



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:15 PM UTC

PDB ID : 3J9Z / pdb_00003j9z
EMDB ID : EMD-6315
Title : Activation of GTP Hydrolysis in mRNA-tRNA Translocation by Elongation Factor G
Authors : Li, W.; Liu, Z.; Koripella, R.K.; Langlois, R.; Sanyal, S.; Frank, J.
Deposited on : 2015-03-27
Resolution : 3.60 Å(reported)
Based on initial model : 3J0U

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:

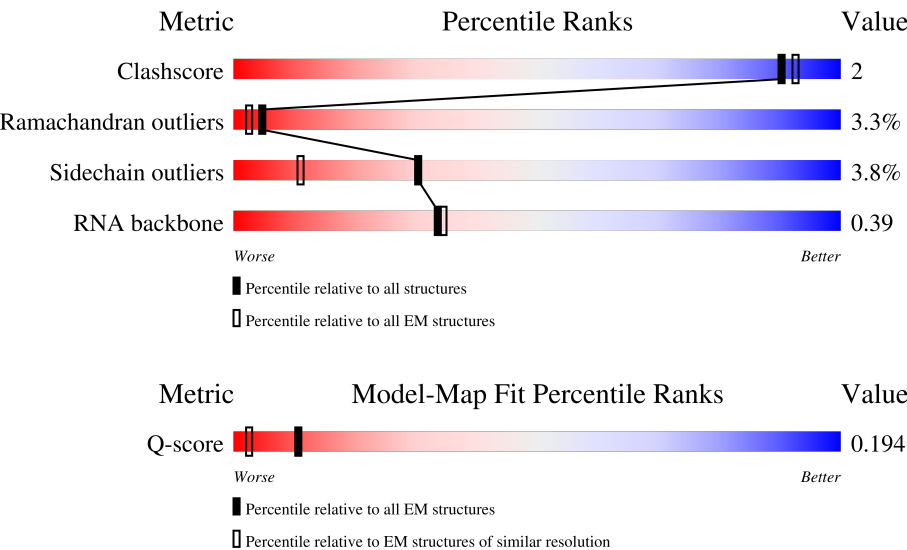
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.60 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	12797 (3.10 - 4.10)

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	SA	1542	42%35%17%7%
2	S6	77	61%21%13%5%
3	S7	74	23%36%24%16%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	SJ	103	
5	SK	128	
6	SL	123	
7	SM	117	
8	SN	100	
9	SO	88	
10	SP	82	
11	SQ	83	
12	SR	74	
13	SS	91	
14	SB	240	
15	ST	86	
16	SU	70	
17	SC	232	
18	SD	205	
19	SE	166	
20	SF	135	
21	SG	178	
22	SH	129	
23	SI	129	
24	S1	702	
25	LA	2904	
26	LB	120	
27	LC	234	
28	LM	114	

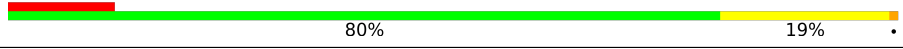
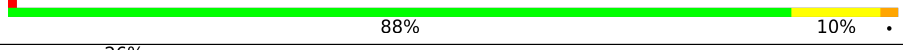
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	LN	272	
30	LO	117	
31	LP	103	
32	LQ	110	
33	LR	100	
34	LS	103	
35	LT	94	
36	LU	84	
37	LV	77	
38	LD	164	
39	LW	63	
40	LX	209	
41	LY	58	
42	L1	56	
43	L2	54	
44	L3	46	
45	L4	64	
46	L5	38	
47	L6	201	
48	LE	141	
49	L7	178	
50	L8	176	
51	L9	149	
52	LF	142	
53	LG	123	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	LH	144	 84% 14% ..
55	LI	136	 86% 13% .
56	LJ	127	 12% 80% 19% .
57	LK	117	 88% 10% .
58	LZ	70	 26% 86% 10% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
59	GTP	S1	801	-	-	X	-

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 156714 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	SA	1542	Total	C	N	O	P	0	0
			33076	14754	6064	10717	1541		

- Molecule 2 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	S6	77	Total	C	N	O	P	0	0
			1639	732	297	534	76		

- Molecule 3 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S7	74	Total	C	N	O	P	0	0
			1577	704	282	518	73		

- Molecule 4 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SJ	103	Total	C	N	O	S	0	0
			825	514	158	151	2		

- Molecule 5 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SK	128	Total	C	N	O	S	0	0
			965	595	196	171	3		

- Molecule 6 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SL	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 7 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SM	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 8 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SN	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 9 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SO	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 10 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SP	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SQ	83	Total	C	N	O	S	0	0
			672	425	124	120	3		

- Molecule 12 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SR	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SS	91	Total	C	N	O	S	0	0
			727	464	139	122	2		

- Molecule 14 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SB	240	Total	C	N	O	S	0	0
			1872	1180	332	352	8		

- Molecule 15 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	ST	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 16 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SU	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 17 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SC	232	Total	C	N	O	S	0	0
			1822	1149	346	323	4		

- Molecule 18 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SD	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 19 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SE	166	Total	C	N	O	S	0	0
			1225	761	232	226	6		

- Molecule 20 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SF	135	Total	C	N	O	S	0	0
			1101	677	198	219	7		

- Molecule 21 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SG	178	Total	C	N	O	S	0	0
			1400	874	269	253	4		

- Molecule 22 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SH	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 23 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SI	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 24 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S1	702	Total	C	N	O	S	0	0
			5431	3420	938	1048	25		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S1	91	ALA	HIS	engineered mutation	UNP P0A6M8

- Molecule 25 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LA	2904	Total	C	N	O	P	0	0
			62333	27808	11464	20158	2903		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LA	1618	U	A	conflict	GB 33357927
LA	2030	C	A	conflict	GB 33357927

- Molecule 26 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LB	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

- Molecule 27 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LC	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 28 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LM	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 29 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LN	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 30 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	LO	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 31 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LP	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 32 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LQ	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 33 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LR	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 34 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LS	103	Total	C	N	O	S	0	0
			789	498	148	143			

- Molecule 35 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LT	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 36 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LU	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 37 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LV	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 38 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LD	164	Total	C	N	O	S	0	0
			1233	776	220	231	6		

- Molecule 39 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LW	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 40 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LX	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 41 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LY	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 42 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L1	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 43 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L2	54	Total	C	N	O	S	0	0
			441	284	81	76			

- Molecule 44 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	L3	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 45 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	L4	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 46 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	L5	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 47 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	L6	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 48 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LE	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 49 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	L7	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 50 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	L8	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 51 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	L9	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 52 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LF	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 53 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LG	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 54 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LH	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 55 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LI	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 56 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LJ	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

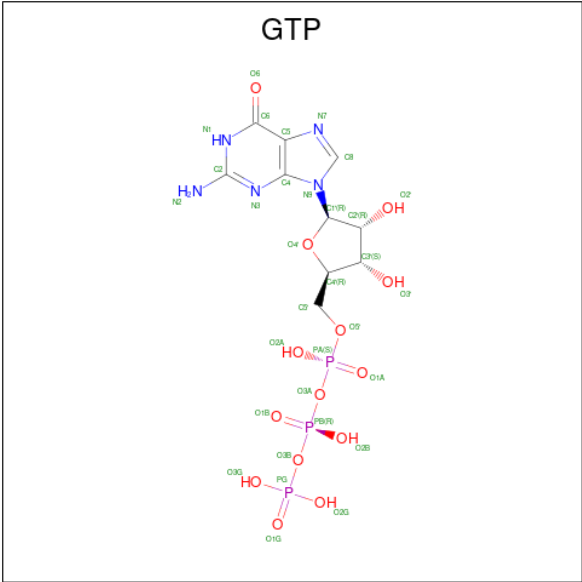
- Molecule 57 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LK	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 58 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LZ	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 59 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

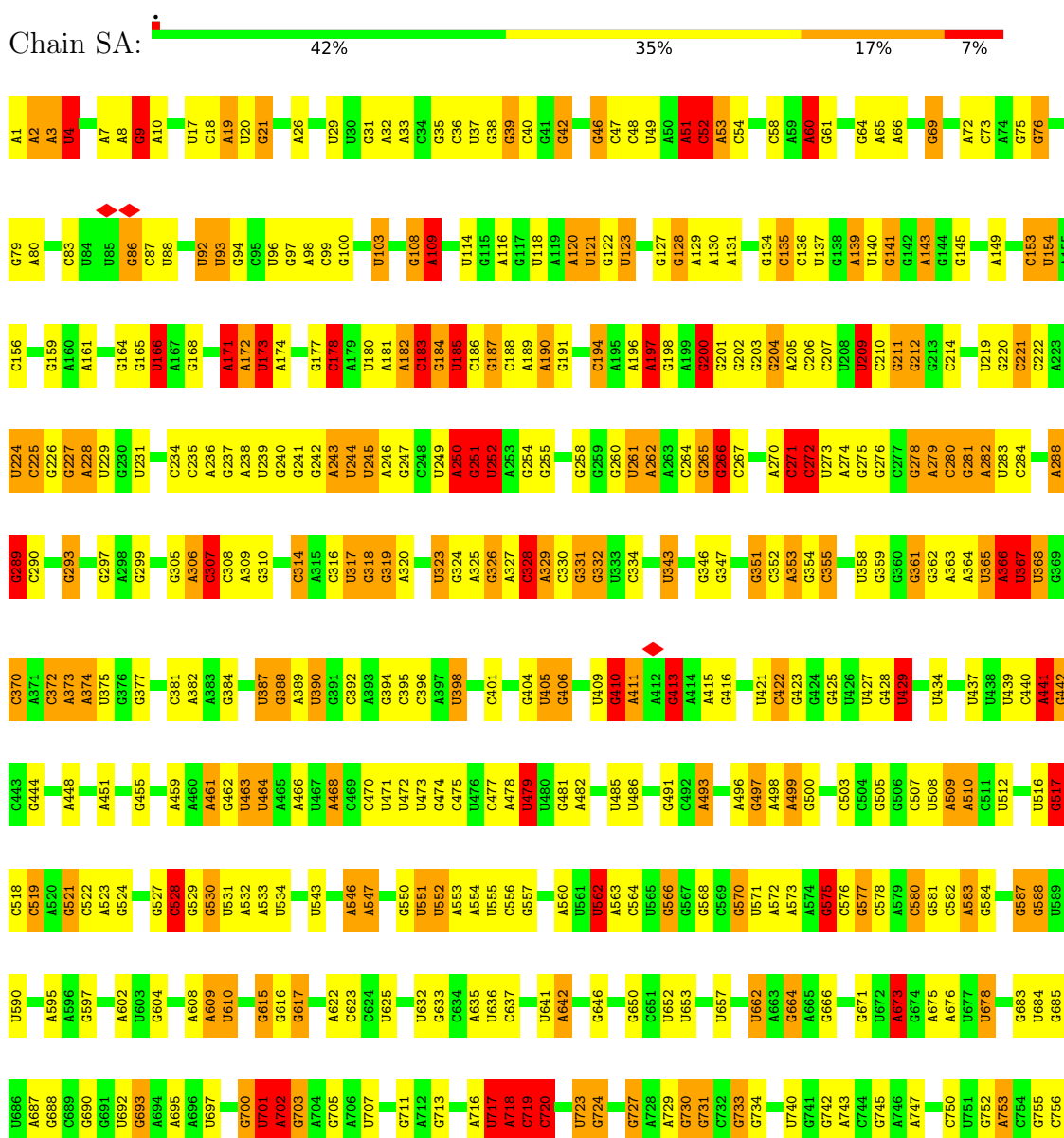


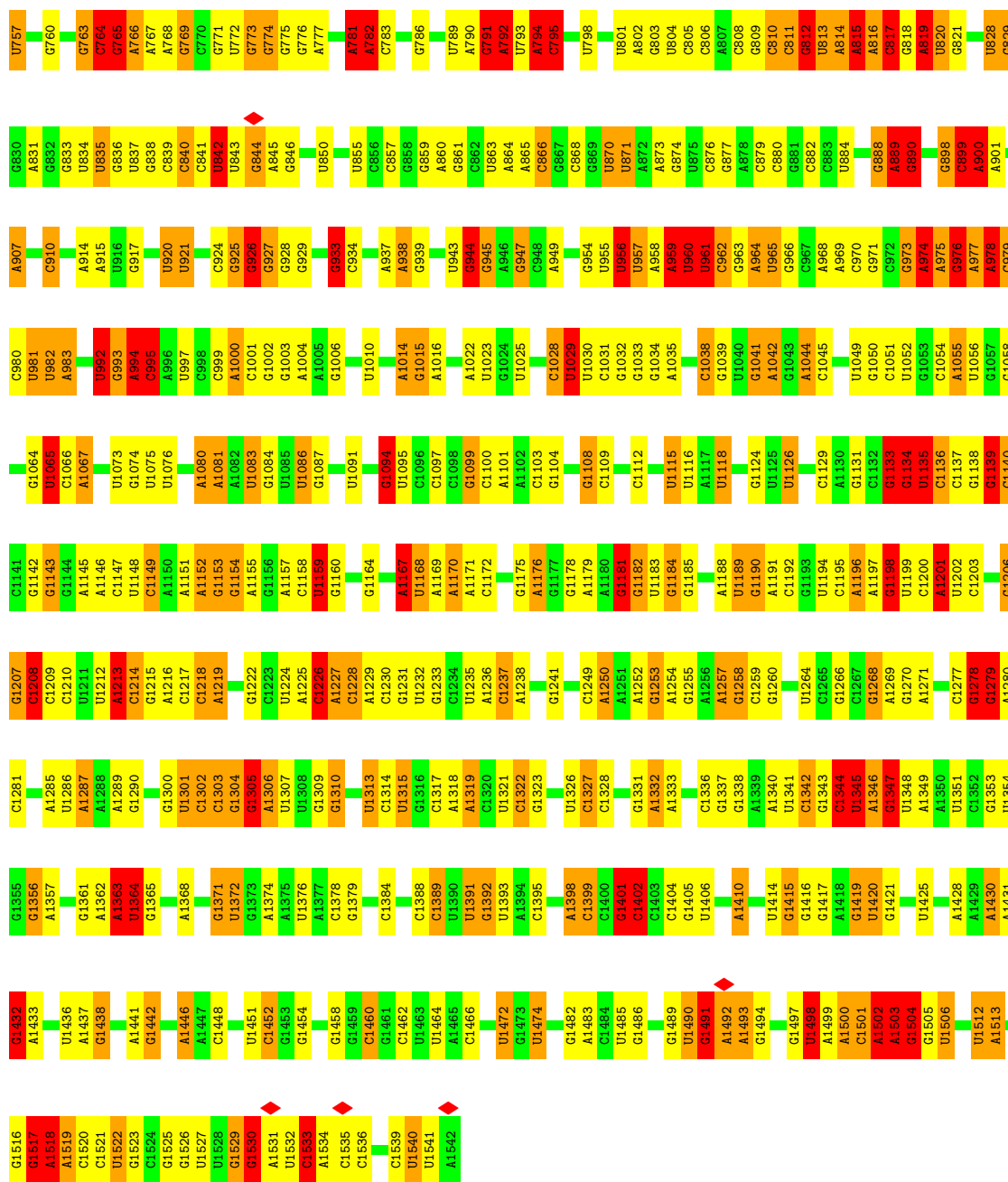
Mol	Chain	Residues	Atoms					AltConf
59	S1	1	Total	C	N	O	P	0
			32	10	5	14	3	

3 Residue-property plots

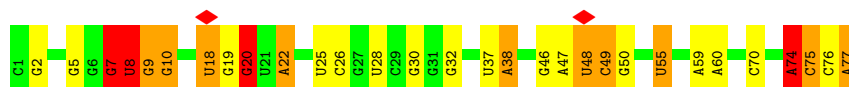
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S ribosomal RNA

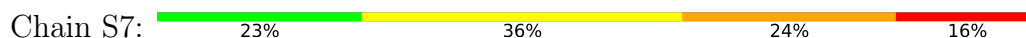


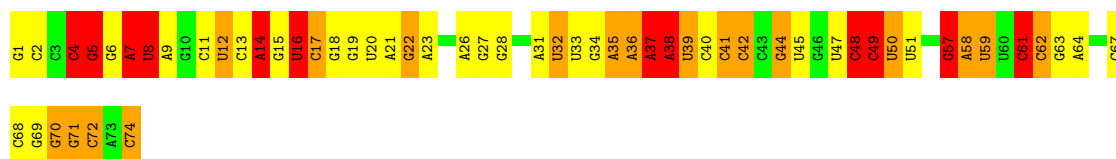


• Molecule 2: P-tRNA

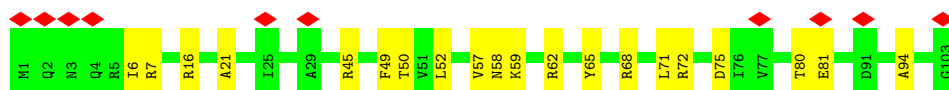
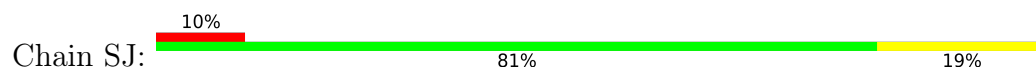


• Molecule 3: E-tRNA

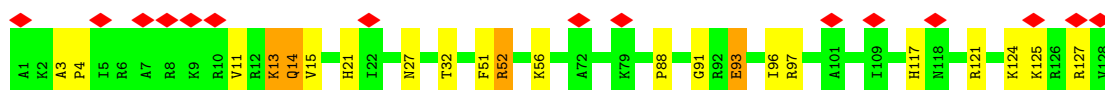
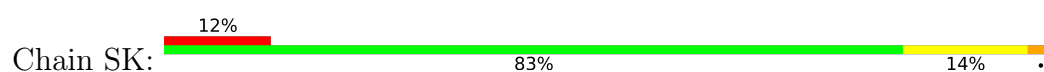




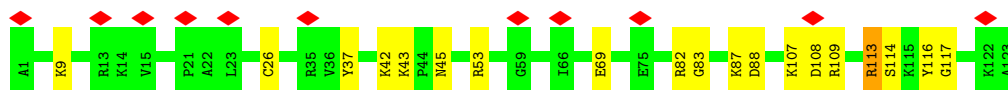
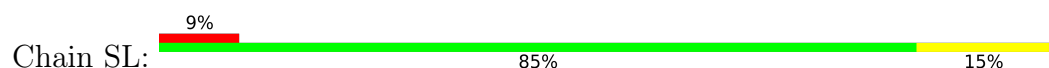
- Molecule 4: 30S ribosomal protein S10



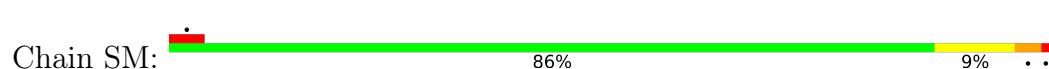
- Molecule 5: 30S ribosomal protein S11



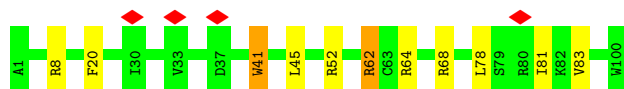
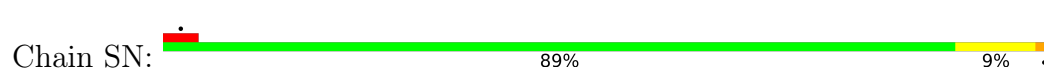
- Molecule 6: 30S ribosomal protein S12



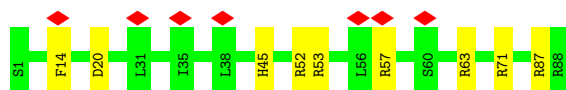
- Molecule 7: 30S ribosomal protein S13



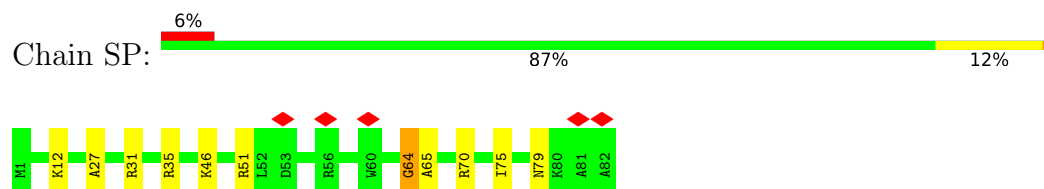
- Molecule 8: 30S ribosomal protein S14



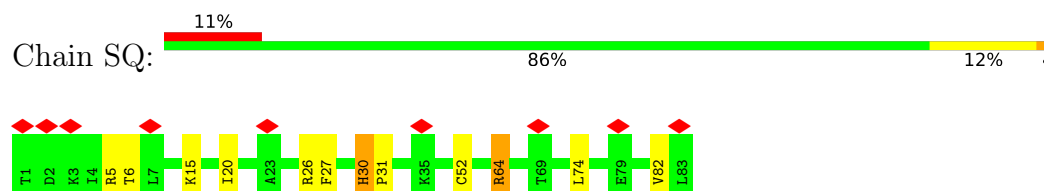
- Molecule 9: 30S ribosomal protein S15



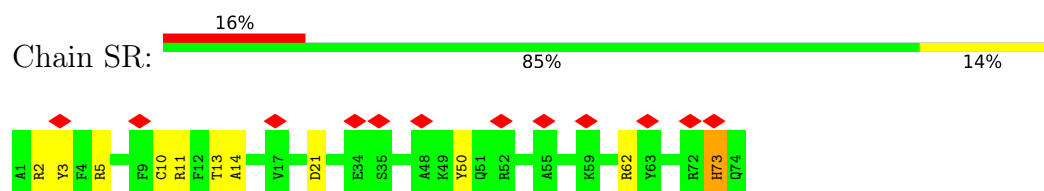
- Molecule 10: 30S ribosomal protein S16



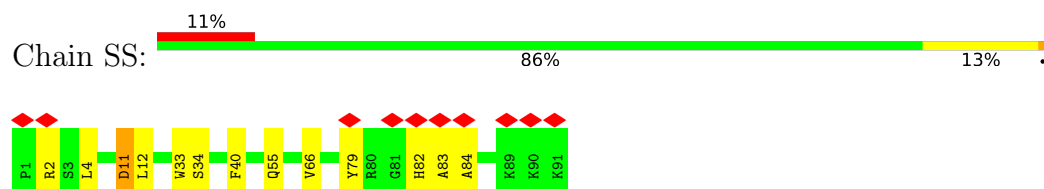
- Molecule 11: 30S ribosomal protein S17



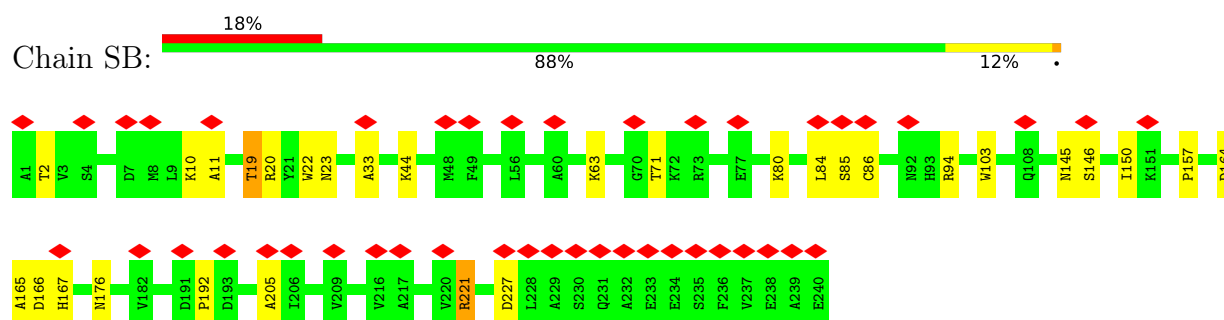
- Molecule 12: 30S ribosomal protein S18



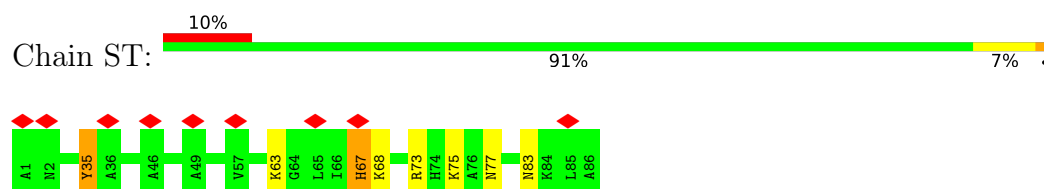
- Molecule 13: 30S ribosomal protein S19



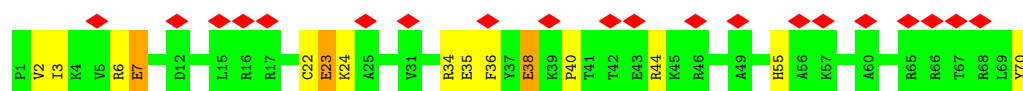
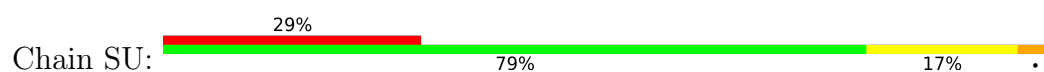
- Molecule 14: 30S ribosomal protein S2



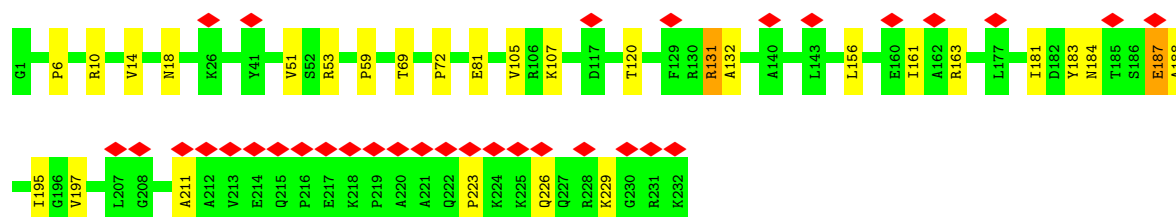
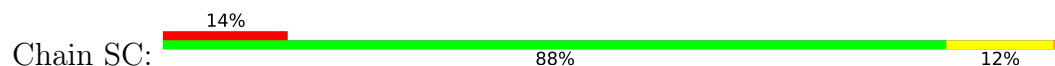
- Molecule 15: 30S ribosomal protein S20



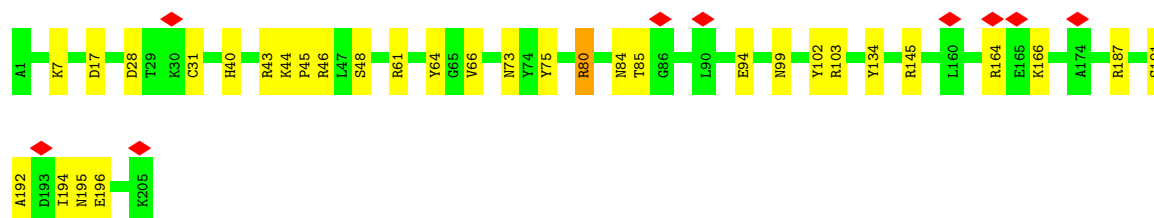
- Molecule 16: 30S ribosomal protein S21



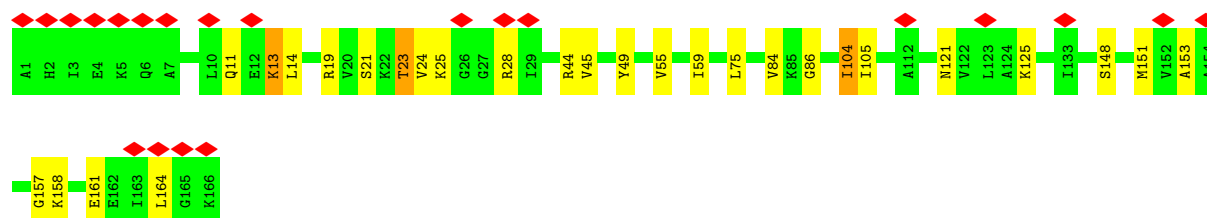
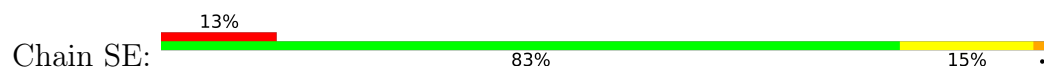
• Molecule 17: 30S ribosomal protein S3



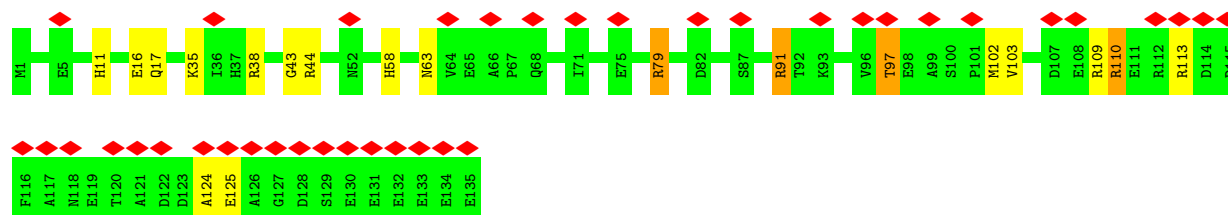
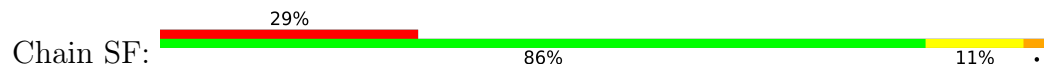
• Molecule 18: 30S ribosomal protein S4



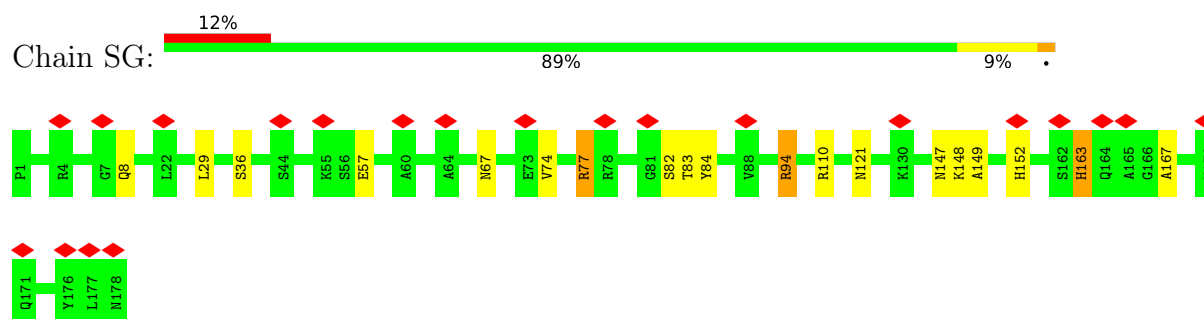
• Molecule 19: 30S ribosomal protein S5



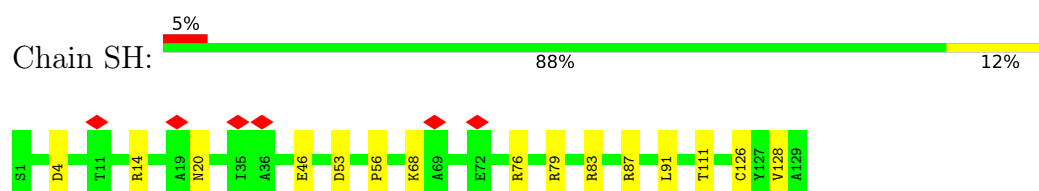
• Molecule 20: 30S ribosomal protein S6



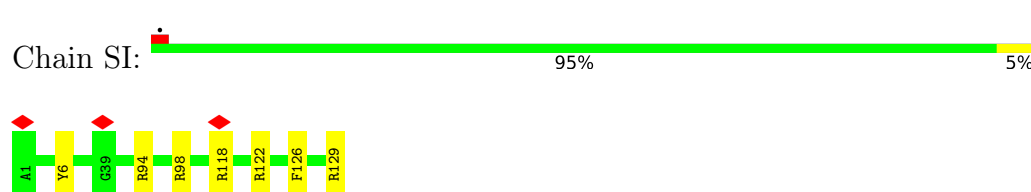
- Molecule 21: 30S ribosomal protein S7



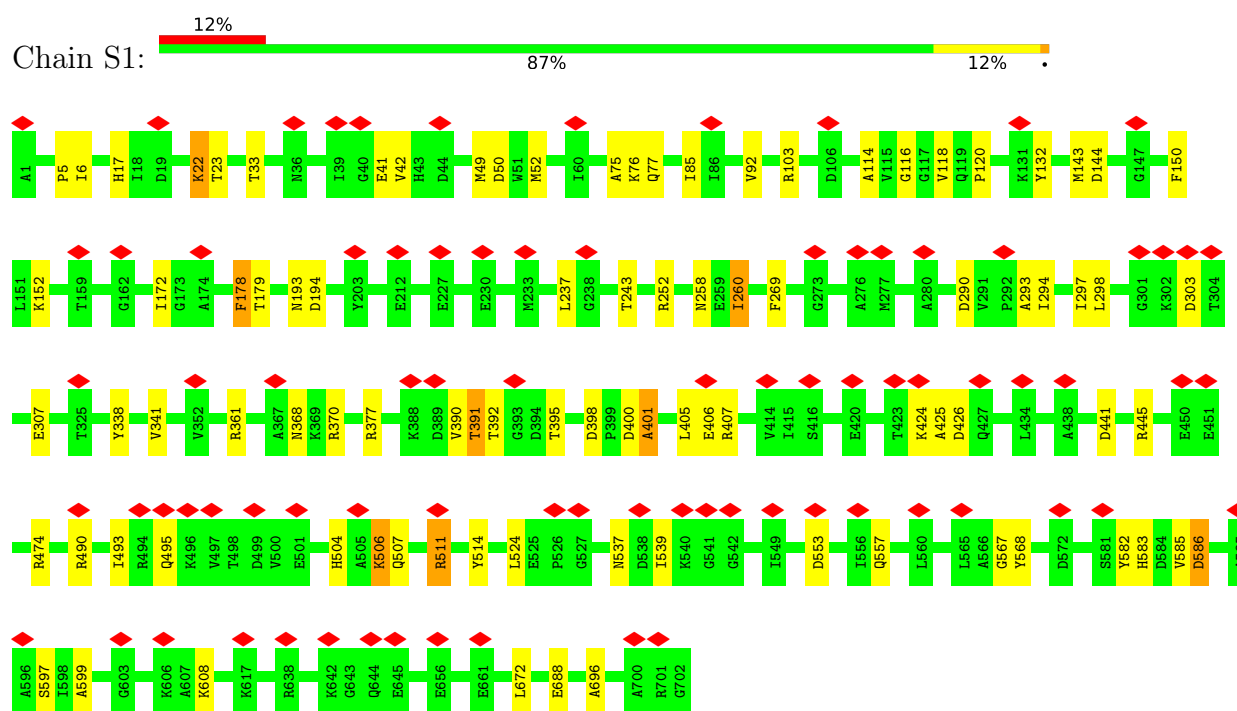
- Molecule 22: 30S ribosomal protein S8



- Molecule 23: 30S ribosomal protein S9

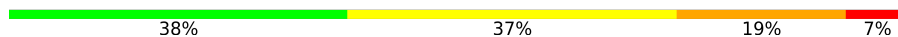


- Molecule 24: Elongation factor G



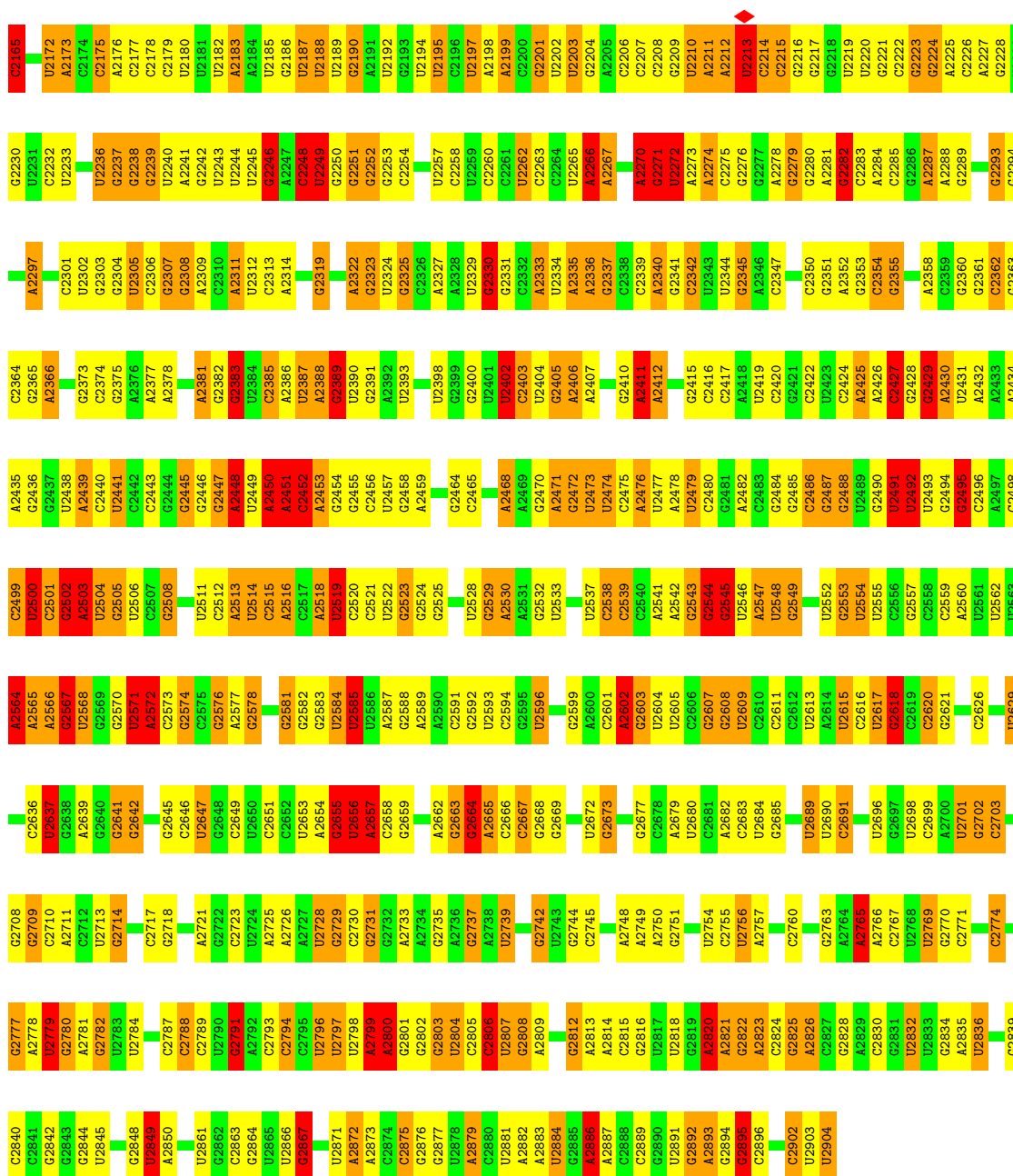
- Molecule 25: 23S ribosomal RNA

Chain LA:



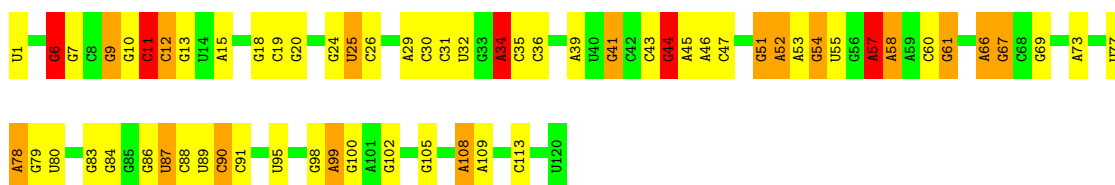
G1	G2	U3	U12	A13	A14	G15	C16	G17	U18	A19	C20	A21	C22	G23	G24	U25	G26	G27	A28	U29	G30	U34	G35	G36	C37	A38	G39	U40	C41	A42	G43	A44	G45	G46	C47	G48	A49	U50	G51	A52	G55	A56	C57	G60	C61	U62	A63	A64	U65	C66	G70	A71	U72	A73
A74	G75	C79	G80	G81	U82	A83	U84	C85	U86	A91	U92	G93	A94	A95	G96	C97	G98	U99	A100	A101	U102	A103	A104	C105	C106	A107	U113	U114	C115	G116	A117	A118	U119	A120	U121	G122	G123	A126	C127	C128	G129	C130	A131	G132	U133	G134	U135	G136	C140	U142	C143	A144	G145	
C147	A152	U153	U154	G160	A161	U162	C163	A164	G169	U170	G175	A176	G177	A181	G185	A186	G187	A190	A191	C192	U193	G194	A195	A196	C197	U198	A199	U200	C201	U202	A203	A204	G205	U206	A207	G212	G215	A216	G220	A221	A222	A223	U224	C225	C228	C229	A144	G230	A145					
G232	A233	C238	G239	A241	G242	U243	A244	G248	C249	G250	A251	G252	A255	G258	A261	A262	G263	A265	G266	C267	G268	C269	A270	G271	C272	G273	U276	G277	U284	A285	G286	U289	G291	U292	U293	A294	G295	U296	G297	A298	G299	A309	A310	A311										
G312	G313	G317	C318	G319	A320	U321	A322	G329	A330	C331	A332	G333	C336	G337	A342	A345	A346	U349	G350	A354	U355	G356	C357	U358	G361	C366	G367	A368	U369	A370	A371	G372	G377	A378	G379	A384	C385	G386	U387	G388	C389	U390	A391	A395										
G396	U397	C398	U399	U403	A404	U405	G406	G411	A412	C413	A419	G424	A428	A429	A430	U431	C435	A436	U437	U441	U442	A443	C444	C445	G446	A447	U451	A452	A453	A454	C455	C456	A457	U458	U459	A460	C461	A462	G463	U464	G465	A466	C467	G468	U469	A470	A471	A472	C475	G476				
A477	A478	U479	A480	A481	A482	A483	C484	C487	A488	G489	C490	A491	A503	A504	A505	U506	A507	C509	C510	U511	G512	A513	A514	A515	C516	U517	A518	U519	A520	U521	A522	C523	A524	U525	A526	C527	A528	A529	U530	A532	G533	U534	G535	U536	G537	A538	U539	G540	A541	C542	G543			
C544	U545	U546	A547	G548	C550	G553	U558	A559	A560	U562	A563	C564	U567	U568	U569	A570	U571	A572	U573	A574	C575	A576	G577	U580	C581	A582	U583	A584	U585	A586	U589	A590	U591	A592	U593	U594	A603	G604	U607	G611	G612	A613	U614	U615	A616	G620	A621	C624						
A631	A632	A633	G636	A637	U639	C640	U641	U642	A643	A644	C645	U646	U647	G648	C649	G650	U651	U652	U653	A654	A655	G656	G662	G663	U664	A665	U666	A667	A668	G669	A670	C671	C672	U673	A674	U675	A676	A677	C680	U681	U682	U683	A684	U685	U686	U687	U688	U689	U694	G695	U696	G697	U697	
G700	G701	U702	U703	G704	A705	U706	G707	G708	G711	G712	A715	U716	G717	A718	C719	G723	U724	G725	G726	A727	U728	G729	A730	G731	G732	G733	A734	A735	G736	G737	G738	U741	U744	G745	U746	U747	G748	A750	A751	A752	U753	U754	U755	A756	G757	C758	U759	G763	A764	G765	U766	U767		
U773	G775	G776	G777	G778	U779	A781	A782	G783	A784	G785	C786	U789	U790	G791	A792	A793	G794	C795	G796	U797	G798	A802	U803	A804	G805	C806	U810	C812	U813	C814	C815	C816	A819	G822	C823	U824	A825	U826	U827	U828	A829	A830	G831	A832	U833	C834	U839	C840	G841					
A844	A845	U846	C848	U852	C853	G857	G858	U860	A861	G862	A863	G864	C865	A866	C867	U868	U869	U870	U871	U872	C873	G874	C875	C876	A877	A878	G881	G882	U883	U884	C885	A886	U887	C888	A891	A892	C893	U894	A895	A896	C897	C898	A899	A900	C901	C902	C903	U906	G907	C908	A909	A910		
A911	C912	U913	G914	C915	G916	A917	A918	U919	A920	G923	G924	A925	G926	U927	U931	A932	A933	U934	C937	G938	G939	G940	A941	A945	C946	A947	C948	G949	C950	G951	U952	C953	G954	U955	G956	C957	U958	C961	C964	C968	G969	U970	A973	G974	A975	U976	G977	A980	A981	C982	A983			
A984	C985	G986	G987	A988	G989	C994	C995	A996	U999	G1002	G1003	U1004	C1005	G1006	C1007	A1008	A1009	U1012	C1013	A1014	U1015	G1016	U1019	C1020	A1021	G1022	G1025	G1026	A1027	A1028	C1029	C1030	G1031	C1034	G1038	C1044	A1048	C1052	G1055	G1056	A1057	U1058	G1059	U1060	U1061	C1062	G1063							
G1064	U1065	A1066	G1067	G1068	A1069	U1070	G1071	C1072	A1073	C1079	A1080	U1081	U1082	A1083	A1084	A1085	A1086	G1087	G1093	U1094	A1095	A1096	U1097	A1098	U1101	C1104	G1107	U1108	U1109	G1110	A1111	G1112	U1113	C1114	G1115	G1116	C1117	U1118	U1119	G1125	A1126	U1127	G1128	A1129	U1130	U1131	U1132	A1133	A1134	C1135	G1136			



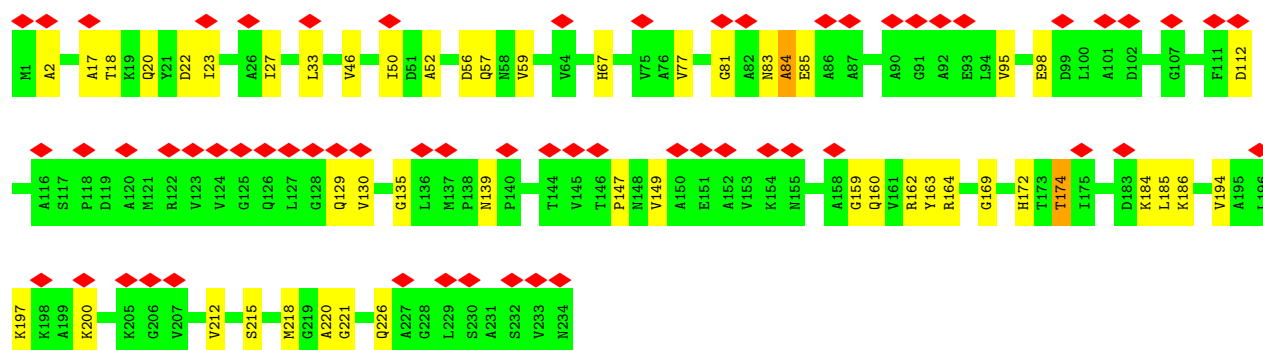
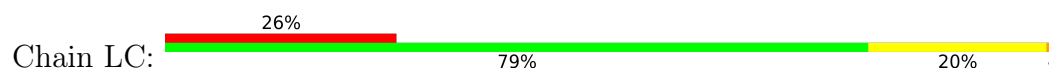


• Molecule 26: 5S ribosomal RNA

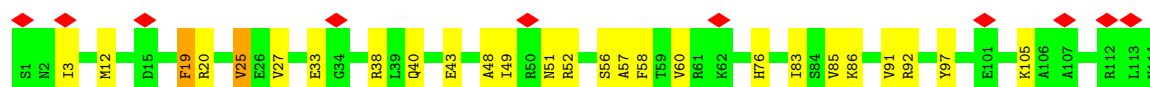
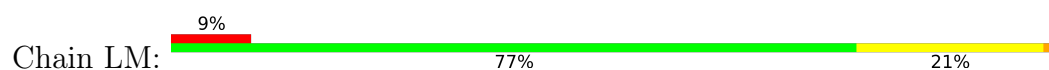
Chain LB: 48% 35% 13%



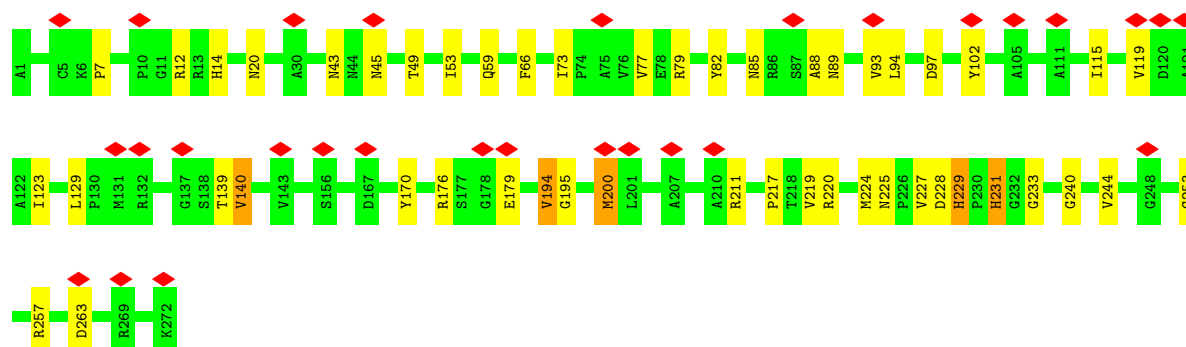
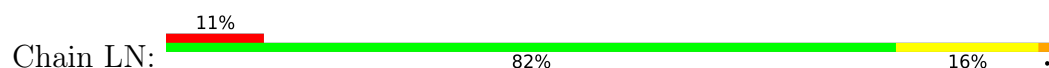
• Molecule 27: 50S ribosomal protein L1



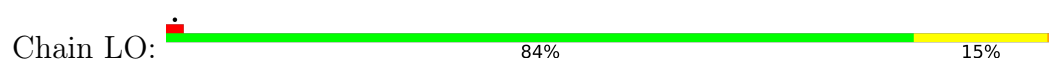
- Molecule 28: 50S ribosomal protein L19



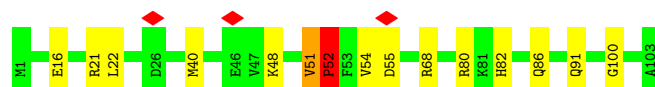
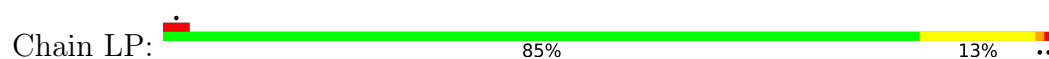
- Molecule 29: 50S ribosomal protein L2



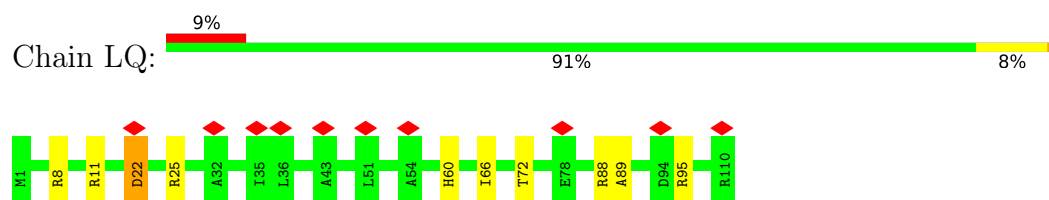
- Molecule 30: 50S ribosomal protein L20



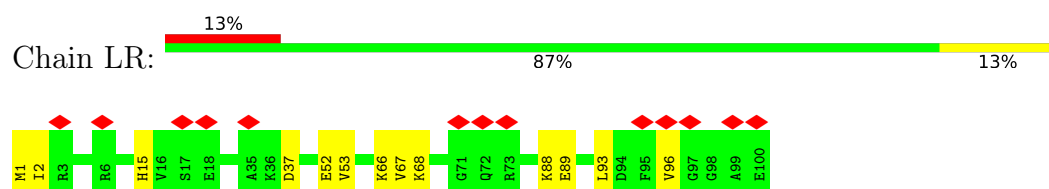
- Molecule 31: 50S ribosomal protein L21



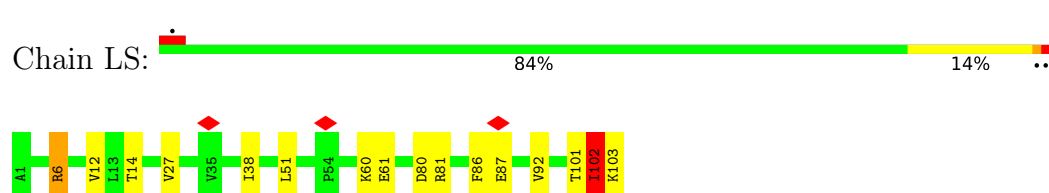
- Molecule 32: 50S ribosomal protein L22



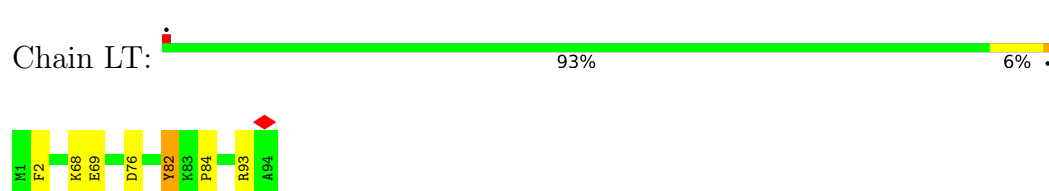
- Molecule 33: 50S ribosomal protein L23



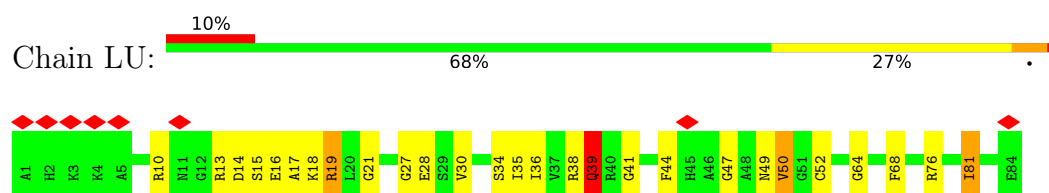
- Molecule 34: 50S ribosomal protein L24



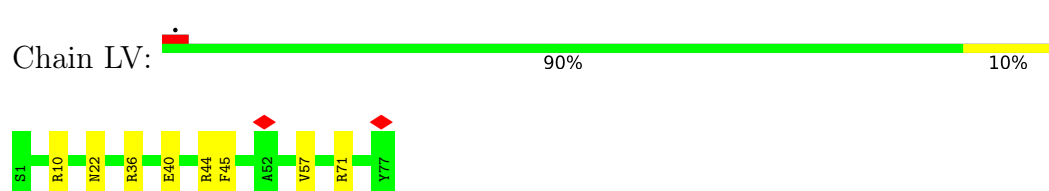
- Molecule 35: 50S ribosomal protein L25



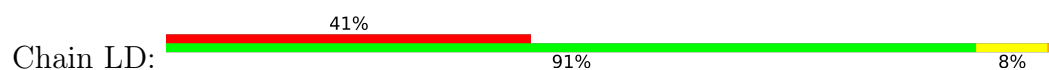
- Molecule 36: 50S ribosomal protein L27

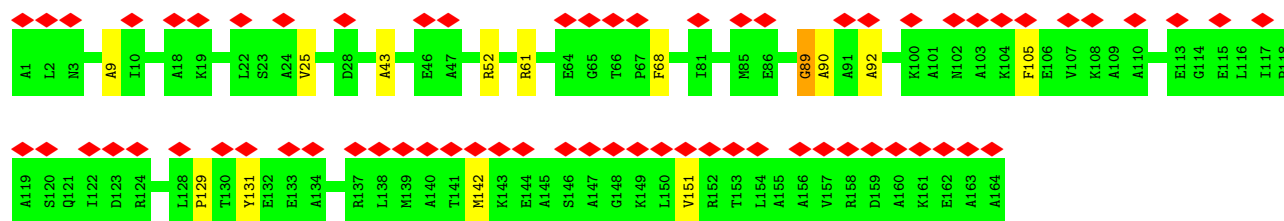


- Molecule 37: 50S ribosomal protein L28

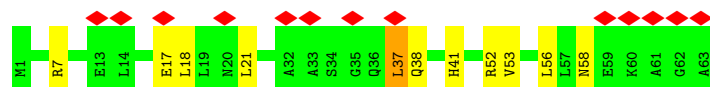
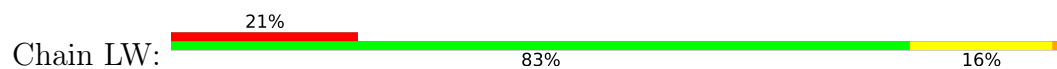


- Molecule 38: 50S ribosomal protein L10

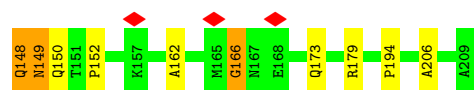
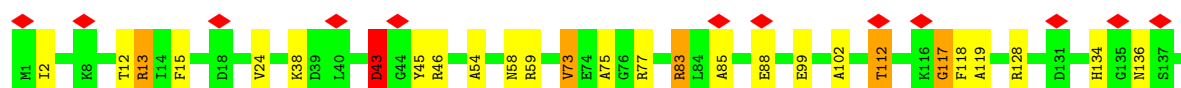
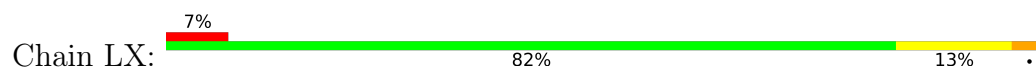




- Molecule 39: 50S ribosomal protein L29



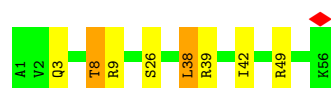
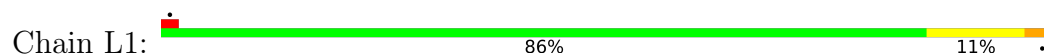
- Molecule 40: 50S ribosomal protein L3



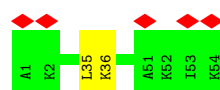
- Molecule 41: 50S ribosomal protein L30



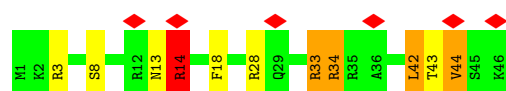
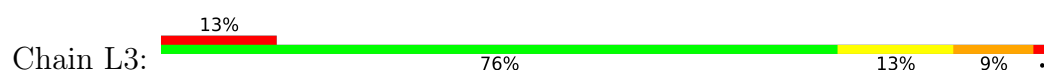
- Molecule 42: 50S ribosomal protein L32



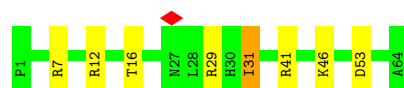
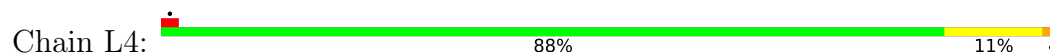
- Molecule 43: 50S ribosomal protein L33



- Molecule 44: 50S ribosomal protein L34



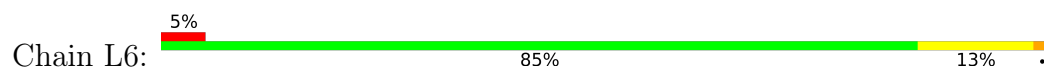
- Molecule 45: 50S ribosomal protein L35



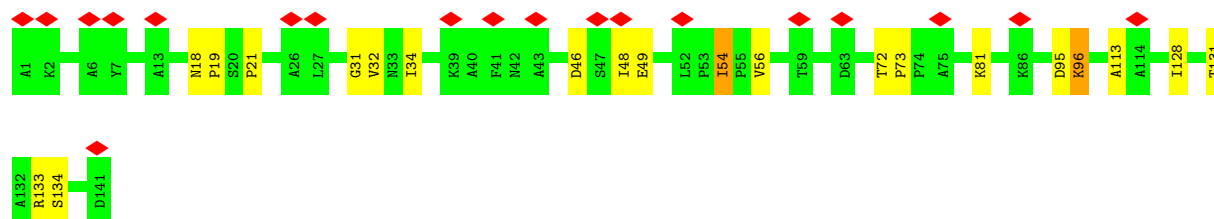
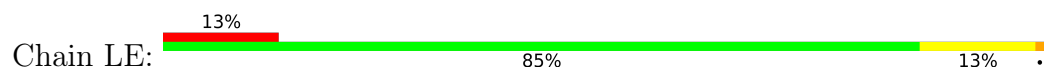
- Molecule 46: 50S ribosomal protein L36



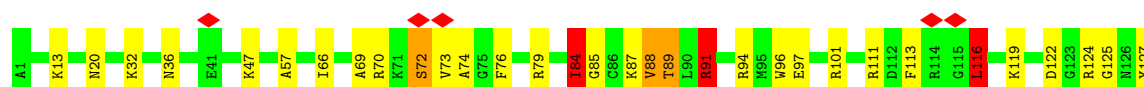
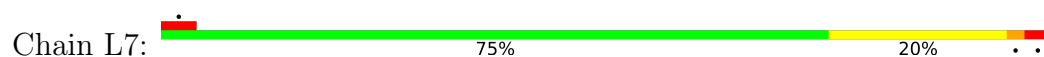
- Molecule 47: 50S ribosomal protein L4



- Molecule 48: 50S ribosomal protein L11

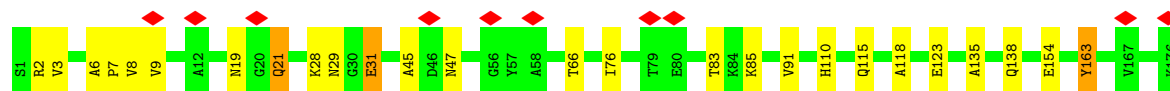
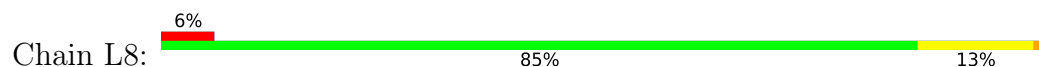


- Molecule 49: 50S ribosomal protein L5

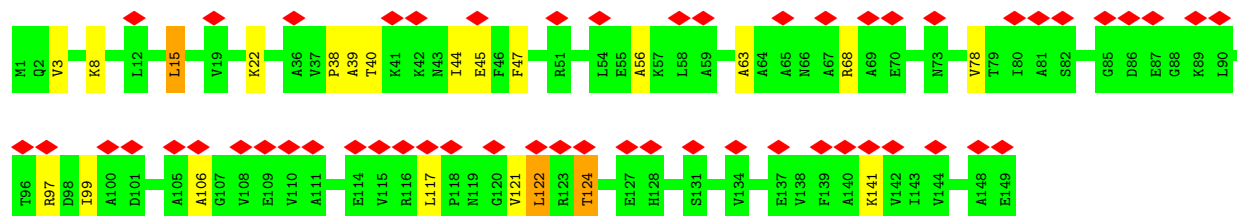
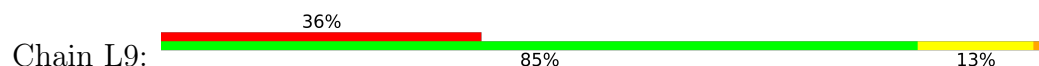




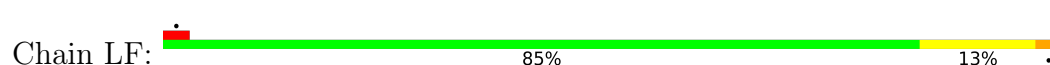
- Molecule 50: 50S ribosomal protein L6



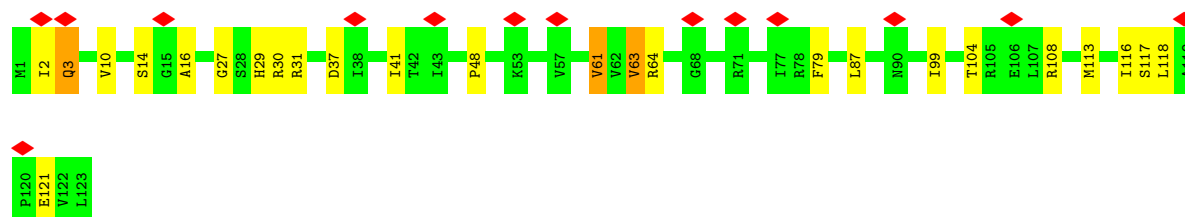
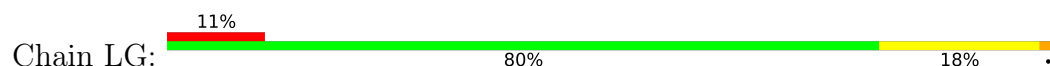
- Molecule 51: 50S ribosomal protein L9



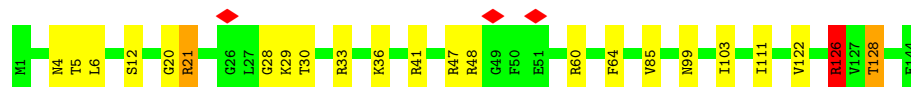
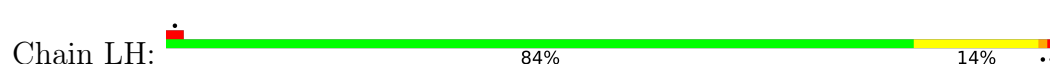
- Molecule 52: 50S ribosomal protein L13



- Molecule 53: 50S ribosomal protein L14

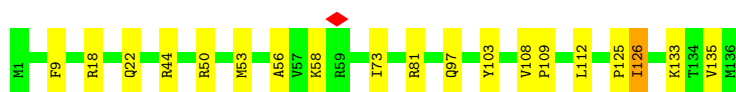


- Molecule 54: 50S ribosomal protein L15



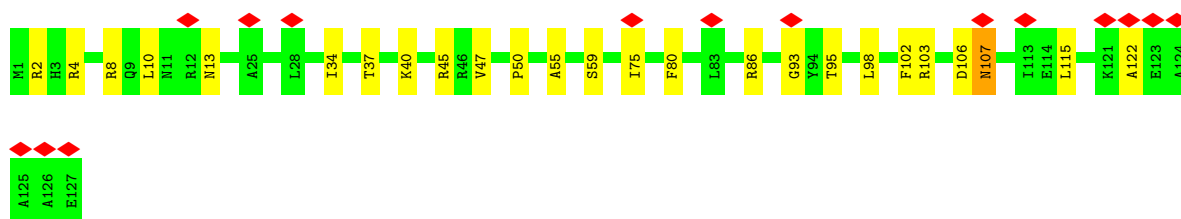
- Molecule 55: 50S ribosomal protein L16

Chain LI:  86% 13%



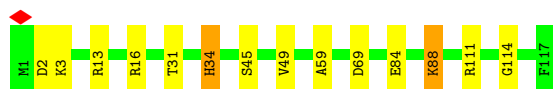
- Molecule 56: 50S ribosomal protein L17

Chain LJ:  12% 80% 19%



- Molecule 57: 50S ribosomal protein L18

Chain LK:  88% 10%



- Molecule 58: 50S ribosomal protein L31

Chain LZ:  26% 86% 10%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	90000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	CTFFIND3 and CTFIT	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	58000	Depositor
Image detector	DIRECT ELECTRON DE-12 (4k x 3k)	Depositor
Maximum map value	0.305	Depositor
Minimum map value	-0.154	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	377.99997, 377.99997, 377.99997	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP

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	SA	1.12	20/37035 (0.1%)	1.46	575/57774 (1.0%)
2	S6	1.06	0/1831	1.36	24/2853 (0.8%)
3	S7	1.10	0/1762	1.53	34/2746 (1.2%)
4	SJ	1.03	0/835	1.58	9/1127 (0.8%)
5	SK	1.03	1/982 (0.1%)	1.59	8/1323 (0.6%)
6	SL	1.03	0/969	1.55	6/1300 (0.5%)
7	SM	0.96	0/919	1.62	6/1226 (0.5%)
8	SN	0.95	0/817	1.61	4/1088 (0.4%)
9	SO	1.00	0/724	1.61	2/966 (0.2%)
10	SP	1.00	0/659	1.57	4/884 (0.5%)
11	SQ	1.00	0/681	1.55	6/913 (0.7%)
12	SR	0.95	0/637	1.53	5/851 (0.6%)
13	SS	0.95	0/744	1.69	6/995 (0.6%)
14	SB	0.91	0/1904	1.65	15/2565 (0.6%)
15	ST	0.95	0/676	1.65	3/895 (0.3%)
16	SU	1.06	0/598	1.75	6/792 (0.8%)
17	SC	1.02	0/1852	1.54	9/2490 (0.4%)
18	SD	0.90	0/1665	1.59	10/2227 (0.4%)
19	SE	1.04	1/1239 (0.1%)	1.65	15/1664 (0.9%)
20	SF	0.99	0/1121	1.61	13/1509 (0.9%)
21	SG	0.97	0/1422	1.60	8/1908 (0.4%)
22	SH	0.96	0/989	1.53	6/1326 (0.5%)
23	SI	0.96	0/1048	1.49	3/1394 (0.2%)
24	S1	0.91	0/5532	1.61	50/7485 (0.7%)
25	LA	1.17	35/69812 (0.1%)	1.47	1142/108912 (1.0%)
26	LB	1.05	1/2869 (0.0%)	1.34	27/4474 (0.6%)
27	LC	0.91	0/1748	1.70	28/2355 (1.2%)
28	LM	1.04	0/929	1.62	11/1242 (0.9%)
29	LN	1.06	0/2131	1.63	20/2863 (0.7%)
30	LO	0.99	0/960	1.69	12/1278 (0.9%)
31	LP	1.03	0/829	1.48	8/1107 (0.7%)
32	LQ	1.10	0/864	1.58	8/1156 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LR	1.02	0/794	1.53	5/1060 (0.5%)
34	LS	0.94	0/797	1.52	7/1062 (0.7%)
35	LT	0.97	0/766	1.45	4/1025 (0.4%)
36	LU	1.05	0/642	1.68	7/848 (0.8%)
37	LV	1.06	0/635	1.63	6/848 (0.7%)
38	LD	0.89	0/1247	1.61	13/1679 (0.8%)
39	LW	0.95	0/510	1.70	9/677 (1.3%)
40	LX	1.10	1/1586 (0.1%)	1.65	17/2134 (0.8%)
41	LY	0.95	0/453	1.66	3/605 (0.5%)
42	L1	1.04	0/450	1.59	0/599
43	L2	1.01	0/448	1.45	0/594
44	L3	1.15	1/380 (0.3%)	1.83	10/498 (2.0%)
45	L4	0.95	0/513	1.66	6/676 (0.9%)
46	L5	1.18	0/303	1.57	1/397 (0.3%)
47	L6	0.95	0/1571	1.62	15/2113 (0.7%)
48	LE	0.85	0/1046	1.66	16/1410 (1.1%)
49	L7	0.93	0/1444	1.71	17/1937 (0.9%)
50	L8	0.93	0/1343	1.54	8/1816 (0.4%)
51	L9	0.91	0/1122	1.61	13/1515 (0.9%)
52	LF	1.09	0/1152	1.64	10/1551 (0.6%)
53	LG	1.14	1/956 (0.1%)	1.56	8/1279 (0.6%)
54	LH	0.97	0/1062	1.60	6/1413 (0.4%)
55	LI	1.03	0/1093	1.59	16/1460 (1.1%)
56	LJ	1.06	0/1021	1.60	3/1364 (0.2%)
57	LK	0.96	0/910	1.57	6/1219 (0.5%)
58	LZ	0.93	0/559	1.64	7/745 (0.9%)
All	All	1.10	61/169586 (0.0%)	1.51	2296/252212 (0.9%)

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
1	SA	2	423
2	S6	0	16
3	S7	0	31
4	SJ	0	7
5	SK	0	5
6	SL	0	9
7	SM	0	4
8	SN	0	5

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
9	SO	0	4
10	SP	0	4
11	SQ	0	4
12	SR	0	3
13	SS	0	2
14	SB	0	3
15	ST	0	2
16	SU	0	3
17	SC	0	7
18	SD	0	6
19	SE	0	8
20	SF	0	6
21	SG	0	4
22	SH	0	3
23	SI	0	4
24	S1	0	19
25	LA	1	941
26	LB	0	21
27	LC	0	4
28	LM	0	5
29	LN	0	9
30	LO	0	4
31	LP	0	1
32	LQ	0	2
34	LS	0	3
35	LT	0	2
36	LU	0	5
37	LV	0	3
38	LD	0	3
39	LW	0	4
40	LX	0	10
41	LY	0	1
42	L1	0	2
44	L3	0	5
45	L4	0	3
46	L5	0	1
47	L6	0	6
48	LE	0	1
49	L7	0	8
50	L8	0	3
51	L9	0	2
52	LF	0	6

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
53	LG	0	4
54	LH	0	5
55	LI	0	1
56	LJ	0	6
57	LK	0	3
58	LZ	0	4
All	All	3	1660

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	LA	2571	U	O3'-P	-8.13	1.49	1.61
44	L3	18	PHE	CA-C	-7.41	1.47	1.52
1	SA	51	A	O3'-P	-7.29	1.50	1.61
19	SE	55	VAL	CA-CB	-7.28	1.50	1.54
25	LA	2665	A	C1'-N9	-6.97	1.37	1.48

The worst 5 of 2296 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	LA	1900	A	P-O3'-C3'	20.44	150.87	120.20
1	SA	51	A	P-O3'-C3'	19.85	149.97	120.20
1	SA	810	C	P-O5'-C5'	17.34	146.91	120.90
25	LA	1420	A	P-O3'-C3'	15.01	142.71	120.20
25	LA	1409	U	P-O5'-C5'	14.91	143.26	120.90

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	SA	1498	U	C3',C4'
25	LA	2251	G	C1'

5 of 1660 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	SA	20	U	Sidechain
1	SA	21	G	Sidechain
1	SA	33	A	Sidechain
1	SA	4	U	Sidechain
1	SA	9	G	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	SA	33076	0	16648	113	0
2	S6	1639	0	837	1	0
3	S7	1577	0	800	5	0
4	SJ	825	0	865	0	0
5	SK	965	0	997	3	0
6	SL	955	0	1019	2	0
7	SM	910	0	981	2	0
8	SN	805	0	847	1	0
9	SO	716	0	742	0	0
10	SP	649	0	666	0	0
11	SQ	672	0	716	0	0
12	SR	626	0	651	0	0
13	SS	727	0	769	2	0
14	SB	1872	0	1885	1	0
15	ST	670	0	722	3	0
16	SU	590	0	631	1	0
17	SC	1822	0	1913	2	0
18	SD	1643	0	1710	2	0
19	SE	1225	0	1273	1	0
20	SF	1101	0	1050	1	0
21	SG	1400	0	1449	2	0
22	SH	979	0	1034	1	0
23	SI	1036	0	1084	0	0
24	S1	5431	0	5403	18	0
25	LA	62333	0	31349	252	0
26	LB	2566	0	1302	10	0
27	LC	1733	0	1824	6	0
28	LM	917	0	965	1	0
29	LN	2092	0	2170	7	0
30	LO	947	0	1022	1	0
31	LP	816	0	839	2	0
32	LQ	857	0	922	1	0
33	LR	787	0	846	0	0
34	LS	789	0	847	1	0
35	LT	753	0	780	0	0
36	LU	634	0	656	4	0
37	LV	625	0	655	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	LD	1233	0	1283	1	0
39	LW	509	0	543	2	0
40	LX	1565	0	1616	2	0
41	LY	449	0	491	1	0
42	L1	444	0	461	5	0
43	L2	441	0	485	0	0
44	L3	377	0	418	0	0
45	L4	504	0	574	0	0
46	L5	302	0	343	0	0
47	L6	1552	0	1619	3	0
48	LE	1032	0	1088	0	0
49	L7	1420	0	1460	4	0
50	L8	1323	0	1374	2	0
51	L9	1111	0	1148	0	0
52	LF	1129	0	1162	7	0
53	LG	947	0	1023	5	0
54	LH	1053	0	1129	2	0
55	LI	1074	0	1157	2	0
56	LJ	1008	0	1045	4	0
57	LK	900	0	935	0	0
58	LZ	549	0	552	1	0
59	S1	32	0	12	16	0
All	All	156714	0	108787	462	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 2.

The worst 5 of 462 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)
24:S1:22:LYS:CE	59:S1:801:GTP:O3G	2.13	0.97
24:S1:23:THR:N	59:S1:801:GTP:O2B	2.08	0.86
24:S1:22:LYS:HE3	59:S1:801:GTP:O3G	1.76	0.85
24:S1:144:ASP:CG	59:S1:801:GTP:HN1	1.89	0.79
21:SG:77:ARG:HE	21:SG:152:HIS:CD2	2.05	0.74

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SJ	101/103 (98%)	98 (97%)	0	3 (3%)	3	25
5	SK	126/128 (98%)	104 (82%)	17 (14%)	5 (4%)	2	20
6	SL	121/123 (98%)	109 (90%)	10 (8%)	2 (2%)	7	35
7	SM	115/117 (98%)	101 (88%)	9 (8%)	5 (4%)	2	18
8	SN	98/100 (98%)	88 (90%)	9 (9%)	1 (1%)	12	45
9	SO	86/88 (98%)	83 (96%)	1 (1%)	2 (2%)	5	30
10	SP	80/82 (98%)	72 (90%)	4 (5%)	4 (5%)	1	16
11	SQ	81/83 (98%)	71 (88%)	8 (10%)	2 (2%)	4	28
12	SR	72/74 (97%)	58 (81%)	11 (15%)	3 (4%)	2	19
13	SS	89/91 (98%)	74 (83%)	10 (11%)	5 (6%)	1	14
14	SB	238/240 (99%)	217 (91%)	13 (6%)	8 (3%)	3	23
15	ST	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	10	41
16	SU	68/70 (97%)	52 (76%)	11 (16%)	5 (7%)	1	9
17	SC	230/232 (99%)	212 (92%)	13 (6%)	5 (2%)	5	30
18	SD	203/205 (99%)	177 (87%)	18 (9%)	8 (4%)	2	20
19	SE	164/166 (99%)	149 (91%)	13 (8%)	2 (1%)	10	41
20	SF	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	16	49
21	SG	176/178 (99%)	158 (90%)	15 (8%)	3 (2%)	7	35
22	SH	127/129 (98%)	121 (95%)	4 (3%)	2 (2%)	7	36
23	SI	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
24	S1	700/702 (100%)	632 (90%)	45 (6%)	23 (3%)	3	24
27	LC	232/234 (99%)	206 (89%)	19 (8%)	7 (3%)	3	25
28	LM	112/114 (98%)	99 (88%)	10 (9%)	3 (3%)	4	27
29	LN	270/272 (99%)	244 (90%)	16 (6%)	10 (4%)	2	21
30	LO	115/117 (98%)	108 (94%)	4 (4%)	3 (3%)	4	27

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	LP	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	6	32
32	LQ	108/110 (98%)	102 (94%)	5 (5%)	1 (1%)	14	46
33	LR	98/100 (98%)	84 (86%)	9 (9%)	5 (5%)	1	15
34	LS	101/103 (98%)	89 (88%)	8 (8%)	4 (4%)	2	20
35	LT	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	11	43
36	LU	82/84 (98%)	56 (68%)	15 (18%)	11 (13%)	0	3
37	LV	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
38	LD	162/164 (99%)	154 (95%)	7 (4%)	1 (1%)	21	54
39	LW	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
40	LX	207/209 (99%)	168 (81%)	25 (12%)	14 (7%)	1	11
41	LY	56/58 (97%)	52 (93%)	3 (5%)	1 (2%)	6	34
42	L1	54/56 (96%)	47 (87%)	5 (9%)	2 (4%)	2	21
43	L2	52/54 (96%)	44 (85%)	7 (14%)	1 (2%)	6	33
44	L3	44/46 (96%)	39 (89%)	2 (4%)	3 (7%)	1	11
45	L4	62/64 (97%)	59 (95%)	2 (3%)	1 (2%)	7	36
46	L5	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
47	L6	199/201 (99%)	172 (86%)	18 (9%)	9 (4%)	2	17
48	LE	139/141 (99%)	123 (88%)	12 (9%)	4 (3%)	3	26
49	L7	176/178 (99%)	137 (78%)	21 (12%)	18 (10%)	0	5
50	L8	174/176 (99%)	156 (90%)	9 (5%)	9 (5%)	1	15
51	L9	147/149 (99%)	132 (90%)	9 (6%)	6 (4%)	2	19
52	LF	140/142 (99%)	122 (87%)	16 (11%)	2 (1%)	9	38
53	LG	121/123 (98%)	107 (88%)	12 (10%)	2 (2%)	7	35
54	LH	142/144 (99%)	129 (91%)	5 (4%)	8 (6%)	1	14
55	LI	134/136 (98%)	122 (91%)	10 (8%)	2 (2%)	8	37
56	LJ	125/127 (98%)	110 (88%)	9 (7%)	6 (5%)	2	16
57	LK	115/117 (98%)	107 (93%)	5 (4%)	3 (3%)	4	27
58	LZ	68/70 (97%)	56 (82%)	10 (15%)	2 (3%)	3	26
All	All	7019/7125 (98%)	6254 (89%)	534 (8%)	231 (3%)	5	24

5 of 231 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	SK	125	LYS
7	SM	62	PHE
16	SU	7	GLU
18	SD	48	SER
18	SD	134	TYR

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	SJ	90/90 (100%)	88 (98%)	2 (2%)	45	65
5	SK	98/98 (100%)	91 (93%)	7 (7%)	13	40
6	SL	103/103 (100%)	100 (97%)	3 (3%)	37	60
7	SM	95/95 (100%)	90 (95%)	5 (5%)	20	48
8	SN	83/83 (100%)	81 (98%)	2 (2%)	43	63
9	SO	76/76 (100%)	75 (99%)	1 (1%)	61	72
10	SP	65/65 (100%)	64 (98%)	1 (2%)	57	70
11	SQ	77/77 (100%)	74 (96%)	3 (4%)	28	54
12	SR	64/64 (100%)	62 (97%)	2 (3%)	35	59
13	SS	78/78 (100%)	77 (99%)	1 (1%)	61	72
14	SB	198/198 (100%)	191 (96%)	7 (4%)	32	57
15	ST	65/65 (100%)	64 (98%)	1 (2%)	57	70
16	SU	60/60 (100%)	56 (93%)	4 (7%)	15	42
17	SC	189/189 (100%)	182 (96%)	7 (4%)	30	56
18	SD	172/172 (100%)	165 (96%)	7 (4%)	27	53
19	SE	125/125 (100%)	116 (93%)	9 (7%)	13	40
20	SF	116/116 (100%)	111 (96%)	5 (4%)	26	52
21	SG	146/146 (100%)	141 (97%)	5 (3%)	32	57
22	SH	104/104 (100%)	101 (97%)	3 (3%)	37	60
23	SI	106/106 (100%)	105 (99%)	1 (1%)	70	76

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	S1	575/575 (100%)	559 (97%)	16 (3%)	38	60
27	LC	181/181 (100%)	174 (96%)	7 (4%)	28	54
28	LM	99/99 (100%)	90 (91%)	9 (9%)	9	33
29	LN	217/217 (100%)	207 (95%)	10 (5%)	24	51
30	LO	89/89 (100%)	87 (98%)	2 (2%)	45	65
31	LP	84/84 (100%)	78 (93%)	6 (7%)	13	40
32	LQ	93/93 (100%)	92 (99%)	1 (1%)	65	74
33	LR	84/84 (100%)	80 (95%)	4 (5%)	23	50
34	LS	84/84 (100%)	79 (94%)	5 (6%)	17	45
35	LT	78/78 (100%)	76 (97%)	2 (3%)	40	62
36	LU	62/62 (100%)	57 (92%)	5 (8%)	11	36
37	LV	67/67 (100%)	67 (100%)	0	100	100
38	LD	122/122 (100%)	121 (99%)	1 (1%)	73	77
39	LW	55/55 (100%)	55 (100%)	0	100	100
40	LX	164/164 (100%)	158 (96%)	6 (4%)	30	56
41	LY	48/48 (100%)	47 (98%)	1 (2%)	47	65
42	L1	47/47 (100%)	45 (96%)	2 (4%)	26	52
43	L2	48/48 (100%)	47 (98%)	1 (2%)	47	65
44	L3	38/38 (100%)	36 (95%)	2 (5%)	20	48
45	L4	51/51 (100%)	49 (96%)	2 (4%)	28	54
46	L5	34/34 (100%)	34 (100%)	0	100	100
47	L6	165/165 (100%)	161 (98%)	4 (2%)	43	63
48	LE	109/109 (100%)	101 (93%)	8 (7%)	13	40
49	L7	149/149 (100%)	140 (94%)	9 (6%)	17	45
50	L8	137/137 (100%)	129 (94%)	8 (6%)	18	46
51	L9	114/114 (100%)	107 (94%)	7 (6%)	17	45
52	LF	116/116 (100%)	113 (97%)	3 (3%)	40	62
53	LG	104/104 (100%)	98 (94%)	6 (6%)	18	46
54	LH	103/103 (100%)	98 (95%)	5 (5%)	22	49
55	LI	109/109 (100%)	106 (97%)	3 (3%)	38	60
56	LJ	103/103 (100%)	99 (96%)	4 (4%)	28	54

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	LK	87/87 (100%)	82 (94%)	5 (6%)	18	46
58	LZ	62/62 (100%)	61 (98%)	1 (2%)	55	69
All	All	5788/5788 (100%)	5567 (96%)	221 (4%)	30	55

5 of 221 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	LN	244	VAL
38	LD	68	PHE
57	LK	88	LYS
53	LG	37	ASP
30	LO	91	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
50	L8	37	ASN
51	L9	20	ASN
55	LI	3	GLN
24	S1	191	ASN
24	S1	119	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	SA	1542/1542 (100%)	314 (20%)	87 (5%)
2	S6	76/77 (98%)	13 (17%)	4 (5%)
25	LA	2903/2904 (99%)	570 (19%)	141 (4%)
26	LB	119/120 (99%)	21 (17%)	11 (9%)
3	S7	73/74 (98%)	29 (39%)	7 (9%)
All	All	4713/4717 (99%)	947 (20%)	250 (5%)

5 of 947 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	SA	2	A
1	SA	3	A
1	SA	4	U
1	SA	7	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	SA	8	A

5 of 250 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	LA	428	A
25	LA	2473	U
25	LA	1142	A
25	LA	2452	C
25	LA	2835	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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	$\# Z > 2$
59	GTP	S1	801	-	33,34,34	3.73	5 (15%)	50,54,54	1.67	11 (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
59	GTP	S1	801	-	-	2/22/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	S1	801	GTP	PB-O3B	20.18	1.81	1.59
59	S1	801	GTP	C5-C6	-3.00	1.33	1.44
59	S1	801	GTP	C5-N7	-2.74	1.33	1.39
59	S1	801	GTP	PG-O3G	-2.04	1.47	1.54
59	S1	801	GTP	PG-O2G	-2.04	1.47	1.54

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	S1	801	GTP	C2-N3-C4	4.85	120.65	112.30
59	S1	801	GTP	C5-C4-N3	-4.58	121.10	128.39
59	S1	801	GTP	C2-N1-C6	-3.79	118.24	125.11
59	S1	801	GTP	N9-C8-N7	-3.02	107.81	113.40
59	S1	801	GTP	N9-C4-N3	2.62	131.18	125.95

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	S1	801	GTP	O4'-C4'-C5'-O5'
59	S1	801	GTP	C3'-C4'-C5'-O5'

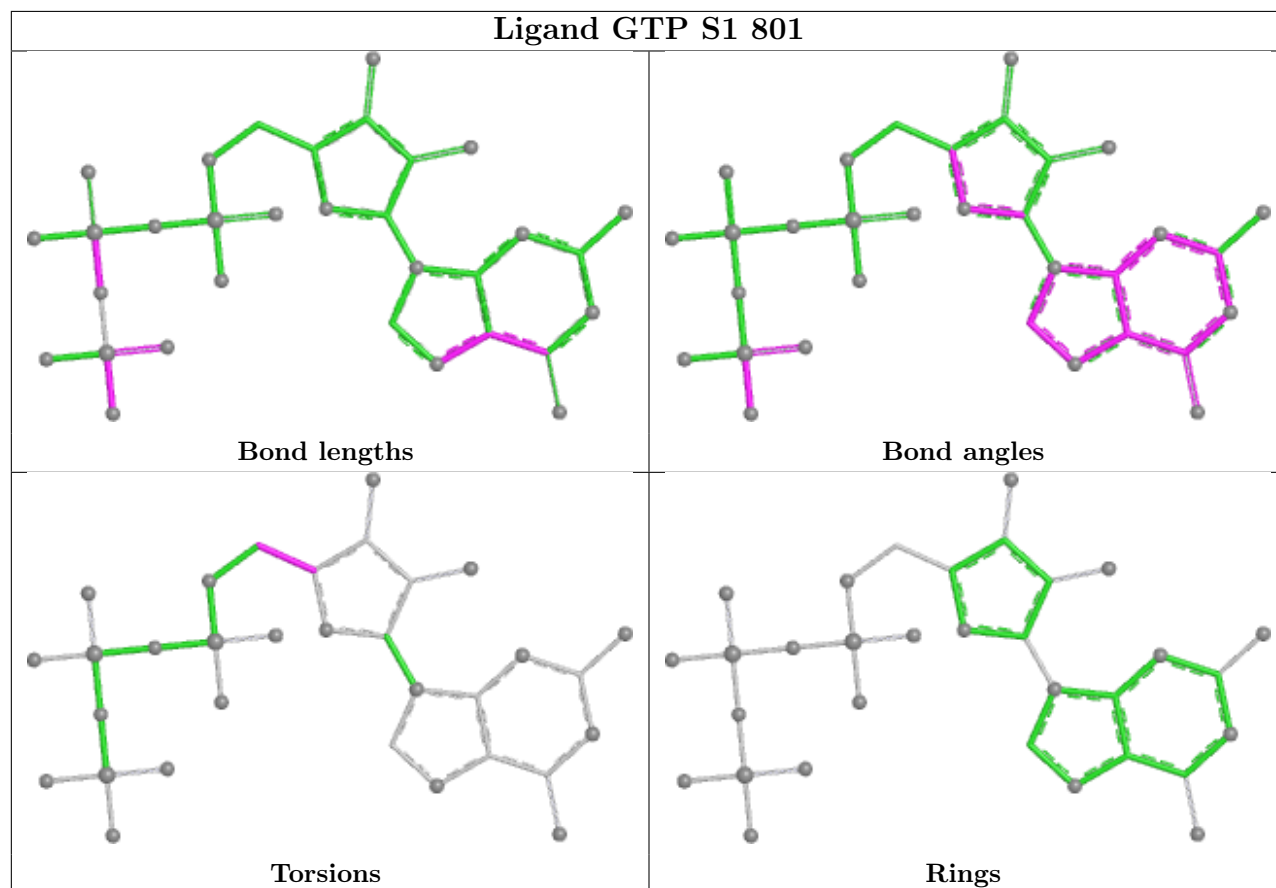
There are no ring outliers.

1 monomer is involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	S1	801	GTP	16	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.

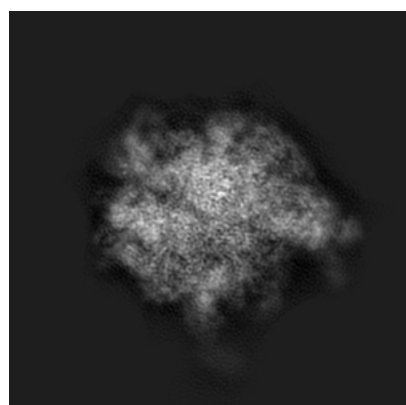
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6315. These allow visual inspection of the internal detail of the map and identification of artifacts.

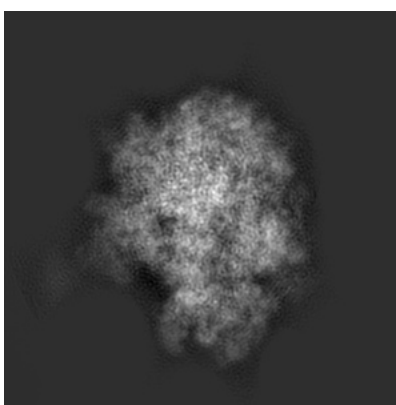
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

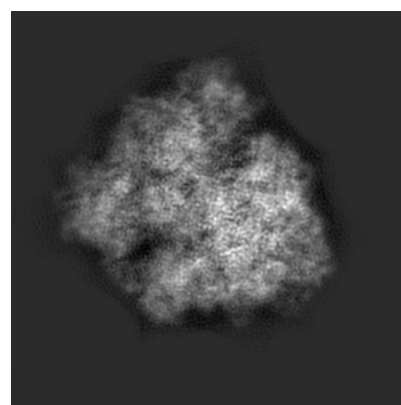
6.1.1 Primary map



X



Y

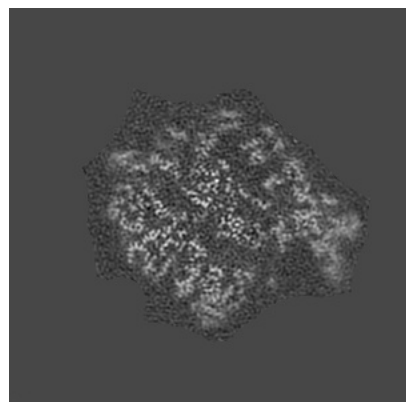


Z

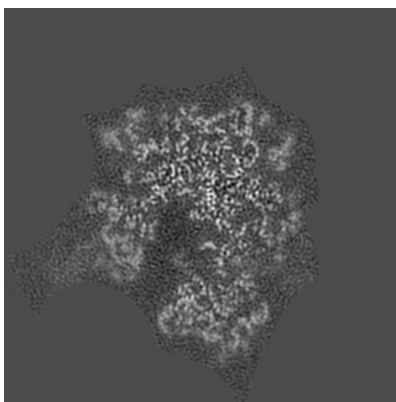
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

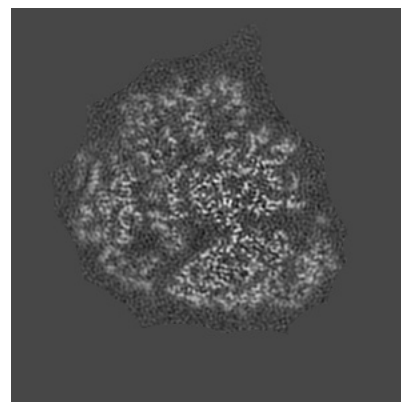
6.2.1 Primary map



X Index: 180



Y Index: 180

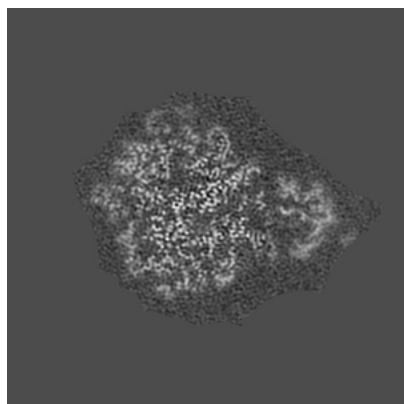


Z Index: 180

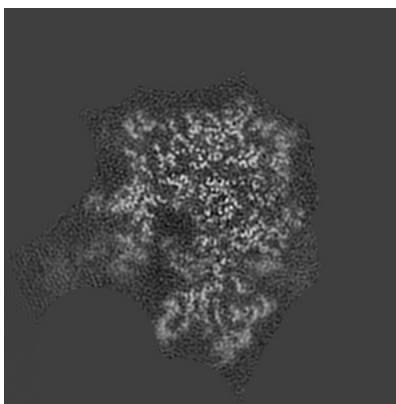
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

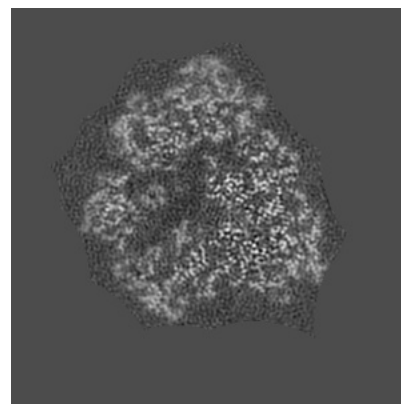
6.3.1 Primary map



X Index: 201



Y Index: 187

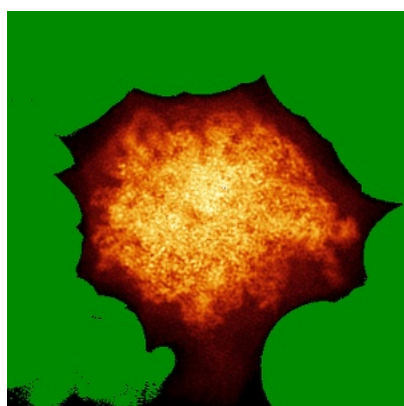


Z Index: 164

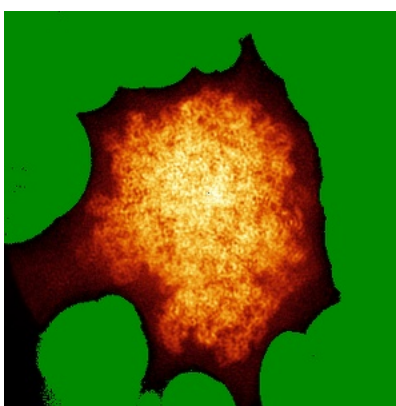
The images above show the largest variance slices of the map in three orthogonal directions.

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

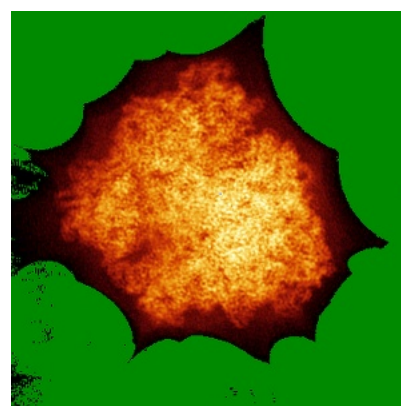
6.4.1 Primary map



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

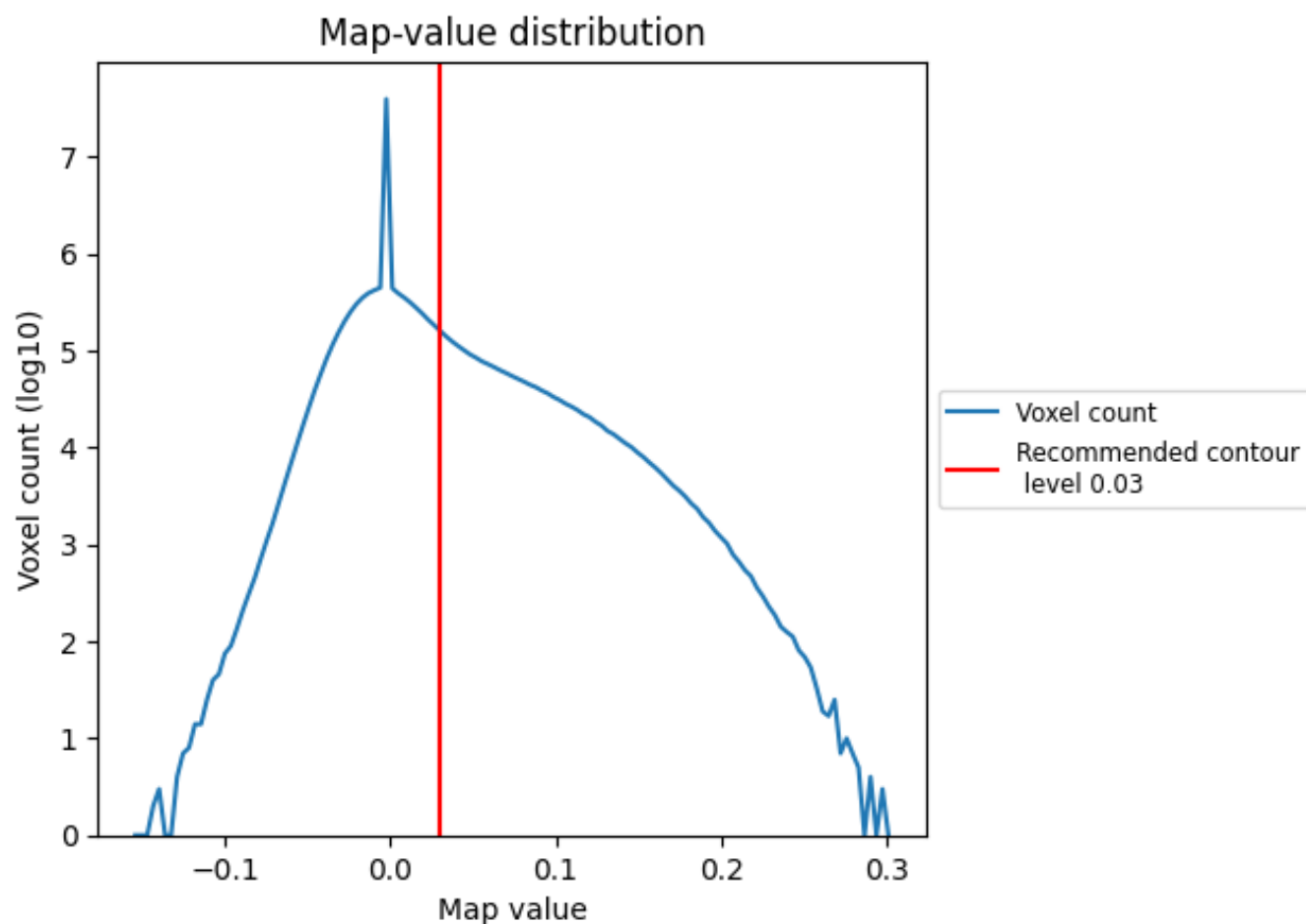
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

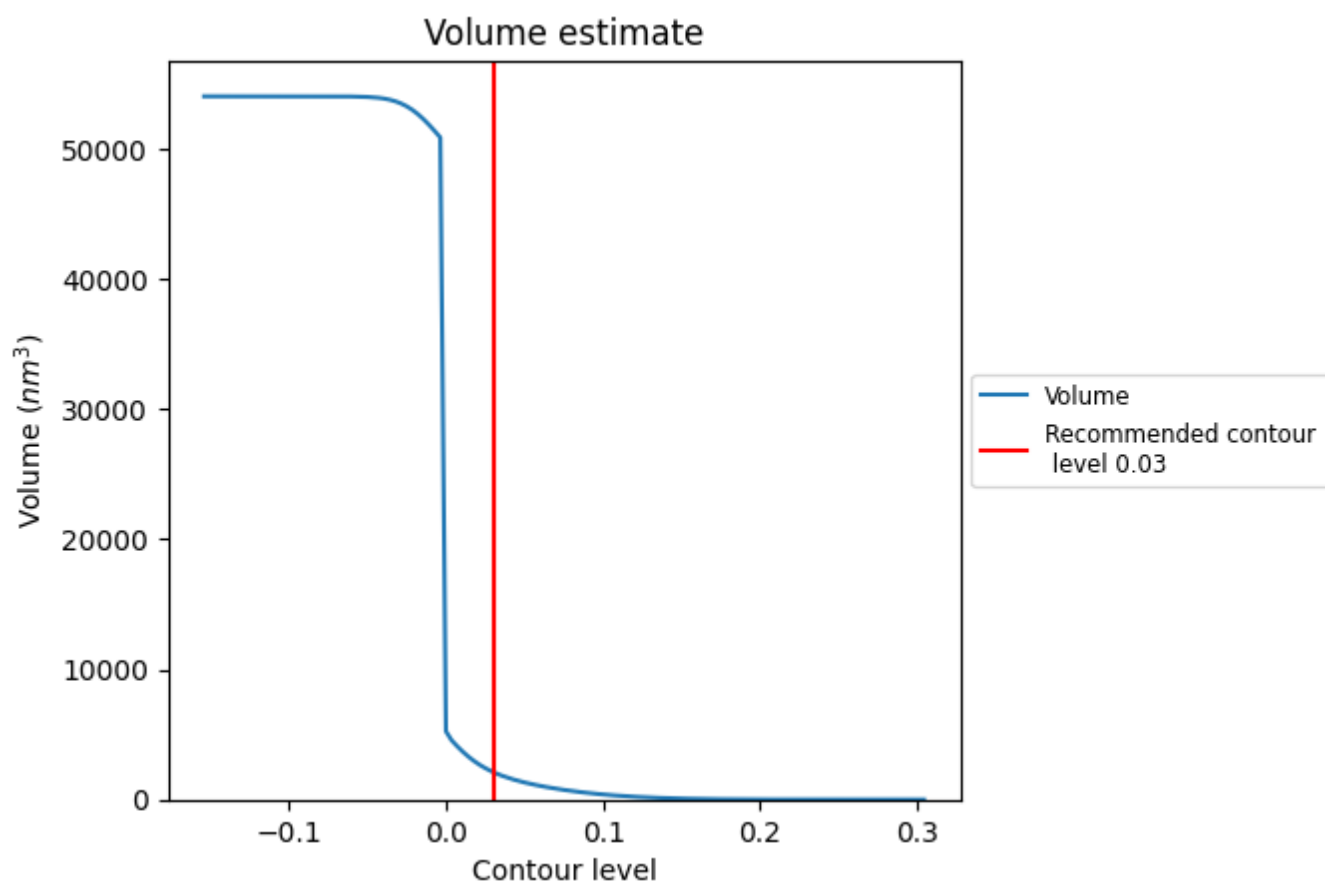
This section contains the results of statistical analysis of the map.

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.

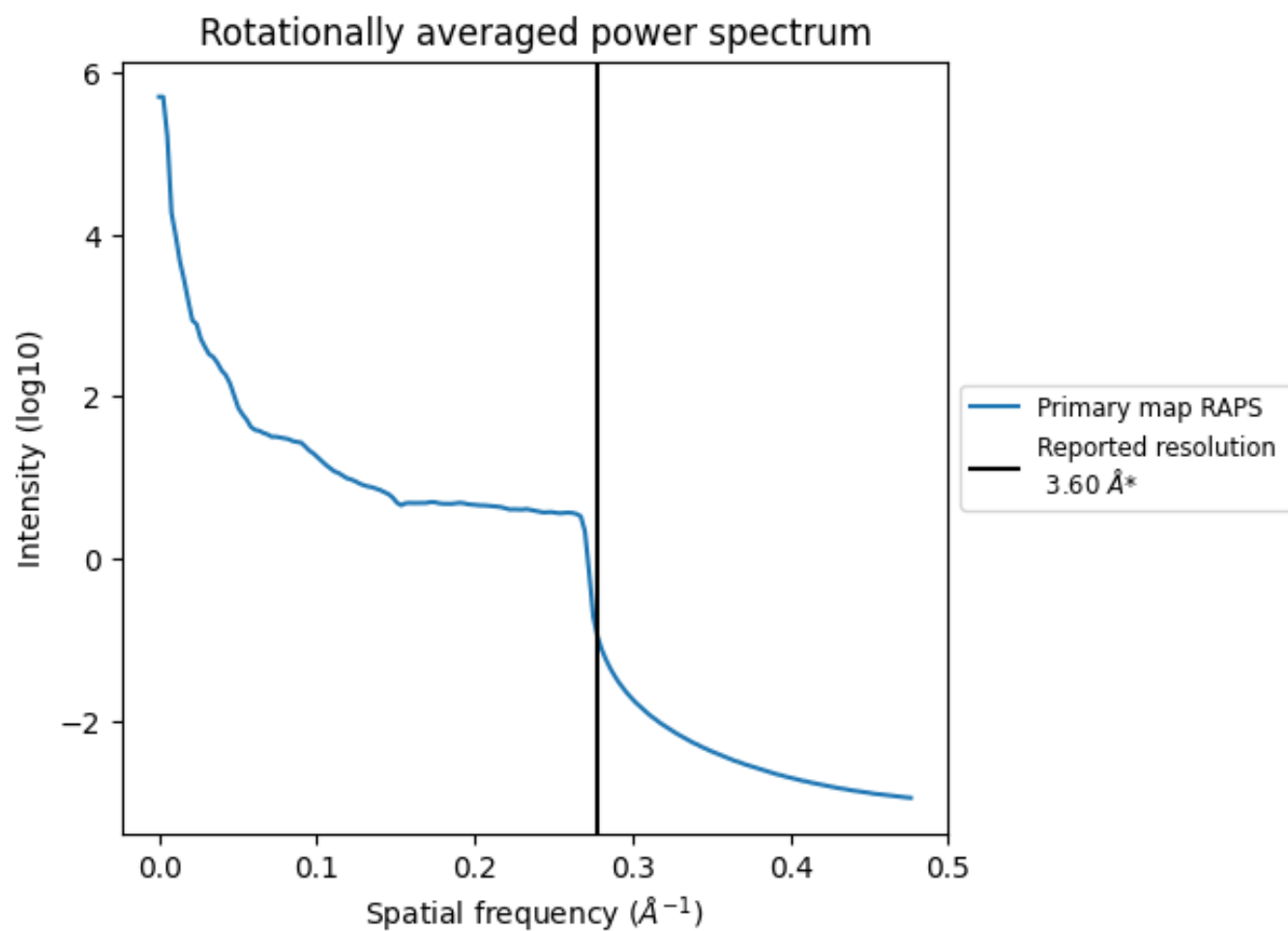
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2119 nm³; this corresponds to an approximate mass of 1915 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 0.278 Å⁻¹

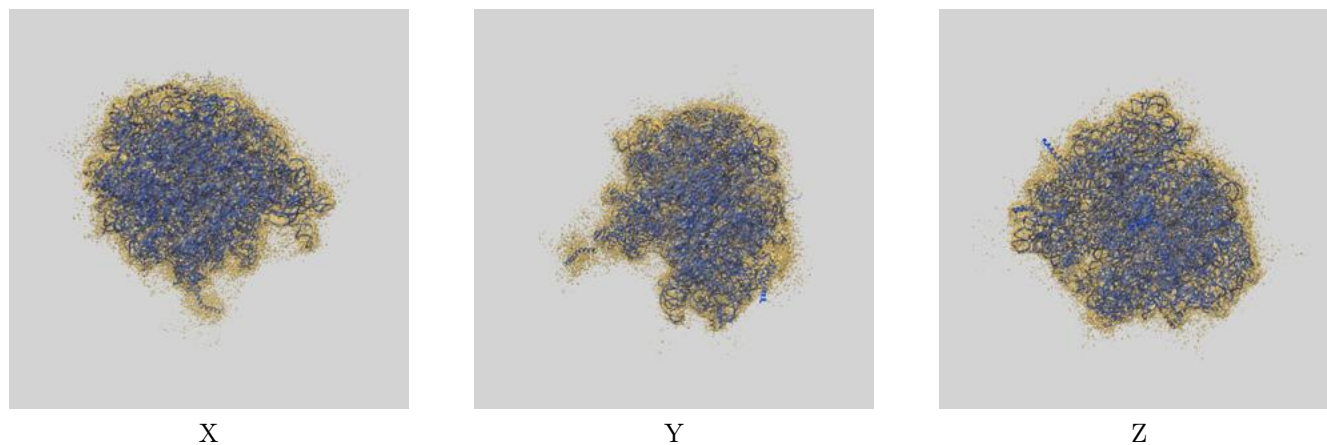
8 Fourier-Shell correlation

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-6315 and PDB model 3J9Z. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



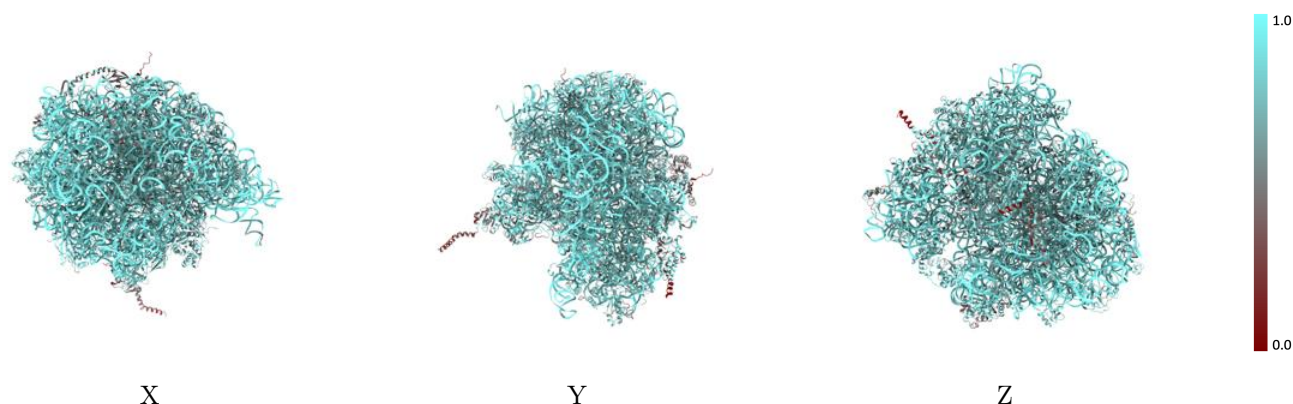
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



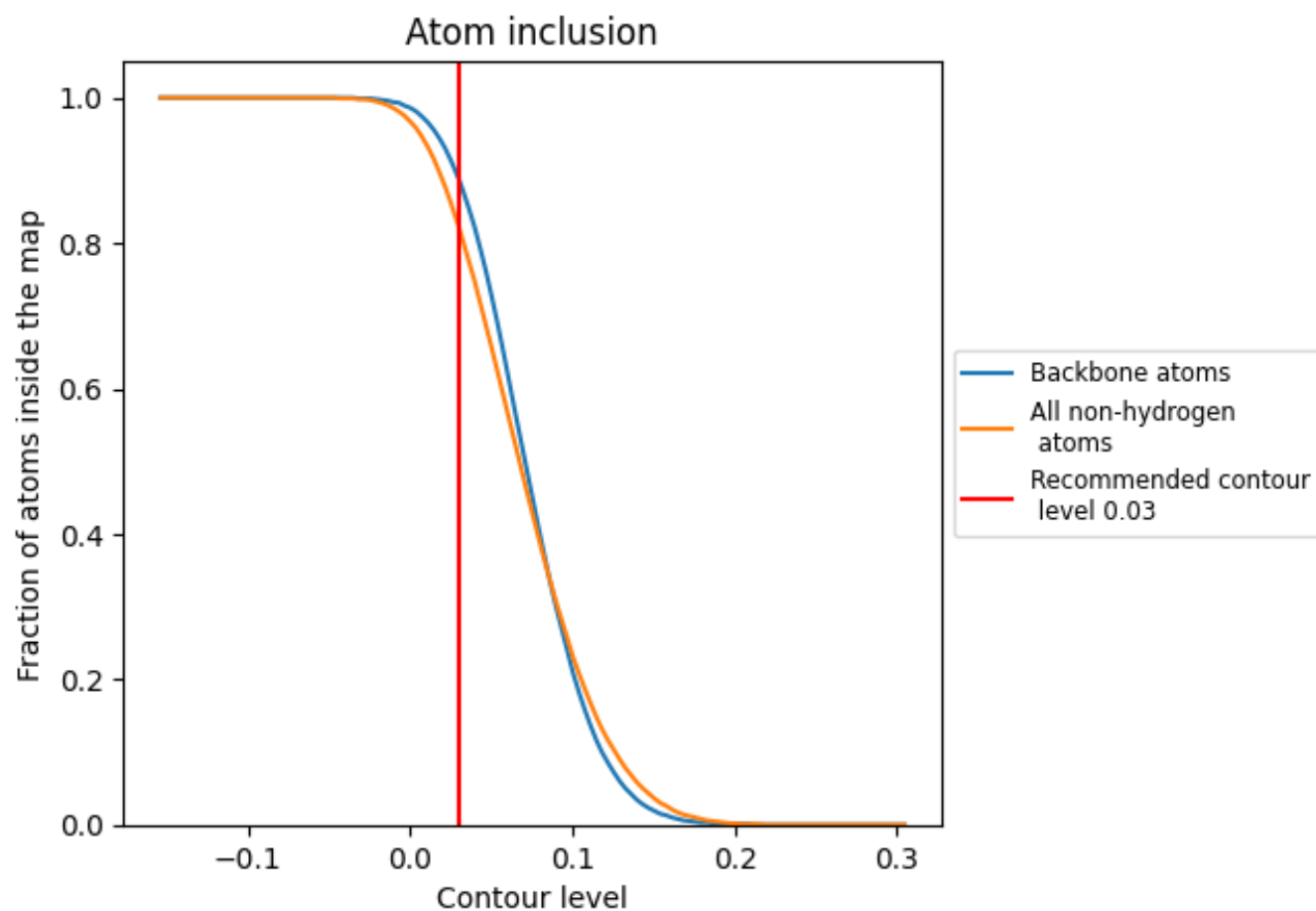
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 82% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8210	 0.1940
L1	 0.7380	 0.1660
L2	 0.7570	 0.2300
L3	 0.6760	 0.1490
L4	 0.7720	 0.2340
L5	 0.7880	 0.2560
L6	 0.7570	 0.1840
L7	 0.8160	 0.2540
L8	 0.8020	 0.2460
L9	 0.5100	 0.1070
LA	 0.8750	 0.2050
LB	 0.9630	 0.2750
LC	 0.6100	 0.1060
LD	 0.4940	 0.1870
LE	 0.7120	 0.1980
LF	 0.7910	 0.2260
LG	 0.6440	 0.1730
LH	 0.7810	 0.2110
LI	 0.8080	 0.2900
LJ	 0.6830	 0.1270
LK	 0.8530	 0.2540
LM	 0.6860	 0.1430
LN	 0.6740	 0.1470
LO	 0.7950	 0.2170
LP	 0.7880	 0.2220
LQ	 0.7140	 0.1760
LR	 0.6780	 0.1130
LS	 0.7900	 0.1340
LT	 0.8500	 0.3110
LU	 0.7280	 0.2380
LV	 0.7350	 0.1800
LW	 0.6800	 0.0770
LX	 0.7220	 0.1850
LY	 0.7990	 0.2660
LZ	 0.6410	 0.1850



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
S1	 0.7010	 0.1850
S6	 0.8650	 0.2260
S7	 0.8100	 0.1550
SA	 0.8840	 0.1920
SB	 0.6410	 0.1240
SC	 0.6850	 0.1890
SD	 0.7720	 0.1700
SE	 0.6680	 0.1570
SF	 0.5730	 0.0870
SG	 0.7070	 0.1740
SH	 0.7160	 0.1140
SI	 0.7600	 0.1720
SJ	 0.7000	 0.1970
SK	 0.6910	 0.1670
SL	 0.7130	 0.1850
SM	 0.7940	 0.2500
SN	 0.8000	 0.2190
SO	 0.6800	 0.0970
SP	 0.7580	 0.1140
SQ	 0.6980	 0.1110
SR	 0.6760	 0.1380
SS	 0.7610	 0.2490
ST	 0.7270	 0.1220
SU	 0.5980	 0.1600