



wwPDB EM Validation Summary Report ⓘ

May 5, 2025 – 11:08 am BST

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:

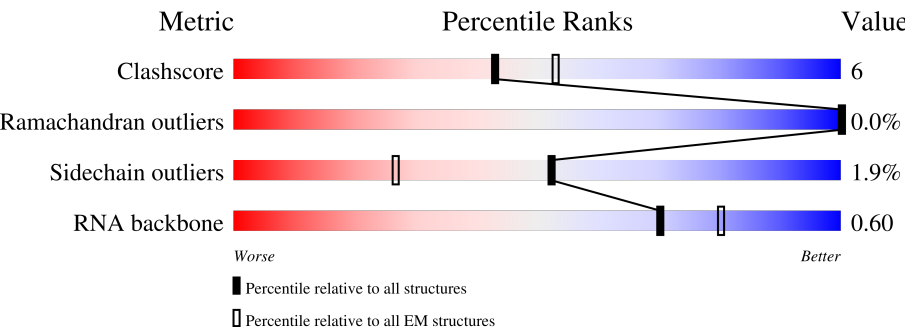
EMDB validation analysis : 0.0.1.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

1 Overall quality at a glance

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

The reported resolution of this entry is 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.









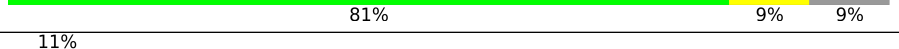
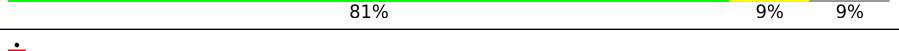
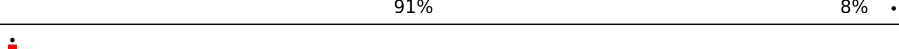
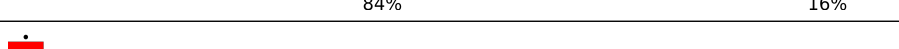
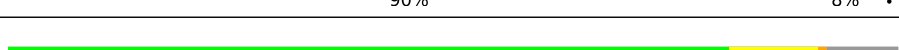

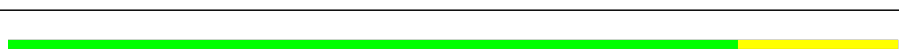

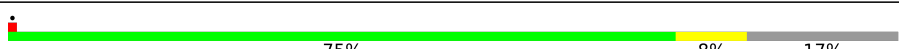





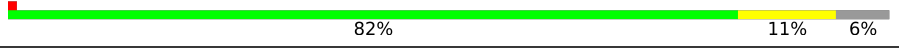




Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	
2	7	121	
3	8	157	
4	B	506	
5	C	314	
6	D	85	
7	E	794	



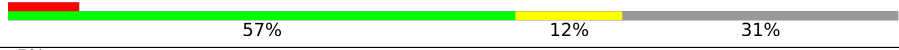



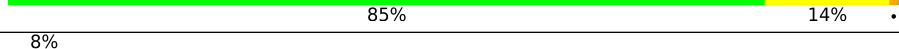
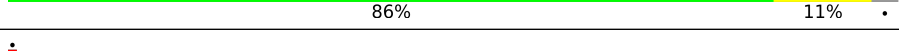
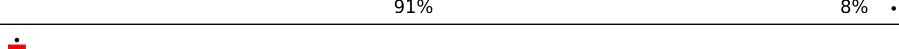
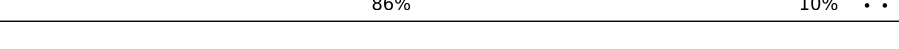
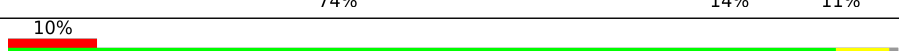
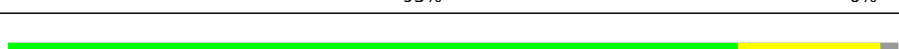

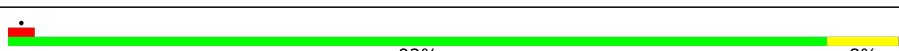
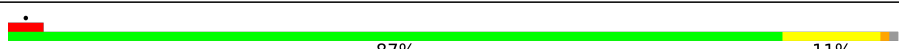





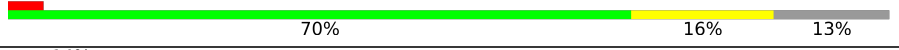
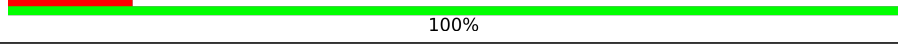

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Mol	Chain	Length	Quality of chain
8	F	1766	
9	G	76	
10	LB	403	
11	LC	427	
12	LD	297	
13	LE	288	
14	LF	248	
15	LG	266	
16	LH	192	
17	LI	214	
18	LJ	178	
19	LL	211	
20	LM	215	
21	LN	204	
22	LO	203	
23	LP	184	
24	LQ	188	
25	LR	196	
26	LS	176	
27	LT	160	
28	LU	128	
29	LV	140	
30	LW	157	
31	LX	156	
32	LY	145	

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Mol	Chain	Length	Quality of chain
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	
54	t	165	
55	A	7	

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	

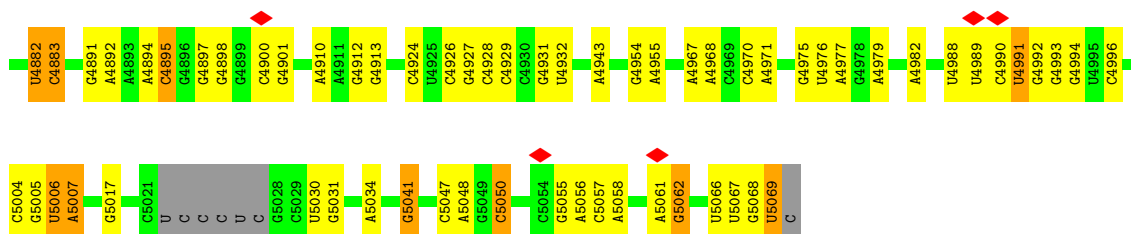
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

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





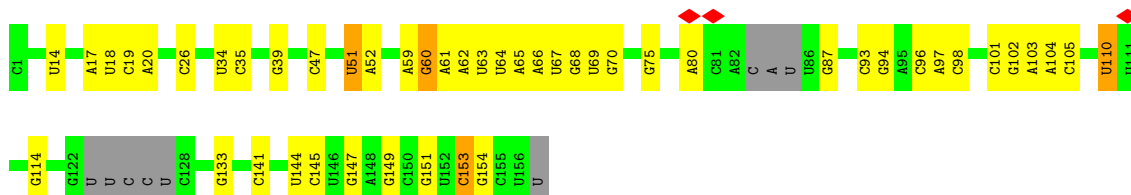
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C	A4655	A4656	G4550	A4449	U4352	G4254	A4157	G4076	G	G3933	A3624	A3647
C	C4748	C4749	C4560	G4454	U4353	A4255	C4162	C4080	G	G3934	A3728	A3648
C	G4750	G4751	U4563	U4457	U4354	C4258	U4163	C4081	C	C3935	A3732	A3652
C	G4754	C4670	U4564	U4458	U4355	U4260	C4164	C4084	C	G3939	A3733	A3653
C	C4755	A4672	U4565	U4459	U4356	U4261	C4165	G4089	C	C3949	U3794	G3654
C	C4757	U4673	U4566	U4460	U4357	C4262	A4170	C4090	G	A3949	C3843	G3659
C	U4758	U4674	C4567	C4461	U4358	C4263	G4173	C4091	G	U3950	U3848	C3660
C	A4568	U4675	U4464	C4462	U4359	U4264	U4174	C4092	C	G3951	A3746	C3661
C	U4569	U4676	U4465	U4463	C4364	G4265	C4177	G4093	C	G3763	A3747	A3662
C	U4570	U4677	C4466	C4464	G4370	G4266	A4178	C4094	C	G3763	A3748	G3663
C	A4571	U4678	C4467	U4445	U4371	G4267	A4179	U4095	C	U3768	A3749	G3664
C	U4572	U4679	C4468	U4446	C4372	G4268	G4183	G4096	C	A	G3768	G3665
G	G4575	U4680	C4469	U4447	C4373	U4269	G4184	C4097	C	A	C3668	C3668
G	C4576	A4681	U4470	U4448	C4374	U4270	U4185	C4098	C	C	C3672	C3673
G	C4577	U4682	U4471	U4449	C4375	U4271	A4186	A4098	C	C	C3681	C3681
G	U4578	U4683	U4472	U4450	C4376	U4272	U4187	G	C	C	G3684	G3684
G	U4579	U4684	U4473	U4451	C4377	U4273	U4188	C	C	C	C3685	C3685
A	U4580	U4685	U4474	U4452	A4378	A4274	U4189	C	C	C	C3686	C3686
G	U4581	U4686	U4475	U4453	A4379	U4275	C4185	C	C	C	C3687	C3687
G	A4584	U4687	U4476	U4454	A4380	U4276	A4186	C	C	C	C3688	C3688
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C	U4589	U4692	U4481	U4459	C4385	U4281	C4191	C	C	C	C3693	C3693
C	U4590	U4693	U4482	U4460	C4386	U4282	C4192	C	C	C	C3694	C3694
C	U4591	U4694	U4483	U4461	C4387	U4283	C4193	C	C	C	C3695	C3695
C	U4592	U4695	U4484	U4462	C4388	U4284	U4194	C	C	C	C3696	C3696
C	U4593	U4696	U4485	U4463	C4389	U4285	C4195	C	C	C	C3697	C3697
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C	C4740	C4740	U4508	U4486	C4412	U4308	C4221	C	C	C	C3720	C3720
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C	C4742	C4742	U4510	U4488	C4414	U4310	C4223	C	C	C	C3722	C3722
C	C4743	C4743	U4511	U4489	C4415	U4311	C4224	C	C	C	C3723	C3723
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C	C4745	C4745	U4513	U4491	C4417	U4313	C4226	C	C	C	C3725	C3725
C	C4746	C4746	U4514	U4492	C4418	U4314	C4227	C	C	C	C3726	C3726
C	C4747	C4747	U4515	U4493	C4419	U4315	C4228	C	C	C	C3727	C3727
C	C4748	C4748	U4516	U4494	C4420	U4316	C4229	C	C	C	C3728	C3728
C	C4749	C4749	U4517	U4495	C4421	U4317	C4230	C	C	C	C3729	C3729
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C	C4771	C4771	U4539	U4517	C4443	U4339	C4252	C	C	C	C3751	C3751
C	C4772	C4772	U4540	U4518	C4444	U4340	C4253	C	C	C	C3752	C3752
C	C4773	C4773	U4541	U4519	C4445	U4341	C4254	C	C	C	C3753	C3753
C	C4774	C4774	U4542	U4520	C4446	U4342	C4255	C	C	C	C3754	C3754
C	C4775	C4775	U4543	U4521	C4447	U4343	C4256	C	C	C	C3755	C3755
C	C4776	C4776	U4544	U4522	C4448	U4344	C4257	C	C	C	C3756	C3756
C	C4777	C4777	U4545	U4523	C4449	U4345	C4258	C	C	C	C3757	C3757
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C	C4779	C4779	U4547	U4525	C4451	U4347	C4260	C	C	C	C3759	C3759
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C	C4781	C4781	U4549	U4527	C4453	U4349	C4262	C	C	C	C3761	C3761
C	C4782	C4782	U4550	U4528	C4454	U4350	C4263	C	C	C	C3762	C3762
C	C4783	C4783	U4551	U4529	C4455	U4351	C4264	C	C	C	C3763	C3763
C	C4784	C4784	U4552	U4530	C4456	U4352	C4265	C	C	C	C3764	C3764
C	C4785	C4785	U4553	U4531	C4457	U4353	C4266	C	C	C	C3765	C3765
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C	C4788	C4788	U4556	U4534	C4460	U4356	C4269	C	C	C	C3768	C3768
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C	C4793	C4793	U4561	U4539	C4465	U4361	C4274	C	C	C	C3773	C3773
C	C4794	C4794	U4562	U4540	C4466	U4362	C4275	C	C	C	C3774	C3774
C	C4795	C4795	U4563	U4541	C4467	U4363	C4276	C	C	C	C3775	C3775
C	C4796	C4796	U4564	U4542	C4468	U4364	C4277	C	C	C	C3776	C3776
C	C4797	C4797	U4565	U4543	C4469	U4365	C4278	C	C	C	C3777	C3777
C	C4798	C4798	U4566	U4544	C4470	U4366	C4279	C	C	C	C3778	C3778
C	C4799	C4799	U4567	U4545	C4471	U4367	C4280	C	C	C	C3779	C3



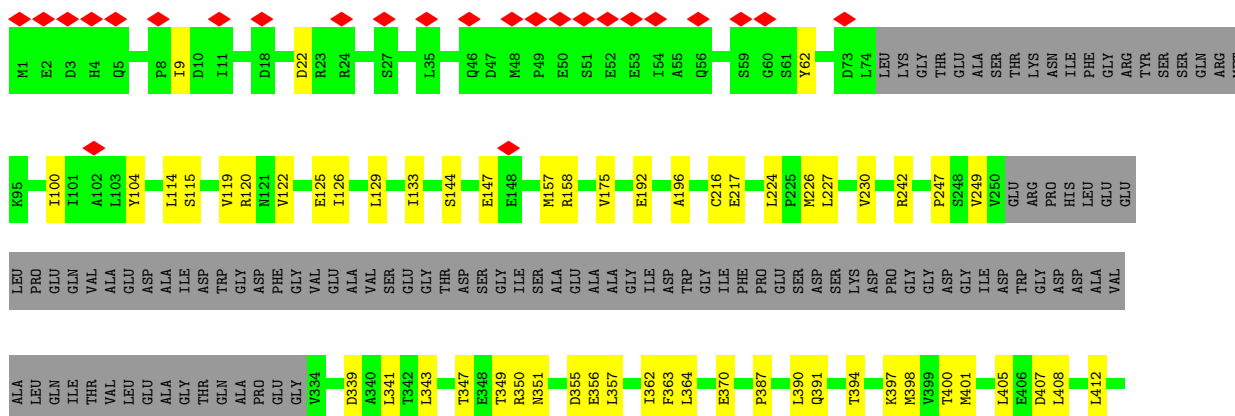
- Molecule 2: 5S rRNA



- Molecule 3: 5.8S rRNA



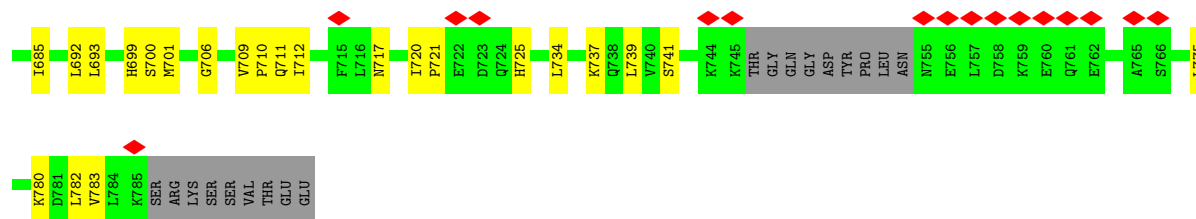
- Molecule 4: CDK5 regulatory subunit-associated protein 3



- Molecule 5: DDRGK domain-containing protein 1

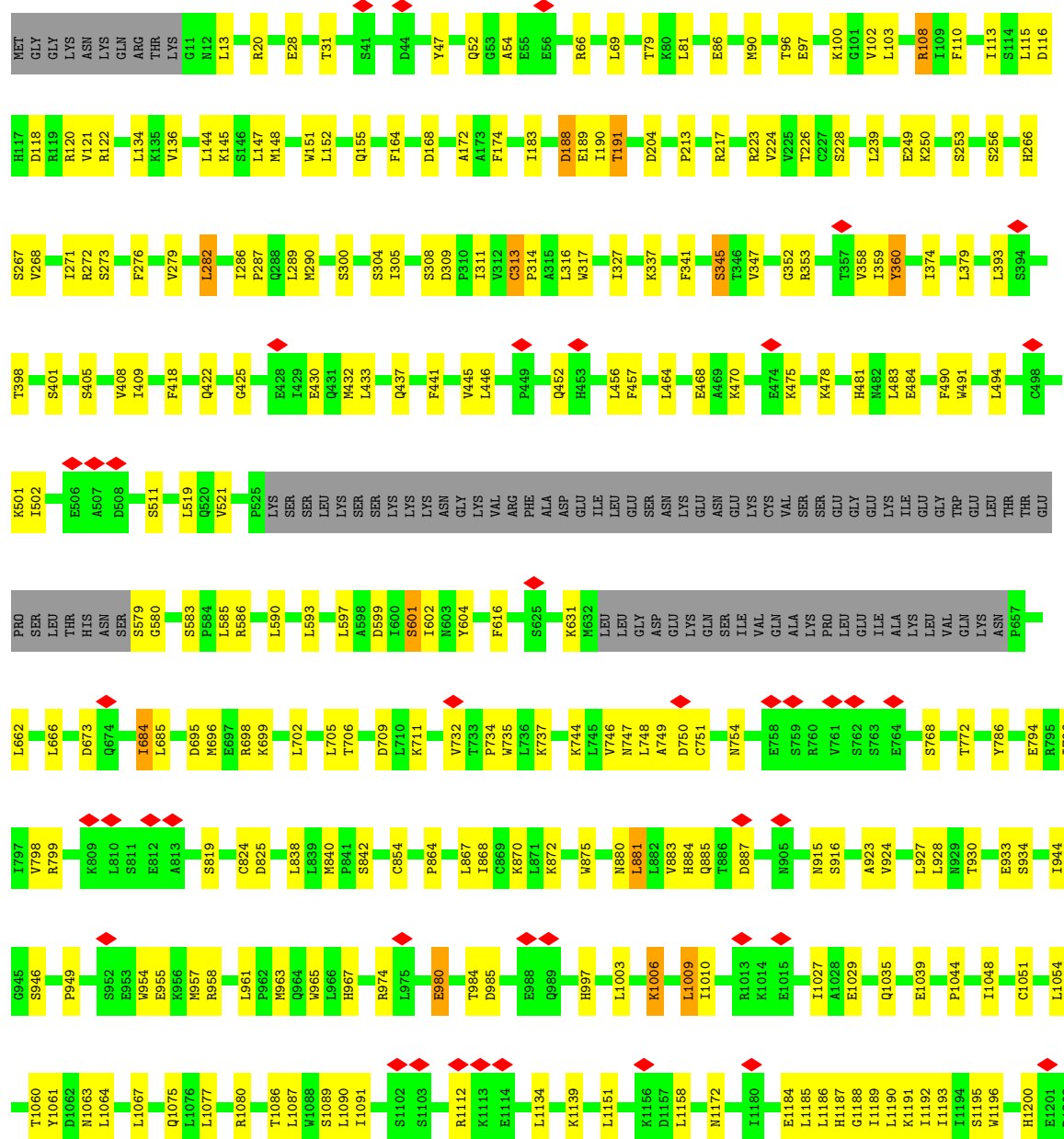


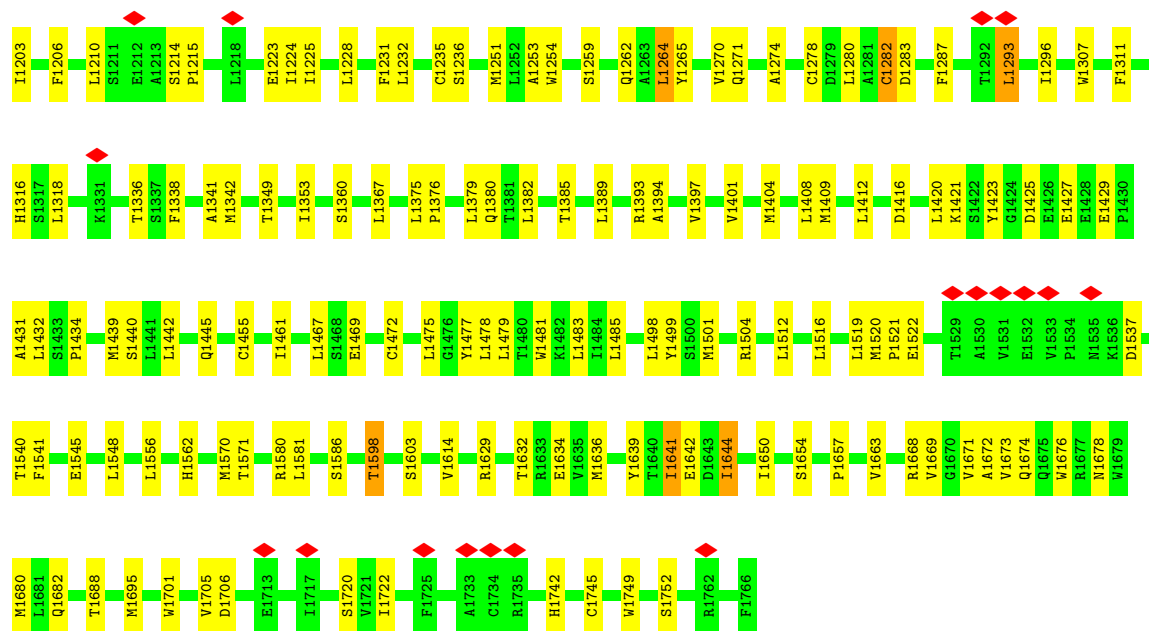




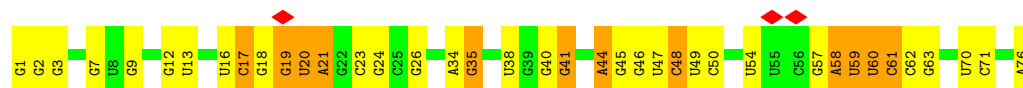
• Molecule 8: E3 ubiquitin-protein ligase listerin

Chain F: 72% 22% 5%

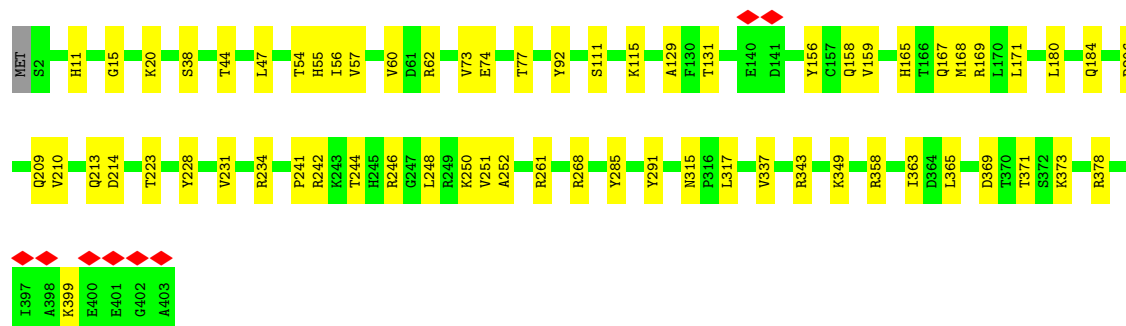
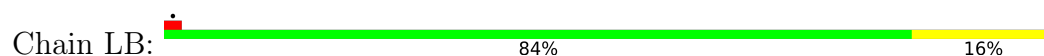




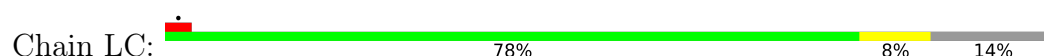
- Molecule 9: tRNA



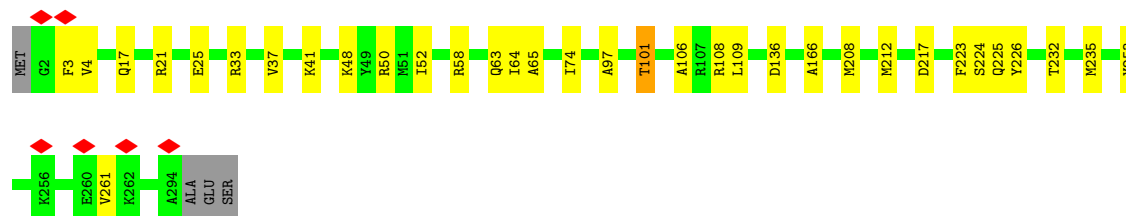
- Molecule 10: 60S ribosomal protein L3



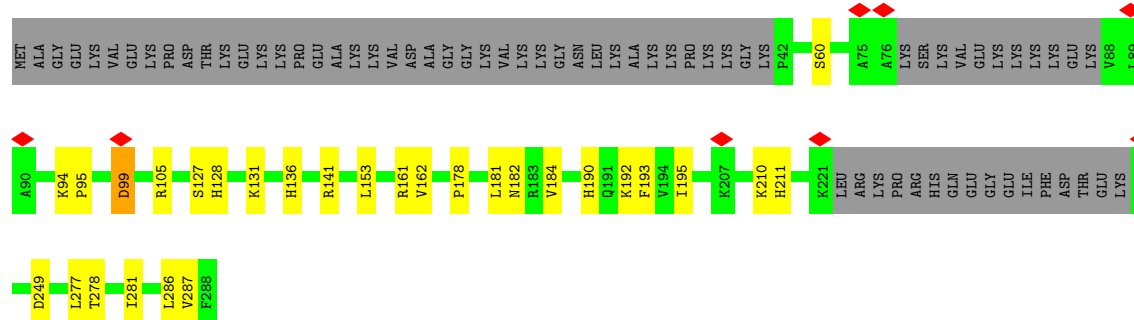
- Molecule 11: 60S ribosomal protein L4



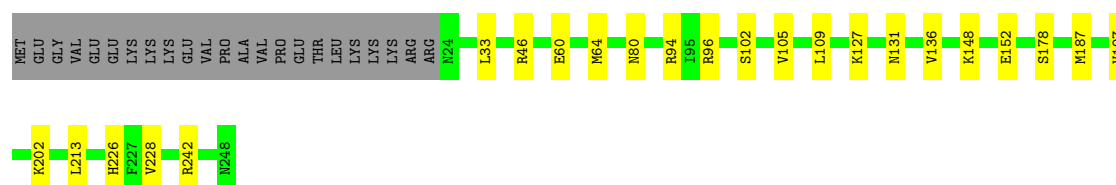
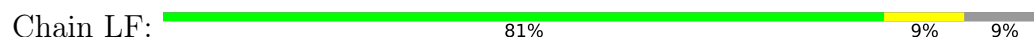
- Molecule 12: 60S ribosomal protein L5



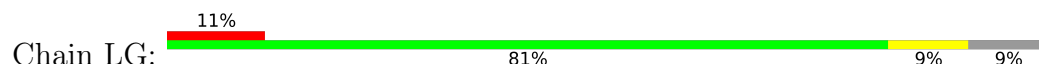
- Molecule 13: Large ribosomal subunit protein eL6

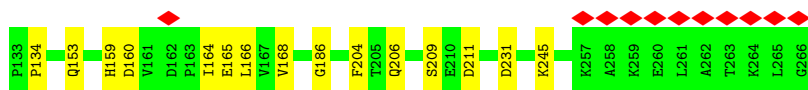


- Molecule 14: Large ribosomal subunit protein uL30



- Molecule 15: 60S ribosomal protein L7a

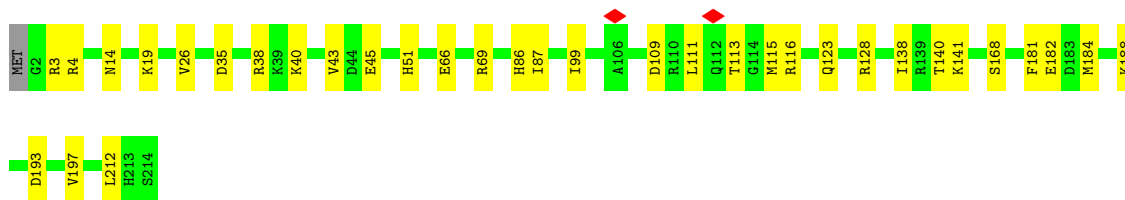
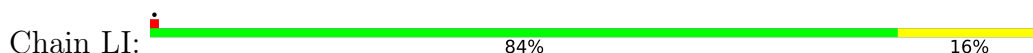




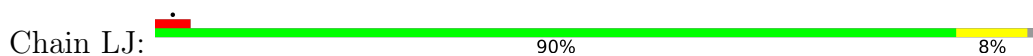
- Molecule 16: 60S ribosomal protein L9



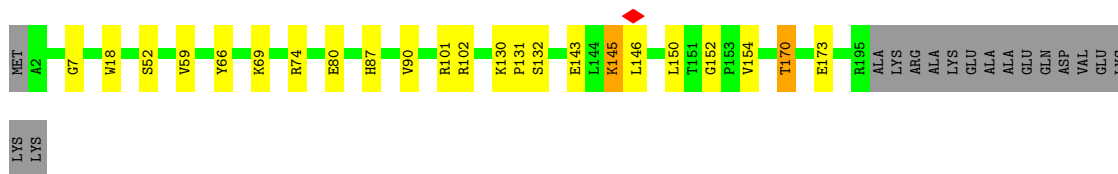
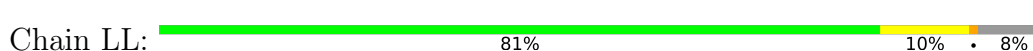
- Molecule 17: Ribosomal protein uL16-like



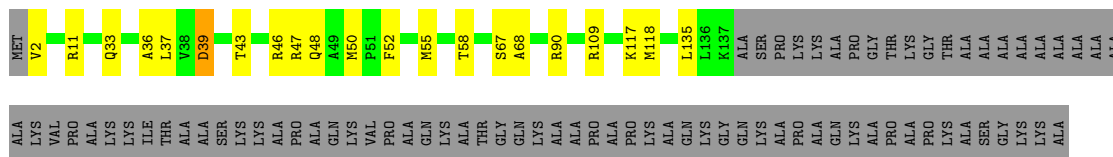
- Molecule 18: 60S ribosomal protein L11




- Molecule 19: 60S ribosomal protein L13

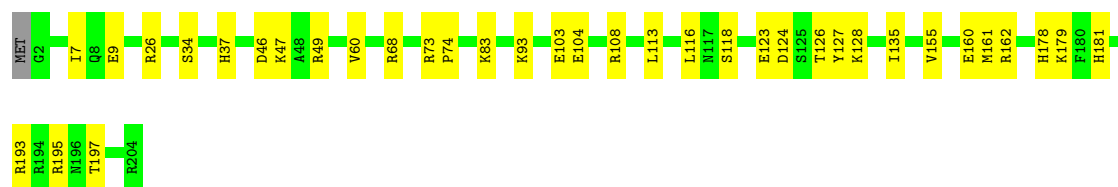


- Molecule 20: 60S ribosomal protein L14




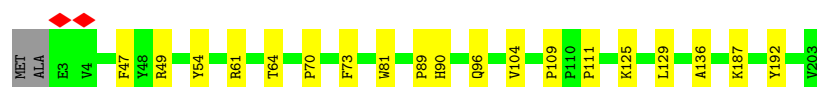
- Molecule 21: 60S ribosomal protein L15

Chain LN:  82% 18%




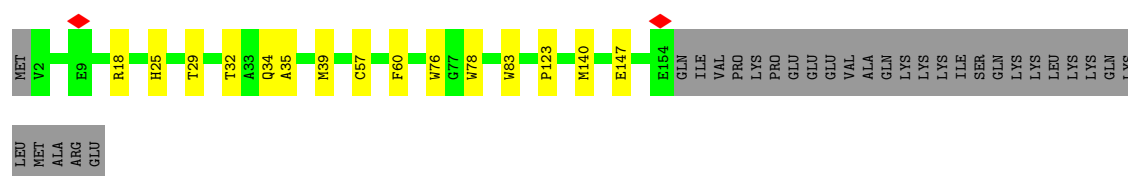
- Molecule 22: 60S ribosomal protein L13a

Chain LO:  90% 9%




- Molecule 23: 60S ribosomal protein L17

Chain LP:  75% 8% 17%



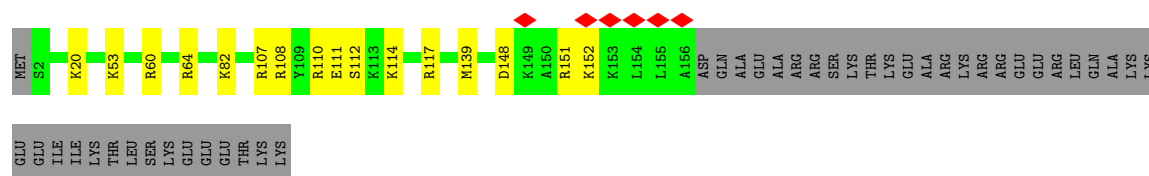
- Molecule 24: 60S ribosomal protein L18

Chain LQ:  86% 13%




- Molecule 25: 60S ribosomal protein L19

Chain LR:  71% 8% 21%




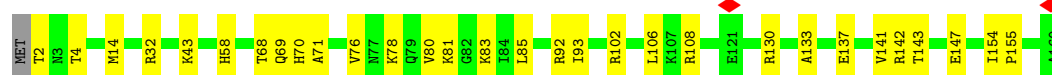
- Molecule 26: 60S ribosomal protein L18a

Chain LS:  86% 14%



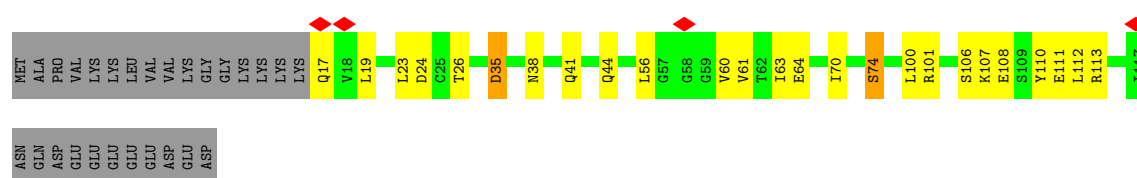
- Molecule 27: 60S ribosomal protein L21

Chain LT:  81% 19%




- Molecule 28: 60S ribosomal protein L22

Chain LU:  59% 18% 21%



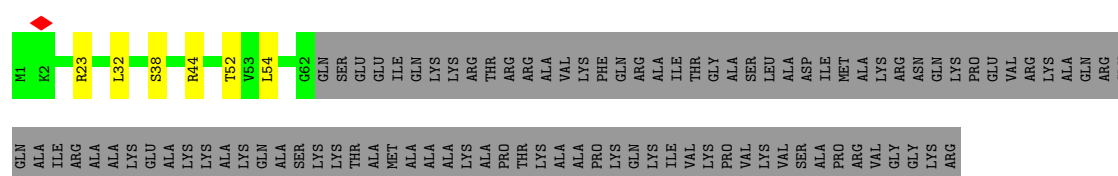
- Molecule 29: 60S ribosomal protein L23

Chain LV:  82% 11% 6%



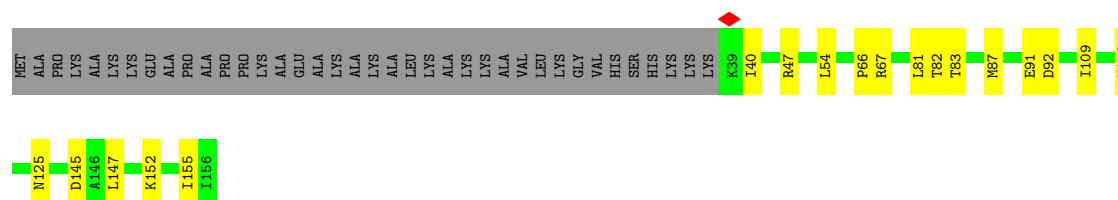
- Molecule 30: 60S ribosomal protein L24

Chain LW:  36% 61%




- Molecule 31: 60S ribosomal protein L23a

Chain LX:  64% 12% 24%



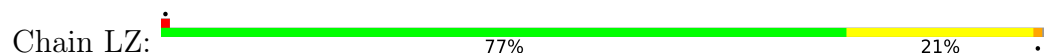
- Molecule 32: 60S ribosomal protein L26

Chain LY:  84% 8% 8%

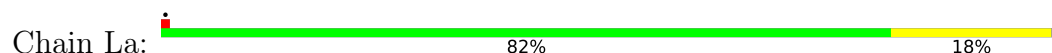




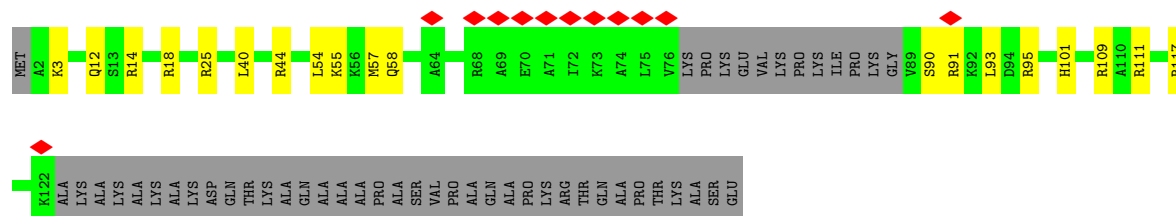
- Molecule 33: 60S ribosomal protein L27



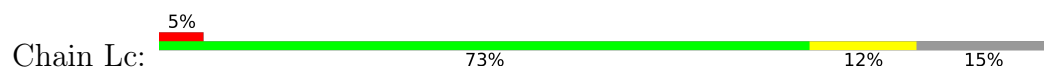
- Molecule 34: 60S ribosomal protein L27a



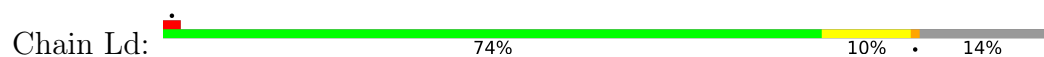
- Molecule 35: 60S ribosomal protein L29



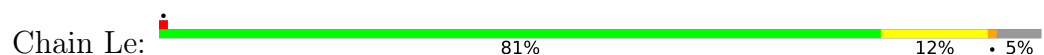
- Molecule 36: 60S ribosomal protein L30

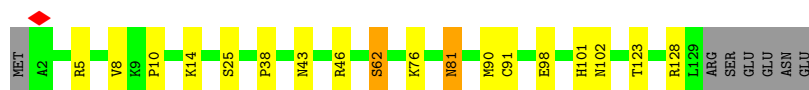


- Molecule 37: 60S ribosomal protein L31



- Molecule 38: 60S ribosomal protein L32





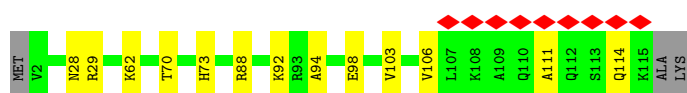
- Molecule 39: 60S ribosomal protein L35a

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% .



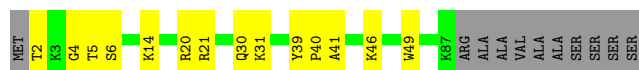
- Molecule 42: 60S ribosomal protein L36

Chain Li: 86% 10% ..



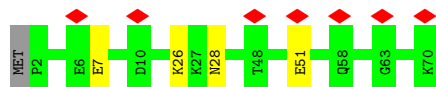
- Molecule 43: 60S ribosomal protein L37

Chain Lj: 74% 14% 11%



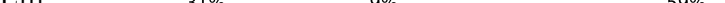
- Molecule 44: 60S ribosomal protein L38

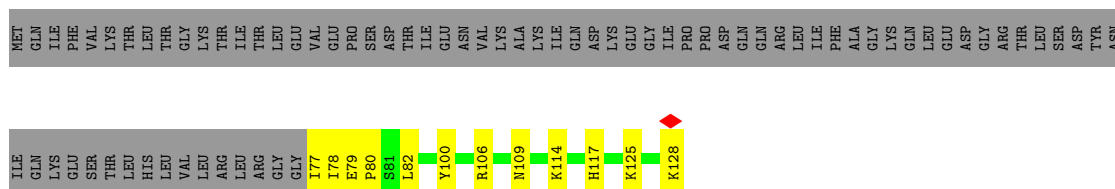
Chain Lk: 10% 93% 6% .



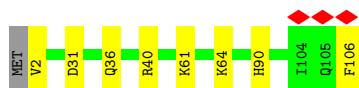
- Molecule 45: 60S ribosomal protein L39

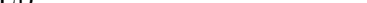
Diagram illustrating the sequence of amino acids (MET, S2, R8, I9, K10, L13, R21, S39, K40, R41, L51) and their corresponding positions (S2, R8, I9, K10, L13, R21, S39, K40, R41, L51). The amino acids are color-coded: MET (grey), S2 (grey), R8 (grey), I9 (red), K10 (red), L13 (grey), R21 (grey), S39 (grey), K40 (red), R41 (grey), and L51 (grey).

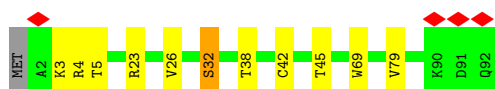
- Chain Lm: 

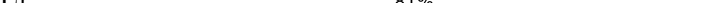


- Chain Lo:  92% 8%



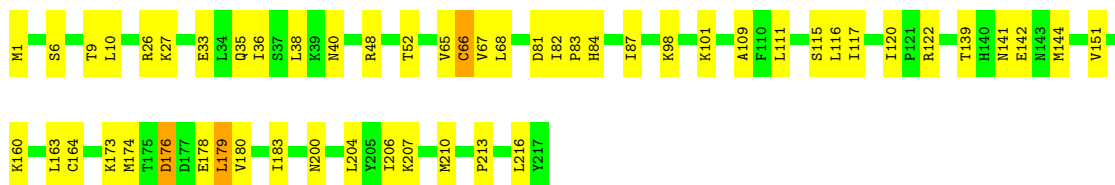
- Chain Lp:  87% 11% ..



- Chain Lr:  81% 10% 9%

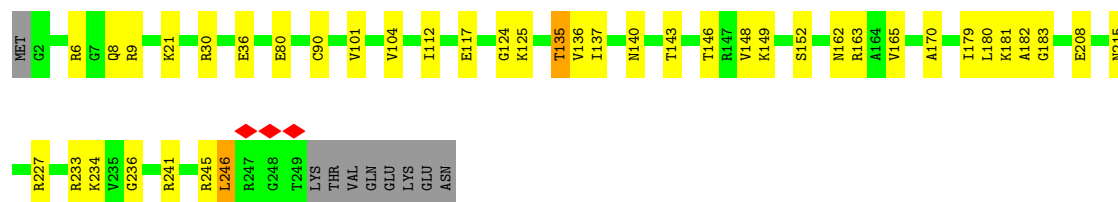


- Chain LZ: 76% 23%

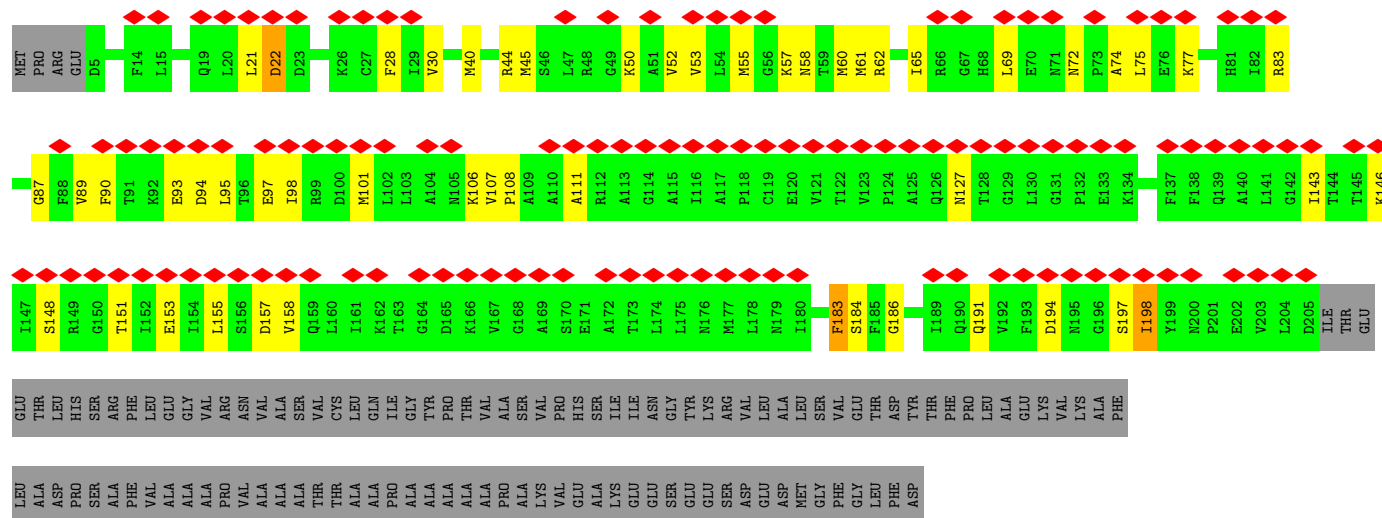
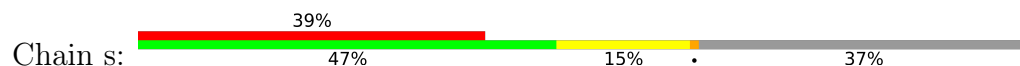


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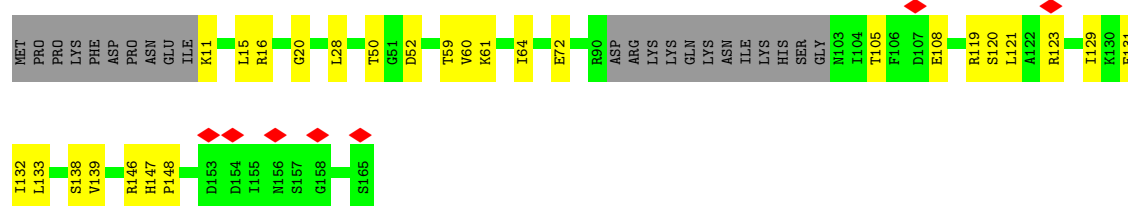
Chain a: 81% 15% ..



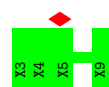
• Molecule 53: 60S acidic ribosomal protein P0



• 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

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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	81
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%)	37	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	66
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

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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

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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	81
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%)	52	79
6	D	66/72 (92%)	65 (98%)	1 (2%)	60	83
7	E	593/704 (84%)	581 (98%)	12 (2%)	50	78
8	F	1533/1611 (95%)	1486 (97%)	47 (3%)	35	68
10	LB	348/349 (100%)	344 (99%)	4 (1%)	70	87
11	LC	306/348 (88%)	305 (100%)	1 (0%)	91	96
12	LD	246/250 (98%)	245 (100%)	1 (0%)	89	95
13	LE	194/252 (77%)	192 (99%)	2 (1%)	73	88
14	LF	194/215 (90%)	191 (98%)	3 (2%)	60	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	LG	203/223 (91%)	198 (98%)	5 (2%)	42	73
16	LH	169/171 (99%)	166 (98%)	3 (2%)	54	80
17	LI	179/181 (99%)	179 (100%)	0	100	100
18	LJ	147/149 (99%)	144 (98%)	3 (2%)	50	78
19	LL	164/177 (93%)	162 (99%)	2 (1%)	67	86
20	LM	116/161 (72%)	113 (97%)	3 (3%)	41	72
21	LN	171/172 (99%)	168 (98%)	3 (2%)	54	80
22	LO	173/174 (99%)	173 (100%)	0	100	100
23	LP	134/163 (82%)	131 (98%)	3 (2%)	47	76
24	LQ	164/165 (99%)	163 (99%)	1 (1%)	84	93
25	LR	138/175 (79%)	138 (100%)	0	100	100
26	LS	156/157 (99%)	153 (98%)	3 (2%)	52	79
27	LT	139/140 (99%)	137 (99%)	2 (1%)	62	83
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%)	52	79
31	LX	106/133 (80%)	104 (98%)	2 (2%)	52	79
32	LY	124/135 (92%)	123 (99%)	1 (1%)	79	90
33	LZ	117/118 (99%)	114 (97%)	3 (3%)	41	72
34	La	120/121 (99%)	120 (100%)	0	100	100
35	Lb	88/126 (70%)	86 (98%)	2 (2%)	45	75
36	Lc	83/97 (86%)	80 (96%)	3 (4%)	30	64
37	Ld	98/110 (89%)	96 (98%)	2 (2%)	50	78
38	Le	114/121 (94%)	110 (96%)	4 (4%)	31	65
39	Lf	88/89 (99%)	86 (98%)	2 (2%)	45	75
40	Lg	98/100 (98%)	98 (100%)	0	100	100
41	Lh	109/110 (99%)	107 (98%)	2 (2%)	54	80
42	Li	86/89 (97%)	85 (99%)	1 (1%)	67	86
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%)	48	77

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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%)	70	87
48	Lp	74/75 (99%)	73 (99%)	1 (1%)	62	83
49	Lr	109/121 (90%)	107 (98%)	2 (2%)	54	80
50	Lz	196/196 (100%)	185 (94%)	11 (6%)	17	49
51	Z	645/962 (67%)	632 (98%)	13 (2%)	50	78
52	a	190/199 (96%)	187 (98%)	3 (2%)	58	82
53	s	169/258 (66%)	165 (98%)	4 (2%)	44	74
54	t	116/137 (85%)	114 (98%)	2 (2%)	56	81
All	All	9356/10749 (87%)	9179 (98%)	177 (2%)	52	79

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 ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

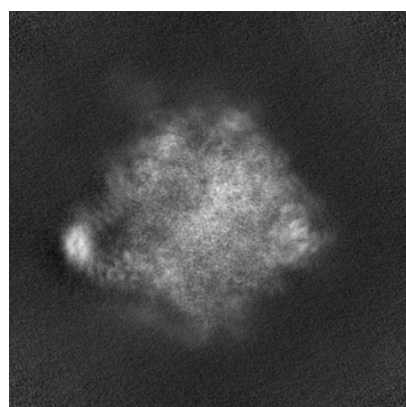
6 Map visualisation [i](#)

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.

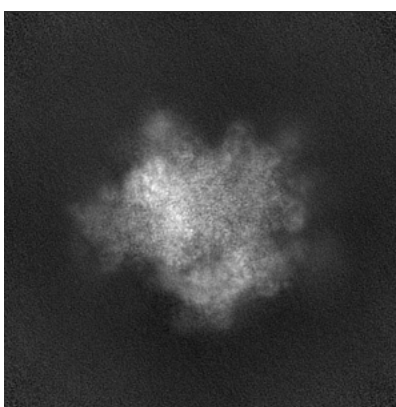
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

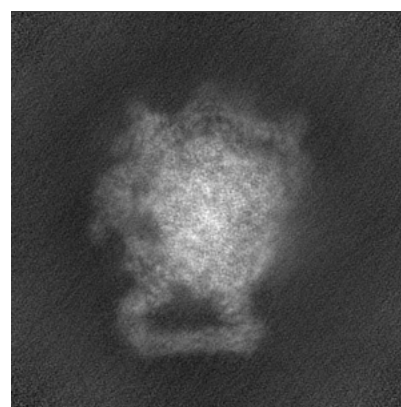
6.1.1 Primary map



X



Y

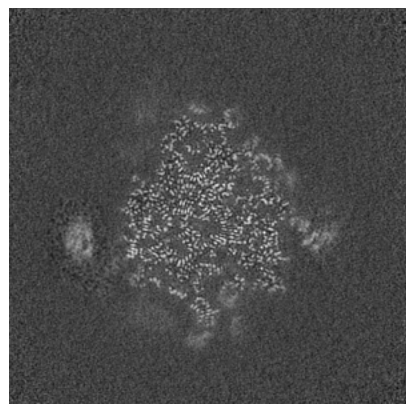


Z

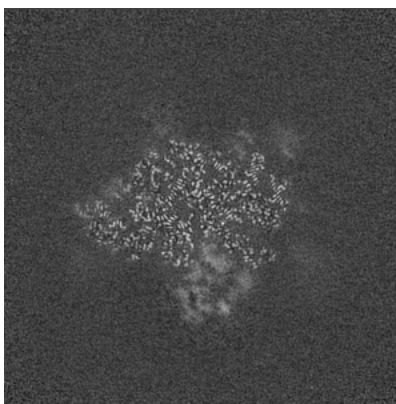
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

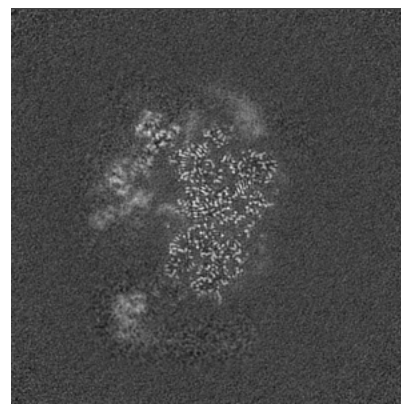
6.2.1 Primary map



X Index: 300



Y Index: 300

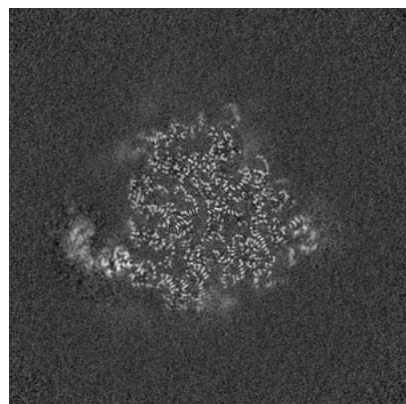


Z Index: 300

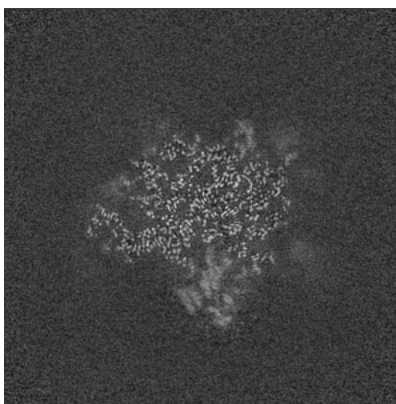
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

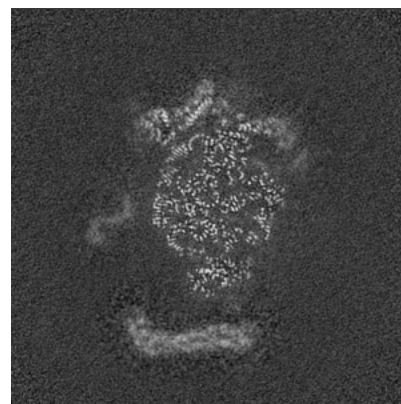
6.3.1 Primary map



X Index: 321



Y Index: 310

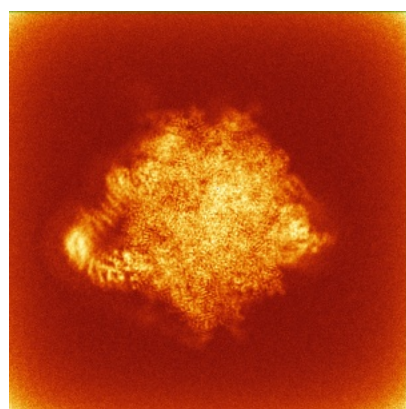


Z Index: 261

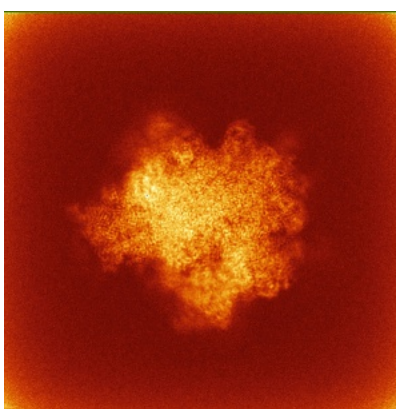
The images above show the largest variance slices of the map in three orthogonal directions.

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

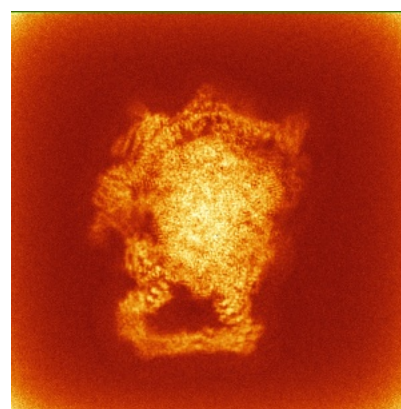
6.4.1 Primary map



X



Y

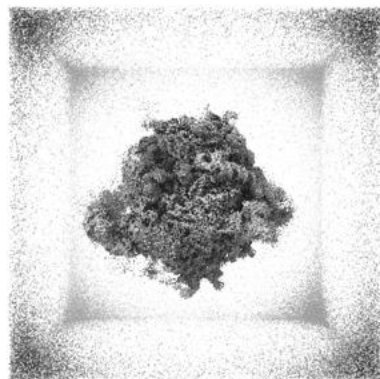


Z

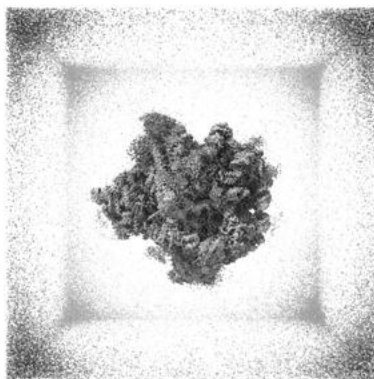
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

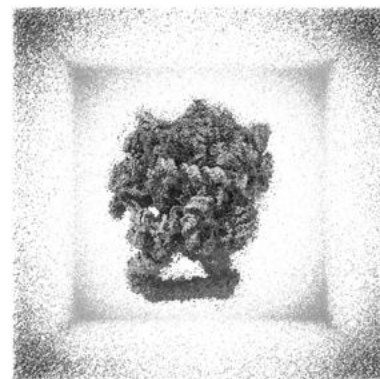
6.5.1 Primary map



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.

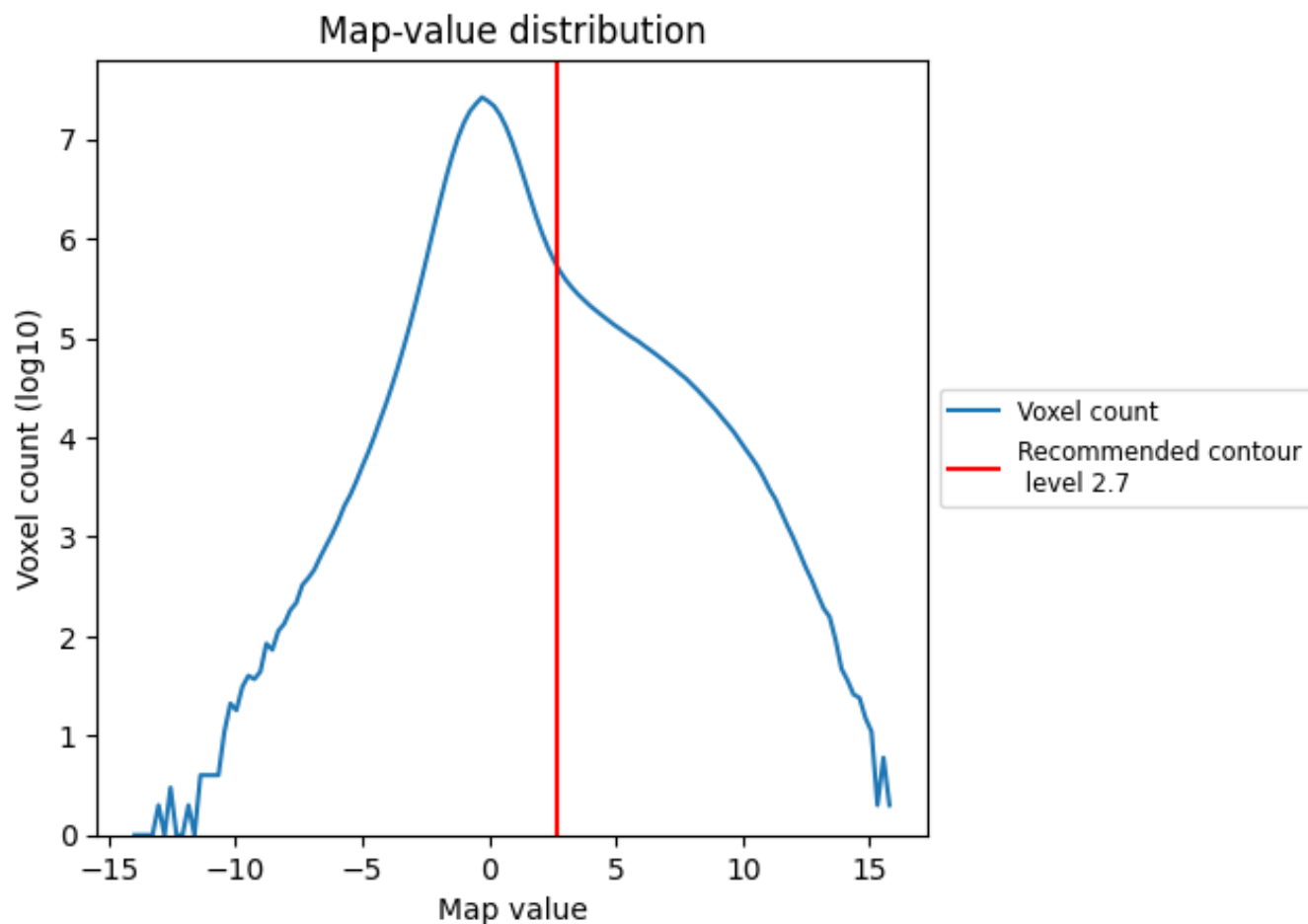
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

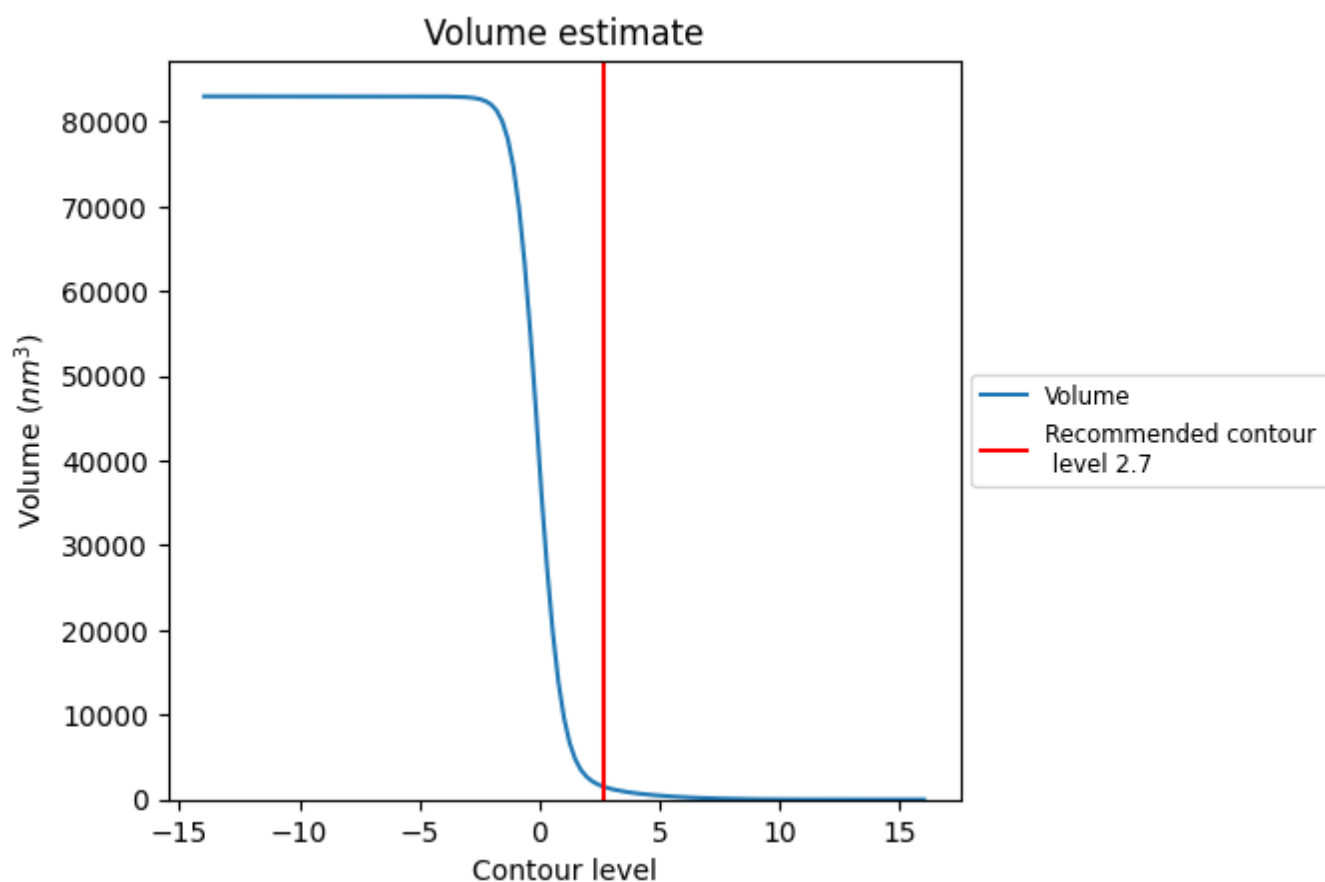
This section contains the results of statistical analysis of the map.

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.

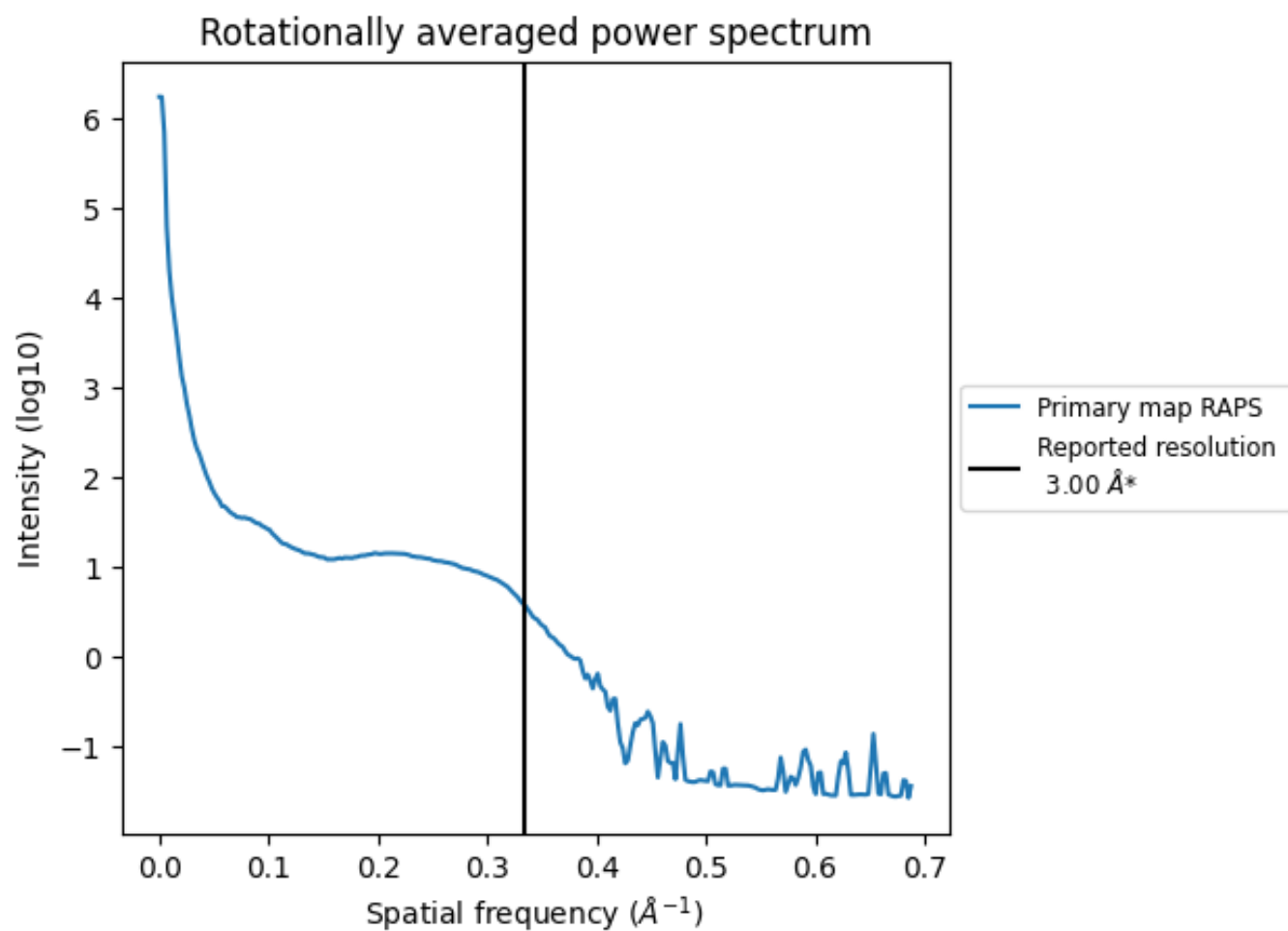
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1497 nm³; 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

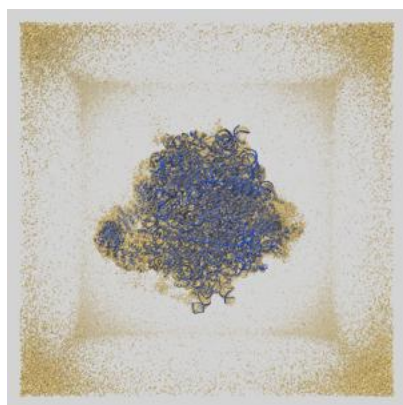
8 Fourier-Shell correlation

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

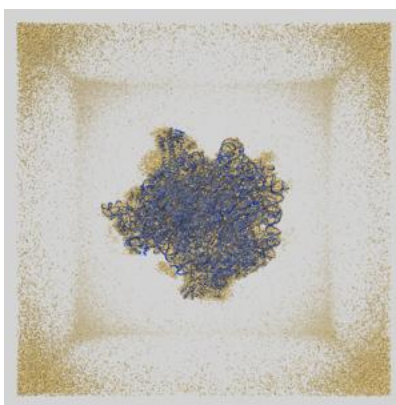
9 Map-model fit [i](#)

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 [15](#).

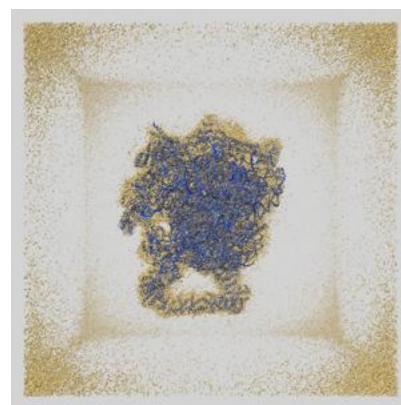
9.1 Map-model overlay [i](#)



X



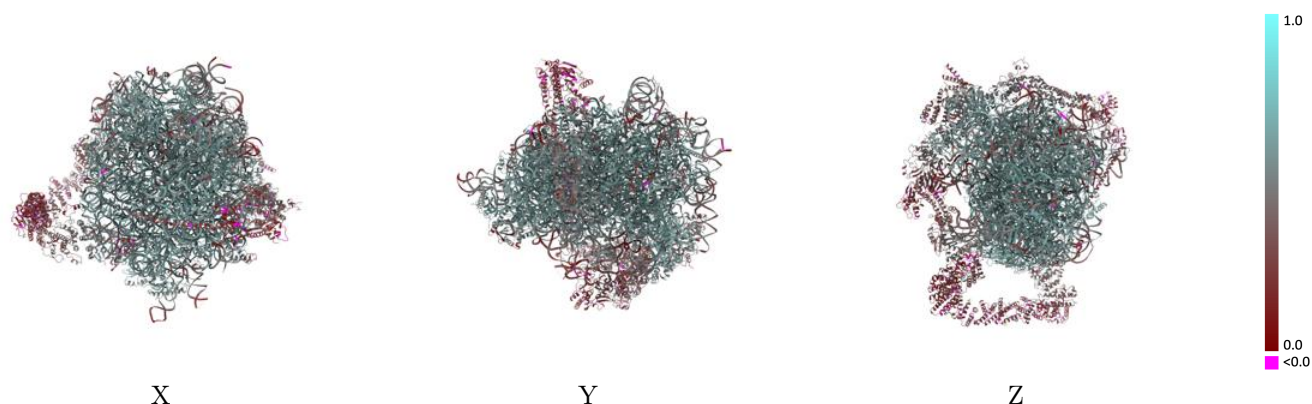
Y



Z

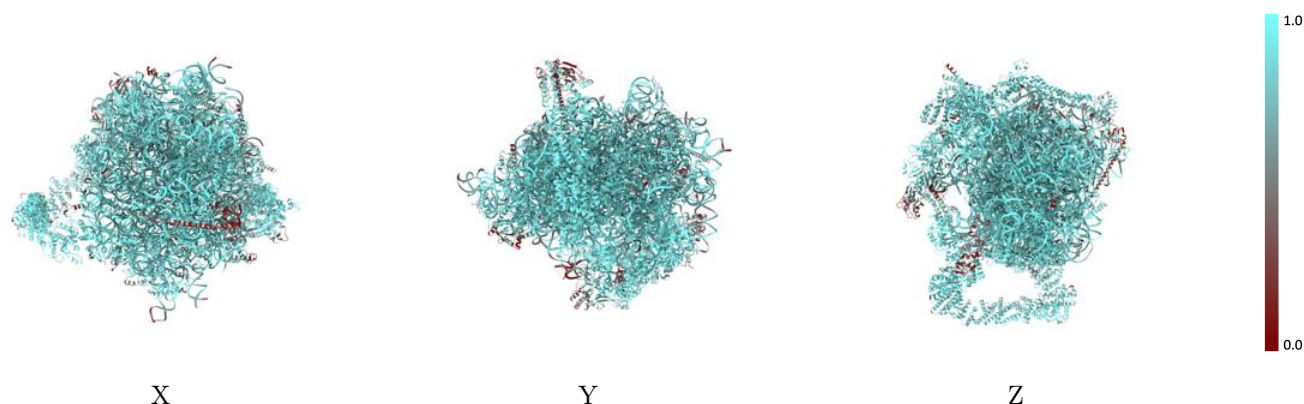
The images above show the 3D surface view of the map at the recommended contour level 2.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



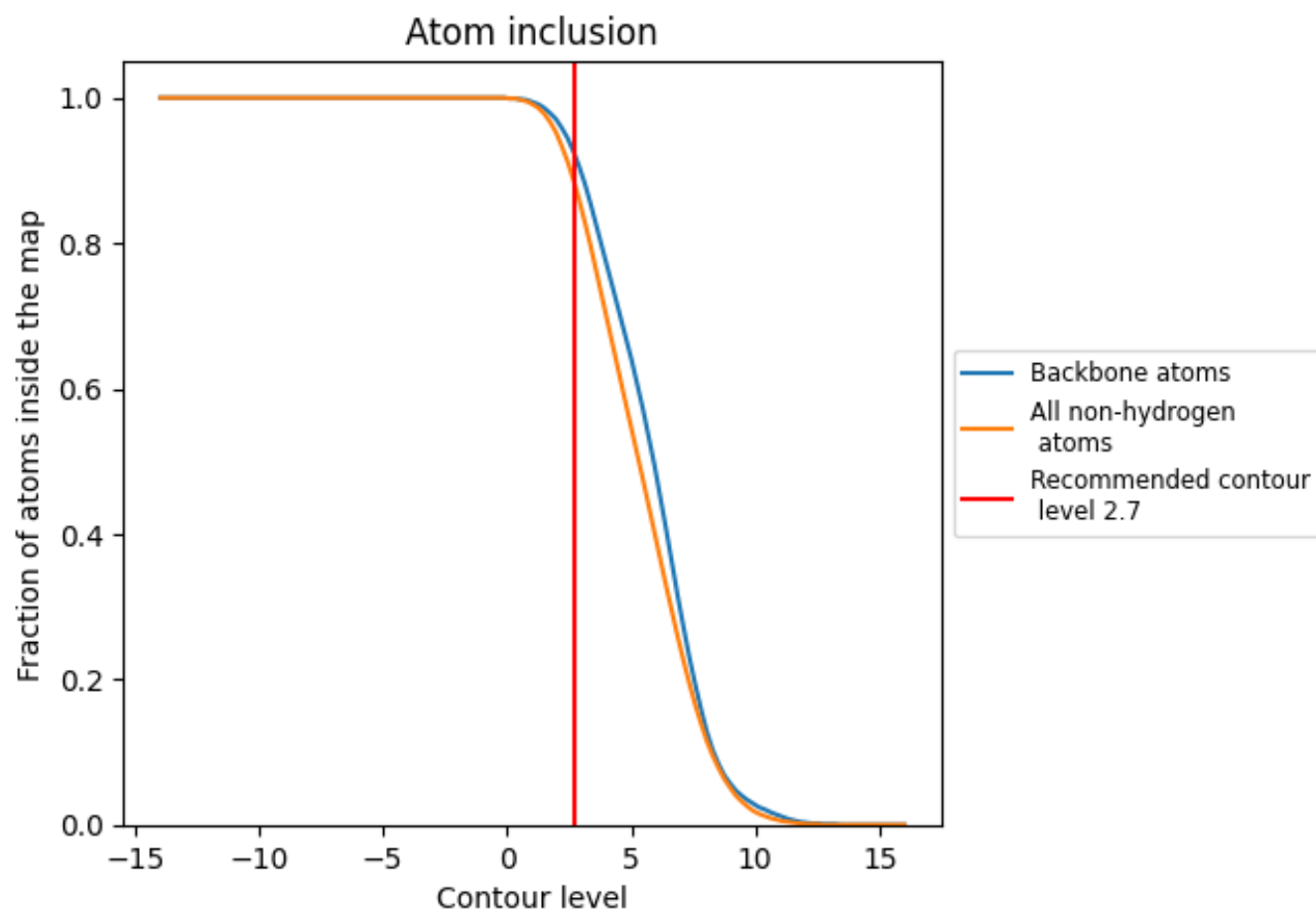
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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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