



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:59 AM UTC

PDB ID : 9GY4 / pdb_00009gy4
EMDB ID : EMD-51681
Title : 60S ribosomal subunit in complex with E3-UFM1 ligase and RQC machinery components NEMF and LTN1 (Composite map)
Authors : Penchev, I.; Gumbin, S.; Becker, T.; Kopito, R.; Beckmann, R.
Deposited on : 2024-10-01
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

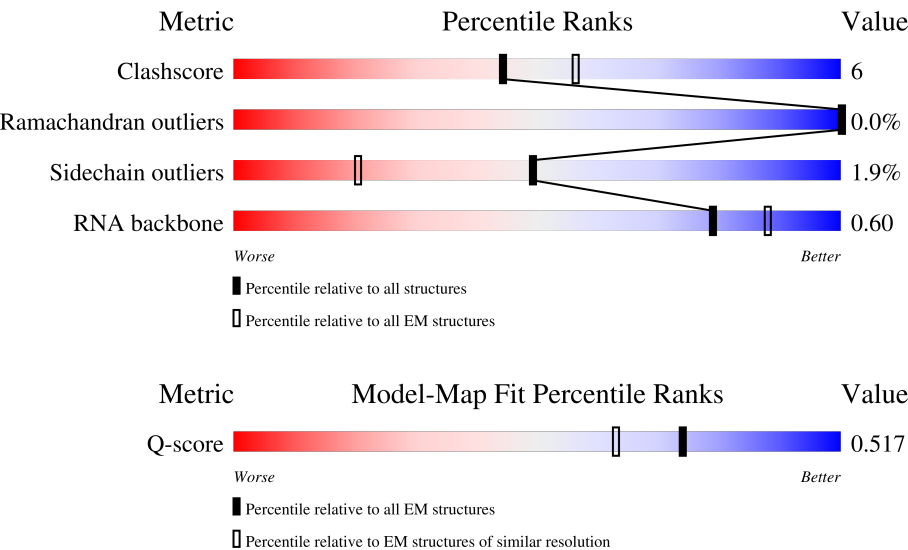
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	5	5070	42%25%30%
2	7	121	73%23%..
3	8	157	64%28%.6%

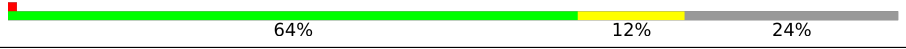
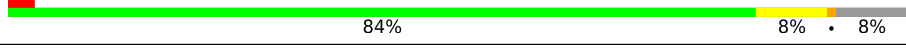
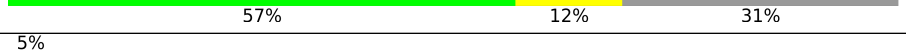
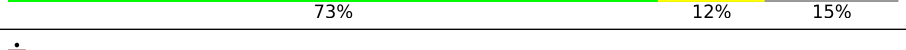
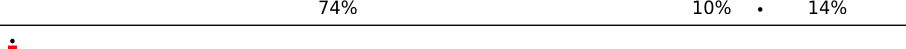
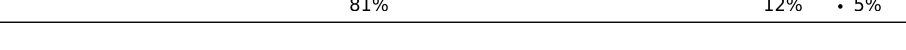
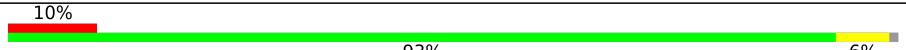
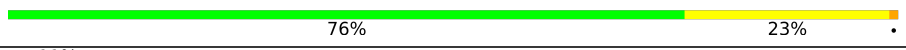
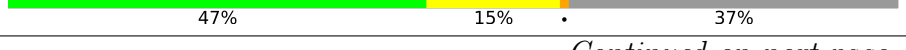
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	B	506	
5	C	314	
6	D	85	
7	E	794	
8	F	1766	
9	G	76	
10	LB	403	
11	LC	427	
12	LD	297	
13	LE	288	
14	LF	248	
15	LG	266	
16	LH	192	
17	LI	214	
18	LJ	178	
19	LL	211	
20	LM	215	
21	LN	204	
22	LO	203	
23	LP	184	
24	LQ	188	
25	LR	196	
26	LS	176	
27	LT	160	
28	LU	128	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	LV	140	
30	LW	157	
31	LX	156	
32	LY	145	
33	LZ	136	
34	La	148	
35	Lb	159	
36	Lc	115	
37	Ld	125	
38	Le	135	
39	Lf	110	
40	Lg	117	
41	Lh	123	
42	Li	105	
43	Lj	97	
44	Lk	70	
45	Ll	51	
46	Lm	128	
47	Lo	106	
48	Lp	92	
49	Lr	137	
50	Lz	217	
51	Z	1076	
52	a	257	
53	s	317	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	t	165	 14% 70% 16% 13%
55	A	7	 14% 100%

2 Entry composition [i](#)

There are 57 unique types of molecules in this entry. The entry contains 169625 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3528	Total	C	N	O	P	0	0
			75663	33699	13869	24568	3527		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	2113	C	G	conflict	GB 86475748
5	4906	U	C	conflict	GB 86475748
5	4910	A	G	conflict	GB 86475748

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	148	Total	C	N	O	P	0	0
			3152	1407	563	1035	147		

- Molecule 4 is a protein called CDK5 regulatory subunit-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	403	Total	C	N	O	S	0	0
			3234	2049	545	624	16		

- Molecule 5 is a protein called DDRGK domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	188	Total	C	N	O	S	0	0
			1547	954	279	313	1		

- Molecule 6 is a protein called Ubiquitin-fold modifier 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	78	Total	C	N	O	S	0	0
			588	382	96	109	1		

- Molecule 7 is a protein called E3 UFM1-protein ligase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	660	Total	C	N	O	S	0	0
			5251	3323	901	1009	18		

- Molecule 8 is a protein called E3 ubiquitin-protein ligase listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	1679	Total	C	N	O	S	0	0
			13415	8627	2194	2514	80		

- Molecule 9 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	76	Total	C	N	O	P	0	0
			1622	721	285	540	76		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	73	G	A	conflict	GB 2736373571
G	74	C	A	conflict	GB 2736373571
G	75	C	U	conflict	GB 2736373571
G	76	A	C	conflict	GB 2736373571

- Molecule 10 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LB	402	Total	C	N	O	S	0	0
			3239	2060	608	557	14		

- Molecule 11 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 12 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 13 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	220	Total	C	N	O	S	0	0
			1765	1136	334	291	4		

- Molecule 14 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 15 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 16 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 17 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	213	Total	C	N	O	S	0	0
			1710	1083	329	284	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	87	ILE	MET	conflict	UNP Q96L21

- Molecule 18 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	175	Total	C	N	O	S	0	0
			1401	882	261	252	6		

- Molecule 19 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LL	194	Total	C	N	O	S	0	0
			1573	987	327	255	4		

- Molecule 20 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LM	136	Total	C	N	O	S	0	0
			1120	719	215	179	7		

- Molecule 21 is a protein called 60S ribosomal protein L15.

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

- Molecule 22 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 23 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 24 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 25 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LR	155	Total	C	N	O	S	0	0
			1294	808	278	199	9		

- Molecule 26 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 27 is a protein called 60S ribosomal protein L21.

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

- Molecule 28 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 29 is a protein called 60S ribosomal protein L23.

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

- Molecule 30 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 31 is a protein called 60S ribosomal protein L23a.

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

- Molecule 32 is a protein called 60S ribosomal protein L26.

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

- Molecule 33 is a protein called 60S ribosomal protein L27.

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

- Molecule 34 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 36 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 37 is a protein called 60S ribosomal protein L31.

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

- Molecule 38 is a protein called 60S ribosomal protein L32.

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

- Molecule 39 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 40 is a protein called 60S ribosomal protein L34.

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

- Molecule 41 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 42 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 43 is a protein called 60S ribosomal protein L37.

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

- Molecule 44 is a protein called 60S ribosomal protein L38.

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

- Molecule 45 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 46 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 47 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lo	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 48 is a protein called 60S ribosomal protein L37a.

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

- Molecule 49 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 50 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lz	217	Total	C	N	O	S	0	0
			1744	1114	314	307	9		

- Molecule 51 is a protein called Ribosome quality control complex subunit NEMF.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Z	731	Total	C	N	O	S	0	0
			5891	3768	1012	1090	21		

- Molecule 52 is a protein called 60S ribosomal protein L8.

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

- Molecule 53 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	201	Total	C	N	O	S	0	0
			1545	983	268	285	9		

- Molecule 54 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	t	143	Total	C	N	O	S	0	0
			1068	665	197	202	4		

- Molecule 55 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	A	7	Total	C	N	O	0	0
			35	21	7	7		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	5	205	Total	Mg	0
			205	205	
56	7	2	Total	Mg	0
			2	2	
56	8	5	Total	Mg	0
			5	5	
56	LI	1	Total	Mg	0
			1	1	
56	LP	1	Total	Mg	0
			1	1	
56	LV	1	Total	Mg	0
			1	1	
56	Le	1	Total	Mg	0
			1	1	
56	Lf	1	Total	Mg	0
			1	1	
56	Lg	1	Total	Mg	0
			1	1	
56	Lj	1	Total	Mg	0
			1	1	

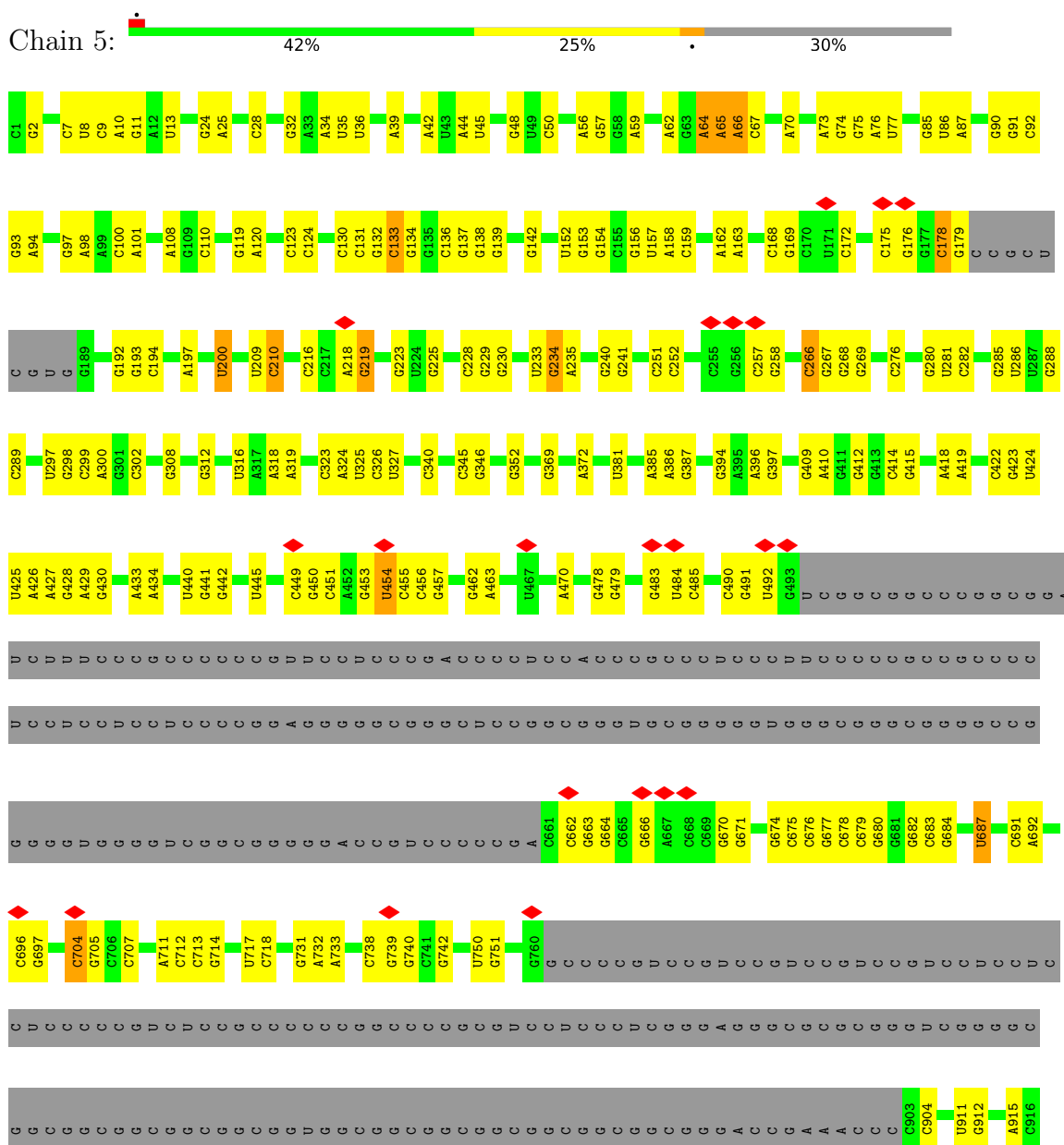
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	Lg	1	Total 1	Zn 1	0
57	Lj	1	Total 1	Zn 1	0
57	Lm	1	Total 1	Zn 1	0
57	Lo	1	Total 1	Zn 1	0
57	Lp	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.

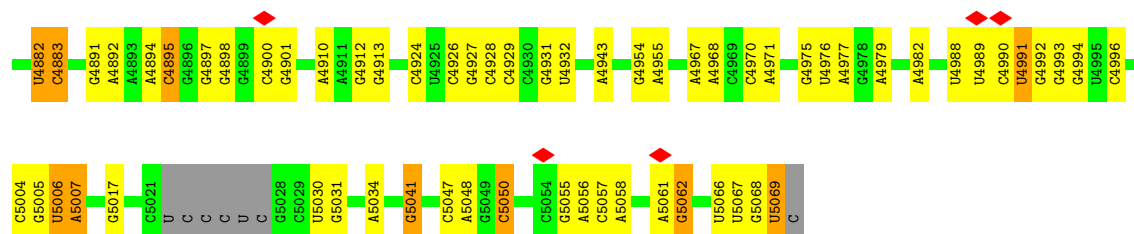
• Molecule 1: 28S rRNA





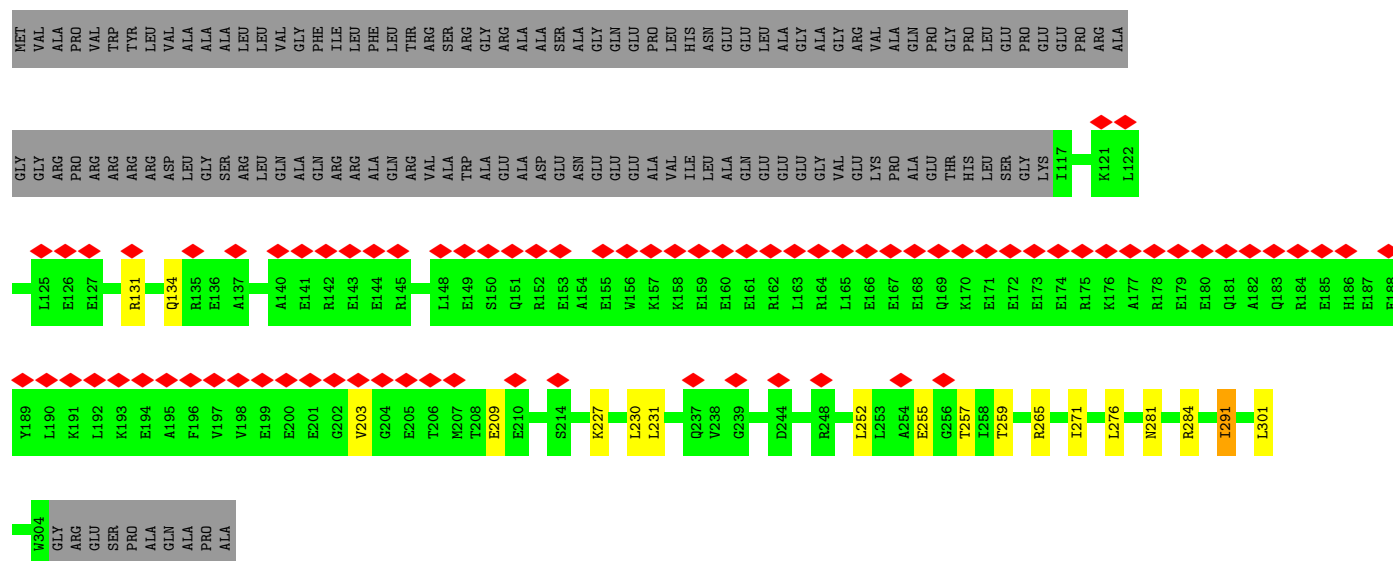


G4745	C4654	G4549	G4448	U4351	A4253	A4156	G4085	C3924	G3823	A3726	A3646
G4748	A4655	G4550	A4449	U4352	G4254	A4157	G4076	G3933	A3824	A3727	A3647
C4749	A4656	C4560	G4454	U4353	A4255	C4162	G4080	G3934	G3838	A3728	A3648
G4750	C4670	U4563	U4457	G4354	C4258	U4163	C4081	G3935	U3839	A3732	A3652
G4751	C4671	C4564	U4458	G4355	C4259	C4164	G4090	G3939	U3840	A3733	A3653
G4754	U4673	U4565	U4459	G4356	U4260	C4165	G4091	G3949	U3843	U3794	G3654
C4755	U4674	U4566	U4460	G4357	C4261	C4166	G4092	A3949	C3843	G3785	G3659
U4756	U4675	G4567	C4461	U4358	C4262	A4170	G4093	U3950	U3848	A3746	G3660
C4757	A4568	U4464	U4465	G4364	U4265	C4171	G4094	G3951	U3849	A3747	G3661
U4758	U4569	U4466	C4466	G4370	G4266	U4174	G4095	A3954	U3855	G3763	A3662
C4759	G4679	C4467	C4467	U4371	G4267	C4177	G4096	G3955	A3856	G3764	G3663
G4760	A4571	C4468	C4468	G4372	G4268	A4178	G4097	G3956	G3867	U3768	G3664
C4761	U4572	U4469	U4469	G4373	A4269	C4179	G4098	U3957	G3868	A	G3665
G4765	G4575	G4472	G4472	C4374	G4270	A4180	G4099	G3958	C3869	A	C3668
C4766	C4576	A4473	A4473	G4375	A4271	C4181	C4096	U3959	G3870	C	G3672
G4768	G4578	A4474	A4474	A4376	G4272	U4182	C4097	A3960	C3871	U	C3673
C4769	U4579	C4475	C4475	A4377	G4273	G4183	A4098	G3961	A3872	A	G3681
U4770	U4580	C4476	C4476	A4378	G4274	U4184	G	A3962	G3873	G	G3684
C4771	C4581	C4477	C4477	A4379	G4275	G4185	C	A3963	G3874	A3766	G3685
G4774	A4584	U4488	U4488	A4380	A4281	A4186	C	U3964	A3877	C3769	G3686
C	G4585	U4489	U4489	A4381	A4282	U4187	C	A3965	G3878	U3770	G3687
C	G4586	C4488	C4488	A4382	G4283	U4188	C	A3966	U3771	U3772	U3688
C	G4587	A4489	A4489	A4383	G4284	U4189	C	U3967	U3773	A3774	G3689
C	A4590	U4490	U4490	A4384	G4285	U4190	C	G3968	A3775	A3775	U3690
C	U4591	C4489	C4489	A4385	G4286	C4191	C	A3972	G3776	A3691	A3692
C	U4592	A4490	A4490	A4386	G4287	A4192	C	G3973	G3777	A3692	A3693
C	C4593	U4491	U4491	A4387	G4288	A4193	C	G3974	U3778	C3696	C3697
C	U4594	A4492	A4492	A4388	G4289	A4194	C	C3975	A3784	U3697	U3698
C	C4595	U4493	U4493	A4389	A4300	A4203	C	C3976	A3785	C3699	C3700
C	U4601	A4494	A4494	A4390	A4301	A4204	C	C	U3786	C3701	A3702
C	G4604	U4495	U4495	A4391	A4302	A4211	C	C	G3703	G3703	U3704
C	A4607	C4496	C4496	A4392	A4303	A4212	C	C	A3799	U3705	G3706
C	G4617	U4497	U4497	A4393	A4304	A4213	C	C	U3805	U3707	U3707
C	U4620	A4498	A4498	A4394	A4305	A4214	C	C	G3806	G3708	G3709
C	G4627	U4499	U4499	A4395	A4306	A4215	C	C	G3809	G3710	A3711
C	G4630	C4499	C4499	U4499	A4307	A4216	C	C	G3810	A3712	U3713
C	U4631	U4500	U4500	U4500	A4308	A4217	C	C	G3811	U3714	G3714
C	U4632	A4501	A4501	A4501	A4309	A4218	C	C	A3812	A3717	A3717
C	A4635	U4502	U4502	A4502	A4310	A4219	C	C	G3813	A3816	A3816
C	U4636	C4503	C4503	A4503	A4311	A4220	C	C	A3814	A3817	A3817
C	G4637	U4504	U4504	A4504	A4312	A4221	C	C	G3815	A3818	U3818
C	U4638	C4505	C4505	A4505	A4313	A4222	C	C	A3816	A3819	G3819
C	U4642	U4506	U4506	A4506	A4314	A4223	C	C	A3817	A3820	A3820
C	C4643	G4507	G4507	A4507	A4315	A4224	C	C	A3818	A3821	A3821
C	A4651	U4508	U4508	A4508	A4316	A4225	C	C	A3819	A3822	A3822
C	G4652	C4509	C4509	A4509	A4317	A4226	C	C	A3820	A3823	A3823
C	U4653	U4510	U4510	A4510	A4318	A4227	C	C	A3821	A3824	A3824
C	G4654	A4511	A4511	A4511	A4319	A4228	C	C	A3822	A3825	A3825
C	A4657	U4512	U4512	A4512	A4320	A4229	C	C	A3823	A3826	A3826
C	C4658	A4513	A4513	A4513	A4321	U4230	C	C	A3824	A3827	A3827
C	G4659	A4514	A4514	A4514	A4322	A4231	C	C	A3825	A3828	A3828
C	U4660	U4515	U4515	A4515	A4323	A4232	C	C	A3826	A3829	A3829
C	A4661	C4516	C4516	A4516	A4324	A4233	C	C	A3827	A3830	A3830
C	G4662	U4517	U4517	A4517	A4325	A4234	C	C	A3828	A3831	A3831
C	U4663	A4518	A4518	A4518	A4326	A4235	C	C	A3829	A3832	A3832
C	C4664	U4519	U4519	A4519	A4327	A4236	C	C	A3830	A3833	A3833
C	G4665	A4520	A4520	A4520	A4328	A4237	C	C	A3831	A3834	A3834
C	A4666	C4521	C4521	A4521	A4329	A4238	C	C	A3832	A3835	A3835
C	U4667	U4522	U4522	A4522	A4330	A4239	C	C	A3833	A3836	A3836
C	G4668	A4523	A4523	A4523	A4331	A4240	C	C	A3834	A3837	A3837
C	C4669	U4524	U4524	A4524	A4332	A4241	C	C	A3835	A3838	A3838
C	U4670	C4525	C4525	A4525	A4333	A4242	C	C	A3836	A3839	A3839
C	G4671	U4526	U4526	A4526	A4334	A4243	C	C	A3837	A3840	A3840
C	A4672	G4527	G4527	A4527	A4335	A4244	C	C	A3838	A3841	A3841
C	U4673	U4528	U4528	A4528	A4336	A4245	C	C	A3839	A3842	A3842
C	C4674	A4529	A4529	A4529	A4337	A4246	C	C	A3840	A3843	A3843
C	G4675	C4530	C4530	A4530	A4338	A4247	C	C	A3841	A3844	A3844
C	U4676	U4632	U4632	A4531	A4339	A4248	C	C	A3842	A3845	A3845
C	A4677	A4635	A4635	A4532	A4340	A4249	C	C	A3843	A3846	A3846
C	G4678	U4636	U4636	A4533	A4341	A4250	C	C	A3844	A3847	A3847
C	C4679	G4637	G4637	A4534	A4342	A4251	C	C	A3845	A3848	A3848
C	U4680	U4638	U4638	A4535	A4343	A4252	C	C	A3846	A3849	A3849
C	A4681	A4642	A4642	A4536	A4344	A4253	C	C	A3847	A3850	A3850
C	G4682	C4643	C4643	A4537	A4345	A4254	C	C	A3848	A3851	A3851
C	C4683	A4643	A4643	A4538	A4346	A4255	C	C	A3849	A3852	A3852
C	U4684	G4644	G4644	A4539	A4347	A4256	C	C	A3850	A3853	A3853
C	G4685	U4645	U4645	A4540	A4348	A4257	C	C	A3851	A3854	A3854
C	A4686	C4645	C4645	A4541	A4349	A4258	C	C	A3852	A3855	A3855
C	U4687	A4646	A4646	A4542	A4350	A4259	C	C	A3853	A3856	A3856
C	G4688	G4647	G4647	A4543	A4351	A4260	C	C	A3854	A3857	A3857
C	C4689	C4648	C4648	A4544	A4352	A4261	C	C	A3855	A3858	A3858
C	A4690	A4649	A4649	A4545	A4353	A4262	C	C	A3856	A3859	A3859
C	U4691	G4650	G4650	A4546	A4354	A4263	C	C	A3857	A3860	A3860
C	A4692	A4651	A4651	A4547	A4355	A4264	C	C	A3858	A3861	A3861
C	G4693	C4652	C4652	A4548	A4356	A4265	C	C	A3859	A3862	A3862
C	U4694	U4653	U4653	A4549	A4357	A4266	C	C	A3860	A3863	A3863
C	C4695	A4654	A4654	A4550	A4358	A4267	C	C	A3861	A3864	A3864
C	G4696	G4655	G4655	A4551	A4359	A4268	C	C	A3862	A3865	A3865
C	U4697	C4656	C4656	A4552	A4360	A4269	C	C	A3863	A3866	A3866
C	A4698	U4657	U4657	A4553	A4361	A4270	C	C	A3864	A3867	A3867
C	G4699	A4658	A4658	A4554	A4362	A4271	C	C	A3865	A3868	A3868
C	U4700	G4659	G4659	A4555	A4363	A4272	C	C	A3866	A3869	A3869
C	C4701	C4660	C4660	A4556	A4364	A4273	C	C	A3867	A3870	A3870
C	A4702	A4661	A4661	A4557	A4365	A4274	C	C	A3868	A3871	A3871
C	G4703	U4662	U4662	A4558	A4366	A4275	C	C	A3869	A3872	A3872
C	U4704	C4663	C4663	A4559	A4367	A4276	C	C	A3870	A3873	A3873
C	A4705	A4664	A4664	A4560	A4368	A4277	C	C	A3871	A3874	A3874
C	G4706	G4665	G4665	A4561	A4369	A4278	C	C	A3872	A3875	A3875
C	C4707	U4666	U4666	A4562	A4370	A4279	C	C	A3873	A3876	A3876
C	A4708	C4667	C4667	A4563	A4371	A4280	C	C	A3874	A3877	A3877
C	U4709	A4668	A4668	A4564	A4372	A4281	C	C	A3875	A3878	A3878
C	G4710	G4669	G4669	A4565	A4373	A4282	C	C	A3876	A3879	A3879
C	C4711	U4670	U4670	A4566	A4374	A4283	C	C	A3877	A3880	A3880
C	U4712	C4671	C4671	A4567	A4375	A4284	C	C	A3878	A3881	A3881
C	G4713	A4672	A4672	A4568	A4376	A4285	C	C	A3879	A3882	A3882
C	C4714	U4673	U4673	A4569	A4377	A4286	C	C	A3880	A3883	A3883
C	A4715	C4674	C4674	A4570	A4378	A4287	C	C	A3881	A3884	A3884
C	U4716	A4675	A4675	A4571	A4379	A4288	C	C	A3882	A3885	A3885
C	G4717	G4676	G4676	A4572	A4380	A4289	C	C	A3883	A3886	A3886
C	C4718	U4677	U4677	A4573	A4381	A4290	C	C	A3884	A3887	A3887
C	U4719	A4678	A4678	A4574	A4382	A4291	C	C	A3885	A3888	A3888
C	G4720	C4679	C4679	A4575	A4383	A4292	C	C	A3886	A3889	A3889
C	A4721	U4680	U4680	A4576	A4384	A4293	C	C	A3887	A3890	A3890
C	C4722	A4681	A4681	A4577	A4385	A4294	C	C	A3888	A3891	A3891
C	U4723	G4682	G4682	A4578	A4386	A4295	C	C	A3889	A3892	A3892
C	A4724	C4683	C4683	A4579	A4387	A4296	C	C	A3890	A3893	A3893
C	C4725	U4684	U4684	A4580	A4388	A4297	C	C	A3891	A3894	A3894
C	G4726	A4685	A4685	A4581	A4389	A4298	C	C	A3892	A3895	A3895
C	U4727	G4686	G4686								

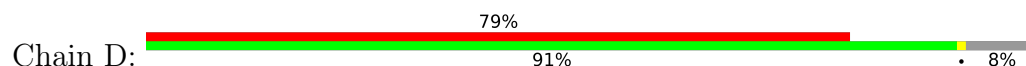


• Molecule 2: 5S rRNA

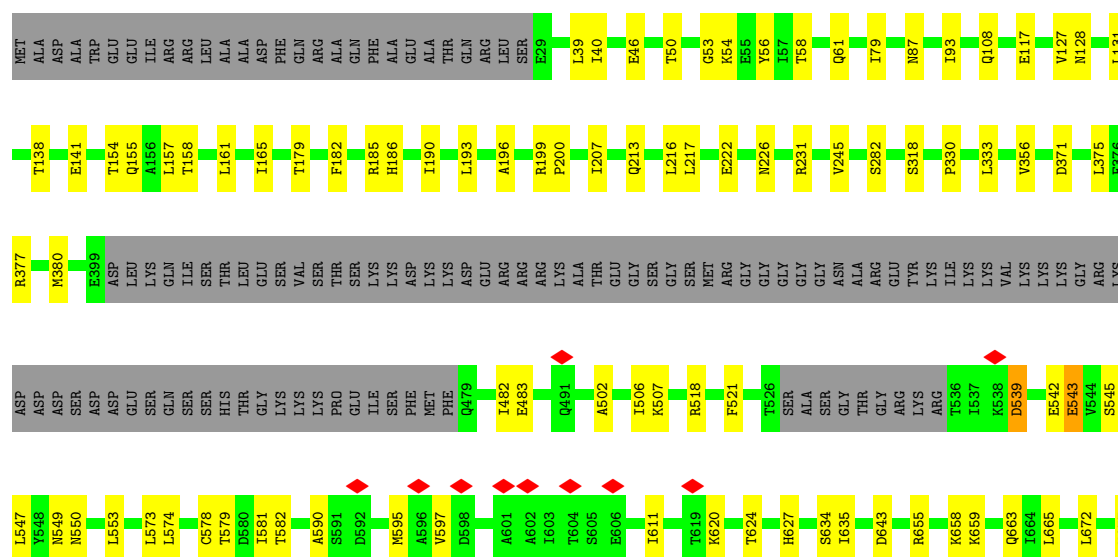


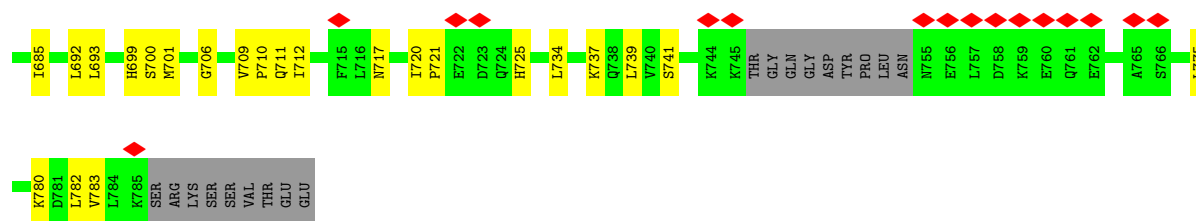


- Molecule 6: Ubiquitin-fold modifier 1



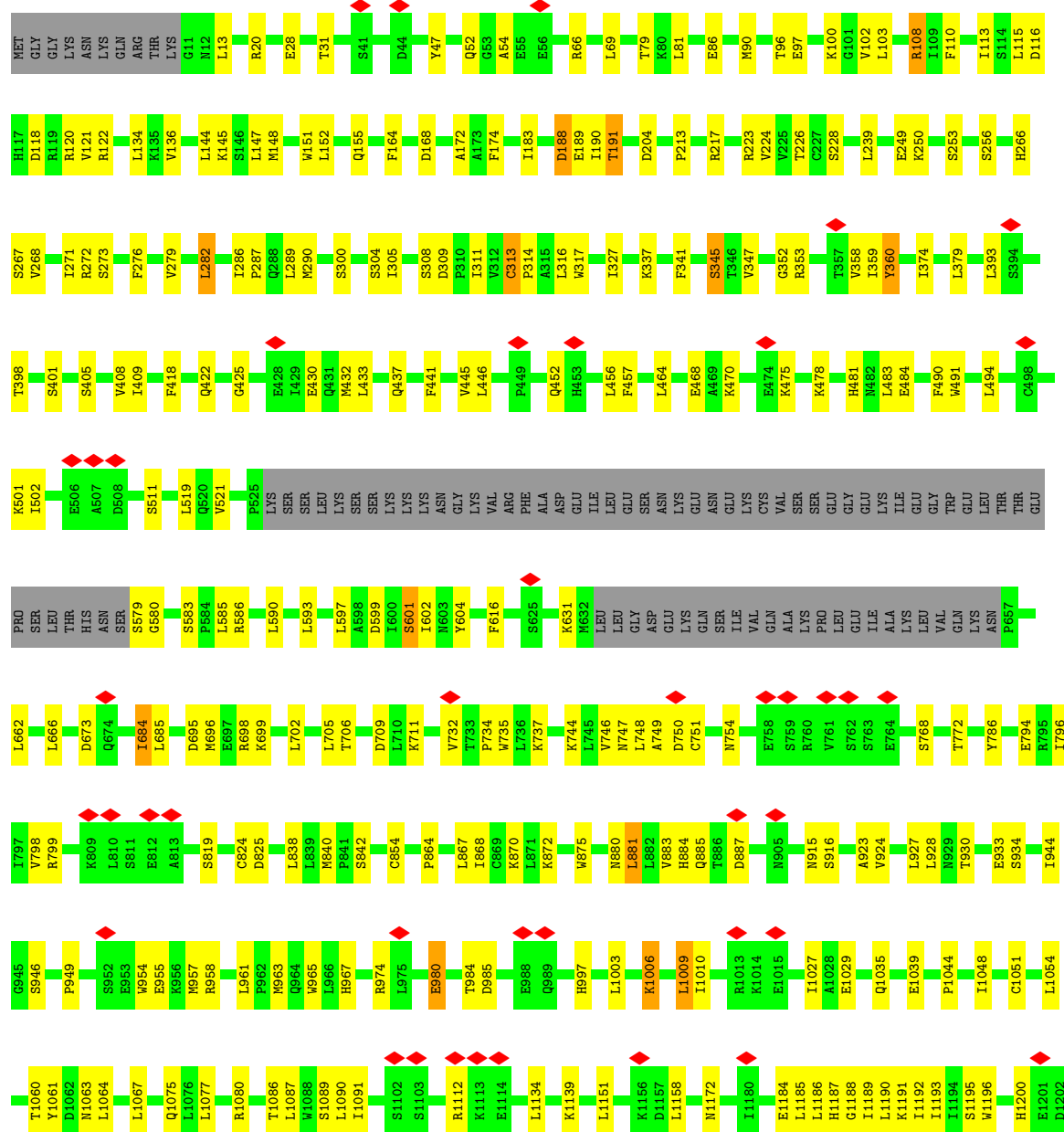
- Molecule 7: E3 UFM1-protein ligase 1

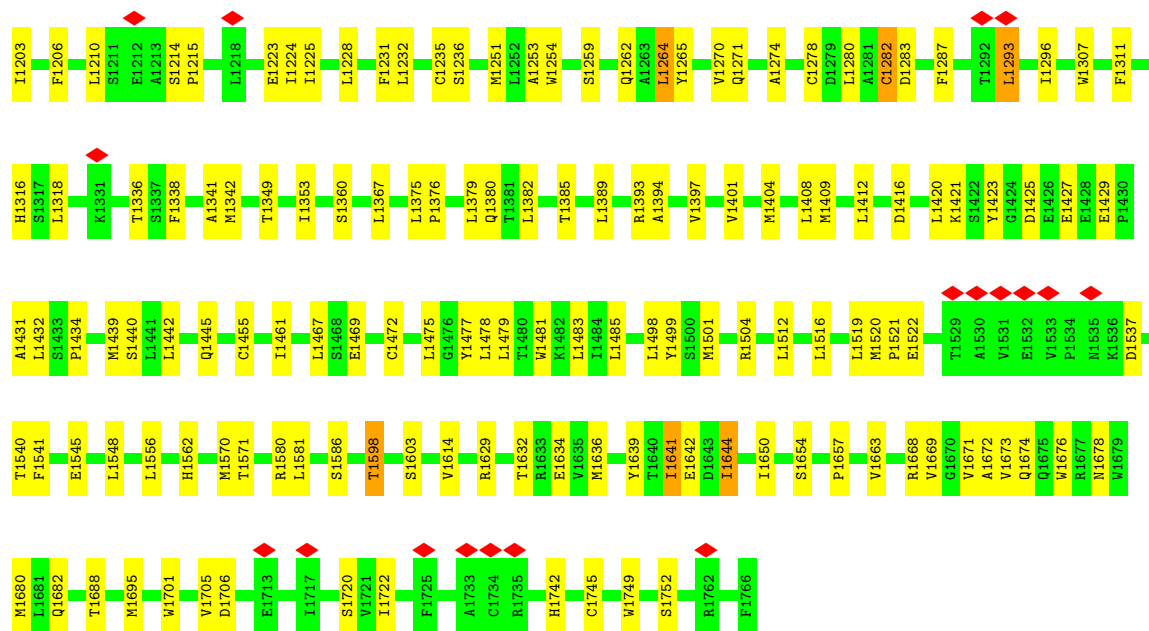




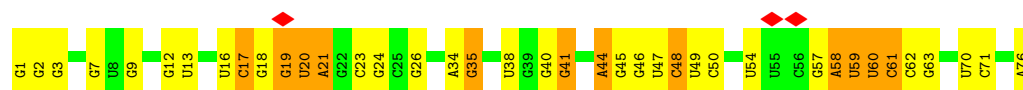
• Molecule 8: E3 ubiquitin-protein ligase listerin

Chain F: 72% 22% 5%

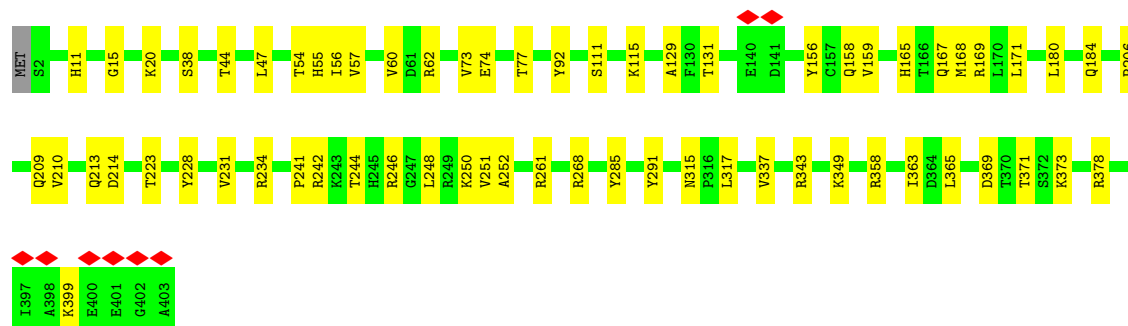
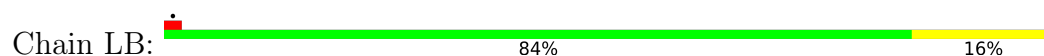




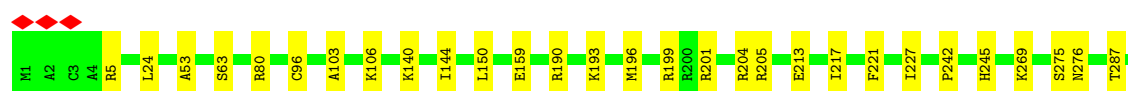
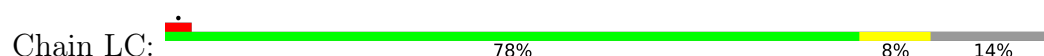
• Molecule 9: tRNA

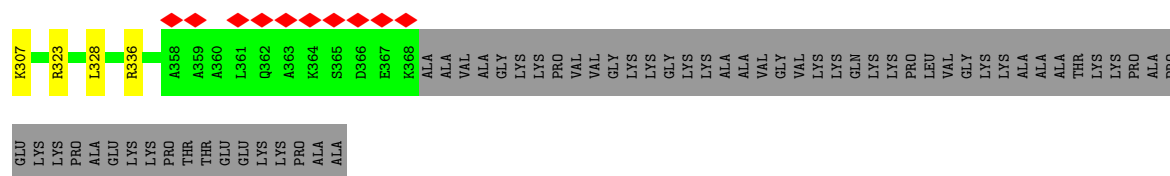


• Molecule 10: 60S ribosomal protein L3

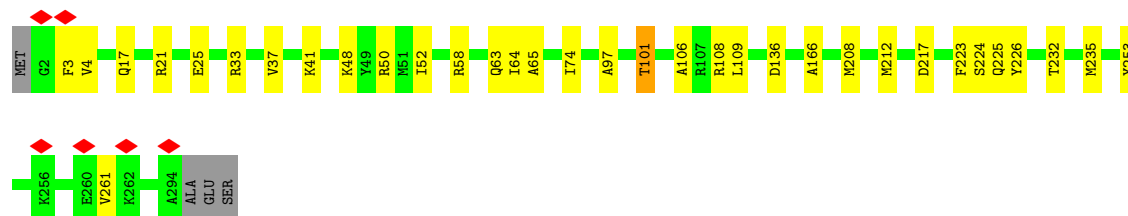


• Molecule 11: 60S ribosomal protein L4

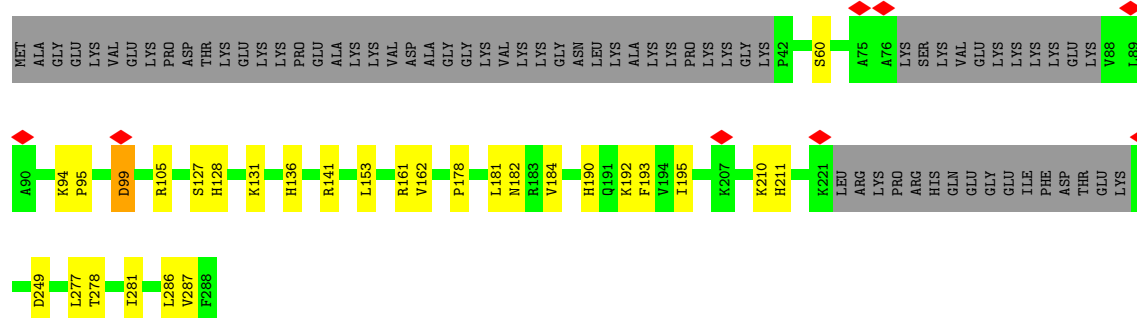




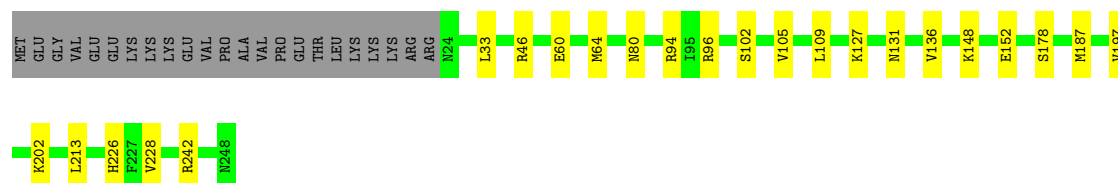
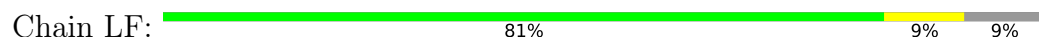
- Molecule 12: 60S ribosomal protein L5



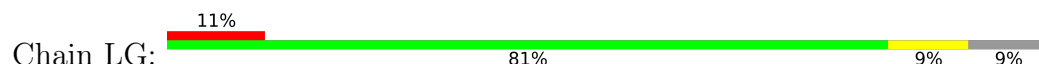
- Molecule 13: Large ribosomal subunit protein eL6



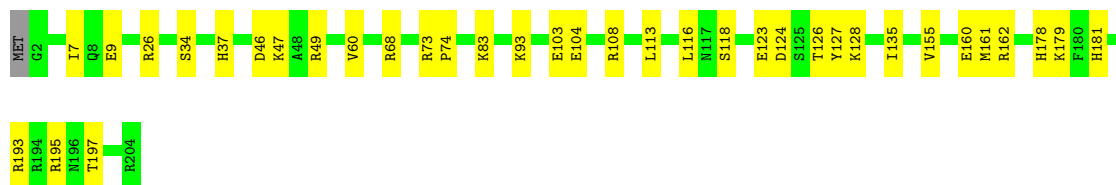
- Molecule 14: Large ribosomal subunit protein uL30



- Molecule 15: 60S ribosomal protein L7a



Chain LN:  82% 18%



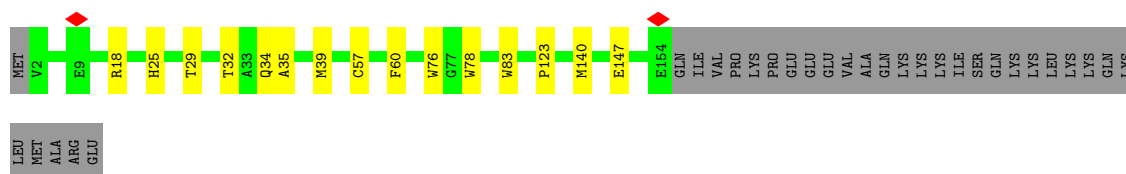
- Molecule 22: 60S ribosomal protein L13a

Chain LO:  90% 9%



- Molecule 23: 60S ribosomal protein L17

Chain LP:  75% 8% 17%



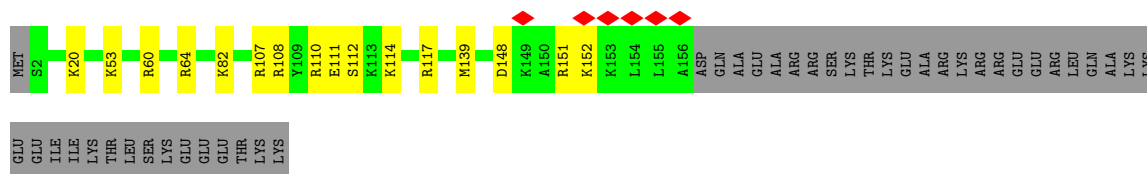
- Molecule 24: 60S ribosomal protein L18

Chain LQ:  86% 13%



- Molecule 25: 60S ribosomal protein L19

Chain LR:  71% 8% 21%



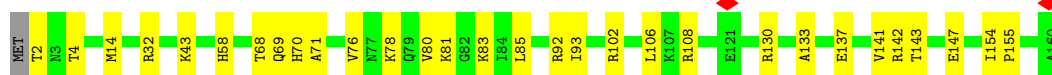
- Molecule 26: 60S ribosomal protein L18a

Chain LS:  86% 14%



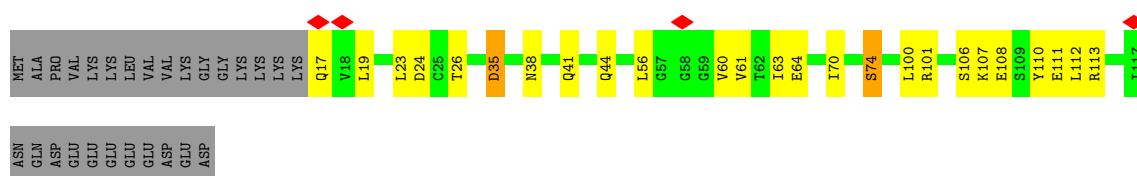
- Molecule 27: 60S ribosomal protein L21

Chain LT:  81% 19% .



- Molecule 28: 60S ribosomal protein L22

Chain LU:  59% 18% . 21%



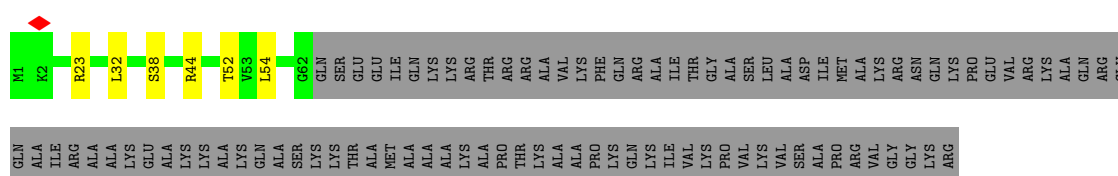
- Molecule 29: 60S ribosomal protein L23

Chain LV:  82% 11% 6%



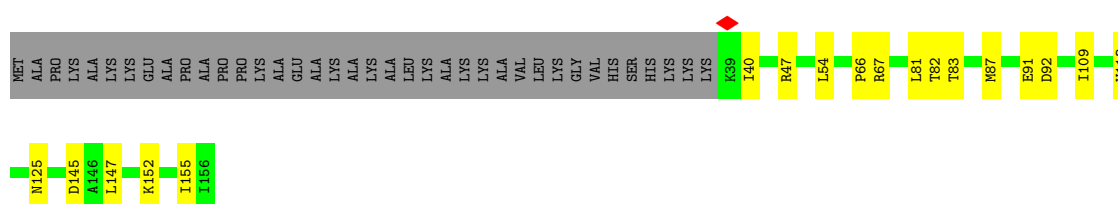
- Molecule 30: 60S ribosomal protein L24

Chain LW:  36% . 61%



- Molecule 31: 60S ribosomal protein L23a

Chain LX:  64% 12% 24%

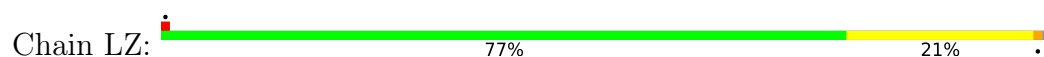


- Molecule 32: 60S ribosomal protein L26

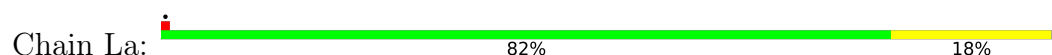
Chain LY:  84% 8% . 8%



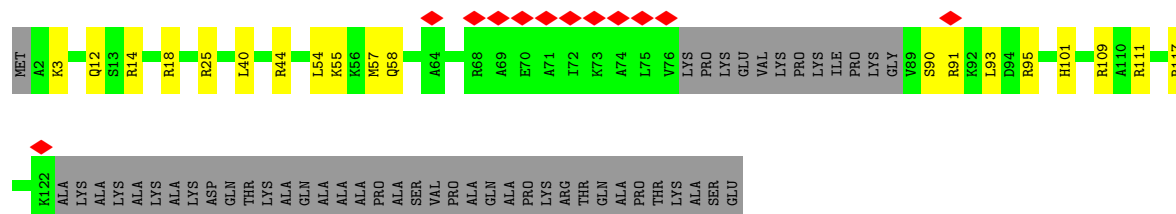
- Molecule 33: 60S ribosomal protein L27



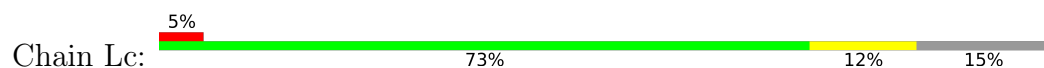
- Molecule 34: 60S ribosomal protein L27a



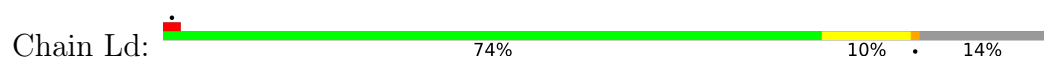
- Molecule 35: 60S ribosomal protein L29



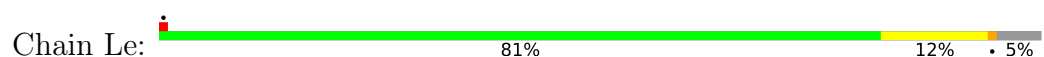
- Molecule 36: 60S ribosomal protein L30

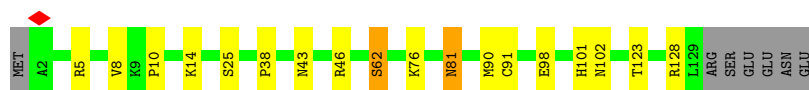


- Molecule 37: 60S ribosomal protein L31



- Molecule 38: 60S ribosomal protein L32





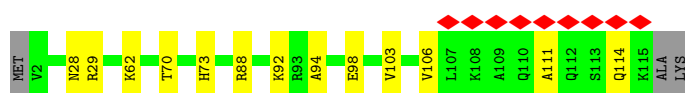
- Molecule 39: 60S ribosomal protein L35a

Chain Lf: 85% 14% ..



- Molecule 40: 60S ribosomal protein L34

Chain Lg: 8% 86% 11% .



- Molecule 41: 60S ribosomal protein L35

Chain Lh: 91% 8% .



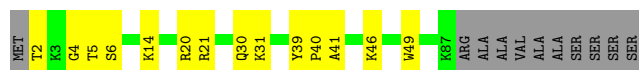
- Molecule 42: 60S ribosomal protein L36

Chain Li: 86% 10% ..



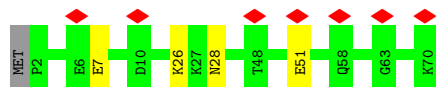
- Molecule 43: 60S ribosomal protein L37

Chain Lj: 74% 14% 11%



- Molecule 44: 60S ribosomal protein L38

Chain Lk: 10% 93% 6% .



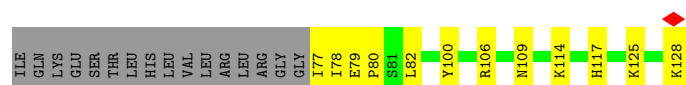
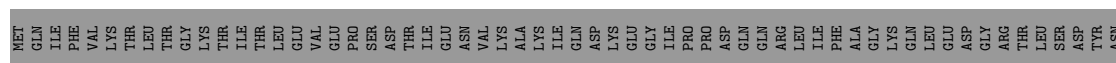
- Molecule 45: 60S ribosomal protein L39

Chain Ll:  82% 16%



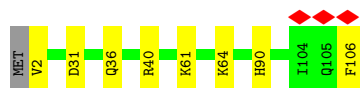
- Molecule 46: Ubiquitin-60S ribosomal protein L40

Chain Lm:  31% 9% 59%



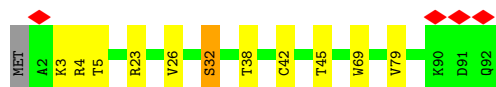
- Molecule 47: 60S ribosomal protein L36a

Chain Lo:  92% 8%



- Molecule 48: 60S ribosomal protein L37a

Chain Lp:  87% 11%



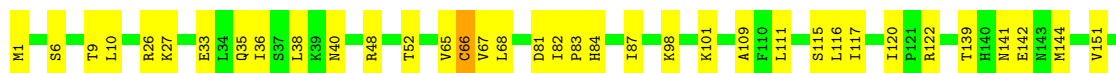
- Molecule 49: 60S ribosomal protein L28

Chain Lr:  81% 10% 9%



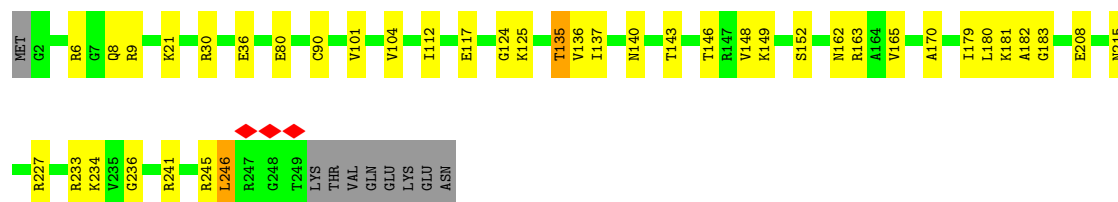
- Molecule 50: 60S ribosomal protein L10a

Chain Lz:  76% 23%

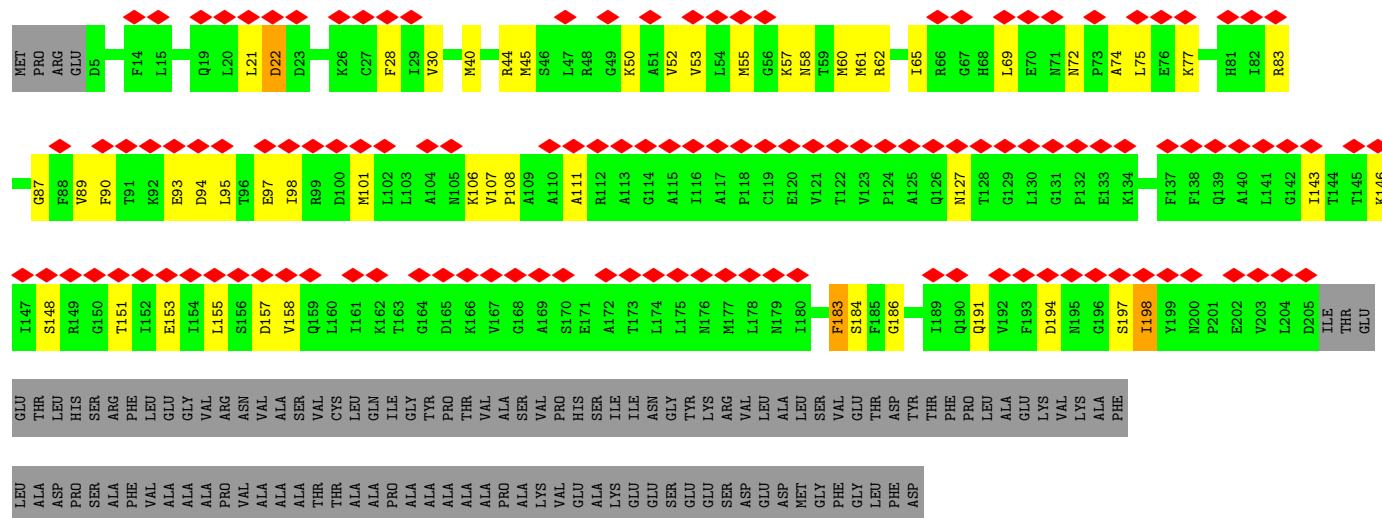
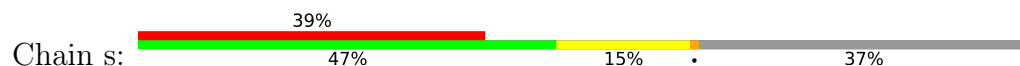


- Molecule 51: Ribosome quality control complex subunit NEMF

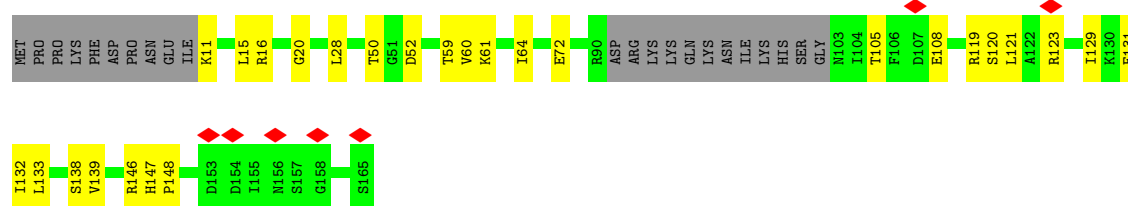
Chain a: 81% 15% ..



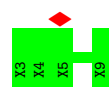
• Molecule 53: 60S acidic ribosomal protein P0



• Molecule 54: Large ribosomal subunit protein uL11



• Molecule 55: Nascent chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8461	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	16.014	Depositor
Minimum map value	-13.967	Depositor
Average map value	0.033	Depositor
Map value standard deviation	1.069	Depositor
Recommended contour level	2.7	Depositor
Map size (Å)	436.2, 436.2, 436.2	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	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	5	0.08	0/84644	0.21	0/132019
2	7	0.08	0/2861	0.19	0/4459
3	8	0.08	0/3520	0.21	0/5481
4	B	0.19	0/3280	0.42	1/4426 (0.0%)
5	C	0.11	0/1560	0.38	0/2085
6	D	0.11	0/601	0.33	0/818
7	E	0.13	0/5322	0.38	0/7181
8	F	0.16	0/13702	0.39	1/18567 (0.0%)
9	G	0.08	0/1810	0.21	0/2821
10	LB	0.11	0/3307	0.37	0/4424
11	LC	0.12	0/2981	0.42	0/4002
12	LD	0.11	0/2428	0.38	0/3252
13	LE	0.13	0/1799	0.41	0/2414
14	LF	0.11	0/1905	0.40	0/2539
15	LG	0.12	0/1960	0.41	0/2637
16	LH	0.11	0/1537	0.37	0/2066
17	LI	0.12	0/1750	0.41	0/2340
18	LJ	0.11	0/1424	0.41	0/1904
19	LL	0.14	0/1604	0.49	0/2149
20	LM	0.10	0/1142	0.37	0/1527
21	LN	0.13	0/1746	0.46	0/2338
22	LO	0.12	0/1682	0.41	0/2250
23	LP	0.11	0/1268	0.40	0/1701
24	LQ	0.14	0/1537	0.48	0/2052
25	LR	0.13	0/1310	0.48	0/1734
26	LS	0.14	0/1493	0.44	0/2003
27	LT	0.14	0/1326	0.44	0/1770
28	LU	0.16	0/839	0.47	0/1126
29	LV	0.11	0/993	0.39	0/1332
30	LW	0.11	0/532	0.40	0/708
31	LX	0.12	0/984	0.42	0/1323
32	LY	0.13	0/1132	0.45	0/1504

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LZ	0.13	0/1130	0.41	0/1507
34	La	0.12	0/1191	0.42	0/1591
35	Lb	0.12	0/889	0.44	0/1175
36	Lc	0.11	0/774	0.34	0/1038
37	Ld	0.13	0/903	0.44	0/1216
38	Le	0.13	0/1071	0.46	0/1429
39	Lf	0.12	0/895	0.43	0/1198
40	Lg	0.13	0/916	0.47	0/1220
41	Lh	0.12	0/1023	0.43	0/1351
42	Li	0.12	0/843	0.46	0/1115
43	Lj	0.13	0/720	0.47	0/952
44	Lk	0.13	0/575	0.39	0/761
45	Ll	0.14	0/454	0.50	0/599
46	Lm	0.13	0/435	0.47	0/575
47	Lo	0.12	0/877	0.40	0/1156
48	Lp	0.10	0/718	0.37	0/953
49	Lr	0.13	0/1017	0.45	0/1364
50	Lz	0.12	0/1772	0.40	0/2375
51	Z	0.19	0/6010	0.42	0/8115
52	a	0.13	0/1936	0.44	0/2596
53	s	0.15	0/1569	0.42	1/2119 (0.0%)
54	t	0.14	0/1081	0.46	0/1460
All	All	0.11	0/180778	0.32	3/262817 (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
51	Z	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	470	PRO	N-CA-C	-6.77	103.79	113.47
53	s	108	PRO	CA-N-CD	-5.96	103.66	112.00
8	F	734	PRO	CA-N-CD	-5.89	103.75	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
51	Z	185	ARG	Sidechain
51	Z	791	ARG	Sidechain

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	5	75663	0	38217	887	0
2	7	2561	0	1295	24	0
3	8	3152	0	1601	33	0
4	B	3234	0	3287	48	0
5	C	1547	0	1543	12	0
6	D	588	0	616	0	0
7	E	5251	0	5358	73	0
8	F	13415	0	13576	248	0
9	G	1622	0	820	20	0
10	LB	3239	0	3376	41	0
11	LC	2927	0	3104	27	0
12	LD	2382	0	2410	26	0
13	LE	1765	0	1917	21	0
14	LF	1870	0	1996	15	0
15	LG	1927	0	2074	16	0
16	LH	1518	0	1601	11	0
17	LI	1710	0	1748	23	0
18	LJ	1401	0	1428	10	0
19	LL	1573	0	1681	16	0
20	LM	1120	0	1187	16	0
21	LN	1701	0	1749	25	0
22	LO	1650	0	1794	12	0
23	LP	1242	0	1269	9	0
24	LQ	1513	0	1628	19	0
25	LR	1294	0	1434	14	0
26	LS	1453	0	1490	15	0
27	LT	1298	0	1366	26	0
28	LU	825	0	850	18	0
29	LV	979	0	1039	12	0
30	LW	519	0	533	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	LX	967	0	1040	14	0
32	LY	1115	0	1205	12	0
33	LZ	1107	0	1182	18	0
34	La	1162	0	1213	22	0
35	Lb	876	0	948	17	0
36	Lc	764	0	804	8	0
37	Ld	888	0	930	9	0
38	Le	1053	0	1147	15	0
39	Lf	876	0	912	12	0
40	Lg	906	0	998	9	0
41	Lh	1015	0	1148	6	0
42	Li	832	0	917	8	0
43	Lj	705	0	737	11	0
44	Lk	569	0	637	3	0
45	Ll	444	0	483	10	0
46	Lm	429	0	465	12	0
47	Lo	863	0	929	5	0
48	Lp	708	0	756	10	0
49	Lr	1002	0	1068	8	0
50	Lz	1744	0	1859	31	0
51	Z	5891	0	5986	106	0
52	a	1898	0	1993	34	0
53	s	1545	0	1599	33	0
54	t	1068	0	1113	23	0
55	A	35	0	10	0	0
56	5	205	0	0	0	0
56	7	2	0	0	0	0
56	8	5	0	0	0	0
56	LI	1	0	0	0	0
56	LP	1	0	0	0	0
56	LV	1	0	0	0	0
56	Le	1	0	0	0	0
56	Lf	1	0	0	0	0
56	Lg	1	0	0	0	0
56	Lj	1	0	0	0	0
57	Lg	1	0	0	0	0
57	Lj	1	0	0	0	0
57	Lm	1	0	0	0	0
57	Lo	1	0	0	0	0
57	Lp	1	0	0	0	0
All	All	169625	0	132066	1852	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 6.

The worst 5 of 1852 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)
1:5:2520:C:O2	1:5:2640:G:N2	2.14	0.80
8:F:286:ILE:HD12	8:F:287:PRO:HD2	1.65	0.78
1:5:1293:G:OP2	1:5:1293:G:N2	2.16	0.78
51:Z:350:LEU:O	51:Z:354:ASN:ND2	2.17	0.78
26:LS:69:GLU:OE1	26:LS:102:THR:N	2.16	0.78

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	
4	B	397/506 (78%)	379 (96%)	18 (4%)	0	100	100
5	C	186/314 (59%)	186 (100%)	0	0	100	100
6	D	76/85 (89%)	75 (99%)	1 (1%)	0	100	100
7	E	652/794 (82%)	633 (97%)	19 (3%)	0	100	100
8	F	1673/1766 (95%)	1619 (97%)	53 (3%)	1 (0%)	48	80
10	LB	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
11	LC	366/427 (86%)	354 (97%)	12 (3%)	0	100	100
12	LD	291/297 (98%)	286 (98%)	4 (1%)	1 (0%)	36	70
13	LE	214/288 (74%)	206 (96%)	8 (4%)	0	100	100
14	LF	223/248 (90%)	218 (98%)	4 (2%)	1 (0%)	30	65
15	LG	239/266 (90%)	232 (97%)	7 (3%)	0	100	100
16	LH	188/192 (98%)	185 (98%)	3 (2%)	0	100	100
17	LI	211/214 (99%)	206 (98%)	5 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	LJ	173/178 (97%)	172 (99%)	1 (1%)	0	100	100
19	LL	192/211 (91%)	188 (98%)	4 (2%)	0	100	100
20	LM	134/215 (62%)	132 (98%)	2 (2%)	0	100	100
21	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
22	LO	199/203 (98%)	197 (99%)	2 (1%)	0	100	100
23	LP	151/184 (82%)	149 (99%)	2 (1%)	0	100	100
24	LQ	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
25	LR	153/196 (78%)	153 (100%)	0	0	100	100
26	LS	173/176 (98%)	169 (98%)	4 (2%)	0	100	100
27	LT	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
28	LU	99/128 (77%)	92 (93%)	7 (7%)	0	100	100
29	LV	129/140 (92%)	127 (98%)	2 (2%)	0	100	100
30	LW	60/157 (38%)	60 (100%)	0	0	100	100
31	LX	116/156 (74%)	115 (99%)	1 (1%)	0	100	100
32	LY	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
33	LZ	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
34	La	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
35	Lb	105/159 (66%)	102 (97%)	3 (3%)	0	100	100
36	Lc	96/115 (84%)	95 (99%)	1 (1%)	0	100	100
37	Ld	105/125 (84%)	102 (97%)	3 (3%)	0	100	100
38	Le	126/135 (93%)	124 (98%)	2 (2%)	0	100	100
39	Lf	107/110 (97%)	107 (100%)	0	0	100	100
40	Lg	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
41	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
42	Li	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
43	Lj	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
44	Lk	67/70 (96%)	67 (100%)	0	0	100	100
45	Ll	48/51 (94%)	48 (100%)	0	0	100	100
46	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
47	Lo	103/106 (97%)	102 (99%)	1 (1%)	0	100	100
48	Lp	89/92 (97%)	88 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	Lr	123/137 (90%)	122 (99%)	1 (1%)	0	100	100
50	Lz	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
51	Z	721/1076 (67%)	700 (97%)	20 (3%)	1 (0%)	48	80
52	a	246/257 (96%)	239 (97%)	7 (3%)	0	100	100
53	s	199/317 (63%)	193 (97%)	6 (3%)	0	100	100
54	t	139/165 (84%)	136 (98%)	3 (2%)	0	100	100
All	All	10603/12427 (85%)	10348 (98%)	251 (2%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	F	360	TYR
12	LD	4	VAL
51	Z	789	PRO
14	LF	197	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	B	360/438 (82%)	349 (97%)	11 (3%)	35	68
5	C	162/254 (64%)	159 (98%)	3 (2%)	50	76
6	D	66/72 (92%)	65 (98%)	1 (2%)	57	80
7	E	593/704 (84%)	581 (98%)	12 (2%)	48	76
8	F	1533/1611 (95%)	1486 (97%)	47 (3%)	35	68
10	LB	348/349 (100%)	344 (99%)	4 (1%)	65	83
11	LC	306/348 (88%)	305 (100%)	1 (0%)	86	91
12	LD	246/250 (98%)	245 (100%)	1 (0%)	84	90
13	LE	194/252 (77%)	192 (99%)	2 (1%)	68	84
14	LF	194/215 (90%)	191 (98%)	3 (2%)	57	80

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	LG	203/223 (91%)	198 (98%)	5 (2%)	42	72
16	LH	169/171 (99%)	166 (98%)	3 (2%)	51	77
17	LI	179/181 (99%)	179 (100%)	0	100	100
18	LJ	147/149 (99%)	144 (98%)	3 (2%)	48	76
19	LL	164/177 (93%)	162 (99%)	2 (1%)	63	82
20	LM	116/161 (72%)	113 (97%)	3 (3%)	40	72
21	LN	171/172 (99%)	168 (98%)	3 (2%)	51	77
22	LO	173/174 (99%)	173 (100%)	0	100	100
23	LP	134/163 (82%)	131 (98%)	3 (2%)	45	74
24	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	88
25	LR	138/175 (79%)	138 (100%)	0	100	100
26	LS	156/157 (99%)	153 (98%)	3 (2%)	50	76
27	LT	139/140 (99%)	137 (99%)	2 (1%)	59	80
28	LU	91/115 (79%)	88 (97%)	3 (3%)	33	67
29	LV	101/107 (94%)	101 (100%)	0	100	100
30	LW	54/126 (43%)	53 (98%)	1 (2%)	50	76
31	LX	106/133 (80%)	104 (98%)	2 (2%)	50	76
32	LY	124/135 (92%)	123 (99%)	1 (1%)	73	86
33	LZ	117/118 (99%)	114 (97%)	3 (3%)	40	72
34	La	120/121 (99%)	120 (100%)	0	100	100
35	Lb	88/126 (70%)	86 (98%)	2 (2%)	44	74
36	Lc	83/97 (86%)	80 (96%)	3 (4%)	31	65
37	Ld	98/110 (89%)	96 (98%)	2 (2%)	48	76
38	Le	114/121 (94%)	110 (96%)	4 (4%)	32	65
39	Lf	88/89 (99%)	86 (98%)	2 (2%)	44	74
40	Lg	98/100 (98%)	98 (100%)	0	100	100
41	Lh	109/110 (99%)	107 (98%)	2 (2%)	51	77
42	Li	86/89 (97%)	85 (99%)	1 (1%)	63	82
43	Lj	73/80 (91%)	73 (100%)	0	100	100
44	Lk	64/65 (98%)	64 (100%)	0	100	100
45	Ll	47/48 (98%)	46 (98%)	1 (2%)	47	75

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	Lm	48/116 (41%)	48 (100%)	0	100	100
47	Lo	93/94 (99%)	92 (99%)	1 (1%)	65	83
48	Lp	74/75 (99%)	73 (99%)	1 (1%)	59	80
49	Lr	109/121 (90%)	107 (98%)	2 (2%)	51	77
50	Lz	196/196 (100%)	185 (94%)	11 (6%)	19	52
51	Z	645/962 (67%)	632 (98%)	13 (2%)	48	76
52	a	190/199 (96%)	187 (98%)	3 (2%)	55	79
53	s	169/258 (66%)	165 (98%)	4 (2%)	43	73
54	t	116/137 (85%)	114 (98%)	2 (2%)	53	78
All	All	9356/10749 (87%)	9179 (98%)	177 (2%)	49	76

5 of 177 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	LU	74	SER
49	Lr	78	VAL
32	LY	12	SER
38	Le	25	SER
50	Lz	115	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
51	Z	488	GLN
51	Z	790	GLN
54	t	137	GLN
15	LG	82	GLN
15	LG	81	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3506/5070 (69%)	445 (12%)	12 (0%)
2	7	119/121 (98%)	6 (5%)	0
3	8	145/157 (92%)	16 (11%)	0
9	G	75/76 (98%)	22 (29%)	2 (2%)
All	All	3845/5424 (70%)	489 (12%)	14 (0%)

5 of 489 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	13	U
1	5	25	A
1	5	39	A
1	5	42	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	2506	G
1	5	4048	A
9	G	44	A
1	5	4699	U
9	G	12	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 224 ligands modelled in this entry, 224 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

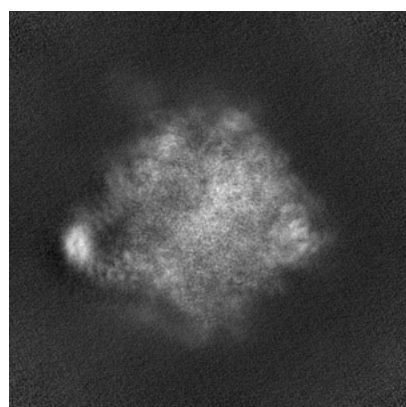
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51681. These allow visual inspection of the internal detail of the map and identification of artifacts.

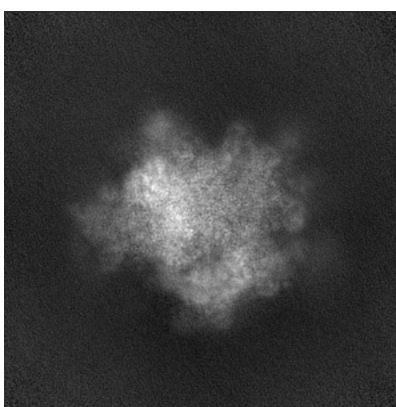
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

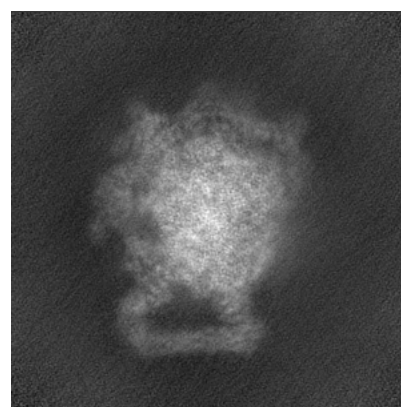
6.1.1 Primary map



X



Y

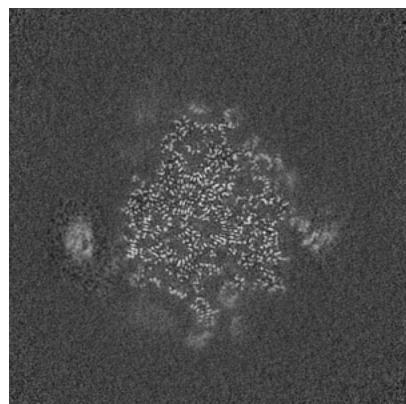


Z

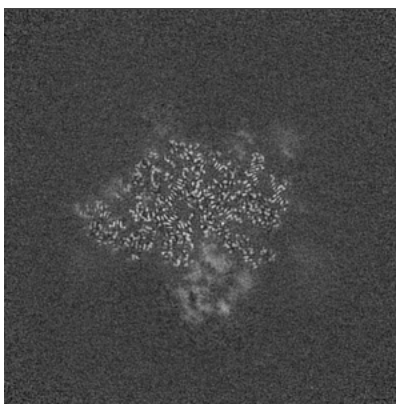
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

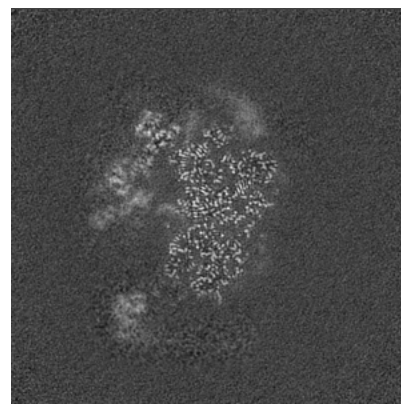
6.2.1 Primary map



X Index: 300



Y Index: 300

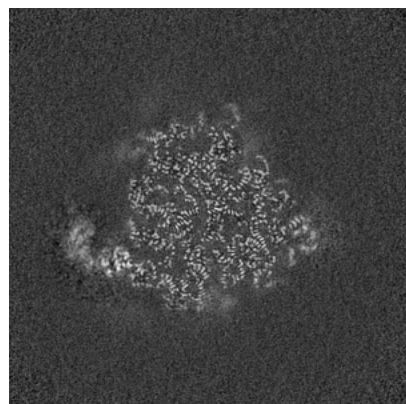


Z Index: 300

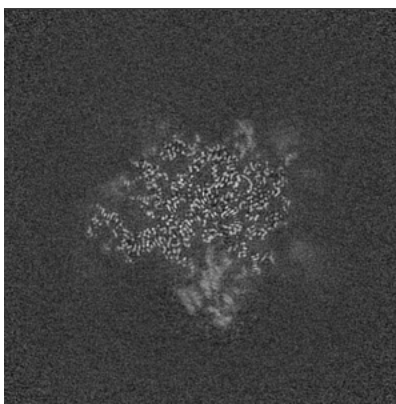
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

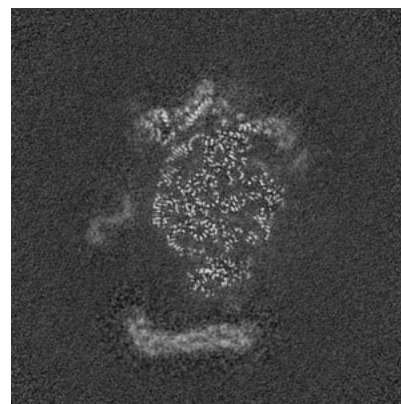
6.3.1 Primary map



X Index: 321



Y Index: 310

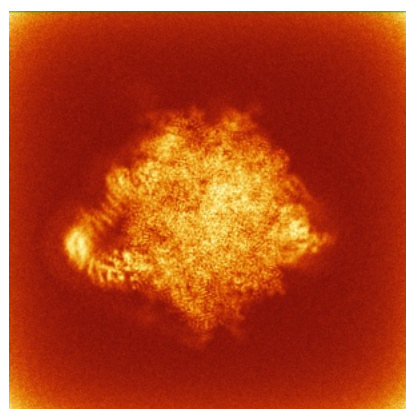


Z Index: 261

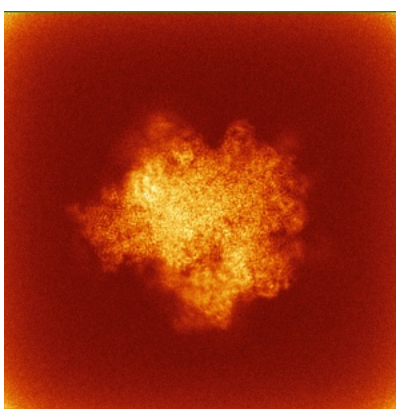
The images above show the largest variance slices of the map in three orthogonal directions.

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

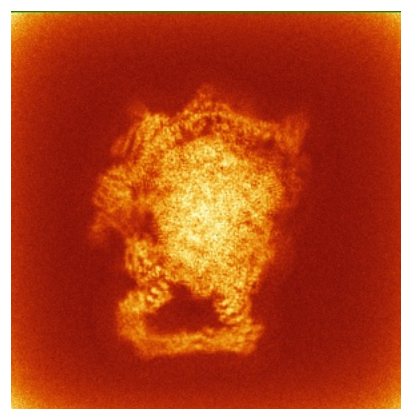
6.4.1 Primary map



X



Y

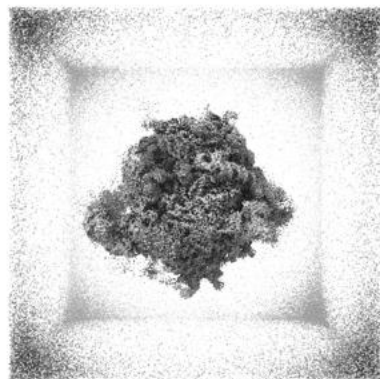


Z

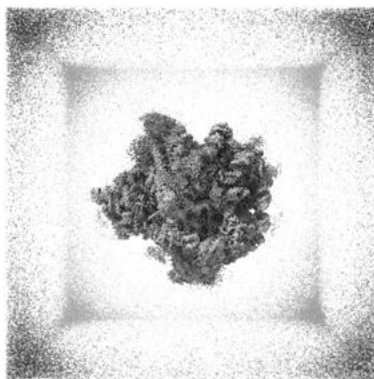
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

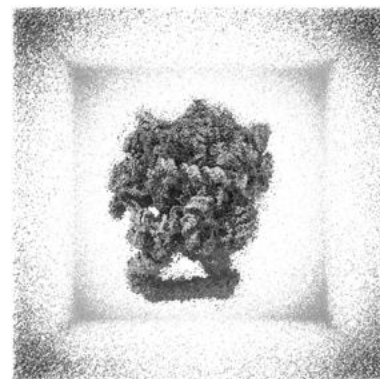
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

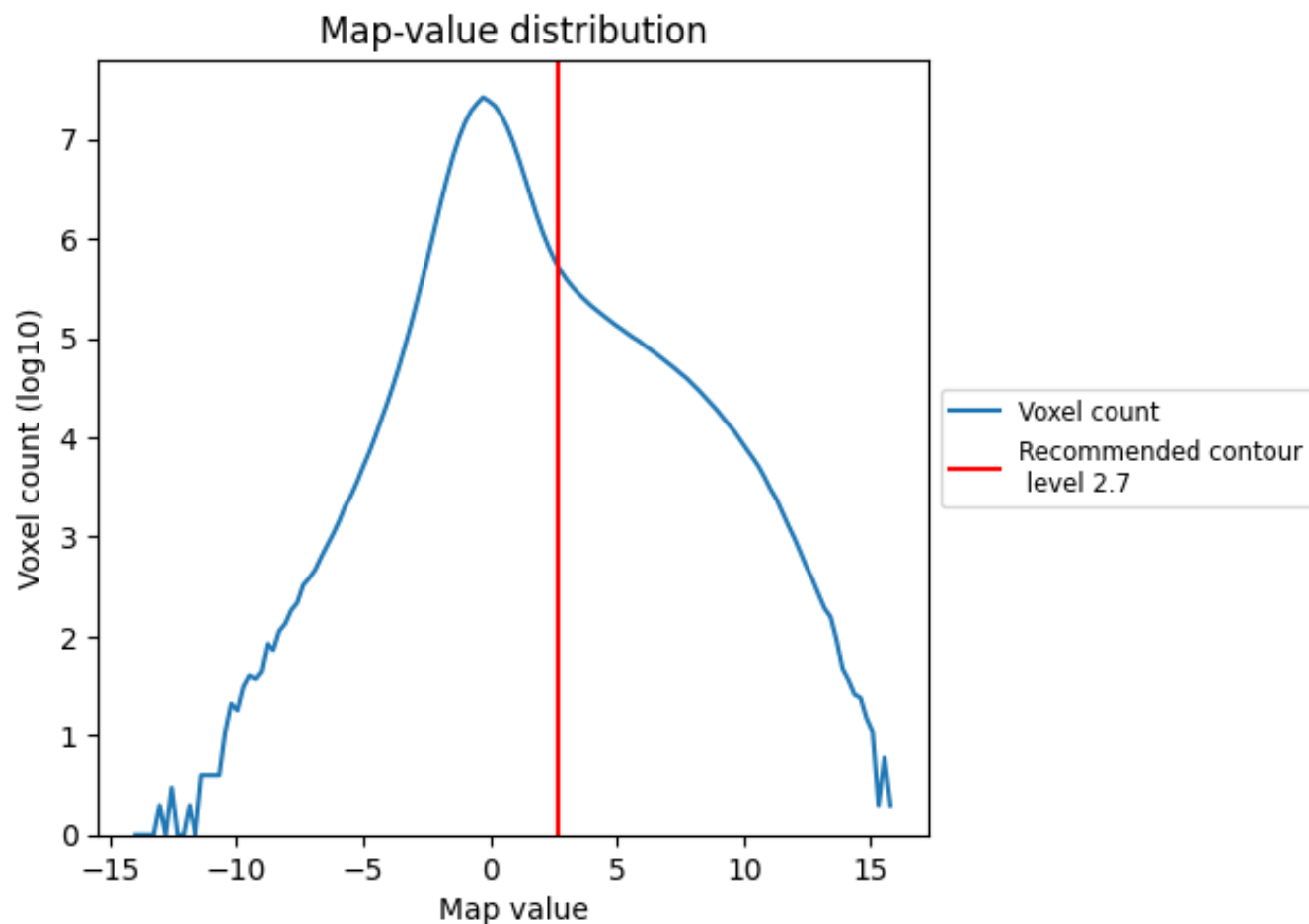
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

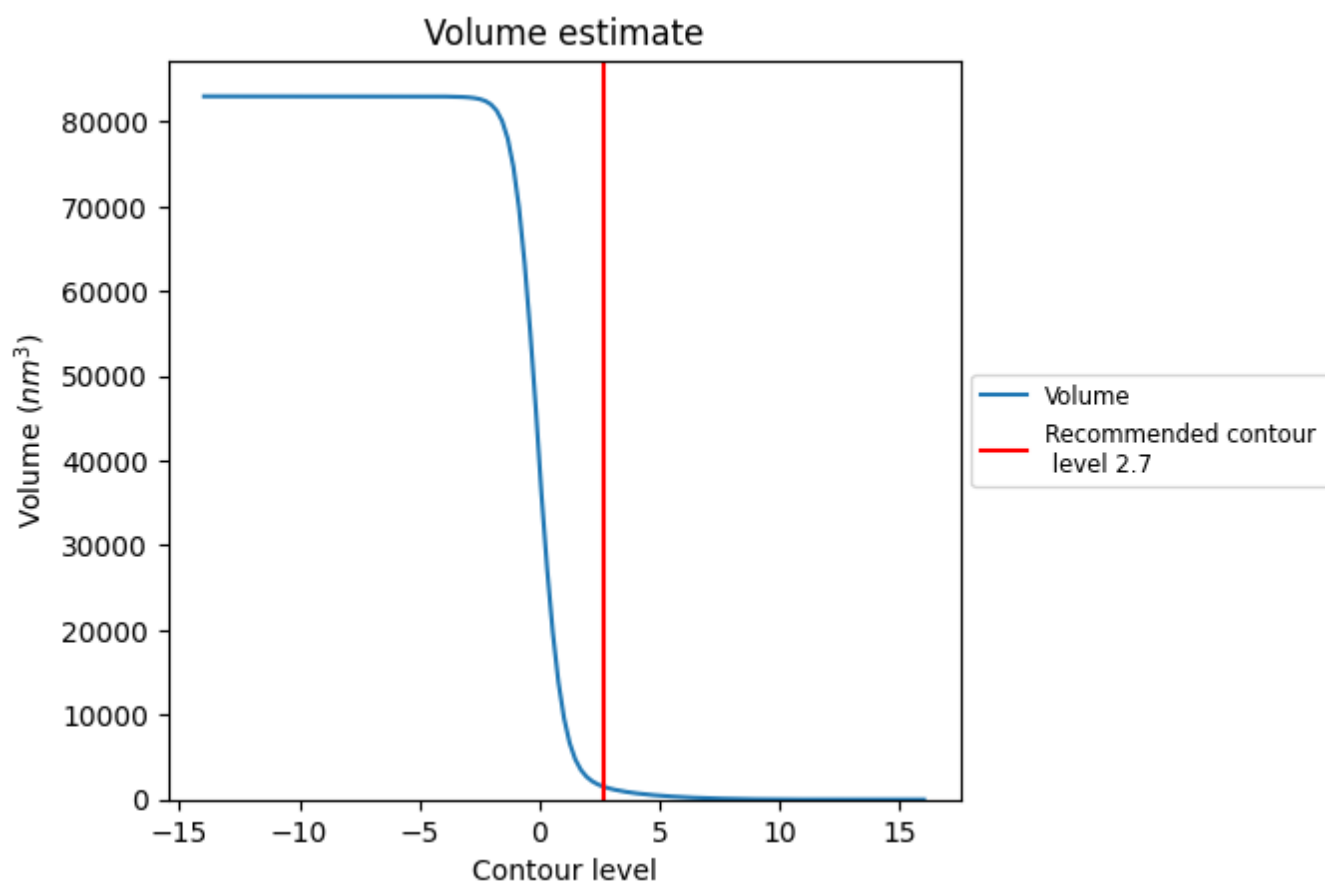
This section contains the results of statistical analysis of the map.

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.

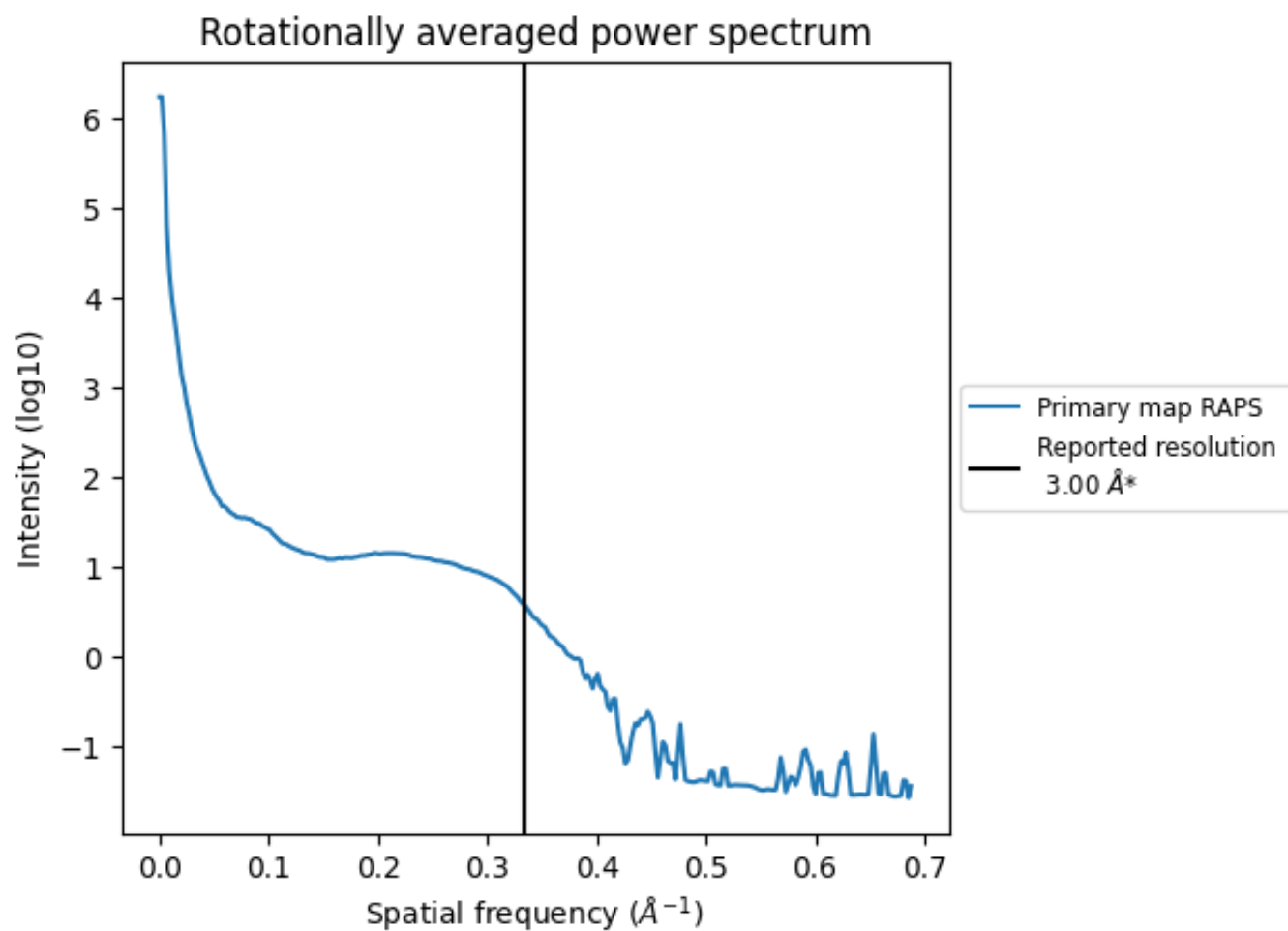
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1497 nm^3 ; this corresponds to an approximate mass of 1352 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 0.333 Å⁻¹

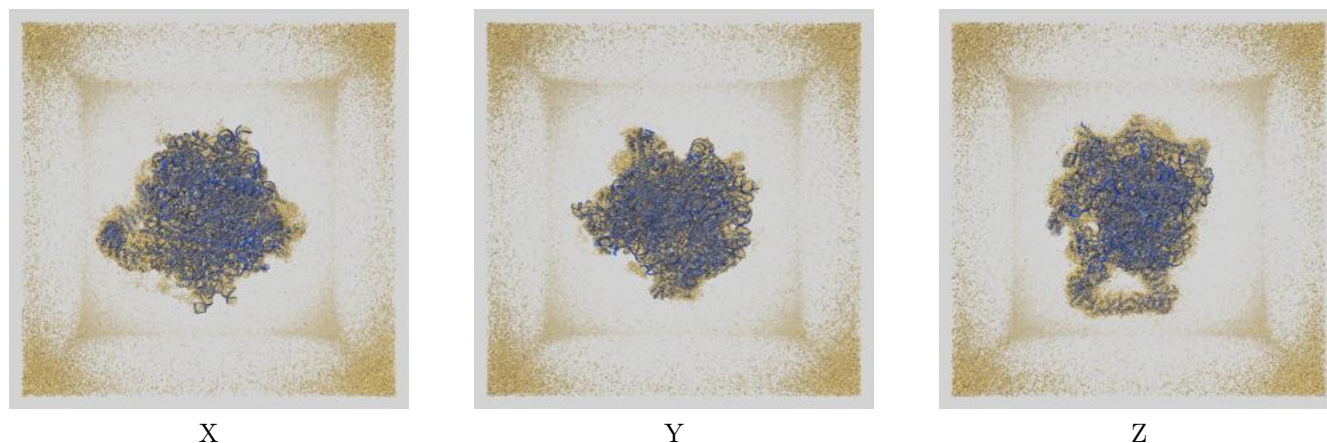
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

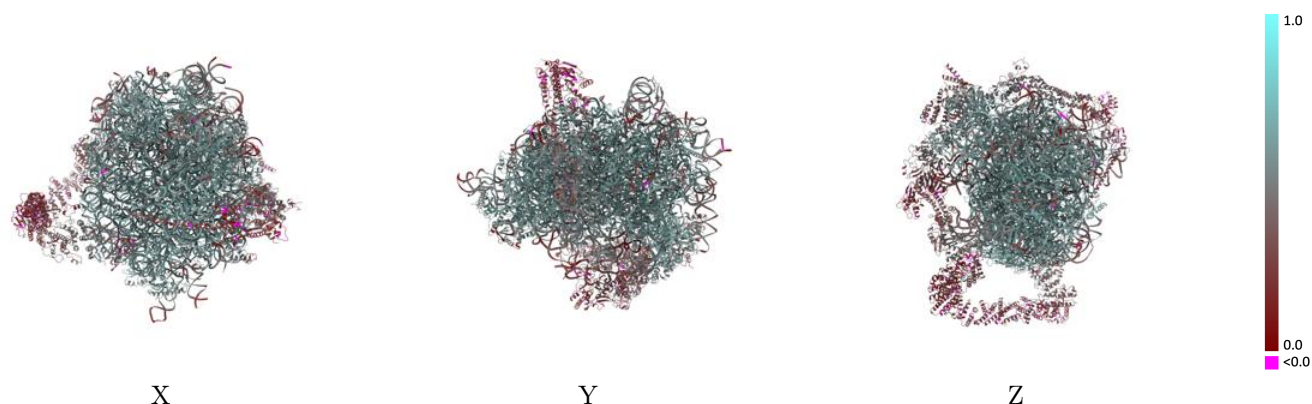
This section contains information regarding the fit between EMDB map EMD-51681 and PDB model 9GY4. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



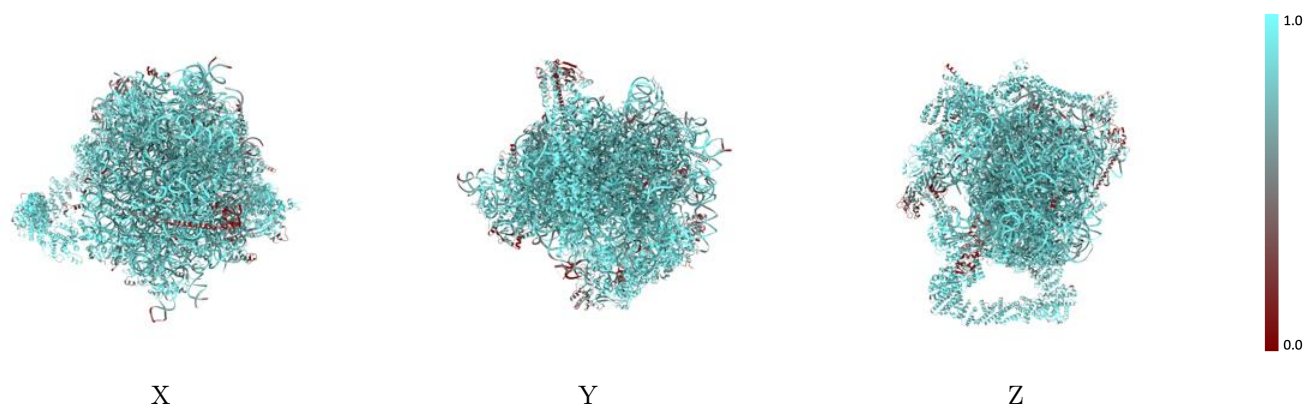
The images above show the 3D surface view of the map at the recommended contour level 2.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



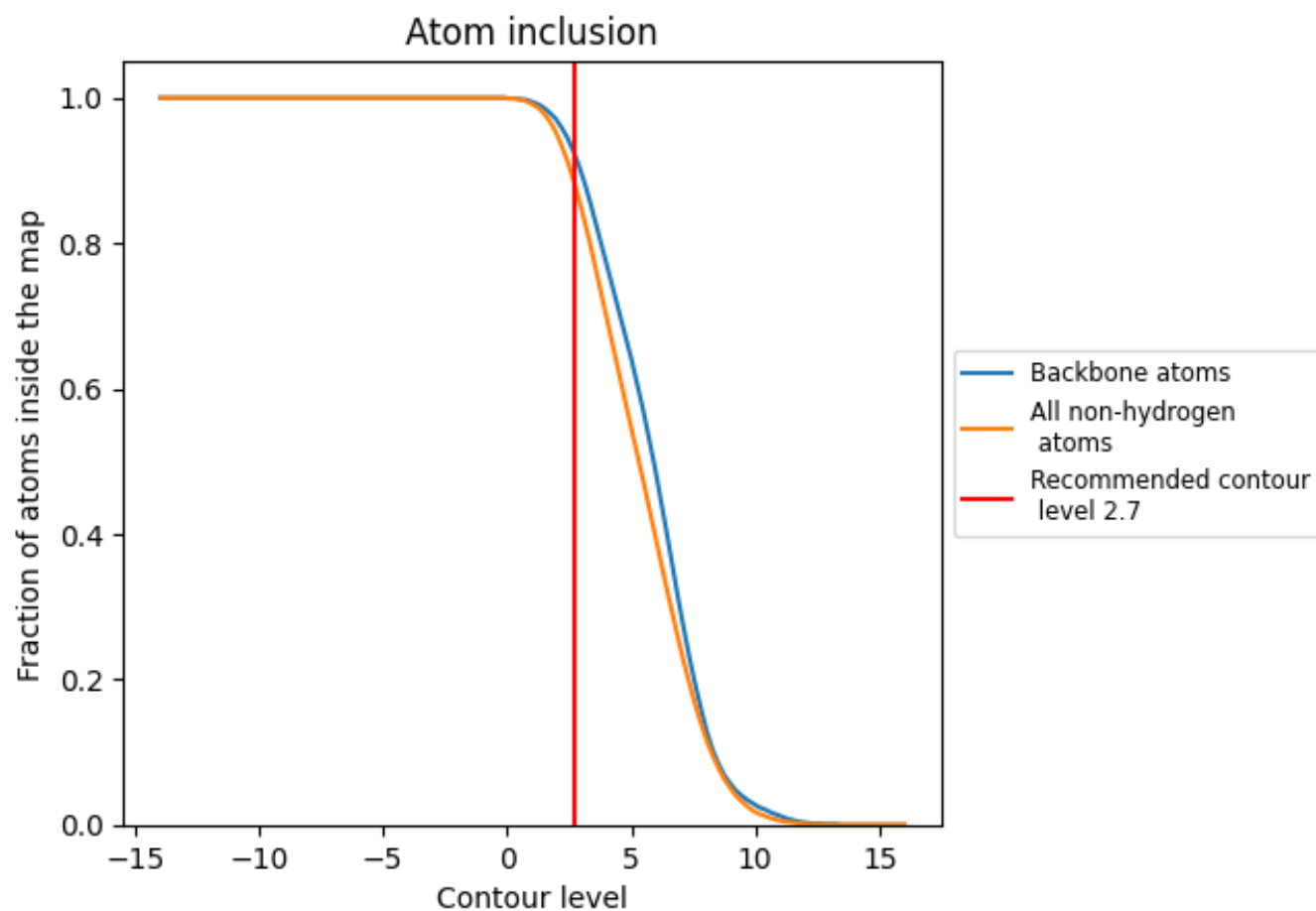
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 88% 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 (2.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8840	 0.5170
5	 0.9160	 0.5490
7	 0.9670	 0.5860
8	 0.9400	 0.5730
A	 0.6860	 0.4700
B	 0.8090	 0.3180
C	 0.5250	 0.2670
D	 0.1940	 0.1560
E	 0.8520	 0.4260
F	 0.8840	 0.2680
G	 0.8680	 0.2640
LB	 0.8980	 0.6150
LC	 0.8910	 0.6040
LD	 0.8700	 0.5830
LE	 0.8500	 0.5820
LF	 0.9190	 0.6200
LG	 0.7870	 0.5580
LH	 0.8880	 0.6050
LI	 0.8870	 0.6020
LJ	 0.8350	 0.5400
LL	 0.9140	 0.5950
LM	 0.9030	 0.6090
LN	 0.9600	 0.6330
LO	 0.9210	 0.6180
LP	 0.9170	 0.6200
LQ	 0.9360	 0.6250
LR	 0.8850	 0.5940
LS	 0.9300	 0.6200
LT	 0.8700	 0.5930
LU	 0.8690	 0.5210
LV	 0.8740	 0.6140
LW	 0.8860	 0.6160
LX	 0.8770	 0.6010
LY	 0.8970	 0.6040
LZ	 0.8750	 0.5920



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
La	 0.9160	 0.6160
Lb	 0.7770	 0.5520
Lc	 0.7960	 0.5830
Ld	 0.9250	 0.5910
Le	 0.9210	 0.6160
Lf	 0.9410	 0.6290
Lg	 0.8630	 0.5890
Lh	 0.8630	 0.6050
Li	 0.8780	 0.5870
Lj	 0.9630	 0.6300
Lk	 0.7380	 0.5640
Ll	 0.9080	 0.6090
Lm	 0.9130	 0.5880
Lo	 0.9150	 0.6090
Lp	 0.8460	 0.6030
Lr	 0.9090	 0.6140
Lz	 0.9150	 0.4760
Z	 0.7370	 0.3290
a	 0.9300	 0.6230
s	 0.3390	 0.3290
t	 0.8240	 0.3820