



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 02:48 AM UTC

PDB ID : 8K82 / pdb_00008k82
EMDB ID : EMD-36945
Title : Cryo-EM structure of the yeast 80S ribosome with tigecycline, Not5 and P-site tRNA
Authors : Buschauer, R.; Beckmann, R.; Cheng, J.
Deposited on : 2023-07-28
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

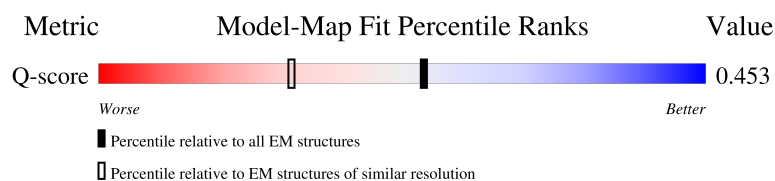
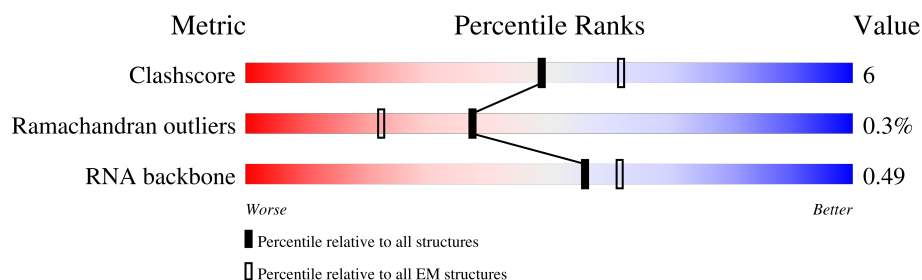
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



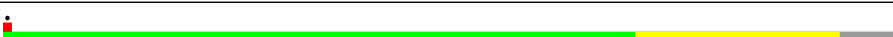
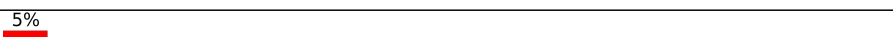
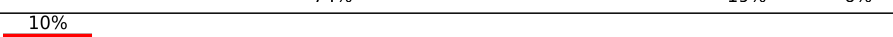
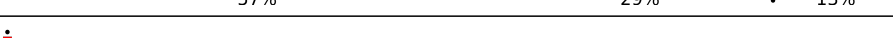
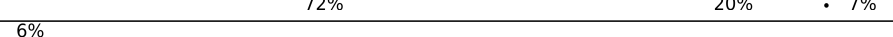
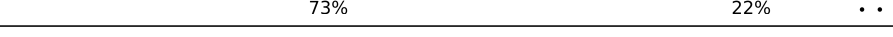
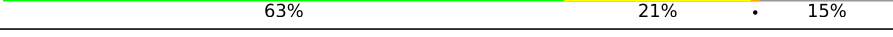
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	C2	1800	
2	C7	3	
3	C5	75	
4	C1	3396	

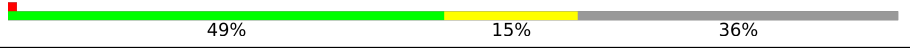
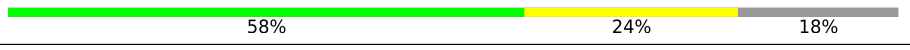
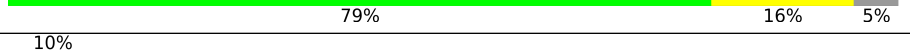
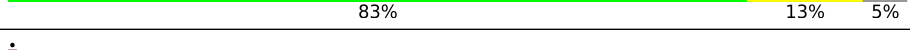
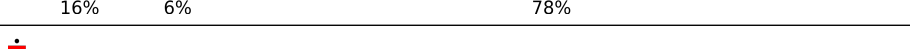
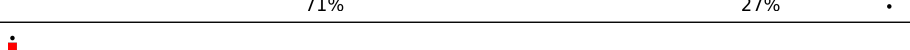
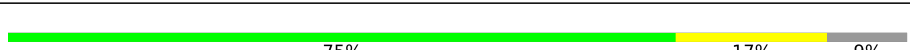
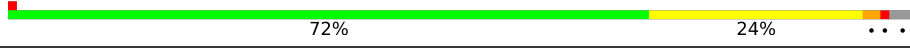
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Mol	Chain	Length	Quality of chain
5	C4	121	
6	C3	158	
7	SA	252	
8	SB	255	
9	SC	254	
10	SD	240	
11	SE	261	
12	SF	225	
13	SG	236	
14	SH	190	
15	SI	200	
16	SJ	197	
17	SK	105	
18	SL	156	
19	SM	143	
20	SN	151	
21	SO	137	
22	SP	142	
23	SQ	143	
24	SR	136	
25	SS	146	
26	ST	144	
27	SU	121	
28	SV	87	
29	SW	130	

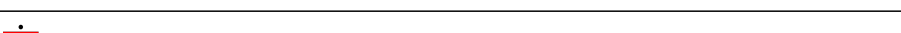
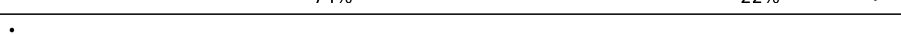
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Mol	Chain	Length	Quality of chain
30	SX	145	
31	SY	135	
32	SZ	108	
33	Sa	119	
34	Sb	82	
35	Sc	67	
36	Sd	56	
37	Se	63	
38	Sf	152	
39	Sg	319	
40	LA	254	
41	LB	387	
42	LC	362	
43	LD	297	
44	LE	176	
45	LF	244	
46	LG	256	
47	LH	191	
48	LI	221	
49	LJ	174	
50	LK	165	
51	LL	199	
52	LM	138	
53	LN	204	
54	LO	199	

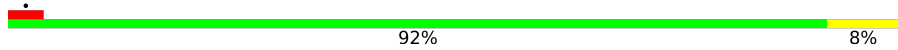
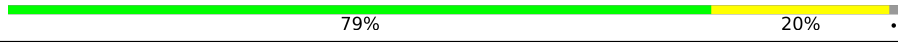
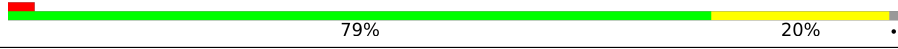
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Mol	Chain	Length	Quality of chain
55	LP	184	
56	LQ	186	
57	LR	189	
58	LS	172	
59	LT	160	
60	LU	121	
61	LV	137	
62	LW	155	
63	LX	142	
64	LY	127	
65	LZ	136	
66	La	149	
67	Lb	59	
68	Lc	105	
69	Ld	113	
70	Le	130	
71	Lf	107	
72	Lg	121	
73	Lh	120	
74	Li	100	
75	Lj	88	
76	Lk	78	
77	Ll	51	
78	Lm	128	
79	L2	25	

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Mol	Chain	Length	Quality of chain
79	Ln	25	 92% 8%
80	Lo	106	 79% 20%
81	Lp	92	 79% 20%
82	L1	217	 60% 92% 6%
83	P0	312	 31% 58% 5% 35%
84	CN	560	 15% 80%

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 205122 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C2	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

- Molecule 2 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C7	3	Total	C	N	O	P	0	0
			65	29	12	21	3		

- Molecule 3 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C5	75	Total	C	N	O	P	0	0
			1624	728	298	523	75		

- Molecule 4 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C1	3204	Total	C	N	O	P	0	0
			68535	30613	12358	22360	3204		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 6 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 7 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SA	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		

- Molecule 8 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SB	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		

- Molecule 9 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SC	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 10 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SD	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 11 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SE	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 12 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SF	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 13 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SG	218	Total	C	N	O	S	0	0
			1755	1102	337	313	3		

- Molecule 14 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	SH	185	Total	C	N	O		
			1486	954	266	266	0	0

- Molecule 15 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SI	188	Total	C	N	O	S		
			1489	925	298	264	2	0	0

- Molecule 16 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SJ	185	Total	C	N	O	S		
			1494	943	289	261	1	0	0

- Molecule 17 is a protein called Small ribosomal subunit protein eS10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SK	92	Total	C	N	O	S		
			741	478	121	140	2	0	0

- Molecule 18 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SL	146	Total	C	N	O	S		
			1168	747	221	197	3	0	0

- Molecule 19 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SM	124	Total	C	N	O	S		
			890	560	156	172	2	0	0

- Molecule 20 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SN	150	Total	C	N	O	S		
			1192	759	224	207	2	0	0

- Molecule 21 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SO	128	Total	C	N	O	S	0	0
			949	582	188	176	3		

- Molecule 22 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SP	119	Total	C	N	O	S	0	0
			939	595	176	161	7		

- Molecule 23 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SQ	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 24 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SR	115	Total	C	N	O	S	0	0
			896	557	172	165	2		

- Molecule 25 is a protein called Small ribosomal subunit protein uS13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 26 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	ST	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 27 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SU	101	Total	C	N	O	S	0	0
			805	512	145	147	1		

- Molecule 28 is a protein called Small ribosomal subunit protein eS21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 29 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 30 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 31 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SY	134	Total	C	N	O		0	0
			1073	676	208	189			

- Molecule 32 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	SZ	69	Total	C	N	O		0	0
			558	357	103	98			

- Molecule 33 is a protein called Small ribosomal subunit protein eS26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Sa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 34 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 35 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Sc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 36 is a protein called Small ribosomal subunit protein uS14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Sd	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 37 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Se	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 38 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Sf	33	Total	C	N	O	S	0	0
			248	153	46	45	4		

- Molecule 39 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Sg	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		

- Molecule 40 is a protein called Large ribosomal subunit protein uL2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LA	252	Total	C	N	O	S	0	0
			1912	1190	388	333	1		

- Molecule 41 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 42 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 43 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LD	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 44 is a protein called Large ribosomal subunit protein eL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LE	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

- Molecule 45 is a protein called Large ribosomal subunit protein uL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LF	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 46 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LG	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 47 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LH	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 48 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LI	209	Total	C	N	O	S	0	0
			1696	1077	321	293	5		

- Molecule 49 is a protein called Large ribosomal subunit protein uL5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LJ	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 50 is a protein called Large ribosomal subunit protein uL11A.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	LK	158	Total	C	N	O	0	0
			778	461	158	159		

- Molecule 51 is a protein called Large ribosomal subunit protein eL13A.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	LL	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 52 is a protein called Large ribosomal subunit protein eL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LM	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 53 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 54 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LO	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 55 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	LP	175	Total	C	N	O	0	0
			1378	856	273	249		

- Molecule 56 is a protein called Large ribosomal subunit protein eL18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 57 is a protein called Large ribosomal subunit protein eL19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LR	174	Total	C	N	O	S	0	0
			1365	843	286	236			

- Molecule 58 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LS	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 59 is a protein called Large ribosomal subunit protein eL21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 60 is a protein called Large ribosomal subunit protein eL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LU	98	Total	C	N	O	S	0	0
			778	505	127	146			

- Molecule 61 is a protein called Large ribosomal subunit protein uL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LV	134	Total	C	N	O	S	0	0
			993	623	187	176	7		

- Molecule 62 is a protein called Large ribosomal subunit protein eL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LW	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 63 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LX	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 64 is a protein called Large ribosomal subunit protein uL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	LY	124	Total	C	N	O		0	0
			976	614	190	172			

- Molecule 65 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	LZ	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 66 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	La	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 67 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Lb	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 68 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Lc	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 69 is a protein called Large ribosomal subunit protein eL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Ld	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 70 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Le	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 71 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lf	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 72 is a protein called Large ribosomal subunit protein eL34A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Lg	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 73 is a protein called Large ribosomal subunit protein uL29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Lh	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 74 is a protein called Large ribosomal subunit protein eL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Li	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 75 is a protein called Large ribosomal subunit protein eL37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Lj	82	Total	C	N	O	S	0	0
			650	396	142	107	5		

- Molecule 76 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	Lk	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 77 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	L1	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 78 is a protein called Ubiquitin-ribosomal protein eL40A fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Lm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 79 is a protein called Large ribosomal subunit protein eL41A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Ln	25	Total	C	N	O	S	0	0
			233	142	63	27	1		
79	L2	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 80 is a protein called Large ribosomal subunit protein eL42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Lo	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 81 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Lp	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 82 is a protein called Large ribosomal subunit protein uL1A.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	L1	204	Total	C	N	O	0	0
			1010	602	204	204		

- Molecule 83 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	P0	203	Total	C	N	O	0	0
			998	592	203	203		

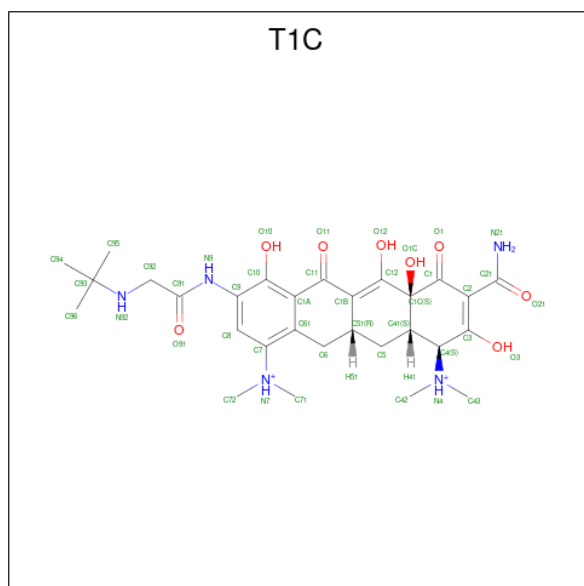
- Molecule 84 is a protein called General negative regulator of transcription subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CN	112	Total	C	N	O	S	0	0
			940	585	170	182	3		

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	C2	89	Total	Mg	0
			89	89	
85	C5	3	Total	Mg	0
			3	3	
85	C1	222	Total	Mg	0
			222	222	
85	C4	1	Total	Mg	0
			1	1	
85	C3	1	Total	Mg	0
			1	1	

- Molecule 86 is TIGECYCLINE (CCD ID: T1C) (formula: C₂₉H₄₁N₅O₈) (labeled as "Ligand of Interest" by depositor).



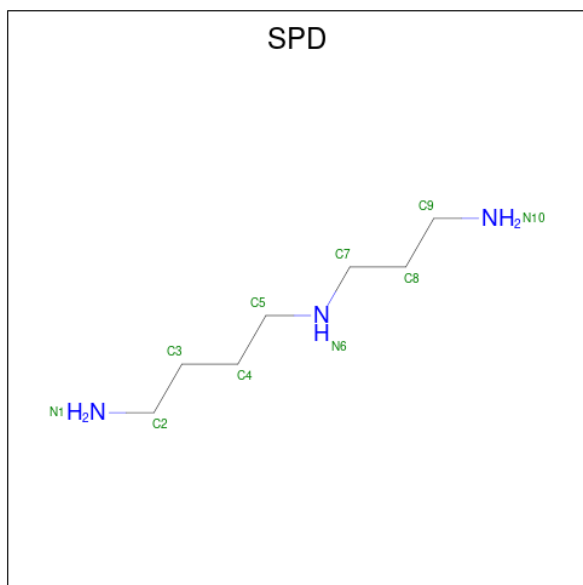
Mol	Chain	Residues	Atoms				AltConf
86	C2	1	Total	C	N	O	0
			42	29	5	8	
86	C1	1	Total	C	N	O	0
			42	29	5	8	
86	C1	1	Total	C	N	O	0
			42	29	5	8	

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Mol	Chain	Residues	Atoms				AltConf
86	C1	1	Total	C	N	O	0
			42	29	5	8	
86	C1	1	Total	C	N	O	0
			42	29	5	8	
86	C1	1	Total	C	N	O	0
			42	29	5	8	

- Molecule 87 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			AltConf
87	C1	1	Total	C	N	0
			10	7	3	

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
88	Sa	1	Total	Zn	0
			1	1	
88	Sb	1	Total	Zn	0
			1	1	
88	Sd	1	Total	Zn	0
			1	1	
88	Sf	1	Total	Zn	0
			1	1	
88	Lg	1	Total	Zn	0
			1	1	

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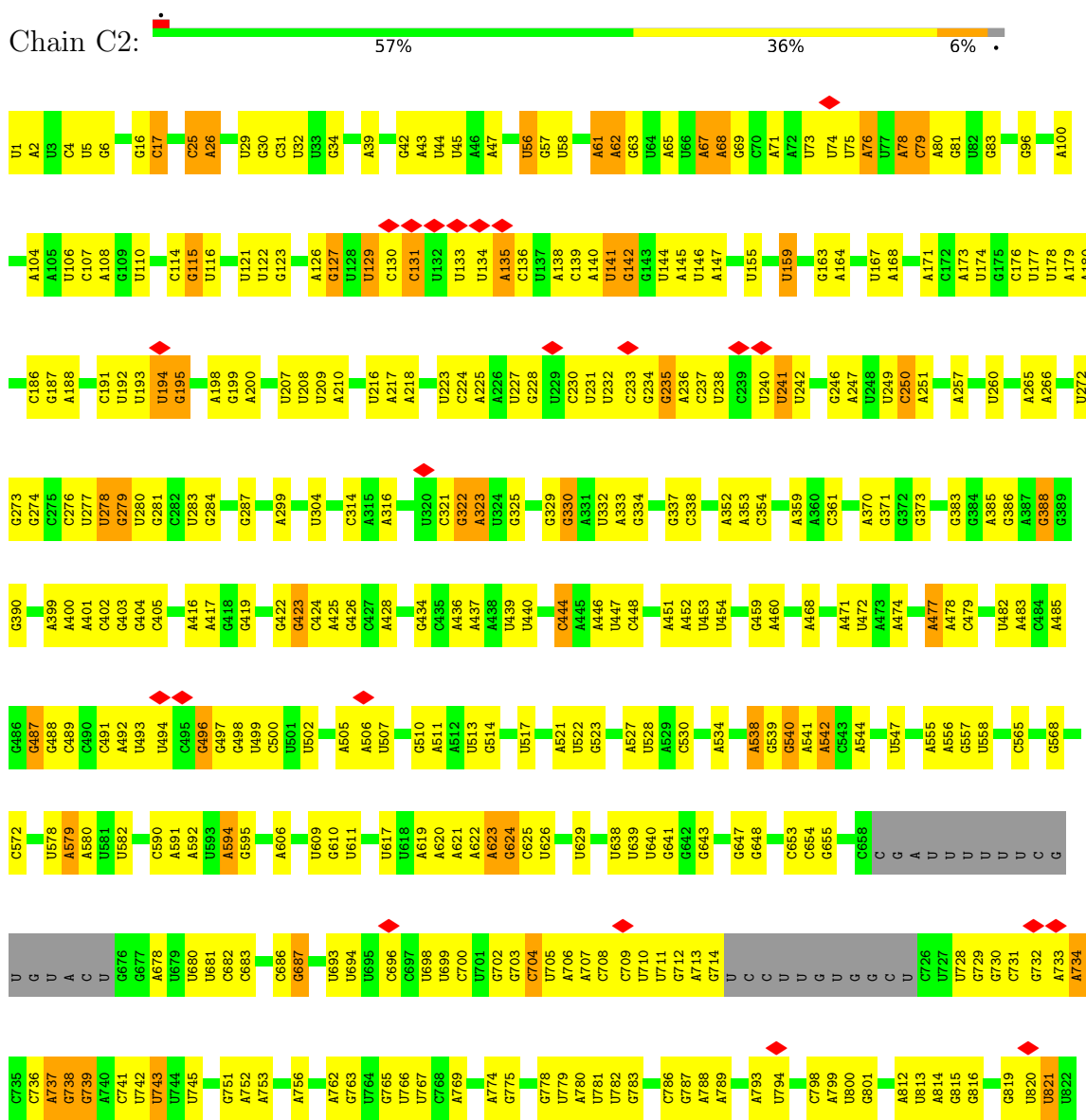
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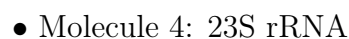
Mol	Chain	Residues	Atoms		AltConf
88	Lj	1	Total 1	Zn 1	0
88	Lm	1	Total 1	Zn 1	0
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0

3 Residue-property plots

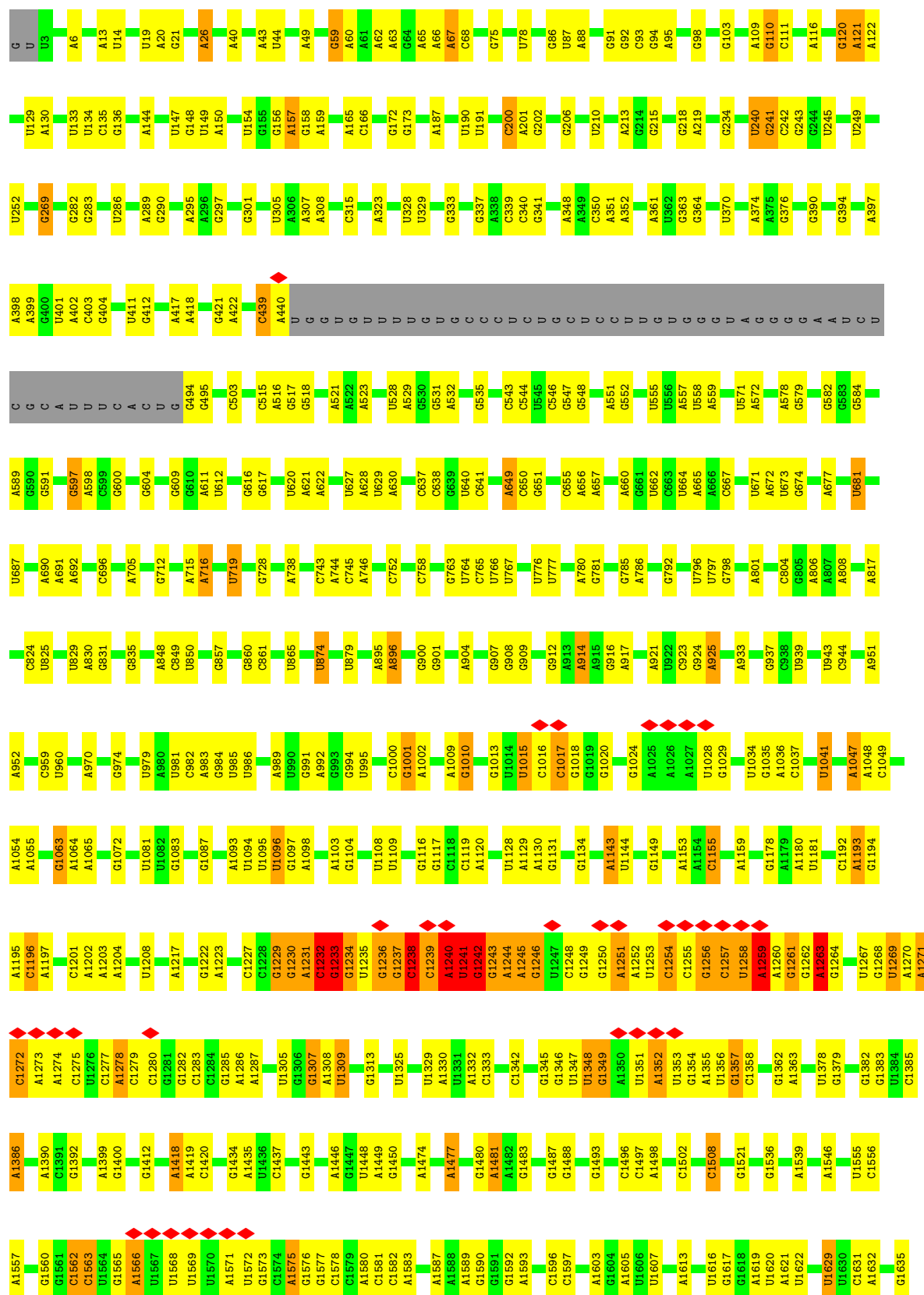
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 18S rRNA

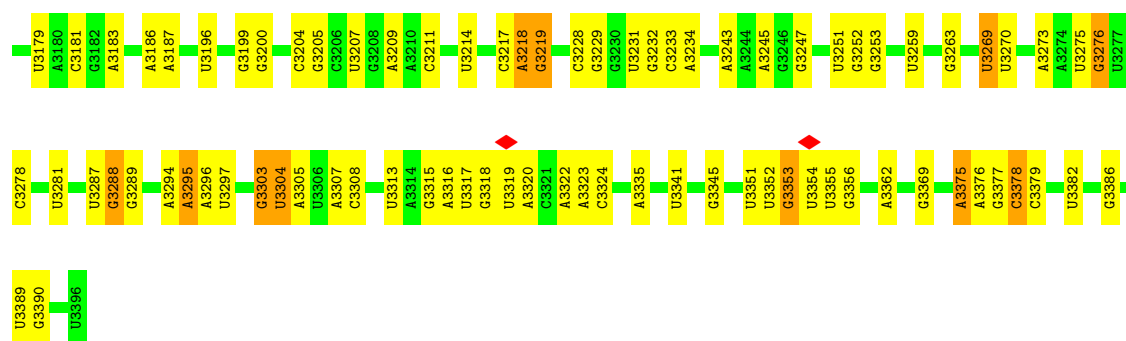




Chain C1: 63% 27% 6%



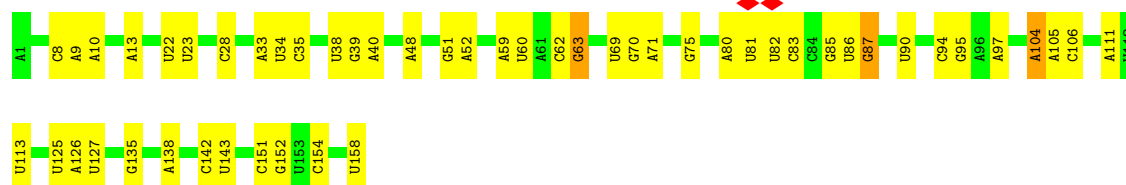




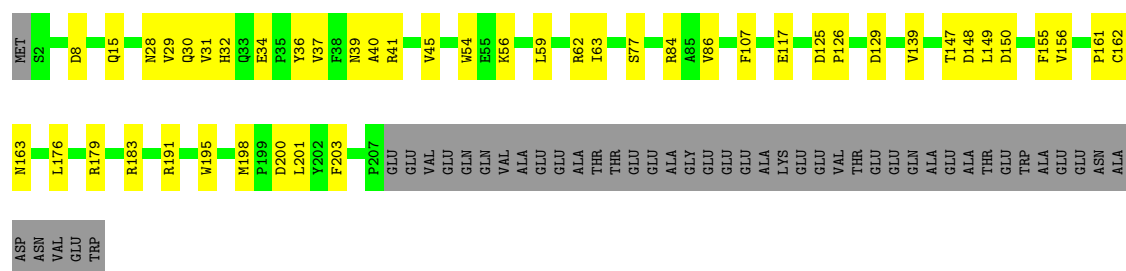
• Molecule 5: 5S rRNA



• Molecule 6: 5.8S rRNA

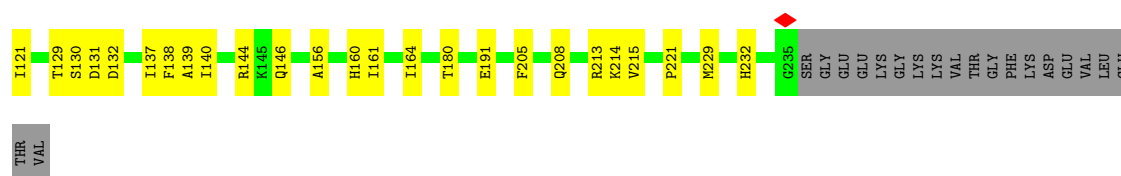


• Molecule 7: Small ribosomal subunit protein uS2A



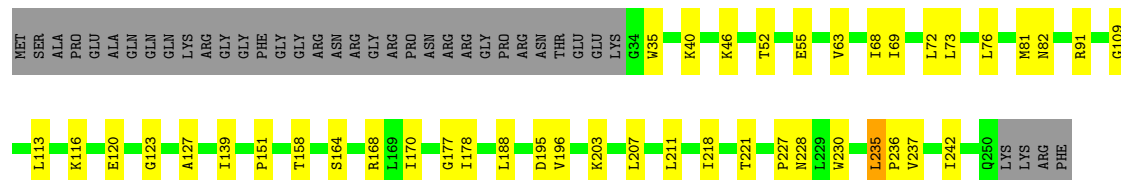
• Molecule 8: 40S ribosomal protein S1-A





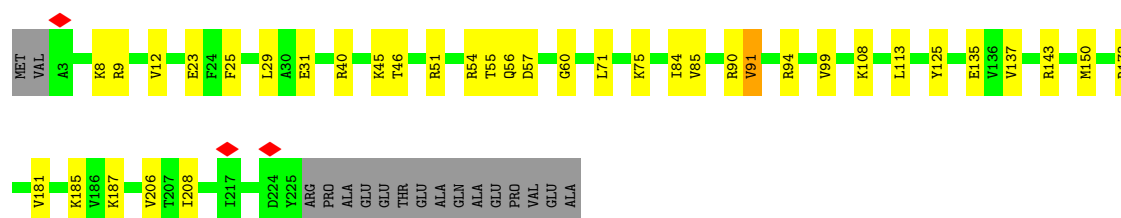
- Molecule 9: 40S ribosomal protein S2

Chain SC: 69% 17% 15%



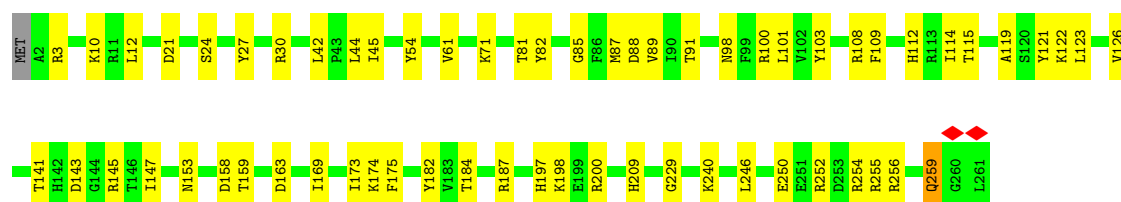
- Molecule 10: Small ribosomal subunit protein uS3

Chain SD: 78% 15% 7%



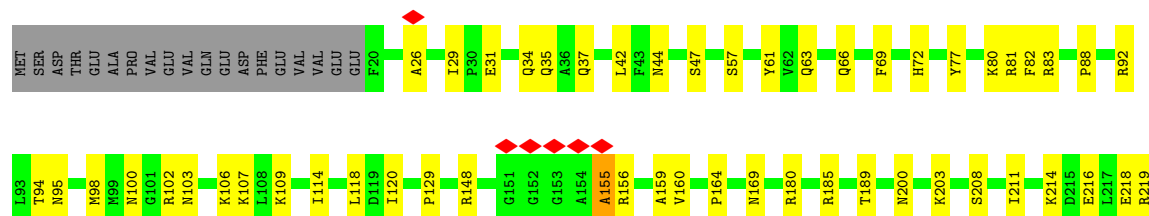
- Molecule 11: 40S ribosomal protein S4-A

Chain SE: 76% 23%



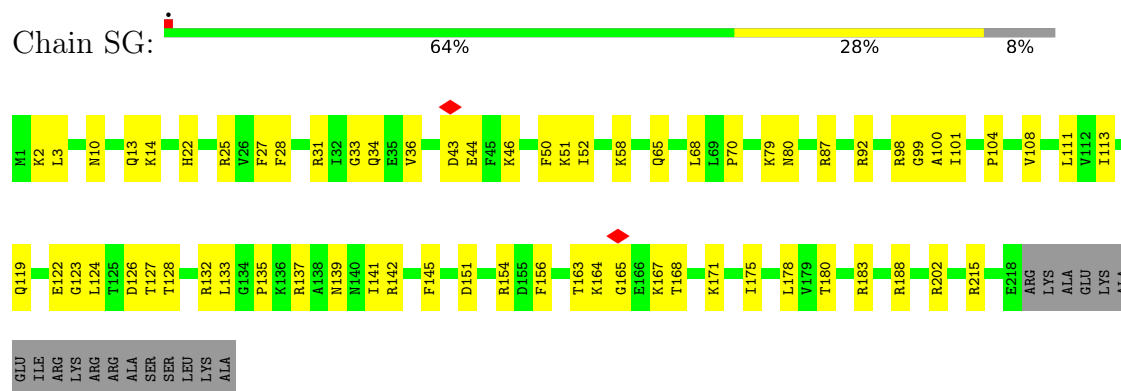
- Molecule 12: Small ribosomal subunit protein uS7

Chain SF: 68% 24% 8%

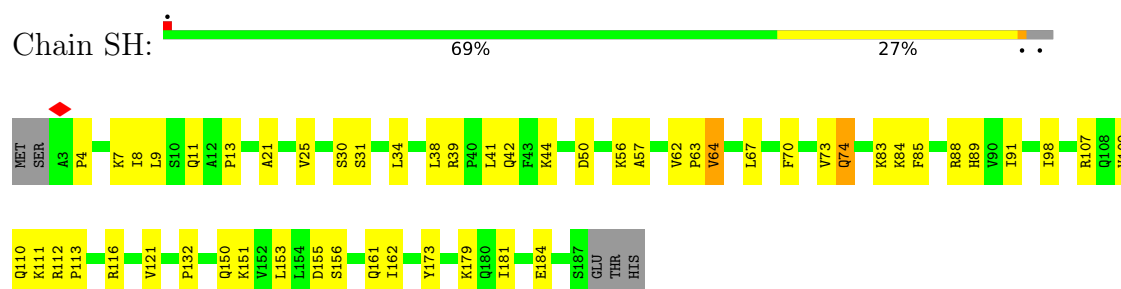




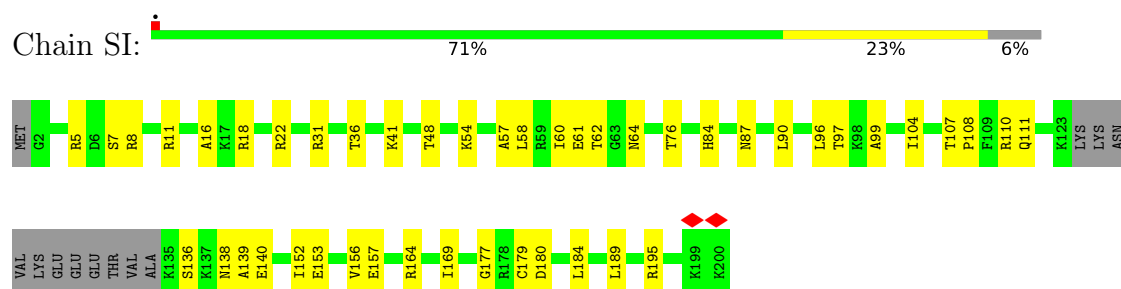
- Molecule 13: 40S ribosomal protein S6-A



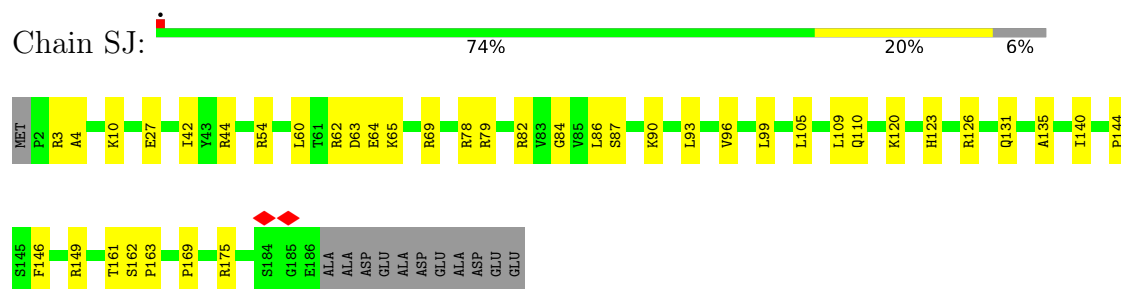
- Molecule 14: 40S ribosomal protein S7-A



- Molecule 15: 40S ribosomal protein S8-A

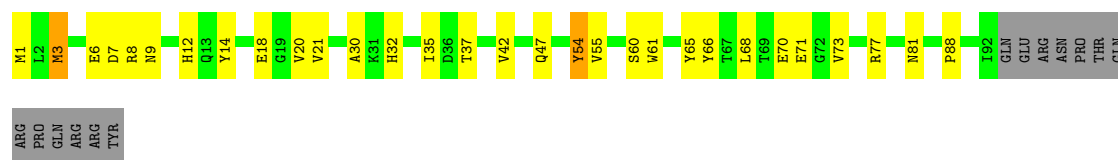


- Molecule 16: 40S ribosomal protein S9-A



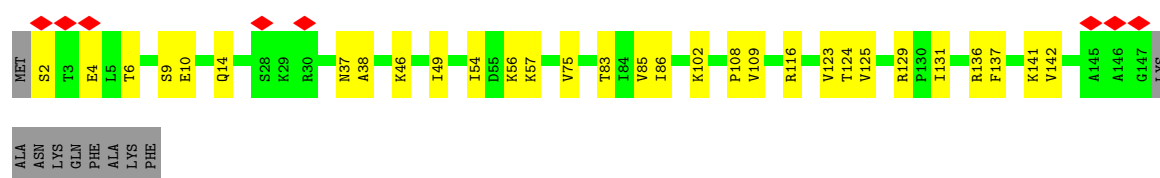
- Molecule 17: Small ribosomal subunit protein eS10A

Chain SK: 



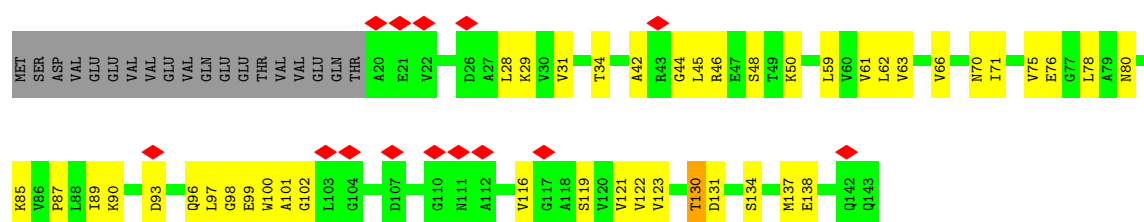
- Molecule 18: Small ribosomal subunit protein uS17A

Chain SL: 



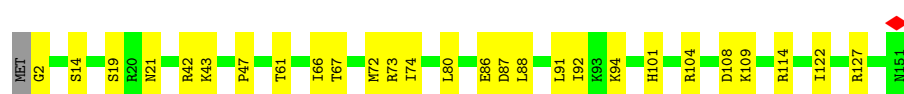
- Molecule 19: Small ribosomal subunit protein eS12

Chain SM: 



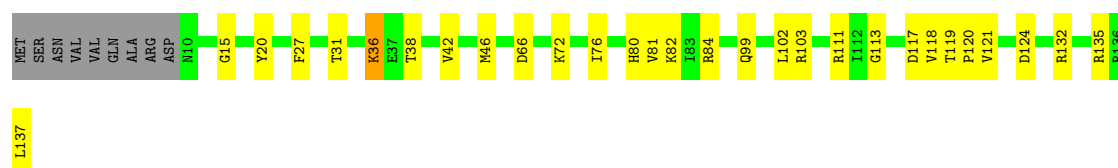
- Molecule 20: 40S ribosomal protein S13

Chain SN: 



- Molecule 21: 40S ribosomal protein S14-A

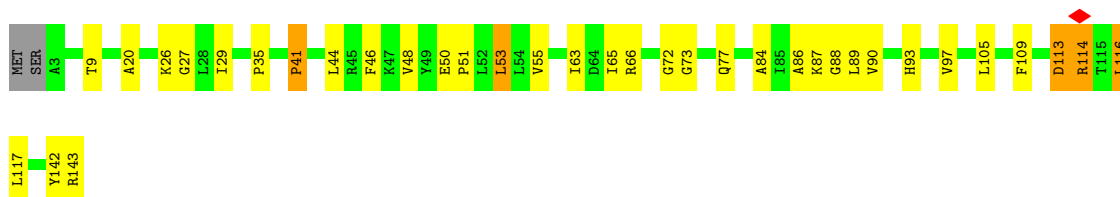
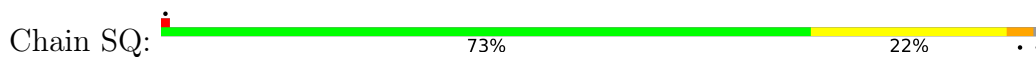
Chain SO: 



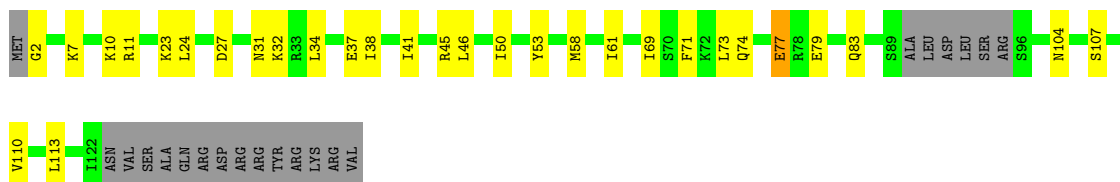
- Molecule 22: Small ribosomal subunit protein uS19

Chain SP: 

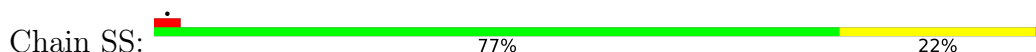
- Molecule 23: Small ribosomal subunit protein uS9A



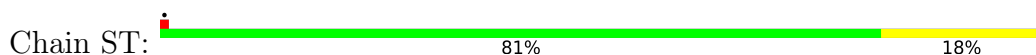
- Molecule 24: Small ribosomal subunit protein eS17A



- Molecule 25: Small ribosomal subunit protein uS13A

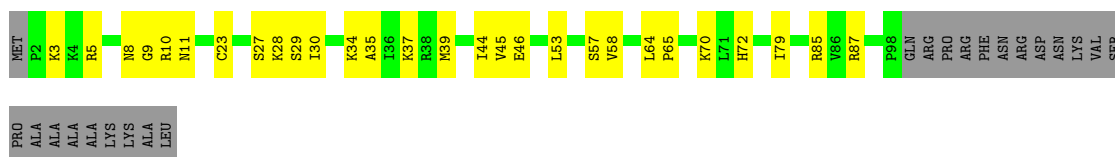


- Molecule 26: Small ribosomal subunit protein eS19A



- Molecule 27: Small ribosomal subunit protein uS10





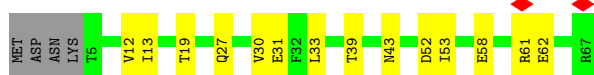
- Molecule 34: 40S ribosomal protein S27-A

Chain Sb: 83% 16%



- Molecule 35: Small ribosomal subunit protein eS28A

Chain Sc: 73% 21% 6%



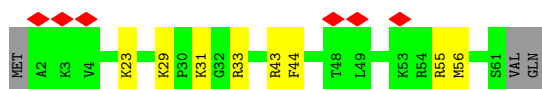
- Molecule 36: Small ribosomal subunit protein uS14A

Chain Sd: 79% 16% 5%



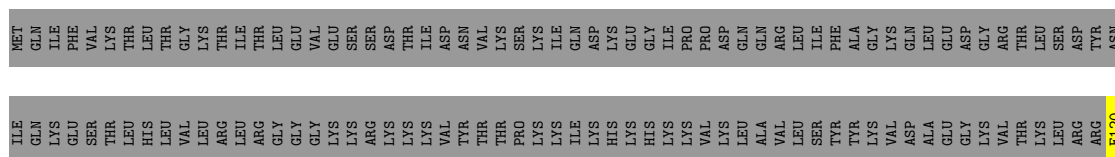
- Molecule 37: 40S ribosomal protein S30-A

Chain Se: 10% 83% 13% 5%



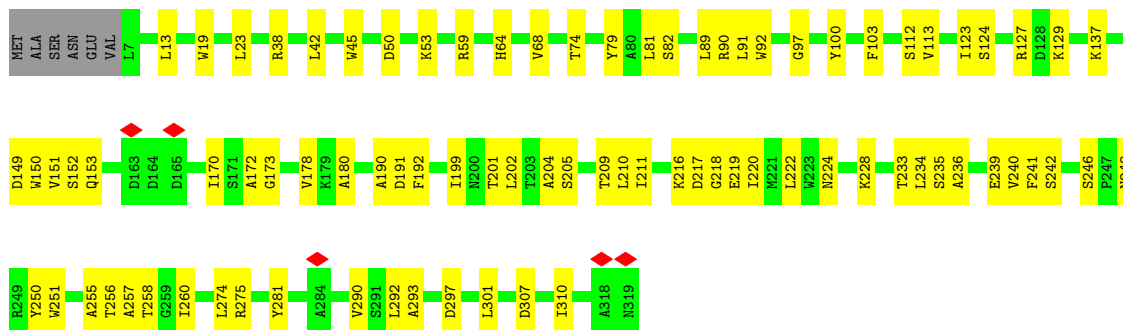
- Molecule 38: Ubiquitin-ribosomal protein eS31 fusion protein

Chain Sf: 16% 6% 78%



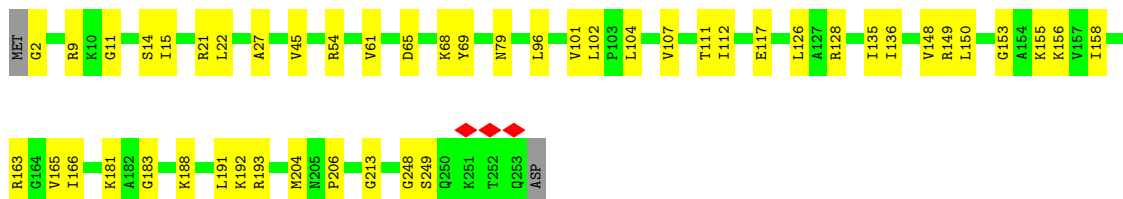
- Molecule 39: Small ribosomal subunit protein RACK1

Chain Sg:  71% 27%



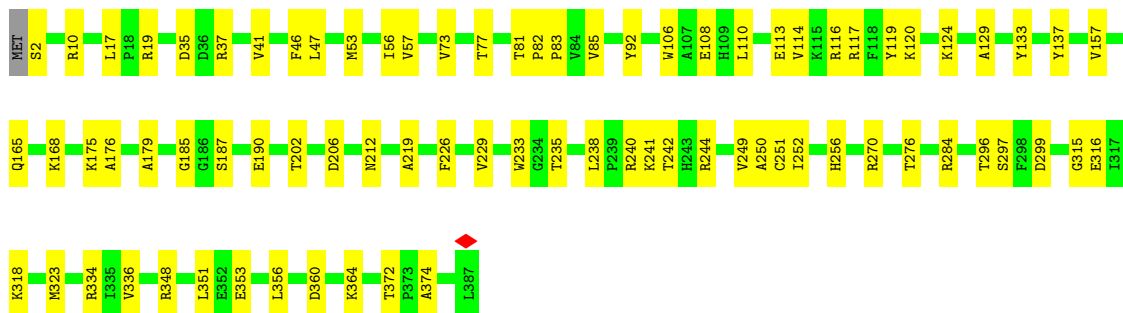
- Molecule 40: Large ribosomal subunit protein uL2A

Chain LA:  80% 19%



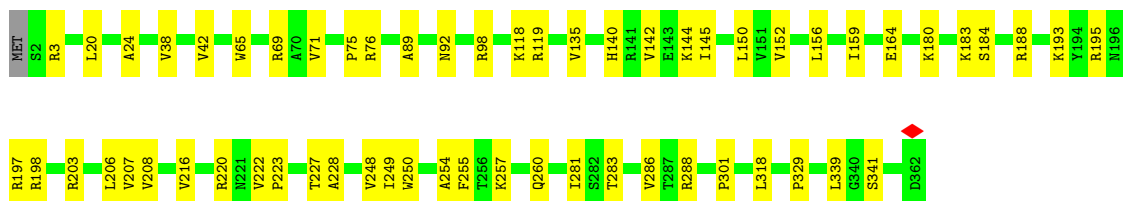
- Molecule 41: Large ribosomal subunit protein uL3

Chain LB:  79% 20%

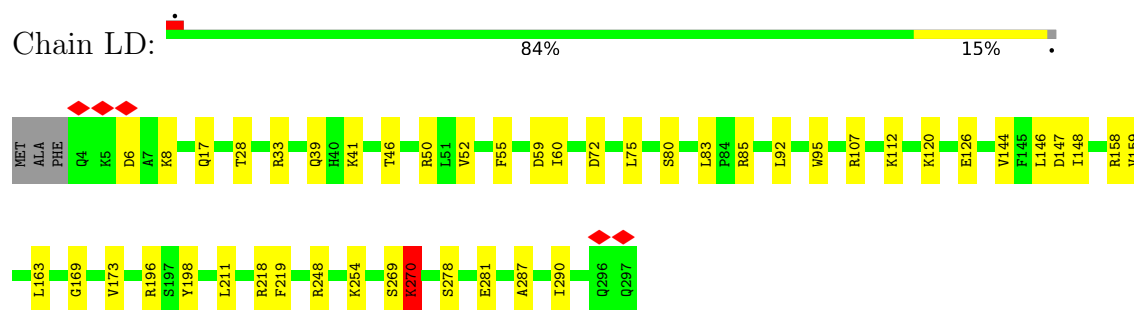


- Molecule 42: Large ribosomal subunit protein uL4A

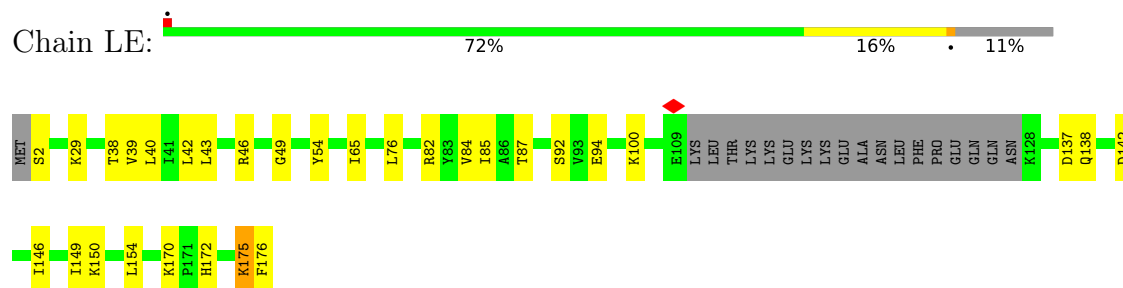
Chain LC:  83% 16%



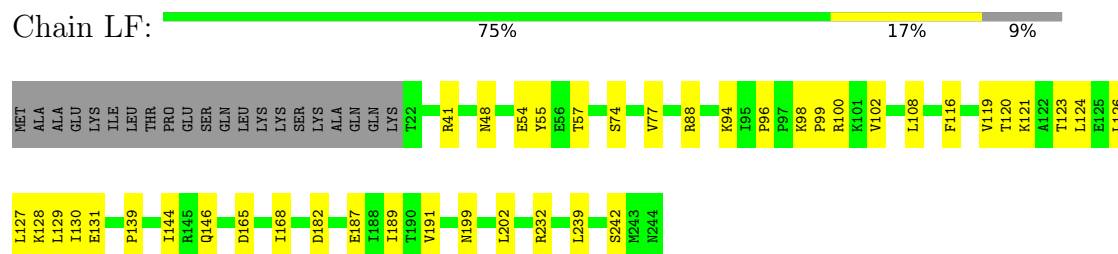
- Molecule 43: Large ribosomal subunit protein uL18



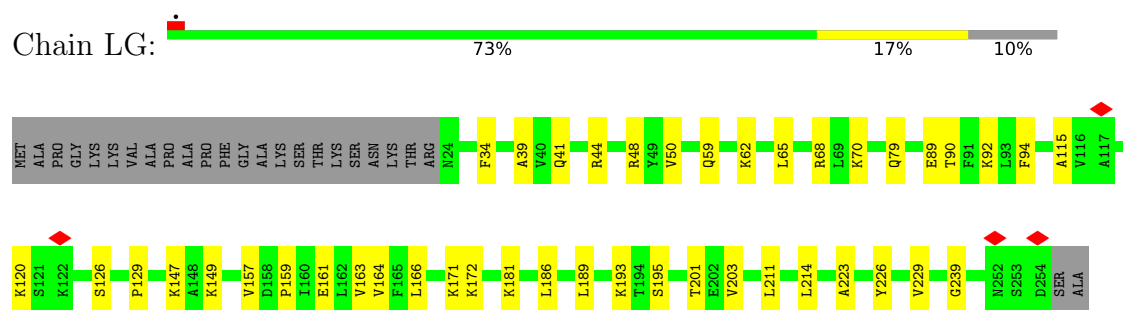
- Molecule 44: Large ribosomal subunit protein eL6A



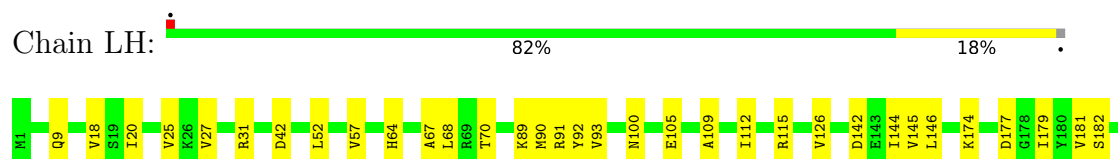
- Molecule 45: Large ribosomal subunit protein uL30A



- Molecule 46: Large ribosomal subunit protein eL8A



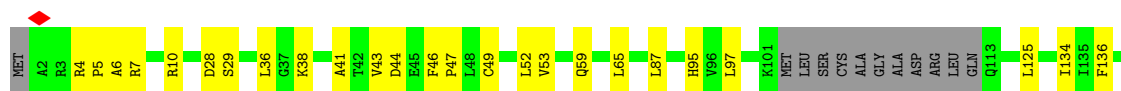
- Molecule 47: Large ribosomal subunit protein uL6A





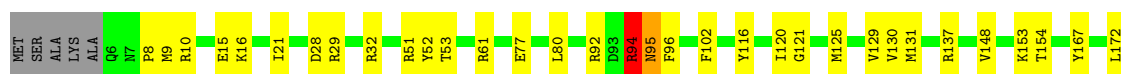
- Molecule 48: Large ribosomal subunit protein uL16

Chain LI: 75% 19% 5%



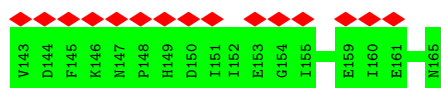
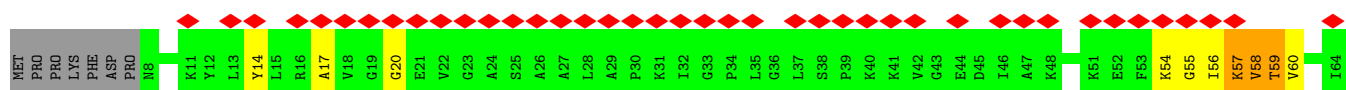
- Molecule 49: Large ribosomal subunit protein uL5A

Chain LJ: 77% 19% ..



- Molecule 50: Large ribosomal subunit protein uL11A

Chain LK: 60% 80% 13%



- Molecule 51: Large ribosomal subunit protein eL13A

Chain LL: 72% 24% ...



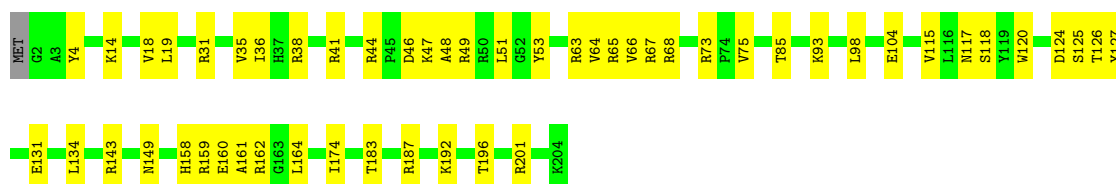
- Molecule 52: Large ribosomal subunit protein eL14A

Chain LM:  88% 11%



- Molecule 53: Large ribosomal subunit protein eL15A

Chain LN:  74% 25%



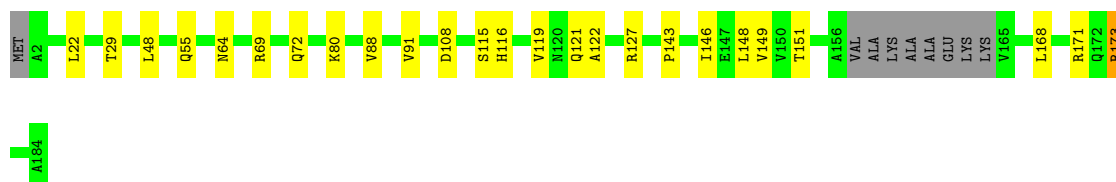
- Molecule 54: Large ribosomal subunit protein uL13A

Chain LO:  84% 15%



- Molecule 55: Large ribosomal subunit protein uL22A

Chain LP:  82% 13% 5%



- Molecule 56: Large ribosomal subunit protein eL18A

Chain LQ:  84% 16%

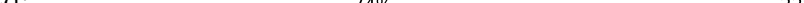


- Molecule 57: Large ribosomal subunit protein eL19A

Chain LR:  77% 15% 8%

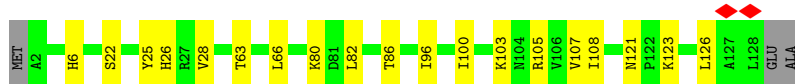
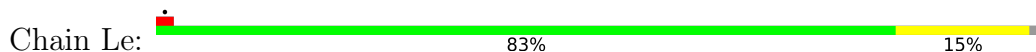




- Chain Ld:  74% 22%



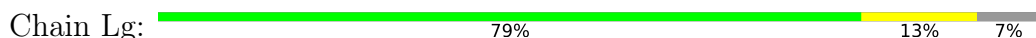
- Molecule 70: Large ribosomal subunit protein eL32



- Molecule 71: Large ribosomal subunit protein eL33A



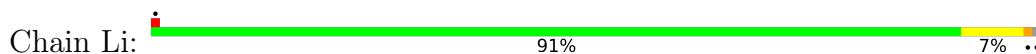
- Molecule 72: Large ribosomal subunit protein eL34A



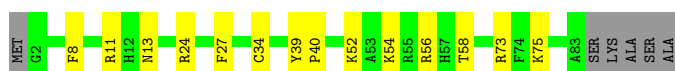
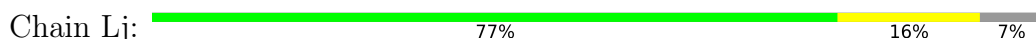
- Molecule 73: Large ribosomal subunit protein uL29A



- Molecule 74: Large ribosomal subunit protein eL36A



- Molecule 75: Large ribosomal subunit protein eL37A



- Molecule 76: Large ribosomal subunit protein eL38

Chain Lk:  76% 22% ..



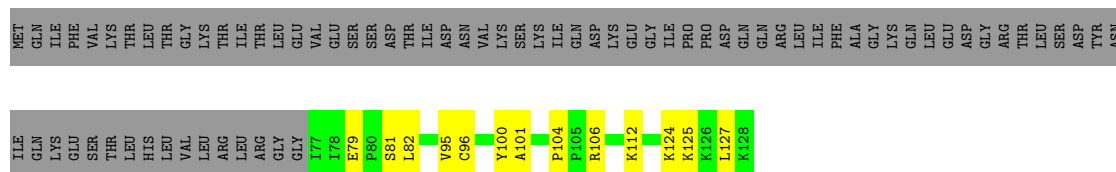
- Molecule 77: Large ribosomal subunit protein eL39

Chain Ll:  84% 14% .

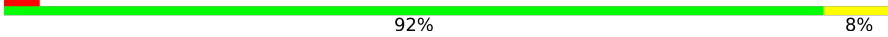


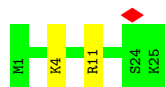
- Molecule 78: Ubiquitin-ribosomal protein eL40A fusion protein

Chain Lm:  30% 10% 59%

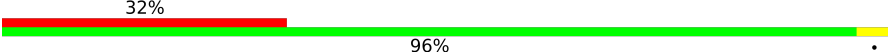


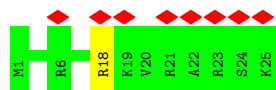
- Molecule 79: Large ribosomal subunit protein eL41A

Chain Ln:  92% 8%



- Molecule 79: Large ribosomal subunit protein eL41A

Chain L2:  32% 96%



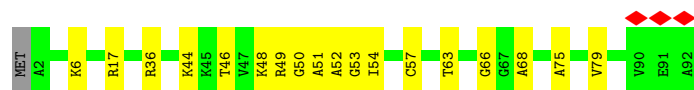
- Molecule 80: Large ribosomal subunit protein eL42A

Chain Lo:  79% 20%

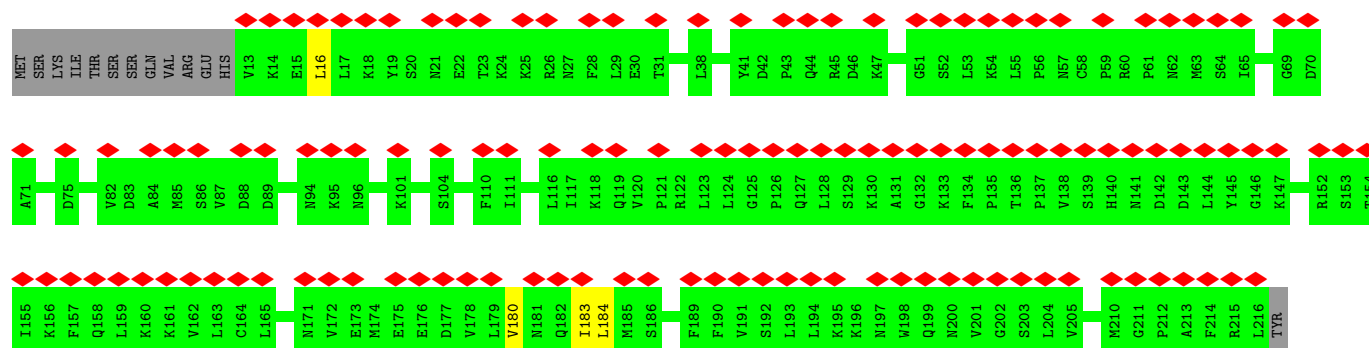


- Molecule 81: Large ribosomal subunit protein eL43A

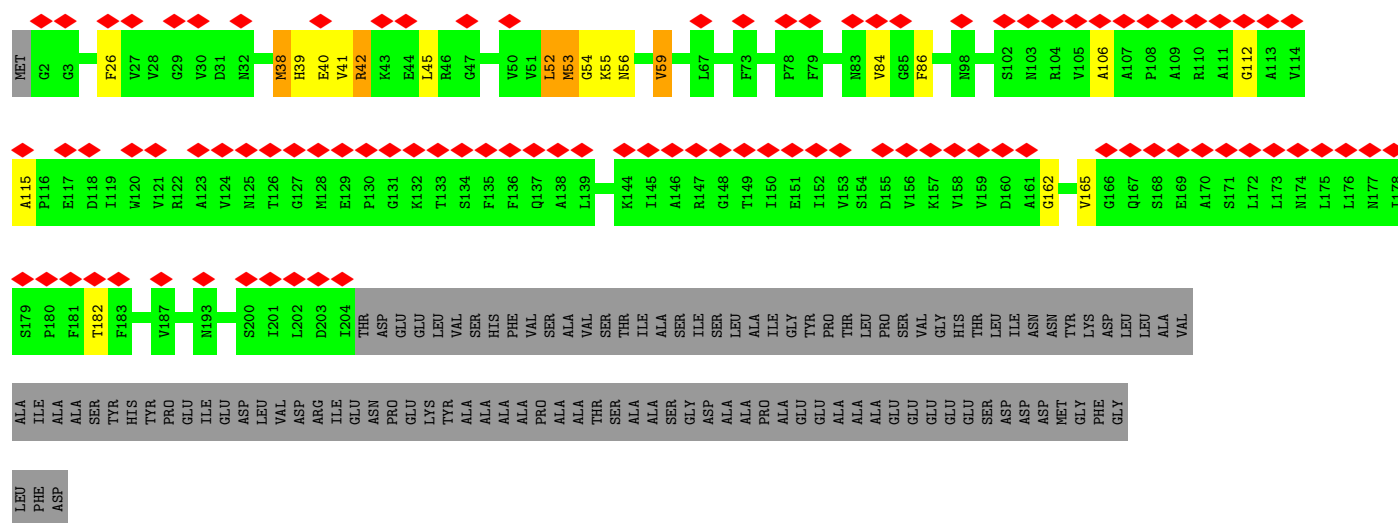
Chain Lp:  79% 20%



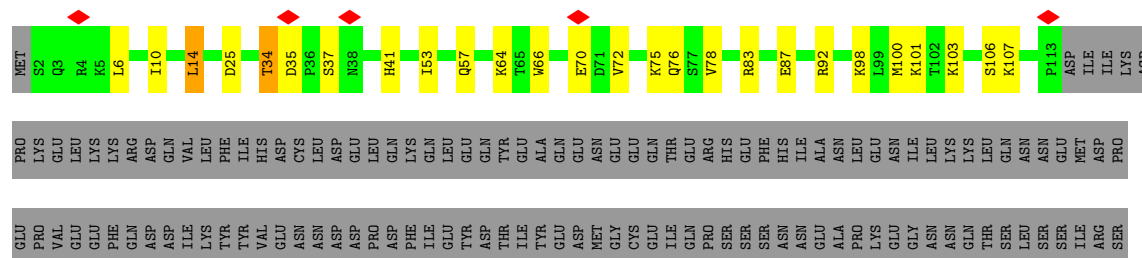
- Molecule 82: Large ribosomal subunit protein uL1A



- Molecule 83: Large ribosomal subunit protein uL10



- Molecule 84: General negative regulator of transcription subunit 5



LYS	PHE	ASN	LEU	PHE	SER
SER	ILE	GLU	TYR	ASP	LYS
TRP	PHE	PRO	LYS	ASN	GLN
LEU	THR	ILE	LEU	THR	GLY
ALA	HIS	THR	LEU	THR	GLN
ARG	TYR	PHE	ASP	LEU	ARG
ARG	GLN	VAL	SER	GLY	SER
CYS	GLY	TYR	LYS	THR	PRO
GLY	SER	PRO	PRO	PRO	LYS
ASN	TYR	TYR	TYR	THR	LYS
ASP	GLU	ASP	MET	THR	LYS
PHE	GLN	VAL	MET	HIS	ALA
VAL	PHE	PRO	GLN	VAL	PRO
TYR	LEU	LEU	PRO	GLN	PRO
ASN	ALA	ASN	LEU	MET	ARG
GLU	ALA	LEU	GLN	LYS	ASP
GLY	ARG	THR	GLU	LYS	VAL
ASP	GLU	ASN	MET	LYS	SER
PHE	LEU	ASN	SER	GLU	ILE
GLY	PHE	GLU	PRO	SER	SER
LYS	LYS	ASN	LYS	GLY	ASP
LEU	ASN	THR	MET	ASN	ARG
	ARG	THR	VAL	ASP	ALA
	ASN	ASN	SER	SER	THR
	TRP	ASN	GLN	GLU	THR
	LEU	LYS	LEU	GLN	PRO
	PHE	PHE	GLU	GLN	ILE
	ASN	GLY	SER	LEU	ALA
	LYS	LYS	SER	ASN	ALA
	VAL	ASP	LEU	PHE	GLY
	ASP	SER	LEU	PRO	VAL
	ARG	LYS	LEU	GLY	ILE
	CYS	LYS	ASN	PRO	SER
	TRP	LYS	PRO	ARG	ALA
	TYR	SER	ASP	THR	SER
	TYR	LYS	SER	ASP	GLN
	LYS	LYS	LEU	SER	LYS
	GLU	ILE	ASP	ALA	ILE
	LEU	LYS	ASP	LYS	SER
	PRO	TYR	PRO	ILE	THR
	GLY	ARG	CYS	ILE	PRO
	GLY	THR	LEU	GLN	THR
	LYS	ALA	PRO	THR	ASP
	SER	ILE	LEU	ASN	THR
	GLU	ILE	SER	ALA	PRO
	GLU	PHE	LEU	ALA	LYS
	GLU	MET	PRO	PHE	HIS
	SER	LYS	HIS	GLN	THR
	TRP	PHE	PRO	ASN	VAL
	ARG	ASP	THR	PRO	LYS
	TYR	LEU	SER	PHO	ASP
	PHE	ASP	ILE	PHE	ASP
	ASP	THR	PHE	ASP	SER
	TYR	LEU	PHE	ASP	ILE
	LYS	PHE	PRO	GLY	TYR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	140917	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.362	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.01	Depositor
Map size ($\text{\AA}$)	406.56, 406.56, 406.56	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.847, 0.847, 0.847	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: T1C, 5MC, SPD, ZN, 2MG, T6A, 1MG, M2G, 1MA, H2U, MG, 7MG

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	C2	0.24	0/42211	0.42	1/65773 (0.0%)
2	C7	0.20	0/72	0.22	0/110
3	C5	0.22	0/1577	0.33	0/2457
4	C1	0.27	0/76717	0.40	19/119611 (0.0%)
5	C4	0.19	0/2883	0.29	0/4491
6	C3	0.25	0/3746	0.34	0/5832
7	SA	0.31	0/1623	0.74	3/2222 (0.1%)
8	SB	0.25	0/1748	0.60	0/2352
9	SC	0.29	0/1665	0.63	0/2263
10	SD	0.31	0/1759	0.70	2/2368 (0.1%)
11	SE	0.32	0/2109	0.69	3/2839 (0.1%)
12	SF	0.28	0/1629	0.66	0/2202
13	SG	0.21	0/1779	0.50	0/2379
14	SH	0.42	0/1511	0.86	0/2036
15	SI	0.39	0/1514	0.70	3/2021 (0.1%)
16	SJ	0.39	0/1519	0.75	2/2035 (0.1%)
17	SK	0.36	0/757	0.80	0/1022
18	SL	0.28	0/1194	0.55	0/1610
19	SM	0.33	0/898	0.95	2/1220 (0.2%)
20	SN	0.29	0/1215	0.62	0/1638
21	SO	0.24	0/960	0.51	0/1290
22	SP	0.48	1/959 (0.1%)	0.86	2/1288 (0.2%)
23	SQ	0.54	0/1125	0.99	7/1510 (0.5%)
24	SR	0.34	0/904	0.71	1/1210 (0.1%)
25	SS	0.27	0/1211	0.73	2/1628 (0.1%)
26	ST	0.29	0/1130	0.61	0/1517
27	SU	0.27	0/815	0.63	0/1102
28	SV	0.24	0/693	0.64	0/935
29	SW	0.31	0/1038	0.61	0/1395
30	SX	0.24	0/1139	0.59	0/1518
31	SY	0.24	0/1087	0.76	3/1449 (0.2%)
32	SZ	0.37	0/566	0.80	0/761

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Sa	0.25	0/782	0.62	0/1047
34	Sb	0.20	0/620	0.66	0/838
35	Sc	0.24	0/499	0.66	1/670 (0.1%)
36	Sd	0.39	0/452	0.65	0/600
37	Se	0.21	0/483	0.63	0/643
38	Sf	0.59	0/253	0.96	0/340
39	Sg	0.31	0/2456	0.75	0/3343
40	LA	0.29	0/1946	0.64	2/2614 (0.1%)
41	LB	0.25	0/3146	0.50	0/4228
42	LC	0.29	0/2800	0.59	0/3790
43	LD	0.25	0/2408	0.55	2/3248 (0.1%)
44	LE	0.28	0/1269	0.63	1/1705 (0.1%)
45	LF	0.27	0/1828	0.57	0/2461
46	LG	0.28	0/1795	0.62	0/2429
47	LH	0.24	0/1531	0.56	0/2062
48	LI	0.27	0/1732	0.63	2/2323 (0.1%)
49	LJ	0.40	0/1374	0.83	0/1842
50	LK	0.85	5/777 (0.6%)	1.20	8/1077 (0.7%)
51	LL	0.30	0/1573	0.68	3/2113 (0.1%)
52	LM	0.24	0/1074	0.46	0/1446
53	LN	0.29	0/1757	0.52	0/2354
54	LO	0.30	0/1585	0.58	0/2128
55	LP	0.31	0/1400	0.56	2/1882 (0.1%)
56	LQ	0.27	0/1465	0.53	0/1965
57	LR	0.27	0/1382	0.57	1/1849 (0.1%)
58	LS	0.26	0/1481	0.52	0/1990
59	LT	0.31	0/1300	0.60	0/1743
60	LU	0.21	0/794	0.47	0/1076
61	LV	0.27	0/1008	0.56	1/1356 (0.1%)
62	LW	0.22	0/533	0.52	0/707
63	LX	0.28	0/974	0.67	0/1314
64	LY	0.23	0/987	0.50	0/1318
65	LZ	0.31	0/1118	0.71	1/1497 (0.1%)
66	La	0.29	0/1204	0.68	2/1612 (0.1%)
67	Lb	0.25	0/473	0.67	0/629
68	Lc	0.22	0/775	0.48	0/1040
69	Ld	0.33	0/897	0.53	0/1205
70	Le	0.25	0/1041	0.60	1/1394 (0.1%)
71	Lf	0.26	0/868	0.53	0/1168
72	Lg	0.44	0/890	0.76	0/1189
73	Lh	0.20	0/974	0.42	0/1297
74	Li	0.25	0/777	0.61	2/1033 (0.2%)
75	Lj	0.31	0/665	0.57	0/882

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Lk	0.25	0/614	0.65	0/822
77	Ll	0.29	0/443	0.59	0/588
78	Lm	0.24	0/423	0.53	0/562
79	L2	0.21	0/234	0.44	0/300
79	Ln	0.24	0/234	0.51	0/300
80	Lo	0.23	0/860	0.55	0/1136
81	Lp	0.29	0/701	0.66	0/934
82	L1	0.31	0/1009	0.83	1/1405 (0.1%)
83	P0	0.54	0/997	1.14	7/1384 (0.5%)
84	CN	0.31	0/950	0.75	5/1260 (0.4%)
All	All	0.28	6/219364 (0.0%)	0.52	92/322222 (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
12	SF	0	1
14	SH	0	1
16	SJ	0	1
19	SM	0	2
21	SO	0	1
23	SQ	0	1
25	SS	0	1
27	SU	0	1
31	SY	0	1
37	Se	0	1
42	LC	0	1
43	LD	0	1
46	LG	0	1
49	LJ	0	1
50	LK	0	5
51	LL	0	2
65	LZ	0	1
66	La	0	2
67	Lb	0	1
74	Li	0	1
81	Lp	0	1
82	L1	0	1
83	P0	0	3
All	All	0	32

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	LK	58	VAL	C-N	9.76	1.48	1.33
50	LK	58	VAL	CA-C	8.17	1.63	1.52
50	LK	59	THR	N-CA	6.87	1.54	1.46
22	SP	52	LYS	C-N	5.67	1.38	1.33
50	LK	57	LYS	C-N	5.63	1.41	1.33

The worst 5 of 92 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C2	322	G	C2'-C3'-O3'	9.77	124.16	109.50
4	C1	1307	G	C2'-C3'-O3'	9.48	123.72	109.50
83	P0	41	VAL	CA-C-N	-9.31	108.08	122.60
83	P0	41	VAL	C-N-CA	-9.31	108.08	122.60
66	La	47	LYS	CA-C-N	8.41	137.61	121.54

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	SF	155	ALA	Peptide
14	SH	64	VAL	Peptide
16	SJ	105	LEU	Mainchain
19	SM	119	SER	Peptide
19	SM	130	THR	Peptide

5.2 Too-close contacts [i](#)

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	C2	37739	0	18986	296	0
2	C7	65	0	33	0	0
3	C5	1624	0	841	9	0
4	C1	68535	0	34437	471	0
5	C4	2579	0	1304	27	0
6	C3	3353	0	1695	24	0
7	SA	1583	0	1578	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	SB	1722	0	1793	29	0
9	SC	1635	0	1723	26	0
10	SD	1734	0	1817	27	0
11	SE	2068	0	2154	51	0
12	SF	1609	0	1675	39	0
13	SG	1755	0	1846	49	0
14	SH	1486	0	1576	34	0
15	SI	1489	0	1525	29	0
16	SJ	1494	0	1573	31	0
17	SK	741	0	691	19	0
18	SL	1168	0	1233	21	0
19	SM	890	0	887	28	0
20	SN	1192	0	1255	21	0
21	SO	949	0	985	22	0
22	SP	939	0	968	24	0
23	SQ	1105	0	1166	28	0
24	SR	896	0	902	23	0
25	SS	1192	0	1222	24	0
26	ST	1112	0	1124	21	0
27	SU	805	0	874	14	0
28	SV	684	0	672	17	0
29	SW	1021	0	1060	13	0
30	SX	1121	0	1196	15	0
31	SY	1073	0	1132	24	0
32	SZ	558	0	598	11	0
33	Sa	769	0	815	24	0
34	Sb	610	0	631	9	0
35	Sc	497	0	535	11	0
36	Sd	442	0	428	8	0
37	Se	475	0	525	6	0
38	Sf	248	0	237	7	0
39	Sg	2403	0	2350	60	0
40	LA	1912	0	1976	42	0
41	LB	3075	0	3142	55	0
42	LC	2748	0	2859	42	0
43	LD	2359	0	2311	33	0
44	LE	1248	0	1339	20	0
45	LF	1791	0	1869	31	0
46	LG	1763	0	1819	30	0
47	LH	1510	0	1576	20	0
48	LI	1696	0	1731	26	0
49	LJ	1353	0	1383	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	LK	778	0	368	24	0
51	LL	1548	0	1613	37	0
52	LM	1059	0	1154	12	0
53	LN	1720	0	1779	37	0
54	LO	1555	0	1659	21	0
55	LP	1378	0	1404	18	0
56	LQ	1441	0	1543	24	0
57	LR	1365	0	1414	24	0
58	LS	1445	0	1487	23	0
59	LT	1276	0	1323	29	0
60	LU	778	0	791	8	0
61	LV	993	0	1040	21	0
62	LW	521	0	551	3	0
63	LX	959	0	1023	9	0
64	LY	976	0	1064	12	0
65	LZ	1092	0	1155	23	0
66	La	1173	0	1215	24	0
67	Lb	462	0	491	6	0
68	Lc	767	0	816	7	0
69	Ld	883	0	918	21	0
70	Le	1020	0	1090	12	0
71	Lf	850	0	880	17	0
72	Lg	880	0	942	12	0
73	Lh	965	0	1067	8	0
74	Li	770	0	846	6	0
75	Lj	650	0	650	13	0
76	Lk	608	0	671	15	0
77	Ll	436	0	475	6	0
78	Lm	417	0	455	11	0
79	L2	233	0	284	1	0
79	Ln	233	0	284	3	0
80	Lo	847	0	914	13	0
81	Lp	694	0	734	15	0
82	L1	1010	0	435	1	0
83	P0	998	0	458	18	0
84	CN	940	0	973	16	0
85	C1	222	0	0	0	0
85	C2	89	0	0	0	0
85	C3	1	0	0	0	0
85	C4	1	0	0	0	0
85	C5	3	0	0	0	0
86	C1	210	0	190	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	C2	42	0	38	0	0
87	C1	10	0	19	0	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sb	1	0	0	0	0
88	Sd	1	0	0	0	0
88	Sf	1	0	0	0	0
All	All	205122	0	150260	2023	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 2023 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)
39:Sg:218:GLY:O	39:Sg:235:SER:HA	1.36	1.25
62:LW:4:GLU:O	62:LW:12:LYS:HA	1.52	1.09
65:LZ:121:ARG:O	65:LZ:125:GLY:HA2	1.55	1.06
81:Lp:53:GLY:HA2	81:Lp:66:GLY:O	1.56	1.05
39:Sg:220:ILE:O	39:Sg:233:THR:HA	1.57	1.04

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
7	SA	204/252 (81%)	179 (88%)	24 (12%)	1 (0%)	24 60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	SB	214/255 (84%)	200 (94%)	14 (6%)	0	100	100
9	SC	215/254 (85%)	205 (95%)	9 (4%)	1 (0%)	24	60
10	SD	221/240 (92%)	196 (89%)	24 (11%)	1 (0%)	24	60
11	SE	258/261 (99%)	234 (91%)	24 (9%)	0	100	100
12	SF	204/225 (91%)	181 (89%)	22 (11%)	1 (0%)	24	60
13	SG	216/236 (92%)	204 (94%)	12 (6%)	0	100	100
14	SH	183/190 (96%)	157 (86%)	24 (13%)	2 (1%)	11	43
15	SI	184/200 (92%)	176 (96%)	8 (4%)	0	100	100
16	SJ	183/197 (93%)	168 (92%)	15 (8%)	0	100	100
17	SK	90/105 (86%)	78 (87%)	7 (8%)	5 (6%)	1	8
18	SL	144/156 (92%)	133 (92%)	11 (8%)	0	100	100
19	SM	122/143 (85%)	86 (70%)	36 (30%)	0	100	100
20	SN	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
21	SO	126/137 (92%)	107 (85%)	19 (15%)	0	100	100
22	SP	117/142 (82%)	99 (85%)	17 (14%)	1 (1%)	14	48
23	SQ	139/143 (97%)	119 (86%)	19 (14%)	1 (1%)	18	53
24	SR	111/136 (82%)	100 (90%)	11 (10%)	0	100	100
25	SS	143/146 (98%)	127 (89%)	16 (11%)	0	100	100
26	ST	141/144 (98%)	134 (95%)	7 (5%)	0	100	100
27	SU	99/121 (82%)	92 (93%)	7 (7%)	0	100	100
28	SV	85/87 (98%)	76 (89%)	9 (11%)	0	100	100
29	SW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
30	SX	142/145 (98%)	131 (92%)	11 (8%)	0	100	100
31	SY	132/135 (98%)	117 (89%)	13 (10%)	2 (2%)	8	35
32	SZ	67/108 (62%)	63 (94%)	4 (6%)	0	100	100
33	Sa	95/119 (80%)	81 (85%)	14 (15%)	0	100	100
34	Sb	79/82 (96%)	69 (87%)	10 (13%)	0	100	100
35	Sc	61/67 (91%)	59 (97%)	2 (3%)	0	100	100
36	Sd	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
37	Se	58/63 (92%)	52 (90%)	6 (10%)	0	100	100
38	Sf	31/152 (20%)	25 (81%)	5 (16%)	1 (3%)	3	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	Sg	311/319 (98%)	277 (89%)	34 (11%)	0	100	100
40	LA	250/254 (98%)	224 (90%)	26 (10%)	0	100	100
41	LB	384/387 (99%)	367 (96%)	17 (4%)	0	100	100
42	LC	359/362 (99%)	325 (90%)	33 (9%)	1 (0%)	36	70
43	LD	292/297 (98%)	276 (94%)	16 (6%)	0	100	100
44	LE	153/176 (87%)	139 (91%)	14 (9%)	0	100	100
45	LF	221/244 (91%)	217 (98%)	4 (2%)	0	100	100
46	LG	229/256 (90%)	206 (90%)	23 (10%)	0	100	100
47	LH	188/191 (98%)	179 (95%)	9 (5%)	0	100	100
48	LI	205/221 (93%)	194 (95%)	11 (5%)	0	100	100
49	LJ	167/174 (96%)	147 (88%)	18 (11%)	2 (1%)	10	40
50	LK	156/165 (94%)	137 (88%)	16 (10%)	3 (2%)	6	30
51	LL	192/199 (96%)	173 (90%)	15 (8%)	4 (2%)	5	27
52	LM	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
53	LN	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
54	LO	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
55	LP	171/184 (93%)	167 (98%)	4 (2%)	0	100	100
56	LQ	183/186 (98%)	175 (96%)	8 (4%)	0	100	100
57	LR	172/189 (91%)	167 (97%)	5 (3%)	0	100	100
58	LS	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
59	LT	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
60	LU	96/121 (79%)	93 (97%)	3 (3%)	0	100	100
61	LV	132/137 (96%)	129 (98%)	3 (2%)	0	100	100
62	LW	61/155 (39%)	59 (97%)	2 (3%)	0	100	100
63	LX	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
64	LY	122/127 (96%)	119 (98%)	3 (2%)	0	100	100
65	LZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
66	La	146/149 (98%)	125 (86%)	19 (13%)	2 (1%)	9	36
67	Lb	56/59 (95%)	48 (86%)	8 (14%)	0	100	100
68	Lc	98/105 (93%)	94 (96%)	4 (4%)	0	100	100
69	Ld	107/113 (95%)	101 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	Le	125/130 (96%)	118 (94%)	7 (6%)	0	100	100
71	Lf	104/107 (97%)	97 (93%)	7 (7%)	0	100	100
72	Lg	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
73	Lh	117/120 (98%)	109 (93%)	8 (7%)	0	100	100
74	Li	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
75	Lj	80/88 (91%)	77 (96%)	3 (4%)	0	100	100
76	Lk	75/78 (96%)	71 (95%)	3 (4%)	1 (1%)	9	38
77	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
78	Lm	50/128 (39%)	50 (100%)	0	0	100	100
79	L2	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
79	Ln	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
80	Lo	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
81	Lp	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
82	L1	202/217 (93%)	149 (74%)	53 (26%)	0	100	100
83	P0	201/312 (64%)	184 (92%)	16 (8%)	1 (0%)	24	60
84	CN	110/560 (20%)	104 (94%)	6 (6%)	0	100	100
All	All	11507/13159 (87%)	10583 (92%)	894 (8%)	30 (0%)	37	70

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	SK	81	ASN
31	SY	32	ARG
49	LJ	95	ASN
51	LL	48	PRO
14	SH	30	SER

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C2	1768/1800 (98%)	472 (26%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C7	2/3 (66%)	0	0
3	C5	74/75 (98%)	13 (17%)	0
4	C1	3201/3396 (94%)	632 (19%)	0
5	C4	120/121 (99%)	11 (9%)	0
6	C3	157/158 (99%)	28 (17%)	0
All	All	5322/5553 (95%)	1156 (21%)	0

5 of 1156 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C2	2	A
1	C2	4	C
1	C2	17	C
1	C2	25	C
1	C2	26	A

There are no RNA pucker outliers to report.

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

9 non-standard protein/DNA/RNA residues are 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
3	H2U	C5	16	3	18,21,22	3.07	5 (27%)	19,30,33	1.49	4 (21%)
3	1MG	C5	9	3	23,26,27	2.91	8 (34%)	33,39,42	1.73	7 (21%)
3	1MA	C5	57	3	21,25,26	2.87	5 (23%)	30,37,40	2.78	8 (26%)
3	2MG	C5	10	3	23,26,27	2.68	9 (39%)	33,38,41	2.44	13 (39%)
3	7MG	C5	45	3	23,26,27	3.49	10 (43%)	27,39,42	2.09	9 (33%)
3	H2U	C5	46	3	18,21,22	3.16	5 (27%)	19,30,33	1.48	4 (21%)
3	5MC	C5	47	3	19,22,23	3.78	8 (42%)	26,32,35	0.99	2 (7%)
3	T6A	C5	36	3,85	31,34,35	2.03	10 (32%)	43,49,52	2.26	10 (23%)
3	M2G	C5	25	3	24,27,28	2.68	9 (37%)	33,40,43	2.09	9 (27%)

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
3	H2U	C5	16	3	-	0/7/38/39	0/2/2/2
3	1MG	C5	9	3	-	2/7/25/26	0/3/3/3
3	1MA	C5	57	3	-	0/7/25/26	0/3/3/3
3	2MG	C5	10	3	-	0/9/27/28	0/3/3/3
3	7MG	C5	45	3	-	0/7/37/38	0/3/3/3
3	H2U	C5	46	3	-	6/7/38/39	0/2/2/2
3	5MC	C5	47	3	-	2/7/25/26	0/2/2/2
3	T6A	C5	36	3,85	-	1/23/41/42	0/3/3/3
3	M2G	C5	25	3	-	0/11/29/30	0/3/3/3

The worst 5 of 69 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C5	46	H2U	C2-N1	9.77	1.49	1.35
3	C5	16	H2U	C2-N1	9.39	1.48	1.35
3	C5	47	5MC	C6-C5	9.08	1.49	1.34
3	C5	57	1MA	C2-N3	8.90	1.46	1.30
3	C5	45	7MG	C8-N9	8.09	1.51	1.45

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C5	57	1MA	C1'-N9-C8	-8.83	101.64	126.73
3	C5	57	1MA	C1'-N9-C4	8.11	150.46	126.49
3	C5	10	2MG	C2-N3-C4	6.58	120.23	112.00
3	C5	36	T6A	N6-C10-N11	6.24	122.35	113.77
3	C5	25	M2G	C1'-N9-C8	-5.64	110.70	126.73

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C5	46	H2U	O4'-C4'-C5'-O5'
3	C5	46	H2U	O4'-C1'-N1-C6
3	C5	46	H2U	C2'-C1'-N1-C2
3	C5	46	H2U	C2'-C1'-N1-C6
3	C5	47	5MC	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C5	45	7MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 332 ligands modelled in this entry, 325 are monoatomic - leaving 7 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
86	T1C	C1	3402	-	45,45,45	1.17	4 (8%)	56,72,72	1.14	4 (7%)
86	T1C	C1	3404	85	45,45,45	1.16	4 (8%)	56,72,72	1.02	3 (5%)
86	T1C	C1	3405	85	45,45,45	1.14	4 (8%)	56,72,72	1.33	6 (10%)
86	T1C	C2	1990	-	45,45,45	1.17	4 (8%)	56,72,72	0.93	2 (3%)
87	SPD	C1	3628	-	9,9,9	0.30	0	8,8,8	0.97	0
86	T1C	C1	3401	-	45,45,45	1.15	4 (8%)	56,72,72	1.44	9 (16%)
86	T1C	C1	3403	85	45,45,45	1.18	4 (8%)	56,72,72	1.06	4 (7%)

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
86	T1C	C1	3402	-	-	13/22/80/80	0/4/4/4
86	T1C	C1	3404	85	-	7/22/80/80	0/4/4/4
86	T1C	C1	3405	85	-	11/22/80/80	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	T1C	C2	1990	-	-	9/22/80/80	0/4/4/4
87	SPD	C1	3628	-	-	5/7/7/7	-
86	T1C	C1	3401	-	-	11/22/80/80	0/4/4/4
86	T1C	C1	3403	85	-	13/22/80/80	0/4/4/4

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	C1	3402	T1C	C21-N21	5.09	1.48	1.33
86	C2	1990	T1C	C21-N21	5.08	1.48	1.33
86	C1	3401	T1C	C21-N21	5.04	1.48	1.33
86	C1	3403	T1C	C21-N21	5.04	1.48	1.33
86	C1	3404	T1C	C21-N21	5.01	1.47	1.33

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	C1	3401	T1C	C11-C1B-C12	4.63	122.47	118.80
86	C1	3405	T1C	C1-C1C-C12	4.47	115.12	109.88
86	C1	3402	T1C	C1C-C1-C2	4.39	122.72	115.75
86	C1	3401	T1C	C1C-C1-C2	4.23	122.47	115.75
86	C1	3405	T1C	C11-C1B-C12	4.09	122.03	118.80

There are no chirality outliers.

5 of 69 torsion outliers are listed below:

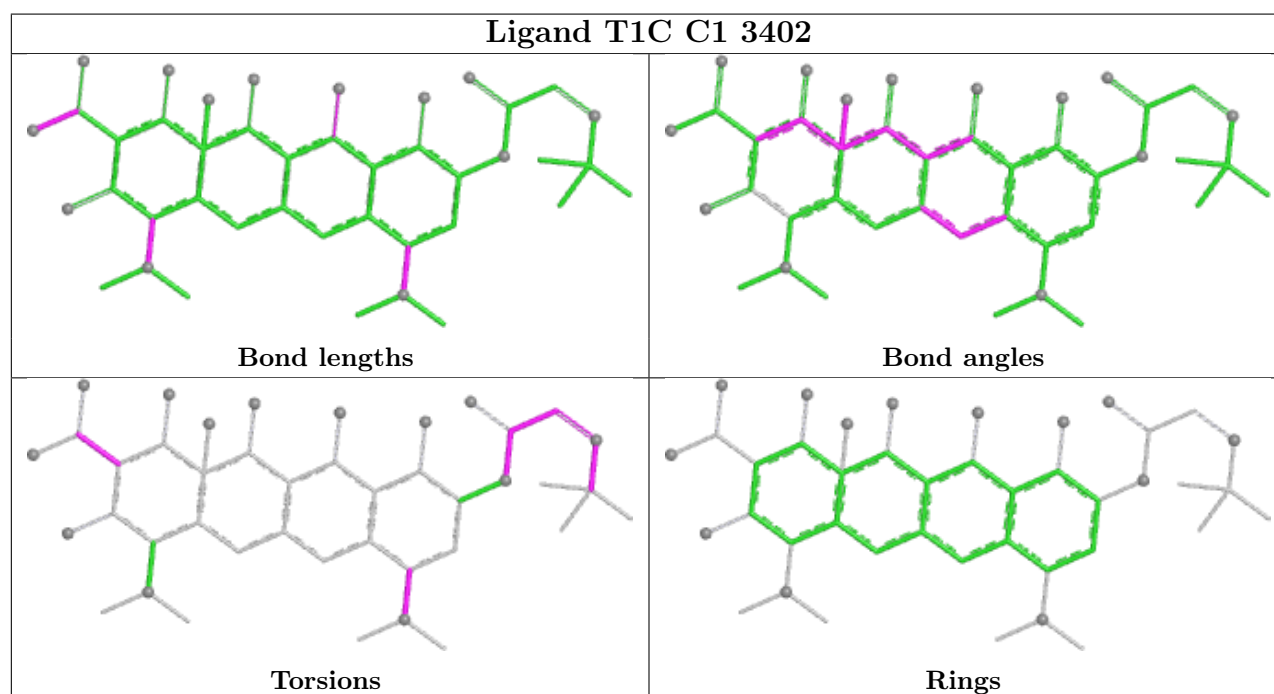
Mol	Chain	Res	Type	Atoms
86	C2	1990	T1C	C92-C91-N9-C9
86	C2	1990	T1C	C3-C2-C21-O21
86	C2	1990	T1C	C3-C2-C21-N21
86	C2	1990	T1C	C1-C2-C21-O21
86	C2	1990	T1C	C1-C2-C21-N21

There are no ring outliers.

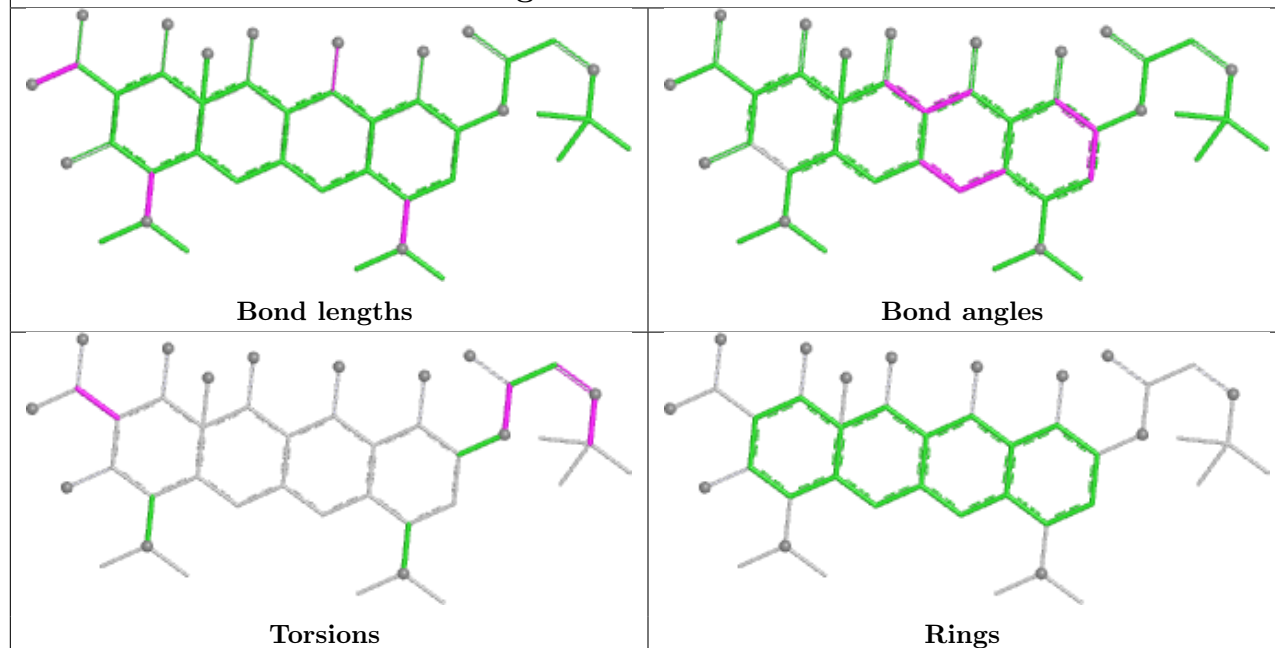
3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	C1	3402	T1C	3	0
86	C1	3404	T1C	1	0
86	C1	3403	T1C	3	0

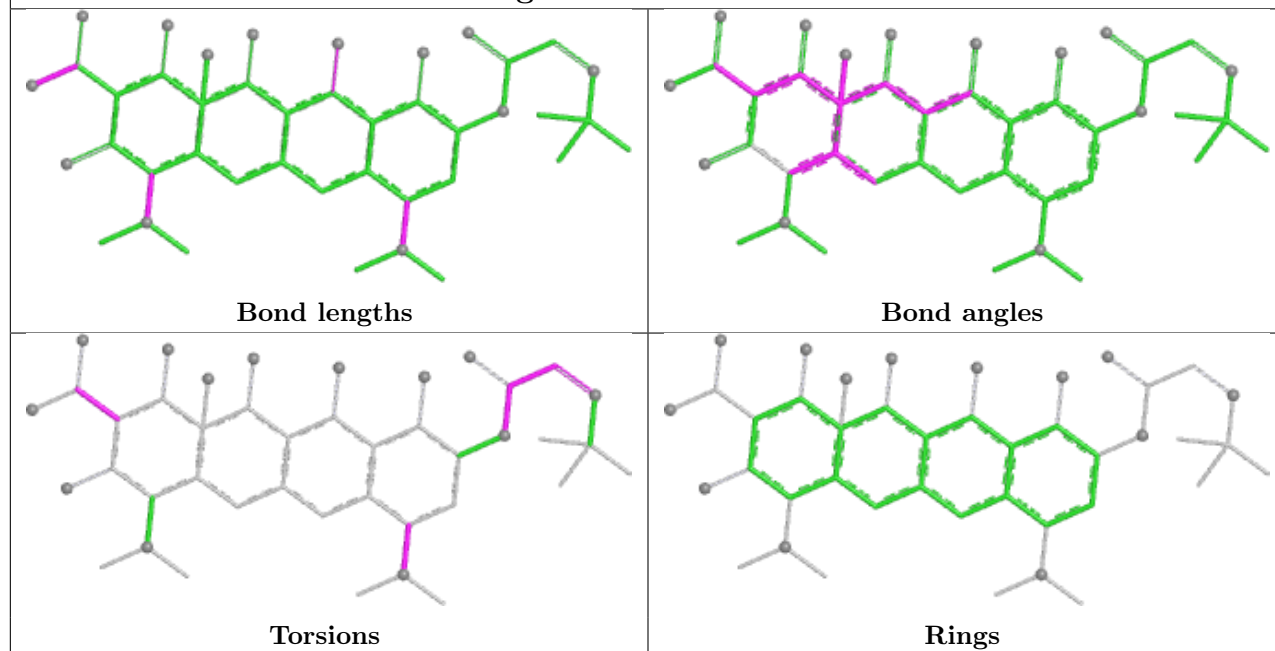
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



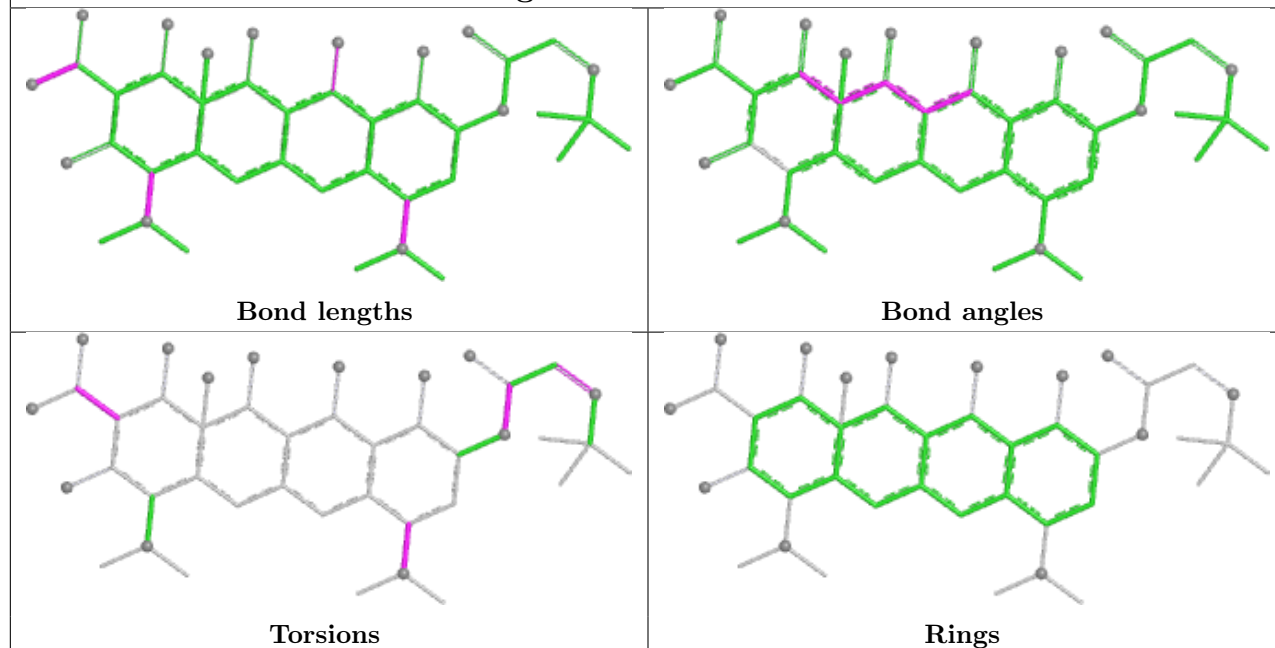
Ligand T1C C1 3404



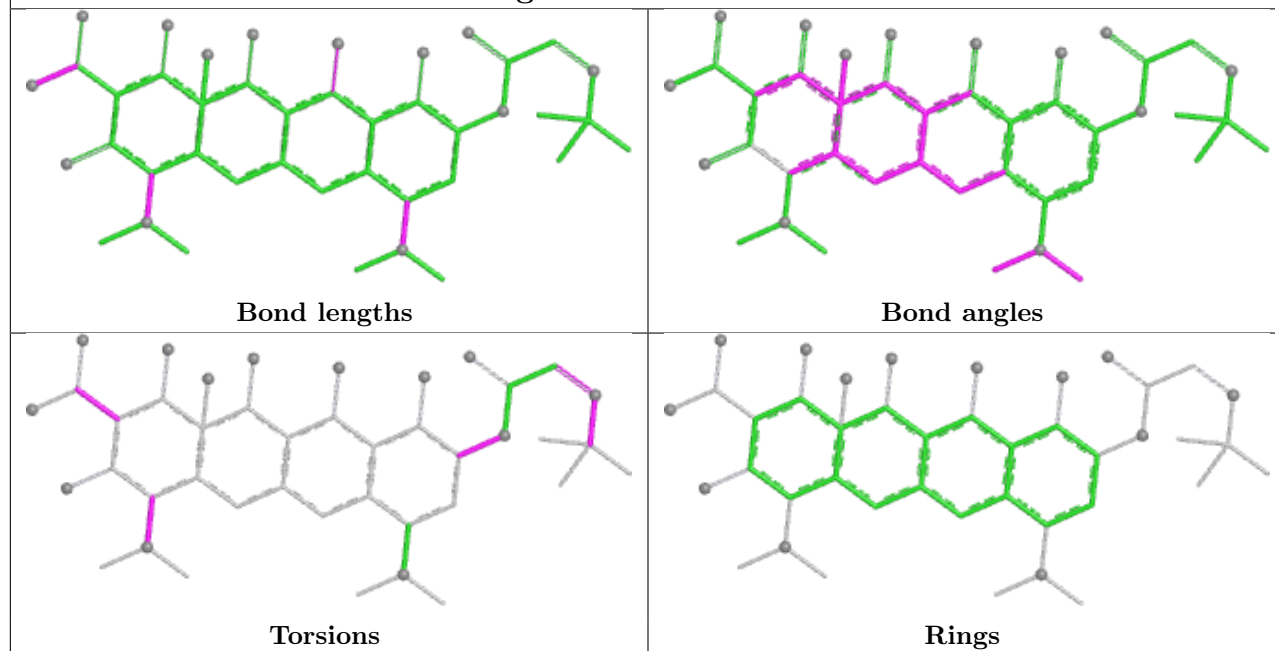
Ligand T1C C1 3405

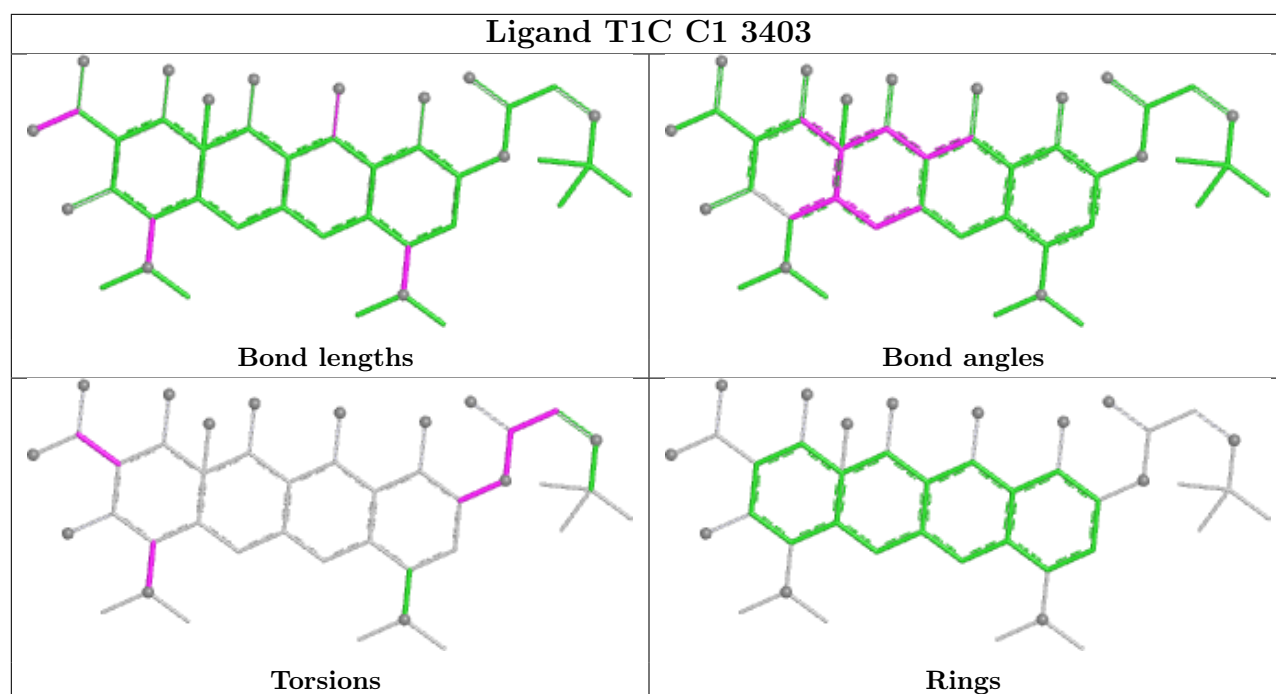


Ligand T1C C2 1990



Ligand T1C C1 3401





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.

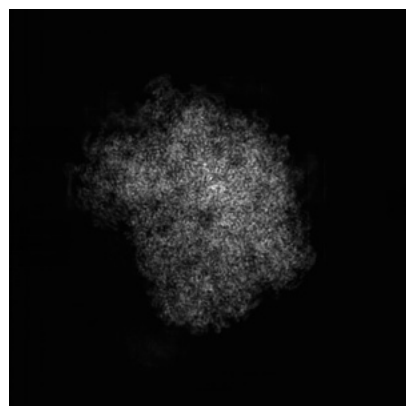
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36945. These allow visual inspection of the internal detail of the map and identification of artifacts.

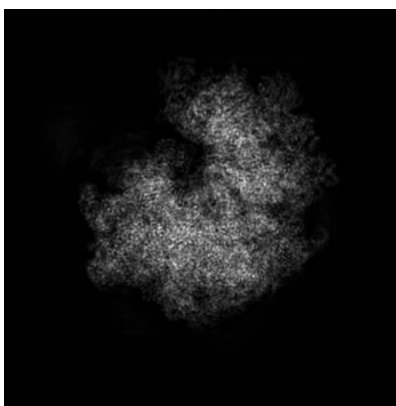
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

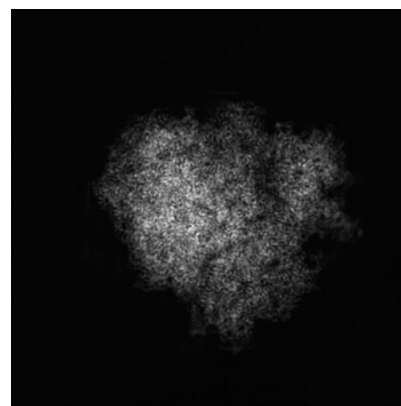
6.1.1 Primary map



X

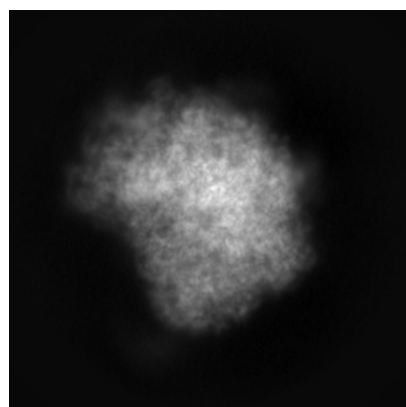


Y

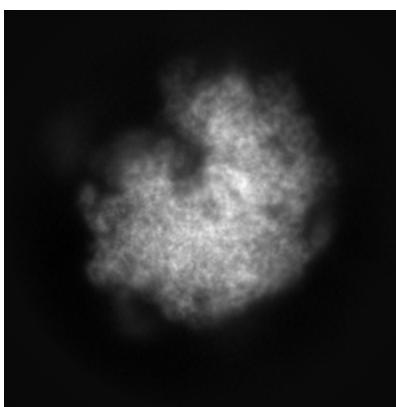


Z

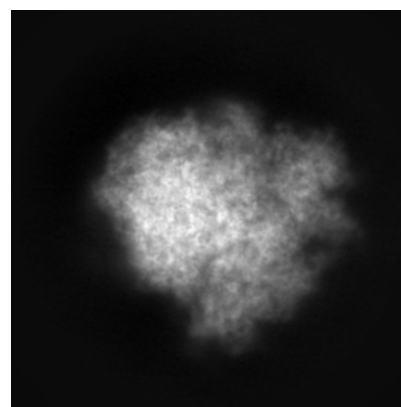
6.1.2 Raw map



X



Y



Z

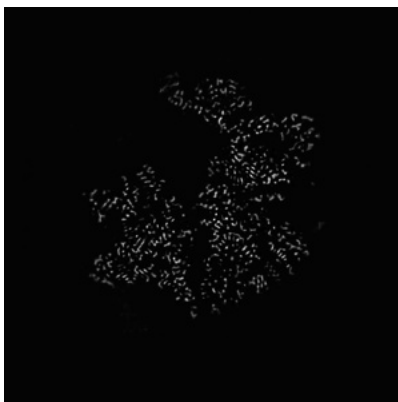
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 240

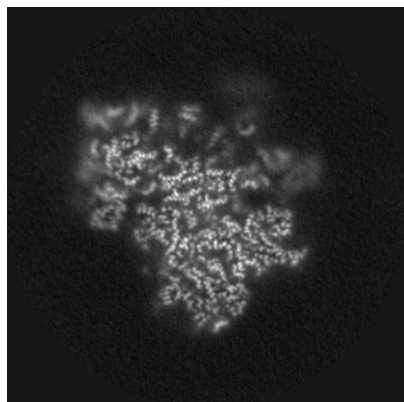


Y Index: 240

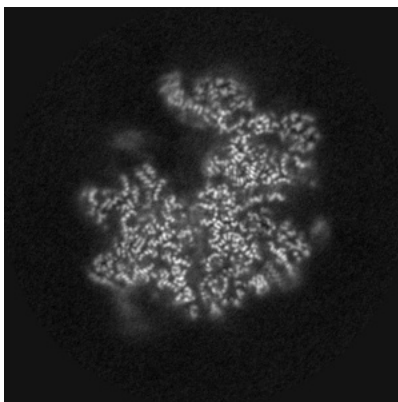


Z Index: 240

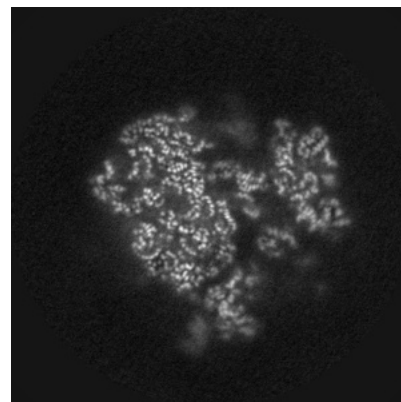
6.2.2 Raw map



X Index: 240



Y Index: 240



Z Index: 240

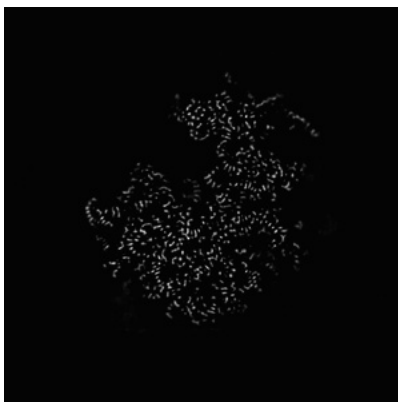
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

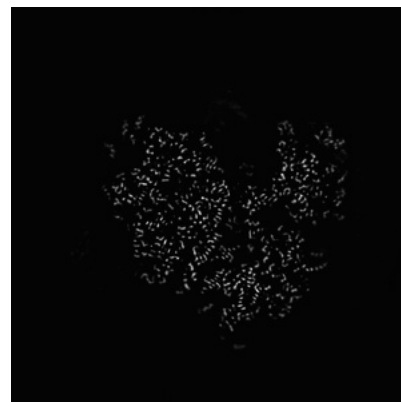
6.3.1 Primary map



X Index: 213

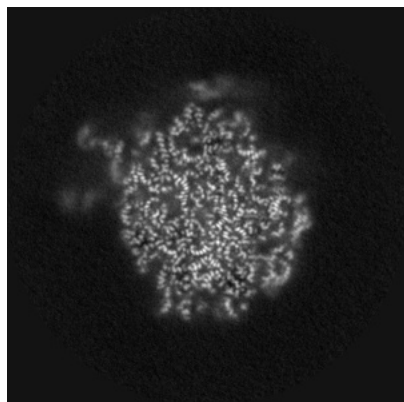


Y Index: 256

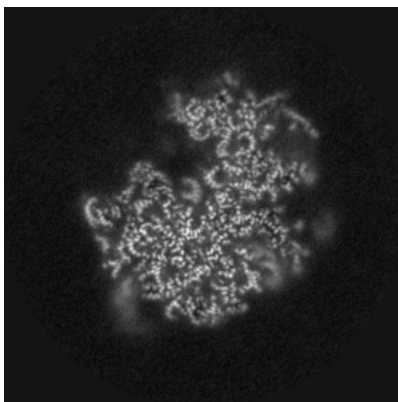


Z Index: 268

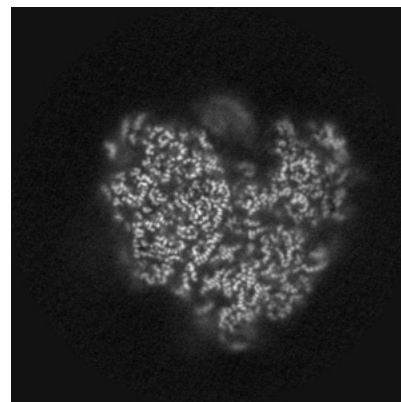
6.3.2 Raw map



X Index: 213



Y Index: 256

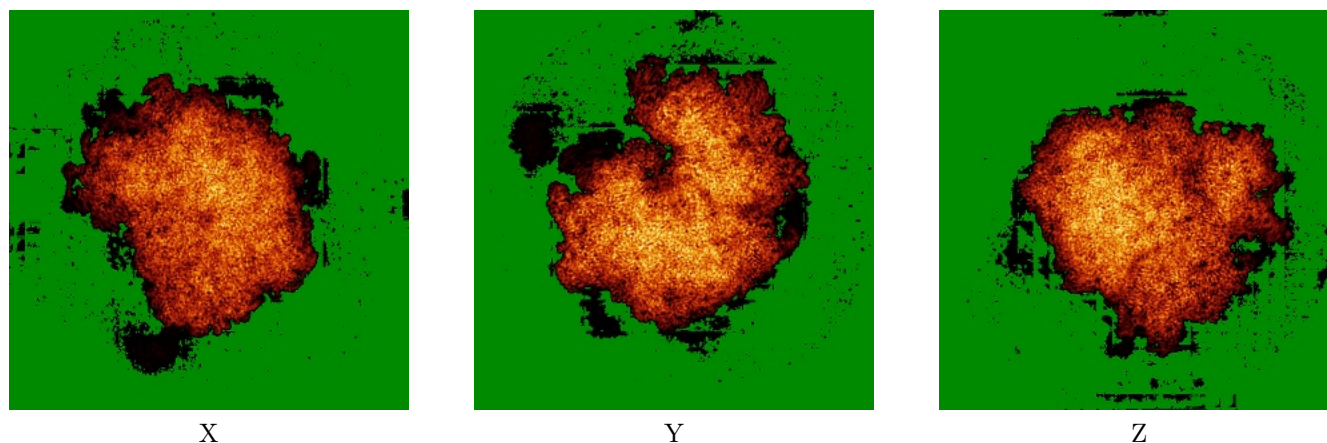


Z Index: 268

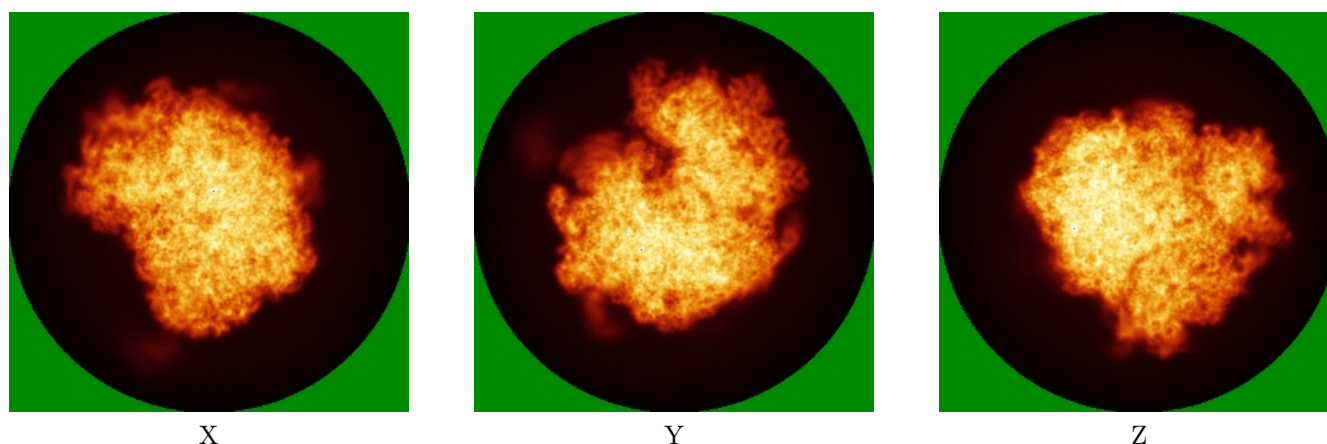
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

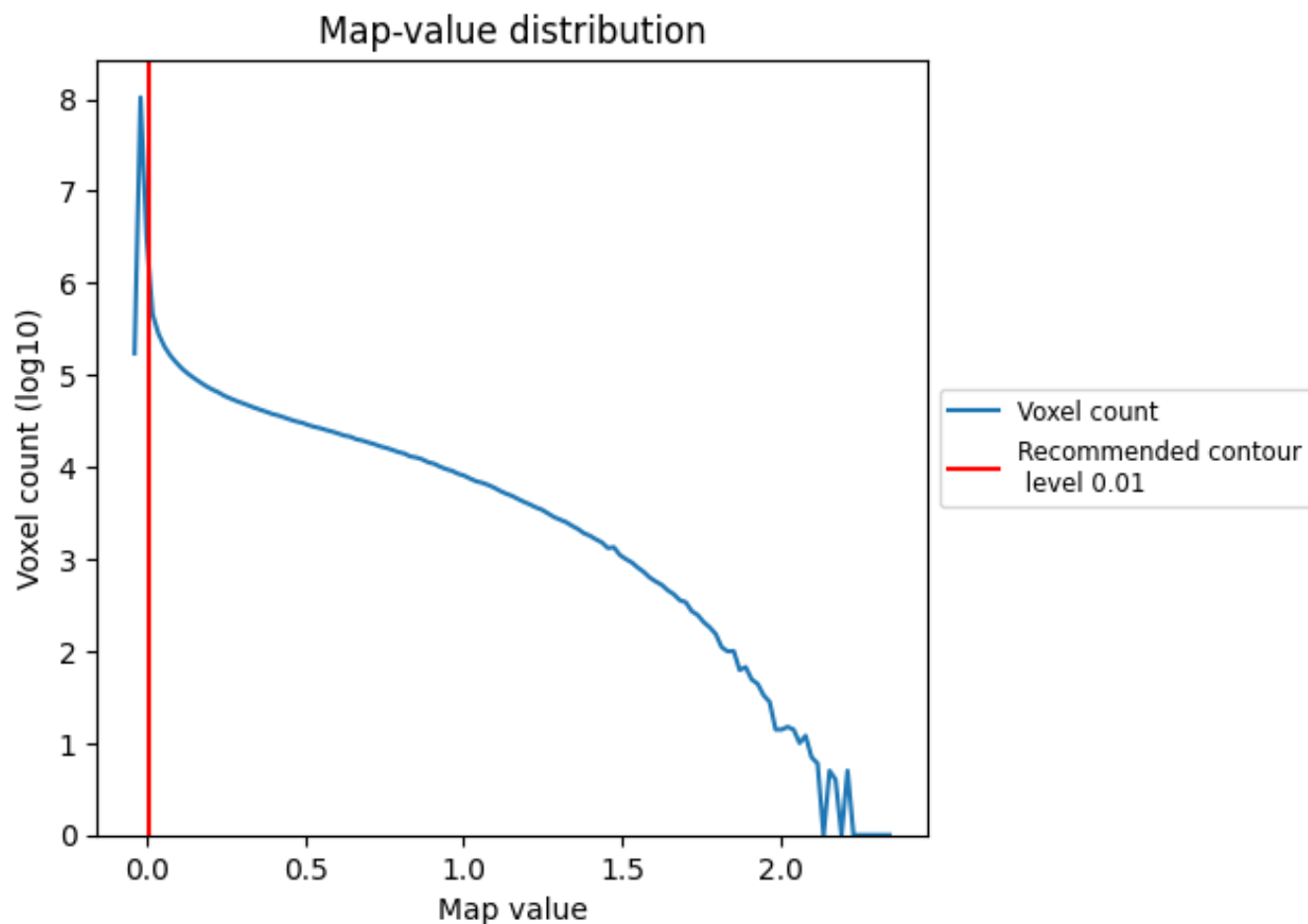
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

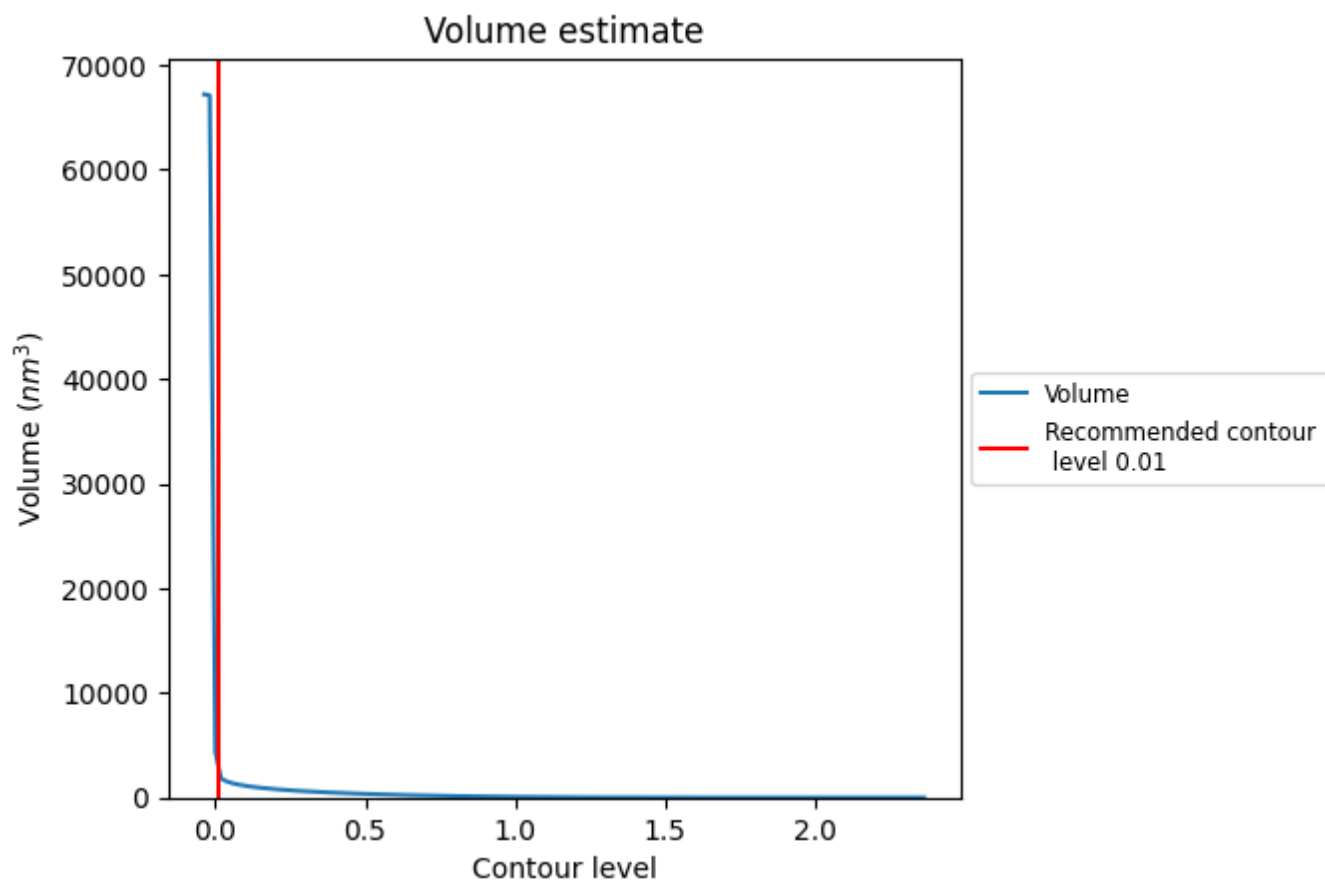
This section contains the results of statistical analysis of the map.

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.

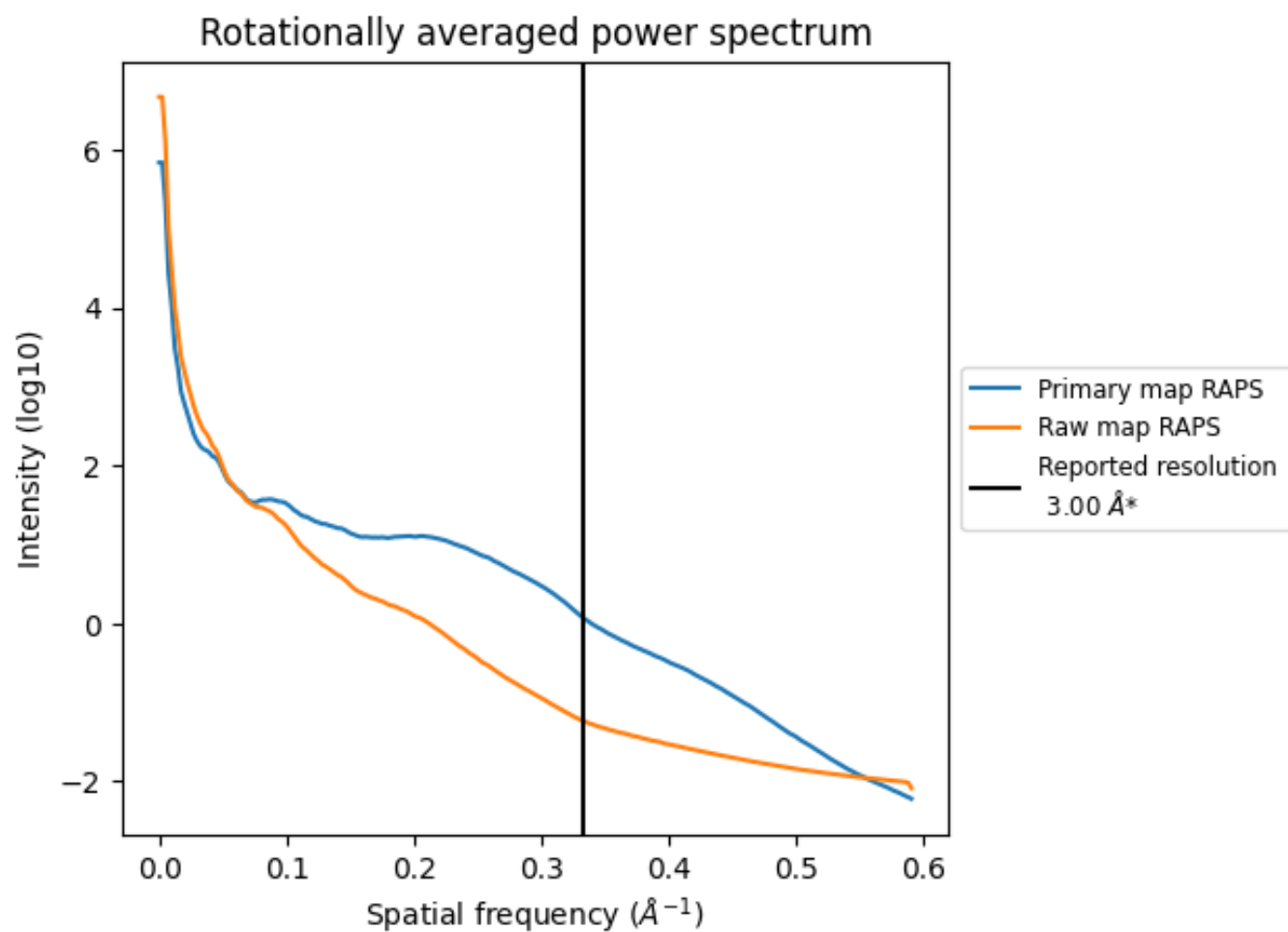
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3065 nm³; this corresponds to an approximate mass of 2769 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 ⓘ

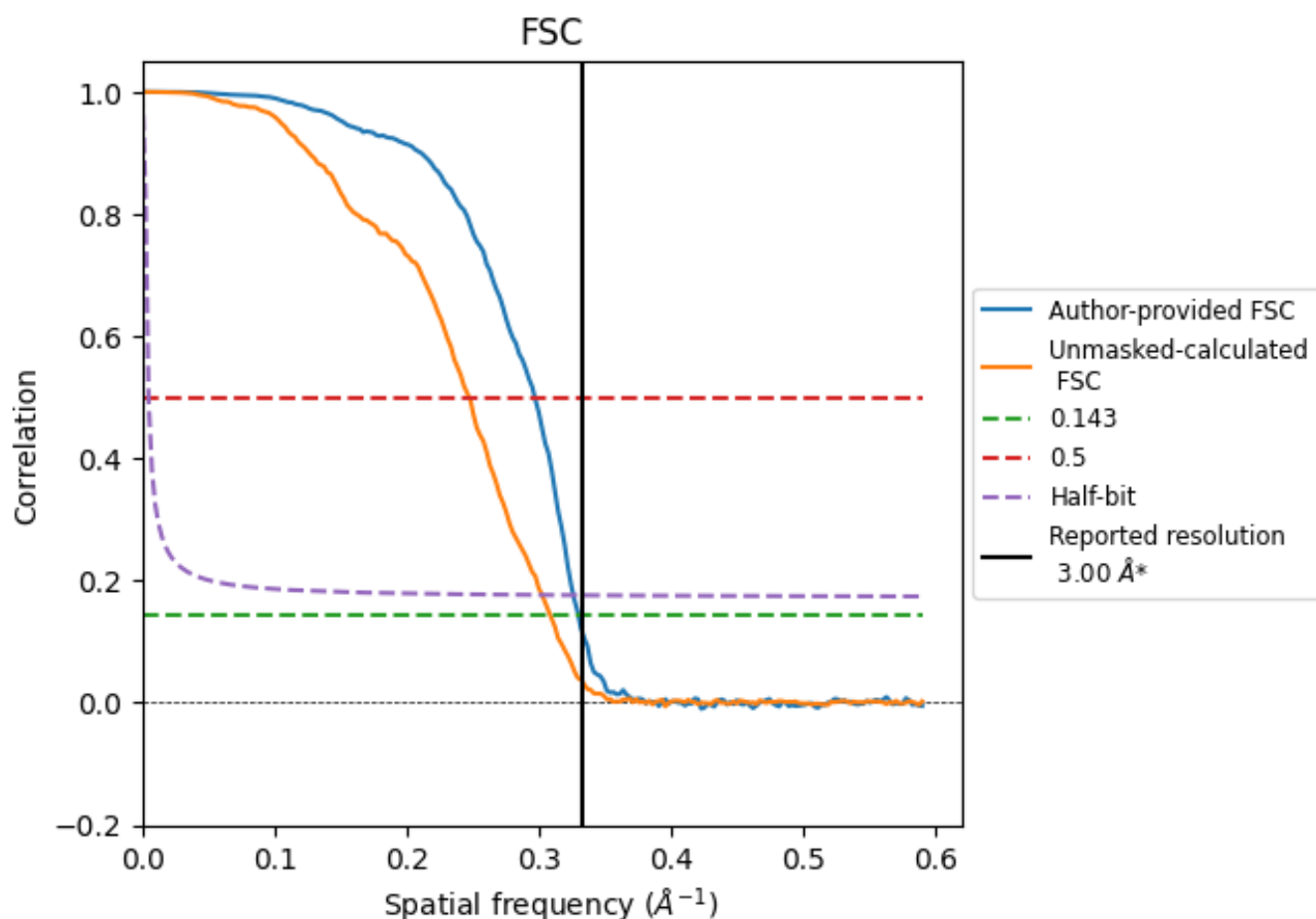


*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

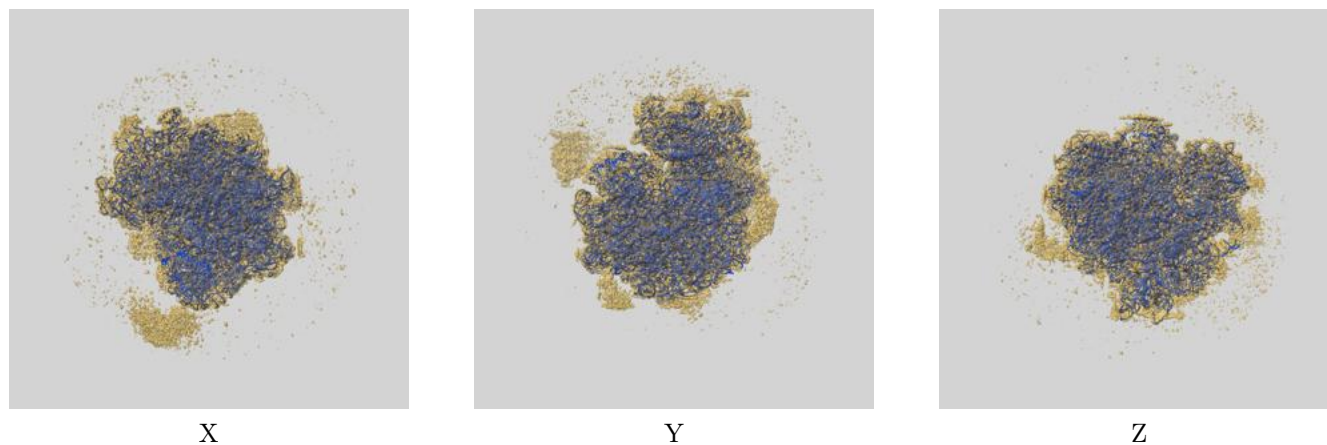
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.03	3.37	3.06
Unmasked-calculated*	3.24	4.04	3.30

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

9 Map-model fit [i](#)

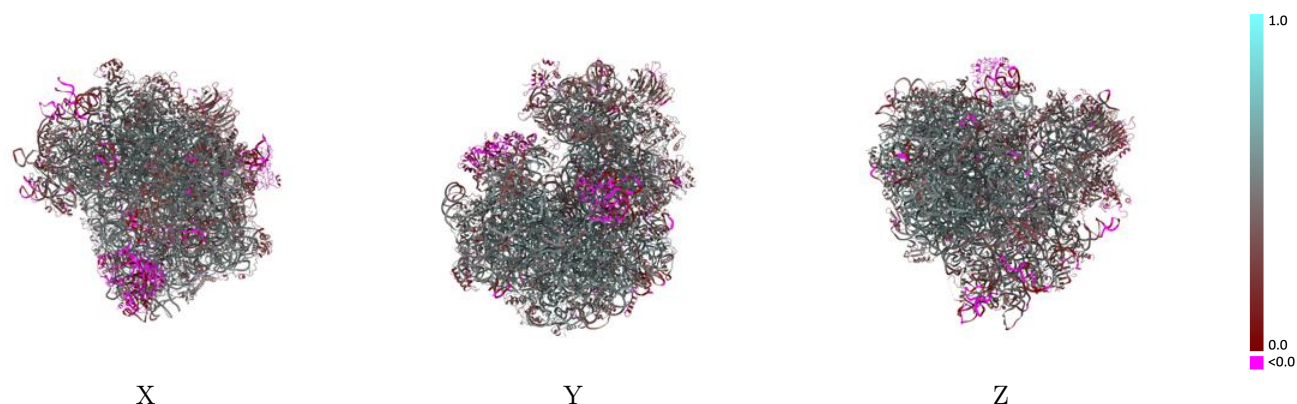
This section contains information regarding the fit between EMDB map EMD-36945 and PDB model 8K82. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

9.1 Map-model overlay [i](#)



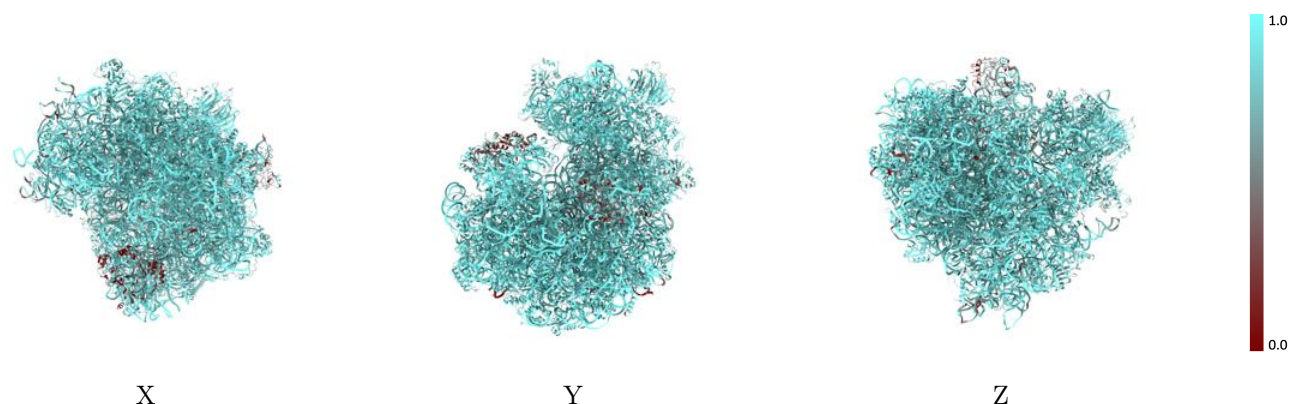
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



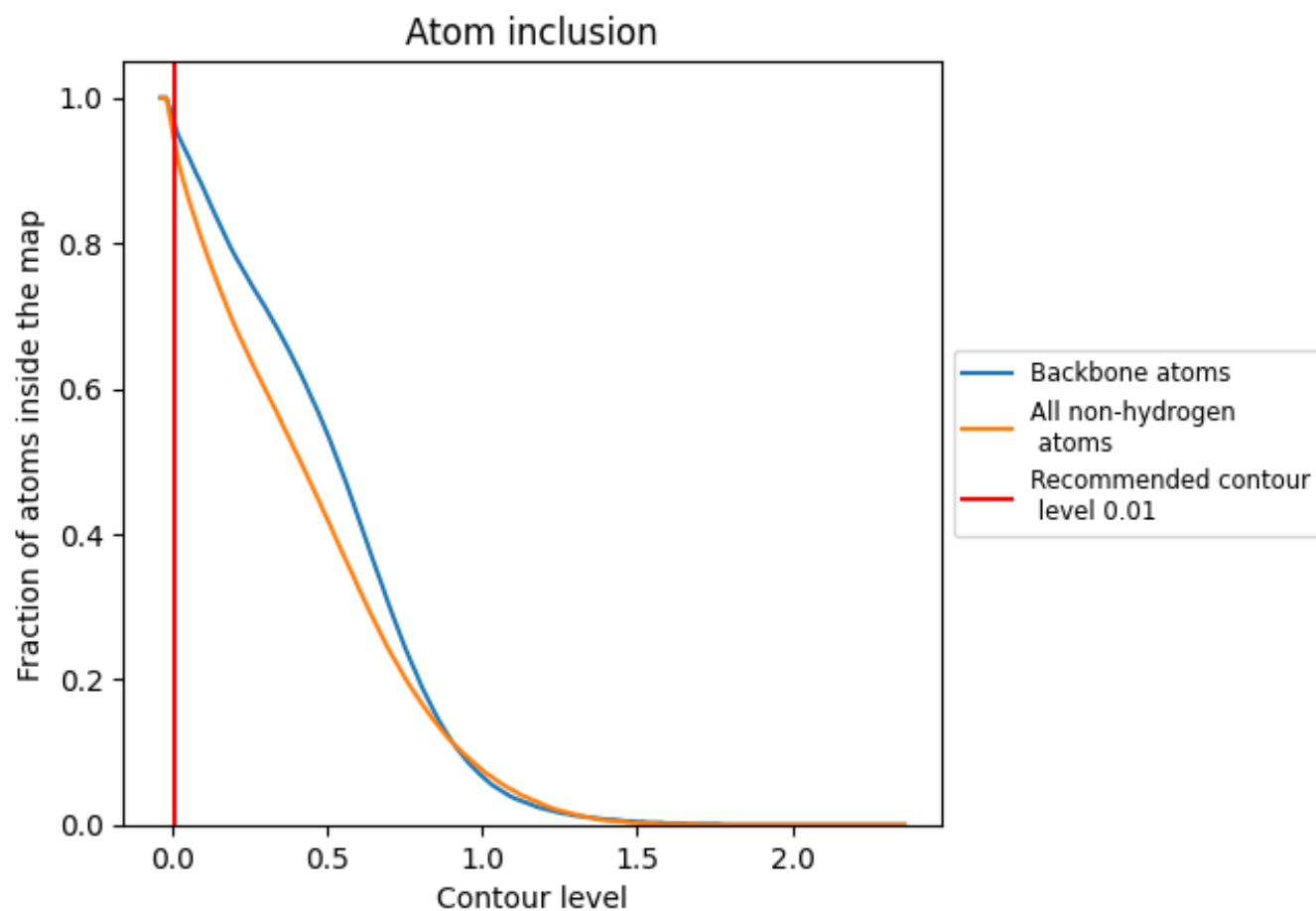
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9330	 0.4530
C1	 0.9650	 0.5090
C2	 0.9580	 0.4620
C3	 0.9820	 0.5350
C4	 0.9920	 0.5310
C5	 0.9480	 0.4580
C7	 1.0000	 0.5590
CN	 0.7270	 0.2950
L1	 0.3790	 -0.0680
L2	 0.6130	 0.2870
LA	 0.9440	 0.5020
LB	 0.9350	 0.4740
LC	 0.9380	 0.4510
LD	 0.8690	 0.3370
LE	 0.9050	 0.3950
LF	 0.9460	 0.4710
LG	 0.9160	 0.4020
LH	 0.9180	 0.4230
LI	 0.9020	 0.4290
LJ	 0.9120	 0.4070
LK	 0.3750	 -0.0300
LL	 0.9300	 0.4450
LM	 0.9250	 0.4390
LN	 0.9590	 0.5190
LO	 0.9550	 0.4860
LP	 0.9350	 0.4850
LQ	 0.9420	 0.4720
LR	 0.9380	 0.4810
LS	 0.9310	 0.4710
LT	 0.9290	 0.4650
LU	 0.9170	 0.4060
LV	 0.9080	 0.4630
LW	 0.9170	 0.4710
LX	 0.9250	 0.4630
LY	 0.9220	 0.4320



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Chain	Atom inclusion	Q-score
LZ	 0.9130	 0.4250
La	 0.9540	 0.4870
Lb	 0.8830	 0.4080
Lc	 0.9020	 0.4380
Ld	 0.8840	 0.4360
Le	 0.9300	 0.4780
Lf	 0.9570	 0.5090
Lg	 0.9320	 0.4900
Lh	 0.9050	 0.4340
Li	 0.9020	 0.4010
Lj	 0.9730	 0.5400
Lk	 0.8990	 0.3960
Ll	 0.9470	 0.4730
Lm	 0.9310	 0.4650
Ln	 0.8910	 0.4330
Lo	 0.9230	 0.4630
Lp	 0.9060	 0.4620
P0	 0.5110	 0.0120
SA	 0.9340	 0.4020
SB	 0.9050	 0.3940
SC	 0.9280	 0.4420
SD	 0.8720	 0.3340
SE	 0.9070	 0.3970
SF	 0.8830	 0.3540
SG	 0.8670	 0.3200
SH	 0.8770	 0.3190
SI	 0.9180	 0.4380
SJ	 0.8970	 0.3920
SK	 0.8860	 0.3090
SL	 0.9110	 0.4550
SM	 0.7640	 0.0910
SN	 0.9200	 0.4400
SO	 0.9260	 0.4350
SP	 0.8630	 0.3220
SQ	 0.9040	 0.3890
SR	 0.9020	 0.3690
SS	 0.8710	 0.3250
ST	 0.8920	 0.3610
SU	 0.8600	 0.3220
SV	 0.9010	 0.3780
SW	 0.9480	 0.4860
SX	 0.8990	 0.4400

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Chain	Atom inclusion	Q-score
SY	 0.8620	 0.3510
SZ	 0.8760	 0.3060
Sa	 0.9260	 0.4570
Sb	 0.9370	 0.4190
Sc	 0.8550	 0.3490
Sd	 0.9340	 0.4670
Se	 0.8040	 0.3400
Sf	 0.7590	 0.0760
Sg	 0.8800	 0.2950