



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:35 PM UTC

PDB ID : 9J9I / pdb_00009j9i
EMDB ID : EMD-61273
Title : High-resolution cryo-EM structure of the Plasmodium falciparum 80S ribosome bound to E-tRNA
Authors : Yan, X.F.; Gao, Y.G.
Deposited on : 2024-08-22
Resolution : 2.46 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

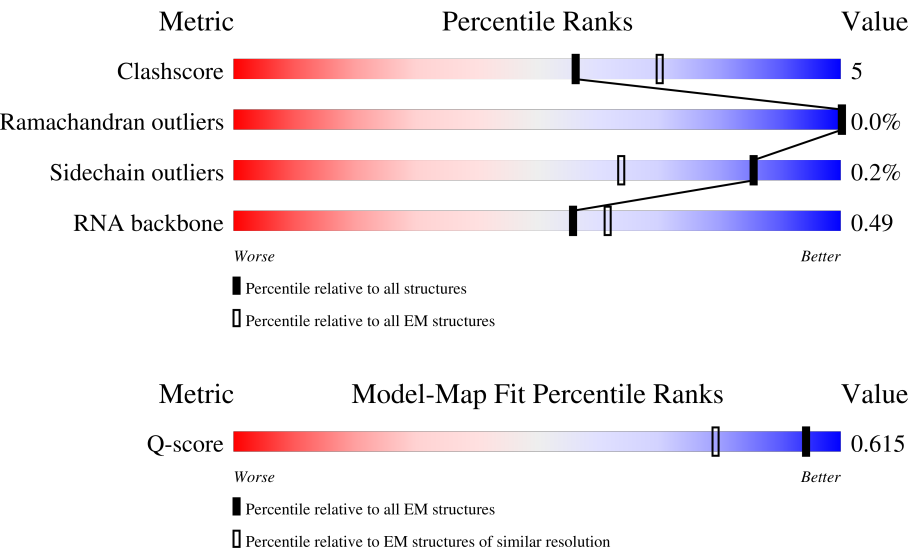
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.46 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.



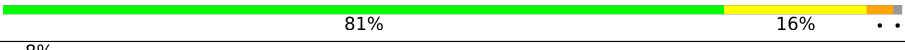
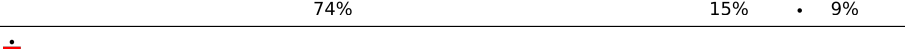
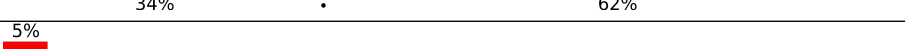
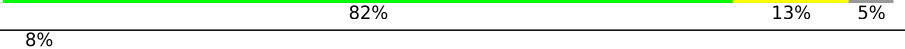
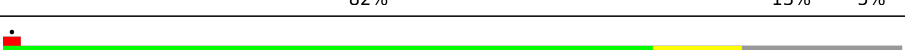
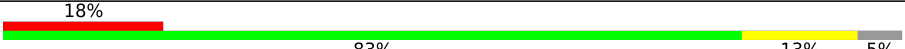
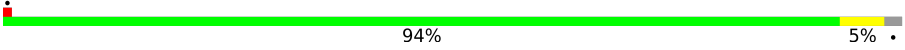
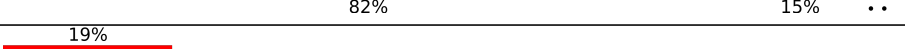
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6014 (1.96 - 2.96)

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	3789	5% 58% 22% • 15%
2	AA	141	47% 68% 15% 17%
3	j	2092	6% 53% 21% 5% 21%

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Mol	Chain	Length	Quality of chain
4	AH	170	
5	B	119	
6	AB	156	
7	k	262	
8	C	159	
9	AC	54	
10	l	263	
11	D	260	
12	0	162	
13	n	189	
14	E	386	
15	1	146	
16	o	261	
17	F	411	
18	2	127	
19	p	272	
20	G	173	
21	3	124	
22	q	306	
23	H	190	
24	4	67	
25	s	194	
26	I	221	
27	5	257	
28	t	130	

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Mol	Chain	Length	Quality of chain
29	J	283	
30	6	108	
31	u	218	
32	K	202	
33	7	120	
34	y	151	
35	L	215	
36	8	131	
37	z	145	
38	M	139	
39	9	140	
40	AD	151	
41	N	165	
42	a	150	
43	AE	161	
44	O	148	
45	b	112	
46	AI	82	
47	P	205	
48	c	92	
49	AQ	74	
50	Q	219	
51	d	87	
52	AK	105	
53	R	294	

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Mol	Chain	Length	Quality of chain
54	e	51	
55	AN	67	
56	S	187	
57	f	128	
58	AP	149	
59	T	182	
60	g	39	
61	m	221	
62	U	184	
63	h	96	
64	r	195	
65	V	161	
66	i	104	
67	v	144	
68	W	203	
69	AJ	133	
70	w	118	
71	X	139	
72	AL	107	
73	x	137	
74	Y	190	
75	AM	82	
76	AF	137	
77	Z	126	
78	AO	58	

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Mol	Chain	Length	Quality of chain
79	AG	145	8% 70% 10% 20%

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 197657 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3203	Total	C	N	O	P	0	0
			68120	30541	12090	22310	3179		

- Molecule 2 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AA	117	Total	C	N	O	S	0	0
			903	573	152	174	4		

- Molecule 3 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	j	1644	Total	C	N	O	P	0	0
			35005	15689	6240	11443	1633		

- Molecule 4 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AH	165	Total	C	N	O	S	0	0
			1353	866	253	232	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	118	Total	C	N	O	P	0	0
			2525	1128	461	818	118		

- Molecule 6 is a protein called 40S ribosomal protein S18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AB	142	Total	C	N	O	S	0	0
			1161	726	228	203	4		

- Molecule 7 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	k	210	Total	C	N	O	S	0	0
			1713	1097	301	303	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	152	Total	C	N	O	P	0	0
			3246	1454	594	1046	152		

- Molecule 9 is a protein called 40S ribosomal protein S29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AC	53	Total	C	N	O	S	0	0
			438	273	91	69	5		

- Molecule 10 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	l	195	Total	C	N	O	S	0	0
			1538	990	266	273	9		

- Molecule 11 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	247	Total	C	N	O	S	0	0
			1866	1166	374	317	9		

- Molecule 12 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

- Molecule 13 is a protein called 40S ribosomal protein S9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	185	Total	C	N	O	S	0	0
			1528	971	295	260	2		

- Molecule 14 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	380	Total	C	N	O	S	0	0
			3061	1948	575	521	17		

- Molecule 15 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	1	145	Total	C	N	O	S	0	0
			1171	758	212	198	3		

- Molecule 16 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	o	257	Total	C	N	O	S	0	0
			2061	1320	377	356	8		

- Molecule 17 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	F	390	Total	C	N	O	S	0	0
			3094	1962	594	527	11		

- Molecule 18 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2	121	Total	C	N	O	S	0	0
			960	607	173	177	3		

- Molecule 19 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	p	224	Total	C	N	O	S	0	0
			1757	1132	307	309	9		

- Molecule 20 is a protein called 60S ribosomal protein L11a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	G	165	Total	C	N	O	S	0	0
			1352	858	253	235	6		

- Molecule 21 is a protein called 60S ribosomal protein L35, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	3	122	Total	C	N	O	S	0	0
			1022	652	200	168	2		

- Molecule 22 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	q	213	Total	C	N	O	S	0	0
			1717	1087	329	295	6		

- Molecule 23 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	H	186	Total	C	N	O	S	0	0
			1468	943	262	256	7		

- Molecule 24 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 25 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	s	188	Total	C	N	O	S	0	0
			1528	982	264	278	4		

- Molecule 26 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	I	207	Total	C	N	O	S	0	0
			1684	1096	298	285	5		

- Molecule 27 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 28 is a protein called 40S ribosomal protein S15A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	t	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 29 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	J	229	Total	C	N	O	S	0	0
			1873	1210	337	319	7		

- Molecule 30 is a protein called 60S ribosomal protein L30e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	6	98	Total	C	N	O	S	0	0
			740	462	132	139	7		

- Molecule 31 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	u	168	Total	C	N	O	S	0	0
			1352	854	257	237	4		

- Molecule 32 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	K	201	Total	C	N	O	S	0	0
			1666	1070	311	277	8		

- Molecule 33 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	97	Total	C	N	O	S	0	0
			802	514	153	130	5		

- Molecule 34 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	y	133	Total	C	N	O	S	0	0
			998	619	192	184	3		

- Molecule 35 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L	211	Total	C	N	O	S	0	0
			1761	1119	349	290	3		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	8	125	Total	C	N	O	S	0	0
			1036	660	206	163	7		

- Molecule 37 is a protein called 40S ribosomal protein S23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	z	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 38 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	M	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 39 is a protein called 60S ribosomal protein L35ae, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	9	105	Total	C	N	O	S	0	0
			858	550	166	139	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AD	148	Total	C	N	O	S	0	0
			1196	766	219	208	3		

- Molecule 41 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	N	148	Total	C	N	O	S	0	0
			1221	793	216	206	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	a	106	Total	C	N	O	S	0	0
			858	530	184	138	6		

- Molecule 43 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AE	147	Total	C	N	O	S	0	0
			1211	775	228	201	7		

- Molecule 44 is a protein called 60S ribosomal protein L27a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	O	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 45 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	b	95	Total	C	N	O	S	0	0
			756	477	150	129			

- Molecule 46 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AI	81	Total	C	N	O	S	0	0
			631	395	113	118	5		

- Molecule 47 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	P	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 48 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	c	89	Total	C	N	O	S	0	0
			705	439	150	111	5		

- Molecule 49 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	AQ	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

- Molecule 50 is a protein called 60S ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Q	192	Total	C	N	O	S	0	0
			1567	997	297	264	9		

- Molecule 51 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	d	76	Total	C	N	O	S	0	0
			636	415	114	105	2		

- Molecule 52 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AK	72	Total	C	N	O	S	0	0
			565	361	100	101	3		

- Molecule 53 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	R	267	Total	C	N	O	S	0	0
			2171	1376	406	383	6		

- Molecule 54 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	e	50	Total	C	N	O	S	0	0
			452	284	104	63	1		

- Molecule 55 is a protein called 40S ribosomal protein S28e, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	AN	58	Total	C	N	O	0	0
			451	282	90	79		

- Molecule 56 is a protein called 60S ribosomal protein L18-2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S	186	Total	C	N	O	S	0	0
			1502	958	299	240	5		

- Molecule 57 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	f	51	Total	C	N	O	S	0	0
			413	255	87	66	5		

- Molecule 58 is a protein called Ribosomal protein S27a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AP	70	Total	C	N	O	S	0	0
			573	368	109	90	6		

- Molecule 59 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	T	181	Total	C	N	O	S	0	0
			1505	949	308	244	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	g	37	Total	C	N	O	S	0	0
			342	210	86	44	2		

- Molecule 61 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	m	213	Total	C	N	O	S	0	0
			1672	1051	315	299	7		

- Molecule 62 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	U	180	Total	C	N	O	S	0	0
			1496	946	289	254	7		

- Molecule 63 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	h	85	Total	C	N	O	S	0	0
			658	417	127	107	7		

- Molecule 64 is a protein called 40S ribosomal protein S5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	r	189	Total	C	N	O	S	0	0
			1487	931	278	268	10		

- Molecule 65 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	V	156	Total	C	N	O	S	0	0
			1279	816	242	215	6		

- Molecule 66 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	i	96	Total	C	N	O	S	0	0
			787	496	154	128	9		

- Molecule 67 is a protein called 40S ribosomal protein S16, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	v	138	Total	C	N	O	S	0	0
			1098	704	200	193	1		

- Molecule 68 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	W	172	Total	C	N	O	S	0	0
			1336	836	270	223	7		

- Molecule 69 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AJ	121	Total	C	N	O	S	0	0
			994	637	190	165	2		

- Molecule 70 is a protein called 40S ribosomal protein S20e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	w	102	Total	C	N	O	S	0	0
			813	508	148	152	5		

- Molecule 71 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	X	97	Total	C	N	O	S	0	0
			824	548	135	139	2		

- Molecule 72 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AL	95	Total	C	N	O	S	0	0
			781	478	169	128	6		

- Molecule 73 is a protein called 40S ribosomal protein S10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	x	98	Total	C	N	O	S	0	0
			839	555	142	140	2		

- Molecule 74 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Y	101	Total	C	N	O	S	0	0
			796	502	144	144	6		

- Molecule 75 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AM	79	Total	C	N	O	S	0	0
			610	384	105	112	9		

- Molecule 76 is a protein called 40S ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AF	118	Total	C	N	O	S	0	0
			963	612	179	168	4		

- Molecule 77 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Z	122	Total	C	N	O	S	0	0
			1005	629	207	166	3		

- Molecule 78 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
78	AO	43	Total	C	N	O	0	0
			345	213	75	57		

- Molecule 79 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	AG	116	Total	C	N	O	S	0	0
			945	602	175	164	4		

- Molecule 80 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
80	A	173	Total	Mg	0
			173	173	
80	j	60	Total	Mg	0
			60	60	
80	AH	1	Total	Mg	0
			1	1	
80	B	3	Total	Mg	0
			3	3	
80	C	7	Total	Mg	0
			7	7	
80	E	1	Total	Mg	0
			1	1	
80	H	1	Total	Mg	0
			1	1	
80	8	1	Total	Mg	0
			1	1	
80	M	1	Total	Mg	0
			1	1	
80	a	1	Total	Mg	0
			1	1	
80	Q	1	Total	Mg	0
			1	1	
80	W	2	Total	Mg	0
			2	2	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
80	AJ	1	Total 1	Mg 1	0
80	X	1	Total 1	Mg 1	0

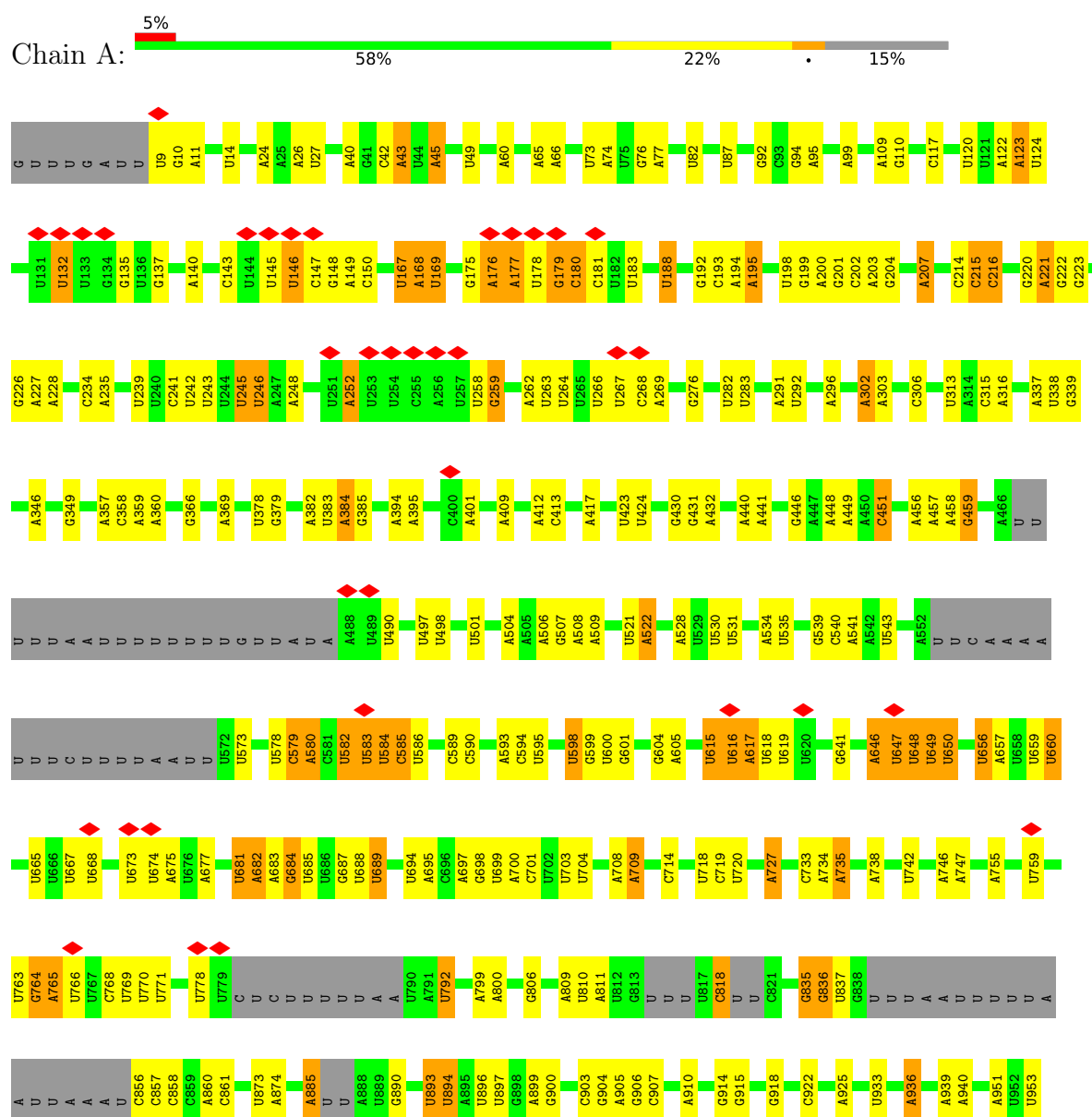
- Molecule 81 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
81	AC	1	Total 1	Zn 1	0
81	a	1	Total 1	Zn 1	0
81	c	1	Total 1	Zn 1	0
81	f	1	Total 1	Zn 1	0
81	h	1	Total 1	Zn 1	0
81	i	1	Total 1	Zn 1	0

3 Residue-property plots

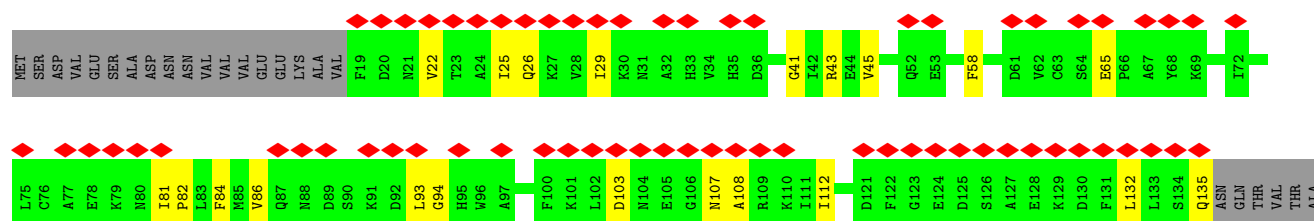
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 28S ribosomal RNA

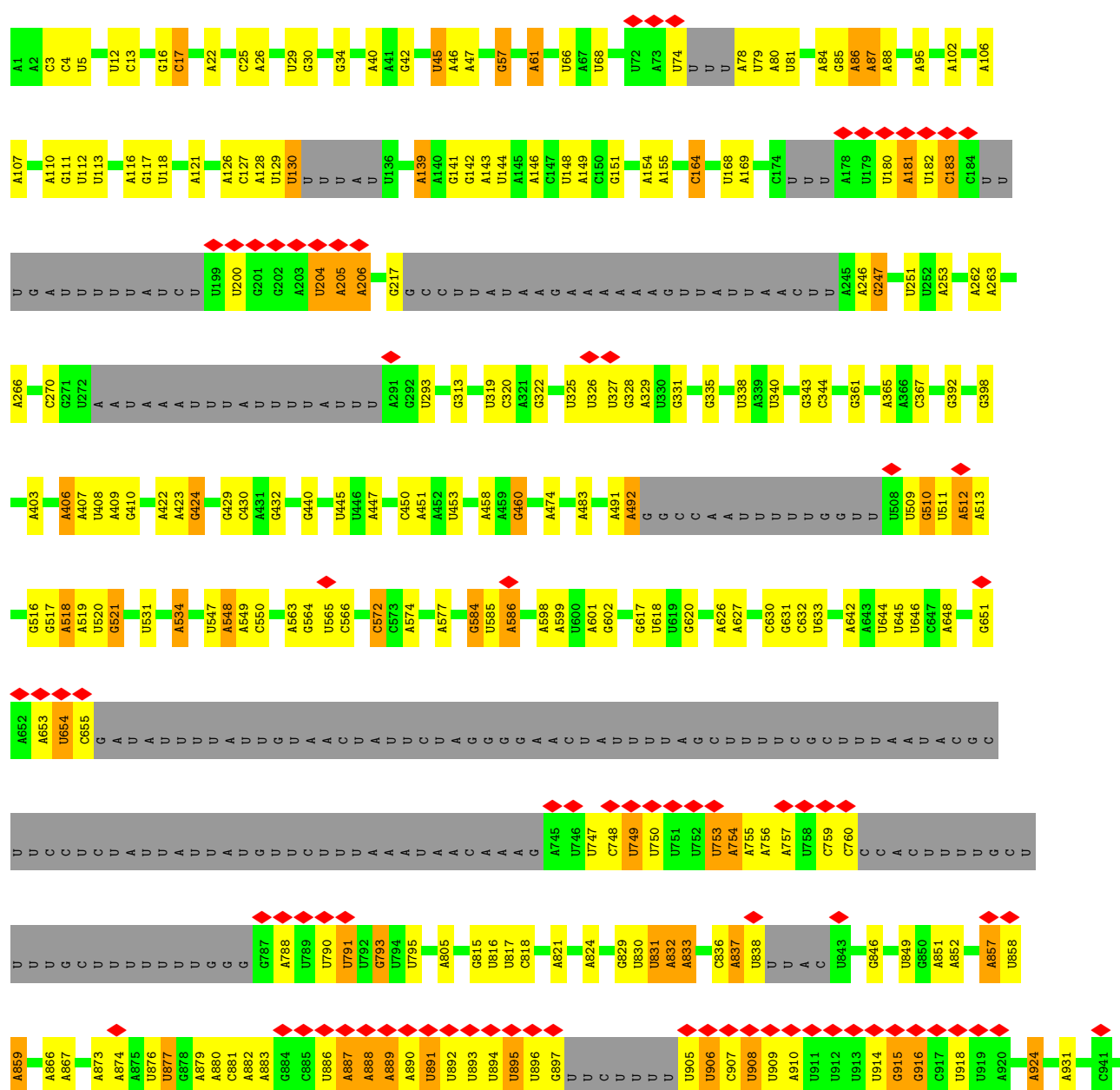


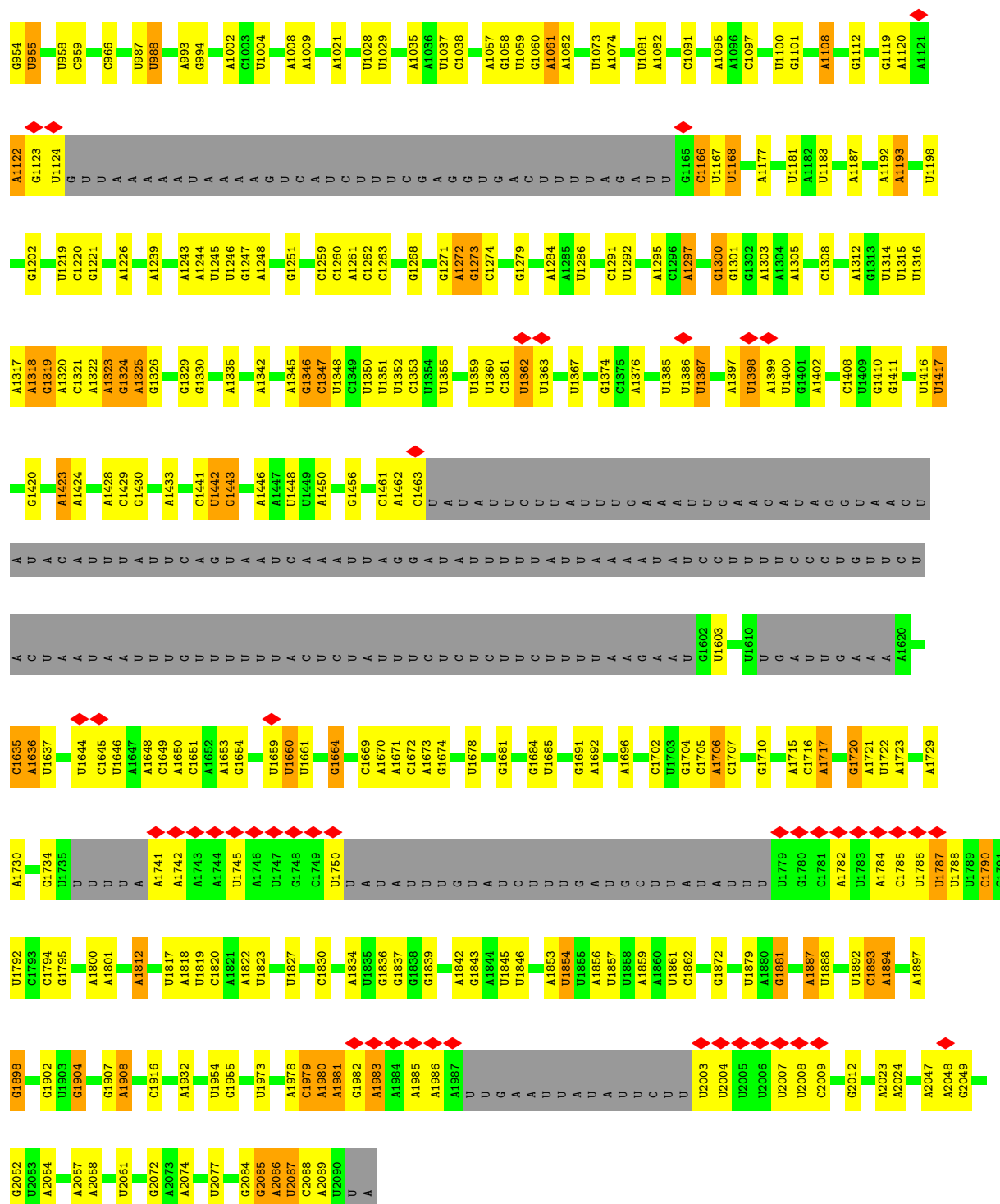






• Molecule 3: 18S ribosomal RNA





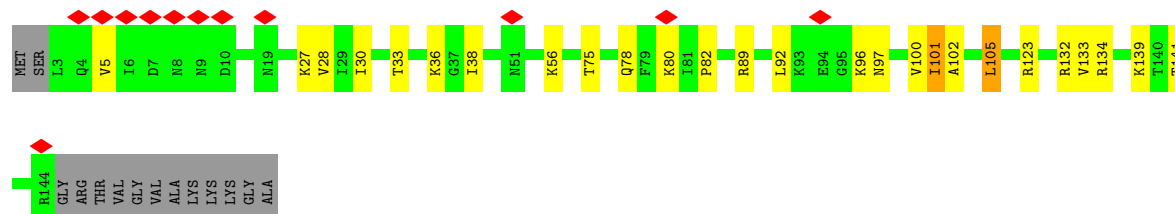
- Molecule 5: 5S ribosomal RNA

Chain B:  81% 16% . .



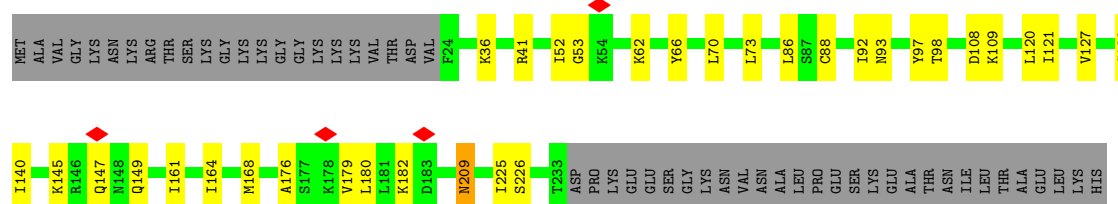
- Molecule 6: 40S ribosomal protein S18, putative

Chain AB:  8% 74% 15% . 9%



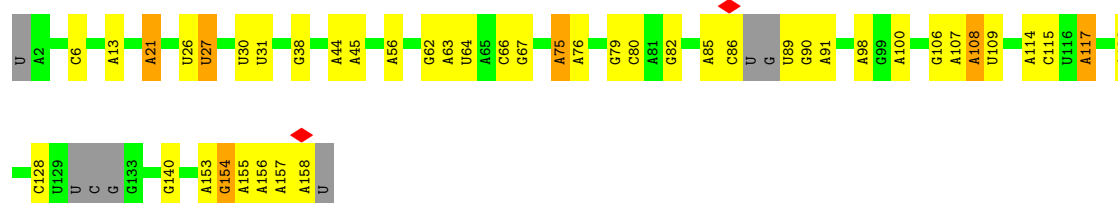
- Molecule 7: Small ribosomal subunit protein eS1

Chain k:  67% 13% 20%



- Molecule 8: 5.8S ribosomal RNA

Chain C:  68% 24% . .



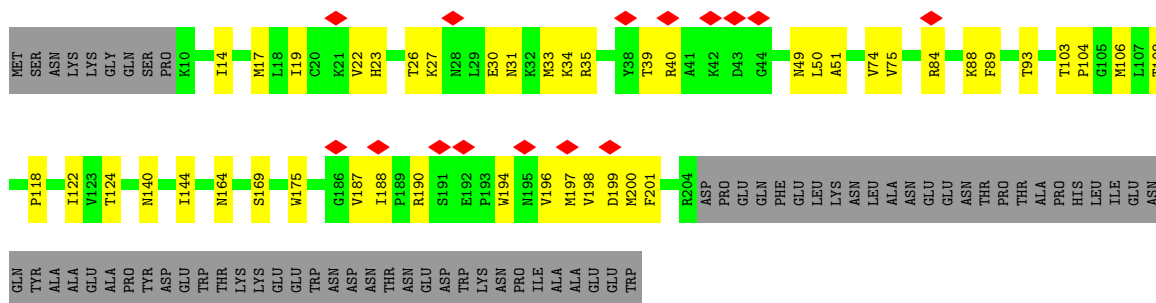
- Molecule 9: 40S ribosomal protein S29, putative

Chain AC:  78% 20% .

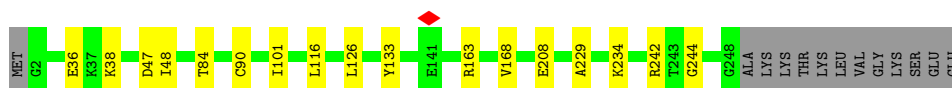


- Molecule 10: Small ribosomal subunit protein uS2

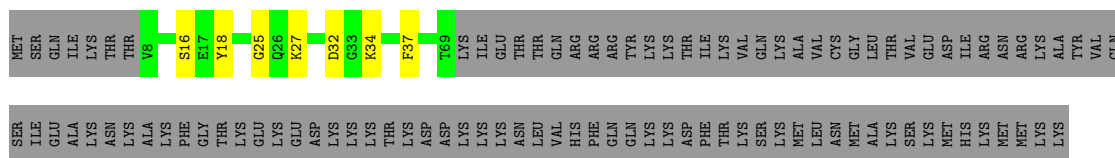
Chain l:  6% 57% 17% 26%



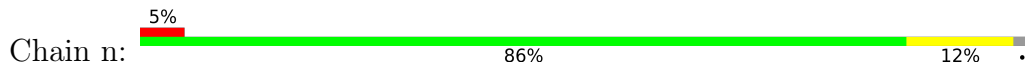
- Molecule 11: 60S ribosomal protein L2



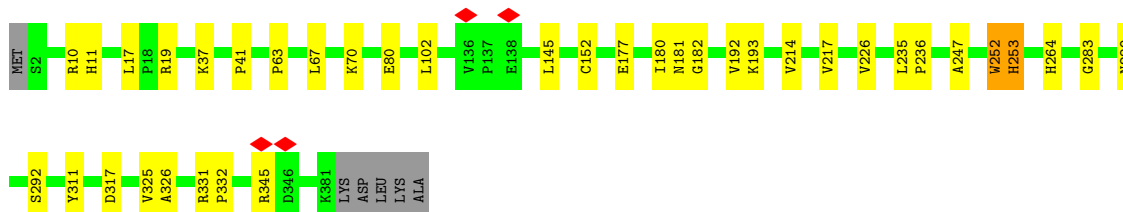
- Molecule 12: 60S ribosomal protein L24, putative



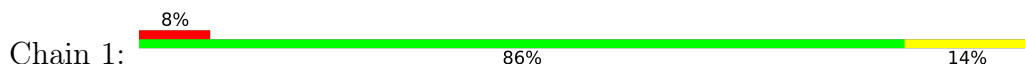
- Molecule 13: 40S ribosomal protein S9, putative

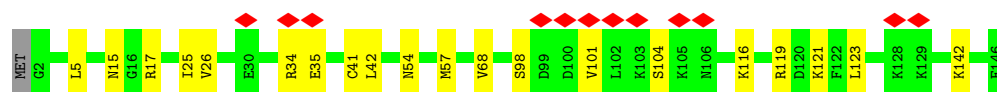


- Molecule 14: 60S ribosomal protein L3

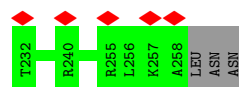
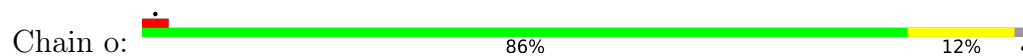


- Molecule 15: 60S ribosomal protein L27

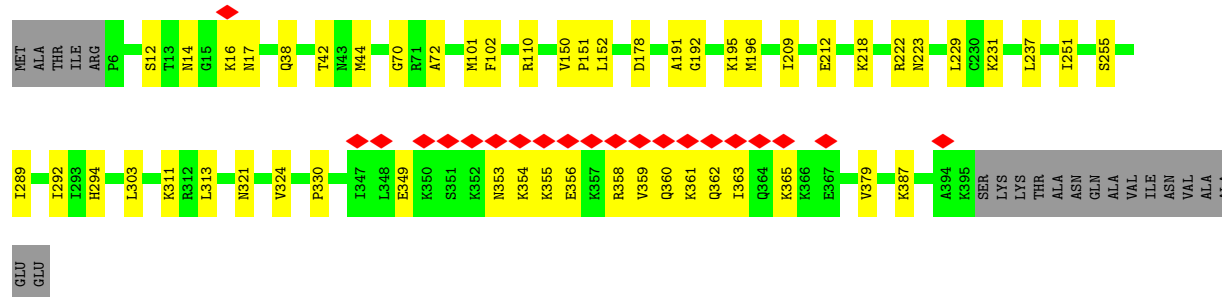
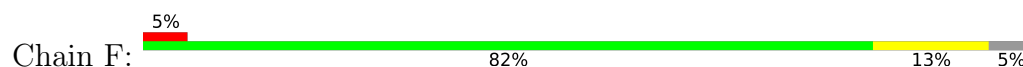




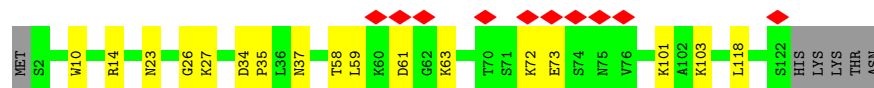
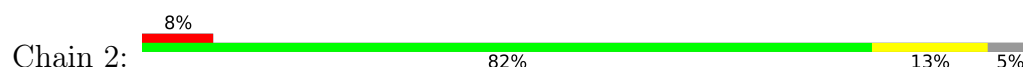
- Molecule 16: 40S ribosomal protein S4



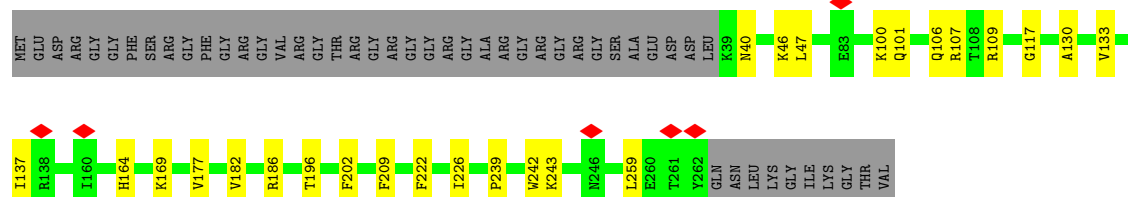
- Molecule 17: 60S ribosomal protein L4



- Molecule 18: 60S ribosomal protein L28

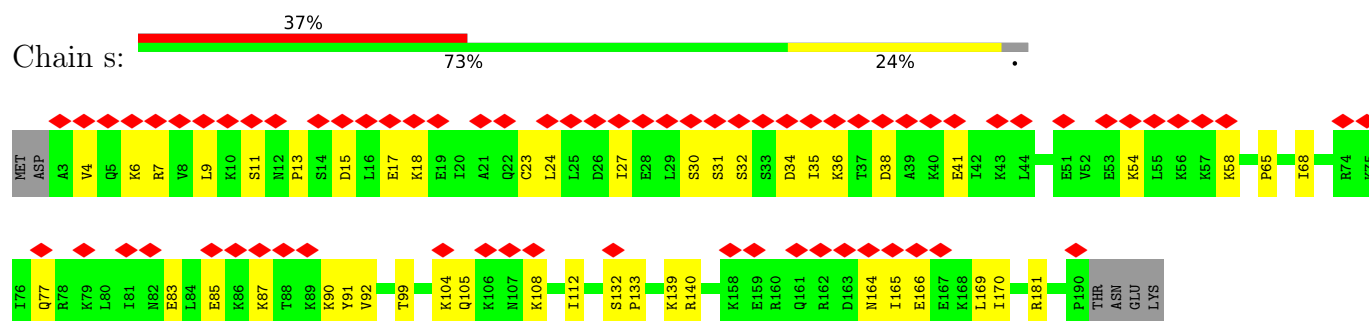


- Molecule 19: 40S ribosomal protein S5

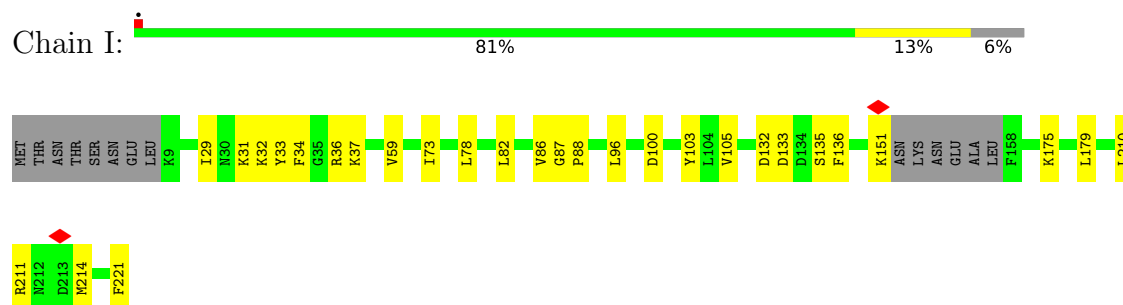


- Molecule 20: 60S ribosomal protein L11a, putative

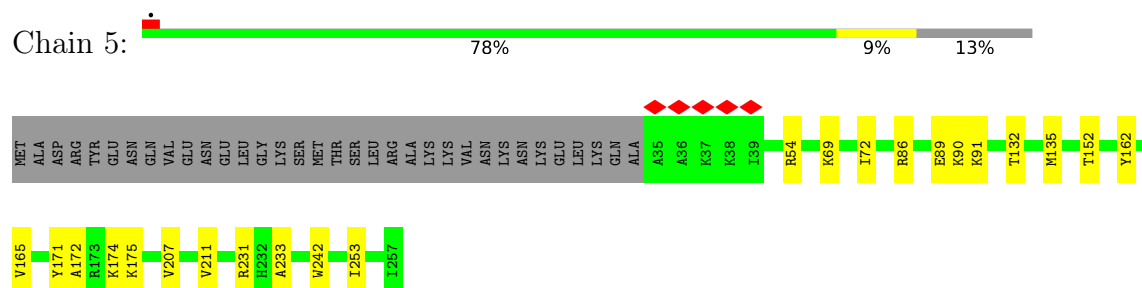
- Molecule 25: 40S ribosomal protein S7



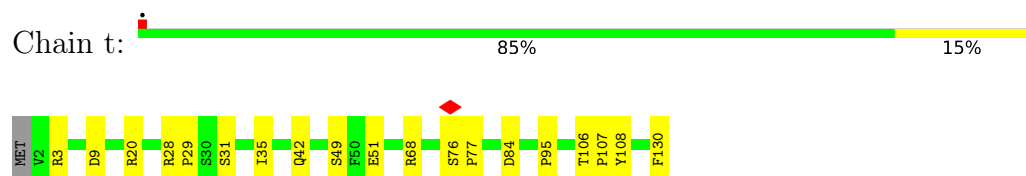
- Molecule 26: 60S ribosomal protein L6, putative



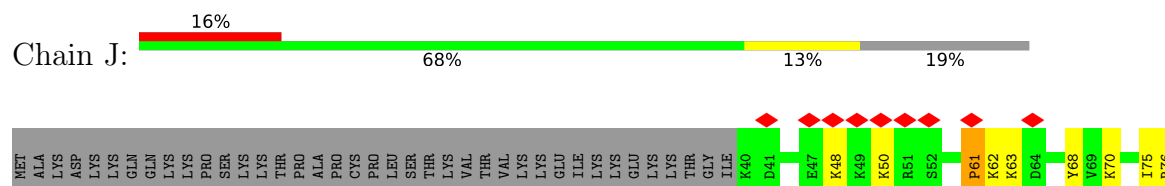
- Molecule 27: 60S ribosomal protein L7, putative

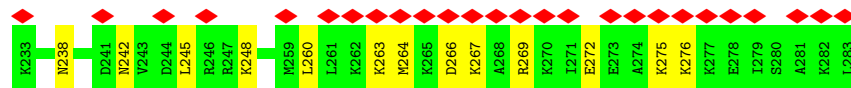


- Molecule 28: 40S ribosomal protein S15A, putative

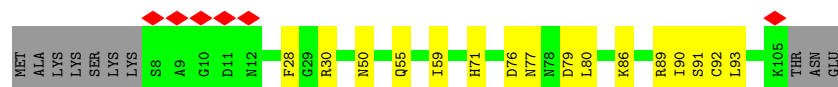
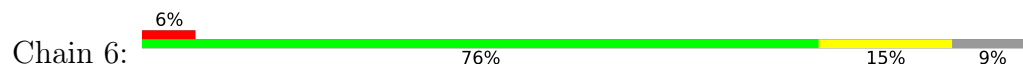


- Molecule 29: 60S ribosomal protein L7a

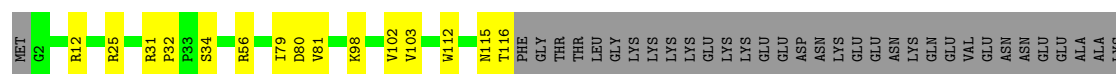




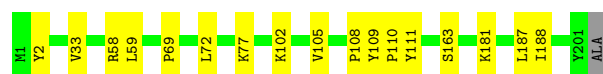
- Molecule 30: 60S ribosomal protein L30e, putative



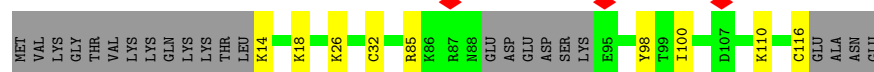
- Molecule 31: 40S ribosomal protein S8



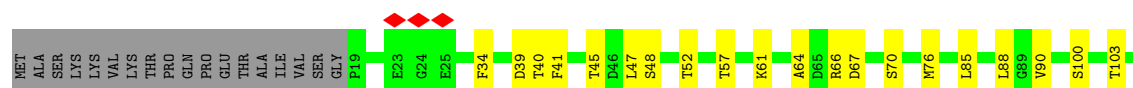
- Molecule 32: 60S ribosomal protein L13, putative



- Molecule 33: 60S ribosomal protein L31

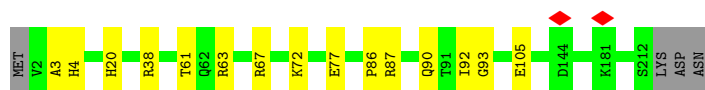


- Molecule 34: 40S ribosomal protein S11



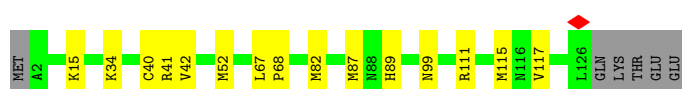
- Molecule 35: 60S ribosomal protein L13

Chain L:  91% 7%



- Molecule 36: 60S ribosomal protein L32

Chain 8:  84% 11% 5%



- Molecule 37: 40S ribosomal protein S23, putative

Chain z:  7% 88% 11%



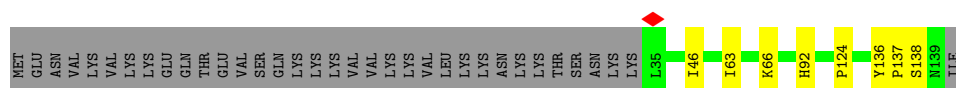
- Molecule 38: 60S ribosomal protein L23, putative

Chain M:  83% 12% 5%



- Molecule 39: 60S ribosomal protein L35ae, putative

Chain 9:  69% 6% 25%



- Molecule 40: 40S ribosomal protein S15

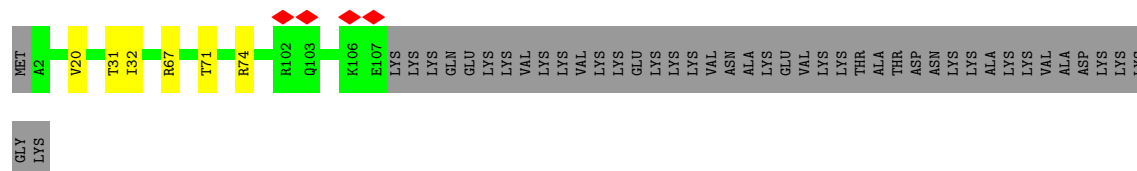
Chain AD:  89% 9%



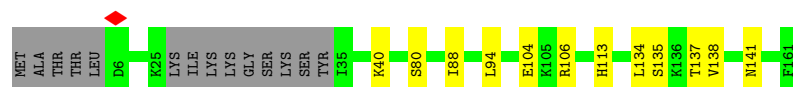
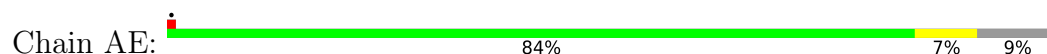
- Molecule 41: 60S ribosomal protein L14, putative

Chain N:  73% 16% 10%

- Molecule 42: 60S ribosomal protein L34



- Molecule 43: 40S ribosomal protein S11, putative



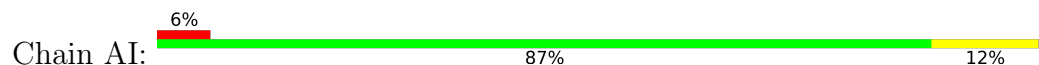
- Molecule 44: 60S ribosomal protein L27a, putative



- Molecule 45: 60S ribosomal protein L36



- Molecule 46: 40S ribosomal protein S21

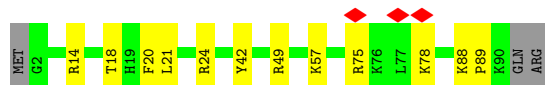
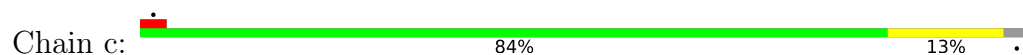


- Molecule 47: Ribosomal protein L15

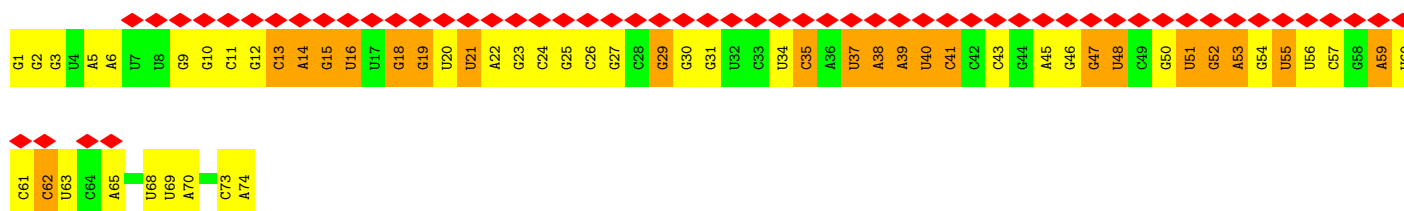
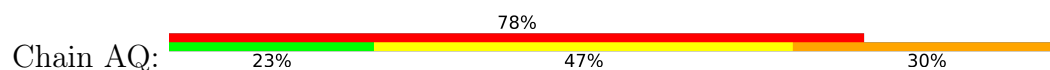




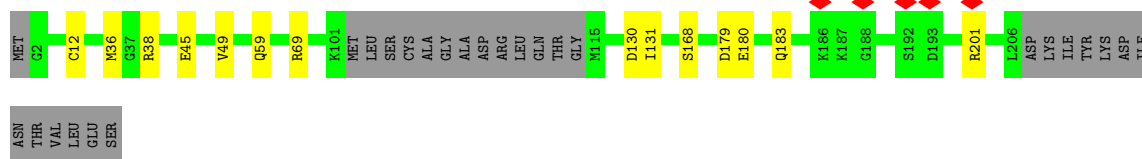
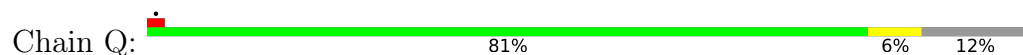
• Molecule 48: Ribosomal protein L37



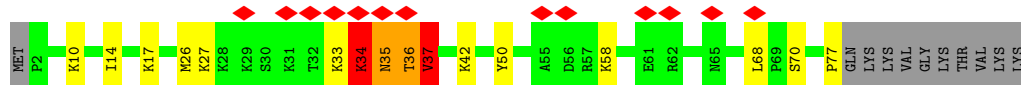
• Molecule 49: tRNA



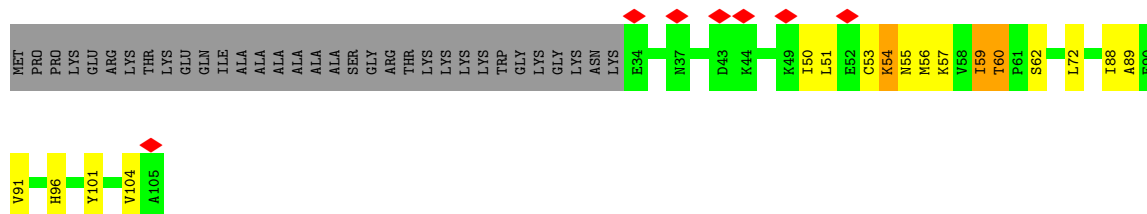
• Molecule 50: 60S ribosomal protein L10, putative

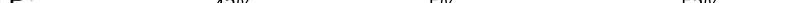


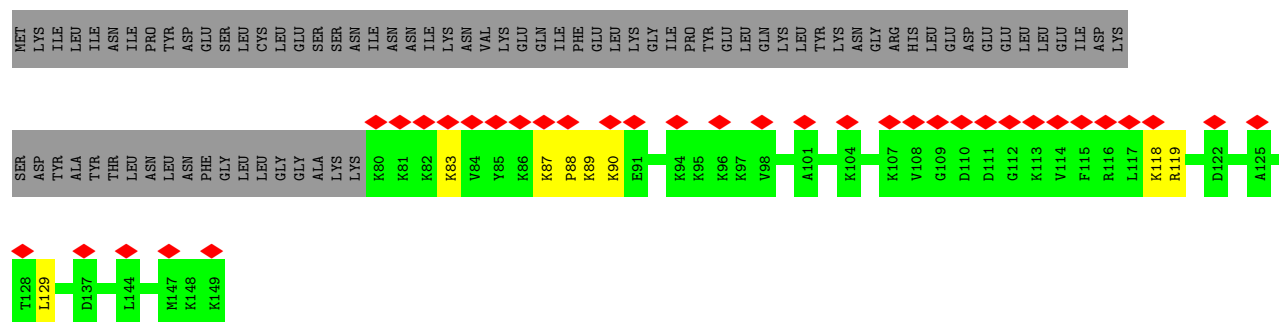
• Molecule 51: 60S ribosomal protein L38



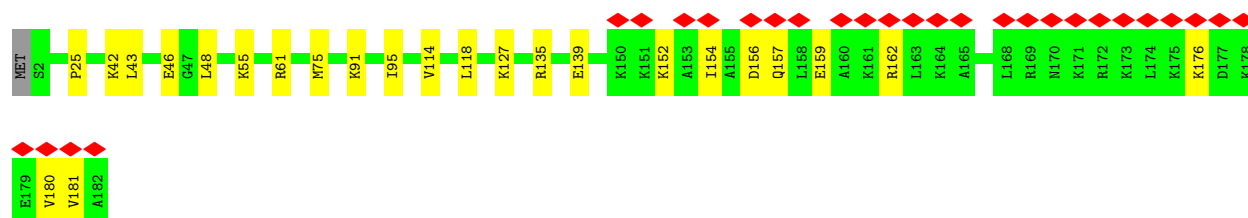
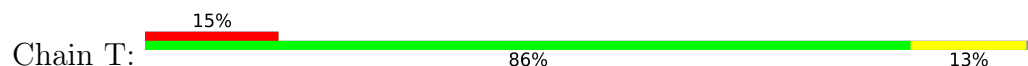
• Molecule 52: 40S ribosomal protein S25



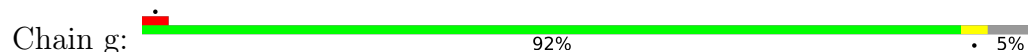
- Chain AP: 



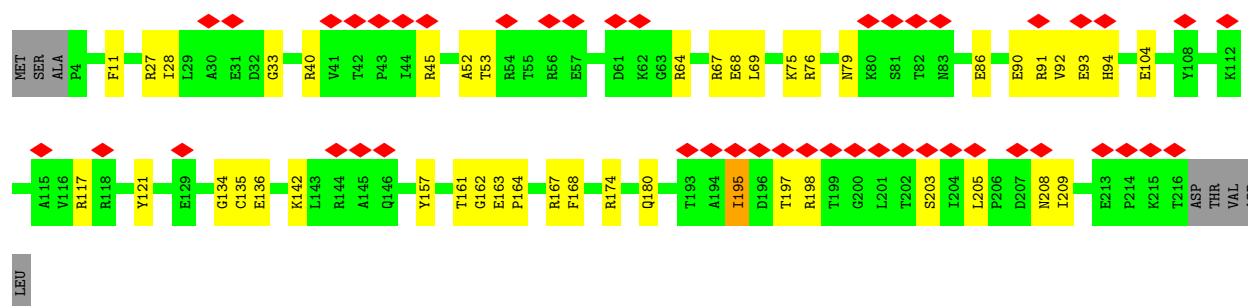
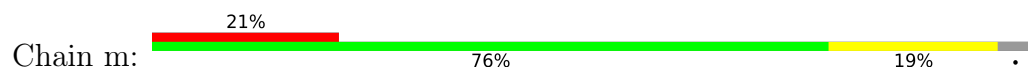
• Molecule 59: 60S ribosomal protein L19



• Molecule 60: 60S ribosomal protein L41



• Molecule 61: 40S ribosomal protein S3



• Molecule 62: 60S ribosomal protein L18a



- Molecule 63: Large ribosomal subunit protein eL43

Chain h:  83% 5% 11%



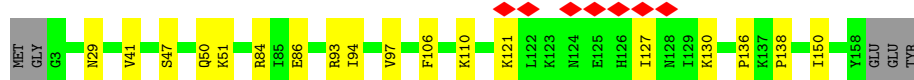
- Molecule 64: 40S ribosomal protein S5, putative

Chain r:  6% 87% 10%



- Molecule 65: 60S ribosomal protein L21

Chain V:  86% 11%



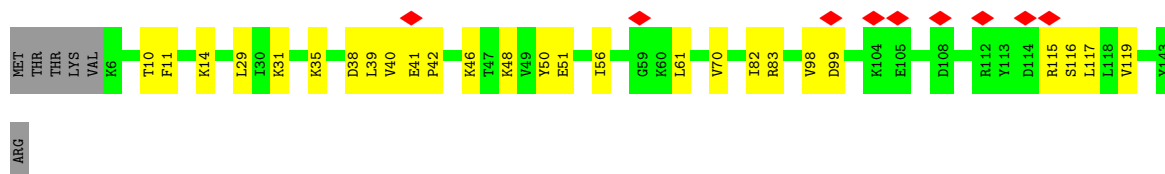
- Molecule 66: Large ribosomal subunit protein eL42

Chain i:  85% 8% 8%



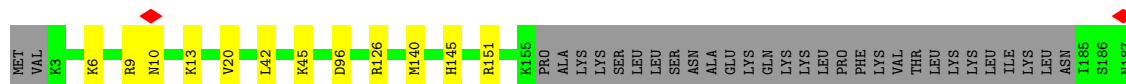
- Molecule 67: 40S ribosomal protein S16, putative

Chain v:  6% 78% 18%

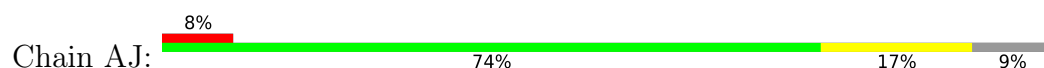


- Molecule 68: 60S ribosomal protein L17, putative

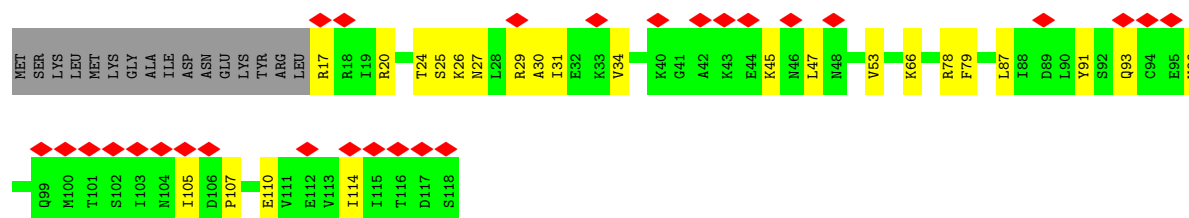
Chain W:  78% 7% 15%



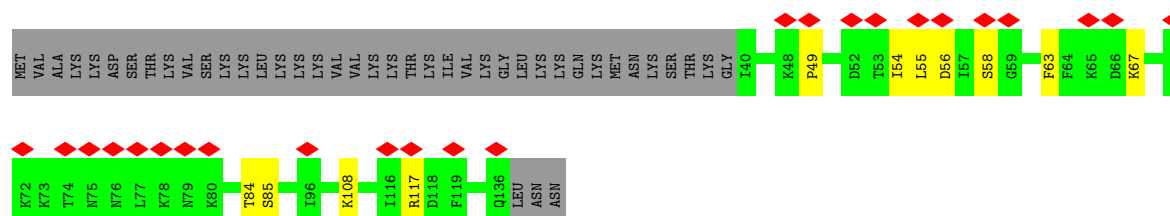
- Molecule 69: 40S ribosomal protein S24



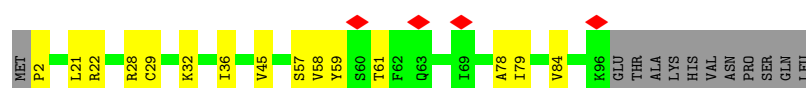
- Molecule 70: 40S ribosomal protein S20e, putative



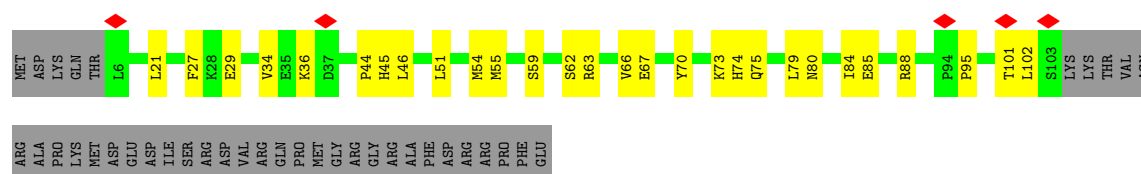
- Molecule 71: Large ribosomal subunit protein eL22



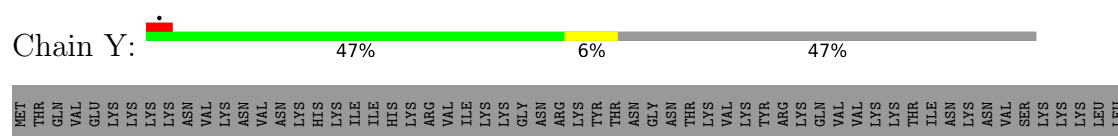
- Molecule 72: 40S ribosomal protein S26



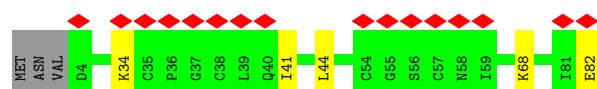
- Molecule 73: 40S ribosomal protein S10, putative



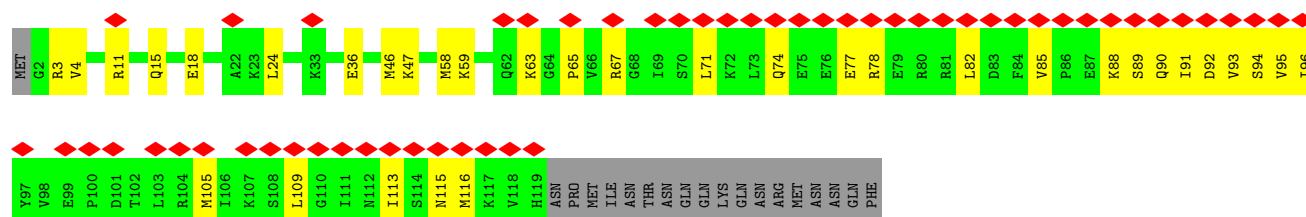
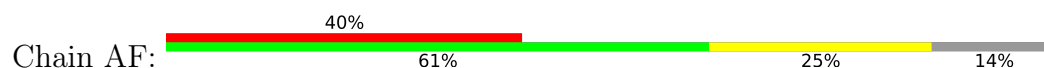
- Molecule 74: 60S ribosomal protein L23



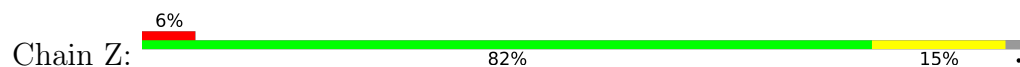
- Molecule 75: 40S ribosomal protein S27



- Molecule 76: 40S ribosomal protein S17, putative



- Molecule 77: 60S ribosomal protein L26, putative



- Molecule 78: Small ribosomal subunit protein eS30



- Molecule 79: 40S ribosomal protein S19

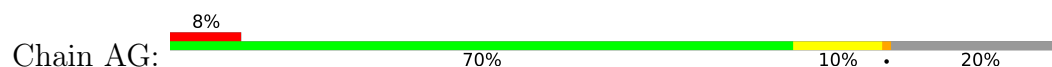


FIG1
GLY
ILE
GLY
ALA
THR
HIS
SER
SER
ARG
PHE
ILE
PRO
LEU
LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	85400	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.037	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	Depositor
Map size ($\text{\AA}$)	465.6, 465.6, 465.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.97, 0.97, 0.97	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.28	1/76208 (0.0%)	0.38	2/118656 (0.0%)
2	AA	0.15	0/916	0.38	0/1233
3	j	0.23	2/39168 (0.0%)	0.33	0/60989
4	AH	0.22	0/1382	0.45	0/1861
5	B	0.25	0/2826	0.32	0/4404
6	AB	0.23	0/1178	0.49	0/1582
7	k	0.25	0/1737	0.58	0/2321
8	C	0.27	0/3633	0.33	0/5654
9	AC	0.20	0/445	0.43	0/590
10	l	0.21	0/1569	0.45	0/2129
11	D	0.28	0/1901	0.53	0/2544
12	o	0.25	0/533	0.50	0/711
13	n	0.24	0/1552	0.48	0/2070
14	E	0.28	0/3129	0.54	0/4195
15	1	0.22	0/1189	0.43	0/1582
16	o	0.25	0/2097	0.52	0/2819
17	F	0.26	0/3144	0.49	0/4205
18	2	0.23	0/973	0.50	0/1298
19	p	0.21	0/1799	0.39	0/2429
20	G	0.22	0/1373	0.44	0/1830
21	3	0.26	0/1033	0.47	0/1367
22	q	0.21	0/1735	0.45	0/2304
23	H	0.26	0/1493	0.53	0/2019
24	4	0.26	0/564	0.54	0/737
25	s	0.20	0/1544	0.43	0/2064
26	I	0.27	0/1707	0.54	0/2274
27	5	0.29	0/1917	0.56	0/2562
28	t	0.25	0/1054	0.44	0/1411
29	J	0.21	0/1901	0.46	0/2537
30	6	0.26	0/748	0.55	0/1001
31	u	0.26	0/1376	0.48	0/1840
32	K	0.27	0/1697	0.47	0/2271

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	7	0.26	0/814	0.46	0/1085
34	y	0.23	0/1012	0.51	0/1358
35	L	0.27	0/1793	0.49	0/2387
36	8	0.26	0/1053	0.54	0/1399
37	z	0.22	0/1149	0.46	0/1532
38	M	0.24	0/1012	0.50	0/1363
39	9	0.32	0/878	0.61	0/1179
40	AD	0.21	0/1217	0.42	0/1627
41	N	0.28	0/1237	0.52	0/1646
42	a	0.26	0/871	0.47	0/1161
43	AE	0.24	0/1238	0.43	0/1652
44	O	0.27	0/1199	0.57	0/1597
45	b	0.29	0/762	0.49	0/1008
46	AI	0.19	0/640	0.39	0/860
47	P	0.28	0/1735	0.52	0/2320
48	c	0.31	0/718	0.60	0/946
49	AQ	0.16	0/1754	0.36	0/2732
50	Q	0.23	0/1602	0.48	0/2142
51	d	0.21	0/645	0.51	0/858
52	AK	0.22	0/572	0.43	0/767
53	R	0.23	0/2204	0.44	0/2946
54	e	0.24	0/462	0.45	0/610
55	AN	0.21	0/452	0.41	0/599
56	S	0.27	0/1530	0.52	0/2040
57	f	0.29	0/418	0.59	0/556
58	AP	0.15	0/583	0.48	0/767
59	T	0.26	0/1521	0.44	0/2012
60	g	0.25	0/347	0.51	0/448
61	m	0.19	0/1691	0.46	0/2265
62	U	0.28	0/1526	0.47	0/2043
63	h	0.24	0/667	0.47	0/887
64	r	0.21	0/1507	0.46	0/2023
65	V	0.24	0/1304	0.42	0/1737
66	i	0.28	0/797	0.51	0/1043
67	v	0.20	0/1113	0.43	0/1487
68	W	0.26	0/1356	0.53	0/1815
69	AJ	0.24	0/1007	0.54	0/1333
70	w	0.18	0/821	0.43	0/1106
71	X	0.19	0/841	0.46	0/1125
72	AL	0.25	0/793	0.51	0/1055
73	x	0.19	0/867	0.47	0/1174
74	Y	0.23	0/805	0.44	0/1074
75	AM	0.21	0/621	0.38	0/834

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AF	0.16	0/974	0.42	0/1301
77	Z	0.26	0/1017	0.49	0/1346
78	AO	0.23	0/348	0.66	0/458
79	AG	0.20	0/963	0.48	2/1287 (0.2%)
All	All	0.25	3/211957 (0.0%)	0.41	4/310479 (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
4	AH	0	1
7	k	0	1
14	E	0	2
21	3	0	1
23	H	0	3
27	5	0	1
37	z	0	1
All	All	0	10

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	j	1346	G	C1'-N9	-6.61	1.37	1.47
3	j	1398	U	C1'-N1	6.33	1.56	1.47
1	A	3599	U	C1'-N1	5.76	1.57	1.48

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	709	A	C4-N9-C1'	6.14	144.73	126.30
1	A	709	A	C8-N9-C1'	-6.09	109.42	127.70
79	AG	71	GLU	CA-C-N	5.75	133.20	121.48
79	AG	71	GLU	C-N-CA	5.75	133.20	121.48

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	3	121	VAL	Peptide

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Mol	Chain	Res	Type	Group
4	AH	141	LYS	Peptide
14	E	252	TRP	Peptide
14	E	253	HIS	Peptide
7	k	97	TYR	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	A	68120	0	34340	464	0
2	AA	903	0	912	16	0
3	j	35005	0	17634	325	0
4	AH	1353	0	1401	17	0
5	B	2525	0	1274	12	0
6	AB	1161	0	1212	27	0
7	k	1713	0	1838	27	0
8	C	3246	0	1639	16	0
9	AC	438	0	451	16	0
10	l	1538	0	1600	36	0
11	D	1866	0	1964	11	0
12	0	521	0	539	6	0
13	n	1528	0	1638	15	0
14	E	3061	0	3205	26	0
15	1	1171	0	1288	16	0
16	o	2061	0	2200	23	0
17	F	3094	0	3333	46	0
18	2	960	0	1016	12	0
19	p	1757	0	1811	19	0
20	G	1352	0	1412	15	0
21	3	1022	0	1147	4	0
22	q	1717	0	1886	27	0
23	H	1468	0	1544	18	0
24	4	555	0	599	5	0
25	s	1528	0	1680	39	0
26	I	1684	0	1849	19	0
27	5	1879	0	2005	16	0
28	t	1037	0	1099	14	0
29	J	1873	0	2055	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	6	740	0	763	13	0
31	u	1352	0	1409	16	0
32	K	1666	0	1789	14	0
33	7	802	0	881	6	0
34	y	998	0	1042	19	0
35	L	1761	0	1896	16	0
36	8	1036	0	1139	11	0
37	z	1129	0	1196	10	0
38	M	996	0	1044	13	0
39	9	858	0	897	10	0
40	AD	1196	0	1294	8	0
41	N	1221	0	1342	25	0
42	a	858	0	908	5	0
43	AE	1211	0	1241	9	0
44	O	1172	0	1230	11	0
45	b	756	0	842	9	0
46	AI	631	0	637	7	0
47	P	1697	0	1802	16	0
48	c	705	0	753	9	0
49	AQ	1571	0	797	45	0
50	Q	1567	0	1607	8	0
51	d	636	0	726	12	0
52	AK	565	0	607	15	0
53	R	2171	0	2257	22	0
54	e	452	0	492	3	0
55	AN	451	0	485	7	0
56	S	1502	0	1636	13	0
57	f	413	0	448	6	0
58	AP	573	0	624	17	0
59	T	1505	0	1671	18	0
60	g	342	0	388	1	0
61	m	1672	0	1778	58	0
62	U	1496	0	1556	13	0
63	h	658	0	723	3	0
64	r	1487	0	1543	18	0
65	V	1279	0	1358	14	0
66	i	787	0	870	6	0
67	v	1098	0	1183	17	0
68	W	1336	0	1345	14	0
69	AJ	994	0	1082	18	0
70	w	813	0	863	20	0
71	X	824	0	882	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	AL	781	0	818	14	0
73	x	839	0	852	31	0
74	Y	796	0	850	8	0
75	AM	610	0	630	4	0
76	AF	963	0	1045	27	0
77	Z	1005	0	1104	14	0
78	AO	345	0	381	3	0
79	AG	945	0	1000	28	0
80	8	1	0	0	0	0
80	A	173	0	0	0	0
80	AH	1	0	0	0	0
80	AJ	1	0	0	0	0
80	B	3	0	0	0	0
80	C	7	0	0	0	0
80	E	1	0	0	0	0
80	H	1	0	0	0	0
80	M	1	0	0	0	0
80	Q	1	0	0	0	0
80	W	2	0	0	0	0
80	X	1	0	0	0	0
80	a	1	0	0	0	0
80	j	60	0	0	0	0
81	AC	1	0	0	0	0
81	a	1	0	0	0	0
81	c	1	0	0	0	0
81	f	1	0	0	0	0
81	h	1	0	0	0	0
81	i	1	0	0	0	0
All	All	197657	0	148277	1674	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 5.

The worst 5 of 1674 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)
61:m:168:PHE:CD2	61:m:195:ILE:HD12	1.48	1.46
61:m:168:PHE:HA	61:m:195:ILE:CD1	1.44	1.46
3:j:1691:G:C5	58:AP:89:LYS:HE2	1.56	1.40
61:m:168:PHE:CG	61:m:195:ILE:HD12	1.73	1.21
61:m:168:PHE:CA	61:m:195:ILE:CD1	2.21	1.18

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	
2	AA	115/141 (82%)	112 (97%)	3 (3%)	0	100	100
4	AH	163/170 (96%)	152 (93%)	11 (7%)	0	100	100
6	AB	140/156 (90%)	125 (89%)	15 (11%)	0	100	100
7	k	208/262 (79%)	182 (88%)	26 (12%)	0	100	100
9	AC	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
10	l	193/263 (73%)	170 (88%)	23 (12%)	0	100	100
11	D	245/260 (94%)	231 (94%)	14 (6%)	0	100	100
12	0	60/162 (37%)	55 (92%)	5 (8%)	0	100	100
13	n	183/189 (97%)	173 (94%)	10 (6%)	0	100	100
14	E	378/386 (98%)	361 (96%)	17 (4%)	0	100	100
15	1	143/146 (98%)	135 (94%)	8 (6%)	0	100	100
16	o	255/261 (98%)	232 (91%)	23 (9%)	0	100	100
17	F	388/411 (94%)	371 (96%)	17 (4%)	0	100	100
18	2	119/127 (94%)	107 (90%)	12 (10%)	0	100	100
19	p	222/272 (82%)	207 (93%)	15 (7%)	0	100	100
20	G	163/173 (94%)	157 (96%)	6 (4%)	0	100	100
21	3	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
22	q	211/306 (69%)	201 (95%)	10 (5%)	0	100	100
23	H	184/190 (97%)	162 (88%)	22 (12%)	0	100	100
24	4	64/67 (96%)	60 (94%)	4 (6%)	0	100	100
25	s	186/194 (96%)	178 (96%)	8 (4%)	0	100	100
26	I	203/221 (92%)	187 (92%)	16 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	5	221/257 (86%)	204 (92%)	17 (8%)	0	100	100
28	t	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
29	J	225/283 (80%)	213 (95%)	11 (5%)	1 (0%)	30	37
30	6	96/108 (89%)	90 (94%)	6 (6%)	0	100	100
31	u	164/218 (75%)	152 (93%)	12 (7%)	0	100	100
32	K	199/202 (98%)	190 (96%)	9 (4%)	0	100	100
33	7	93/120 (78%)	90 (97%)	3 (3%)	0	100	100
34	y	131/151 (87%)	114 (87%)	17 (13%)	0	100	100
35	L	209/215 (97%)	198 (95%)	11 (5%)	0	100	100
36	8	123/131 (94%)	116 (94%)	7 (6%)	0	100	100
37	z	142/145 (98%)	134 (94%)	8 (6%)	0	100	100
38	M	130/139 (94%)	119 (92%)	11 (8%)	0	100	100
39	9	103/140 (74%)	86 (84%)	17 (16%)	0	100	100
40	AD	146/151 (97%)	140 (96%)	6 (4%)	0	100	100
41	N	146/165 (88%)	131 (90%)	15 (10%)	0	100	100
42	a	104/150 (69%)	104 (100%)	0	0	100	100
43	AE	143/161 (89%)	138 (96%)	5 (4%)	0	100	100
44	O	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
45	b	91/112 (81%)	84 (92%)	7 (8%)	0	100	100
46	AI	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
47	P	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
48	c	87/92 (95%)	78 (90%)	9 (10%)	0	100	100
50	Q	188/219 (86%)	169 (90%)	19 (10%)	0	100	100
51	d	74/87 (85%)	69 (93%)	3 (4%)	2 (3%)	4	2
52	AK	70/105 (67%)	68 (97%)	2 (3%)	0	100	100
53	R	261/294 (89%)	247 (95%)	14 (5%)	0	100	100
54	e	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
55	AN	54/67 (81%)	54 (100%)	0	0	100	100
56	S	184/187 (98%)	173 (94%)	11 (6%)	0	100	100
57	f	49/128 (38%)	47 (96%)	2 (4%)	0	100	100
58	AP	68/149 (46%)	64 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	T	179/182 (98%)	177 (99%)	2 (1%)	0	100	100
60	g	35/39 (90%)	33 (94%)	2 (6%)	0	100	100
61	m	211/221 (96%)	198 (94%)	12 (6%)	1 (0%)	24	32
62	U	178/184 (97%)	173 (97%)	5 (3%)	0	100	100
63	h	83/96 (86%)	80 (96%)	3 (4%)	0	100	100
64	r	187/195 (96%)	173 (92%)	14 (8%)	0	100	100
65	V	154/161 (96%)	148 (96%)	6 (4%)	0	100	100
66	i	94/104 (90%)	85 (90%)	9 (10%)	0	100	100
67	v	136/144 (94%)	130 (96%)	6 (4%)	0	100	100
68	W	168/203 (83%)	156 (93%)	12 (7%)	0	100	100
69	AJ	119/133 (90%)	104 (87%)	15 (13%)	0	100	100
70	w	100/118 (85%)	93 (93%)	7 (7%)	0	100	100
71	X	95/139 (68%)	88 (93%)	7 (7%)	0	100	100
72	AL	93/107 (87%)	86 (92%)	7 (8%)	0	100	100
73	x	96/137 (70%)	86 (90%)	10 (10%)	0	100	100
74	Y	99/190 (52%)	95 (96%)	4 (4%)	0	100	100
75	AM	77/82 (94%)	75 (97%)	2 (3%)	0	100	100
76	AF	116/137 (85%)	113 (97%)	3 (3%)	0	100	100
77	Z	120/126 (95%)	117 (98%)	3 (2%)	0	100	100
78	AO	41/58 (71%)	37 (90%)	4 (10%)	0	100	100
79	AG	114/145 (79%)	110 (96%)	3 (3%)	1 (1%)	14	17
All	All	10591/12228 (87%)	9914 (94%)	672 (6%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
51	d	34	LYS
51	d	37	VAL
79	AG	17	TYR
29	J	61	PRO
61	m	195	ILE

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	
2	AA	100/121 (83%)	100 (100%)	0	100	100
4	AH	147/151 (97%)	146 (99%)	1 (1%)	76	84
6	AB	127/136 (93%)	125 (98%)	2 (2%)	55	69
7	k	195/238 (82%)	194 (100%)	1 (0%)	81	87
9	AC	47/48 (98%)	47 (100%)	0	100	100
10	l	167/227 (74%)	167 (100%)	0	100	100
11	D	191/202 (95%)	191 (100%)	0	100	100
12	0	53/146 (36%)	53 (100%)	0	100	100
13	n	164/167 (98%)	164 (100%)	0	100	100
14	E	335/340 (98%)	335 (100%)	0	100	100
15	1	131/132 (99%)	131 (100%)	0	100	100
16	o	233/237 (98%)	233 (100%)	0	100	100
17	F	336/352 (96%)	336 (100%)	0	100	100
18	2	112/118 (95%)	112 (100%)	0	100	100
19	p	191/222 (86%)	191 (100%)	0	100	100
20	G	147/155 (95%)	147 (100%)	0	100	100
21	3	113/115 (98%)	113 (100%)	0	100	100
22	q	189/279 (68%)	188 (100%)	1 (0%)	81	87
23	H	165/173 (95%)	165 (100%)	0	100	100
24	4	60/61 (98%)	60 (100%)	0	100	100
25	s	177/183 (97%)	177 (100%)	0	100	100
26	I	189/203 (93%)	189 (100%)	0	100	100
27	5	201/231 (87%)	201 (100%)	0	100	100
28	t	115/116 (99%)	115 (100%)	0	100	100
29	J	211/260 (81%)	211 (100%)	0	100	100
30	6	83/92 (90%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	u	148/193 (77%)	148 (100%)	0	100	100
32	K	182/182 (100%)	182 (100%)	0	100	100
33	7	91/112 (81%)	91 (100%)	0	100	100
34	y	104/119 (87%)	104 (100%)	0	100	100
35	L	190/194 (98%)	190 (100%)	0	100	100
36	8	114/120 (95%)	114 (100%)	0	100	100
37	z	120/121 (99%)	120 (100%)	0	100	100
38	M	106/110 (96%)	106 (100%)	0	100	100
39	9	92/127 (72%)	92 (100%)	0	100	100
40	AD	132/133 (99%)	132 (100%)	0	100	100
41	N	137/152 (90%)	136 (99%)	1 (1%)	76	84
42	a	89/128 (70%)	89 (100%)	0	100	100
43	AE	131/144 (91%)	131 (100%)	0	100	100
44	O	121/122 (99%)	121 (100%)	0	100	100
45	b	82/97 (84%)	82 (100%)	0	100	100
46	AI	69/70 (99%)	69 (100%)	0	100	100
47	P	179/180 (99%)	179 (100%)	0	100	100
48	c	73/77 (95%)	73 (100%)	0	100	100
50	Q	167/190 (88%)	167 (100%)	0	100	100
51	d	73/83 (88%)	69 (94%)	4 (6%)	19	28
52	AK	64/88 (73%)	59 (92%)	5 (8%)	11	14
53	R	229/254 (90%)	229 (100%)	0	100	100
54	e	47/48 (98%)	47 (100%)	0	100	100
55	AN	46/54 (85%)	46 (100%)	0	100	100
56	S	158/159 (99%)	157 (99%)	1 (1%)	78	86
57	f	45/114 (40%)	45 (100%)	0	100	100
58	AP	62/135 (46%)	62 (100%)	0	100	100
59	T	161/163 (99%)	161 (100%)	0	100	100
60	g	34/35 (97%)	34 (100%)	0	100	100
61	m	181/188 (96%)	181 (100%)	0	100	100
62	U	162/166 (98%)	162 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	h	70/80 (88%)	70 (100%)	0	100	100
64	r	160/165 (97%)	160 (100%)	0	100	100
65	V	140/144 (97%)	140 (100%)	0	100	100
66	i	88/93 (95%)	88 (100%)	0	100	100
67	v	116/122 (95%)	116 (100%)	0	100	100
68	W	130/178 (73%)	130 (100%)	0	100	100
69	AJ	105/115 (91%)	104 (99%)	1 (1%)	68	77
70	w	95/109 (87%)	95 (100%)	0	100	100
71	X	92/131 (70%)	92 (100%)	0	100	100
72	AL	87/98 (89%)	87 (100%)	0	100	100
73	x	94/129 (73%)	94 (100%)	0	100	100
74	Y	90/177 (51%)	90 (100%)	0	100	100
75	AM	73/76 (96%)	73 (100%)	0	100	100
76	AF	108/127 (85%)	108 (100%)	0	100	100
77	Z	111/115 (96%)	111 (100%)	0	100	100
78	AO	36/47 (77%)	36 (100%)	0	100	100
79	AG	105/130 (81%)	104 (99%)	1 (1%)	68	77
All	All	9468/10799 (88%)	9450 (100%)	18 (0%)	85	92

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
52	AK	60	THR
79	AG	20	VAL
69	AJ	46	LYS
51	d	36	THR
52	AK	59	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
43	AE	14	GLN
54	e	11	GLN
43	AE	130	GLN
50	Q	73	ASN

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Mol	Chain	Res	Type
59	T	85	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3173/3789 (83%)	580 (18%)	23 (0%)
3	j	1626/2092 (77%)	324 (19%)	0
49	AQ	73/74 (98%)	33 (45%)	2 (2%)
5	B	117/119 (98%)	11 (9%)	0
8	C	149/159 (93%)	30 (20%)	0
All	All	5138/6233 (82%)	978 (19%)	25 (0%)

5 of 978 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	14	U
1	A	40	A
1	A	43	A
1	A	45	A
1	A	49	U

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1538	U
1	A	2523	U
49	AQ	51	U
1	A	1773	U
1	A	2665	A

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

Of 260 ligands modelled in this entry, 260 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

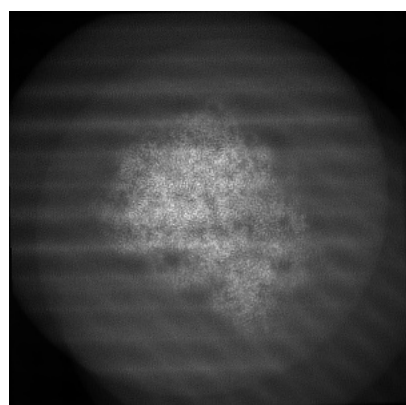
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61273. These allow visual inspection of the internal detail of the map and identification of artifacts.

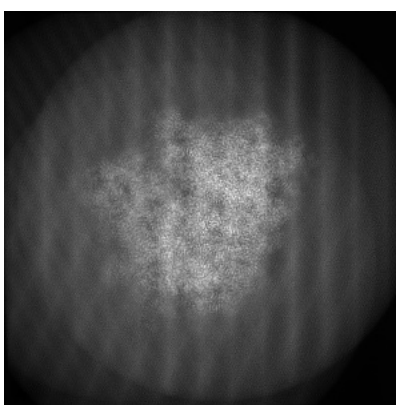
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

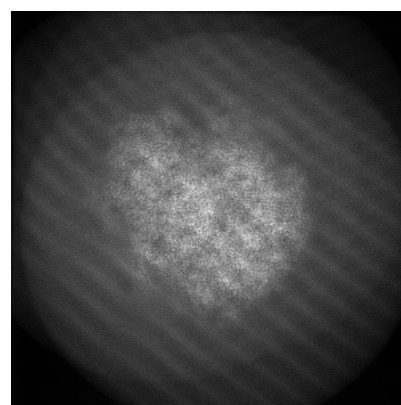
6.1.1 Primary map



X



Y

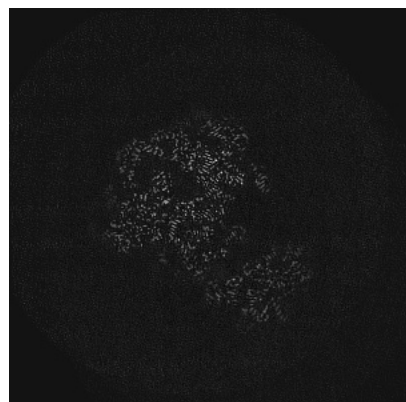


Z

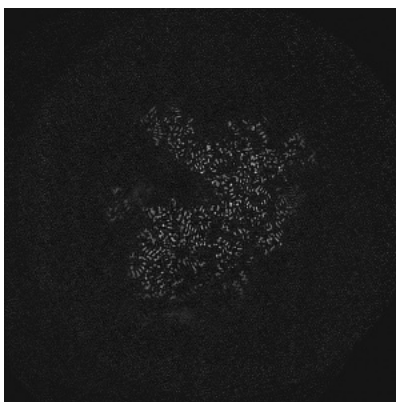
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

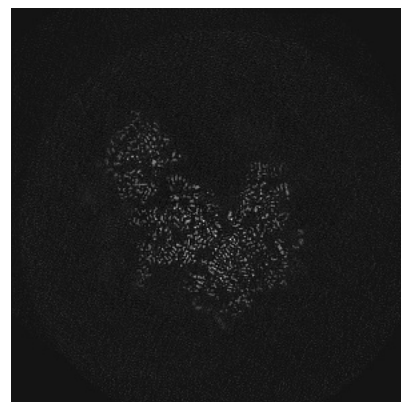
6.2.1 Primary map



X Index: 240



Y Index: 240

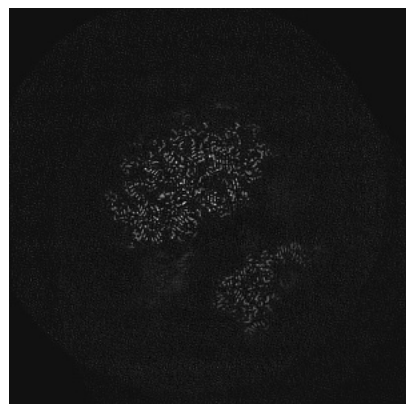


Z Index: 240

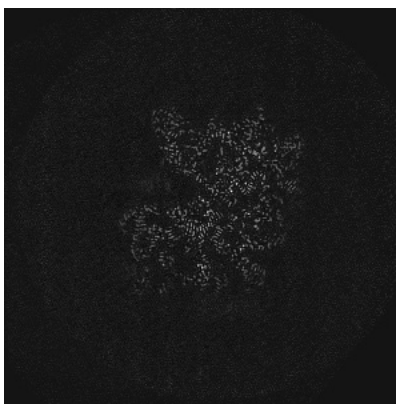
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

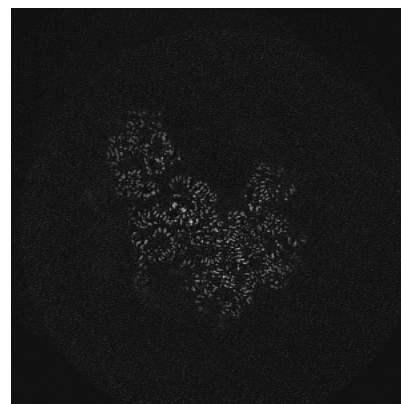
6.3.1 Primary map



X Index: 282



Y Index: 223

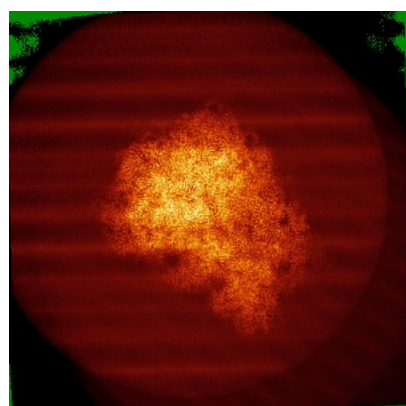


Z Index: 235

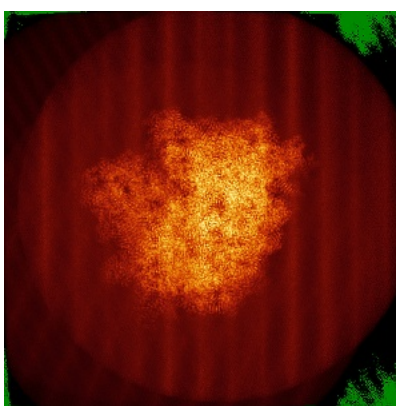
The images above show the largest variance slices of the map in three orthogonal directions.

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

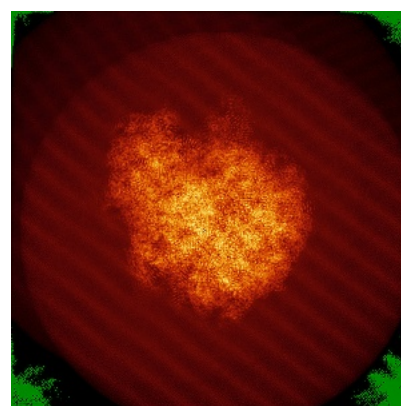
6.4.1 Primary map



X



Y



Z

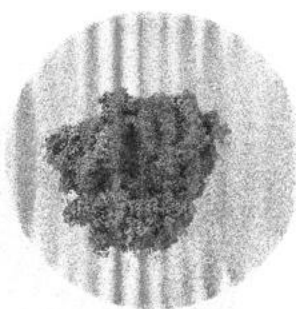
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

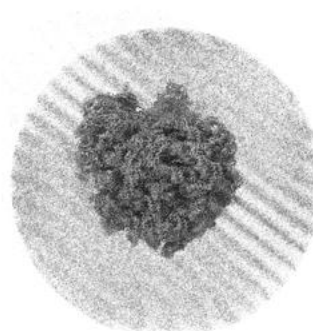
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

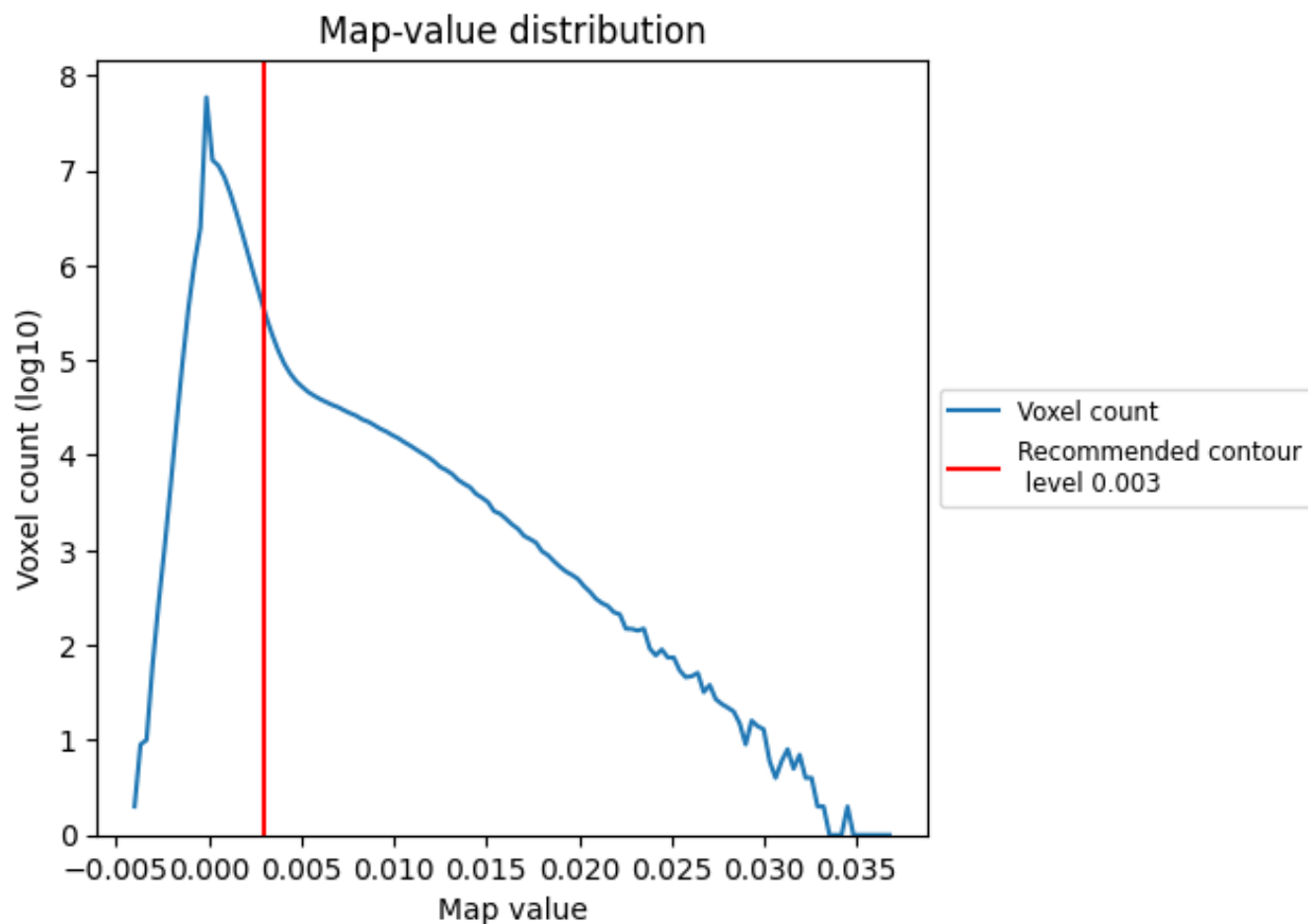
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

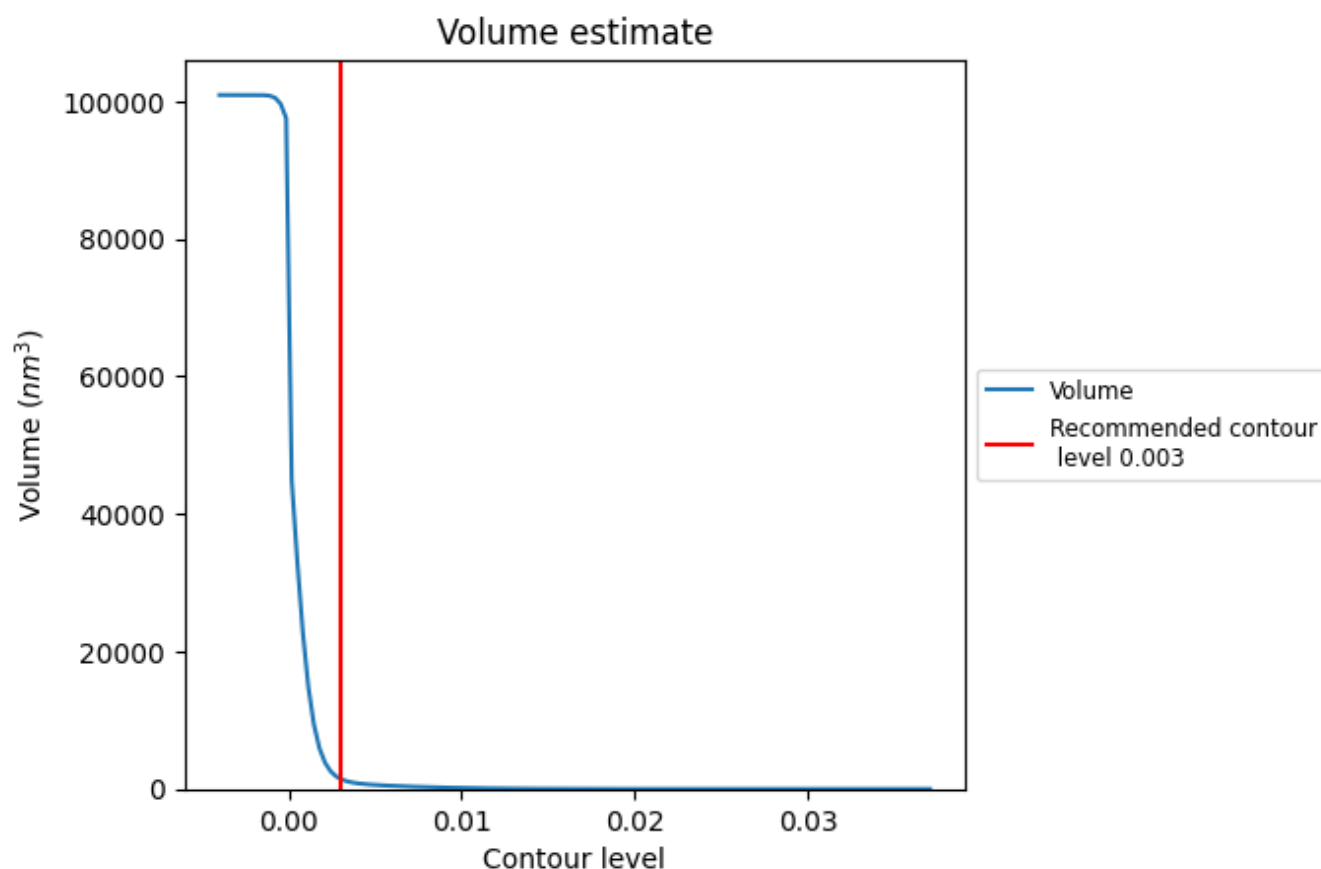
This section contains the results of statistical analysis of the map.

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.

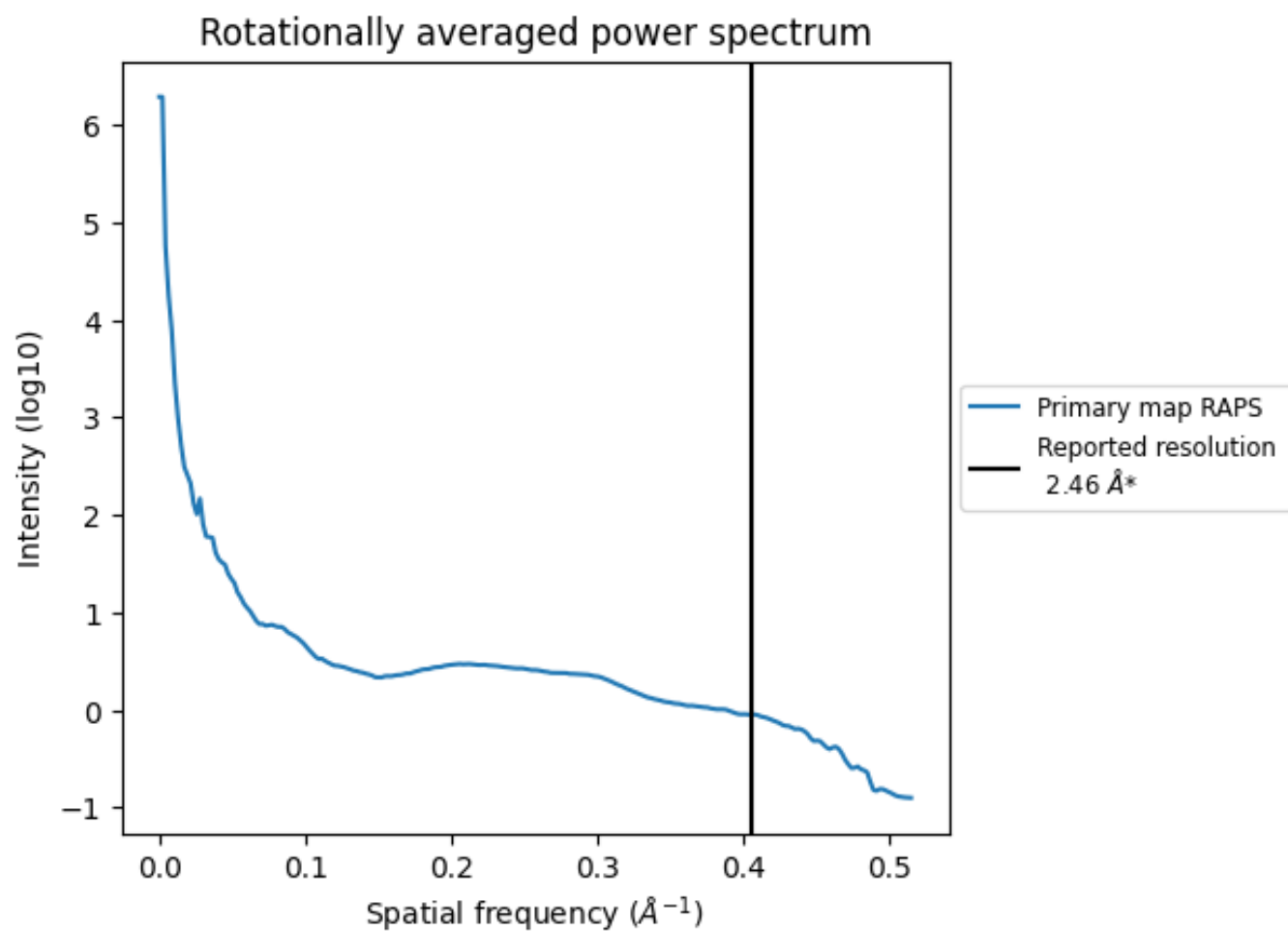
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1460 nm^3 ; this corresponds to an approximate mass of 1318 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 0.407 Å⁻¹

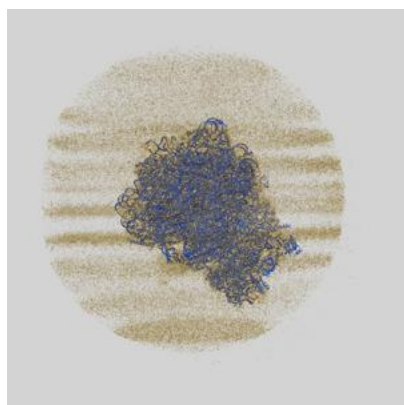
8 Fourier-Shell correlation

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

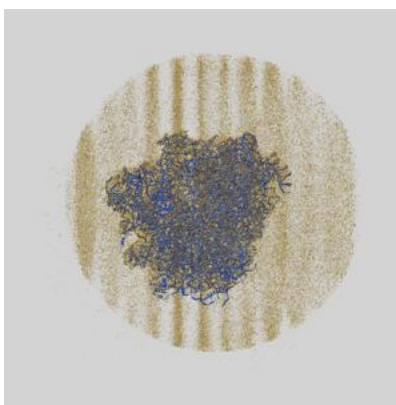
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61273 and PDB model 9J9I. Per-residue inclusion information can be found in section [3](#) on page [20](#).

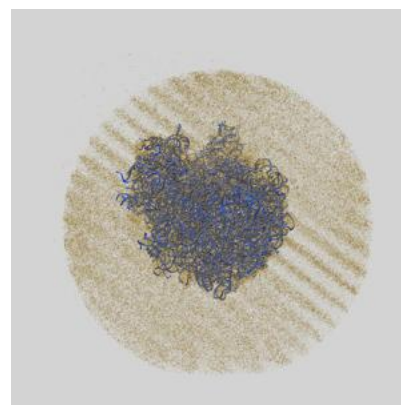
9.1 Map-model overlay [i](#)



X



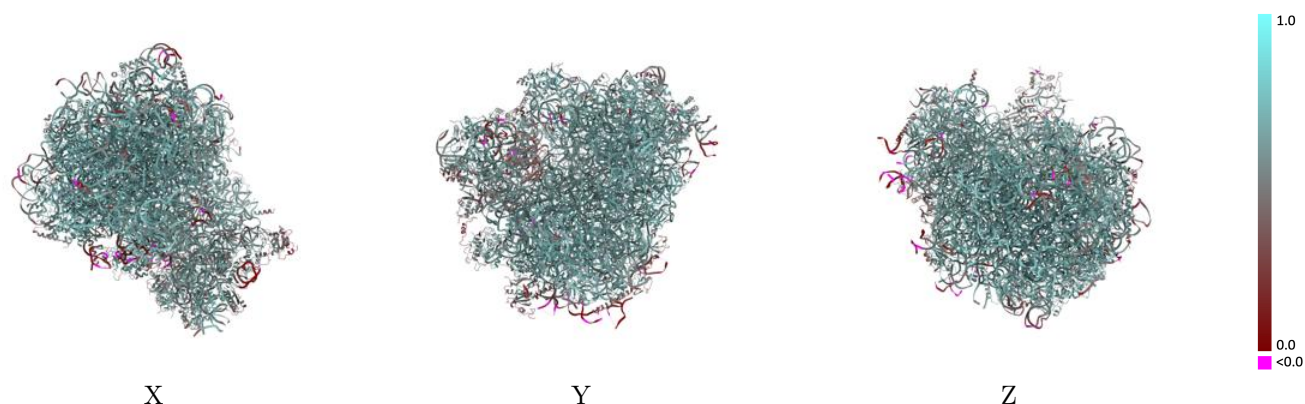
Y



Z

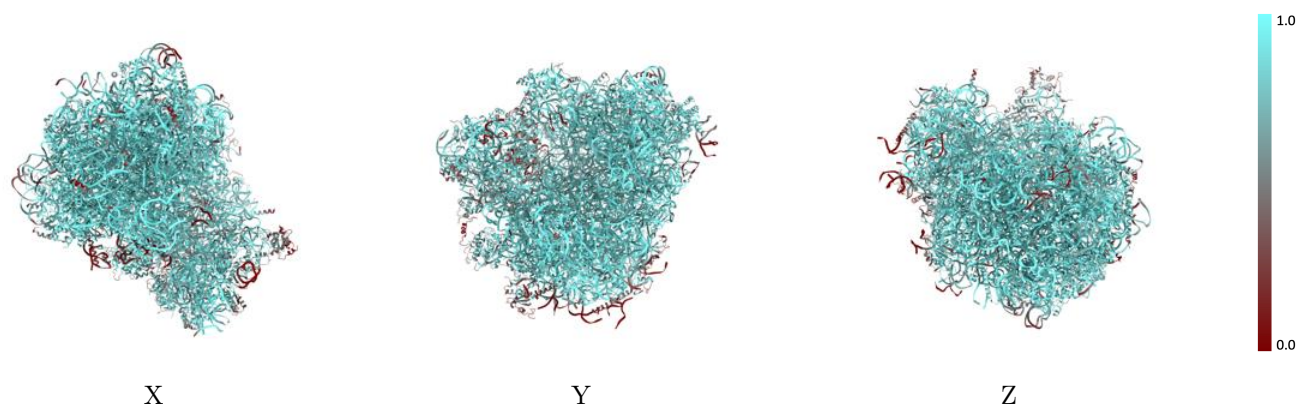
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



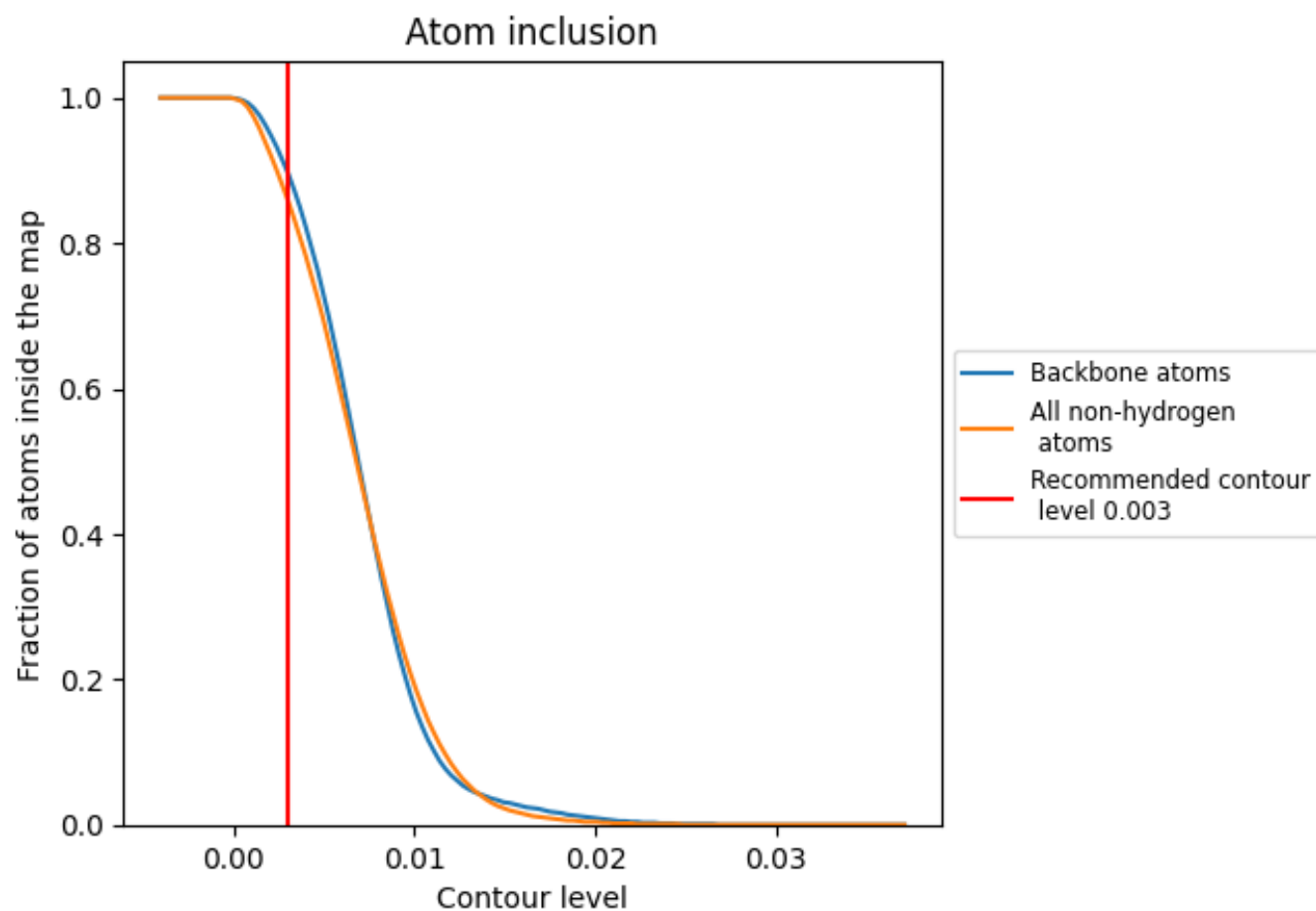
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.003).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8610	 0.6150
0	 0.8940	 0.6290
1	 0.7340	 0.5480
2	 0.8170	 0.5980
3	 0.8540	 0.6160
4	 0.7390	 0.5400
5	 0.9100	 0.6560
6	 0.8380	 0.6080
7	 0.8920	 0.6470
8	 0.9160	 0.6780
9	 0.9300	 0.6770
A	 0.9150	 0.6460
AA	 0.3420	 0.3710
AB	 0.7540	 0.5370
AC	 0.8650	 0.6130
AD	 0.8540	 0.6230
AE	 0.9180	 0.6600
AF	 0.4180	 0.3980
AG	 0.7540	 0.5720
AH	 0.7900	 0.5730
AI	 0.7770	 0.5960
AJ	 0.7840	 0.5600
AK	 0.6830	 0.5430
AL	 0.8570	 0.6230
AM	 0.7070	 0.5590
AN	 0.6670	 0.4990
AO	 0.7050	 0.5300
AP	 0.4060	 0.3920
AQ	 0.2690	 0.2050
B	 0.9740	 0.6660
C	 0.9450	 0.6620
D	 0.9400	 0.6910
E	 0.9210	 0.6670
F	 0.8680	 0.6390
G	 0.6470	 0.4920



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Chain	Atom inclusion	Q-score
H	 0.9060	 0.6400
I	 0.8220	 0.5910
J	 0.6760	 0.5260
K	 0.9250	 0.6730
L	 0.8940	 0.6580
M	 0.9150	 0.6690
N	 0.8290	 0.6010
O	 0.9480	 0.6890
P	 0.9670	 0.7110
Q	 0.8650	 0.6280
R	 0.7920	 0.5860
S	 0.9420	 0.6930
T	 0.7800	 0.5820
U	 0.9270	 0.6690
V	 0.8680	 0.6530
W	 0.9270	 0.6600
X	 0.5980	 0.4610
Y	 0.8410	 0.6040
Z	 0.8180	 0.5910
a	 0.8830	 0.6380
b	 0.8530	 0.6190
c	 0.9180	 0.6560
d	 0.7050	 0.5350
e	 0.8040	 0.6090
f	 0.9000	 0.6530
g	 0.9150	 0.6370
h	 0.9390	 0.6830
i	 0.9100	 0.6690
j	 0.8770	 0.5990
k	 0.7890	 0.5800
l	 0.7450	 0.5650
m	 0.6180	 0.4890
n	 0.8380	 0.6090
o	 0.8750	 0.6300
p	 0.8550	 0.6260
q	 0.5630	 0.4760
r	 0.8140	 0.5730
s	 0.5100	 0.4500
t	 0.9300	 0.6660
u	 0.8780	 0.6140
v	 0.7740	 0.5480
w	 0.6330	 0.4870

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Chain	Atom inclusion	Q-score
x	 0.7550	 0.5350
y	 0.8480	 0.6030
z	 0.8540	 0.6260