



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 01:42 AM UTC

PDB ID : 4V8T / pdb_00004v8t
EMDB ID : EMD-2169
Title : Cryo-EM Structure of the 60S Ribosomal Subunit in Complex with Arx1 and Rei1
Authors : Greber, B.J.; Boehringer, D.; Montellese, C.; Ban, N.
Deposited on : 2012-08-07
Resolution : 8.10 Å (reported)
Based on initial models : 3U5I, 3U5H

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:

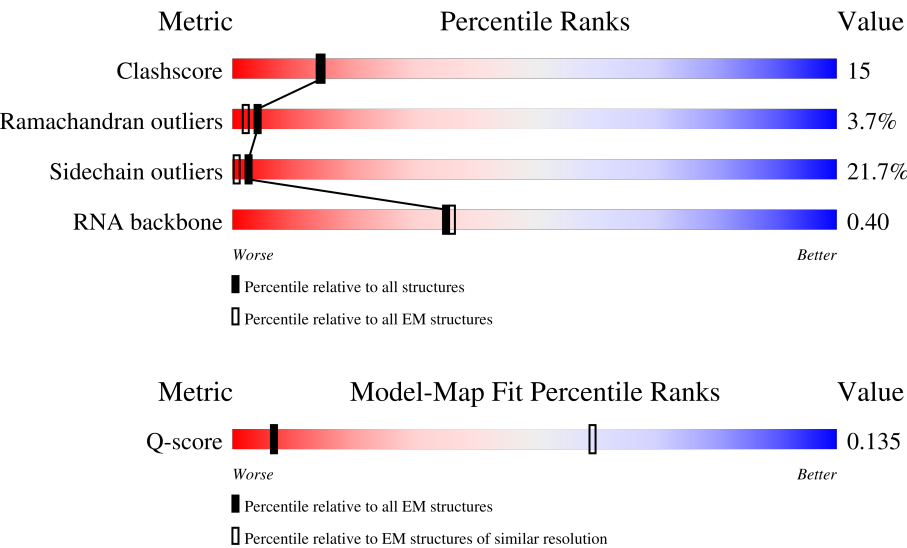
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.10 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	342 (7.60 - 8.60)

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	A	254	37% 54% 32% 11% ..
2	B	387	17% 52% 34% 11% .
3	C	362	17% 51% 31% 15% .

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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	176	
6	F	244	
7	G	256	
8	H	191	
9	I	221	
10	J	174	
11	K	155	
12	L	199	
13	M	138	
14	N	204	
15	O	219	
16	P	184	
17	Q	186	
18	R	189	
19	S	172	
20	T	160	
21	U	121	
22	V	137	
23	W	155	
24	X	142	
25	Y	127	
26	Z	136	
27	a	149	
28	b	59	

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Mol	Chain	Length	Quality of chain
29	c	105	
30	d	113	
31	e	130	
32	f	107	
33	g	121	
34	h	120	
35	i	100	
36	j	88	
37	k	78	
38	l	51	
39	m	128	
40	n	25	
41	o	106	
42	p	92	
43	q	312	
44	r	153	
45	s	46	
46	t	614	
47	1	114	
48	5	3396	
49	7	121	
50	8	158	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
51	ZN	o	501	-	-	X	-

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 130050 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 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	252	Total	C	N	O	S	0	0
			1912	1190	388	333	1		

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 3 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 7 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	213	Total	C	N	O	S	0	0
			1722	1094	325	297	6		

- Molecule 10 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	150	Total	C	N	O	0	0
			750	450	150	150		

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	L	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 13 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 15 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	197	Total	C	N	O	S	197	0
			3119	2008	581	528	2		

- Molecule 16 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	155	Total	C	N	O	S	0	0
			1227	764	238	225			

- Molecule 17 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 18 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	188	Total	C	N	O	S	0	0
			1521	935	326	260			

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 20 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	98	Total	C	N	O	0	0
			778	505	127	146		

- Molecule 22 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 23 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	135	Total	C	N	O	S	0	0
			1038	651	206	180	1		

- Molecule 24 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 25 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Y	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 26 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 27 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 28 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	b	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 30 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 31 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 32 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 33 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 34 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 35 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 36 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 37 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	77	Total	C	N	O	S	0	0
			608	388	114	106			

- Molecule 38 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 39 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 40 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 41 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 42 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 43 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	143	Total	C	N	O	S	0	0
			1077	687	192	195	3		

- Molecule 44 is a protein called RIBOSOMAL PROTEIN P1 ALPHA, Large ribosomal subunit protein P1A.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	r	47	Total	C	N	O	0	0
			235	141	47	47		

- Molecule 45 is a protein called RIBOSOMAL PROTEIN P2 BETA.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	s	46	Total	C	N	O	0	0
			230	138	46	46		

- Molecule 46 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	380	Total	C	N	O	S	0	0
			2938	1853	511	563	11		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	-20	HIS	-	expression tag	UNP Q03862
t	-19	HIS	-	expression tag	UNP Q03862
t	-18	HIS	-	expression tag	UNP Q03862
t	-17	HIS	-	expression tag	UNP Q03862
t	-16	HIS	-	expression tag	UNP Q03862
t	-15	HIS	-	expression tag	UNP Q03862
t	-14	ASP	-	expression tag	UNP Q03862
t	-13	TYR	-	expression tag	UNP Q03862
t	-12	ASP	-	expression tag	UNP Q03862
t	-11	ILE	-	expression tag	UNP Q03862
t	-10	PRO	-	expression tag	UNP Q03862

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Chain	Residue	Modelled	Actual	Comment	Reference
t	-9	THR	-	expression tag	UNP Q03862
t	-8	THR	-	expression tag	UNP Q03862
t	-7	GLU	-	expression tag	UNP Q03862
t	-6	ASN	-	expression tag	UNP Q03862
t	-5	LEU	-	expression tag	UNP Q03862
t	-4	TYR	-	expression tag	UNP Q03862
t	-3	PHE	-	expression tag	UNP Q03862
t	-2	GLN	-	expression tag	UNP Q03862
t	-1	GLY	-	expression tag	UNP Q03862
t	0	ALA	-	expression tag	UNP Q03862

- Molecule 47 is a RNA chain called ES27 OF THE 25S RRNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
47	1	114	Total	P	0	114
			114	114		

- Molecule 48 is a RNA chain called 25S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	3150	Total	C	N	O	P	0	0
			67376	30095	12145	21987	3149		

- Molecule 49 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	7	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 50 is a RNA chain called 5.8S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	8	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
51	j	1	Total	Zn	0
			1	1	
51	m	1	Total	Zn	0
			1	1	

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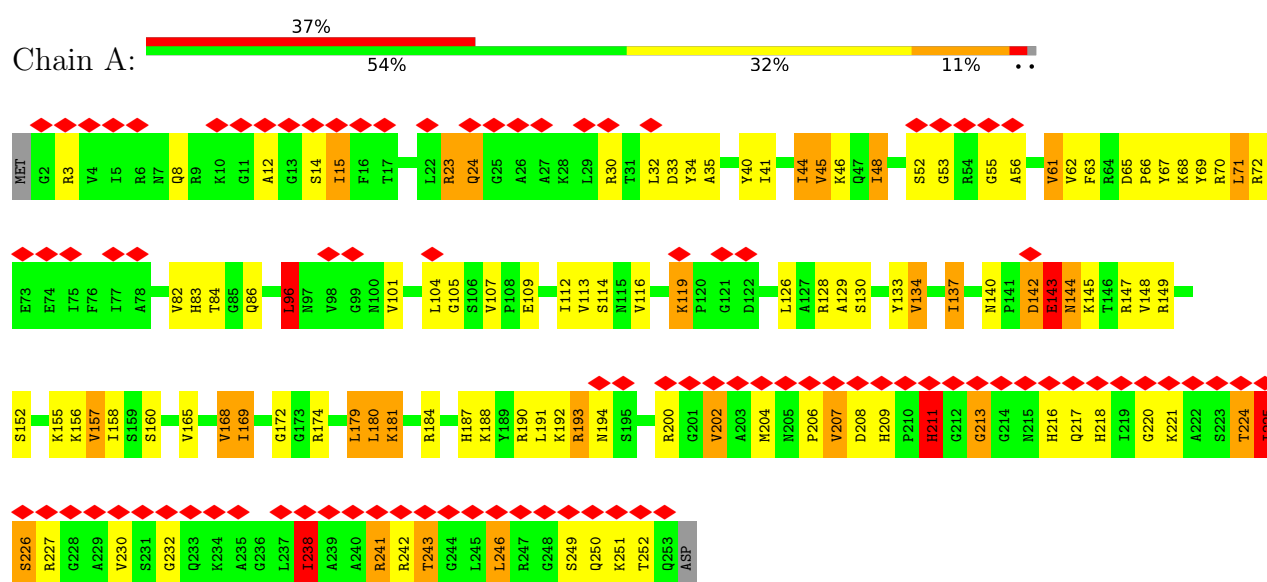
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Mol	Chain	Residues	Atoms		AltConf
51	o	1	Total 1	Zn 1	0
51	p	1	Total 1	Zn 1	0

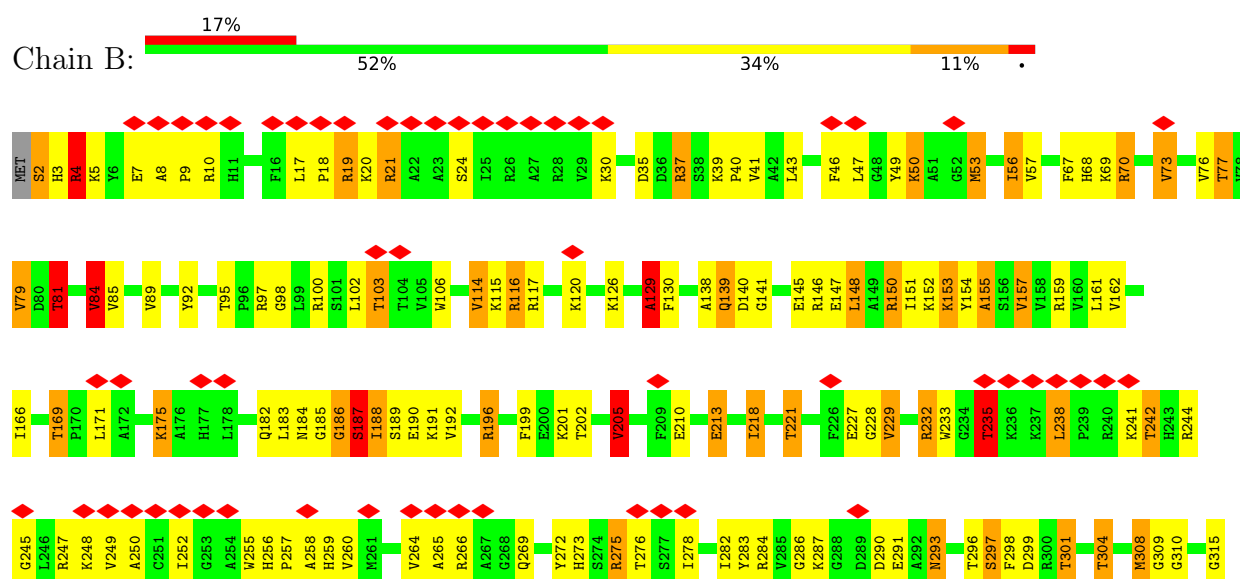
3 Residue-property plots

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

• Molecule 1: 60S ribosomal protein L2-A

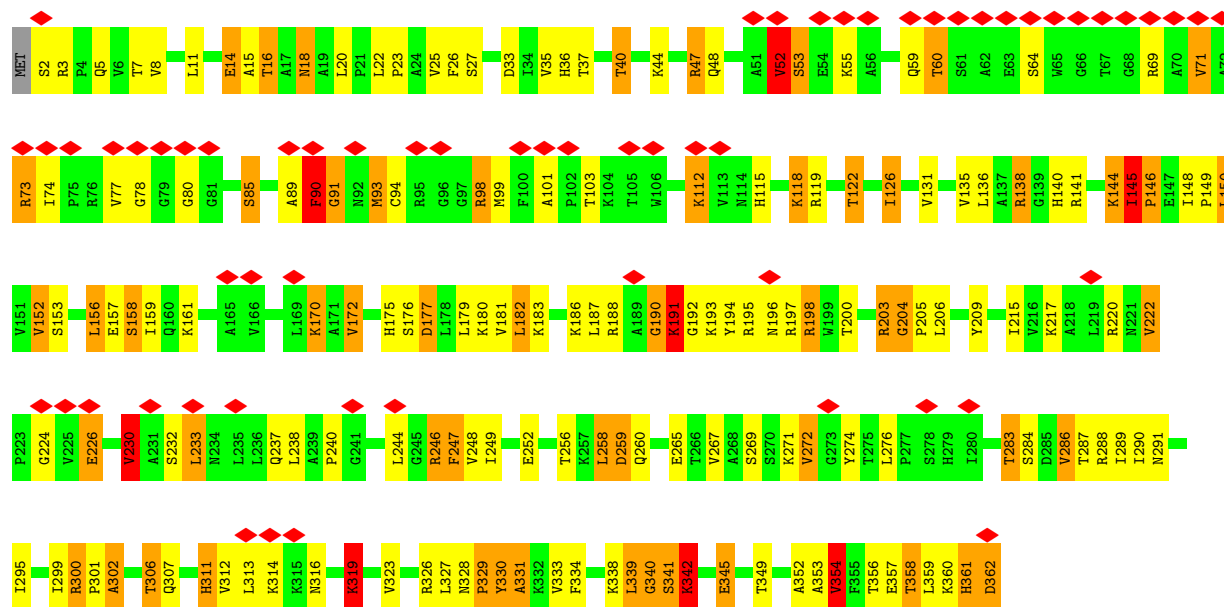


• Molecule 2: 60S ribosomal protein L3

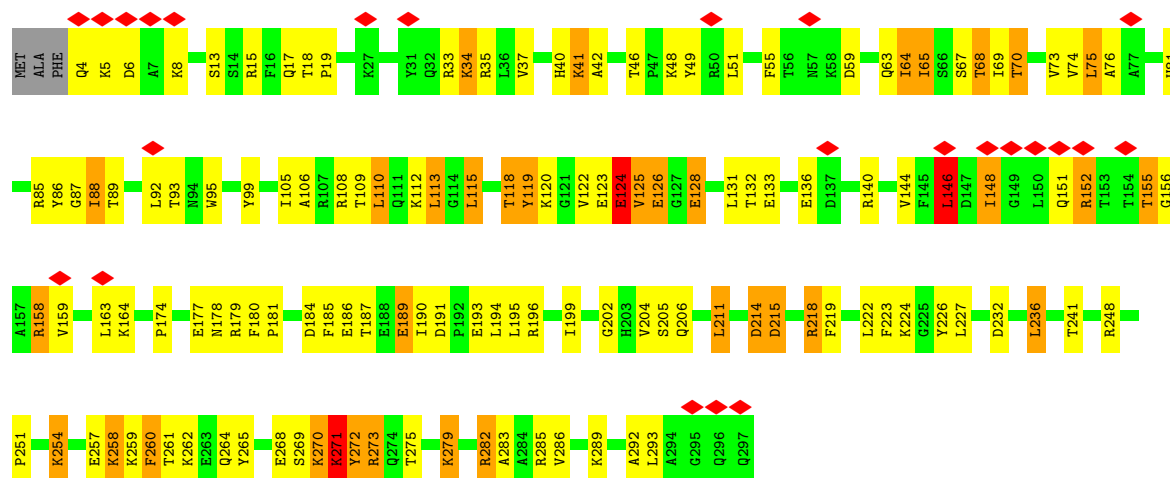




• Molecule 3: 60S ribosomal protein L4-A

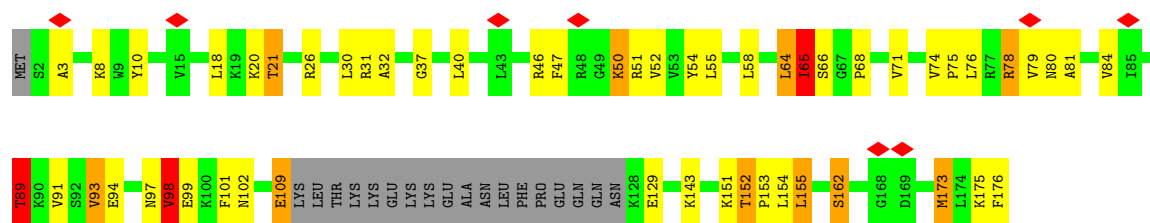


• Molecule 4: 60S ribosomal protein L5

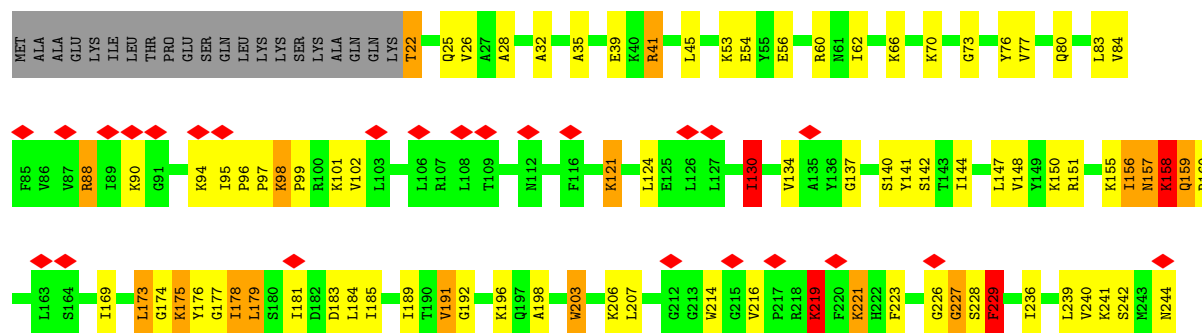


• Molecule 5: 60S ribosomal protein L6-A

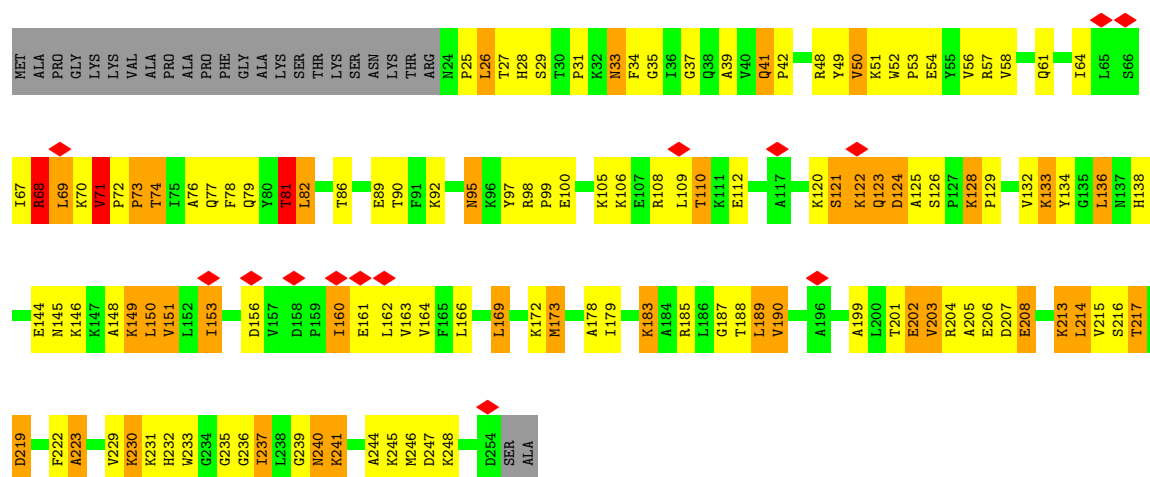




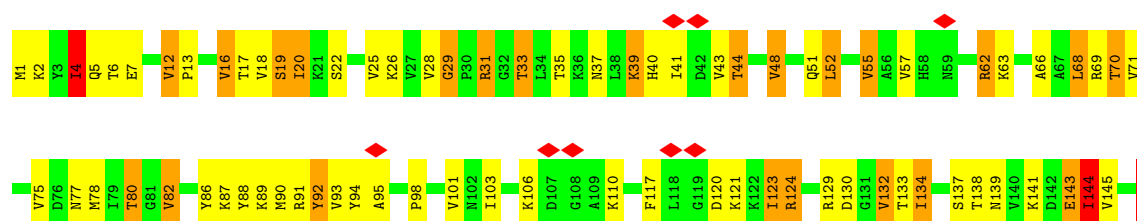
• Molecule 6: 60S ribosomal protein L7-A

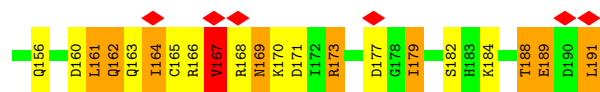


• Molecule 7: 60S ribosomal protein L8-A

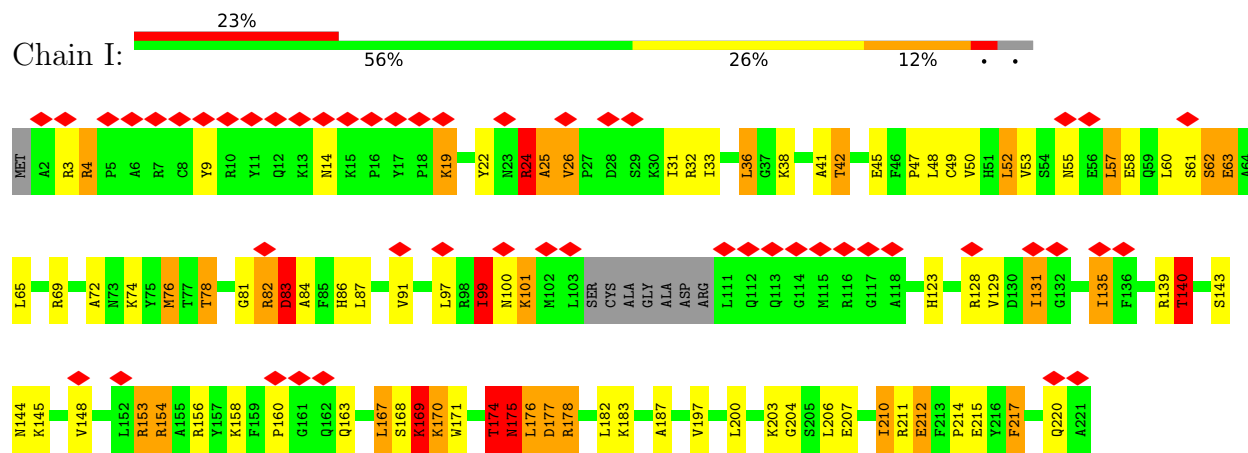


• Molecule 8: 60S ribosomal protein L9-A

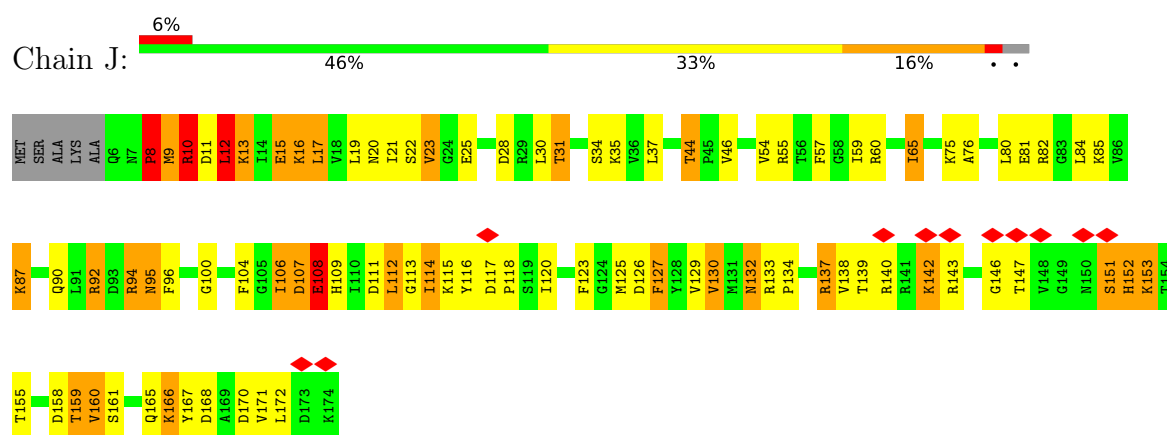




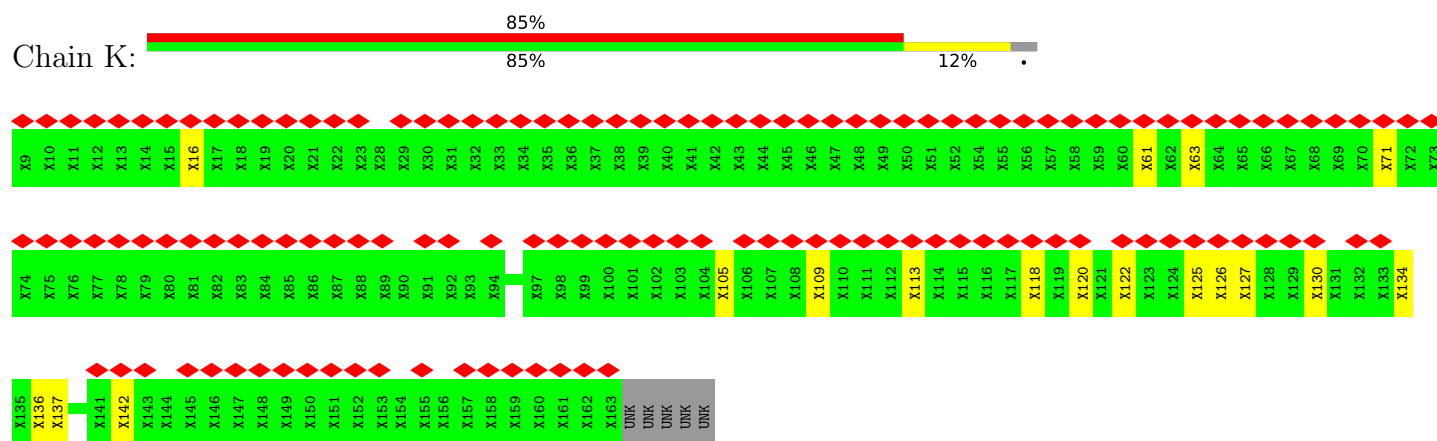
• Molecule 9: 60S ribosomal protein L10



• Molecule 10: 60S ribosomal protein L11-A

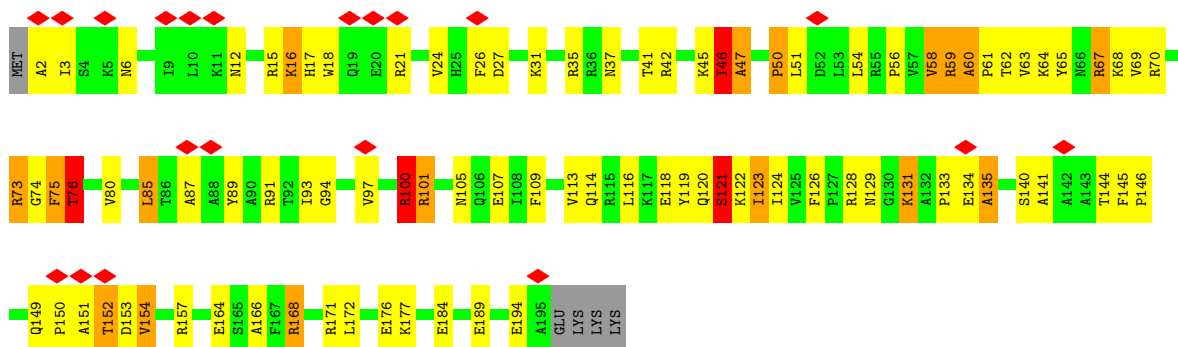


• Molecule 11: 60S RIBOSOMAL PROTEIN L12

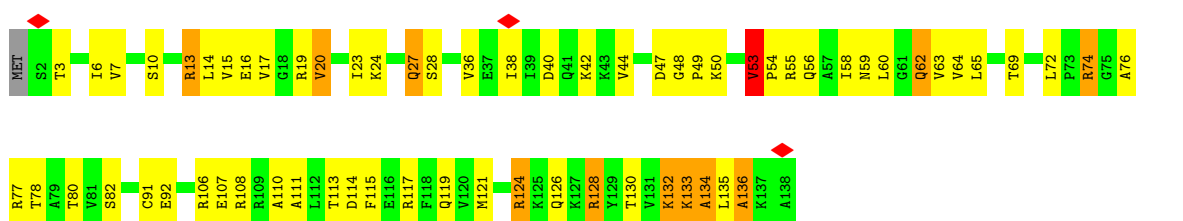


• Molecule 12: 60S ribosomal protein L13-A

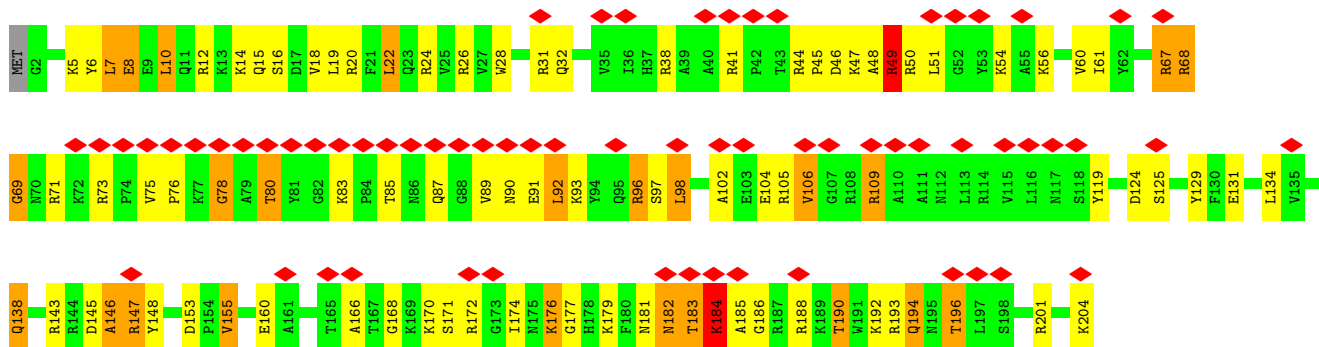




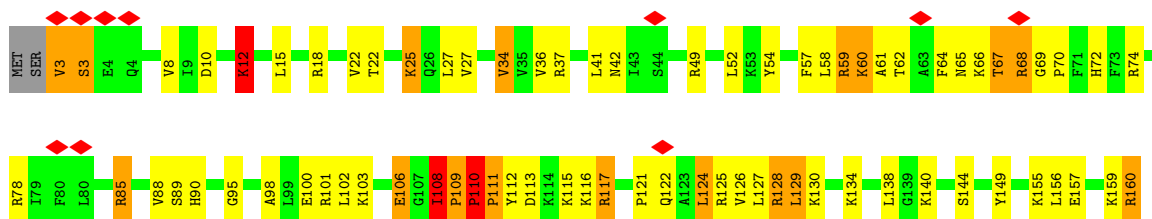
• Molecule 13: 60S ribosomal protein L14-A

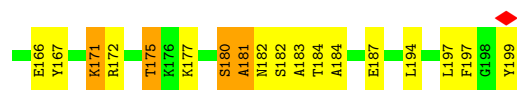


• Molecule 14: 60S ribosomal protein L15-A

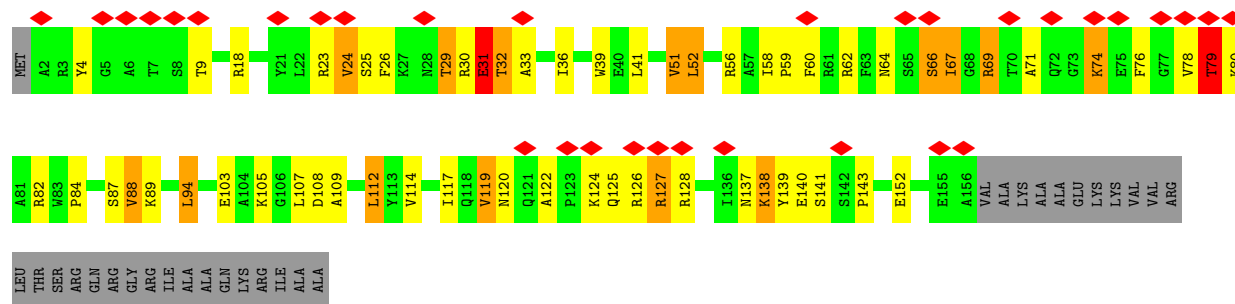


• Molecule 15: Large ribosomal subunit protein uL13A

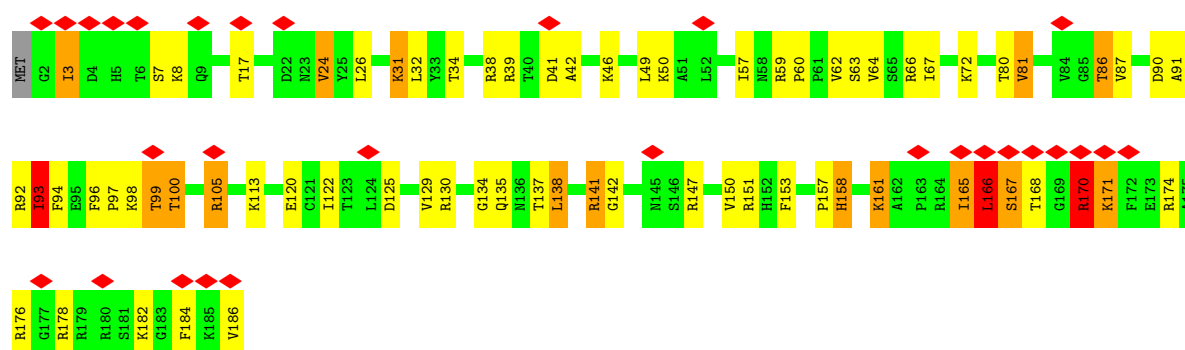




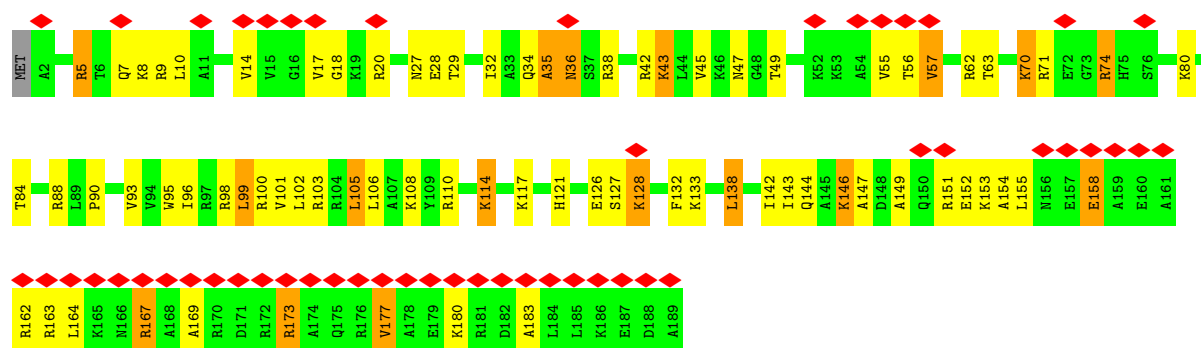
• Molecule 16: 60S ribosomal protein L17-A



• Molecule 17: 60S ribosomal protein L18-A

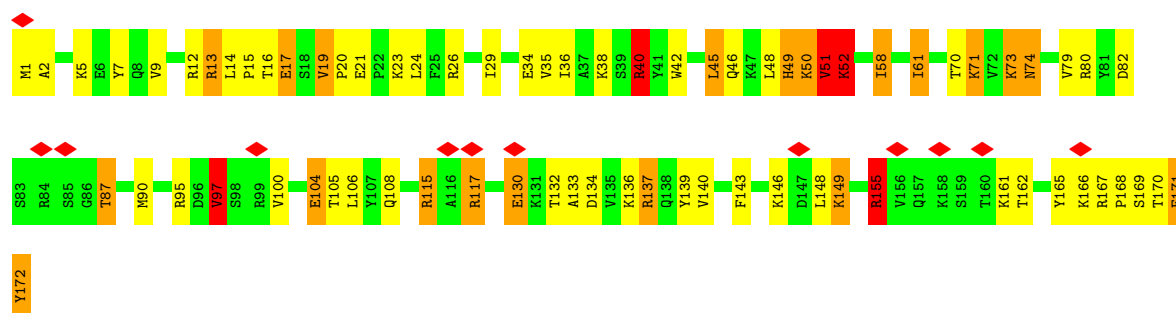


• Molecule 18: 60S ribosomal protein L19-A

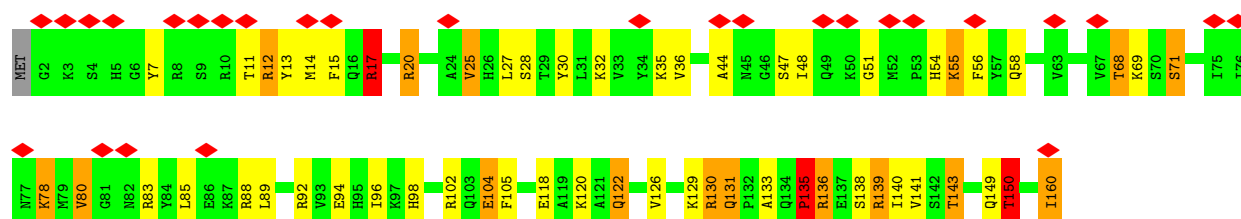


• Molecule 19: 60S ribosomal protein L20-A

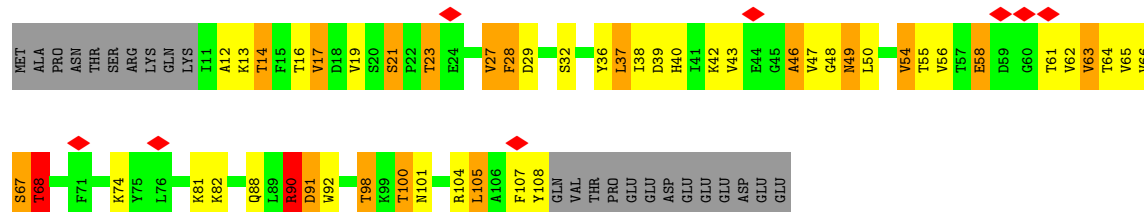




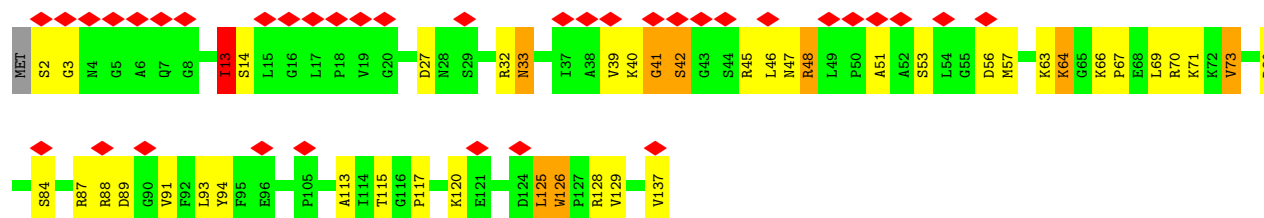
- Molecule 20: 60S ribosomal protein L21-A



- Molecule 21: 60S ribosomal protein L22-A

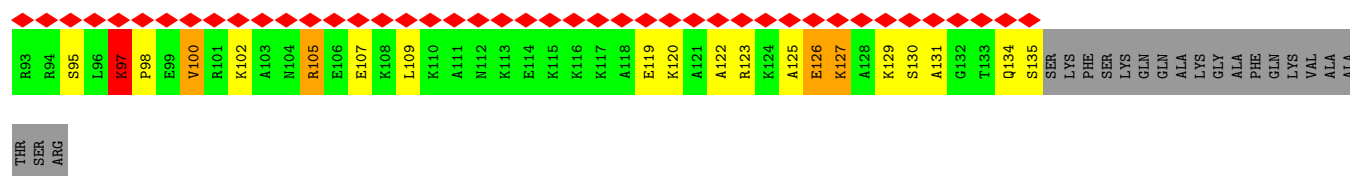


- Molecule 22: 60S ribosomal protein L23-A

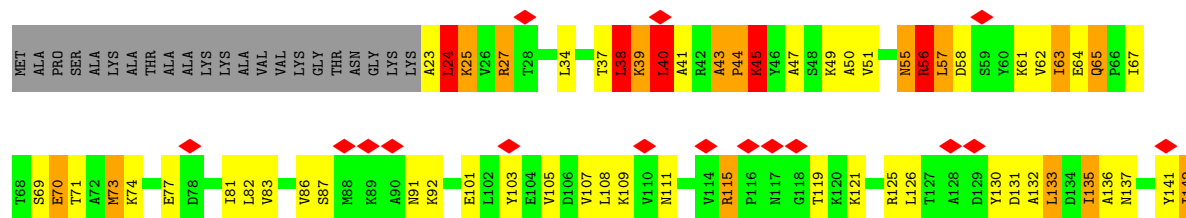


- Molecule 23: 60S ribosomal protein L24-A

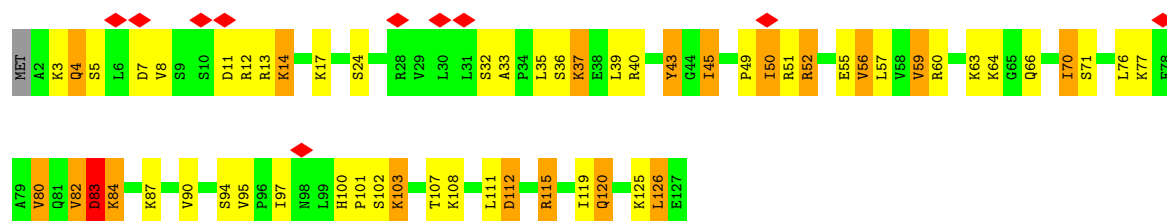




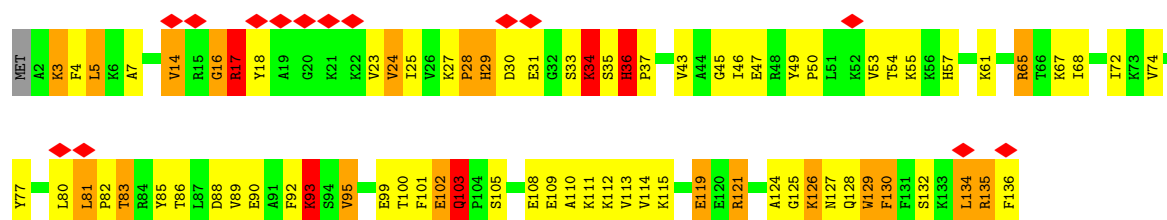
- Molecule 24: 60S ribosomal protein L25



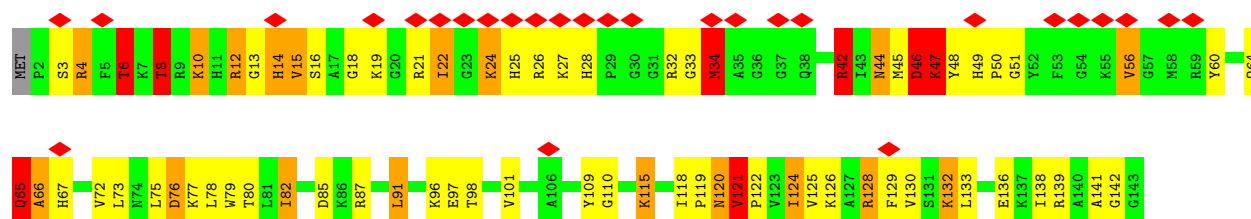
- Molecule 25: 60S ribosomal protein L26-A



- Molecule 26: 60S ribosomal protein L27-A

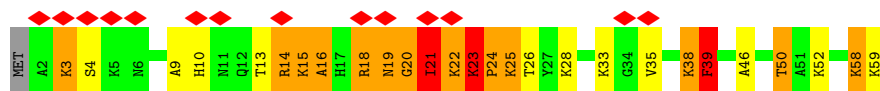


- Molecule 27: 60S ribosomal protein L28

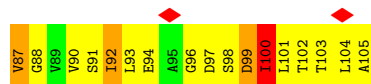
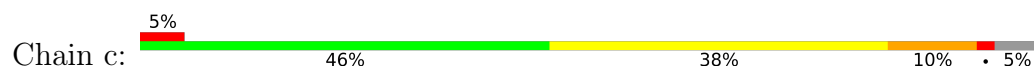




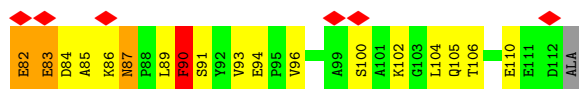
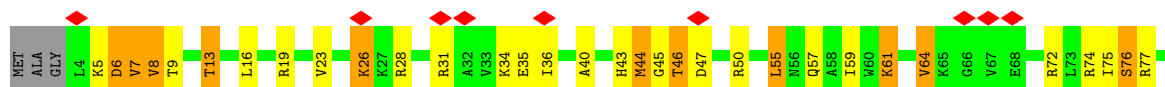
- Molecule 28: 60S ribosomal protein L29



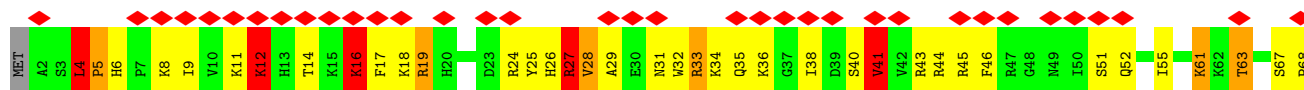
- Molecule 29: 60S ribosomal protein L30



- Molecule 30: 60S ribosomal protein L31-A

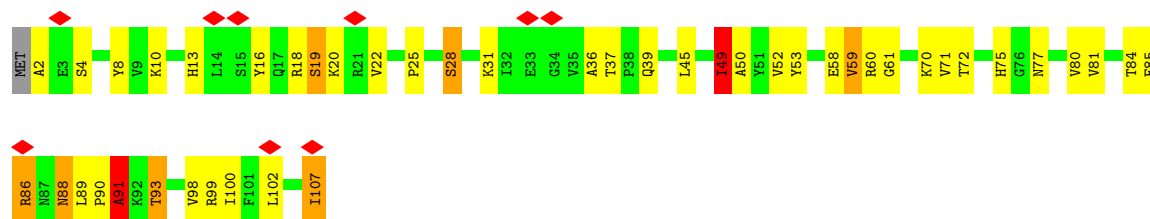


- Molecule 31: 60S ribosomal protein L32

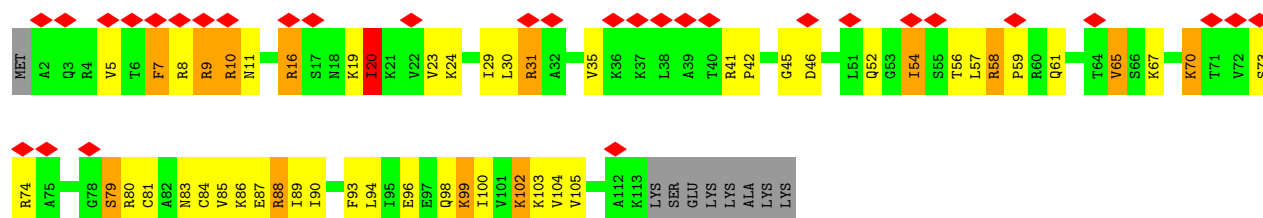


- Molecule 32: 60S ribosomal protein L33-A

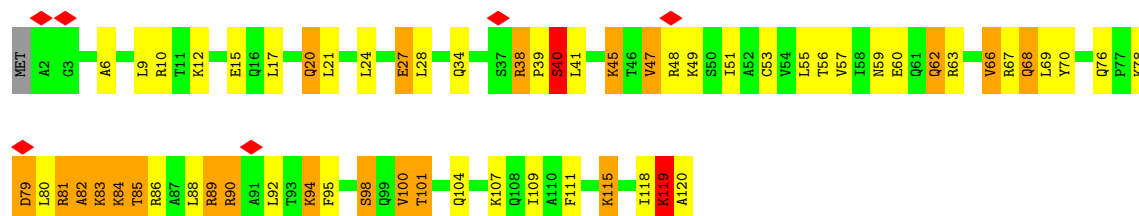




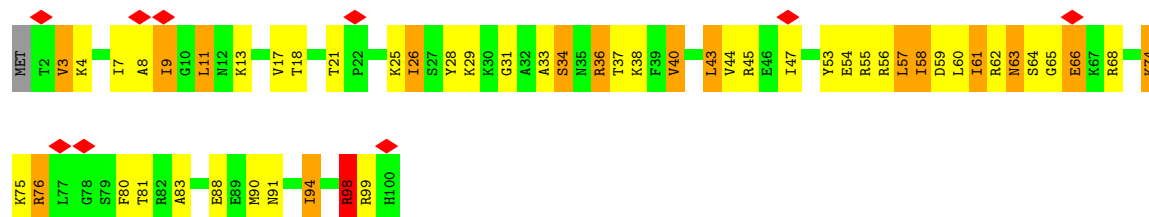
- Molecule 33: 60S ribosomal protein L34-A



- Molecule 34: 60S ribosomal protein L35-A



- Molecule 35: 60S ribosomal protein L36-A

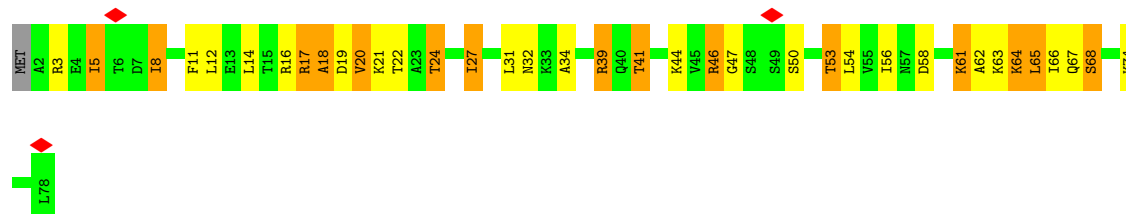


- Molecule 36: 60S ribosomal protein L37-A

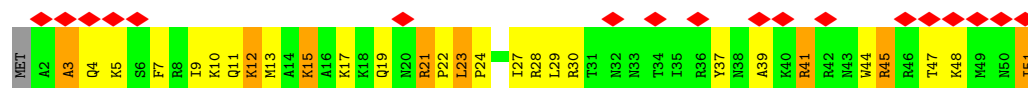




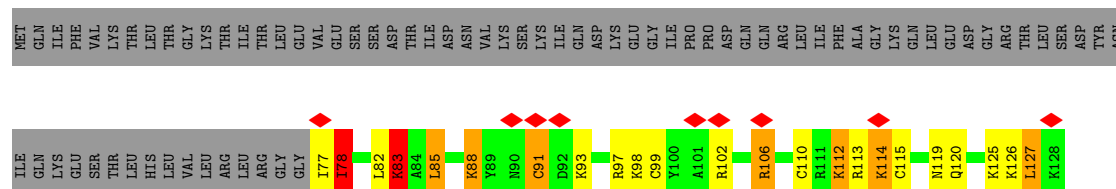
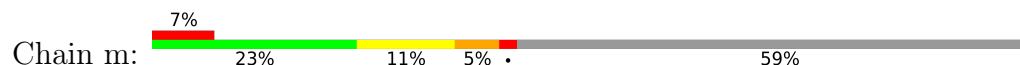
- Molecule 37: 60S ribosomal protein L38



- Molecule 38: 60S ribosomal protein L39



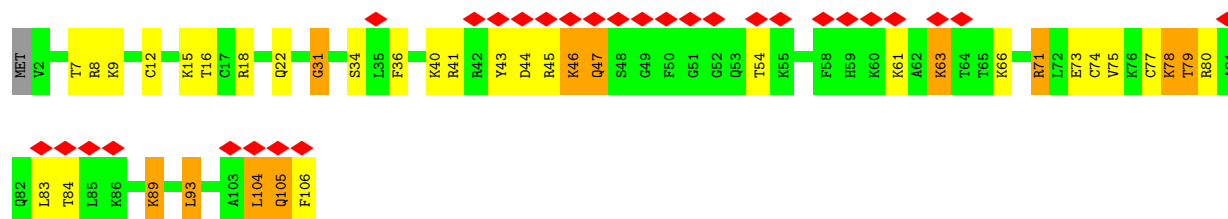
- Molecule 39: Ubiquitin-60S ribosomal protein L40

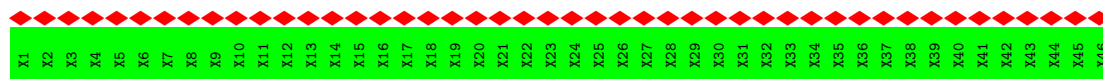


- Molecule 40: 60S ribosomal protein L41-A

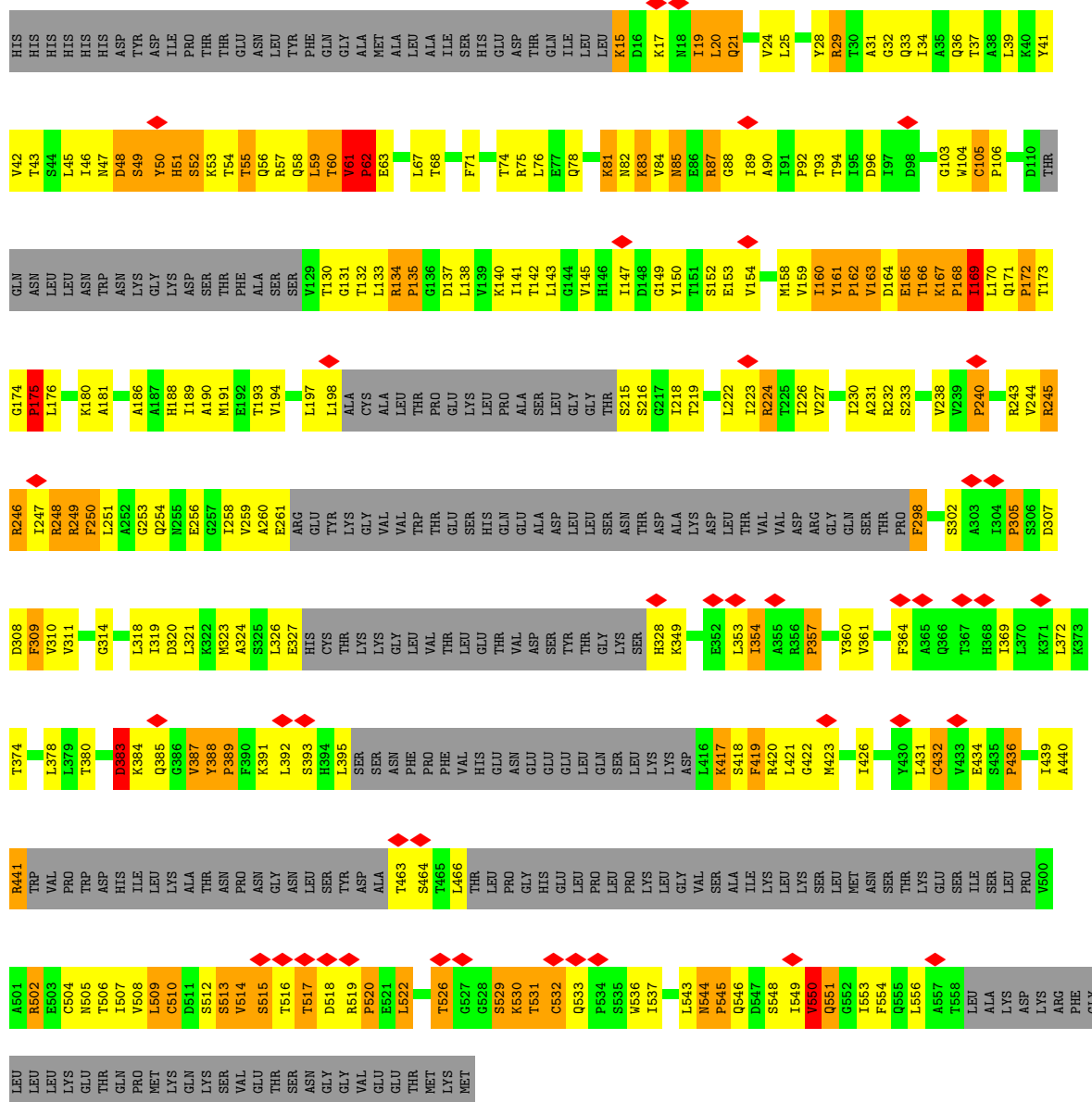
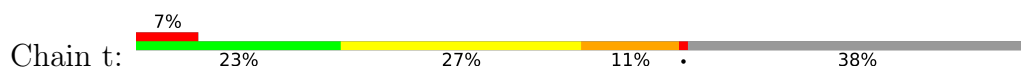


- Molecule 41: 60S ribosomal protein L42-A

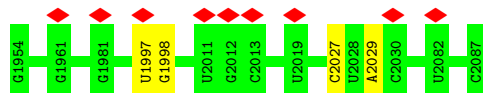




• Molecule 46: Probable metalloprotease ARX1



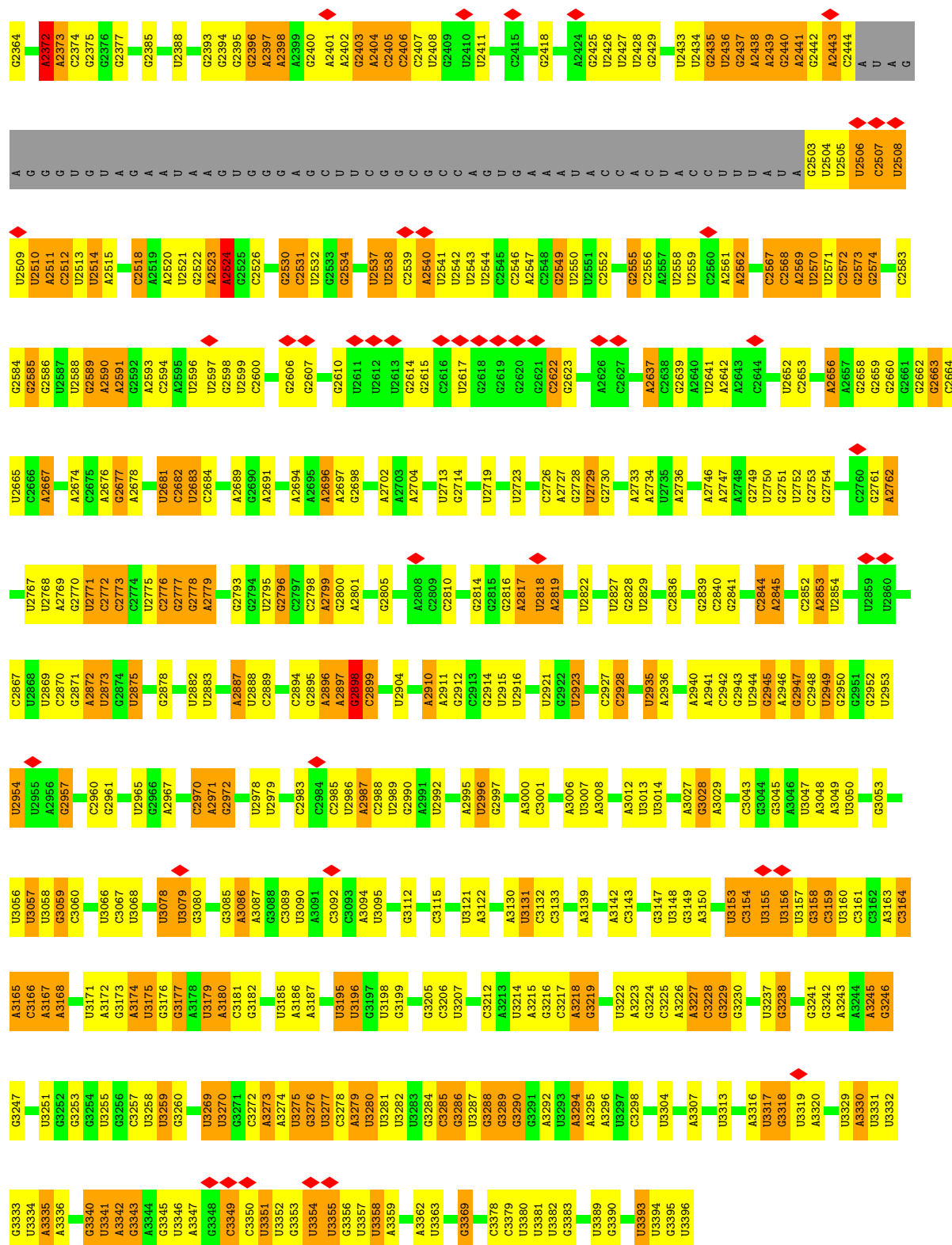
• Molecule 47: ES27 OF THE 25S RRNA



Chain 5: 49% 30% 13% 7%





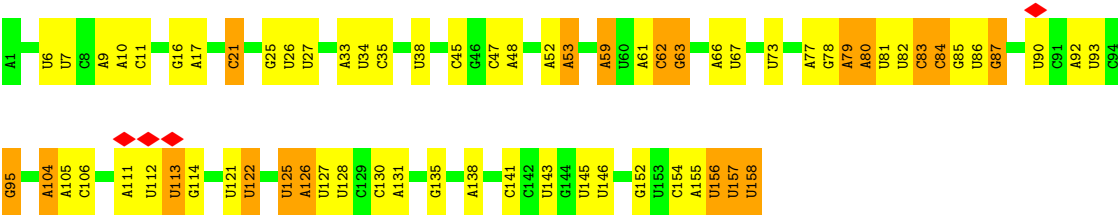


• Molecule 49: 5S RIBOSOMAL RNA

Chain 7: 57% 40%



• Molecule 50: 5.8S RIBOSOMAL RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	84113	Depositor
Resolution determination method	Not provided	
CTF correction method	PER FRAME	Depositor
Microscope	FEI TECNAI 20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	83000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	425.313	Depositor
Minimum map value	-221.732	Depositor
Average map value	-13.190	Depositor
Map value standard deviation	29.801	Depositor
Recommended contour level	35	Depositor
Map size ($\text{\AA}$)	405.44, 405.44, 405.44	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.81, 1.81, 1.81	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	1.11	4/1946 (0.2%)	1.43	18/2614 (0.7%)
2	B	1.23	4/3146 (0.1%)	1.44	26/4228 (0.6%)
3	C	1.12	6/2800 (0.2%)	1.43	34/3790 (0.9%)
4	D	1.02	1/2408 (0.0%)	1.27	21/3248 (0.6%)
5	E	1.07	0/1269	1.37	11/1705 (0.6%)
6	F	1.17	2/1828 (0.1%)	1.43	26/2461 (1.1%)
7	G	0.78	0/1795	1.18	14/2429 (0.6%)
8	H	1.17	0/1539	1.45	13/2073 (0.6%)
9	I	1.11	0/1758	1.38	12/2358 (0.5%)
10	J	0.99	1/1374 (0.1%)	1.36	17/1842 (0.9%)
12	L	1.06	3/1573 (0.2%)	1.40	19/2113 (0.9%)
13	M	1.18	0/1074	1.36	9/1446 (0.6%)
14	N	0.99	2/1757 (0.1%)	1.30	14/2354 (0.6%)
15	O	0.64	0/3159	0.95	14/4205 (0.3%)
16	P	1.34	3/1250 (0.2%)	1.41	6/1683 (0.4%)
17	Q	1.08	1/1465 (0.1%)	1.42	10/1965 (0.5%)
18	R	0.94	0/1538	1.21	5/2050 (0.2%)
19	S	1.20	3/1481 (0.2%)	1.43	17/1990 (0.9%)
20	T	1.16	2/1300 (0.2%)	1.35	6/1743 (0.3%)
21	U	0.67	0/794	1.20	8/1076 (0.7%)
22	V	1.25	2/1018 (0.2%)	1.42	6/1369 (0.4%)
23	W	0.99	0/1052	1.22	7/1398 (0.5%)
24	X	0.87	0/974	1.25	7/1314 (0.5%)
25	Y	0.94	0/1004	1.31	6/1341 (0.4%)
26	Z	0.65	0/1118	1.18	9/1497 (0.6%)
27	a	1.20	6/1204 (0.5%)	1.59	29/1612 (1.8%)
28	b	1.20	2/473 (0.4%)	1.61	10/629 (1.6%)
29	c	0.72	0/775	1.11	3/1040 (0.3%)
30	d	1.11	1/897 (0.1%)	1.32	8/1205 (0.7%)
31	e	1.23	4/1041 (0.4%)	1.58	9/1394 (0.6%)
32	f	1.34	6/868 (0.7%)	1.40	6/1168 (0.5%)
33	g	0.87	0/890	1.26	3/1189 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	h	0.81	0/974	1.15	2/1297 (0.2%)
35	i	0.84	0/777	1.17	2/1033 (0.2%)
36	j	1.02	0/696	1.35	4/923 (0.4%)
37	k	0.66	0/614	1.07	1/822 (0.1%)
38	l	1.03	0/443	1.28	0/588
39	m	1.29	0/423	1.42	5/562 (0.9%)
40	n	1.05	0/234	1.25	2/300 (0.7%)
41	o	0.95	0/860	1.24	0/1136
42	p	1.01	1/701 (0.1%)	1.39	8/934 (0.9%)
43	q	0.62	0/1092	1.11	5/1474 (0.3%)
46	t	5.60	20/2985 (0.7%)	4.28	206/4053 (5.1%)
48	5	0.82	25/75414 (0.0%)	0.66	13/117575 (0.0%)
49	7	0.78	0/2883	0.63	0/4491
50	8	0.66	0/3746	0.61	0/5832
All	All	1.22	99/138410 (0.1%)	1.12	651/203549 (0.3%)

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
1	A	0	2
3	C	0	1
4	D	0	1
5	E	0	1
6	F	0	2
15	O	0	2
19	S	0	1
22	V	0	1
25	Y	0	1
26	Z	0	1
27	a	0	3
28	b	0	1
46	t	0	6
48	5	0	1
All	All	0	24

The worst 5 of 99 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	t	168	PRO	N-CD	120.82	3.16	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	t	545	PRO	N-CD	120.55	3.16	1.47
46	t	162	PRO	N-CD	120.19	3.16	1.47
46	t	172	PRO	N-CD	118.17	3.13	1.47
46	t	520	PRO	N-CD	117.30	3.12	1.47

The worst 5 of 651 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	81	LYS	O-C-N	-96.20	4.54	122.87
46	t	544	ASN	O-C-N	-71.67	32.42	121.29
46	t	520	PRO	N-CA-CB	51.27	148.48	103.36
46	t	15	LYS	O-C-N	-50.72	41.85	123.00
46	t	168	PRO	N-CA-CB	50.42	148.65	103.27

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	143	GLU	Peptide
1	A	211	HIS	Peptide
3	C	91	GLY	Peptide
4	D	271	LYS	Peptide
5	E	129	GLU	Peptide

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	A	1912	0	1976	87	0
2	B	3075	0	3142	122	0
3	C	2748	0	2859	102	0
4	D	2359	0	2311	91	0
5	E	1248	0	1339	38	0
6	F	1791	0	1869	48	0
7	G	1763	0	1819	76	0
8	H	1518	0	1587	67	0
9	I	1722	0	1755	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	1353	0	1383	56	0
11	K	750	0	185	11	0
12	L	1548	0	1613	61	0
13	M	1059	0	1154	38	0
14	N	1720	0	1779	67	0
15	O	3119	0	3302	96	0
16	P	1227	0	1236	33	0
17	Q	1441	0	1543	48	0
18	R	1521	0	1617	44	0
19	S	1445	0	1487	51	0
20	T	1276	0	1323	53	0
21	U	778	0	791	25	0
22	V	1003	0	1048	28	0
23	W	1038	0	1071	23	0
24	X	959	0	1020	77	0
25	Y	993	0	1081	30	0
26	Z	1092	0	1155	59	0
27	a	1173	0	1215	57	0
28	b	462	0	491	16	0
29	c	767	0	816	36	0
30	d	883	0	918	28	0
31	e	1020	0	1090	41	0
32	f	850	0	880	30	0
33	g	880	0	945	36	0
34	h	965	0	1067	45	0
35	i	770	0	846	26	0
36	j	681	0	683	24	0
37	k	608	0	671	25	0
38	l	436	0	475	22	0
39	m	417	0	455	17	0
40	n	233	0	284	8	0
41	o	847	0	915	31	0
42	p	694	0	734	26	0
43	q	1077	0	1041	34	0
44	r	235	0	50	5	0
45	s	230	0	49	0	0
46	t	2938	0	2995	639	0
47	1	114	0	0	10	0
48	5	67376	0	33833	1170	0
49	7	2579	0	1303	38	0
50	8	3353	0	1695	49	0
51	j	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	m	1	0	0	0	0
51	o	1	0	0	2	0
51	p	1	0	0	0	0
All	All	130050	0	94896	3381	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 15.

The worst 5 of 3381 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)
17:Q:171:LYS:NZ	17:Q:171:LYS:CE	1.67	1.55
46:t:82:ASN:HD21	47:1:2029:A:P	1.32	1.52
46:t:198:LEU:HD13	46:t:319:ILE:CD1	1.43	1.49
10:J:8:PRO:CB	10:J:8:PRO:CG	1.75	1.49
24:X:137:ASN:CG	46:t:420:ARG:NH2	1.69	1.49

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	A	250/254 (98%)	213 (85%)	30 (12%)	7 (3%)	4	24
2	B	384/387 (99%)	341 (89%)	34 (9%)	9 (2%)	5	28
3	C	359/362 (99%)	306 (85%)	32 (9%)	21 (6%)	1	14
4	D	292/297 (98%)	267 (91%)	19 (6%)	6 (2%)	5	30
5	E	153/176 (87%)	134 (88%)	15 (10%)	4 (3%)	4	25
6	F	221/244 (91%)	201 (91%)	15 (7%)	5 (2%)	5	28
7	G	229/256 (90%)	181 (79%)	27 (12%)	21 (9%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	189/191 (99%)	172 (91%)	13 (7%)	4 (2%)	5	30
9	I	209/221 (95%)	175 (84%)	22 (10%)	12 (6%)	1	14
10	J	167/174 (96%)	135 (81%)	19 (11%)	13 (8%)	1	10
12	L	192/199 (96%)	161 (84%)	20 (10%)	11 (6%)	1	14
13	M	135/138 (98%)	124 (92%)	10 (7%)	1 (1%)	18	56
14	N	201/204 (98%)	182 (90%)	13 (6%)	6 (3%)	3	23
15	O	352/219 (161%)	324 (92%)	18 (5%)	10 (3%)	4	24
16	P	153/184 (83%)	142 (93%)	9 (6%)	2 (1%)	9	42
17	Q	183/186 (98%)	168 (92%)	9 (5%)	6 (3%)	3	21
18	R	186/189 (98%)	167 (90%)	16 (9%)	3 (2%)	7	38
19	S	170/172 (99%)	163 (96%)	6 (4%)	1 (1%)	21	59
20	T	157/160 (98%)	146 (93%)	9 (6%)	2 (1%)	9	42
21	U	96/121 (79%)	80 (83%)	13 (14%)	3 (3%)	3	22
22	V	134/137 (98%)	124 (92%)	8 (6%)	2 (2%)	8	40
23	W	133/155 (86%)	106 (80%)	19 (14%)	8 (6%)	1	13
24	X	118/142 (83%)	103 (87%)	7 (6%)	8 (7%)	1	11
25	Y	124/127 (98%)	107 (86%)	12 (10%)	5 (4%)	2	18
26	Z	133/136 (98%)	107 (80%)	13 (10%)	13 (10%)	0	7
27	a	146/149 (98%)	123 (84%)	18 (12%)	5 (3%)	3	21
28	b	56/59 (95%)	44 (79%)	7 (12%)	5 (9%)	0	8
29	c	98/105 (93%)	87 (89%)	8 (8%)	3 (3%)	3	22
30	d	107/113 (95%)	88 (82%)	13 (12%)	6 (6%)	1	14
31	e	125/130 (96%)	109 (87%)	10 (8%)	6 (5%)	2	16
32	f	104/107 (97%)	96 (92%)	5 (5%)	3 (3%)	3	23
33	g	110/121 (91%)	93 (84%)	13 (12%)	4 (4%)	2	20
34	h	117/120 (98%)	99 (85%)	14 (12%)	4 (3%)	3	21
35	i	97/100 (97%)	77 (79%)	13 (13%)	7 (7%)	1	11
36	j	85/88 (97%)	75 (88%)	8 (9%)	2 (2%)	4	27
37	k	75/78 (96%)	61 (81%)	10 (13%)	4 (5%)	1	15
38	l	48/51 (94%)	41 (85%)	6 (12%)	1 (2%)	5	30
39	m	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	n	23/25 (92%)	22 (96%)	0	1 (4%)	2	17
41	o	103/106 (97%)	90 (87%)	11 (11%)	2 (2%)	6	32
42	p	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
43	q	139/312 (45%)	111 (80%)	21 (15%)	7 (5%)	1	16
46	t	376/614 (61%)	354 (94%)	14 (4%)	8 (2%)	5	30
All	All	6868/7529 (91%)	6028 (88%)	588 (9%)	252 (4%)	4	20

5 of 252 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	LEU
2	B	129	ALA
2	B	140	ASP
2	B	347	SER
3	C	14	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/196 (98%)	149 (78%)	43 (22%)	1	6
2	B	321/323 (99%)	242 (75%)	79 (25%)	1	4
3	C	288/289 (100%)	213 (74%)	75 (26%)	0	3
4	D	243/245 (99%)	185 (76%)	58 (24%)	1	4
5	E	135/153 (88%)	113 (84%)	22 (16%)	2	10
6	F	187/205 (91%)	158 (84%)	29 (16%)	2	12
7	G	177/208 (85%)	136 (77%)	41 (23%)	1	5
8	H	171/171 (100%)	128 (75%)	43 (25%)	0	4
9	I	179/187 (96%)	134 (75%)	45 (25%)	0	4
10	J	147/150 (98%)	113 (77%)	34 (23%)	1	5
12	L	154/159 (97%)	126 (82%)	28 (18%)	2	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	M	108/109 (99%)	80 (74%)	28 (26%)	0	3
14	N	175/176 (99%)	139 (79%)	36 (21%)	1	6
15	O	323/179 (180%)	254 (79%)	69 (21%)	1	6
16	P	125/146 (86%)	98 (78%)	27 (22%)	1	6
17	Q	150/151 (99%)	121 (81%)	29 (19%)	1	7
18	R	153/154 (99%)	113 (74%)	40 (26%)	0	3
19	S	156/156 (100%)	119 (76%)	37 (24%)	1	4
20	T	136/137 (99%)	107 (79%)	29 (21%)	1	6
21	U	85/107 (79%)	60 (71%)	25 (29%)	0	2
22	V	104/105 (99%)	93 (89%)	11 (11%)	6	21
23	W	100/129 (78%)	83 (83%)	17 (17%)	2	10
24	X	104/118 (88%)	77 (74%)	27 (26%)	0	3
25	Y	109/110 (99%)	81 (74%)	28 (26%)	0	3
26	Z	115/116 (99%)	87 (76%)	28 (24%)	1	4
27	a	118/119 (99%)	90 (76%)	28 (24%)	1	4
28	b	46/47 (98%)	32 (70%)	14 (30%)	0	2
29	c	84/88 (96%)	65 (77%)	19 (23%)	1	6
30	d	94/97 (97%)	72 (77%)	22 (23%)	1	5
31	e	109/111 (98%)	85 (78%)	24 (22%)	1	6
32	f	90/91 (99%)	80 (89%)	10 (11%)	6	20
33	g	95/103 (92%)	70 (74%)	25 (26%)	0	3
34	h	103/105 (98%)	75 (73%)	28 (27%)	0	3
35	i	80/82 (98%)	51 (64%)	29 (36%)	0	1
36	j	70/71 (99%)	55 (79%)	15 (21%)	1	6
37	k	67/69 (97%)	50 (75%)	17 (25%)	0	3
38	l	45/46 (98%)	30 (67%)	15 (33%)	0	2
39	m	47/116 (40%)	35 (74%)	12 (26%)	0	3
40	n	23/23 (100%)	13 (56%)	10 (44%)	0	0
41	o	90/91 (99%)	72 (80%)	18 (20%)	1	7
42	p	71/72 (99%)	59 (83%)	12 (17%)	2	10
43	q	105/254 (41%)	74 (70%)	31 (30%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	t	332/539 (62%)	331 (100%)	1 (0%)	86	86
All	All	5806/6303 (92%)	4548 (78%)	1258 (22%)	3	6

5 of 1258 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	Z	134	LEU
37	k	31	LEU
27	a	132	LYS
26	Z	127	ASN
32	f	70	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
10	J	95	ASN
43	q	36	GLN
18	R	34	GLN
38	l	33	ASN
46	t	82	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
47	1	0/114	-	-
48	5	3145/3396 (92%)	747 (23%)	129 (4%)
49	7	120/121 (99%)	18 (15%)	0
50	8	157/158 (99%)	33 (21%)	3 (1%)
All	All	3422/3789 (90%)	798 (23%)	132 (3%)

5 of 798 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
48	5	14	U
48	5	15	C
48	5	16	A
48	5	26	A
48	5	38	U

5 of 132 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	5	3155	U
48	5	3228	C
50	8	126	A
48	5	1284	C
48	5	1241	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
11	K	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	52:UNK	C	54:UNK	N	3.86
1	K	23:UNK	C	28:UNK	N	3.48

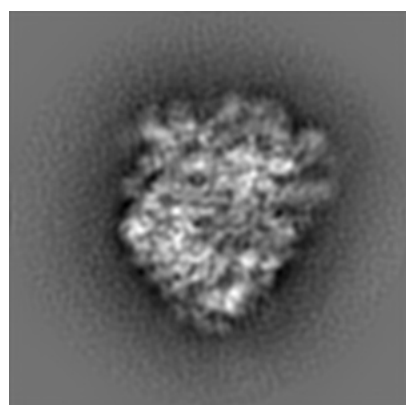
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2169. These allow visual inspection of the internal detail of the map and identification of artifacts.

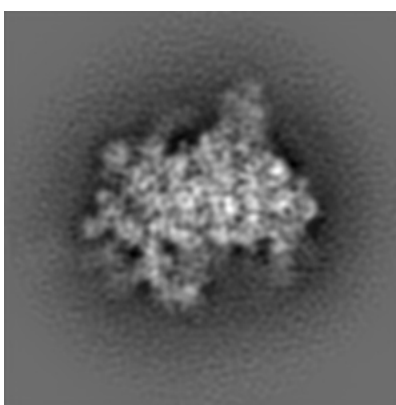
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

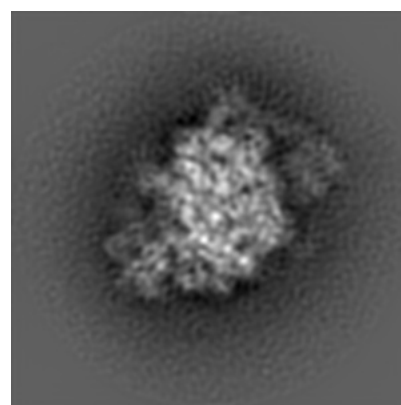
6.1.1 Primary map



X



Y

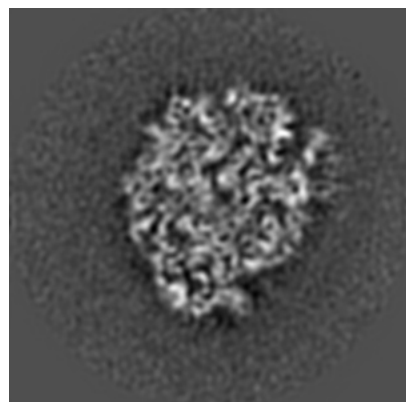


Z

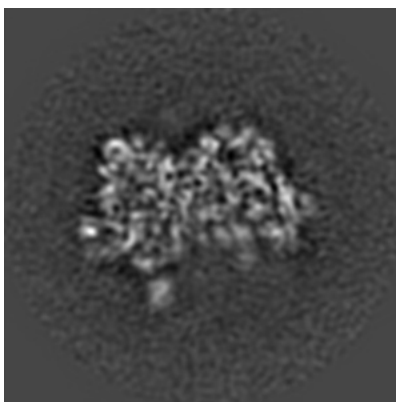
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

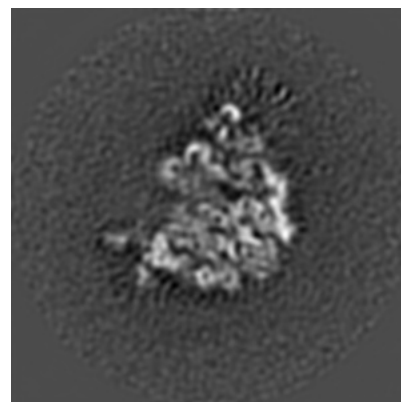
6.2.1 Primary map



X Index: 112



Y Index: 112

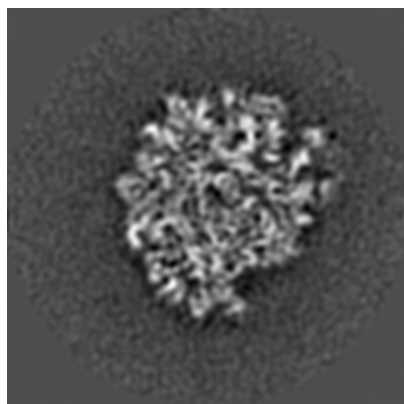


Z Index: 112

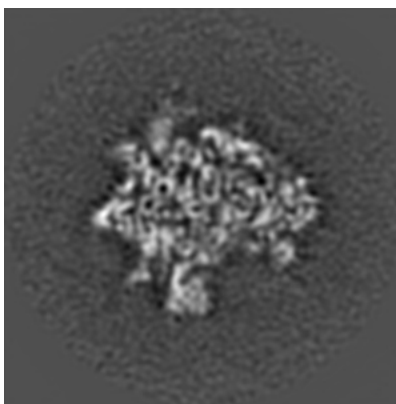
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

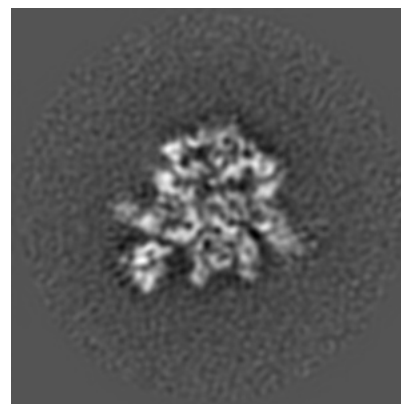
6.3.1 Primary map



X Index: 115



Y Index: 95

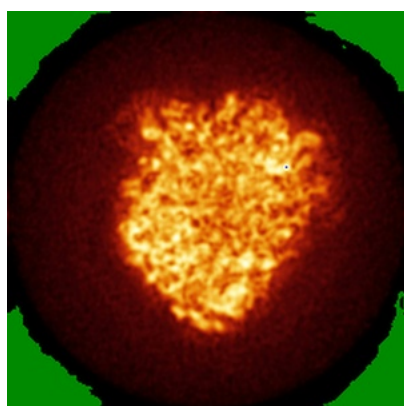


Z Index: 84

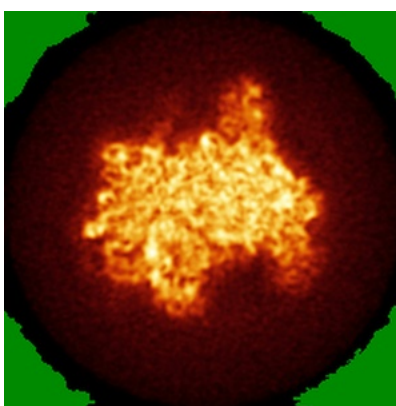
The images above show the largest variance slices of the map in three orthogonal directions.

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

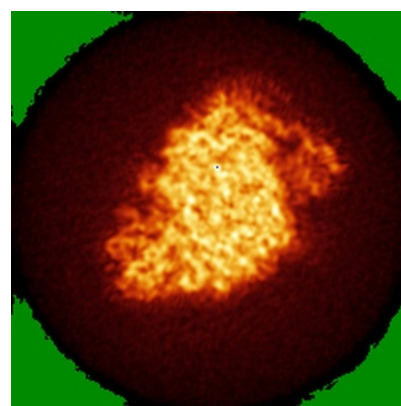
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 35.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

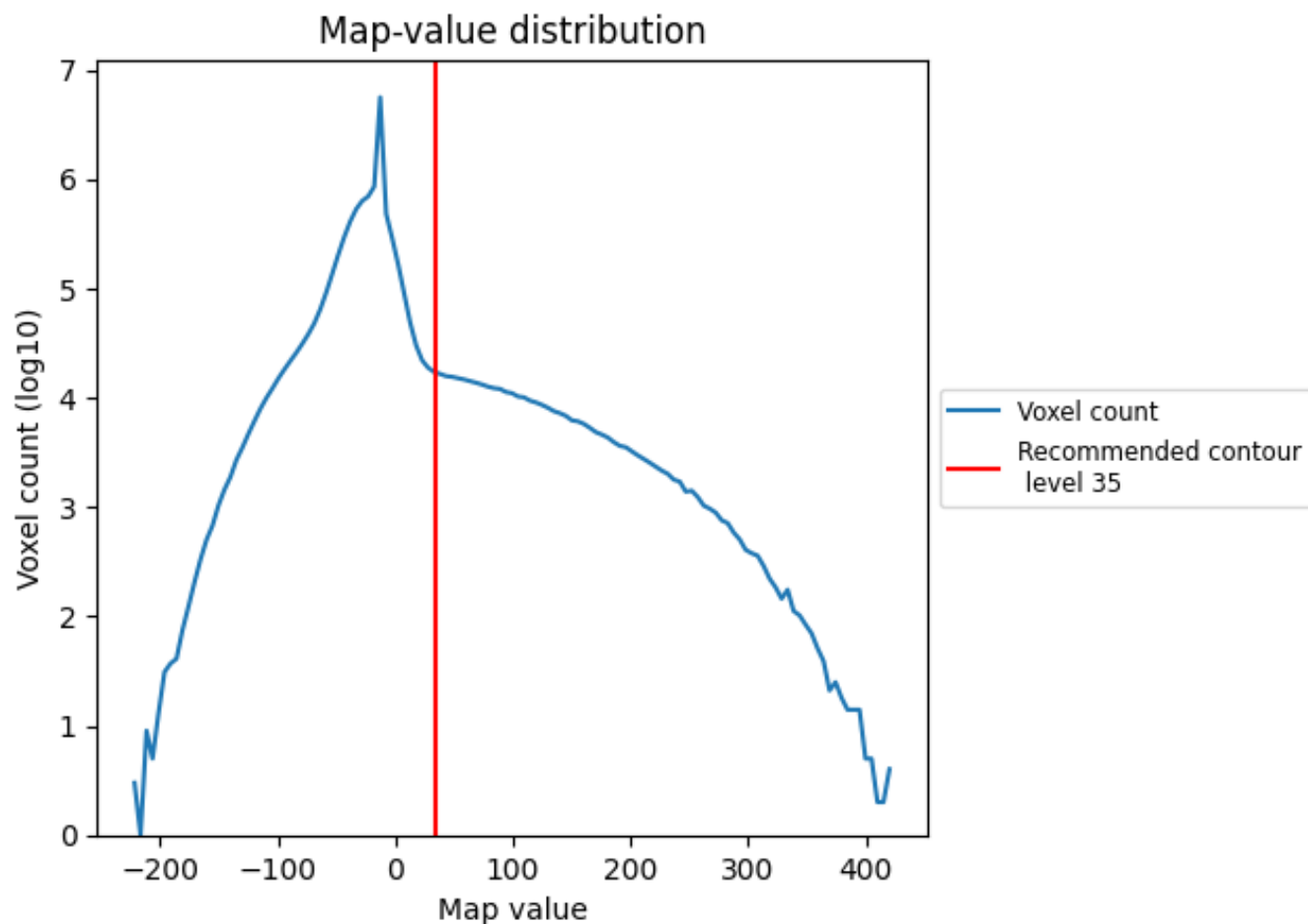
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

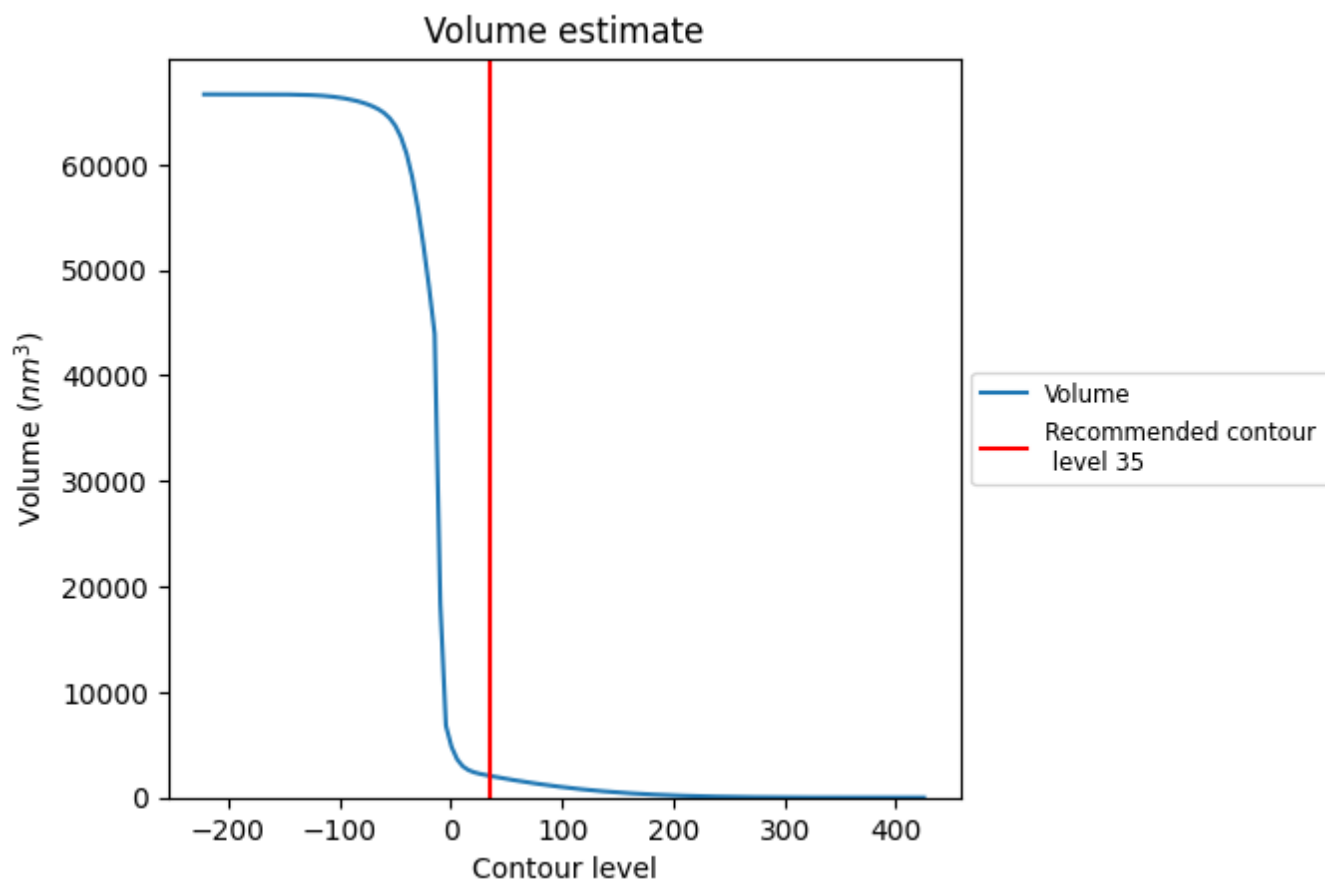
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

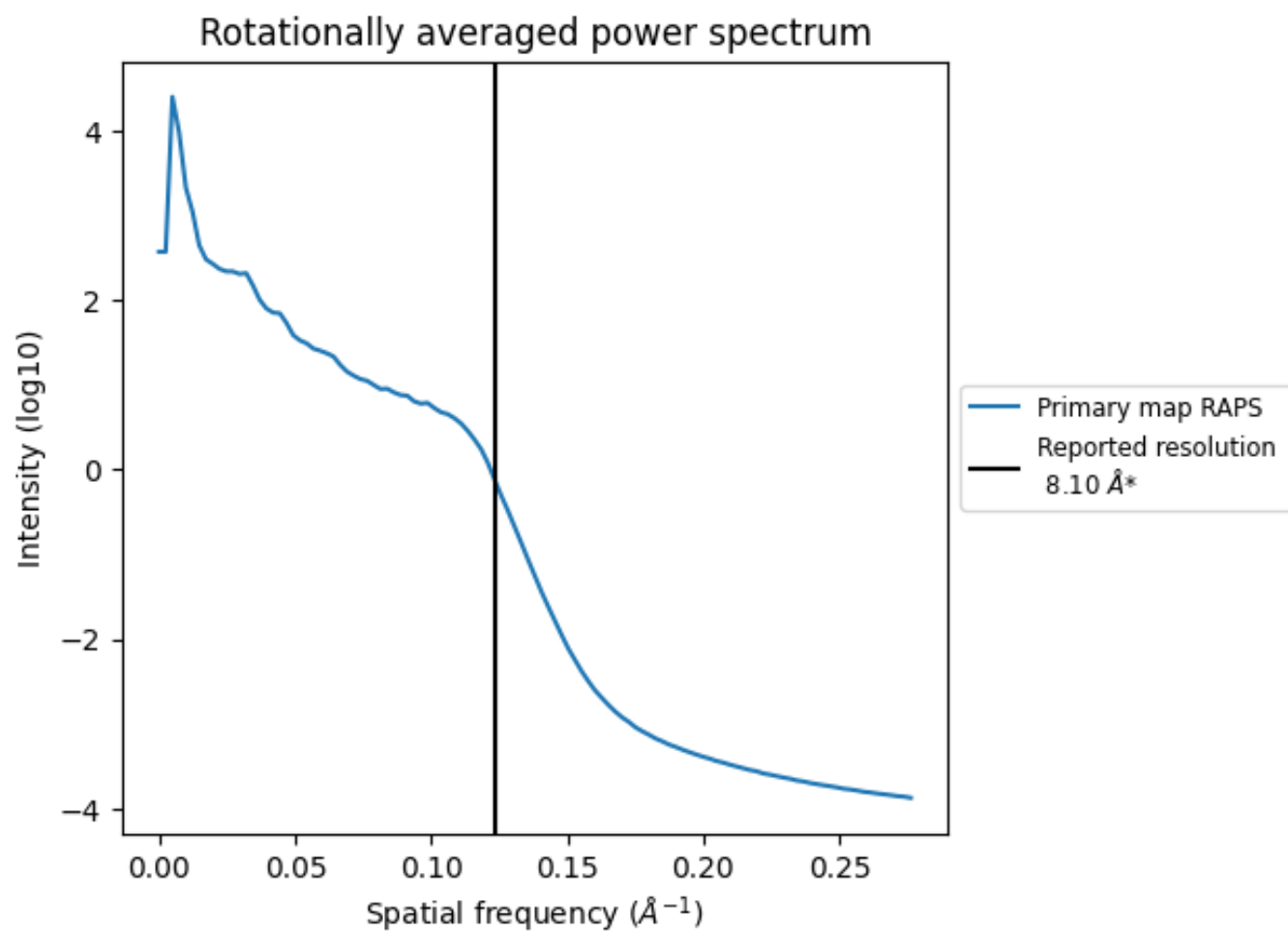
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2057 nm^3 ; this corresponds to an approximate mass of 1858 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 0.123 Å⁻¹

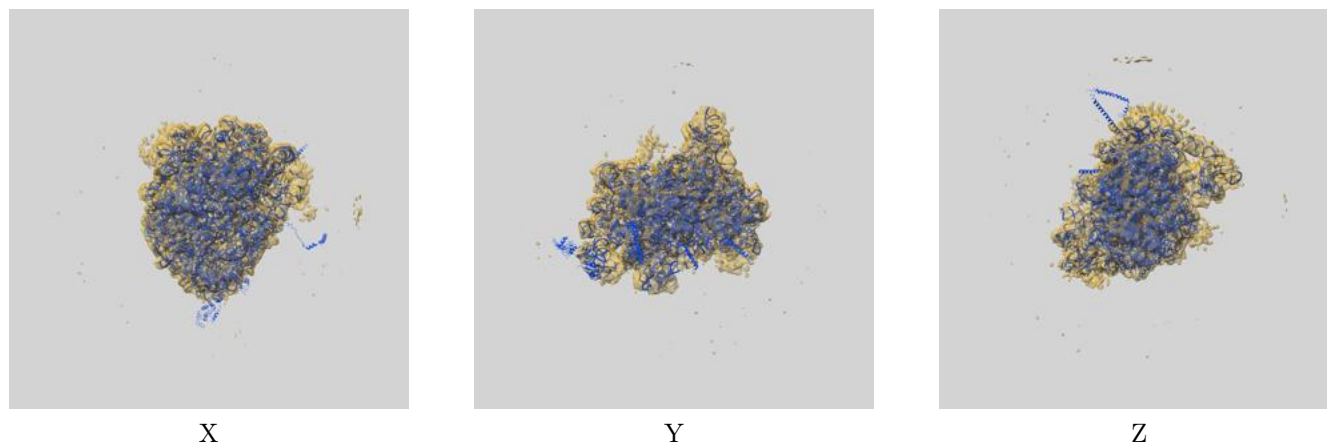
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

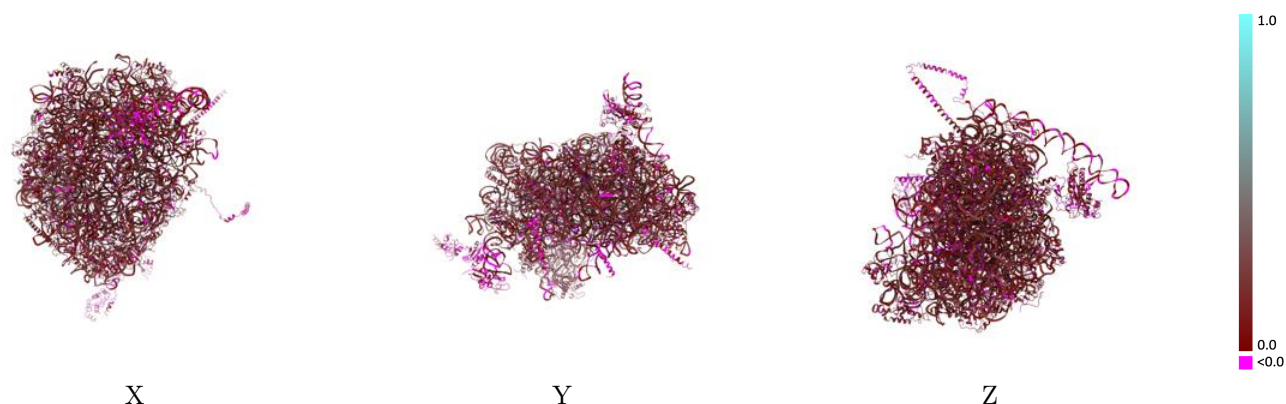
This section contains information regarding the fit between EMDB map EMD-2169 and PDB model 4V8T. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



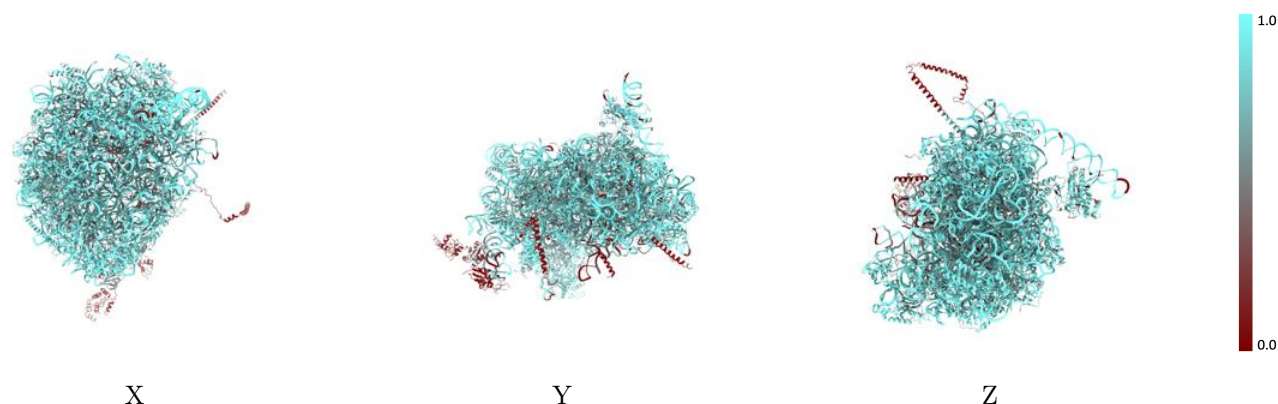
The images above show the 3D surface view of the map at the recommended contour level 35.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



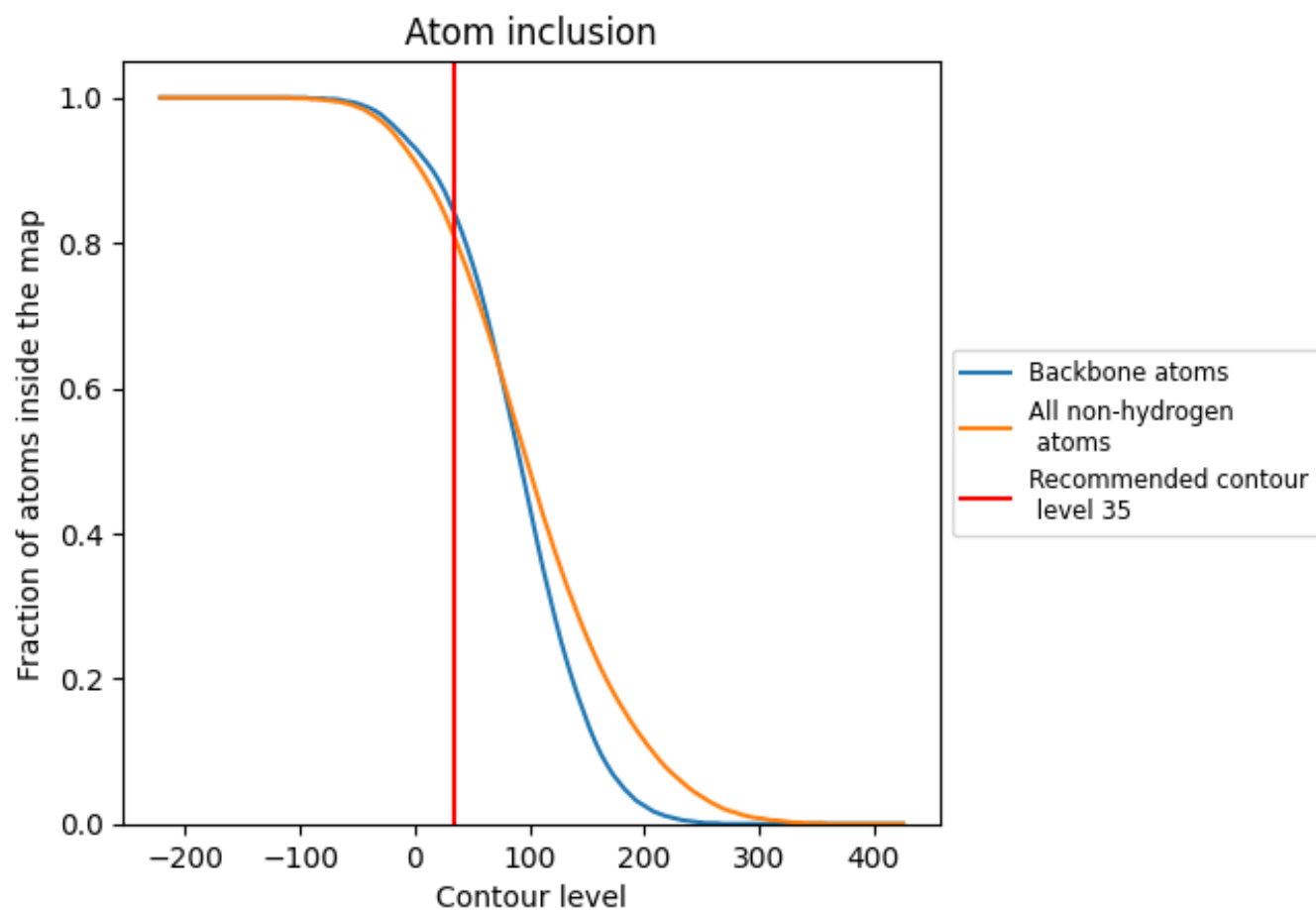
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 81% 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 (35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8060	 0.1350
1	 0.9210	 0.0730
5	 0.8850	 0.1540
7	 0.9700	 0.1670
8	 0.9200	 0.1690
A	 0.5420	 0.0710
B	 0.7000	 0.1060
C	 0.7170	 0.1120
D	 0.8100	 0.1160
E	 0.8080	 0.1310
F	 0.7420	 0.1380
G	 0.8230	 0.1300
H	 0.8120	 0.1290
I	 0.6820	 0.0940
J	 0.8520	 0.1170
K	 0.1310	 0.0320
L	 0.7830	 0.1380
M	 0.8550	 0.1500
N	 0.5560	 0.0810
O	 0.7690	 0.1420
P	 0.6700	 0.1020
Q	 0.6930	 0.1130
R	 0.5720	 0.1050
S	 0.7620	 0.1180
T	 0.7100	 0.1150
U	 0.7660	 0.1080
V	 0.6610	 0.1040
W	 0.3990	 0.0710
X	 0.7100	 0.1280
Y	 0.7650	 0.1130
Z	 0.7740	 0.1330
a	 0.6720	 0.1030
b	 0.6130	 0.1190
c	 0.7960	 0.1400
d	 0.7210	 0.1200



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Chain	Atom inclusion	Q-score
e	 0.6100	 0.1120
f	 0.7350	 0.1050
g	 0.5900	 0.0950
h	 0.7940	 0.1410
i	 0.7570	 0.1360
j	 0.6720	 0.0960
k	 0.8340	 0.1360
l	 0.5300	 0.1020
m	 0.7150	 0.1130
n	 0.0000	 -0.0490
o	 0.6250	 0.0810
p	 0.7700	 0.1110
q	 0.2200	 0.0110
r	 0.0000	 0.0090
s	 0.0000	 0.0190
t	 0.8060	 0.0840