



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:16 PM UTC

PDB ID : 9J9H / pdb_00009j9h
EMDB ID : EMD-61272
Title : High-resolution cryo-EM structure of the Plasmodium falciparum 80S ribosome bound to RACK1 and E-tRNA
Authors : Yan, X.F.; Gao, Y.G.
Deposited on : 2024-08-22
Resolution : 2.45 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

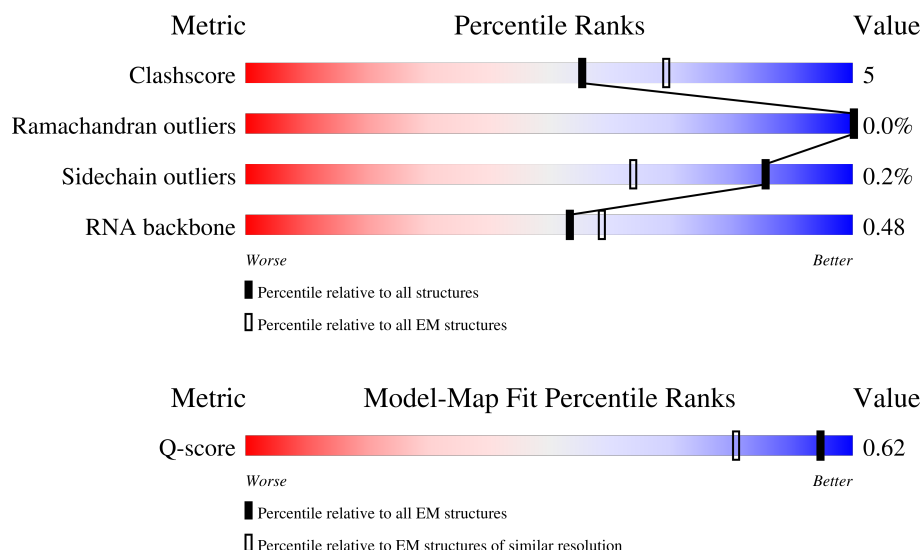
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.45 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	5931 (1.96 - 2.95)

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	3788	5% 58% 22% 5% 15%
2	0	162	28% 10% 62%
3	q	306	22% 55% 15% 30%

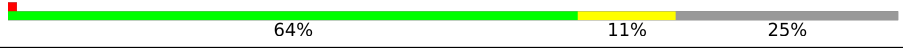
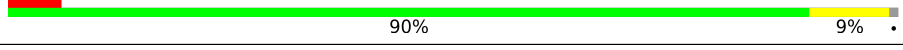
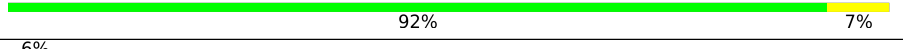
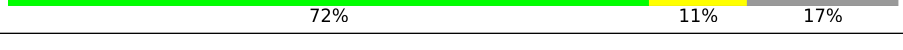
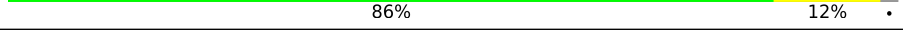
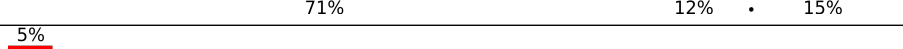
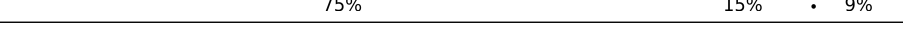
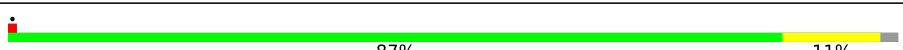
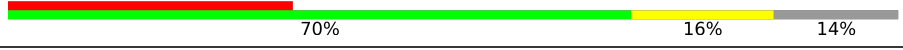
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Mol	Chain	Length	Quality of chain
4	AQ	74	
5	B	119	
6	1	146	
7	r	195	
8	AR	323	
9	C	159	
10	2	127	
11	s	194	
12	D	260	
13	3	124	
14	t	130	
15	E	386	
16	4	67	
17	u	218	
18	F	411	
19	5	257	
20	v	144	
21	G	173	
22	6	108	
23	w	118	
24	H	190	
25	7	120	
26	x	137	
27	I	221	
28	8	131	

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Mol	Chain	Length	Quality of chain
29	y	151	
30	J	283	
31	9	140	
32	z	145	
33	K	202	
34	a	150	
35	AA	141	
36	L	215	
37	b	112	
38	AB	156	
39	M	139	
40	c	92	
41	AC	54	
42	N	165	
43	d	87	
44	AD	151	
45	O	148	
46	e	51	
47	AE	161	
48	P	205	
49	f	128	
50	AF	137	
51	Q	219	
52	g	39	
53	AG	145	

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Mol	Chain	Length	Quality of chain
54	R	294	
55	h	96	
56	AH	170	
57	S	187	
58	i	104	
59	AI	82	
60	T	182	
61	j	2092	
62	AJ	133	
63	U	184	
64	k	262	
65	AK	105	
66	V	161	
67	l	263	
68	AL	107	
69	W	203	
70	m	221	
71	AM	82	
72	X	139	
73	n	189	
74	AN	67	
75	Y	190	
76	o	261	
77	AO	58	
78	Z	126	

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Mol	Chain	Length	Quality of chain
79	p	272	 15% 68% 14% 18%
80	AP	149	 15% 37% 10% 53%

2 Entry composition [i](#)

There are 82 unique types of molecules in this entry. The entry contains 200146 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 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

- Molecule 3 is a protein called 40S ribosomal protein S6.

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

- Molecule 4 is a RNA chain called tRNA.

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

- 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 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1	145	Total	C	N	O	S	0	0
			1171	758	212	198	3		

- Molecule 7 is a protein called 40S ribosomal protein S5, putative.

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

- Molecule 8 is a protein called Receptor for activated c kinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AR	323	Total	C	N	O	S	0	0
			2509	1583	426	488	12		

- Molecule 9 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 10 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	2	121	Total	C	N	O	S	0	0
			960	607	173	177	3		

- Molecule 11 is a protein called 40S ribosomal protein S7.

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

- Molecule 12 is a protein called 60S ribosomal protein L2.

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

- Molecule 13 is a protein called 60S ribosomal protein L35, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	3	122	Total	C	N	O	S	0	0
			1022	652	200	168	2		

- Molecule 14 is a protein called 40S ribosomal protein S15A, putative.

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

- Molecule 15 is a protein called 60S ribosomal protein L3.

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

- Molecule 16 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 17 is a protein called 40S ribosomal protein S8.

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

- Molecule 18 is a protein called 60S ribosomal protein L4.

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

- Molecule 19 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 20 is a protein called 40S ribosomal protein S16, putative.

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

- Molecule 21 is a protein called 60S ribosomal protein L11a, putative.

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

- Molecule 22 is a protein called 60S ribosomal protein L30e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	6	98	Total	C	N	O	S	0	0
			740	462	132	139	7		

- Molecule 23 is a protein called 40S ribosomal protein S20e, putative.

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

- Molecule 24 is a protein called 60S ribosomal protein L6, putative.

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

- Molecule 25 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	7	97	Total	C	N	O	S	0	0
			802	514	153	130	5		

- Molecule 26 is a protein called 40S ribosomal protein S10, putative.

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

- Molecule 27 is a protein called 60S ribosomal protein L6, putative.

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

- Molecule 28 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	8	125	Total	C	N	O	S	0	0
			1036	660	206	163	7		

- Molecule 29 is a protein called 40S ribosomal protein S11.

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

- Molecule 30 is a protein called 60S ribosomal protein L7a.

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

- Molecule 31 is a protein called 60S ribosomal protein L35ae, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	9	105	Total	C	N	O	S	0	0
			858	550	166	139	3		

- Molecule 32 is a protein called 40S ribosomal protein S23, putative.

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

- Molecule 33 is a protein called 60S ribosomal protein L13, putative.

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

- Molecule 34 is a protein called 60S ribosomal protein L34.

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

- Molecule 35 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 36 is a protein called 60S ribosomal protein L13.

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

- Molecule 37 is a protein called 60S ribosomal protein L36.

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

- Molecule 38 is a protein called 40S ribosomal protein S18, putative.

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

- Molecule 39 is a protein called 60S ribosomal protein L23, putative.

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

- Molecule 40 is a protein called Ribosomal protein L37.

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

- Molecule 41 is a protein called 40S ribosomal protein S29, putative.

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

- Molecule 42 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	N	146	Total	C	N	O	S	0	0
			1203	782	211	204	6		

- Molecule 43 is a protein called 60S ribosomal protein L38.

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

- Molecule 44 is a protein called 40S ribosomal protein S15.

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

- Molecule 45 is a protein called 60S ribosomal protein L27a, putative.

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

- Molecule 46 is a protein called 60S ribosomal protein L39.

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

- Molecule 47 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AE	147	Total	C	N	O	S	0	0
			1214	778	228	201	7		

- Molecule 48 is a protein called Ribosomal protein L15.

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

- Molecule 49 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 50 is a protein called 40S ribosomal protein S17, putative.

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

- Molecule 51 is a protein called 60S ribosomal protein L10, putative.

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

- Molecule 52 is a protein called 60S ribosomal protein L41.

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

- Molecule 53 is a protein called 40S ribosomal protein S19.

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

- Molecule 54 is a protein called 60S ribosomal protein L5, putative.

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

- Molecule 55 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 56 is a protein called 40S ribosomal protein S19.

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

- Molecule 57 is a protein called 60S ribosomal protein L18-2, putative.

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

- Molecule 58 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 59 is a protein called 40S ribosomal protein S21.

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

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

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

- Molecule 61 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 62 is a protein called 40S ribosomal protein S24.

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

- Molecule 63 is a protein called 60S ribosomal protein L18a.

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

- Molecule 64 is a protein called Small ribosomal subunit protein eS1.

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

- Molecule 65 is a protein called 40S ribosomal protein S25.

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

- Molecule 66 is a protein called 60S ribosomal protein L21.

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

- Molecule 67 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 68 is a protein called 40S ribosomal protein S26.

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

- Molecule 69 is a protein called 60S ribosomal protein L17, putative.

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

- Molecule 70 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	m	213	Total	C	N	O	S	0	0
			1667	1047	315	298	7		

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

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

- Molecule 72 is a protein called Large ribosomal subunit protein eL22.

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

- Molecule 73 is a protein called 40S ribosomal protein S9, putative.

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

- Molecule 74 is a protein called 40S ribosomal protein S28e, putative.

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

- Molecule 75 is a protein called 60S ribosomal protein L23.

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

- Molecule 76 is a protein called 40S ribosomal protein S4.

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

- Molecule 77 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 78 is a protein called 60S ribosomal protein L26, putative.

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

- Molecule 79 is a protein called 40S ribosomal protein S5.

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

- Molecule 80 is a protein called Ribosomal protein S27a, putative.

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

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	A	172	Total	Mg	0
			172	172	
81	0	1	Total	Mg	0
			1	1	
81	B	3	Total	Mg	0
			3	3	
81	C	8	Total	Mg	0
			8	8	
81	8	1	Total	Mg	0
			1	1	
81	a	1	Total	Mg	0
			1	1	
81	M	1	Total	Mg	0
			1	1	
81	c	1	Total	Mg	0
			1	1	
81	Q	1	Total	Mg	0
			1	1	

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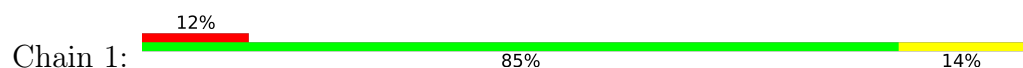
Mol	Chain	Residues	Atoms		AltConf
81	AH	1	Total 1	Mg 1	0
81	j	59	Total 59	Mg 59	0
81	k	1	Total 1	Mg 1	0
81	V	1	Total 1	Mg 1	0
81	W	1	Total 1	Mg 1	0
81	X	1	Total 1	Mg 1	0
81	o	1	Total 1	Mg 1	0

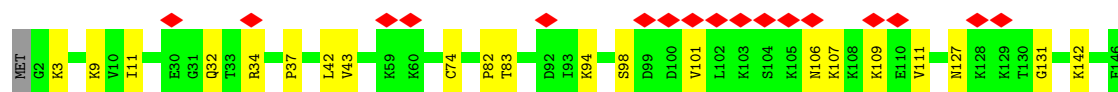
- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

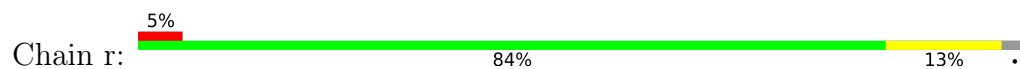




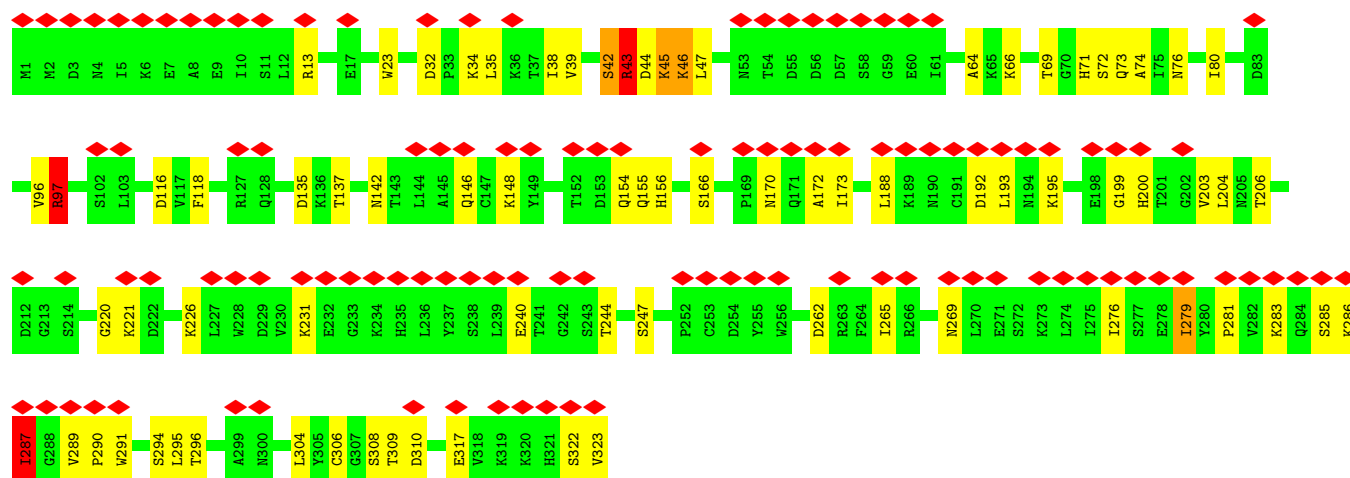
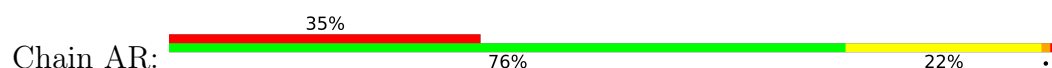




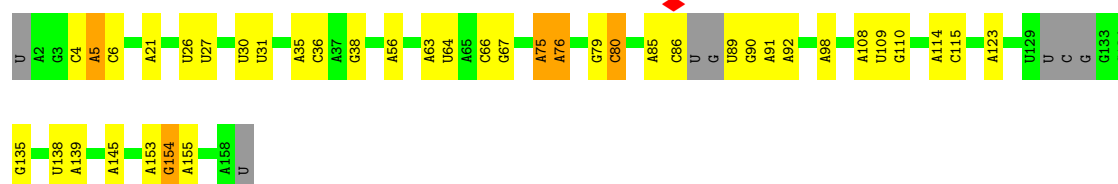
- Molecule 7: 40S ribosomal protein S5, putative



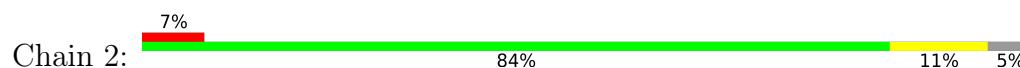
- Molecule 8: Receptor for activated c kinase



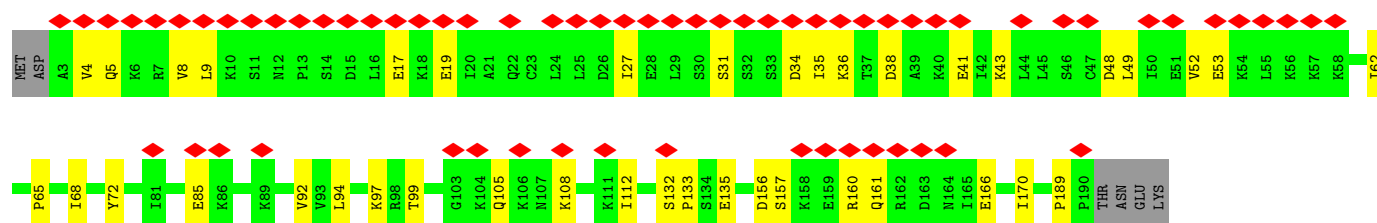
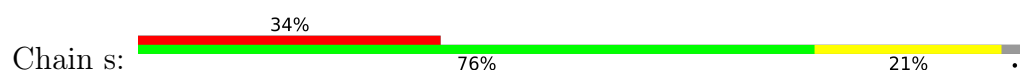
- Molecule 9: 5.8S ribosomal RNA



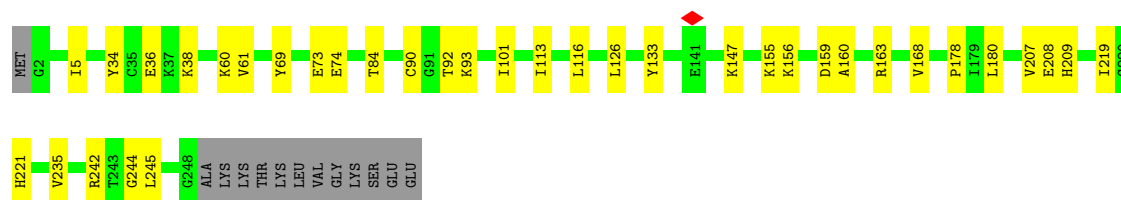
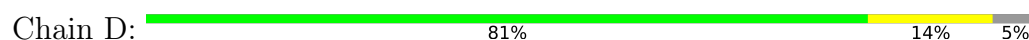
- Molecule 10: 60S ribosomal protein L28



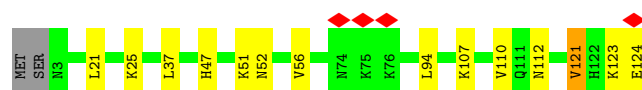
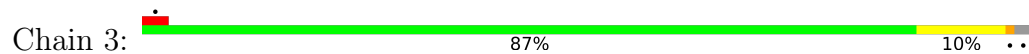
- Molecule 11: 40S ribosomal protein S7



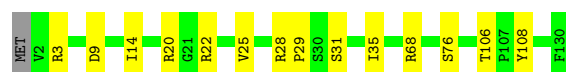
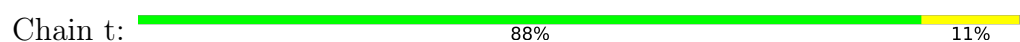
- Molecule 12: 60S ribosomal protein L2



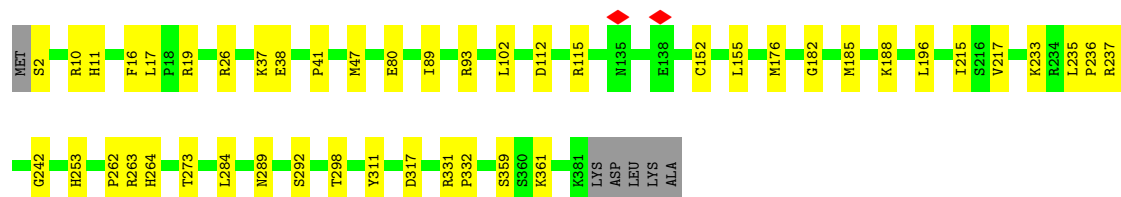
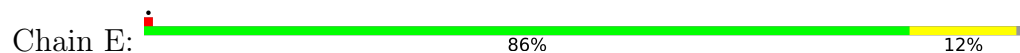
- Molecule 13: 60S ribosomal protein L35, putative



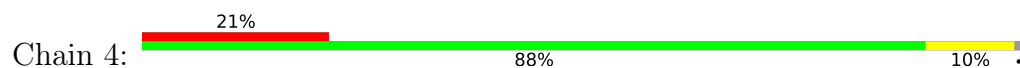
- Molecule 14: 40S ribosomal protein S15A, putative

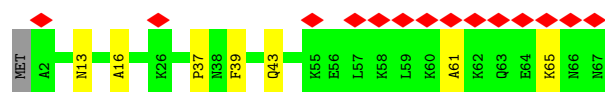


- Molecule 15: 60S ribosomal protein L3

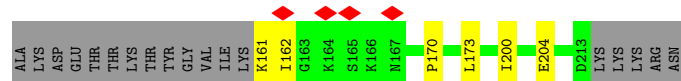
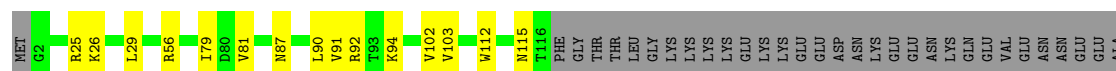


- Molecule 16: 60S ribosomal protein L29

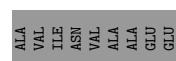
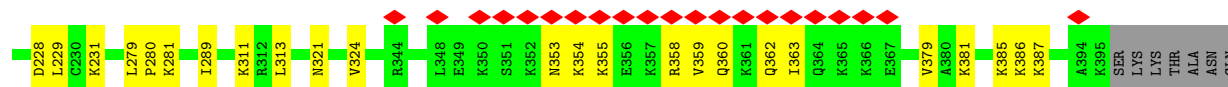
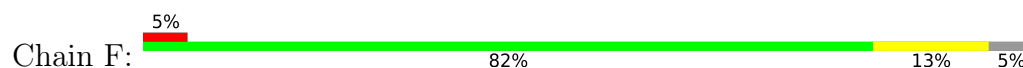




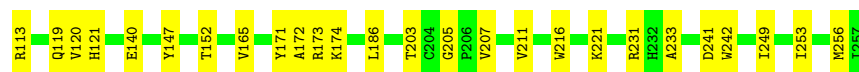
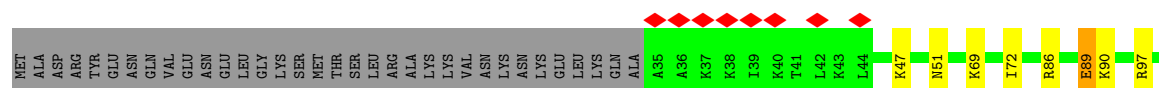
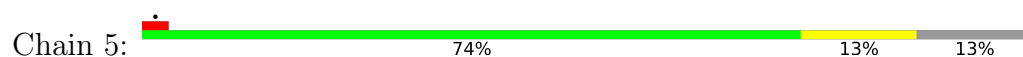
- Molecule 17: 40S ribosomal protein S8



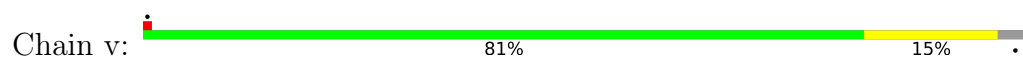
- Molecule 18: 60S ribosomal protein L4



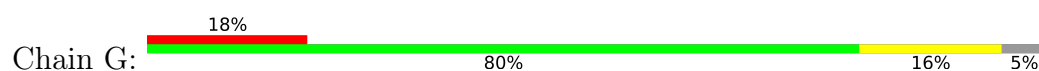
- Molecule 19: 60S ribosomal protein L7, putative

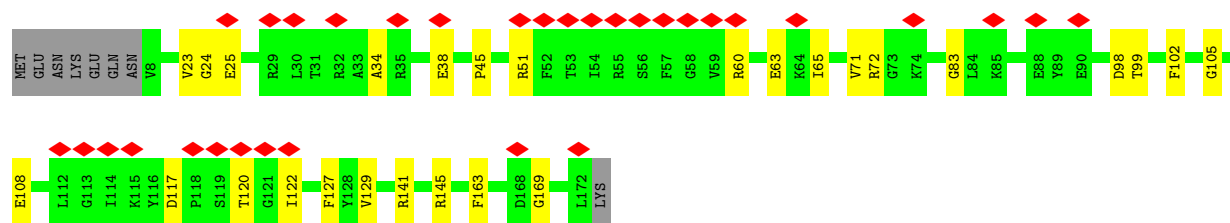


- Molecule 20: 40S ribosomal protein S16, putative

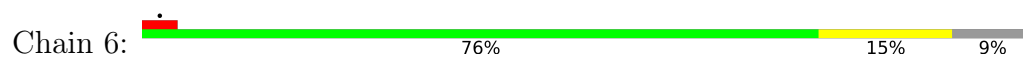


- Molecule 21: 60S ribosomal protein L11a, putative

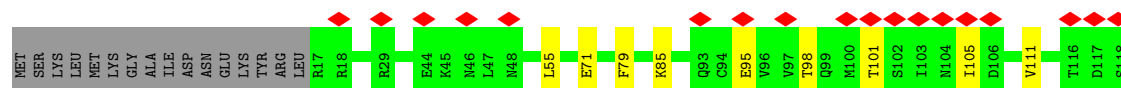
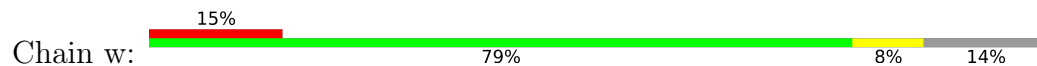




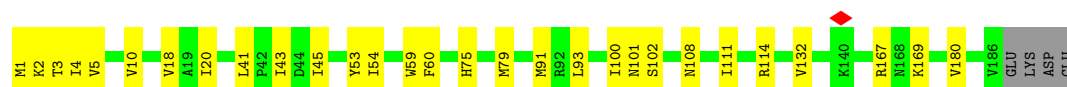
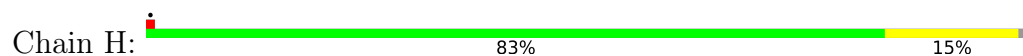
- Molecule 22: 60S ribosomal protein L30e, putative



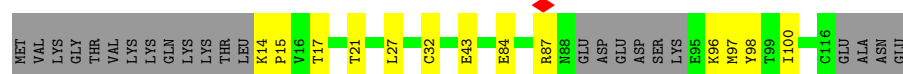
- Molecule 23: 40S ribosomal protein S20e, putative



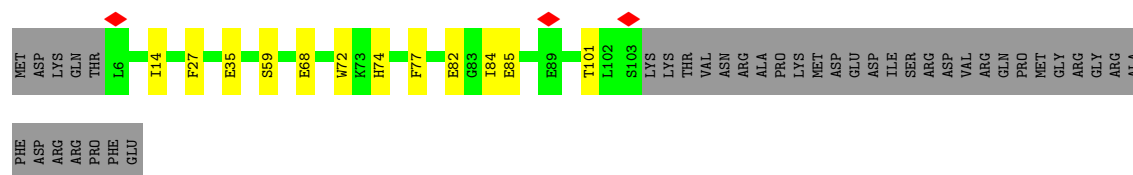
- Molecule 24: 60S ribosomal protein L6, putative



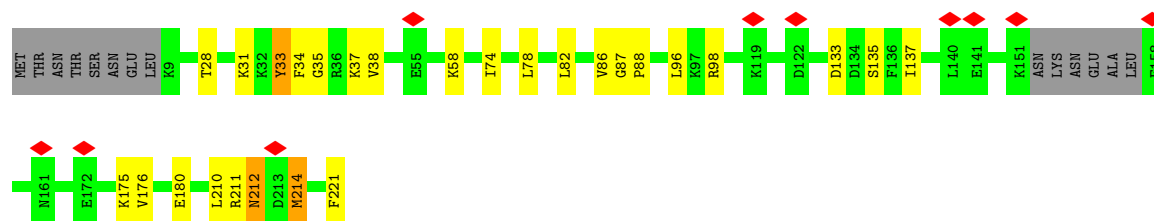
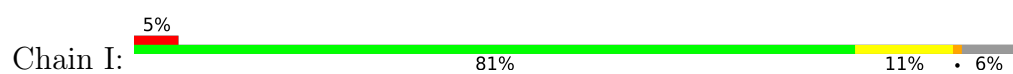
- Molecule 25: 60S ribosomal protein L31



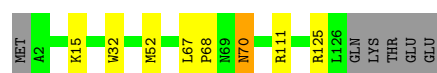
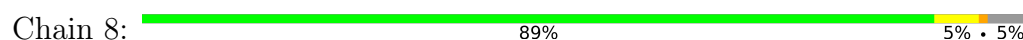
- Molecule 26: 40S ribosomal protein S10, putative



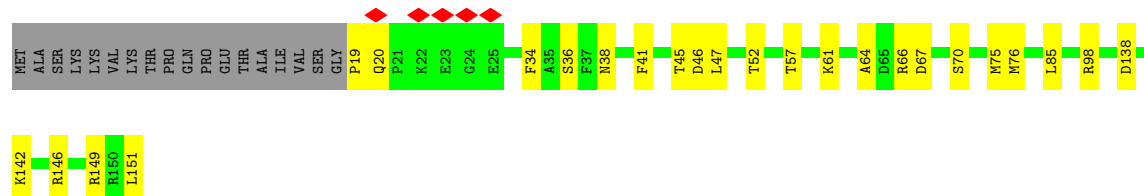
- Molecule 27: 60S ribosomal protein L6, putative



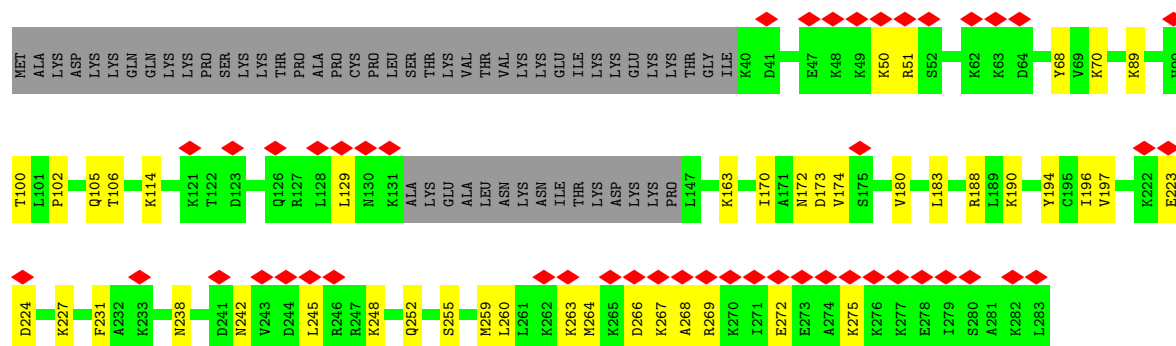
- Molecule 28: 60S ribosomal protein L32



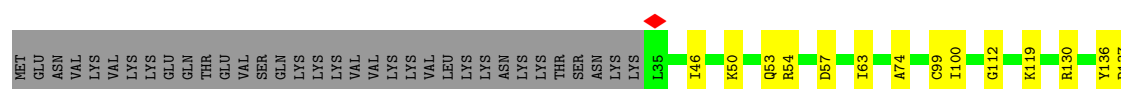
- Molecule 29: 40S ribosomal protein S11



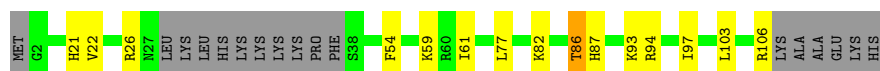
- Molecule 30: 60S ribosomal protein L7a



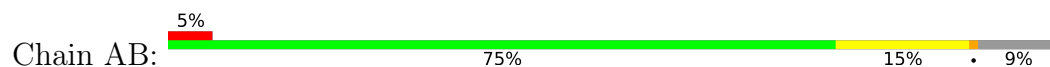
- Molecule 31: 60S ribosomal protein L35ae, putative



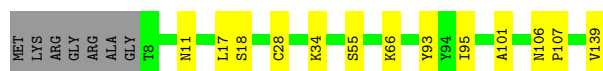
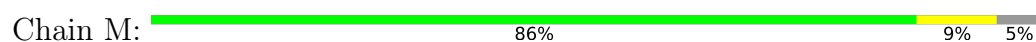




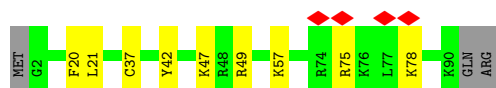
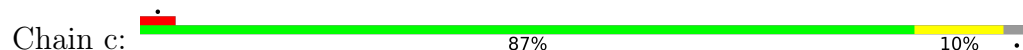
- Molecule 38: 40S ribosomal protein S18, putative



- Molecule 39: 60S ribosomal protein L23, putative



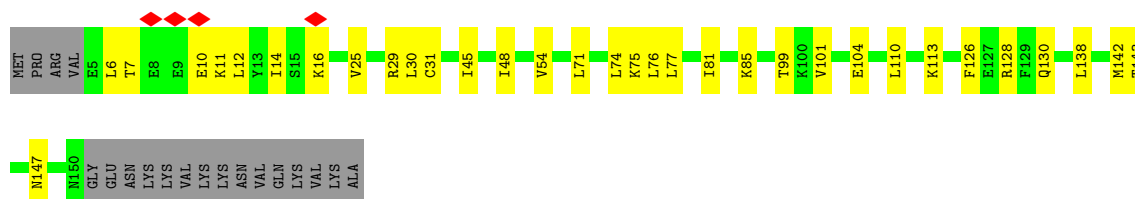
- Molecule 40: Ribosomal protein L37



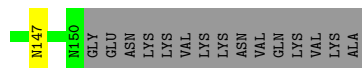
- Molecule 41: 40S ribosomal protein S29, putative



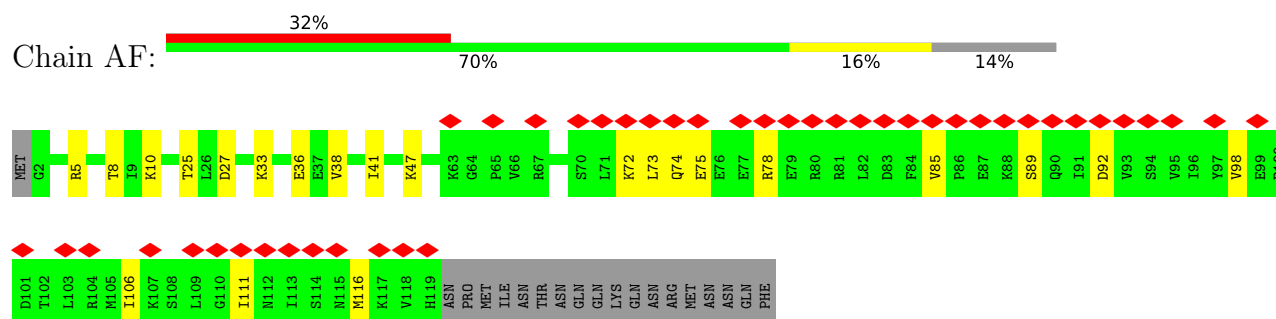
- Molecule 42: 60S ribosomal protein L14, putative



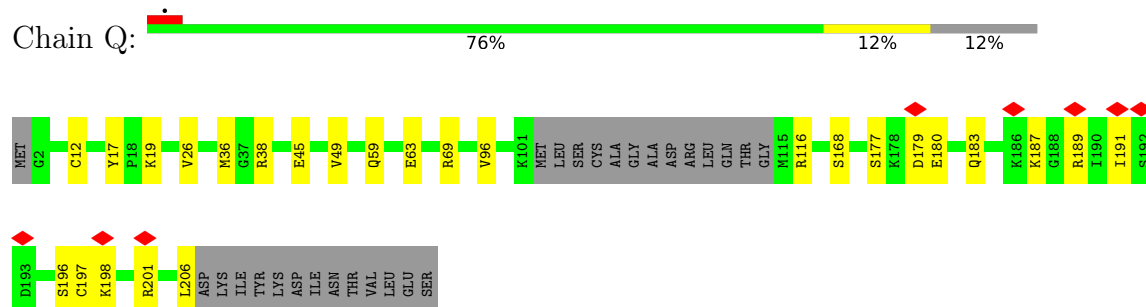
- Molecule 43: 60S ribosomal protein L38



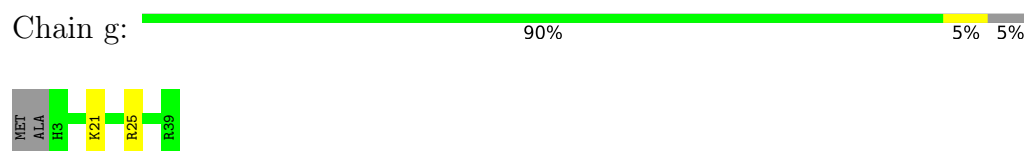
- Molecule 50: 40S ribosomal protein S17, putative



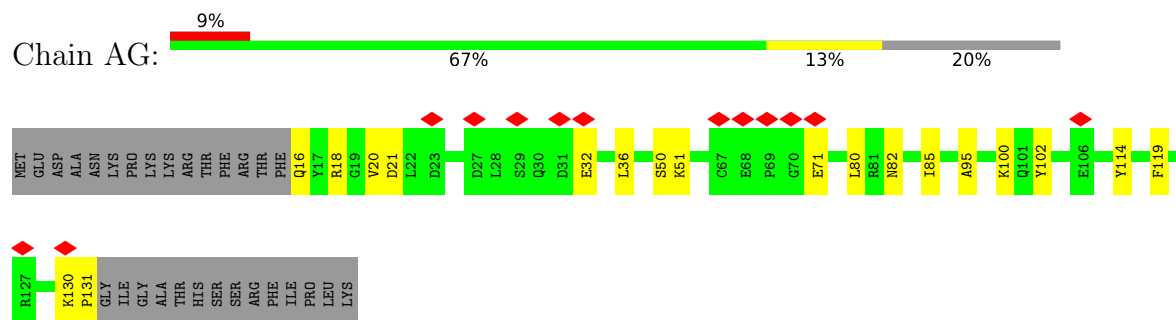
- Molecule 51: 60S ribosomal protein L10, putative



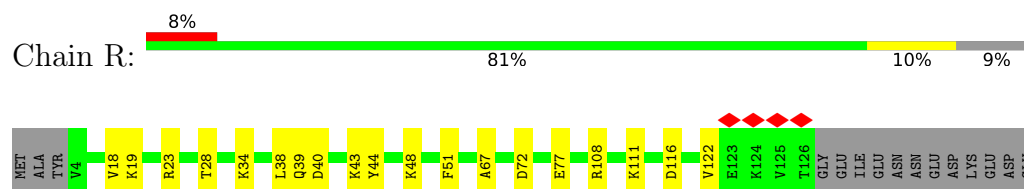
- Molecule 52: 60S ribosomal protein L41

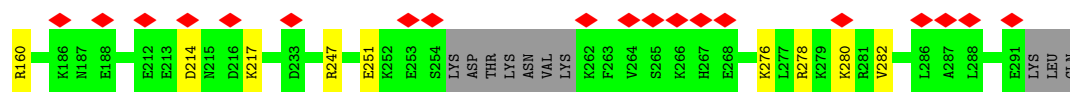


- Molecule 53: 40S ribosomal protein S19

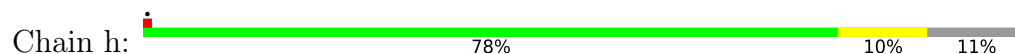


- Molecule 54: 60S ribosomal protein L5, putative

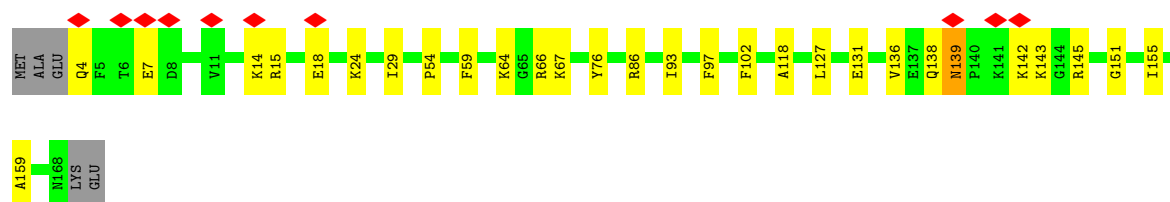
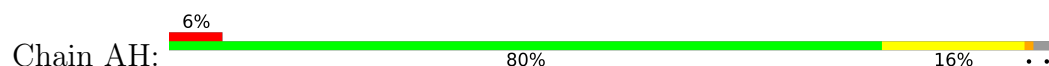




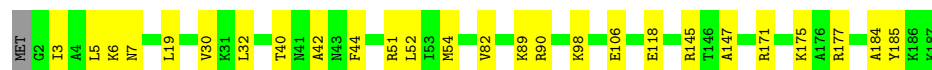
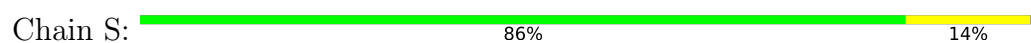
- Molecule 55: Large ribosomal subunit protein eL43



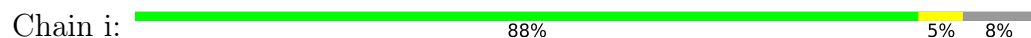
- Molecule 56: 40S ribosomal protein S19



- Molecule 57: 60S ribosomal protein L18-2, putative



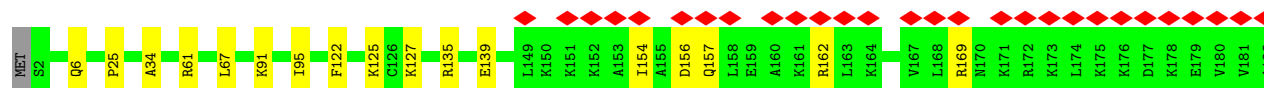
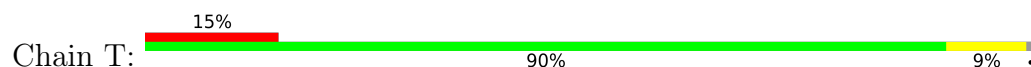
- Molecule 58: Large ribosomal subunit protein eL42



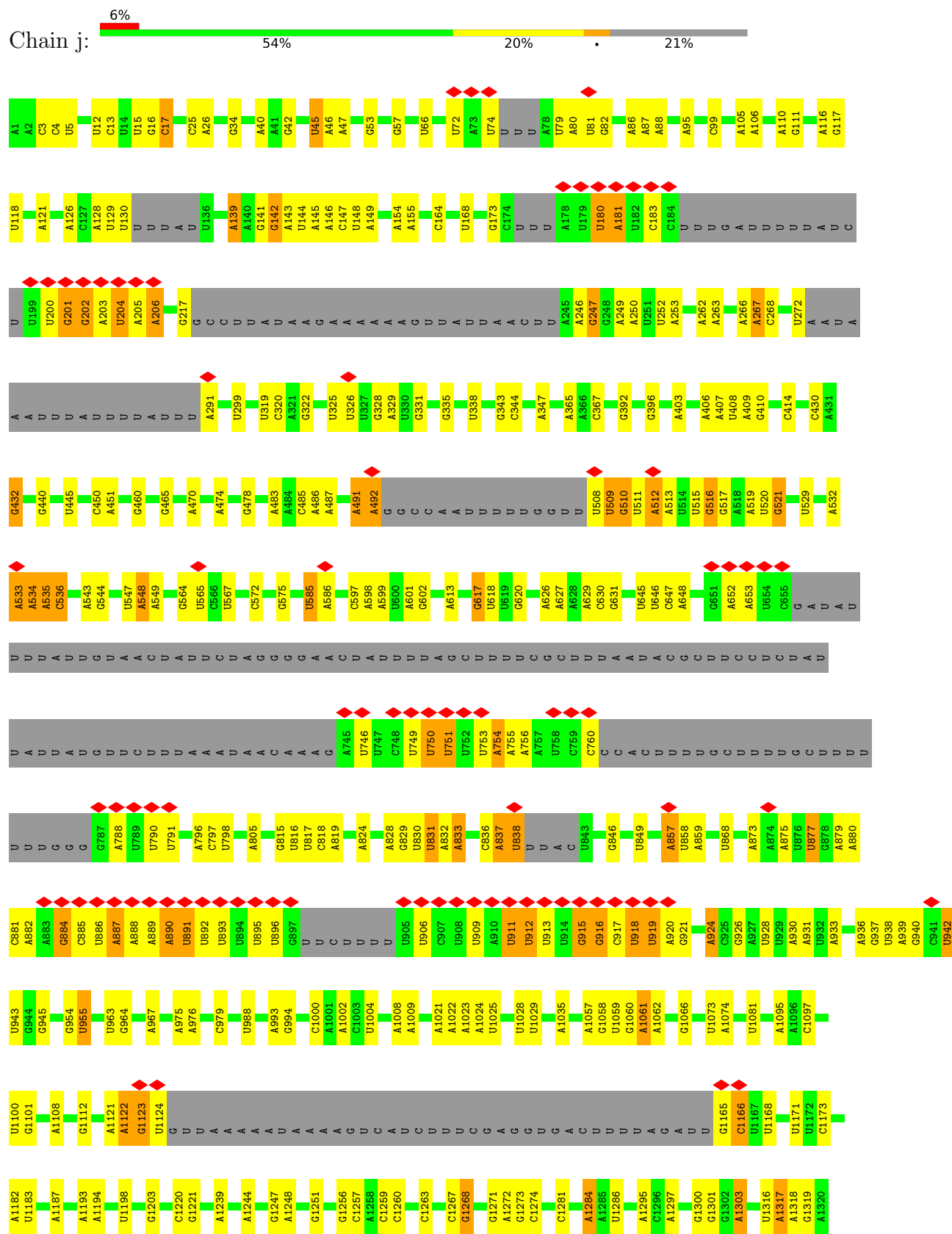
- Molecule 59: 40S ribosomal protein S21

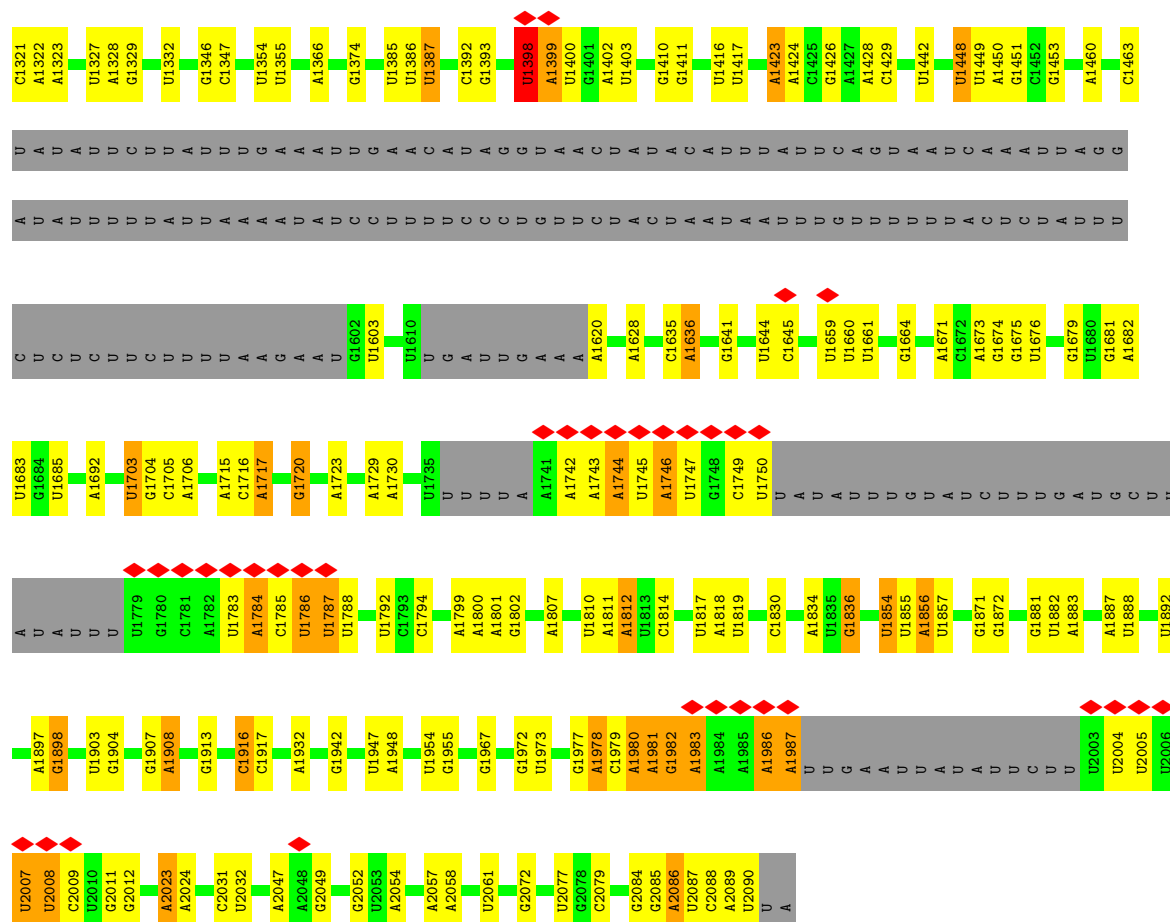


- Molecule 60: 60S ribosomal protein L19

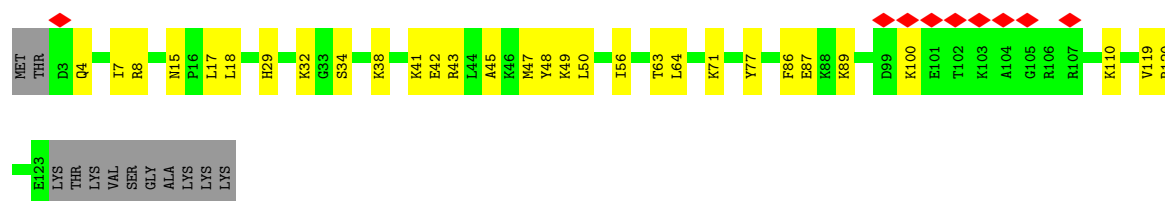


• Molecule 61: 18S ribosomal RNA

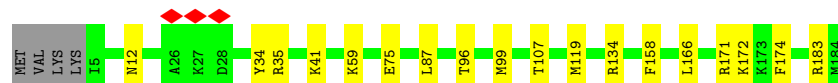
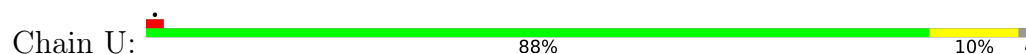




• Molecule 62: 40S ribosomal protein S24

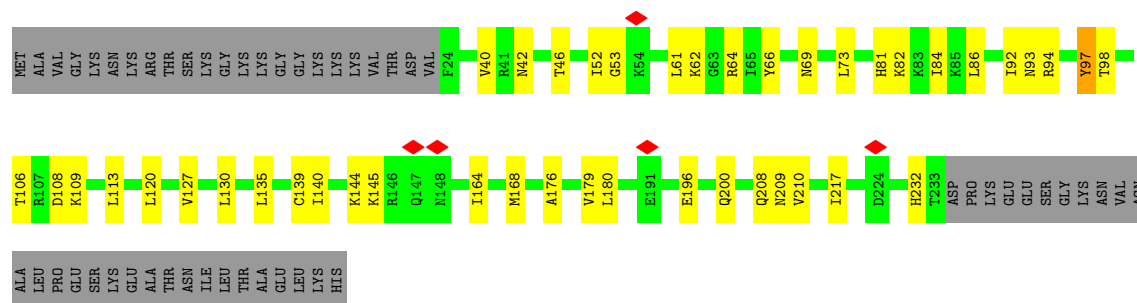


• Molecule 63: 60S ribosomal protein L18a



• Molecule 64: Small ribosomal subunit protein eS1

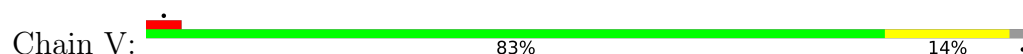




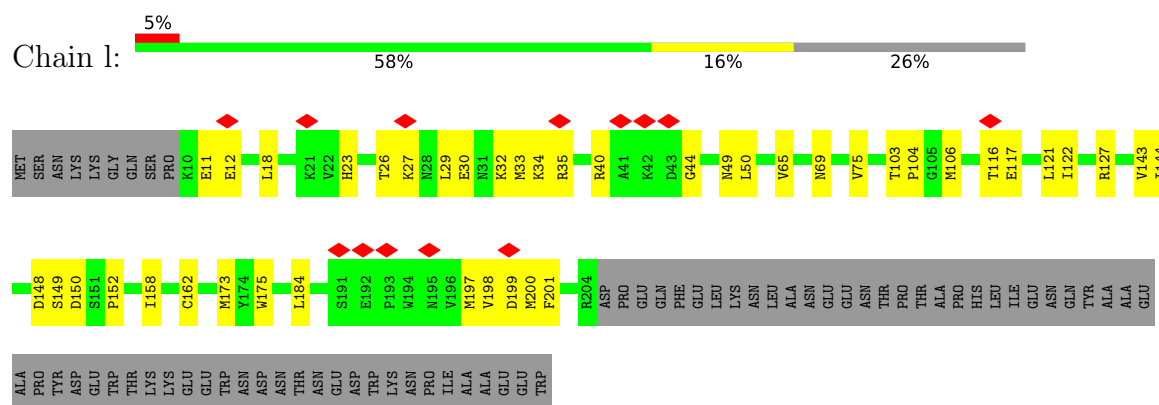
• Molecule 65: 40S ribosomal protein S25



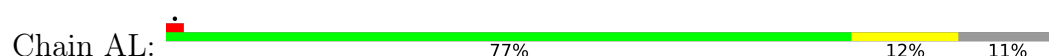
• Molecule 66: 60S ribosomal protein L21



• Molecule 67: Small ribosomal subunit protein uS2

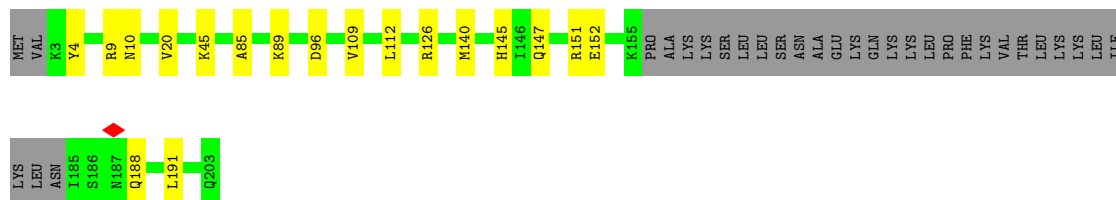


• Molecule 68: 40S ribosomal protein S26



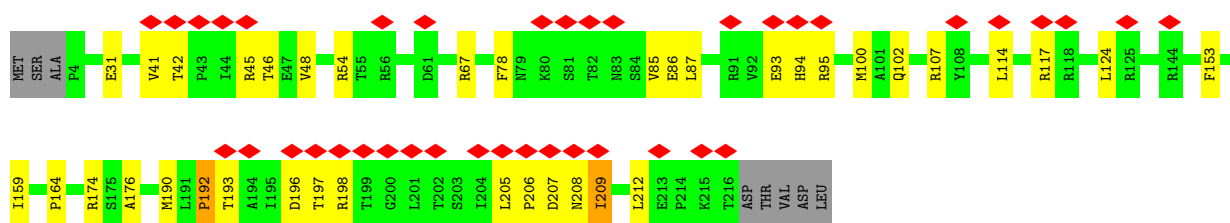
- Molecule 69: 60S ribosomal protein L17, putative

Chain W:  76% 9% 15%

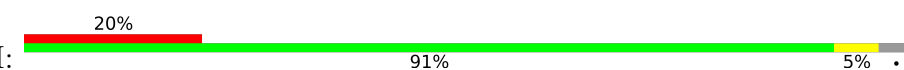


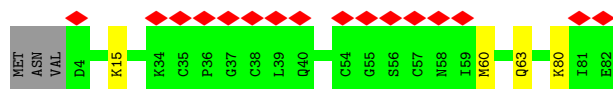
- Molecule 70: 40S ribosomal protein S3

Chain m:  18% 79% 16% . .



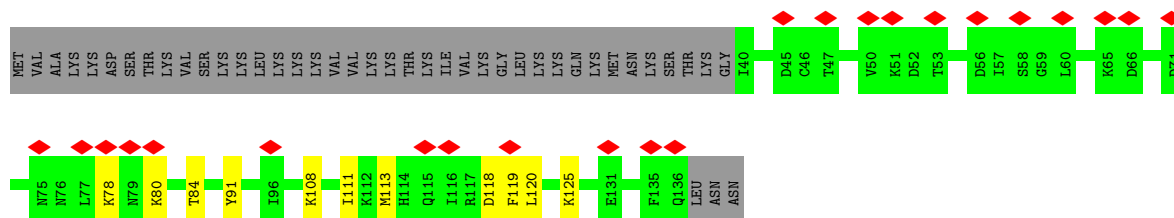
- Molecule 71: 40S ribosomal protein S27

Chain AM:  20% 91% 5% .



- Molecule 72: Large ribosomal subunit protein eL22

Chain X:  17% 62% 8% 30%

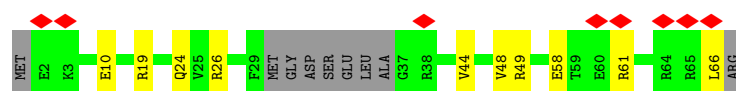
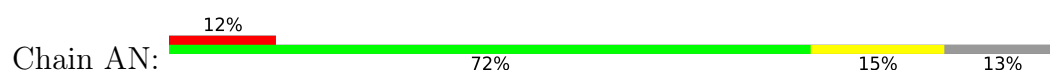


- Molecule 73: 40S ribosomal protein S9, putative

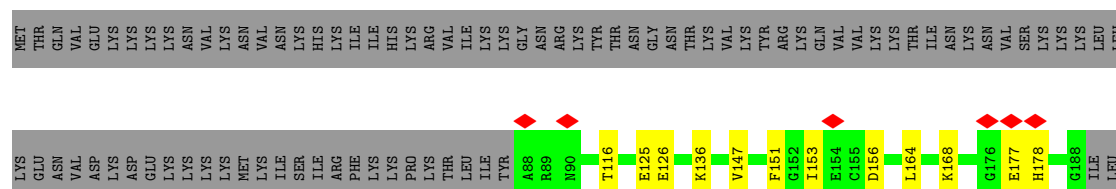
Chain n:  5% 86% 12% .



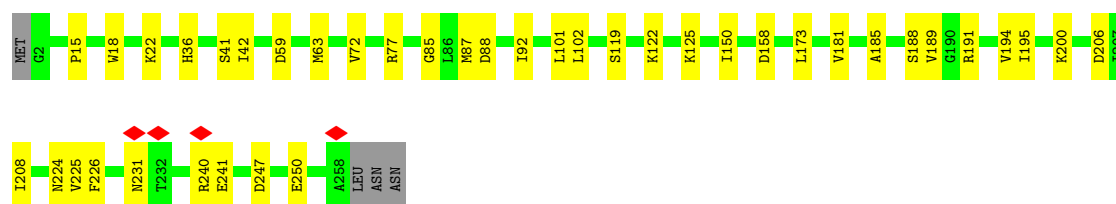
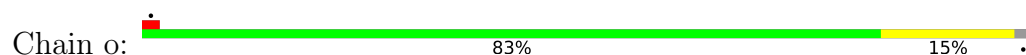
- Molecule 74: 40S ribosomal protein S28e, putative



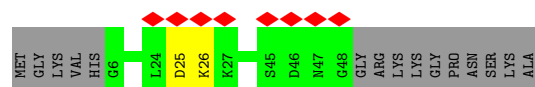
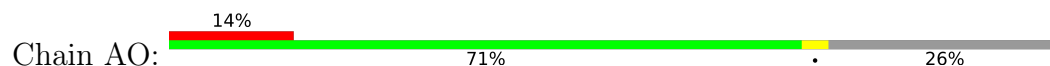
- Molecule 75: 60S ribosomal protein L23



- Molecule 76: 40S ribosomal protein S4



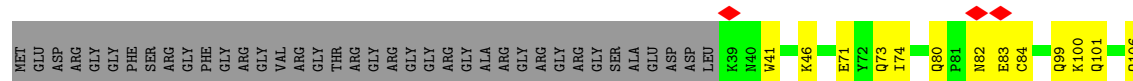
- Molecule 77: Small ribosomal subunit protein eS30

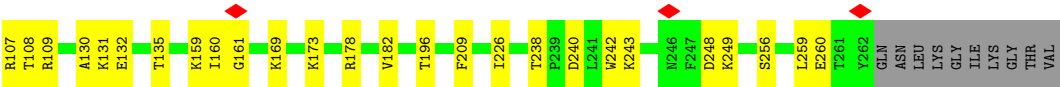


- Molecule 78: 60S ribosomal protein L26, putative

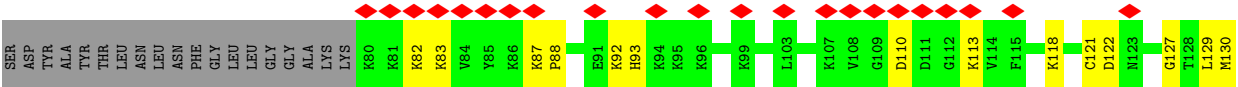
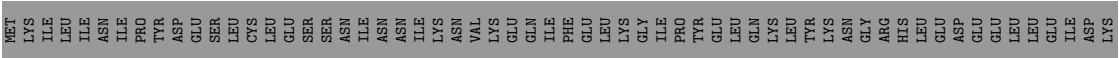
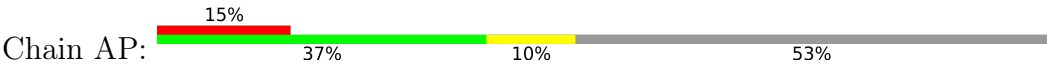


- Molecule 79: 40S ribosomal protein S5





● Molecule 80: Ribosomal protein S27a, putative



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	98057	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	0.038	Depositor
Minimum map value	-0.005	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: ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.28	2/76208 (0.0%)	0.39	2/118656 (0.0%)
2	0	0.23	0/533	0.46	0/711
3	q	0.20	0/1735	0.45	0/2304
4	AQ	0.16	0/1754	0.30	0/2732
5	B	0.25	0/2826	0.33	0/4404
6	1	0.22	0/1189	0.42	0/1582
7	r	0.29	0/1507	0.51	0/2023
8	AR	0.55	4/2565 (0.2%)	0.78	12/3488 (0.3%)
9	C	0.28	0/3633	0.36	0/5654
10	2	0.23	0/973	0.44	0/1298
11	s	0.18	0/1544	0.38	0/2064
12	D	0.27	0/1901	0.48	0/2544
13	3	0.27	0/1033	0.49	0/1367
14	t	0.24	0/1054	0.45	0/1411
15	E	0.25	0/3129	0.47	0/4195
16	4	0.25	0/564	0.46	0/737
17	u	0.25	0/1376	0.48	1/1840 (0.1%)
18	F	0.26	0/3144	0.46	0/4205
19	5	0.27	0/1917	0.50	0/2562
20	v	0.30	0/1113	0.53	0/1487
21	G	0.22	0/1373	0.45	0/1830
22	6	0.26	0/748	0.50	0/1001
23	w	0.28	0/821	0.52	0/1106
24	H	0.25	0/1493	0.49	0/2019
25	7	0.26	0/814	0.48	0/1085
26	x	0.30	0/867	0.60	1/1174 (0.1%)
27	I	0.23	0/1707	0.45	0/2274
28	8	0.27	0/1053	0.51	0/1399
29	y	0.23	0/1012	0.51	0/1358
30	J	0.21	0/1901	0.45	0/2537
31	9	0.28	0/878	0.54	0/1179
32	z	0.22	0/1149	0.43	0/1532

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	K	0.26	0/1697	0.45	0/2271
34	a	0.26	0/871	0.47	0/1161
35	AA	0.20	0/916	0.41	0/1233
36	L	0.26	0/1793	0.49	0/2387
37	b	0.25	0/762	0.45	0/1008
38	AB	0.32	0/1178	0.64	2/1582 (0.1%)
39	M	0.22	0/1012	0.43	0/1363
40	c	0.29	0/718	0.57	0/946
41	AC	0.31	0/445	0.53	0/590
42	N	0.26	0/1219	0.47	0/1622
43	d	0.25	0/645	0.52	0/858
44	AD	0.23	0/1217	0.41	0/1627
45	O	0.28	0/1199	0.54	0/1597
46	e	0.23	0/462	0.40	0/610
47	AE	0.23	0/1241	0.43	0/1656
48	P	0.30	0/1735	0.54	0/2320
49	f	0.25	0/418	0.49	0/556
50	AF	0.23	0/974	0.41	0/1301
51	Q	0.23	0/1602	0.43	0/2142
52	g	0.26	0/347	0.48	0/448
53	AG	0.31	0/963	0.60	2/1287 (0.2%)
54	R	0.24	0/2204	0.44	0/2946
55	h	0.26	0/667	0.48	0/887
56	AH	0.31	0/1382	0.55	0/1861
57	S	0.27	0/1530	0.52	0/2040
58	i	0.26	0/797	0.47	0/1043
59	AI	0.20	0/640	0.38	0/860
60	T	0.24	0/1521	0.47	0/2012
61	j	0.27	1/39168 (0.0%)	0.36	0/60989
62	AJ	0.23	0/1007	0.54	0/1333
63	U	0.27	0/1526	0.46	0/2043
64	k	0.23	0/1737	0.54	0/2321
65	AK	0.38	0/572	0.54	0/767
66	V	0.24	0/1304	0.40	0/1737
67	l	0.21	0/1569	0.43	0/2129
68	AL	0.25	0/793	0.47	0/1055
69	W	0.26	0/1356	0.51	0/1815
70	m	0.27	0/1686	0.52	0/2258
71	AM	0.22	0/621	0.37	0/834
72	X	0.18	0/841	0.41	0/1125
73	n	0.24	0/1552	0.47	0/2070
74	AN	0.30	0/452	0.50	0/599
75	Y	0.25	0/805	0.44	0/1074

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	o	0.24	0/2097	0.49	0/2819
77	AO	0.22	0/348	0.53	0/458
78	Z	0.27	0/1017	0.54	0/1346
79	p	0.23	0/1799	0.40	0/2429
80	AP	0.21	0/583	0.50	0/767
All	All	0.27	7/214502 (0.0%)	0.42	20/313940 (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
8	AR	0	1
13	3	0	1
15	E	0	2
19	5	0	2
27	I	0	2
32	z	0	1
57	S	0	1
62	AJ	0	1
64	k	0	1
All	All	0	12

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	AR	279	ILE	C-N	14.93	1.53	1.33
8	AR	97	ARG	C-N	11.76	1.49	1.33
8	AR	96	VAL	C-N	-10.44	1.20	1.33
1	A	3566	C	C1'-N1	7.42	1.59	1.48
8	AR	38	ILE	C-N	7.36	1.44	1.33

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	AR	287	ILE	N-CA-C	14.55	139.61	109.34
8	AR	96	VAL	O-C-N	-14.47	107.93	122.98
8	AR	96	VAL	CA-C-N	12.96	142.58	121.58
8	AR	96	VAL	C-N-CA	12.96	142.58	121.58
8	AR	97	ARG	O-C-N	7.89	133.04	123.26

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	3	121	VAL	Peptide
19	5	89	GLU	Peptide
8	AR	97	ARG	Mainchain
15	E	16	PHE	Peptide
15	E	253	HIS	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	34331	512	0
2	0	521	0	539	10	0
3	q	1717	0	1886	31	0
4	AQ	1571	0	797	32	0
5	B	2525	0	1274	14	0
6	1	1171	0	1288	13	0
7	r	1487	0	1543	18	0
8	AR	2509	0	2472	59	0
9	C	3246	0	1641	12	0
10	2	960	0	1016	8	0
11	s	1528	0	1680	30	0
12	D	1866	0	1964	25	0
13	3	1022	0	1147	10	0
14	t	1037	0	1099	9	0
15	E	3061	0	3205	29	0
16	4	555	0	599	5	0
17	u	1352	0	1409	17	0
18	F	3094	0	3333	40	0
19	5	1879	0	2005	28	0
20	v	1098	0	1183	13	0
21	G	1352	0	1412	18	0
22	6	740	0	763	13	0
23	w	813	0	863	7	0
24	H	1468	0	1544	17	0
25	7	802	0	881	9	0
26	x	839	0	852	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	I	1684	0	1849	19	0
28	8	1036	0	1139	6	0
29	y	998	0	1042	18	0
30	J	1873	0	2055	30	0
31	9	858	0	897	10	0
32	z	1129	0	1196	7	0
33	K	1666	0	1789	10	0
34	a	858	0	908	8	0
35	AA	903	0	912	13	0
36	L	1761	0	1896	22	0
37	b	756	0	842	10	0
38	AB	1161	0	1212	18	0
39	M	996	0	1044	10	0
40	c	705	0	753	7	0
41	AC	438	0	451	4	0
42	N	1203	0	1320	25	0
43	d	636	0	726	9	0
44	AD	1196	0	1294	11	0
45	O	1172	0	1230	14	0
46	e	452	0	492	4	0
47	AE	1214	0	1250	10	0
48	P	1697	0	1802	16	0
49	f	413	0	448	7	0
50	AF	963	0	1045	23	0
51	Q	1567	0	1607	17	0
52	g	342	0	388	1	0
53	AG	945	0	1000	10	0
54	R	2171	0	2257	23	0
55	h	658	0	723	8	0
56	AH	1353	0	1401	22	0
57	S	1502	0	1636	18	0
58	i	787	0	870	4	0
59	AI	631	0	637	6	0
60	T	1505	0	1671	12	0
61	j	35005	0	17635	238	0
62	AJ	994	0	1082	28	0
63	U	1496	0	1556	14	0
64	k	1713	0	1838	32	0
65	AK	565	0	607	5	0
66	V	1279	0	1358	17	0
67	l	1538	0	1600	33	0
68	AL	781	0	818	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	W	1336	0	1345	13	0
70	m	1667	0	1764	30	0
71	AM	610	0	630	4	0
72	X	824	0	882	7	0
73	n	1528	0	1638	14	0
74	AN	451	0	485	8	0
75	Y	796	0	850	10	0
76	o	2061	0	2199	25	0
77	AO	345	0	381	1	0
78	Z	1005	0	1104	25	0
79	p	1757	0	1811	25	0
80	AP	573	0	624	9	0
81	0	1	0	0	0	0
81	8	1	0	0	0	0
81	A	172	0	0	0	0
81	AH	1	0	0	0	0
81	B	3	0	0	0	0
81	C	8	0	0	0	0
81	M	1	0	0	0	0
81	Q	1	0	0	0	0
81	V	1	0	0	0	0
81	W	1	0	0	0	0
81	X	1	0	0	0	0
81	a	1	0	0	0	0
81	c	1	0	0	0	0
81	j	59	0	0	0	0
81	k	1	0	0	0	0
81	o	1	0	0	0	0
82	AC	1	0	0	0	0
82	a	1	0	0	0	0
82	c	1	0	0	0	0
82	f	1	0	0	0	0
82	h	1	0	0	0	0
82	i	1	0	0	0	0
All	All	200146	0	150715	1729	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 1729 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)
8:AR:322:SER:O	8:AR:323:VAL:CG2	1.75	1.34
70:m:205:LEU:HD12	70:m:206:PRO:HD2	1.34	1.08
1:A:3747:U:H2'	1:A:3748:U:O4'	1.59	1.03
8:AR:322:SER:O	8:AR:323:VAL:HG23	0.83	1.00
70:m:164:PRO:HG3	70:m:206:PRO:HG3	1.45	0.98

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	0	60/162 (37%)	57 (95%)	3 (5%)	0	100	100
3	q	211/306 (69%)	194 (92%)	17 (8%)	0	100	100
6	1	143/146 (98%)	134 (94%)	9 (6%)	0	100	100
7	r	187/195 (96%)	172 (92%)	15 (8%)	0	100	100
8	AR	321/323 (99%)	290 (90%)	31 (10%)	0	100	100
10	2	119/127 (94%)	105 (88%)	14 (12%)	0	100	100
11	s	186/194 (96%)	174 (94%)	12 (6%)	0	100	100
12	D	245/260 (94%)	230 (94%)	15 (6%)	0	100	100
13	3	120/124 (97%)	109 (91%)	11 (9%)	0	100	100
14	t	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
15	E	378/386 (98%)	360 (95%)	18 (5%)	0	100	100
16	4	64/67 (96%)	58 (91%)	6 (9%)	0	100	100
17	u	164/218 (75%)	151 (92%)	13 (8%)	0	100	100
18	F	388/411 (94%)	365 (94%)	23 (6%)	0	100	100
19	5	221/257 (86%)	205 (93%)	16 (7%)	0	100	100
20	v	136/144 (94%)	128 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	G	163/173 (94%)	155 (95%)	8 (5%)	0	100	100
22	6	96/108 (89%)	87 (91%)	9 (9%)	0	100	100
23	w	100/118 (85%)	90 (90%)	10 (10%)	0	100	100
24	H	184/190 (97%)	164 (89%)	20 (11%)	0	100	100
25	7	93/120 (78%)	91 (98%)	2 (2%)	0	100	100
26	x	96/137 (70%)	83 (86%)	13 (14%)	0	100	100
27	I	203/221 (92%)	185 (91%)	18 (9%)	0	100	100
28	8	123/131 (94%)	115 (94%)	8 (6%)	0	100	100
29	y	131/151 (87%)	111 (85%)	20 (15%)	0	100	100
30	J	225/283 (80%)	213 (95%)	12 (5%)	0	100	100
31	9	103/140 (74%)	89 (86%)	14 (14%)	0	100	100
32	z	142/145 (98%)	135 (95%)	7 (5%)	0	100	100
33	K	199/202 (98%)	191 (96%)	8 (4%)	0	100	100
34	a	104/150 (69%)	101 (97%)	3 (3%)	0	100	100
35	AA	115/141 (82%)	107 (93%)	8 (7%)	0	100	100
36	L	209/215 (97%)	198 (95%)	11 (5%)	0	100	100
37	b	91/112 (81%)	82 (90%)	8 (9%)	1 (1%)	11	12
38	AB	140/156 (90%)	116 (83%)	23 (16%)	1 (1%)	18	24
39	M	130/139 (94%)	118 (91%)	12 (9%)	0	100	100
40	c	87/92 (95%)	78 (90%)	9 (10%)	0	100	100
41	AC	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
42	N	144/165 (87%)	132 (92%)	12 (8%)	0	100	100
43	d	74/87 (85%)	69 (93%)	5 (7%)	0	100	100
44	AD	146/151 (97%)	140 (96%)	6 (4%)	0	100	100
45	O	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
46	e	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
47	AE	143/161 (89%)	137 (96%)	6 (4%)	0	100	100
48	P	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
49	f	49/128 (38%)	47 (96%)	2 (4%)	0	100	100
50	AF	116/137 (85%)	114 (98%)	2 (2%)	0	100	100
51	Q	188/219 (86%)	169 (90%)	19 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	g	35/39 (90%)	32 (91%)	3 (9%)	0	100	100
53	AG	114/145 (79%)	110 (96%)	4 (4%)	0	100	100
54	R	261/294 (89%)	243 (93%)	18 (7%)	0	100	100
55	h	83/96 (86%)	78 (94%)	5 (6%)	0	100	100
56	AH	163/170 (96%)	150 (92%)	13 (8%)	0	100	100
57	S	184/187 (98%)	170 (92%)	14 (8%)	0	100	100
58	i	94/104 (90%)	84 (89%)	10 (11%)	0	100	100
59	AI	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
60	T	179/182 (98%)	177 (99%)	2 (1%)	0	100	100
62	AJ	119/133 (90%)	104 (87%)	15 (13%)	0	100	100
63	U	178/184 (97%)	170 (96%)	8 (4%)	0	100	100
64	k	208/262 (79%)	176 (85%)	32 (15%)	0	100	100
65	AK	70/105 (67%)	64 (91%)	6 (9%)	0	100	100
66	V	154/161 (96%)	146 (95%)	8 (5%)	0	100	100
67	l	193/263 (73%)	170 (88%)	23 (12%)	0	100	100
68	AL	93/107 (87%)	86 (92%)	7 (8%)	0	100	100
69	W	168/203 (83%)	156 (93%)	12 (7%)	0	100	100
70	m	211/221 (96%)	189 (90%)	21 (10%)	1 (0%)	24	32
71	AM	77/82 (94%)	73 (95%)	4 (5%)	0	100	100
72	X	95/139 (68%)	87 (92%)	8 (8%)	0	100	100
73	n	183/189 (97%)	171 (93%)	12 (7%)	0	100	100
74	AN	54/67 (81%)	54 (100%)	0	0	100	100
75	Y	99/190 (52%)	95 (96%)	4 (4%)	0	100	100
76	o	255/261 (98%)	227 (89%)	28 (11%)	0	100	100
77	AO	41/58 (71%)	37 (90%)	4 (10%)	0	100	100
78	Z	120/126 (95%)	116 (97%)	4 (3%)	0	100	100
79	p	222/272 (82%)	210 (95%)	12 (5%)	0	100	100
80	AP	68/149 (46%)	64 (94%)	4 (6%)	0	100	100
All	All	10910/12551 (87%)	10100 (93%)	807 (7%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
37	b	86	THR
38	AB	103	ASN
70	m	192	PRO

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	0	53/146 (36%)	53 (100%)	0	100	100
3	q	189/279 (68%)	188 (100%)	1 (0%)	81	87
6	1	131/132 (99%)	131 (100%)	0	100	100
7	r	160/165 (97%)	160 (100%)	0	100	100
8	AR	287/287 (100%)	282 (98%)	5 (2%)	53	67
10	2	112/118 (95%)	112 (100%)	0	100	100
11	s	177/183 (97%)	177 (100%)	0	100	100
12	D	191/202 (95%)	191 (100%)	0	100	100
13	3	113/115 (98%)	113 (100%)	0	100	100
14	t	115/116 (99%)	115 (100%)	0	100	100
15	E	335/340 (98%)	335 (100%)	0	100	100
16	4	60/61 (98%)	60 (100%)	0	100	100
17	u	148/193 (77%)	148 (100%)	0	100	100
18	F	336/352 (96%)	336 (100%)	0	100	100
19	5	201/231 (87%)	201 (100%)	0	100	100
20	v	116/122 (95%)	116 (100%)	0	100	100
21	G	147/155 (95%)	147 (100%)	0	100	100
22	6	83/92 (90%)	83 (100%)	0	100	100
23	w	95/109 (87%)	95 (100%)	0	100	100
24	H	165/173 (95%)	165 (100%)	0	100	100
25	7	91/112 (81%)	91 (100%)	0	100	100
26	x	94/129 (73%)	94 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	I	189/203 (93%)	188 (100%)	1 (0%)	81	87
28	8	114/120 (95%)	113 (99%)	1 (1%)	70	81
29	y	104/119 (87%)	104 (100%)	0	100	100
30	J	211/260 (81%)	211 (100%)	0	100	100
31	9	92/127 (72%)	92 (100%)	0	100	100
32	z	120/121 (99%)	120 (100%)	0	100	100
33	K	182/182 (100%)	182 (100%)	0	100	100
34	a	89/128 (70%)	89 (100%)	0	100	100
35	AA	100/121 (83%)	100 (100%)	0	100	100
36	L	190/194 (98%)	190 (100%)	0	100	100
37	b	82/97 (84%)	82 (100%)	0	100	100
38	AB	127/136 (93%)	127 (100%)	0	100	100
39	M	106/110 (96%)	106 (100%)	0	100	100
40	c	73/77 (95%)	73 (100%)	0	100	100
41	AC	47/48 (98%)	47 (100%)	0	100	100
42	N	135/152 (89%)	134 (99%)	1 (1%)	76	84
43	d	73/83 (88%)	72 (99%)	1 (1%)	59	72
44	AD	132/133 (99%)	132 (100%)	0	100	100
45	O	121/122 (99%)	121 (100%)	0	100	100
46	e	47/48 (98%)	47 (100%)	0	100	100
47	AE	132/144 (92%)	132 (100%)	0	100	100
48	P	179/180 (99%)	179 (100%)	0	100	100
49	f	45/114 (40%)	45 (100%)	0	100	100
50	AF	108/127 (85%)	108 (100%)	0	100	100
51	Q	167/190 (88%)	167 (100%)	0	100	100
52	g	34/35 (97%)	34 (100%)	0	100	100
53	AG	105/130 (81%)	101 (96%)	4 (4%)	29	43
54	R	229/254 (90%)	229 (100%)	0	100	100
55	h	70/80 (88%)	70 (100%)	0	100	100
56	AH	147/151 (97%)	145 (99%)	2 (1%)	59	72
57	S	158/159 (99%)	158 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	i	88/93 (95%)	88 (100%)	0	100	100
59	AI	69/70 (99%)	69 (100%)	0	100	100
60	T	161/163 (99%)	161 (100%)	0	100	100
62	AJ	105/115 (91%)	105 (100%)	0	100	100
63	U	162/166 (98%)	162 (100%)	0	100	100
64	k	195/238 (82%)	195 (100%)	0	100	100
65	AK	64/88 (73%)	61 (95%)	3 (5%)	23	35
66	V	140/144 (97%)	140 (100%)	0	100	100
67	l	167/227 (74%)	167 (100%)	0	100	100
68	AL	87/98 (89%)	87 (100%)	0	100	100
69	W	130/178 (73%)	130 (100%)	0	100	100
70	m	179/188 (95%)	177 (99%)	2 (1%)	65	76
71	AM	73/76 (96%)	73 (100%)	0	100	100
72	X	92/131 (70%)	92 (100%)	0	100	100
73	n	164/167 (98%)	164 (100%)	0	100	100
74	AN	46/54 (85%)	46 (100%)	0	100	100
75	Y	90/177 (51%)	90 (100%)	0	100	100
76	o	233/237 (98%)	233 (100%)	0	100	100
77	AO	36/47 (77%)	36 (100%)	0	100	100
78	Z	111/115 (96%)	111 (100%)	0	100	100
79	p	191/222 (86%)	191 (100%)	0	100	100
80	AP	62/135 (46%)	62 (100%)	0	100	100
All	All	9752/11086 (88%)	9731 (100%)	21 (0%)	85	92

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	AH	138	GLN
65	AK	57	LYS
70	m	209	ILE
65	AK	59	ILE
65	AK	56	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
56	AH	139	ASN
66	V	49	GLN
58	i	14	ASN
62	AJ	31	ASN
68	AL	40	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3171/3788 (83%)	588 (18%)	24 (0%)
4	AQ	73/74 (98%)	28 (38%)	1 (1%)
5	B	117/119 (98%)	9 (7%)	1 (0%)
61	j	1626/2092 (77%)	334 (20%)	0
9	C	149/159 (93%)	28 (18%)	1 (0%)
All	All	5136/6232 (82%)	987 (19%)	27 (0%)

5 of 987 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	A
1	A	14	U
1	A	40	A
1	A	43	A
1	A	45	A

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1538	U
1	A	1961	U
4	AQ	62	C
1	A	1841	U
1	A	2180	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 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.

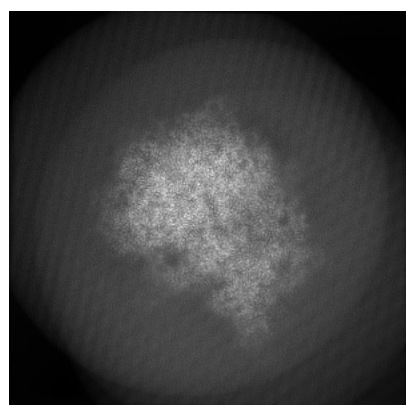
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61272. These allow visual inspection of the internal detail of the map and identification of artifacts.

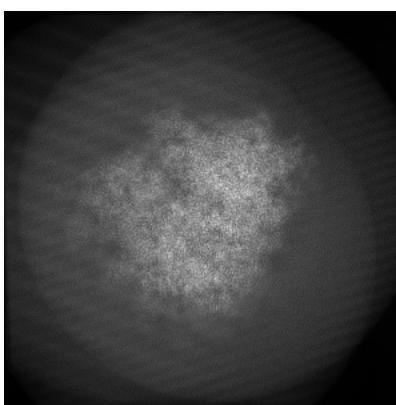
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

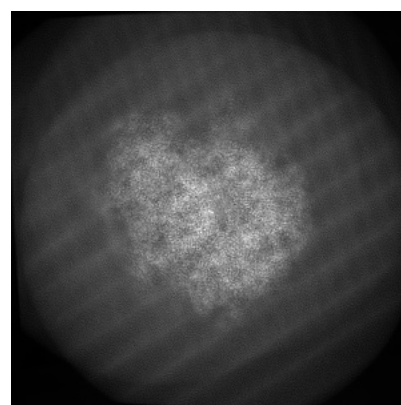
6.1.1 Primary map



X



Y

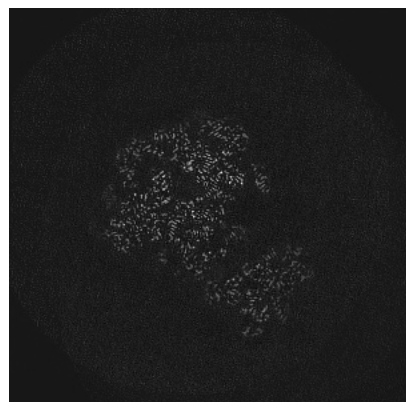


Z

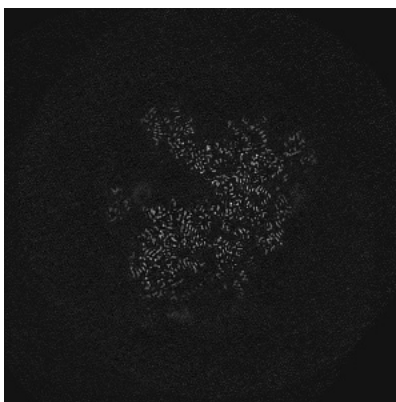
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

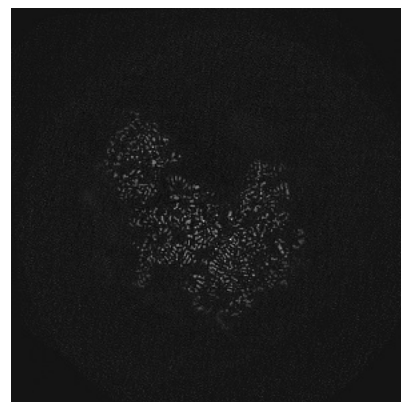
6.2.1 Primary map



X Index: 240



Y Index: 240

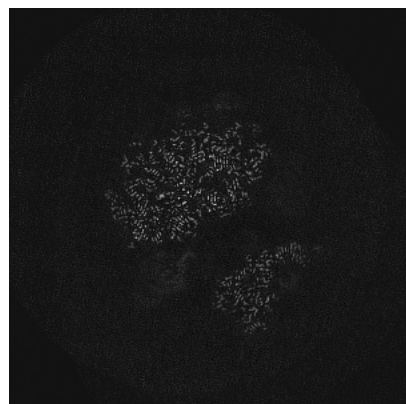


Z Index: 240

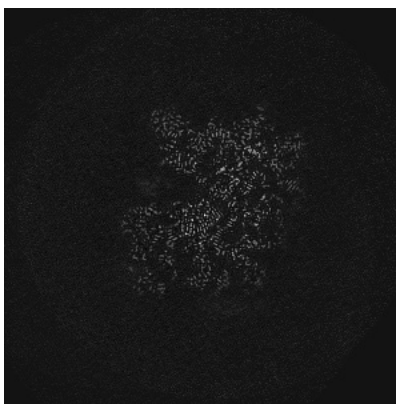
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

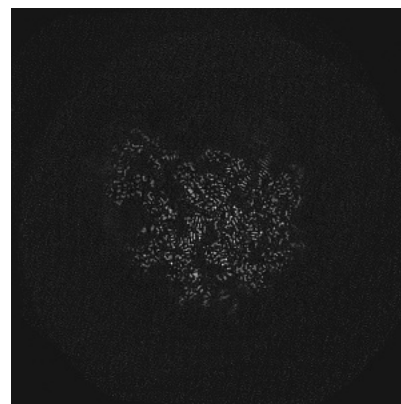
6.3.1 Primary map



X Index: 282



Y Index: 224

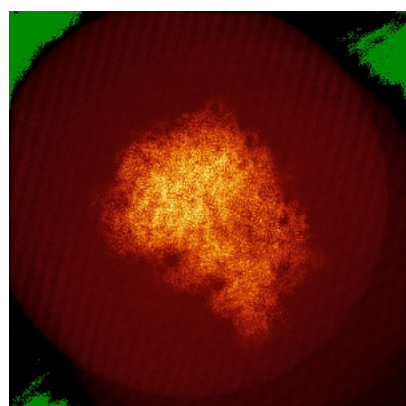


Z Index: 272

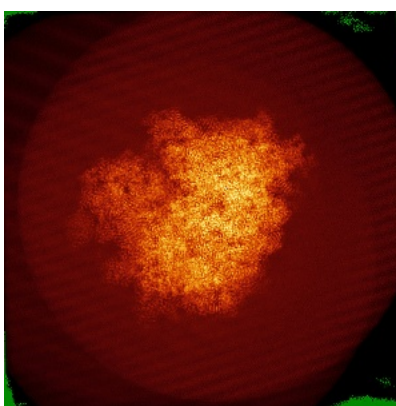
The images above show the largest variance slices of the map in three orthogonal directions.

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

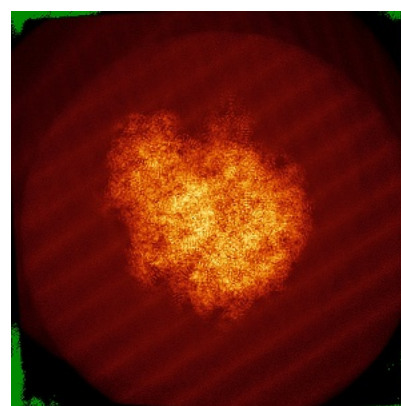
6.4.1 Primary map



X



Y

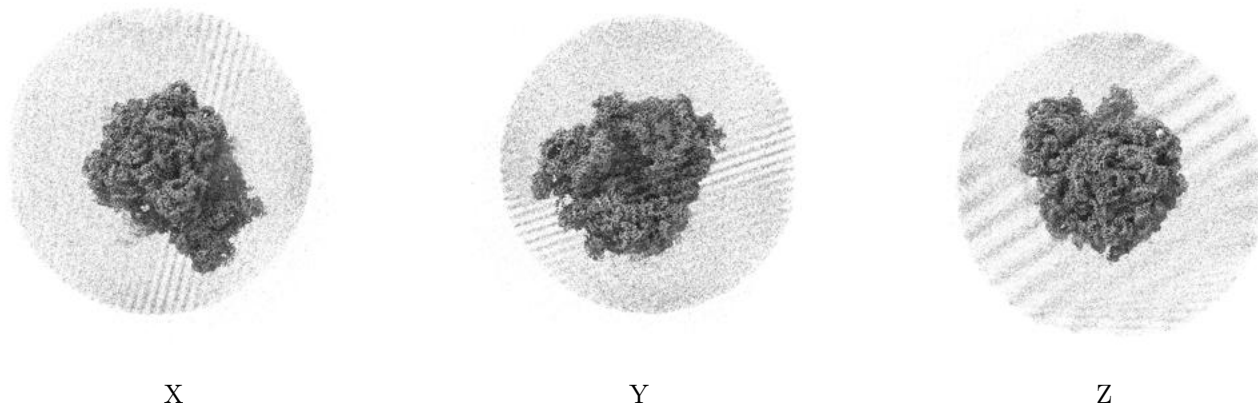


Z

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 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

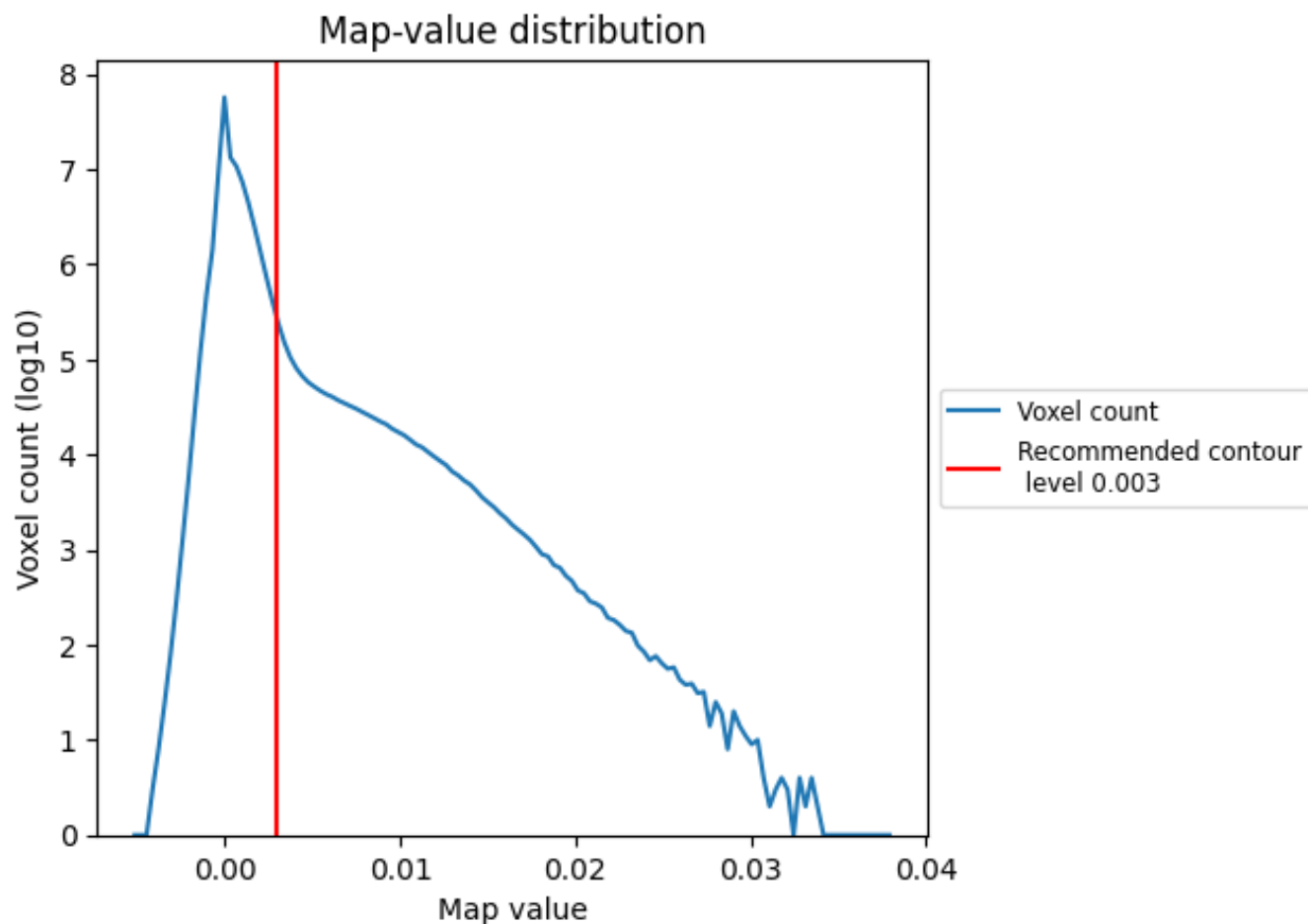
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

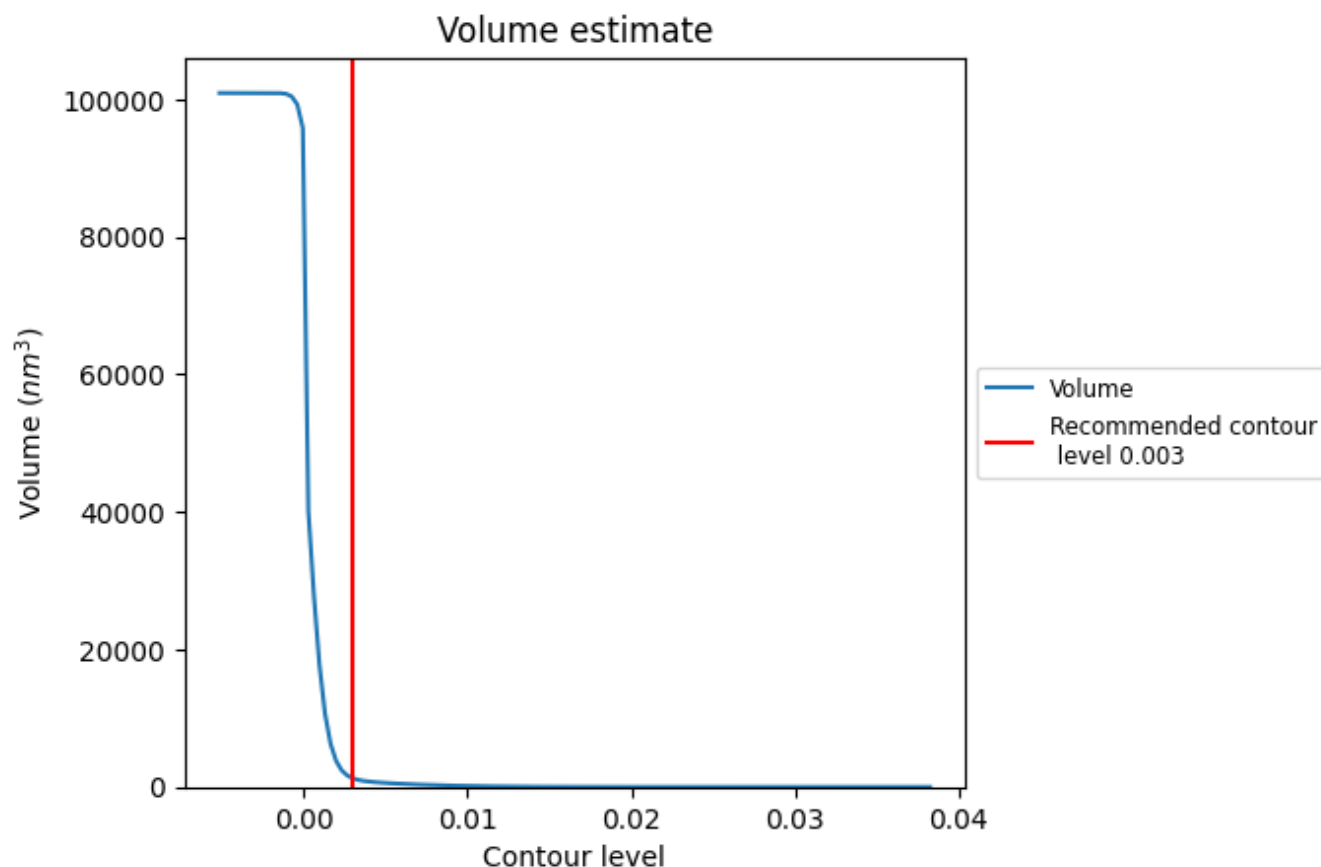
This section contains the results of statistical analysis of the map.

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.

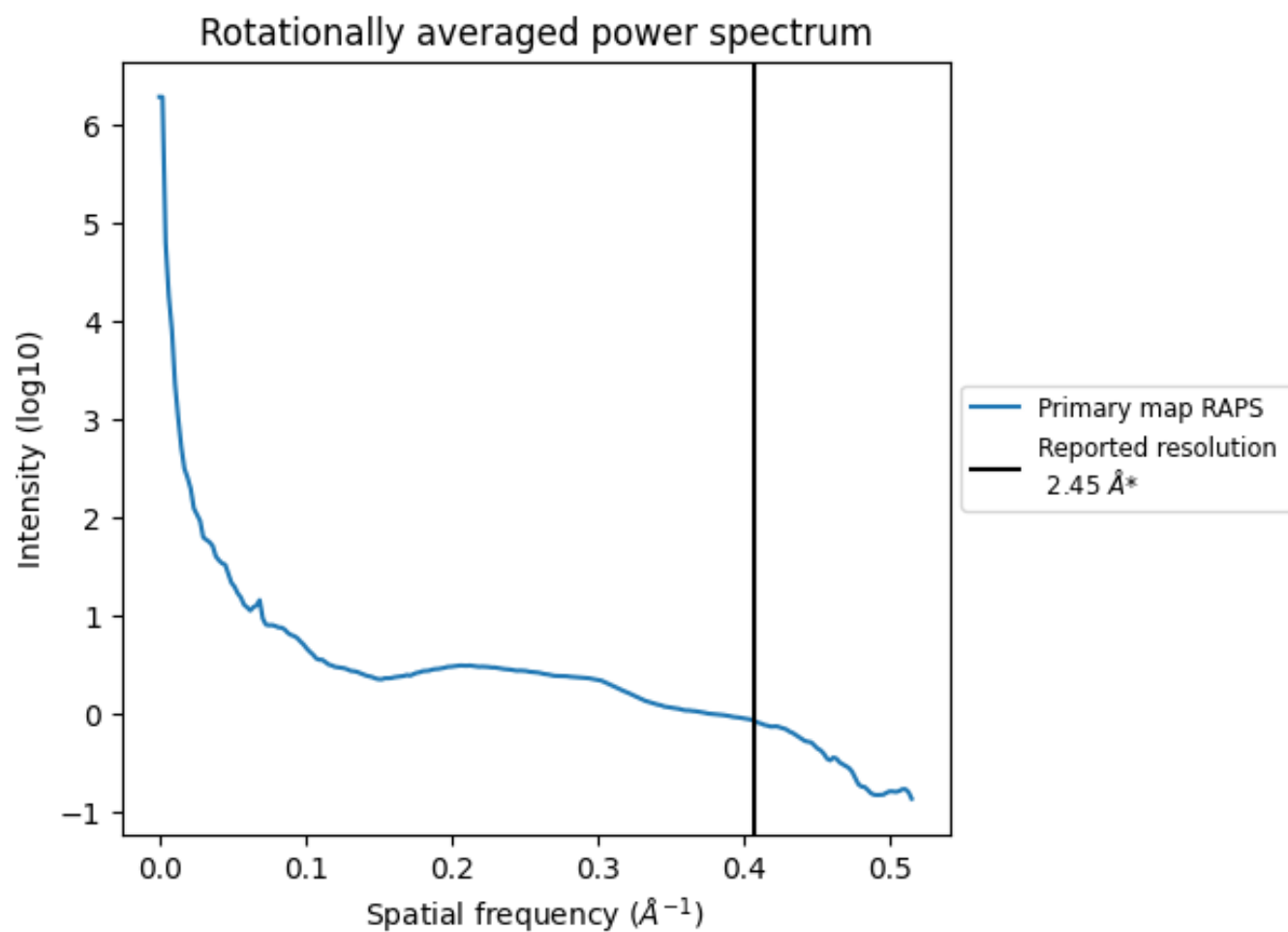
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1259 nm^3 ; this corresponds to an approximate mass of 1137 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 0.408 Å⁻¹

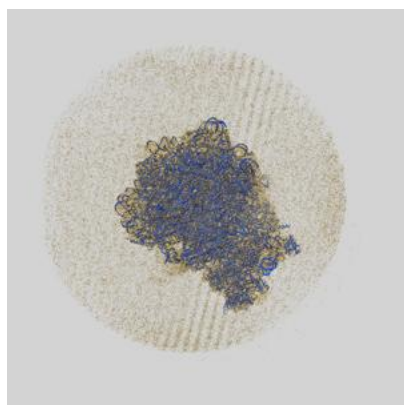
8 Fourier-Shell correlation

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

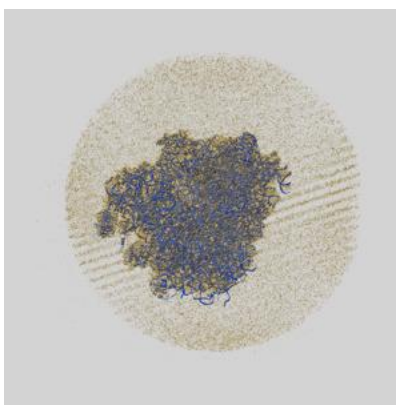
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61272 and PDB model 9J9H. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

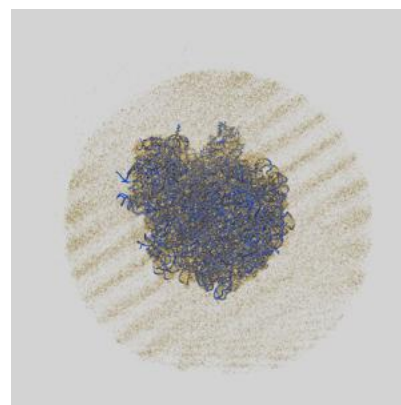
9.1 Map-model overlay [i](#)



X



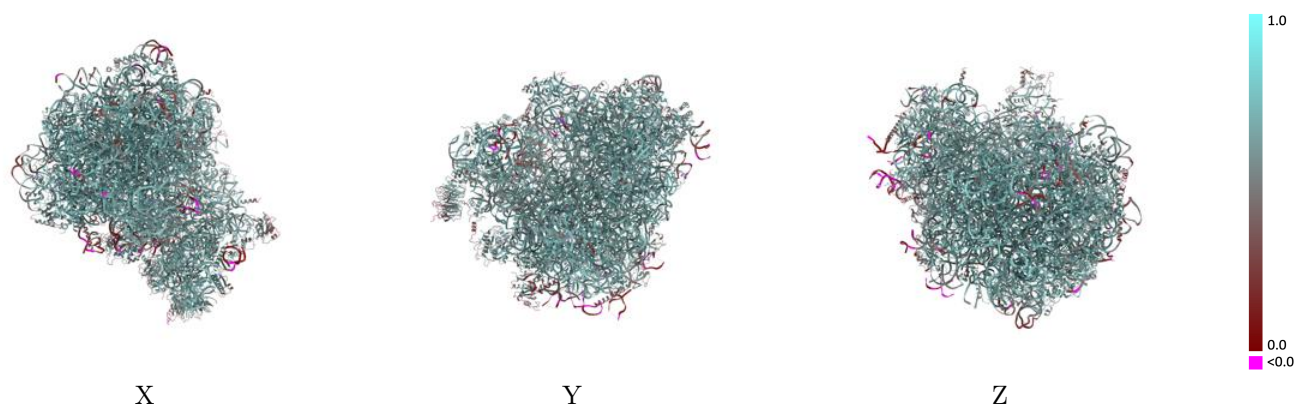
Y



Z

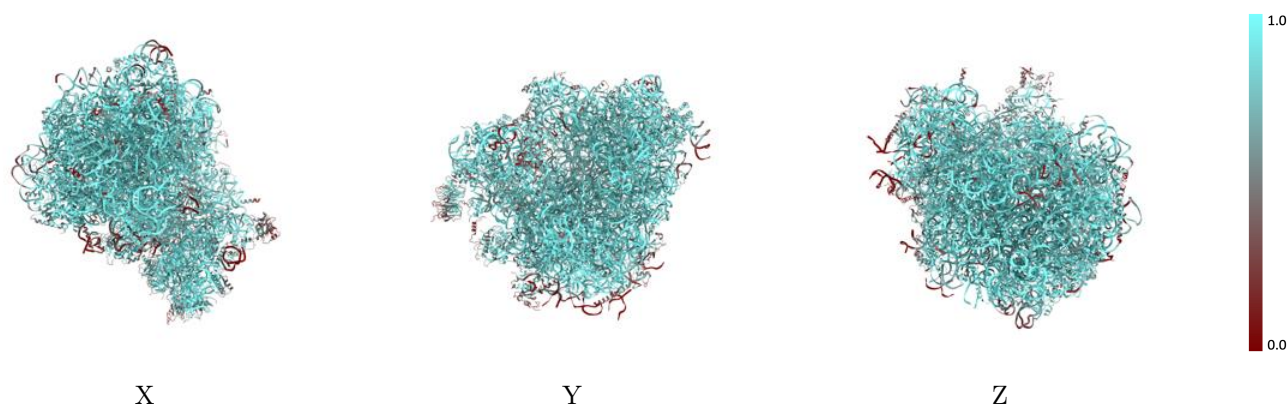
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



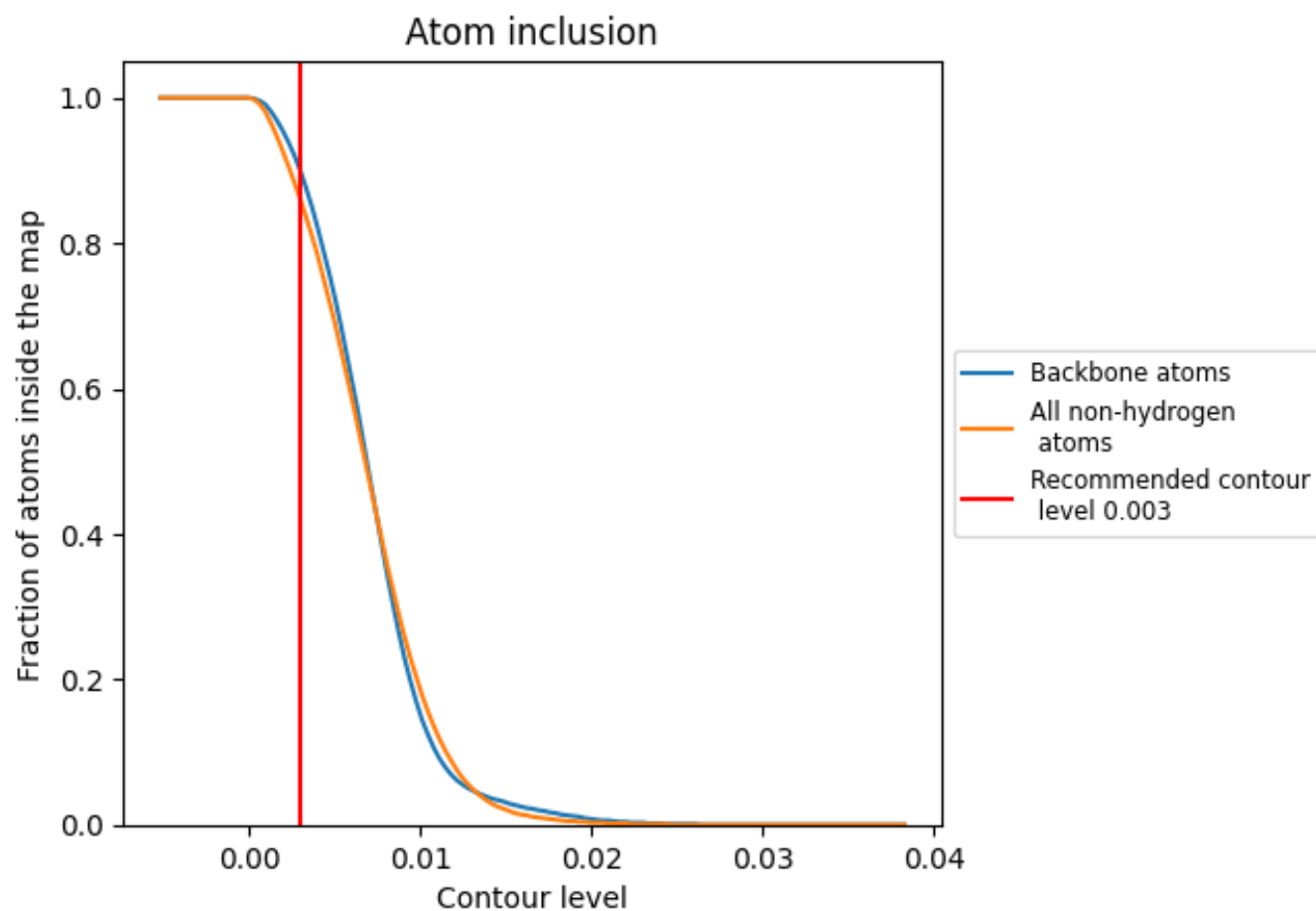
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.6200
0	 0.8830	 0.6190
1	 0.7390	 0.5490
2	 0.8070	 0.6020
3	 0.8410	 0.6140
4	 0.7210	 0.5290
5	 0.8920	 0.6450
6	 0.8270	 0.5930
7	 0.8920	 0.6430
8	 0.8990	 0.6710
9	 0.9210	 0.6690
A	 0.9120	 0.6450
AA	 0.3460	 0.3950
AB	 0.7890	 0.5690
AC	 0.9150	 0.6710
AD	 0.8560	 0.6270
AE	 0.9110	 0.6700
AF	 0.5510	 0.4900
AG	 0.7830	 0.5890
AH	 0.8450	 0.6060
AI	 0.8110	 0.6070
AJ	 0.7780	 0.5780
AK	 0.7020	 0.5310
AL	 0.8590	 0.6270
AM	 0.6960	 0.5580
AN	 0.7010	 0.5000
AO	 0.7020	 0.5290
AP	 0.5000	 0.4450
AQ	 0.3000	 0.2700
AR	 0.5130	 0.4660
B	 0.9740	 0.6680
C	 0.9500	 0.6650
D	 0.9470	 0.6870
E	 0.9130	 0.6560
F	 0.8660	 0.6390



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Chain	Atom inclusion	Q-score
G	 0.6390	 0.4850
H	 0.8890	 0.6320
I	 0.7960	 0.5700
J	 0.6730	 0.5370
K	 0.9170	 0.6730
L	 0.8900	 0.6540
M	 0.9170	 0.6640
N	 0.8430	 0.5990
O	 0.9400	 0.6880
P	 0.9690	 0.7080
Q	 0.8460	 0.6280
R	 0.7870	 0.5840
S	 0.9280	 0.6820
T	 0.7760	 0.5840
U	 0.9220	 0.6650
V	 0.8730	 0.6570
W	 0.9230	 0.6670
X	 0.5860	 0.4770
Y	 0.8360	 0.6010
Z	 0.8360	 0.5930
a	 0.8640	 0.6300
b	 0.8380	 0.6060
c	 0.9160	 0.6670
d	 0.7180	 0.5280
e	 0.8040	 0.6030
f	 0.8970	 0.6450
g	 0.9050	 0.6470
h	 0.9390	 0.6830
i	 0.9100	 0.6700
j	 0.8960	 0.6260
k	 0.7990	 0.5900
l	 0.7480	 0.5710
m	 0.6540	 0.5270
n	 0.8300	 0.6150
o	 0.8680	 0.6270
p	 0.8660	 0.6270
q	 0.5740	 0.4890
r	 0.8290	 0.5880
s	 0.5420	 0.4740
t	 0.9220	 0.6580
u	 0.8850	 0.6230
v	 0.8530	 0.6250

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Chain	Atom inclusion	Q-score
w	 0.7000	 0.5530
x	 0.8070	 0.5780
y	 0.8590	 0.6120
z	 0.8680	 0.6310