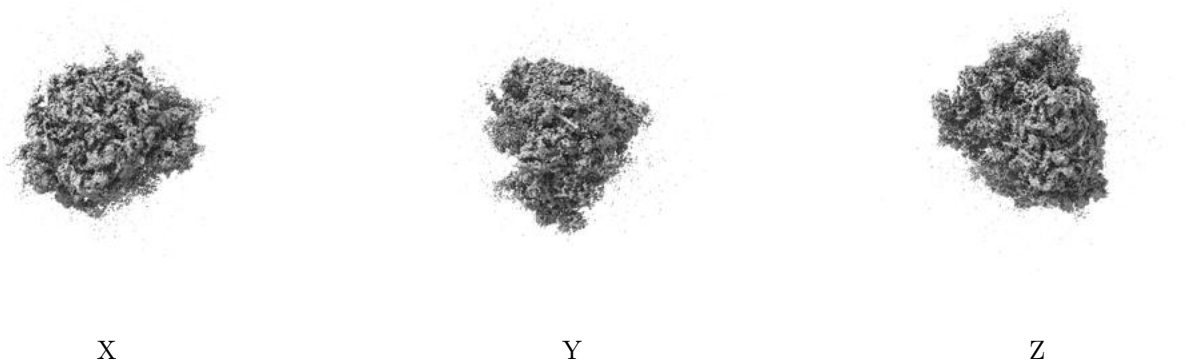


Z

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.

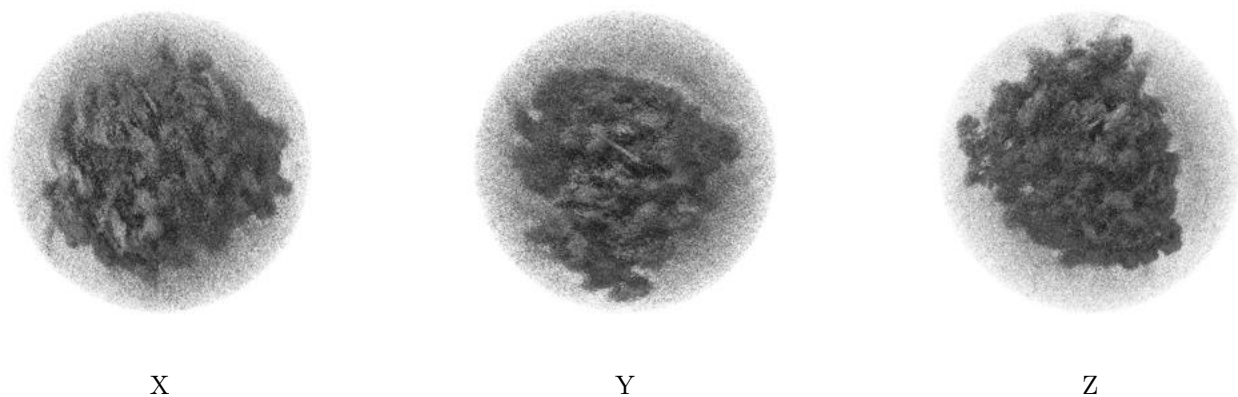
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. 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.

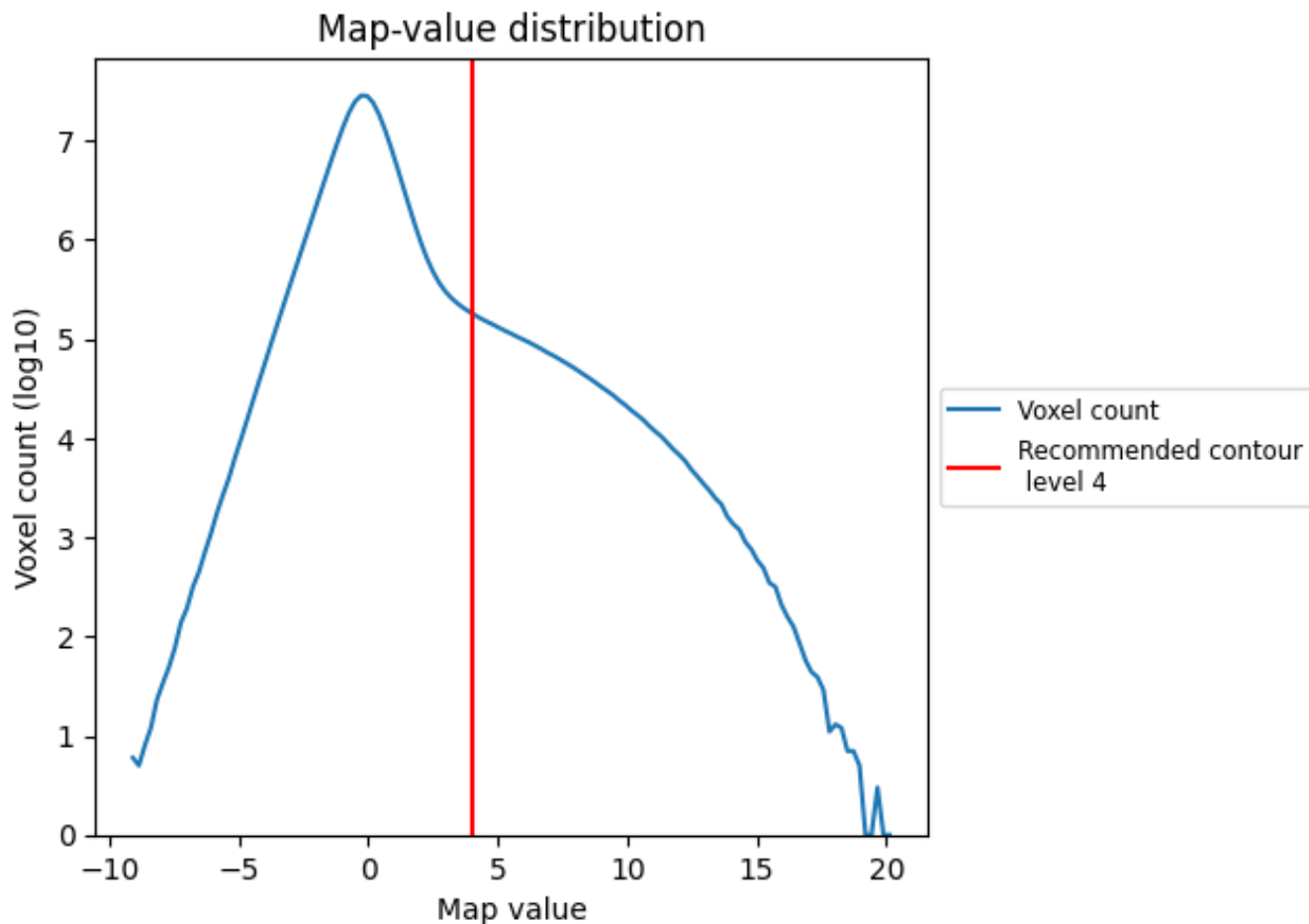
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

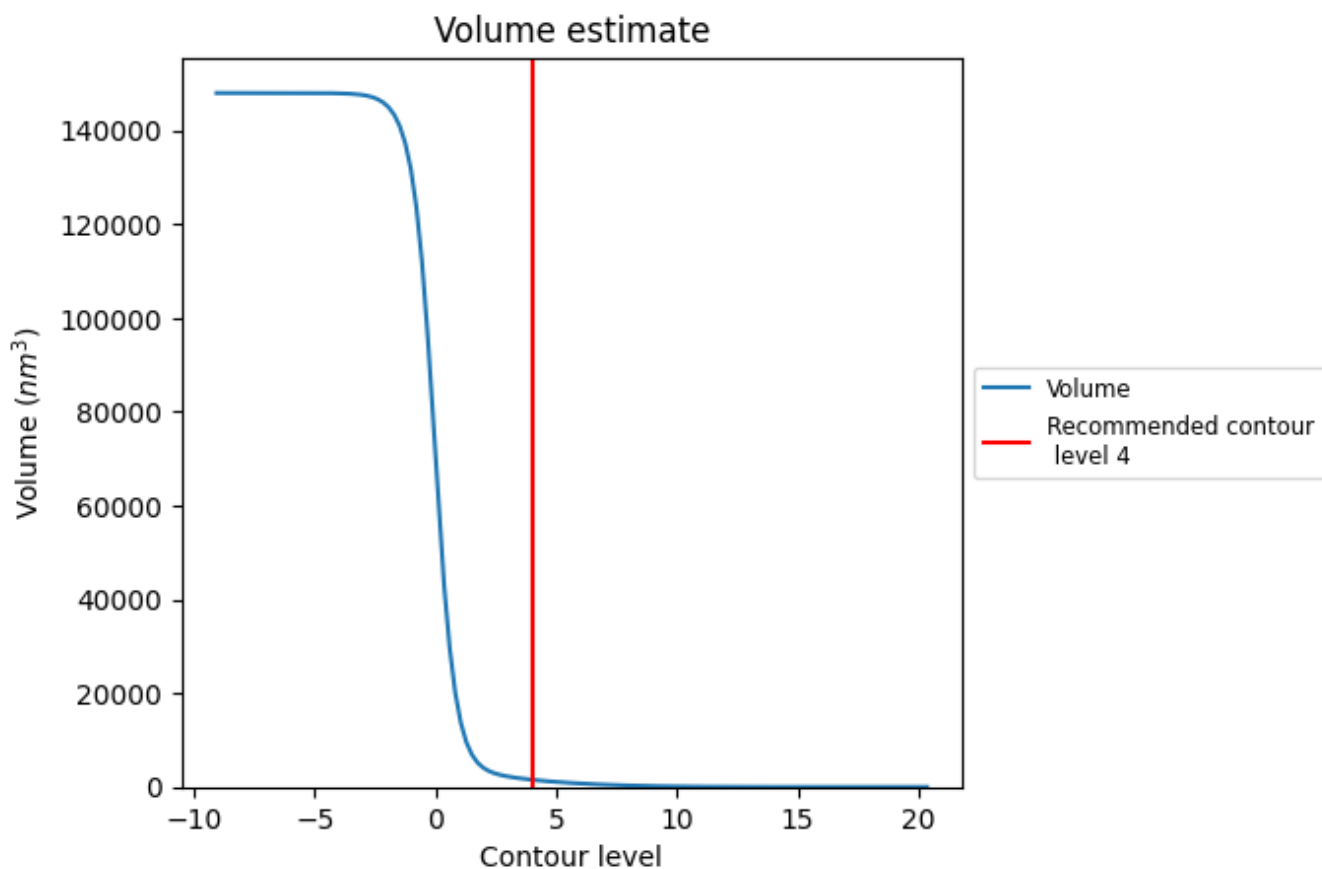
This section contains the results of statistical analysis of the map.

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.

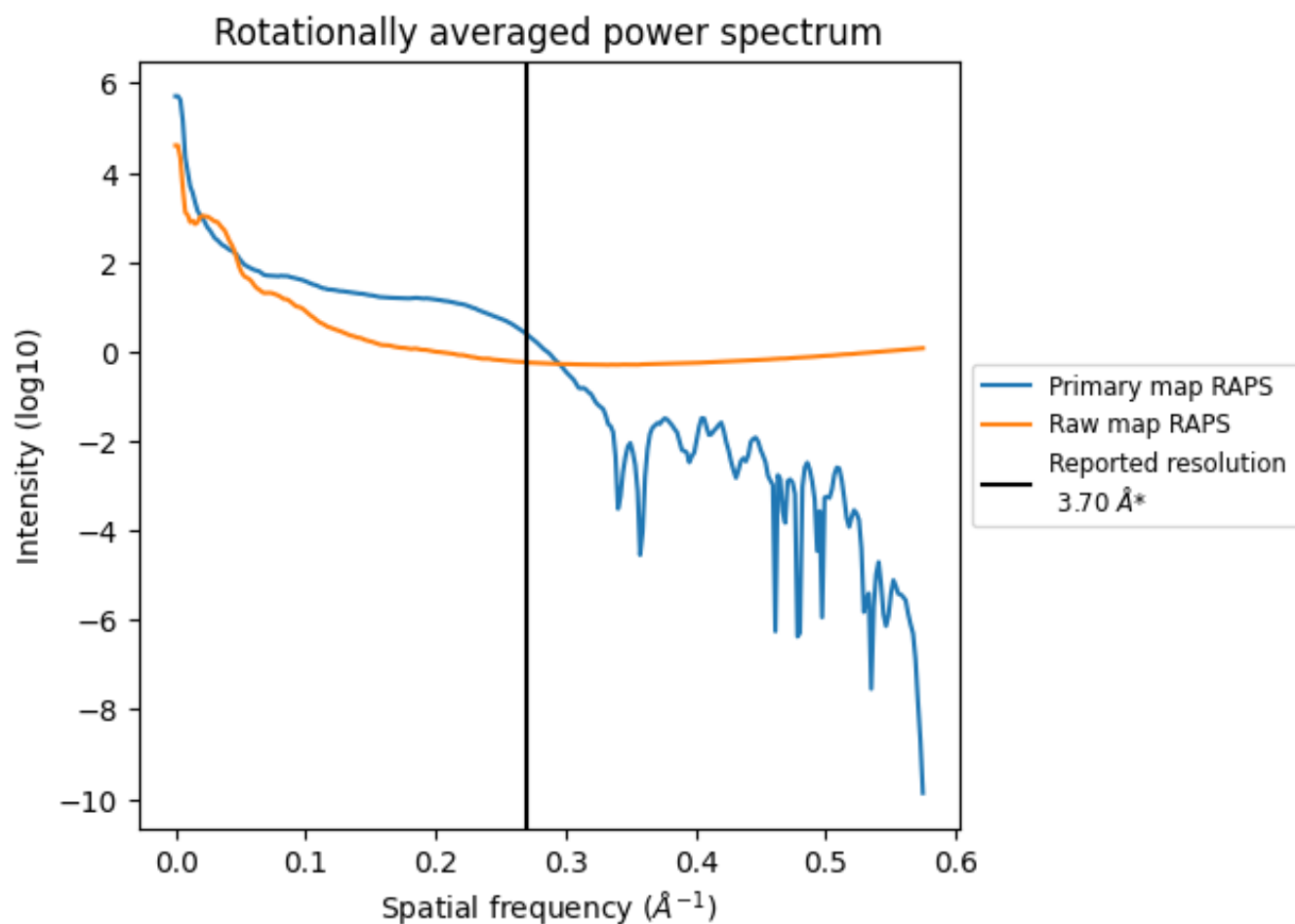
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1530 nm^3 ; this corresponds to an approximate mass of 1382 kDa.

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

7.3 Rotationally averaged power spectrum i

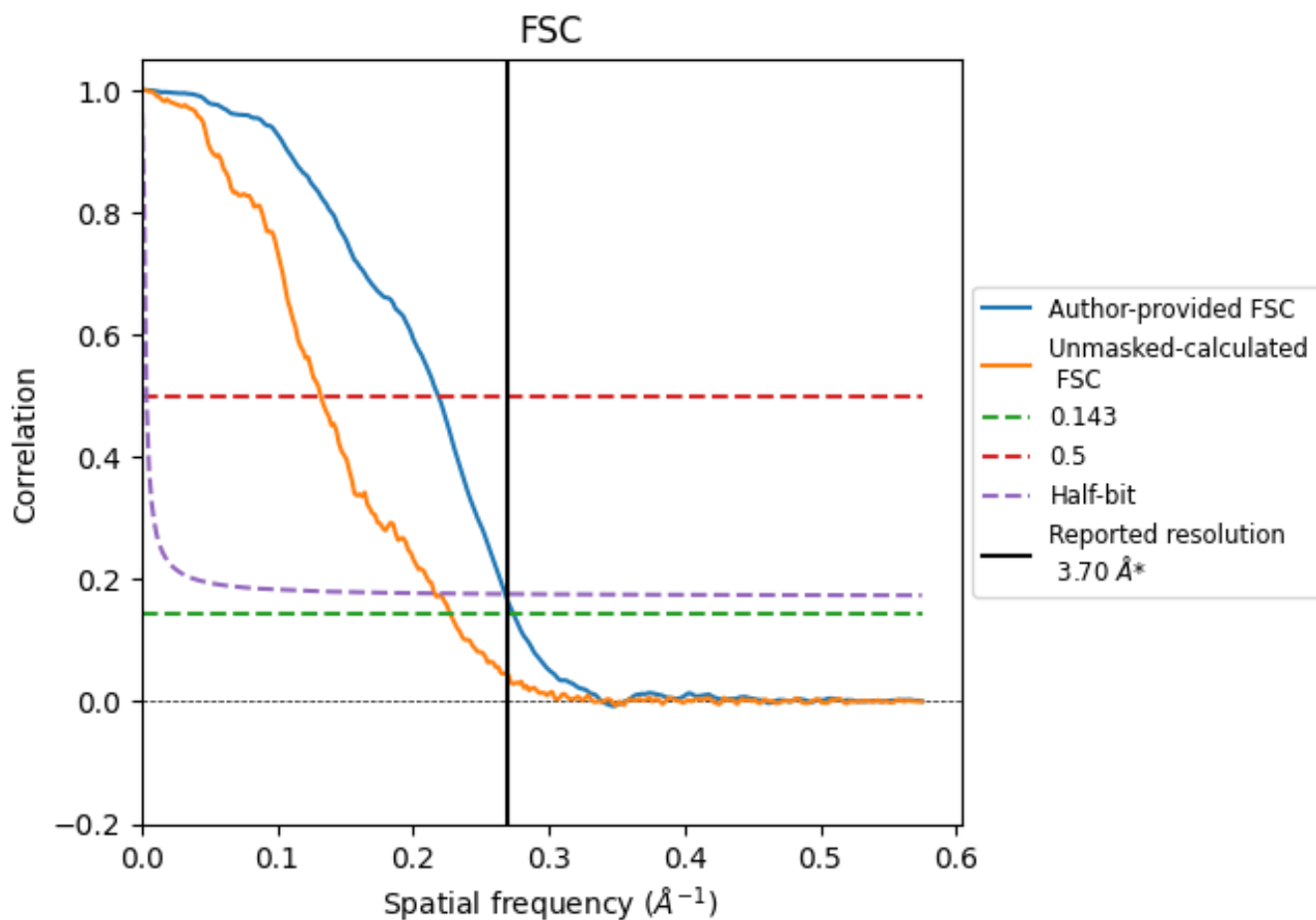


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates

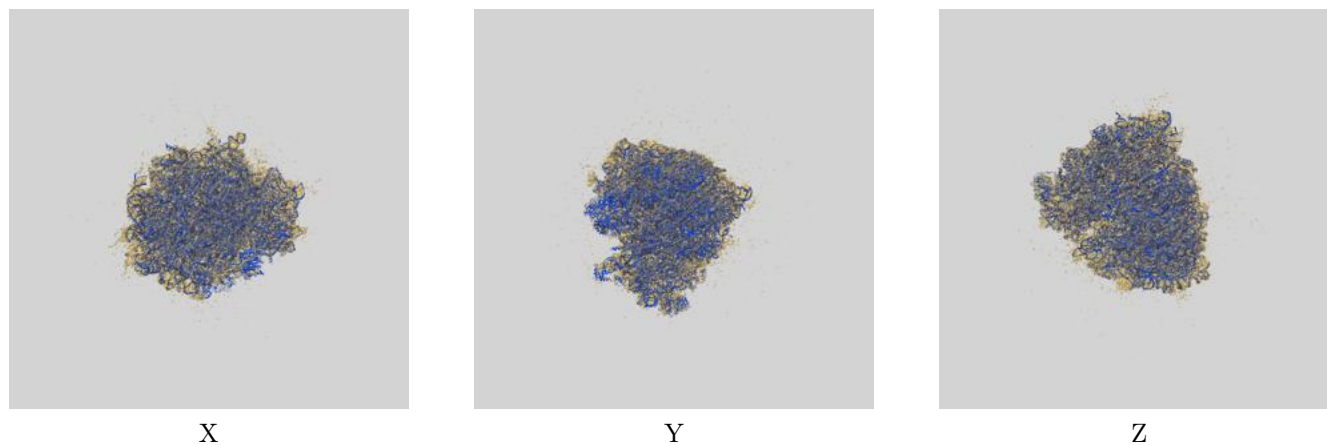
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.65	4.57	3.73
Unmasked-calculated*	4.40	7.58	4.63

*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 4.40 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

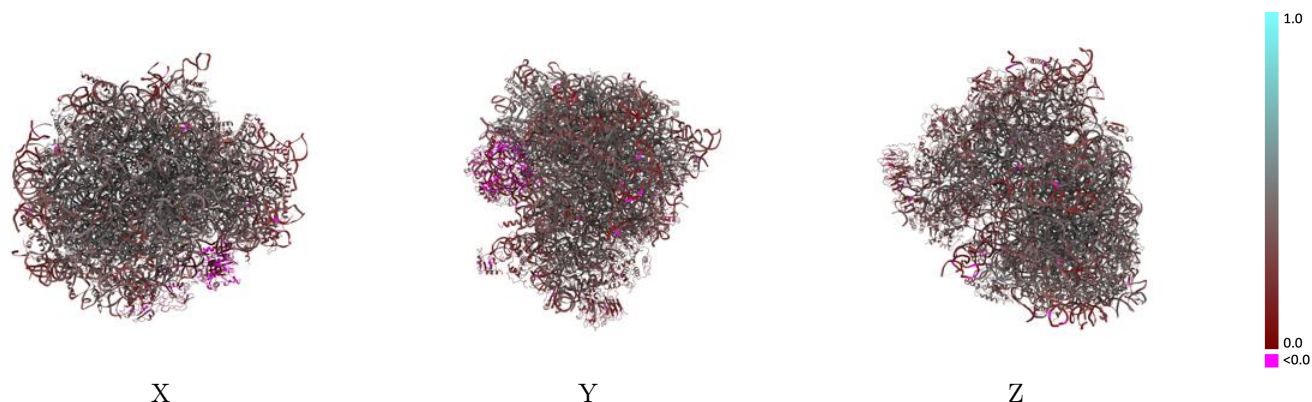
This section contains information regarding the fit between EMDB map EMD-44464 and PDB model 9BDP. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay [i](#)



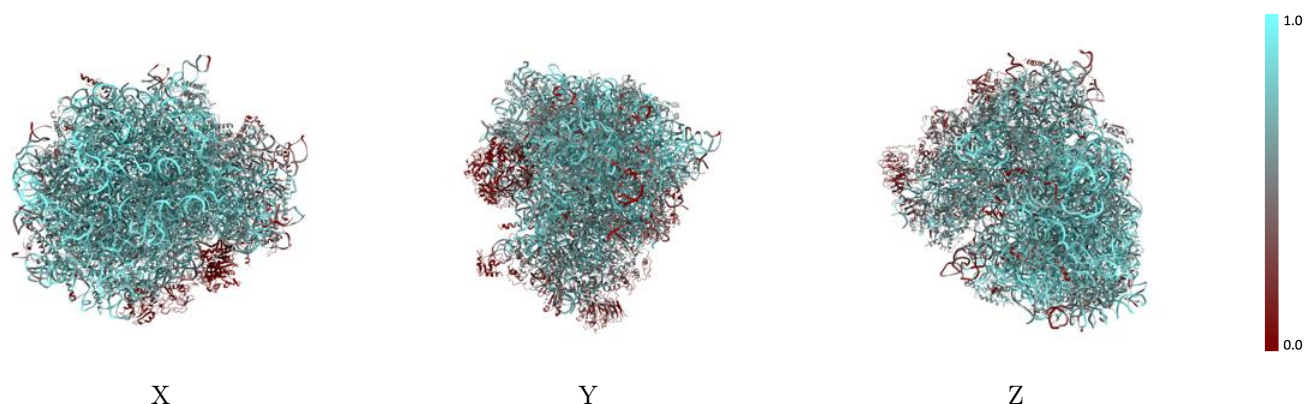
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



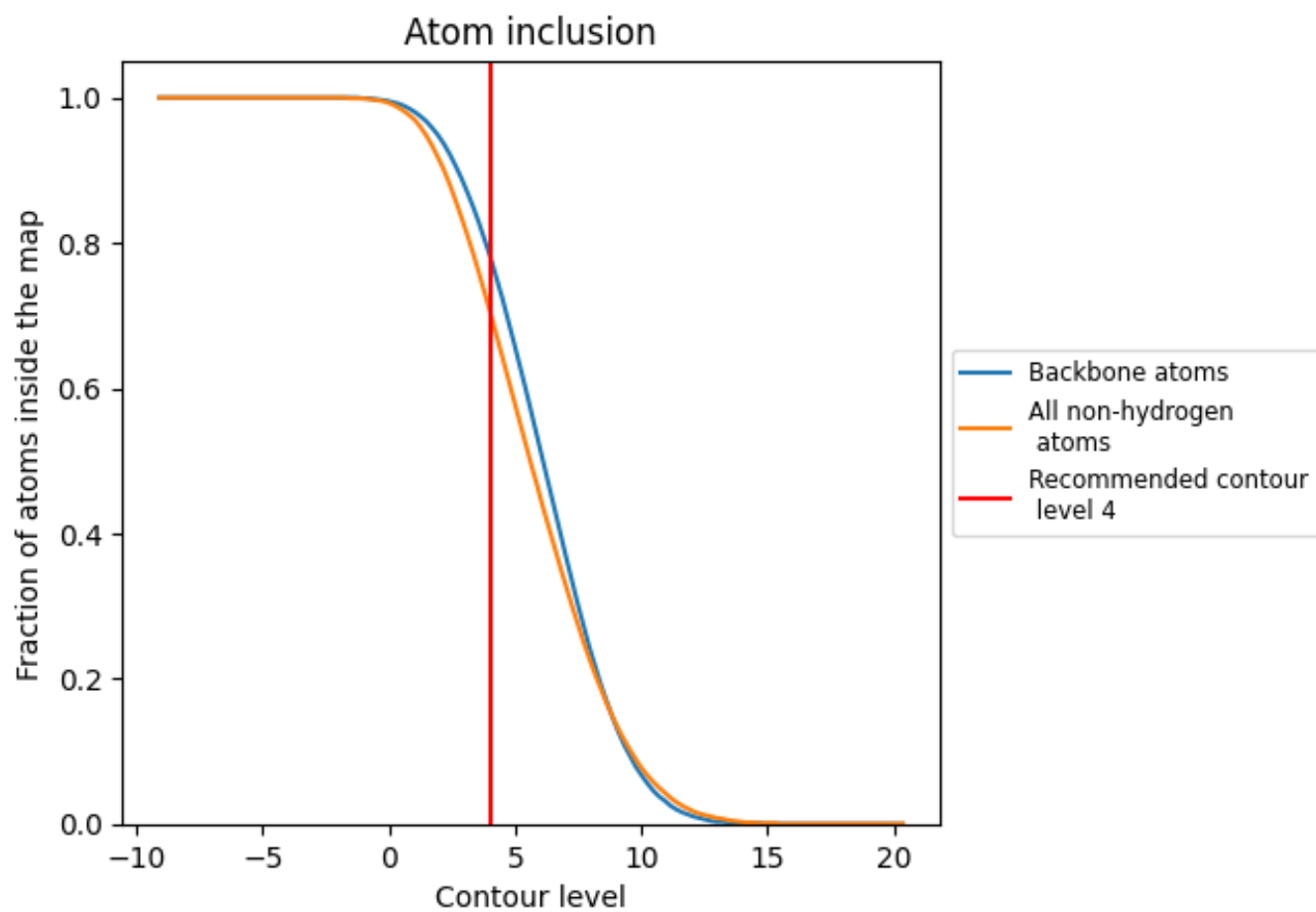
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 71% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7070	 0.3710
A18S	 0.8020	 0.3650
A28S	 0.8540	 0.3900
A58S	 0.8930	 0.3940
A5S	 0.9280	 0.4160
AL02	 0.6990	 0.4450
AL03	 0.6830	 0.4310
AL04	 0.6820	 0.4290
AL05	 0.6660	 0.3730
AL06	 0.5940	 0.3810
AL07	 0.6570	 0.4250
AL08	 0.4750	 0.3510
AL09	 0.6200	 0.3940
AL10	 0.6680	 0.4200
AL11	 0.6350	 0.3730
AL12	 0.1360	 0.2020
AL13	 0.6380	 0.3960
AL14	 0.6610	 0.3880
AL15	 0.7010	 0.4320
AL16	 0.6700	 0.4240
AL17	 0.7170	 0.4400
AL18	 0.6800	 0.4360
AL19	 0.6450	 0.4000
AL20	 0.6620	 0.4310
AL21	 0.6590	 0.4320
AL22	 0.5410	 0.3500
AL23	 0.6700	 0.4420
AL24	 0.6660	 0.4200
AL25	 0.6480	 0.4080
AL26	 0.6720	 0.4040
AL27	 0.6060	 0.3840
AL28	 0.7330	 0.4460
AL29	 0.4970	 0.3600
AL30	 0.6170	 0.3910
AL31	 0.6790	 0.4190























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Chain	Atom inclusion	Q-score
AL32	 0.6800	 0.4510
AL33	 0.6900	 0.4450
AL34	 0.6740	 0.4190
AL35	 0.6330	 0.3790
AL36	 0.6470	 0.3870
AL37	 0.7770	 0.4440
AL38	 0.5150	 0.3620
AL39	 0.6980	 0.4210
AL40	 0.6840	 0.4240
AL41	 0.5140	 0.4230
AL42	 0.6690	 0.4210
AL43	 0.6860	 0.4200
ALNW	 0.6900	 0.4290
ALP0	 0.0820	 0.1970
ANG	 0.4830	 0.3540
ARAC	 0.2510	 0.2460
AS00	 0.4630	 0.3390
AS01	 0.5760	 0.3690
AS02	 0.5380	 0.3750
AS03	 0.4160	 0.3380
AS04	 0.5210	 0.3680
AS05	 0.5220	 0.3420
AS06	 0.4680	 0.3210
AS07	 0.3610	 0.3130
AS08	 0.5410	 0.3700
AS09	 0.5570	 0.3360
AS10	 0.3460	 0.2420
AS11	 0.5860	 0.4080
AS12	 0.0660	 0.1980
AS13	 0.5750	 0.3770
AS14	 0.6070	 0.3830
AS15	 0.4480	 0.2870
AS16	 0.4510	 0.3020
AS17	 0.3890	 0.3350
AS18	 0.5370	 0.3250
AS19	 0.4990	 0.3260
AS20	 0.3280	 0.2980
AS21	 0.4280	 0.3290
AS22	 0.5220	 0.3930
AS23	 0.5830	 0.4150
AS24	 0.4830	 0.2960
AS25	 0.4940	 0.3140

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Chain	Atom inclusion	Q-score
AS26	 0.6110	 0.3950
AS27	 0.4790	 0.3230
AS28	 0.5620	 0.3540
AS29	 0.4690	 0.3440
AS30	 0.4910	 0.3350
EF1A	 0.0490	 0.0510
ETRN	 0.5710	 0.2240
MRNA	 0.5070	 0.3350
PTRN	 0.7540	 0.3330
TIRN	 0.4890	 0.1550