



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 11:37 PM UTC

PDB ID : 6Y6X / pdb_00006y6x
EMDB ID : EMD-10709
Title : Tetracenomycin X bound to the human ribosome
Authors : Buschauer, R.; Cheng, J.; Berninghausen, O.; Beckmann, R.; Wilson, D.N.
Deposited on : 2020-02-27
Resolution : 2.80 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:

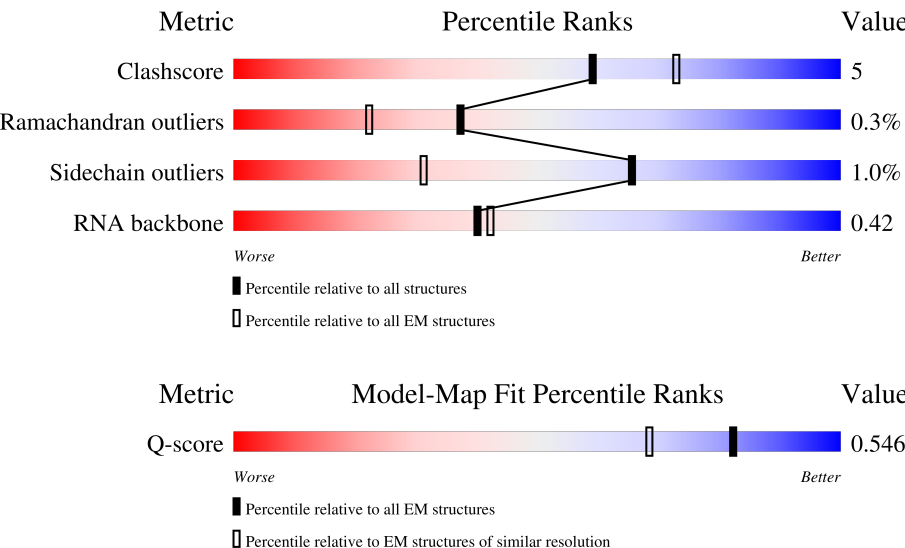
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.80 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.



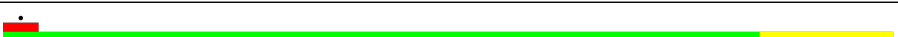
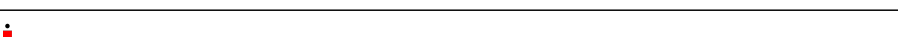
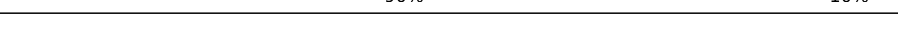
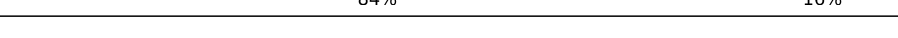
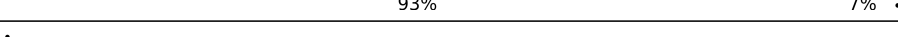
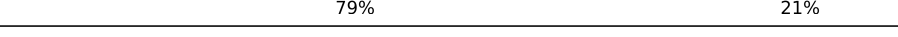
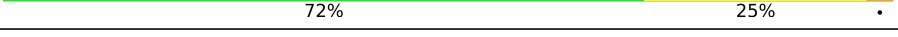
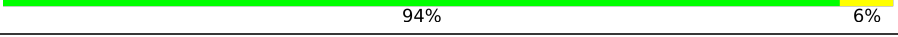
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	L5	5069	
2	L7	120	
3	L8	156	

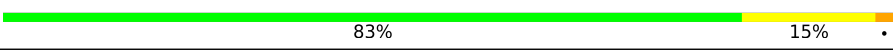
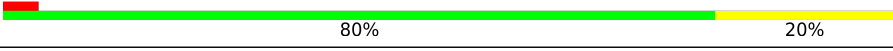
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	LA	248	
5	LB	397	
6	LC	368	
7	LD	293	
8	LE	247	
9	LF	225	
10	LG	241	
11	LH	190	
12	LI	213	
13	LJ	176	
14	LL	210	
15	LM	139	
16	LN	203	
17	LO	201	
18	LP	153	
19	LQ	187	
20	LR	187	
21	LS	175	
22	LT	159	
23	LU	99	
24	LV	131	
25	LW	124	
26	LX	120	
27	LY	134	
28	LZ	135	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	La	147	 81% 19%
30	Lb	121	 8% 71% 18% 10%
31	Lc	98	 7% 85% 14%
32	Ld	107	 86% 14%
33	Le	128	 80% 17%
34	Lf	109	 89% 10%
35	Lg	114	 84% 16%
36	Lh	122	 82% 18%
37	Li	102	 88% 12%
38	Lj	86	 83% 15%
39	Lk	69	 80% 20%
40	Ll	50	 80% 20%
41	Lm	52	 79% 19%
42	Ln	24	 88% 12%
43	Lo	105	 5% 76% 24%
44	Lp	91	 88% 11%
45	Lr	125	 86% 14%
46	Lz	217	 90% 75% 23%

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 140991 atoms, of which 22 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	L5	3773	Total	C	N	O	P	0	0
			80136	35654	14588	26122	3772		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	2113	C	G	conflict	GB NR_003287

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called 60S ribosomal protein L8.

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

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	397	Total	C	N	O	S	0	0
			3202	2039	602	547	14		

- Molecule 6 is a protein called 60S ribosomal protein L4.

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

- Molecule 7 is a protein called 60S ribosomal protein L5.

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

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

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

- Molecule 10 is a protein called 60S ribosomal protein L7a.

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

- Molecule 11 is a protein called 60S ribosomal protein L9.

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

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

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

- Molecule 17 is a protein called 60S ribosomal protein L13a.

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

- Molecule 18 is a protein called 60S ribosomal protein L17.

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

- Molecule 19 is a protein called 60S ribosomal protein L18.

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

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	187	Total	C	N	O	S	0	0
			1434	889	305	231	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

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

- Molecule 22 is a protein called 60S ribosomal protein L21.

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

- Molecule 23 is a protein called 60S ribosomal protein L22.

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

- Molecule 24 is a protein called 60S ribosomal protein L23.

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

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	124	Total	C	N	O	S	0	0
			833	519	164	147	3		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

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

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

- Molecule 30 is a protein called 60S ribosomal protein L29.

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

- Molecule 31 is a protein called 60S ribosomal protein L30.

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

- Molecule 32 is a protein called 60S ribosomal protein L31.

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

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

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

- Molecule 36 is a protein called 60S ribosomal protein L35.

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

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

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

- Molecule 38 is a protein called 60S ribosomal protein L37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

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

- Molecule 45 is a protein called 60S ribosomal protein L28.

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

- Molecule 46 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lz	217	Total	C	N	O	S	0	0
			1738	1110	312	307	9		

- Molecule 47 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

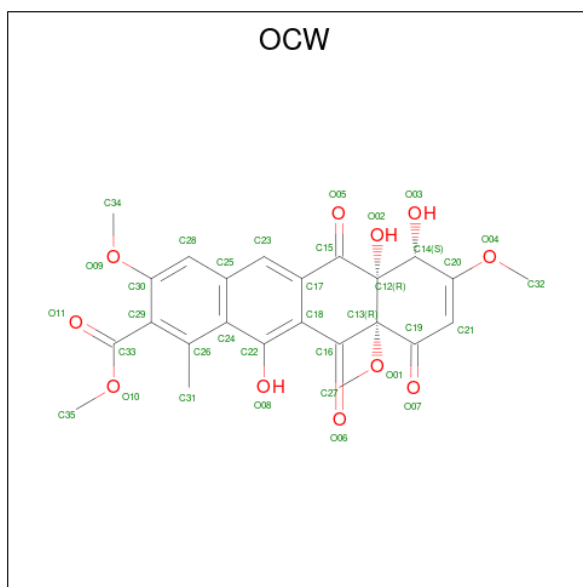
Mol	Chain	Residues	Atoms		AltConf
47	L5	214	Total	Mg	0
			214	214	
47	L7	3	Total	Mg	0
			3	3	
47	L8	4	Total	Mg	0
			4	4	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
47	LA	1	Total	Mg	0
			1	1	
47	LI	1	Total	Mg	0
			1	1	
47	LP	1	Total	Mg	0
			1	1	
47	LT	1	Total	Mg	0
			1	1	
47	LV	1	Total	Mg	0
			1	1	
47	Le	1	Total	Mg	0
			1	1	
47	Lg	1	Total	Mg	0
			1	1	
47	Lj	1	Total	Mg	0
			1	1	

- Molecule 48 is Tetracenomycin X (CCD ID: OCW) (formula: $C_{24}H_{22}O_{11}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
48	L5	1	Total	C	H	O	0
			57	24	22	11	

- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

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





C4996	C4900	C	A4762	A4656	U4530	G4391	G4168	G4076	G4011	G3951	U3838	G3722
U5001	C4901	G	U4763	U4657	U4531	A4394	G4169	A4077	G4012	A3952	G3839	A3726
U5006	A4909	G	A4764	G4658	U4532	A4394	C4171		G4013	G3953	C3841	A3727
G5009	A4910	A	G4659	G4659		G4405	U4174	G4081	G4014	A3954	U3851	A3728
C5013	A4911	G	C4670	C4537	C4538	C4413	G4175	U4083	C4015	G3955	A3861	U3729
A5014	C4912	G	C4671	C4545	A4415	A4414	G4183	U4085	C4016	G3956	A3862	A3732
G5017	C4913	G	C4672	A4546	A4415	A4415	G4187	G4086	G4017	U3957	A3862	A3733
U5022	C4914	C	C4775	C4547	C4775	U4419	G4191	G4088	G4018	U3959	A3867	U3734
C5024	C4918	G	G4776	C4548	C4776	U4422	G4191	G4089	C4019	C3961	C3868	G3735
C5029	C4922	U	C	C4549	C	A4422	G4191		U4020	A3962	C3869	A3736
U5030	C4923	G	U	C4550	C	C4426	U4194	G4092	C4021	A3963	C3870	A3737
G5031	C4924	G	A4687	U4556	U4556	C4426	U4194	G4093	C4022	A3963	A3876	A3746
U5034	C4925	C	C4688	C4567	C4567	U4431	G4196	G4094	G4023	U3964	A3877	A3747
C5040	C4926	C	C4688	C4568	C4568	U4432	G4197	G4095	G4024	A3965	A3878	A3748
G5041	C4927	C	C4693	C4569	C4569	U4441	A4203	G4096	C4025	A3966	G3879	G3750
A5042	C4928	C	C4694	C4570	C4570	A4441	A4203	G4097	G4026	U3967	G3880	G3751
A5043	C4931	C	C4695	C4571	C4571	A4441	A4203	A4098	G4027	U3968	G3881	C3752
C5047	C4934	C	U4699	C4572	C4572	U4448	U4208	G4099	C4027	G3969	G3885	G3753
G5050	C4935	G	A4704	C4573	C4573	A4448	U4210	C4100	G4028	C3970	G3887	G3754
C5054	C4936	C	C4705	U4574	U4574	A4452	A4219	C4102	C4029	A3972	A3890	G3757
U5059	C4937	G	G4706	C4575	C4575	C4453	A4220	C4103	C4030	G3973	A3892	U3758
C5061	C4940	C	A4707	C4576	C4576	U4457	A4221	G4104	U4031	C3974	A3897	A3759
G5062	C4941	C	C4708	C4577	C4577	U4457	A4222	A4105	G4032	C3975	U3897	A3760
G5063	C4942	G	U4709	C4578	C4578	U4457	A4222	G4106	C4033	C3976	G3897	C3761
C5069	A4943	G	C4712	C4583	C4583	U4463	A4225	C4107	G4034	C3977	G3897	G3765
U4946	U4946	A	C4712	C4584	C4584	U4463	A4225	C4107	G4034	C3978	G3900	A3766
U4947	U4947	C	C4712	C4585	C4585	U4463	A4225	C4107	G4034	C3978	A3901	A3767
C5064	C4960	C	C4725	C4586	C4586	U4463	A4225	C4107	G4034	C3978	A3906	U3768
G5065	C4961	C	C4725	C4587	C4587	U4463	A4225	C4107	G4034	C3978	G3907	U3770
A5061	C4962	C	C4725	C4588	C4588	U4463	A4225	C4107	G4034	C3978	A3908	C3771
G5062	C4963	C	C4725	C4589	C4589	U4463	A4225	C4107	G4034	C3978	C3909	A3774
C5069	C4964	C	C4725	C4590	C4590	U4463	A4225	C4107	G4034	C3978	C3911	A3775
U4966	U4966	C	C4725	C4591	C4591	U4463	A4225	C4107	G4034	C3978	U3915	G3776
A4968	U4967	C	C4725	C4592	C4592	U4463	A4225	C4107	G4034	C3978	G3916	G3777
C4973	U4973	C	C4725	C4593	C4593	U4463	A4225	C4107	G4034	C3978	A3917	U3786
U4976	U4976	C	C4725	C4594	C4594	U4463	A4225	C4107	G4034	C3978	G3918	C3788
C4980	C4980	C	C4725	C4595	C4595	U4463	A4225	C4107	G4034	C3978	G3938	U3802
U4985	U4985	C	C4725	C4596	C4596	U4463	A4225	C4107	G4034	C3978	G3939	G3811
U4988	U4988	C	C4725	C4597	C4597	U4463	A4225	C4107	G4034	C3978	U3940	C3812
U4989	U4989	C	C4725	C4598	C4598	U4463	A4225	C4107	G4034	C3978	G3941	A3813
C4990	C4990	C	C4725	C4599	C4599	U4463	A4225	C4107	G4034	C3978	A3942	U3814
U4991	U4991	C	C4725	C4600	C4600	U4463	A4225	C4107	G4034	C3978	A3943	A3817
G4992	G4992	C	C4725	C4601	C4601	U4463	A4225	C4107	G4034	C3978	A3944	U3818
C4993	C4993	C	C4725	C4602	C4602	U4463	A4225	C4107	G4034	C3978	A3945	G3946
											A3947	U3819
											A3948	G3818
											A3949	U3819
											U3950	G3823

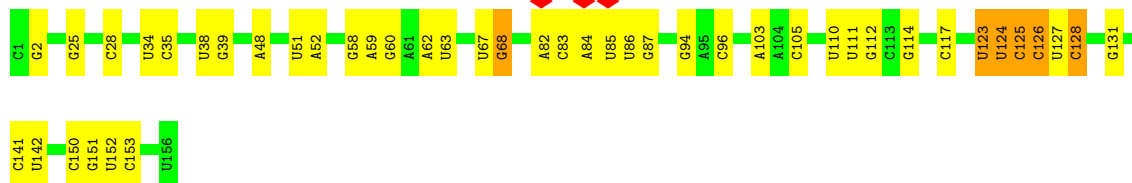
- Molecule 2: 5S ribosomal RNA

Chain L7:  82% 17% .



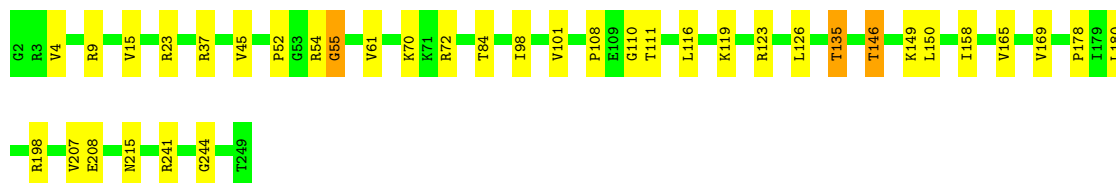
- Molecule 3: 5.8S ribosomal RNA

Chain L8:  71% 25% .



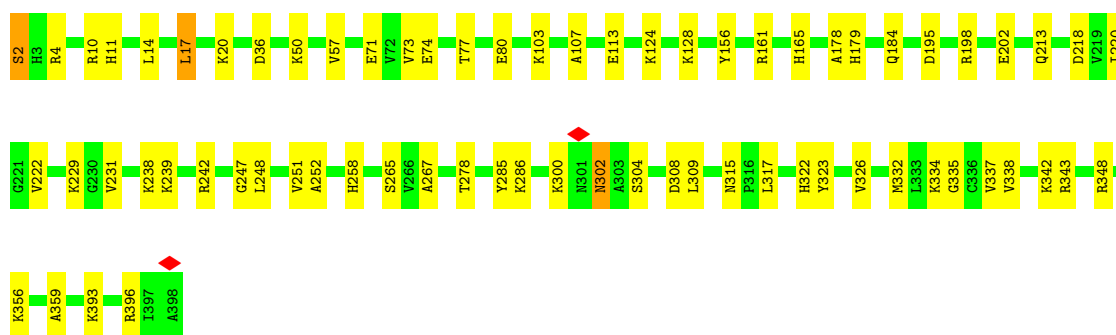
- Molecule 4: 60S ribosomal protein L8

Chain LA:  85% 14% .



- Molecule 5: 60S ribosomal protein L3

Chain LB:  82% 17% .



- Molecule 6: 60S ribosomal protein L4

Chain LC:  85% 15% .

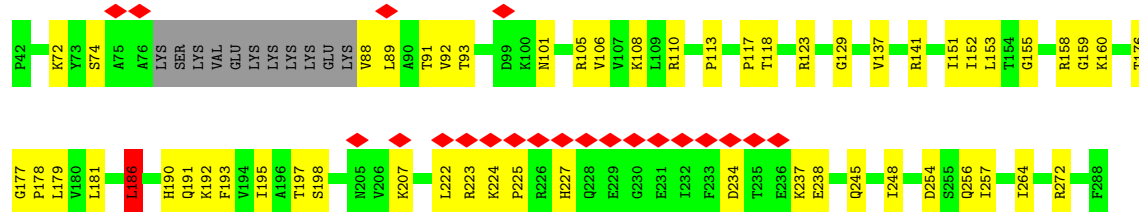
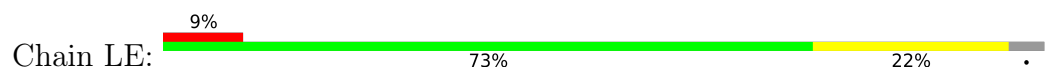




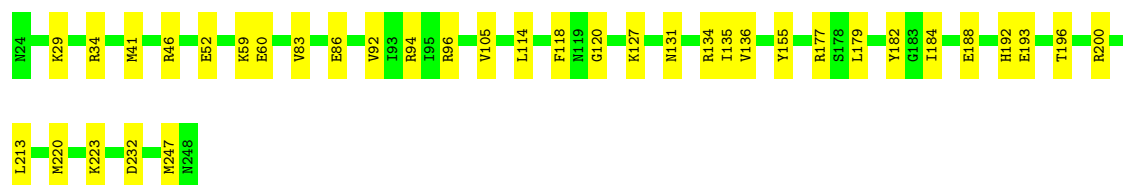
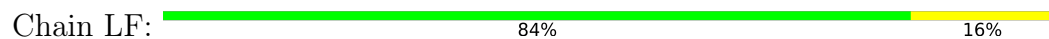
- Molecule 7: 60S ribosomal protein L5



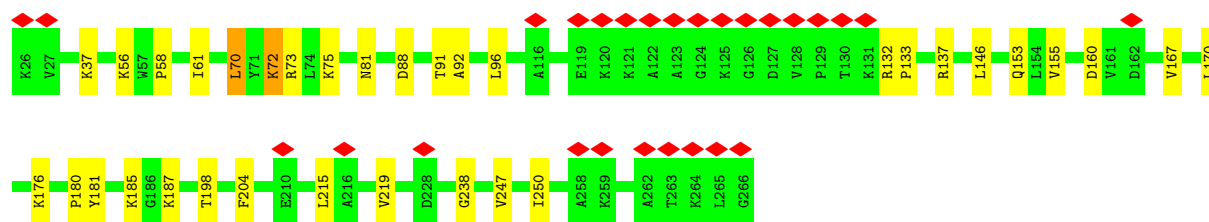
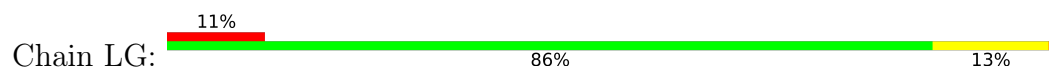
- Molecule 8: 60S ribosomal protein L6



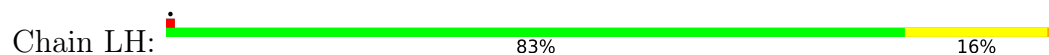
- Molecule 9: 60S ribosomal protein L7

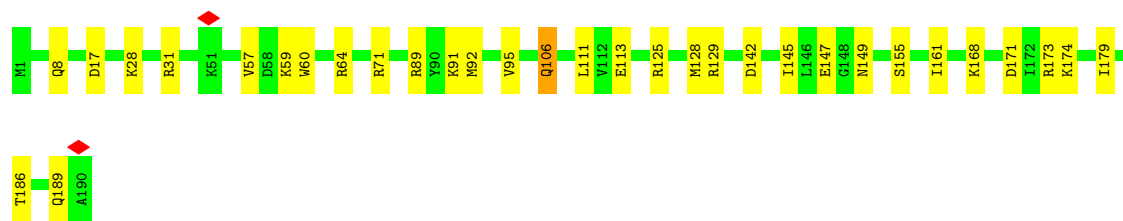


- Molecule 10: 60S ribosomal protein L7a

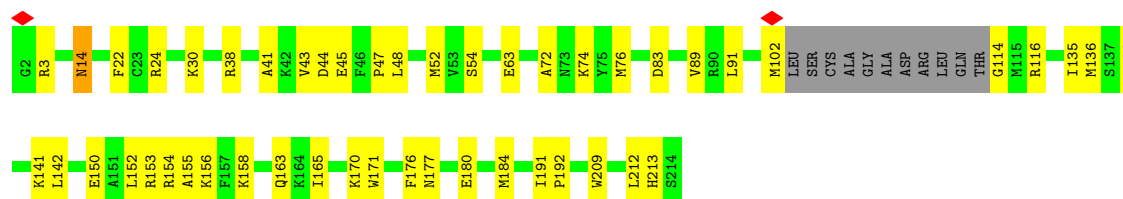


- Molecule 11: 60S ribosomal protein L9

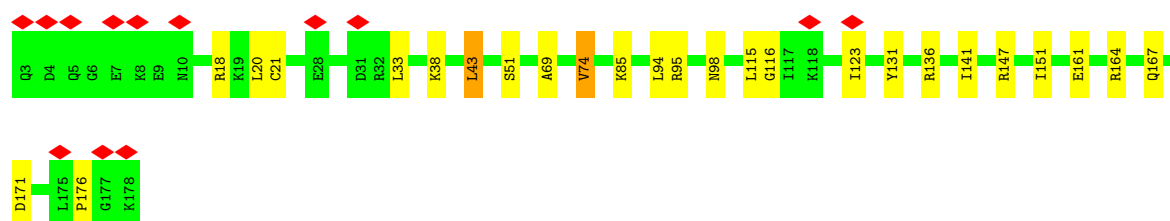
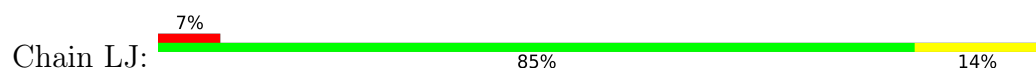




- Molecule 12: 60S ribosomal protein L10-like



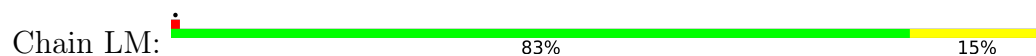
- Molecule 13: 60S ribosomal protein L11



- Molecule 14: 60S ribosomal protein L13



- Molecule 15: 60S ribosomal protein L14



- Molecule 16: 60S ribosomal protein L15

Chain LN:  86% 13%



- Molecule 17: 60S ribosomal protein L13a

Chain LO:  90% 10%



- Molecule 18: 60S ribosomal protein L17

Chain LP:  84% 16%

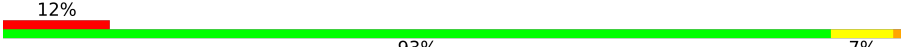


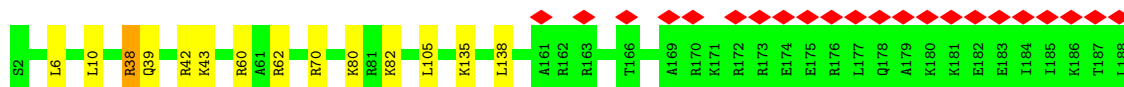
- Molecule 19: 60S ribosomal protein L18

Chain LQ:  90% 10%



- Molecule 20: 60S ribosomal protein L19

Chain LR:  12% 93% 7%



- Molecule 21: 60S ribosomal protein L18a

Chain LS:  83% 15%

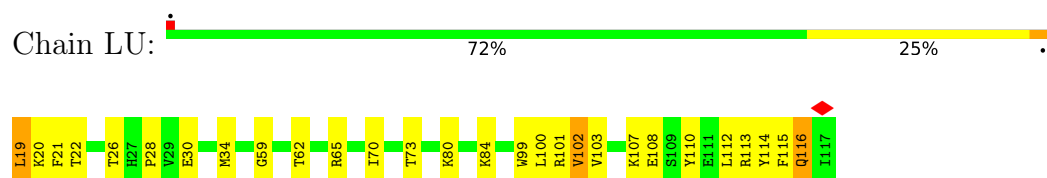


- Molecule 22: 60S ribosomal protein L21

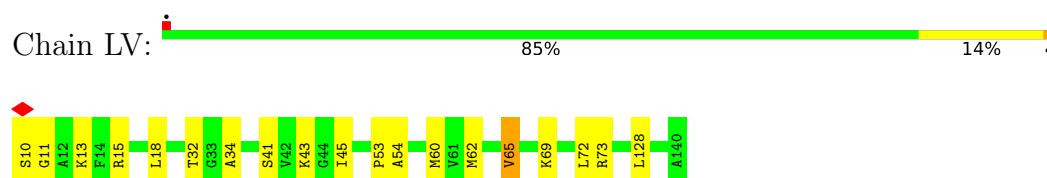
Chain LT:  79% 21%



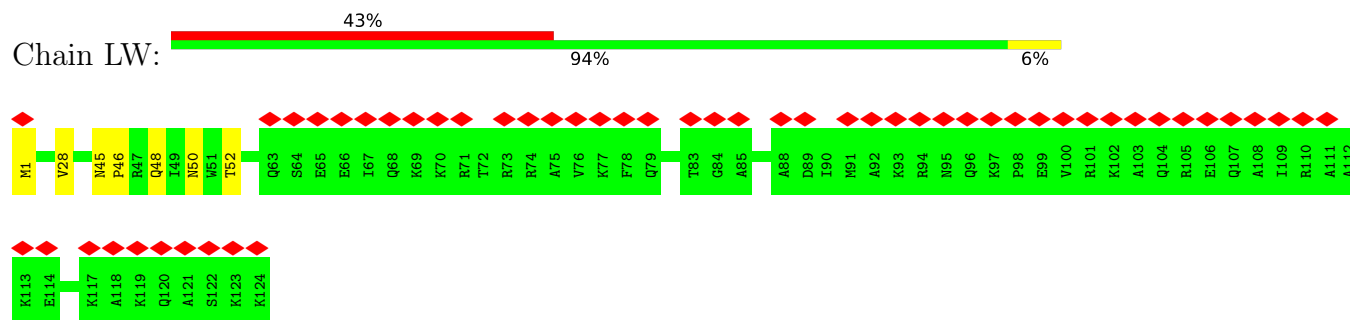
- Molecule 23: 60S ribosomal protein L22



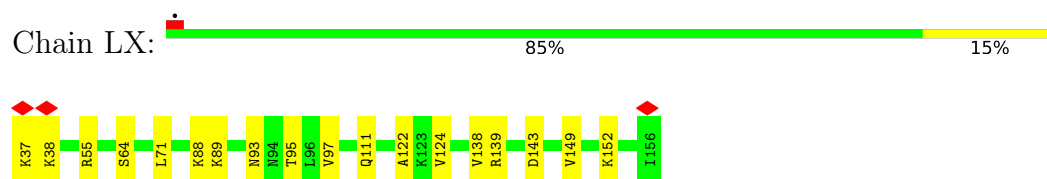
- Molecule 24: 60S ribosomal protein L23



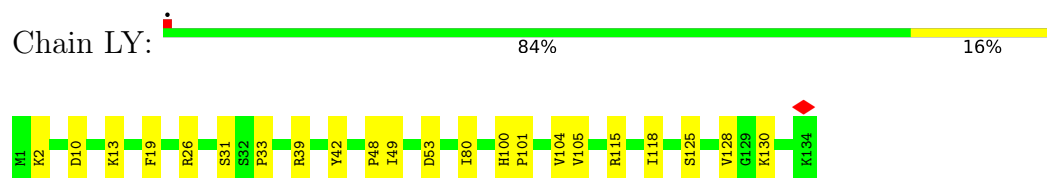
- Molecule 25: 60S ribosomal protein L24



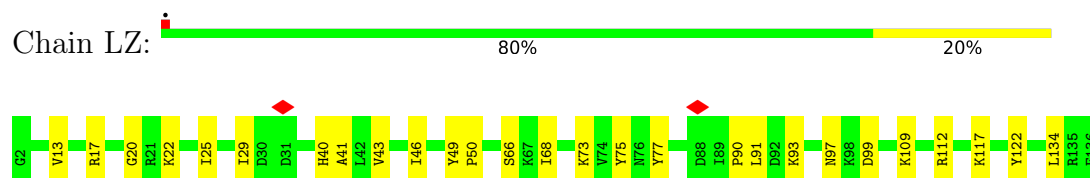
- Molecule 26: 60S ribosomal protein L23a



- Molecule 27: 60S ribosomal protein L26



- Molecule 28: 60S ribosomal protein L27



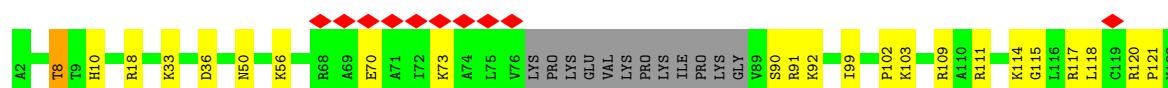
- Molecule 29: 60S ribosomal protein L27a

Chain La:  81% 19%



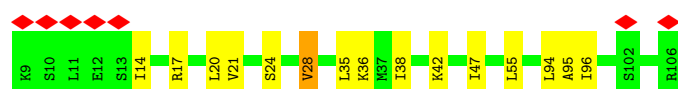
- Molecule 30: 60S ribosomal protein L29

Chain Lb:  8% 71% 18% 10%



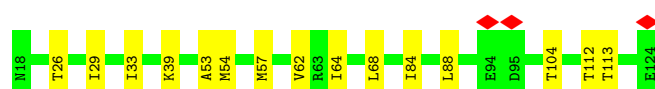
- Molecule 31: 60S ribosomal protein L30

Chain Lc:  7% 85% 14%



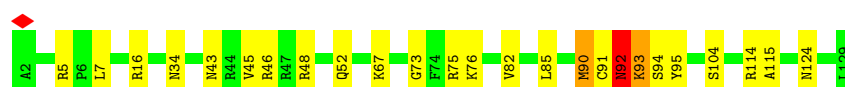
- Molecule 32: 60S ribosomal protein L31

Chain Ld:  86% 14%



- Molecule 33: 60S ribosomal protein L32

Chain Le:  80% 17%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf:  89% 10%

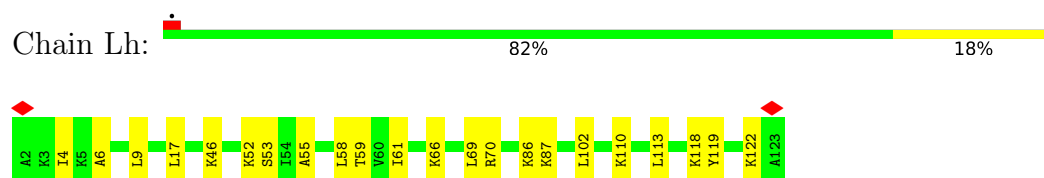


- Molecule 35: 60S ribosomal protein L34

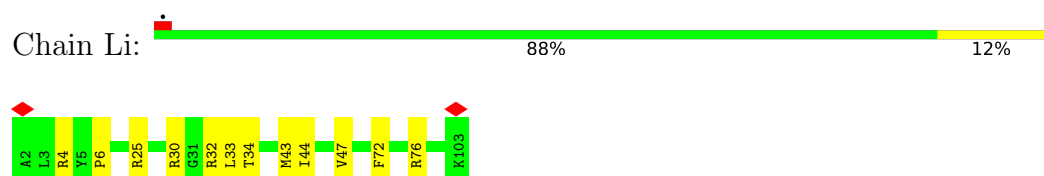
Chain Lg:  84% 16%



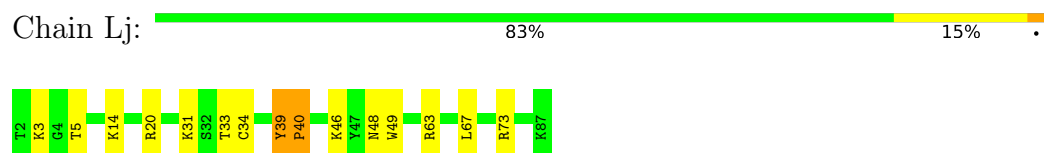
• Molecule 36: 60S ribosomal protein L35



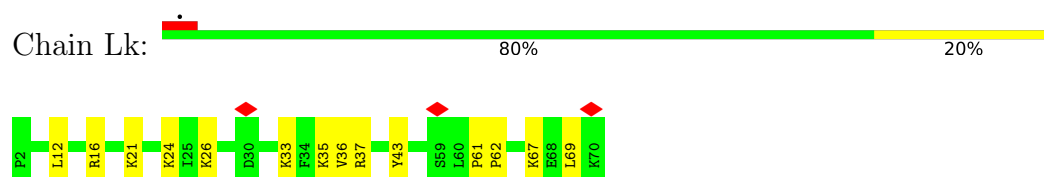
• Molecule 37: 60S ribosomal protein L36



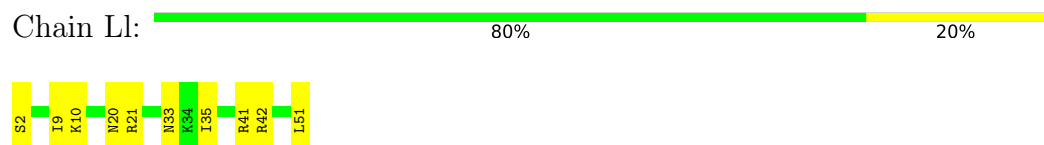
• Molecule 38: 60S ribosomal protein L37



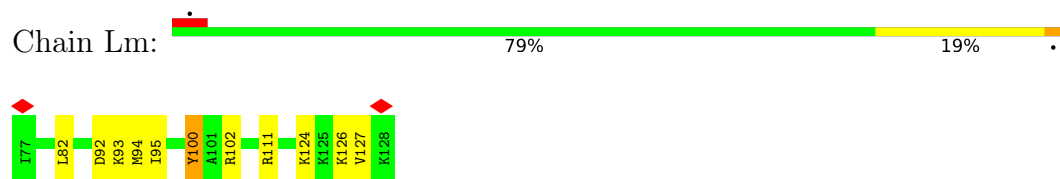
• Molecule 39: 60S ribosomal protein L38



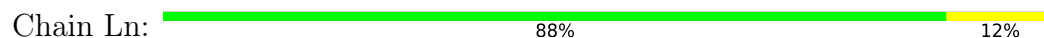
• Molecule 40: 60S ribosomal protein L39



• Molecule 41: Ubiquitin-60S ribosomal protein L40

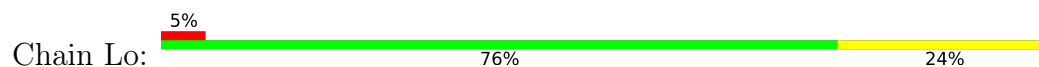


• Molecule 42: 60S ribosomal protein L41

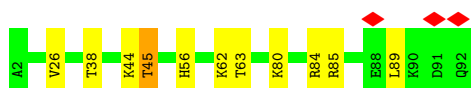




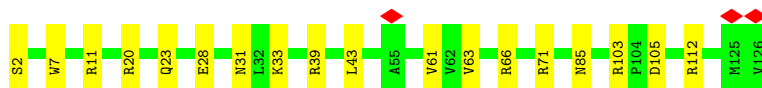
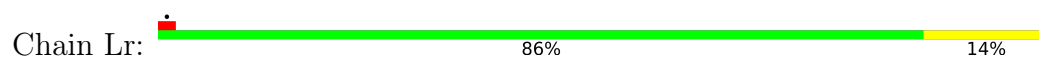
- Molecule 43: 60S ribosomal protein L36a



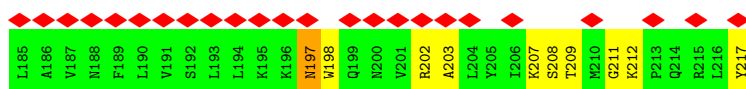
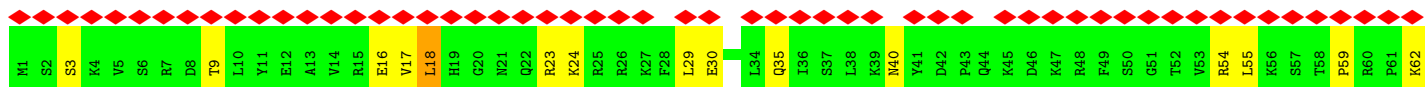
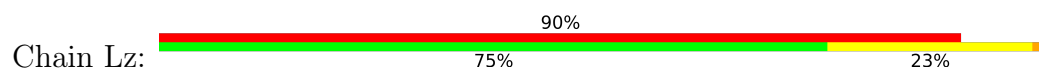
- Molecule 44: 60S ribosomal protein L37a



- Molecule 45: 60S ribosomal protein L28



- Molecule 46: 60S ribosomal protein L10a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	302737	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.604	Depositor
Minimum map value	-0.200	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	487.8, 487.8, 487.8	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OCW, 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	L5	0.33	0/89592	0.47	4/139681 (0.0%)
2	L7	0.31	0/2861	0.41	0/4459
3	L8	0.32	0/3701	0.45	0/5766
4	LA	0.37	0/1936	0.68	2/2596 (0.1%)
5	LB	0.36	0/3270	0.67	0/4377
6	LC	0.37	0/2981	0.71	3/4002 (0.1%)
7	LD	0.30	0/2428	0.63	0/3252
8	LE	0.34	0/1942	0.74	1/2606 (0.0%)
9	LF	0.36	0/1905	0.66	0/2539
10	LG	0.35	0/1960	0.68	0/2637
11	LH	0.37	0/1537	0.69	0/2066
12	LI	0.33	0/1673	0.63	0/2233
13	LJ	0.35	0/1433	0.85	1/1915 (0.1%)
14	LL	0.35	0/1732	0.67	0/2315
15	LM	0.32	0/1161	0.69	2/1554 (0.1%)
16	LN	0.36	0/1746	0.68	0/2338
17	LO	0.34	0/1682	0.56	0/2250
18	LP	0.36	0/1268	0.62	0/1701
19	LQ	0.34	0/1537	0.65	0/2052
20	LR	0.35	0/1450	0.65	2/1935 (0.1%)
21	LS	0.34	0/1493	0.59	0/2003
22	LT	0.37	0/1326	0.70	0/1770
23	LU	0.34	0/823	0.76	0/1104
24	LV	0.33	0/993	0.64	0/1332
25	LW	0.34	0/846	0.62	0/1146
26	LX	0.34	0/1002	0.64	0/1345
27	LY	0.34	0/1132	0.66	0/1504
28	LZ	0.33	0/1130	0.71	0/1507
29	La	0.35	0/1191	0.61	0/1591
30	Lb	0.29	0/889	0.70	0/1175
31	Lc	0.31	0/774	0.68	0/1038
32	Ld	0.34	0/903	0.66	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
33	Le	0.39	0/1071	0.71	1/1429 (0.1%)
34	Lf	0.37	0/895	0.63	0/1198
35	Lg	0.33	0/916	0.61	0/1220
36	Lh	0.29	0/1023	0.62	0/1351
37	Li	0.30	0/843	0.59	0/1115
38	Lj	0.37	0/720	0.71	0/952
39	Lk	0.31	0/575	0.62	0/761
40	Ll	0.35	0/454	0.67	0/599
41	Lm	0.34	0/435	0.72	0/575
42	Ln	0.27	0/231	0.74	1/294 (0.3%)
43	Lo	0.31	0/876	0.58	0/1156
44	Lp	0.34	0/718	0.60	0/953
45	Lr	0.33	0/1017	0.66	0/1364
46	Lz	0.36	0/1766	0.78	1/2367 (0.0%)
All	All	0.33	0/151837	0.54	18/224339 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	LA	0	2
5	LB	0	3
8	LE	0	1
11	LH	0	2
12	LI	0	1
13	LJ	0	1
14	LL	0	1
15	LM	0	2
17	LO	0	1
21	LS	0	1
22	LT	0	1
34	Lf	0	2
36	Lh	0	1
38	Lj	0	1
45	Lr	0	1
46	Lz	0	1
All	All	0	22

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	LM	87	ALA	CA-C-N	6.84	134.62	121.54
15	LM	87	ALA	C-N-CA	6.84	134.62	121.54
6	LC	2	ALA	CA-C-N	6.66	133.68	121.70
6	LC	2	ALA	C-N-CA	6.66	133.68	121.70
6	LC	277	TYR	N-CA-C	6.64	119.76	109.07

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	110	GLY	Peptide
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	2	SER	Peptide
5	LB	258	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	L5	80136	0	40377	490	0
2	L7	2561	0	1295	7	0
3	L8	3314	0	1683	16	0
4	LA	1898	0	1993	24	0
5	LB	3202	0	3343	50	0
6	LC	2927	0	3104	41	0
7	LD	2382	0	2410	24	0
8	LE	1904	0	2055	34	0
9	LF	1870	0	1996	25	0
10	LG	1927	0	2074	28	0
11	LH	1518	0	1601	22	0
12	LI	1634	0	1670	35	0
13	LJ	1410	0	1441	18	0
14	LL	1701	0	1818	25	0
15	LM	1138	0	1204	15	0
16	LN	1701	0	1749	16	0
17	LO	1650	0	1794	15	0
18	LP	1242	0	1269	15	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	LQ	1513	0	1628	12	0
20	LR	1434	0	1459	12	0
21	LS	1453	0	1490	24	0
22	LT	1298	0	1366	24	0
23	LU	809	0	833	37	0
24	LV	979	0	1039	10	0
25	LW	833	0	702	4	0
26	LX	985	0	1066	13	0
27	LY	1115	0	1205	14	0
28	LZ	1107	0	1182	16	0
29	La	1162	0	1213	22	0
30	Lb	876	0	948	18	0
31	Lc	764	0	804	9	0
32	Ld	888	0	930	11	0
33	Le	1053	0	1147	20	0
34	Lf	876	0	912	6	0
35	Lg	906	0	1002	13	0
36	Lh	1015	0	1148	19	0
37	Li	832	0	917	8	0
38	Lj	705	0	737	15	0
39	Lk	569	0	637	8	0
40	Ll	444	0	483	9	0
41	Lm	429	0	465	8	0
42	Ln	230	0	276	1	0
43	Lo	862	0	931	19	0
44	Lp	708	0	756	11	0
45	Lr	1002	0	1068	15	0
46	Lz	1738	0	1845	47	0
47	L5	214	0	0	0	0
47	L7	3	0	0	0	0
47	L8	4	0	0	0	0
47	LA	1	0	0	0	0
47	LI	1	0	0	0	0
47	LP	1	0	0	0	0
47	LT	1	0	0	0	0
47	LV	1	0	0	0	0
47	Le	1	0	0	0	0
47	Lg	1	0	0	0	0
47	Lj	1	0	0	0	0
48	L5	35	22	0	3	0
49	Lg	1	0	0	0	0
49	Lj	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	Lm	1	0	0	0	0
49	Lo	1	0	0	0	0
49	Lp	1	0	0	0	0
All	All	140969	22	101065	1080	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 1080 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)
46:Lz:68:LEU:HD12	46:Lz:90:LEU:HD21	1.26	1.11
1:L5:1176:C:H42	1:L5:1184:A:N6	1.55	1.04
1:L5:1176:C:N4	1:L5:1184:A:H61	1.55	1.04
23:LU:103:VAL:HG21	23:LU:113:ARG:HE	1.20	1.04
31:Lc:20:LEU:O	31:Lc:24:SER:HB3	1.57	1.04

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	LA	246/248 (99%)	221 (90%)	24 (10%)	1 (0%)	30 60
5	LB	395/397 (100%)	366 (93%)	27 (7%)	2 (0%)	24 55
6	LC	366/368 (100%)	336 (92%)	30 (8%)	0	100 100
7	LD	291/293 (99%)	275 (94%)	16 (6%)	0	100 100
8	LE	232/247 (94%)	208 (90%)	23 (10%)	1 (0%)	30 60
9	LF	223/225 (99%)	215 (96%)	8 (4%)	0	100 100
10	LG	239/241 (99%)	218 (91%)	21 (9%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	LH	188/190 (99%)	168 (89%)	20 (11%)	0	100	100
12	LI	198/213 (93%)	184 (93%)	14 (7%)	0	100	100
13	LJ	174/176 (99%)	155 (89%)	18 (10%)	1 (1%)	21	51
14	LL	208/210 (99%)	192 (92%)	16 (8%)	0	100	100
15	LM	137/139 (99%)	127 (93%)	9 (7%)	1 (1%)	18	47
16	LN	201/203 (99%)	189 (94%)	10 (5%)	2 (1%)	12	38
17	LO	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
18	LP	151/153 (99%)	140 (93%)	10 (7%)	1 (1%)	18	47
19	LQ	185/187 (99%)	174 (94%)	11 (6%)	0	100	100
20	LR	185/187 (99%)	180 (97%)	5 (3%)	0	100	100
21	LS	173/175 (99%)	162 (94%)	11 (6%)	0	100	100
22	LT	157/159 (99%)	146 (93%)	10 (6%)	1 (1%)	21	51
23	LU	97/99 (98%)	82 (84%)	13 (13%)	2 (2%)	5	20
24	LV	129/131 (98%)	120 (93%)	9 (7%)	0	100	100
25	LW	122/124 (98%)	117 (96%)	5 (4%)	0	100	100
26	LX	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
27	LY	132/134 (98%)	124 (94%)	8 (6%)	0	100	100
28	LZ	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
29	La	145/147 (99%)	135 (93%)	9 (6%)	1 (1%)	18	47
30	Lb	105/121 (87%)	98 (93%)	7 (7%)	0	100	100
31	Lc	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
32	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
33	Le	126/128 (98%)	118 (94%)	6 (5%)	2 (2%)	7	27
34	Lf	107/109 (98%)	98 (92%)	7 (6%)	2 (2%)	6	22
35	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
36	Lh	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
38	Lj	84/86 (98%)	77 (92%)	6 (7%)	1 (1%)	10	34
39	Lk	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
40	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
41	Lm	50/52 (96%)	49 (98%)	0	1 (2%)	6	21

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	Ln	22/24 (92%)	22 (100%)	0	0	100	100
43	Lo	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
44	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
45	Lr	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
46	Lz	215/217 (99%)	171 (80%)	43 (20%)	1 (0%)	24	55
All	All	6696/6822 (98%)	6206 (93%)	470 (7%)	20 (0%)	37	66

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
23	LU	116	GLN
33	Le	73	GLY
33	Le	92	ASN
34	Lf	80	ASN

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	LA	190/190 (100%)	184 (97%)	6 (3%)	34	70
5	LB	345/345 (100%)	345 (100%)	0	100	100
6	LC	306/306 (100%)	305 (100%)	1 (0%)	86	95
7	LD	246/247 (100%)	244 (99%)	2 (1%)	73	90
8	LE	209/220 (95%)	204 (98%)	5 (2%)	43	77
9	LF	194/194 (100%)	193 (100%)	1 (0%)	81	93
10	LG	203/205 (99%)	201 (99%)	2 (1%)	68	88
11	LH	169/169 (100%)	168 (99%)	1 (1%)	78	92
12	LI	172/180 (96%)	172 (100%)	0	100	100
13	LJ	148/148 (100%)	147 (99%)	1 (1%)	76	91
14	LL	176/176 (100%)	175 (99%)	1 (1%)	78	92

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	LM	118/118 (100%)	116 (98%)	2 (2%)	53	83
16	LN	171/171 (100%)	169 (99%)	2 (1%)	63	87
17	LO	173/173 (100%)	172 (99%)	1 (1%)	78	92
18	LP	134/134 (100%)	134 (100%)	0	100	100
19	LQ	164/164 (100%)	160 (98%)	4 (2%)	43	77
20	LR	133/166 (80%)	133 (100%)	0	100	100
21	LS	156/156 (100%)	154 (99%)	2 (1%)	61	86
22	LT	139/139 (100%)	138 (99%)	1 (1%)	76	91
23	LU	89/89 (100%)	87 (98%)	2 (2%)	45	78
24	LV	101/101 (100%)	100 (99%)	1 (1%)	68	88
25	LW	56/103 (54%)	55 (98%)	1 (2%)	51	82
26	LX	108/108 (100%)	107 (99%)	1 (1%)	70	89
27	LY	124/124 (100%)	124 (100%)	0	100	100
28	LZ	117/117 (100%)	117 (100%)	0	100	100
29	La	120/120 (100%)	119 (99%)	1 (1%)	73	90
30	Lb	88/101 (87%)	87 (99%)	1 (1%)	65	87
31	Lc	83/83 (100%)	82 (99%)	1 (1%)	63	87
32	Ld	98/98 (100%)	98 (100%)	0	100	100
33	Le	114/114 (100%)	111 (97%)	3 (3%)	40	75
34	Lf	88/88 (100%)	87 (99%)	1 (1%)	65	87
35	Lg	98/98 (100%)	97 (99%)	1 (1%)	68	88
36	Lh	109/109 (100%)	109 (100%)	0	100	100
37	Li	86/86 (100%)	85 (99%)	1 (1%)	63	87
38	Lj	73/73 (100%)	73 (100%)	0	100	100
39	Lk	64/64 (100%)	64 (100%)	0	100	100
40	Ll	47/47 (100%)	47 (100%)	0	100	100
41	Lm	48/48 (100%)	47 (98%)	1 (2%)	47	79
42	Ln	23/23 (100%)	23 (100%)	0	100	100
43	Lo	93/93 (100%)	93 (100%)	0	100	100
44	Lp	74/74 (100%)	73 (99%)	1 (1%)	59	85
45	Lr	109/109 (100%)	107 (98%)	2 (2%)	51	82

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
46	Lz	194/196 (99%)	189 (97%)	5 (3%)	40 75
All	All	5750/5867 (98%)	5695 (99%)	55 (1%)	65 88

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	LQ	83	VAL
25	LW	28	VAL
46	Lz	197	ASN
45	Lr	63	VAL
21	LS	85	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 104 such sidechains are listed below:

Mol	Chain	Res	Type
19	LQ	162	HIS
29	La	39	HIS
46	Lz	71	GLN
21	LS	122	HIS
25	LW	17	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3705/5069 (73%)	964 (26%)	19 (0%)
2	L7	119/120 (99%)	15 (12%)	0
3	L8	155/156 (99%)	33 (21%)	0
All	All	3979/5345 (74%)	1012 (25%)	19 (0%)

5 of 1012 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	15	A
1	L5	17	A
1	L5	25	A
1	L5	26	C

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	3614	G
1	L5	4378	A
1	L5	4913	G
1	L5	4045	G
1	L5	2019	C

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 235 ligands modelled in this entry, 234 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
48	OCW	L5	5315	47	35,38,38	1.85	12 (34%)	44,61,61	2.57	10 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
48	OCW	L5	5315	47	-	5/13/62/62	0/4/4/4

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	L5	5315	OCW	C17-C18	-4.32	1.34	1.41
48	L5	5315	OCW	O10-C33	2.80	1.39	1.33
48	L5	5315	OCW	O04-C20	2.67	1.40	1.35
48	L5	5315	OCW	O05-C15	-2.65	1.17	1.21
48	L5	5315	OCW	O06-C16	-2.50	1.18	1.21

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	L5	5315	OCW	O04-C20-C14	10.50	118.75	110.07
48	L5	5315	OCW	O04-C20-C21	-8.38	118.55	126.02
48	L5	5315	OCW	C19-C21-C20	-4.17	116.20	120.97
48	L5	5315	OCW	C31-C26-C29	-3.30	117.05	121.61
48	L5	5315	OCW	O09-C30-C28	-3.03	121.32	125.16

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	L5	5315	OCW	C14-C20-O04-C32
48	L5	5315	OCW	C29-C33-O10-C35
48	L5	5315	OCW	O11-C33-O10-C35
48	L5	5315	OCW	C19-C13-O01-C27
48	L5	5315	OCW	C12-C13-O01-C27

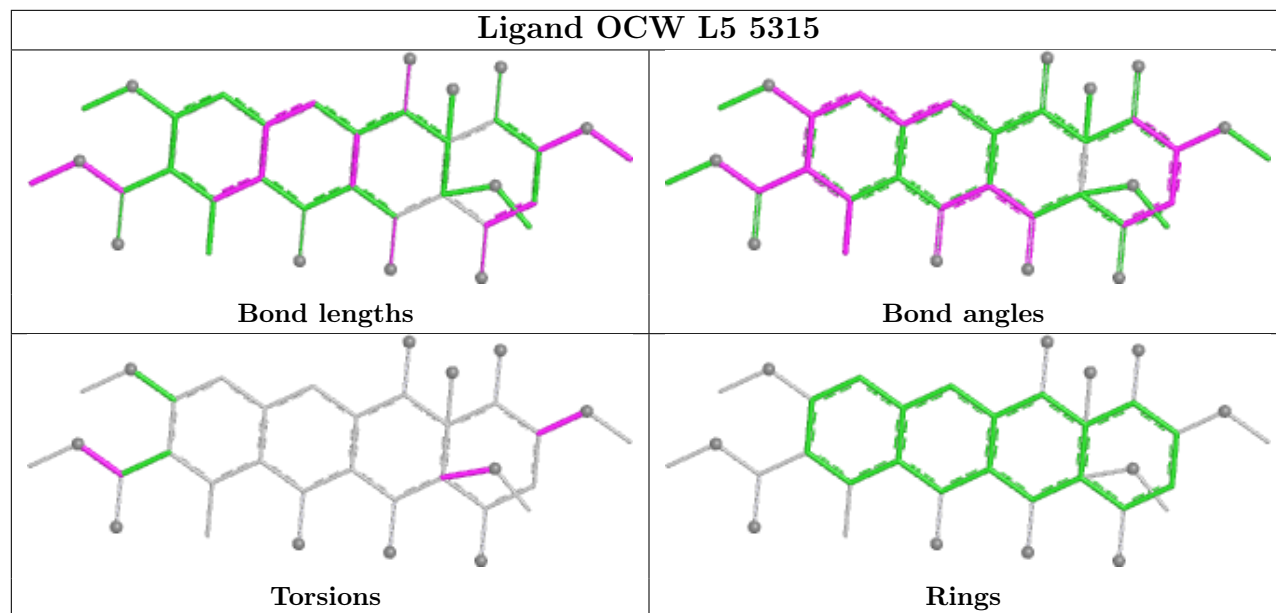
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
48	L5	5315	OCW	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

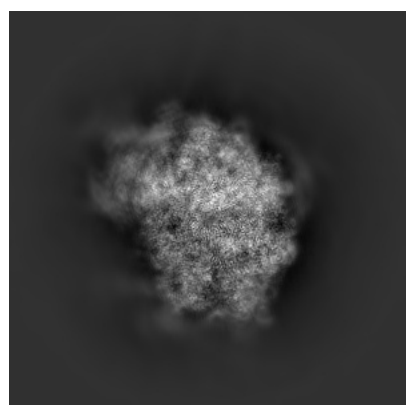
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10709. These allow visual inspection of the internal detail of the map and identification of artifacts.

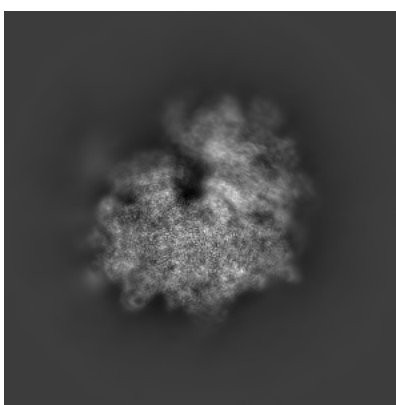
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

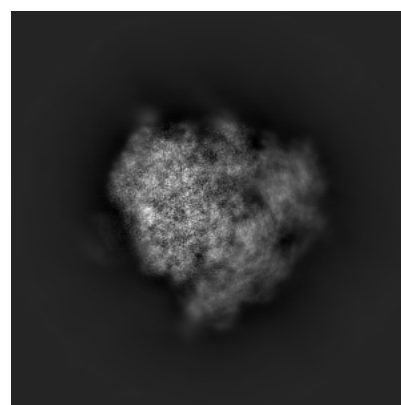
6.1.1 Primary map



X



Y

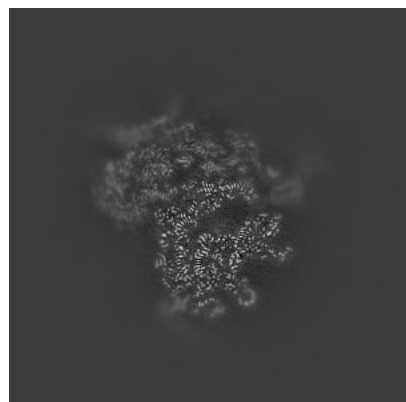


Z

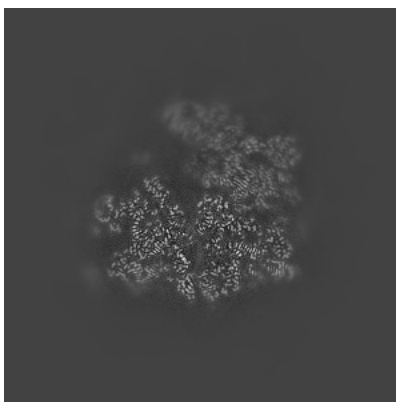
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

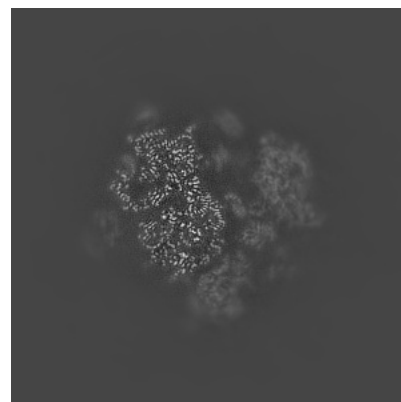
6.2.1 Primary map



X Index: 225



Y Index: 225

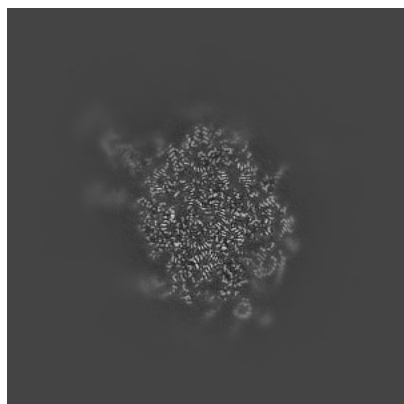


Z Index: 225

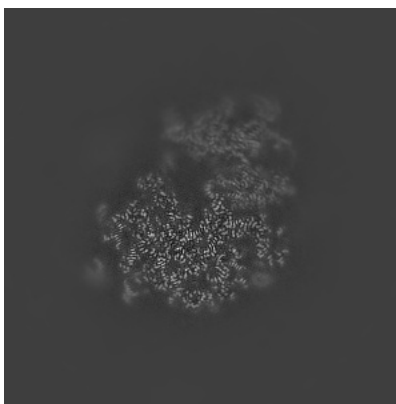
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

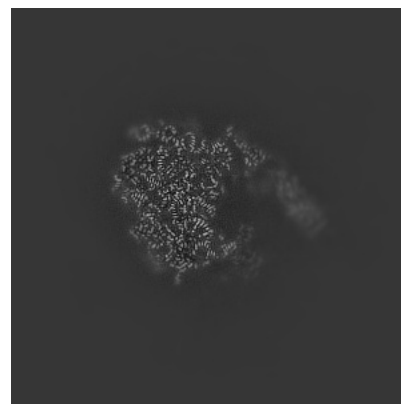
6.3.1 Primary map



X Index: 198



Y Index: 240

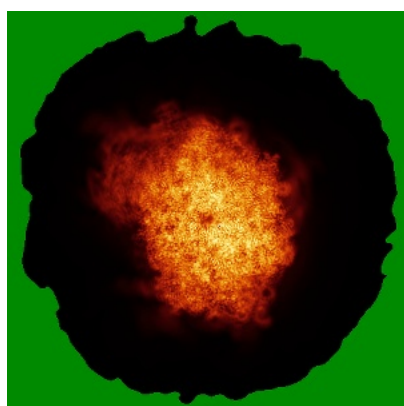


Z Index: 193

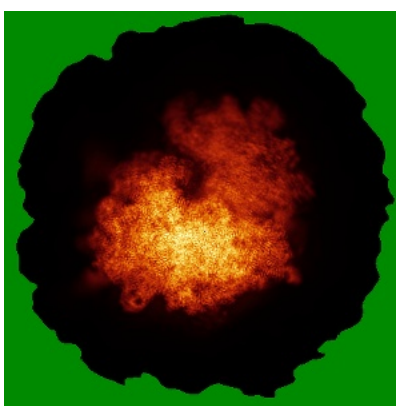
The images above show the largest variance slices of the map in three orthogonal directions.

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

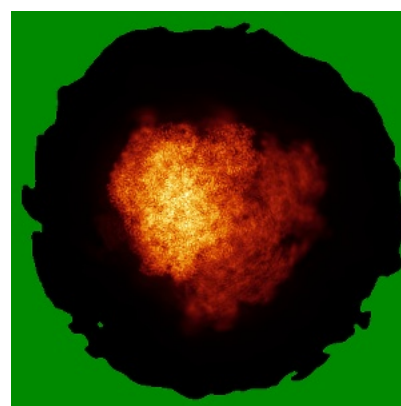
6.4.1 Primary map



X



Y

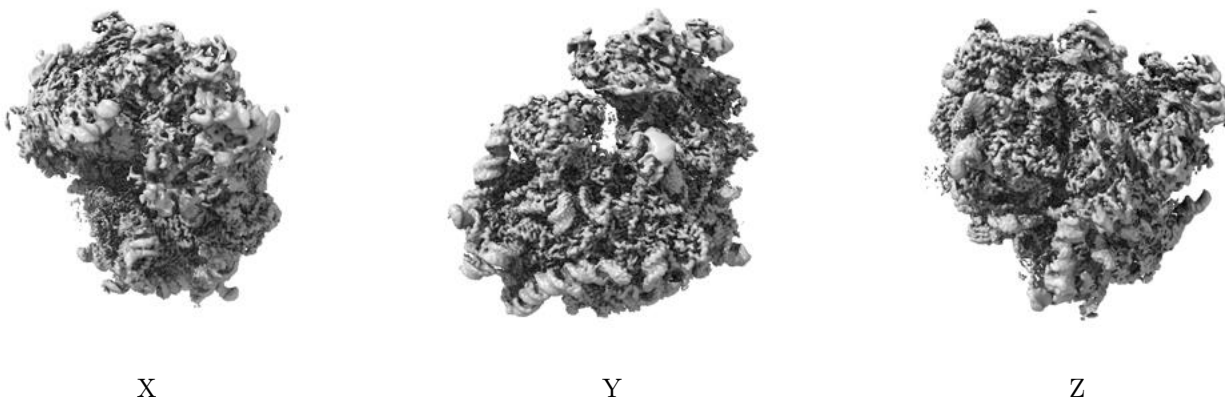


Z

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

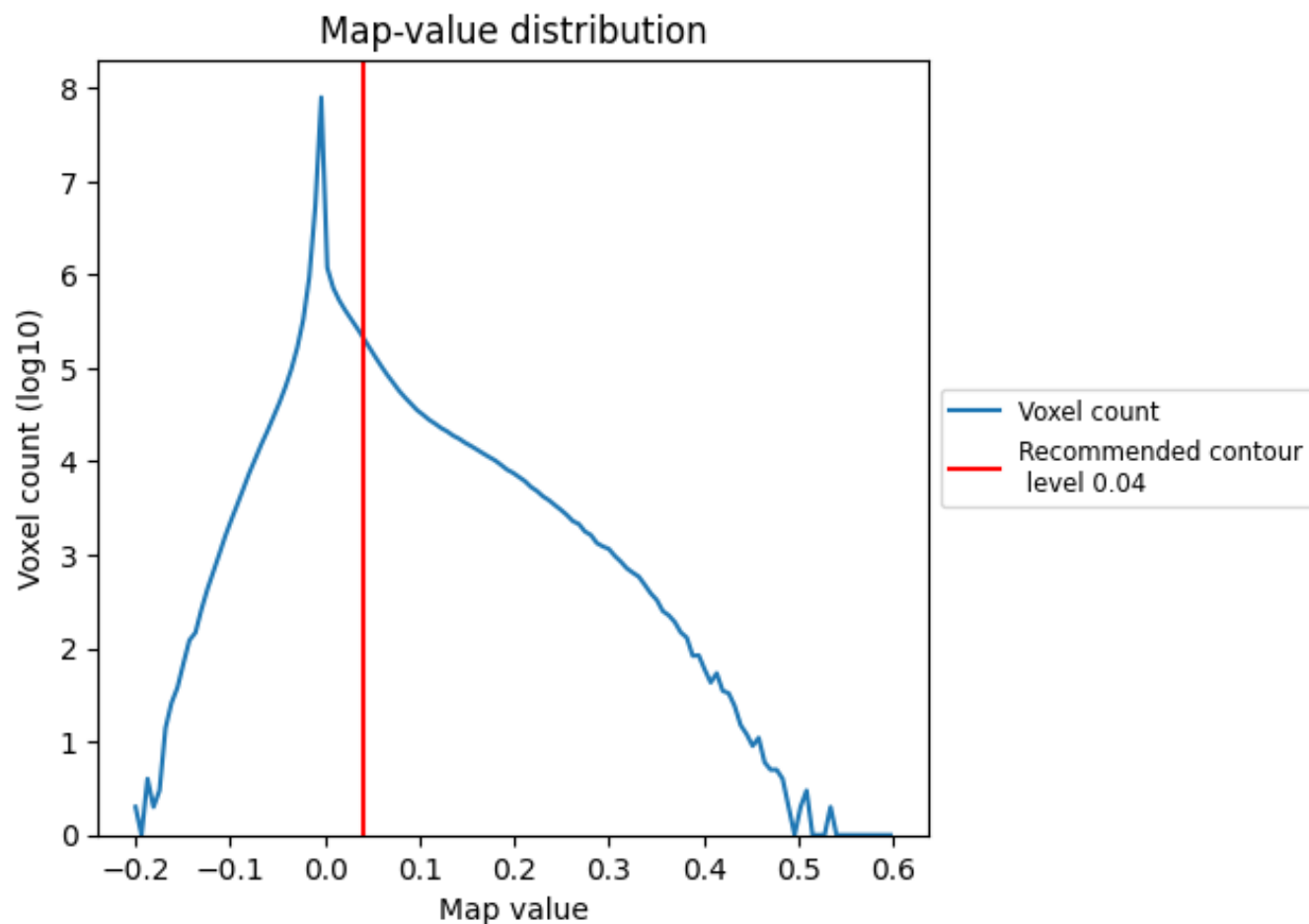
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

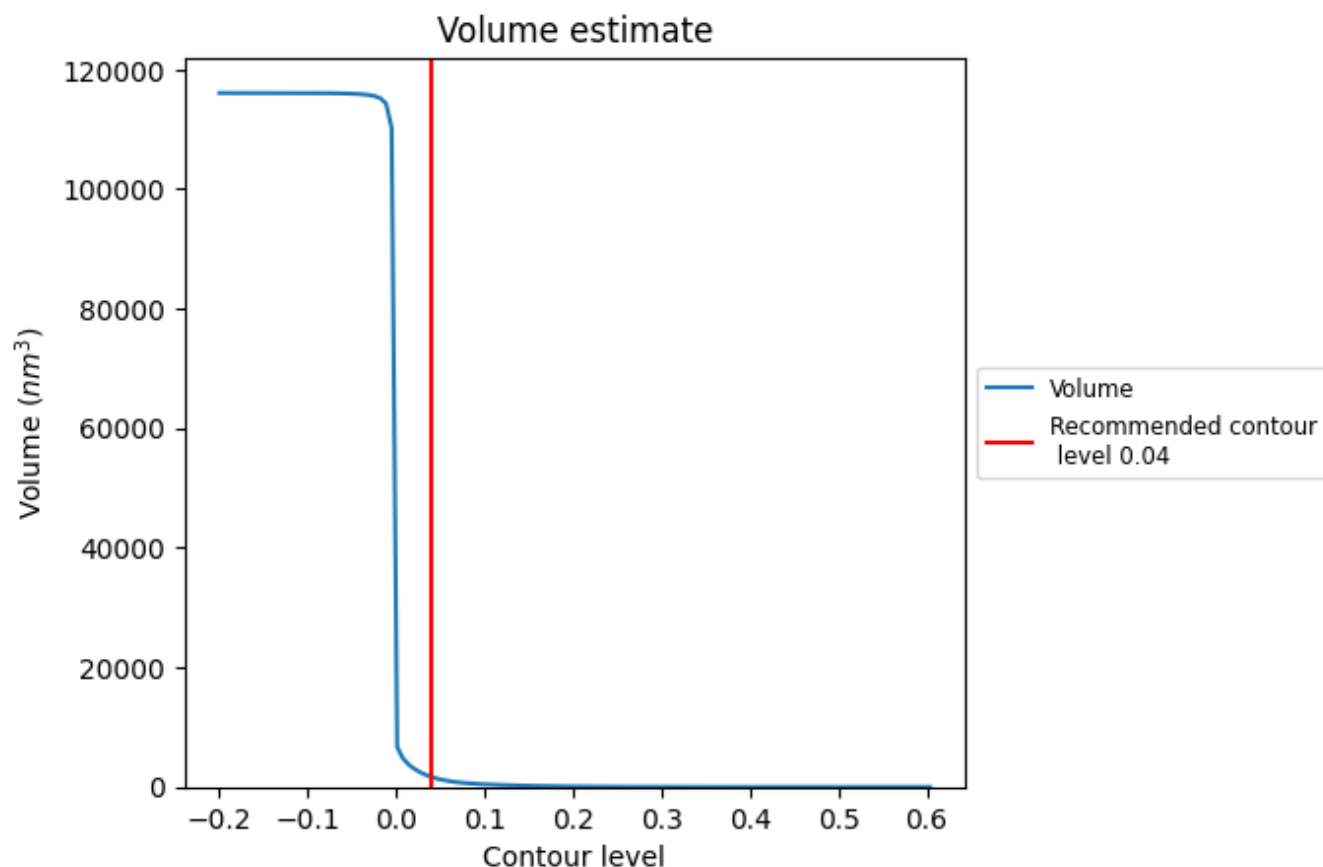
This section contains the results of statistical analysis of the map.

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.

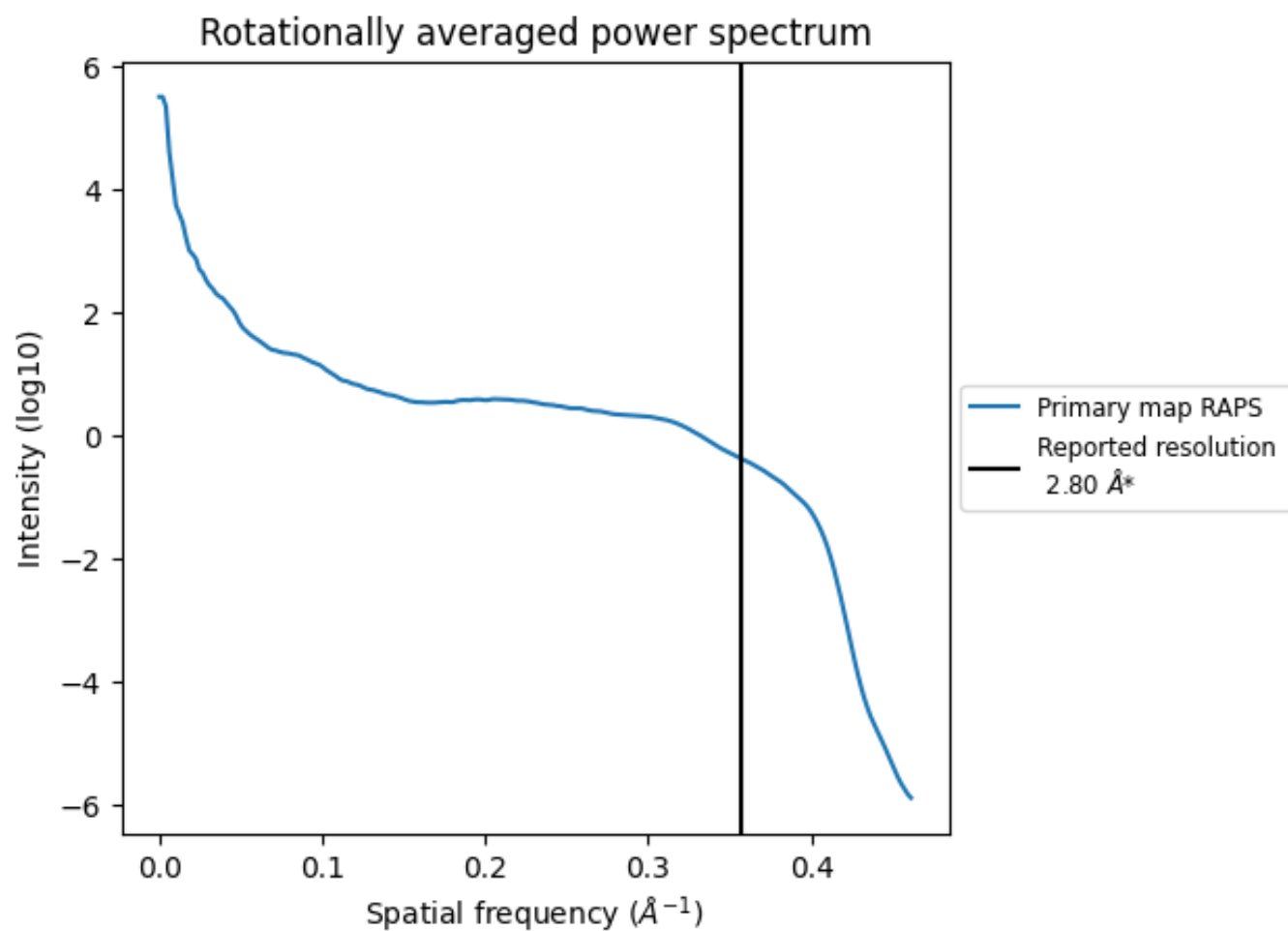
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1664 nm^3 ; this corresponds to an approximate mass of 1503 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 ⓘ

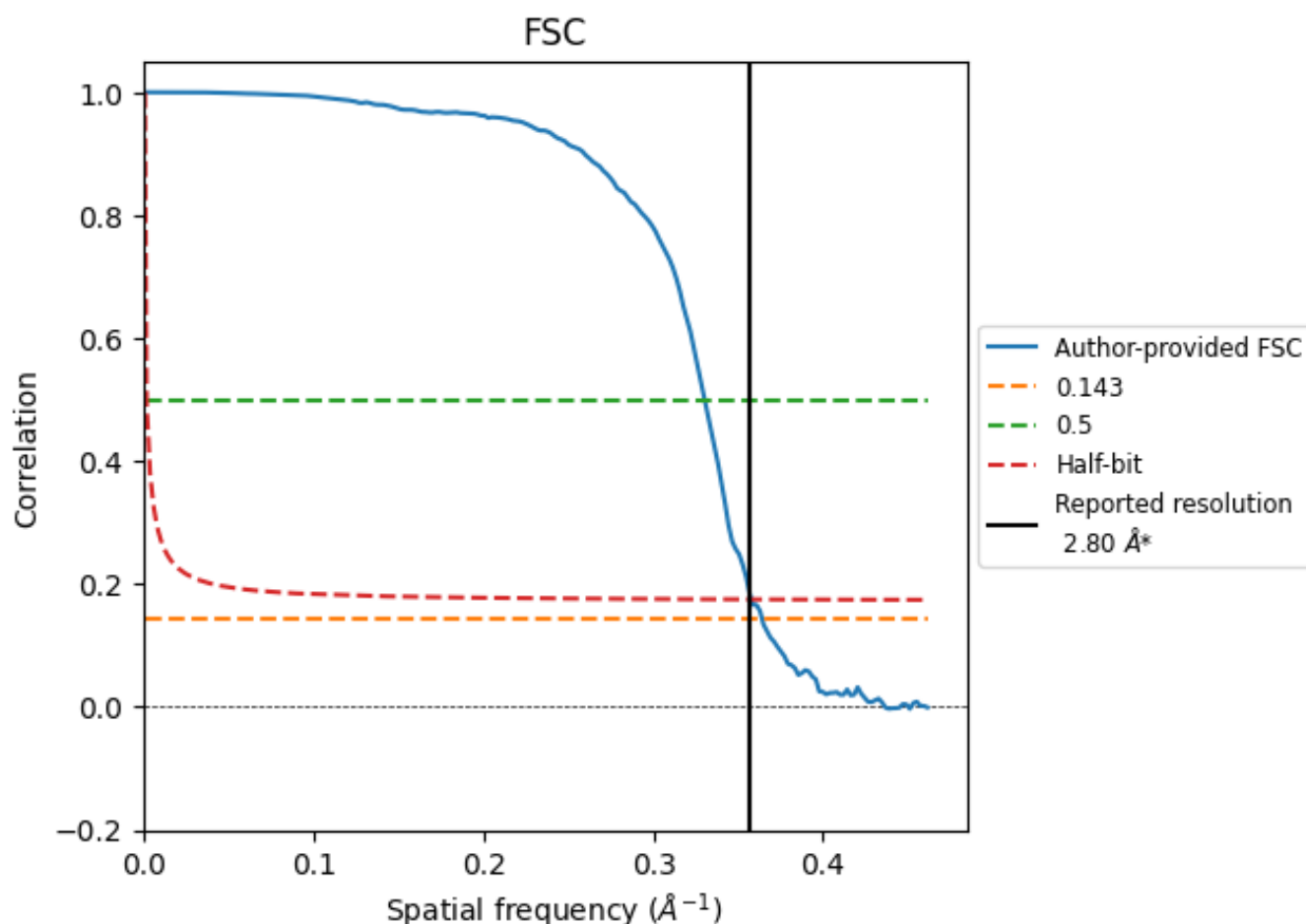


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

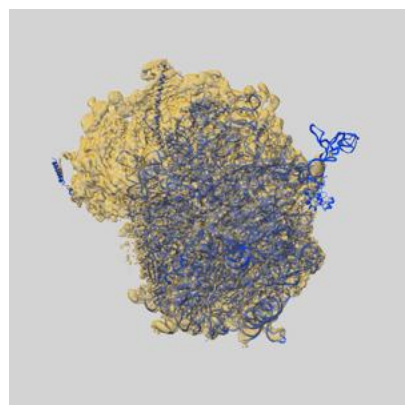
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.75	3.03	2.79
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

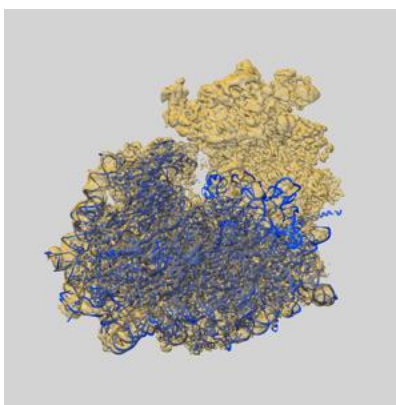
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10709 and PDB model 6Y6X. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

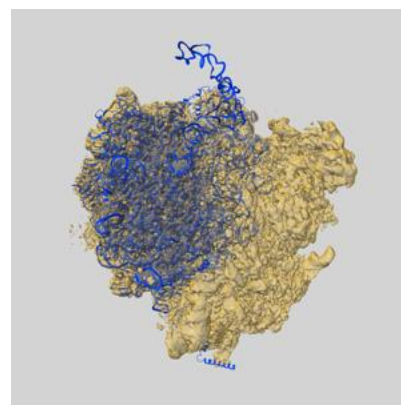
9.1 Map-model overlay [i](#)



X



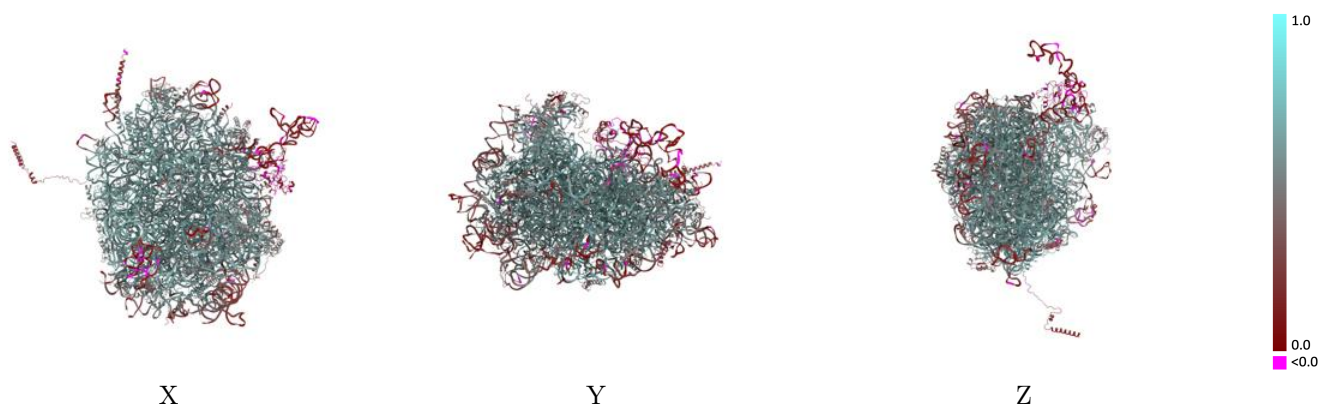
Y



Z

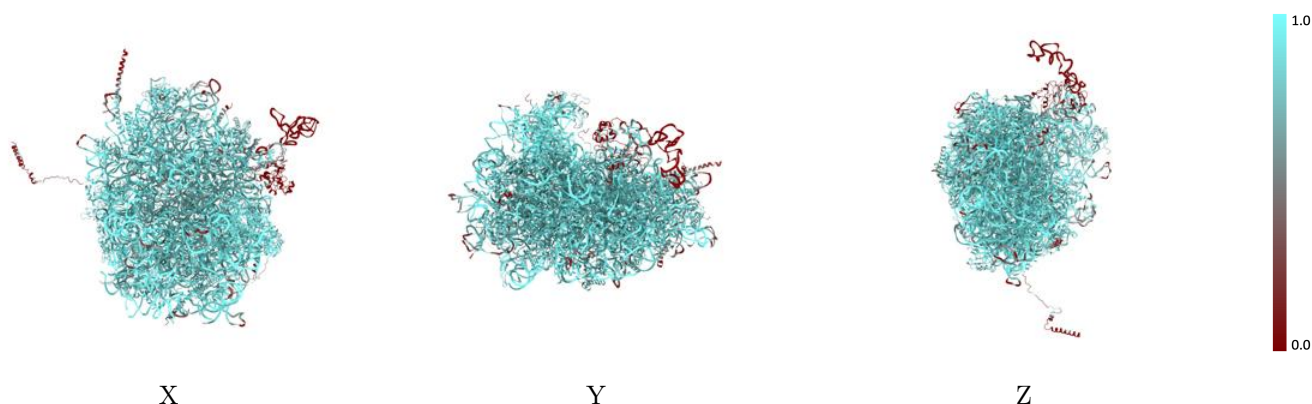
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



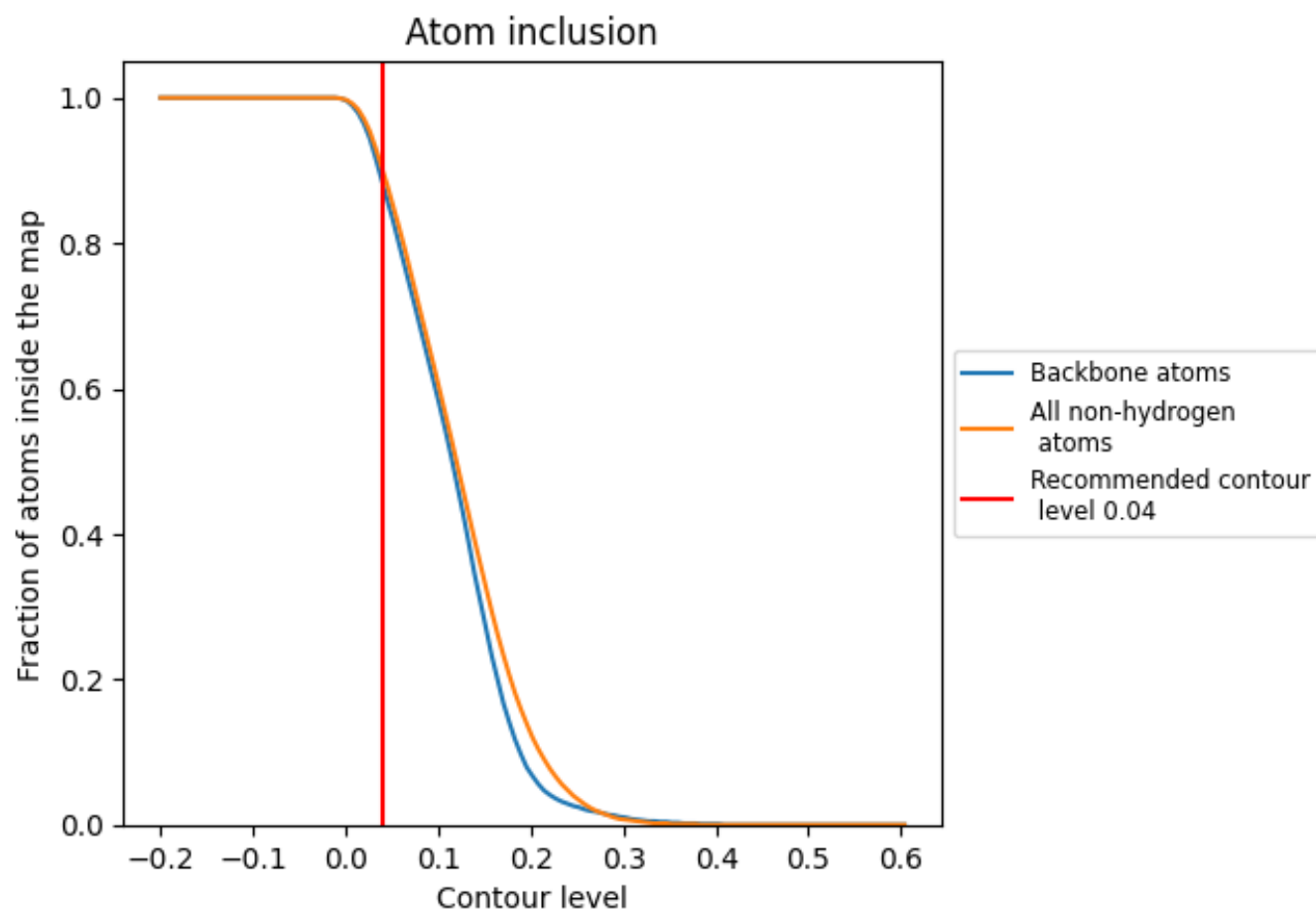
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 90% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9010	 0.5460
L5	 0.9290	 0.5420
L7	 0.9950	 0.6130
L8	 0.9590	 0.5830
LA	 0.9370	 0.6240
LB	 0.9150	 0.5970
LC	 0.9010	 0.5750
LD	 0.8980	 0.5270
LE	 0.8070	 0.4820
LF	 0.9190	 0.6020
LG	 0.7920	 0.4790
LH	 0.8980	 0.5650
LI	 0.9030	 0.5830
LJ	 0.7800	 0.4410
LL	 0.8610	 0.5380
LM	 0.9080	 0.5560
LN	 0.9540	 0.6290
LO	 0.9250	 0.6100
LP	 0.9240	 0.6070
LQ	 0.9320	 0.6100
LR	 0.8440	 0.5400
LS	 0.9470	 0.6150
LT	 0.8960	 0.5650
LU	 0.8240	 0.4590
LV	 0.9110	 0.6080
LW	 0.6220	 0.4360
LX	 0.8690	 0.5510
LY	 0.8780	 0.5440
LZ	 0.8540	 0.4840
La	 0.9440	 0.6160
Lb	 0.7900	 0.4940
Lc	 0.8390	 0.5160
Ld	 0.8890	 0.5720
Le	 0.9240	 0.6110
Lf	 0.9360	 0.6290



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Lg	 0.8840	 0.5830
Lh	 0.8560	 0.5260
Li	 0.8580	 0.5420
Lj	 0.9480	 0.6220
Lk	 0.7770	 0.4580
Ll	 0.9170	 0.5900
Lm	 0.8990	 0.5780
Ln	 0.8520	 0.5420
Lo	 0.8580	 0.5800
Lp	 0.8550	 0.5980
Lr	 0.9180	 0.5710
Lz	 0.0890	 0.0730