



wwPDB EM Validation Summary Report ⓘ

Oct 11, 2025 – 08:29 am BST

PDB ID : 9HL9 / pdb_00009hl9
EMDB ID : EMD-52247
Title : CRYO-EM STRUCTURE OF LEISHMANIA MAJOR 80S RIBOSOME
WITH P/E-site tRNA AND mRNA : LM14Cs1H3 sKO STRAIN
Authors : Rajan, K.S.; Yonath, A.
Deposited on : 2024-12-04
Resolution : 2.50 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.dev129
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

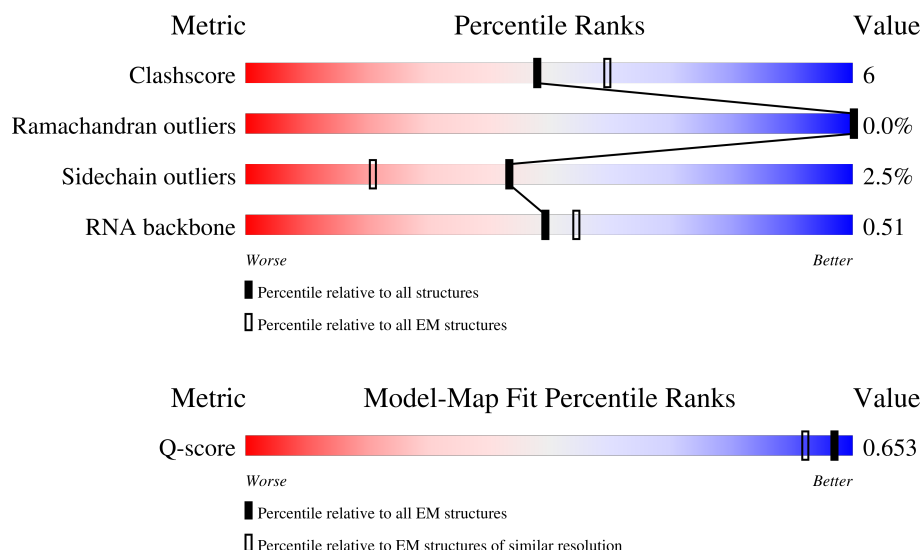
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.50 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.





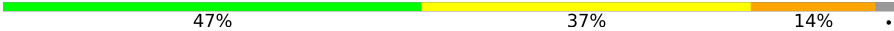








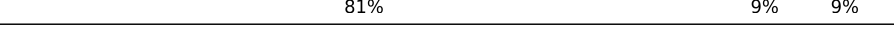







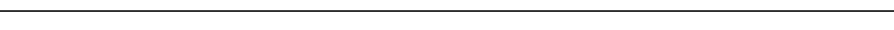

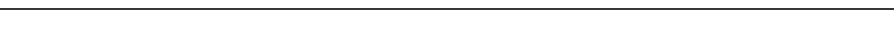
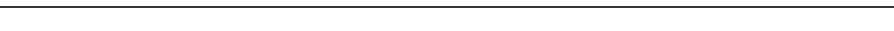


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	7115 (2.00 - 3.00)

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	L1	1782	
2	L2	1526	
3	L3	216	











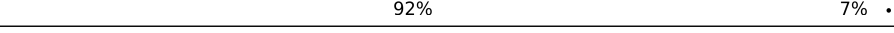
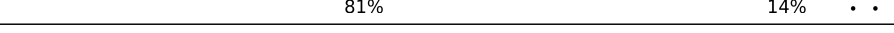
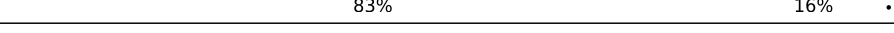


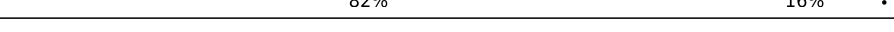









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Mol	Chain	Length	Quality of chain
4	L4	184	 56% 38% 6%
5	L5	135	 50% 32% 7% 12%
6	L6	73	 47% 37% 14% .
7	L7	171	 52% 38% 6% .
8	L8	124	 63% 31% . .
9	LA	260	 89% 10% .
10	LB	419	 87% 10% .
11	LC	373	 83% 14% ..
12	LD	188	 79% 14% . 7%
13	LE	190	 78% 19% ..
14	LF	195	 58% 17% . 24%
15	LG	264	 81% 9% 9%
16	LH	222	 90% 9% .
17	LI	220	 88% 9% .
18	LJ	139	 86% 11% .
19	LK	175	 79% 17% .
20	LL	145	 86% 14% .
21	LM	204	 89% 9% .
22	LN	213	 80% 14% 6%
23	LO	305	 85% 12% ..
24	LP	198	 90% 9% ..
25	LQ	254	 72% 7% 21%
26	LR	179	 87% 11% ..
27	LS	159	 87% 11% ..
28	LT	166	 78% 12% . 9%


























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Mol	Chain	Length	Quality of chain
29	LU	129	 74%19%5%
30	LV	145	 74%8%18%
31	LW	143	 64%21%15%
32	LX	124	 64%5%31%
33	LY	134	 79%20%.
34	LZ	147	 86%12%.
35	La	127	 86%11%..
36	Lb	70	 91%6%.
37	Lc	252	 82%8%9%
38	Ld	104	 79%11%10%
39	Le	188	 92%7%.
40	Lf	133	 81%14%..
41	Lg	144	 83%16%..
42	Lh	168	 65%10%24%
43	Li	105	 85%11%.
44	Lj	83	 82%16%.
45	Lk	83	 81%11%8%
46	Ll	51	 82%16%.
47	Lm	128	 30%9%59%
48	Ln	34	 88%6%..
49	Lo	92	 85%11%..
50	Lp	106	 74%17%8%
51	S3	78	 51%36%6%6%
52	S4	76	 33%51%13%.
53	S5	13	 46%23%31%










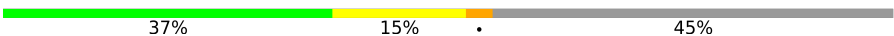
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Mol	Chain	Length	Quality of chain
54	SA	264	
55	SB	246	
56	SC	219	
57	SD	190	
58	SE	273	
59	SF	265	
60	SG	249	
61	SH	190	
62	SI	200	
63	SJ	130	
64	SK	220	
65	SL	149	
66	SM	116	
67	SN	168	
68	SO	144	
69	SP	143	
70	SQ	141	
71	SR	153	
72	SS	57	
73	ST	151	
74	SU	173	
75	SV	143	
76	SW	152	
77	SX	161	
78	SY	164	

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Mol	Chain	Length	Quality of chain
79	SZ	137	 77%18%5%
80	Sa	120	 58%10%32%
81	Sb	112	 82%10%7%
82	Sc	86	 70%29%.
83	Sd	87	 70%6%24%
84	Se	66	 74%18%8%
85	Sf	152	 25%. 71%
86	Sg	312	 70%25%. .
87	Sh	235	 30%11%59%
88	S1	2204	 37%15%. 45%

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 199587 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 LSUa_rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L1	1674	Total	C	N	O	P	1	0
			35924	16058	6567	11624	1675		

- Molecule 2 is a RNA chain called LSUb_rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L2	1153	Total	C	N	O	P	1	0
			24694	11055	4451	8034	1154		

- Molecule 3 is a RNA chain called SR1_rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L3	181	Total	C	N	O	P	0	0
			3834	1715	659	1279	181		

- Molecule 4 is a RNA chain called SR2_rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L4	184	Total	C	N	O	P	0	0
			3937	1756	712	1285	184		

- Molecule 5 is a RNA chain called SR4_rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L5	119	Total	C	N	O	P	0	0
			2533	1130	450	834	119		

- Molecule 6 is a RNA chain called SR6_rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L6	71	Total	C	N	O	P	0	0
			1506	675	271	489	71		

- Molecule 7 is a RNA chain called 5.8S_rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L7	165	Total	C	N	O	P	0	0
			3511	1573	621	1153	164		

- Molecule 8 is a RNA chain called 5S_rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L8	120	Total	C	N	O	P	0	0
			2551	1141	454	836	120		

- Molecule 9 is a protein called Putative 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LA	258	Total	C	N	O	S	0	0
			1962	1223	400	329	10		

- Molecule 10 is a protein called Putative ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LB	404	Total	C	N	O	S	0	0
			3216	2024	638	541	13		

- Molecule 11 is a protein called Putative ribosomal protein L1a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	366	Total	C	N	O	S	0	0
			2820	1761	561	483	15		

- Molecule 12 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	175	Total	C	N	O	S	0	0
			1387	875	261	243	8		

- Molecule 13 is a protein called Putative 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	186	Total	C	N	O	S	0	0
			1477	936	273	262	6		

- Molecule 14 is a protein called Putative 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	148	Total	C	N	O	S	0	0
			1144	726	215	201	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	239	Total	C	N	O	S	1	0
			1903	1198	377	321	7		

- Molecule 16 is a protein called Putative 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	221	Total	C	N	O	S	0	0
			1767	1123	353	284	7		

- Molecule 17 is a protein called Putative 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	214	Total	C	N	O	S	0	0
			1695	1056	342	289	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	203	ARG	ASN	conflict	UNP E9AEA8

- Molecule 18 is a protein called Putative 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	135	Total	C	N	O	S	0	0
			1012	638	191	177	6		

- Molecule 19 is a protein called Putative 40S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	169	Total	C	N	O	S	0	0
			1336	833	264	231	8		

- Molecule 20 is a protein called Putative 60S ribosomal protein L27A/L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	144	Total	C	N	O	S	0	0
			1124	707	226	185	6		

- Molecule 21 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	203	Total	C	N	O	S	0	0
			1711	1079	362	262	8		

- Molecule 22 is a protein called Putative 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	201	Total	C	N	O	S	0	0
			1634	1030	324	265	15		

- Molecule 23 is a protein called Putative 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LO	298	Total	C	N	O	S	0	0
			2329	1480	437	406	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	197	Total	C	N	O	S	0	0
			1539	968	307	258	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	201	Total	C	N	O	S	0	0
			1682	1035	367	274	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LR	178	Total	C	N	O	S	0	0
			1455	925	279	246	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LS	158	Total	C	N	O	S	0	0
			1261	803	245	209	4		

- Molecule 28 is a protein called Putative 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LT	151	Total	C	N	O	S	0	0
			1211	757	240	203	11		

- Molecule 29 is a protein called Putative 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LU	122	Total	C	N	O	S	0	0
			960	624	176	157	3		

- Molecule 30 is a protein called Putative 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LV	119	Total	C	N	O	S	0	0
			953	604	181	166	2		

- Molecule 31 is a protein called Putative 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LW	121	Total	C	N	O	S	0	0
			967	603	200	160	4		

- Molecule 32 is a protein called Putative ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LX	85	Total	C	N	O	S	0	0
			714	461	140	109	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LY	133	Total	C	N	O	S	0	0
			1067	684	215	165	3		

- Molecule 34 is a protein called Putative 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LZ	145	Total	C	N	O	S	0	0
			1117	685	238	189	5		

- Molecule 35 is a protein called Putative 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	La	124	Total	C	N	O	S	0	0
			1032	644	214	170	4		

- Molecule 36 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lb	68	Total	C	N	O	S	0	0
			546	335	125	86			

- Molecule 37 is a protein called Putative 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lc	229	Total	C	N	O	S	0	0
			1862	1185	358	308	11		

- Molecule 38 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ld	94	Total	C	N	O	S	0	0
			720	449	131	135	5		

- Molecule 39 is a protein called Putative 60S ribosomal subunit protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Le	186	Total	C	N	O	S	0	0
			1469	922	296	247	4		

- Molecule 40 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lf	128	Total	C	N	O	S	0	0
			1046	658	210	174	4		

- Molecule 41 is a protein called Putative ribosomal protein l35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lg	143	Total	C	N	O	S	0	0
			1149	714	240	190	5		

- Molecule 42 is a protein called Putative 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lh	127	Total	C	N	O	S	0	0
			1029	633	224	166	6		

- Molecule 43 is a protein called Putative 60S Ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Li	101	Total	C	N	O	S	0	0
			799	503	162	132	2		

- Molecule 44 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lj	81	Total	C	N	O	S	0	0
			672	409	154	103	6		

- Molecule 45 is a protein called Putative ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lk	76	Total	C	N	O	S	0	0
			595	376	116	100	3		

- Molecule 46 is a protein called Putative 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ll	50	Total	C	N	O	S	0	0
			446	288	94	63	1		

- Molecule 47 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lm	52	Total	C	N	O	S	0	0
			418	263	85	64	6		

- Molecule 48 is a protein called Putative 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ln	33	Total	C	N	O	S	0	0
			296	181	76	37	2		

- Molecule 49 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lo	89	Total	C	N	O	S	0	0
			693	431	143	113	6		

- Molecule 50 is a protein called Putative 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lp	97	Total	C	N	O	S	0	0
			784	496	158	125	5		

- Molecule 51 is a RNA chain called P-site_tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S3	73	Total	C	N	O	P	0	0
			1556	694	282	507	73		

- Molecule 52 is a RNA chain called E-site_tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S4	74	Total	C	N	O	P	0	0
			1574	703	280	518	73		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S4	3	G	C	conflict	GB 1851743410
S4	70	C	G	conflict	GB 1851743410

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S5	9	Total	C	N	O	P	0	0
			187	84	30	64	9		

- Molecule 54 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SA	236	Total	C	N	O	S	0	0
			1898	1188	361	338	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SA	22	GLU	-	insertion	UNP Q4FX73
SA	?	-	ARG	deletion	UNP Q4FX73

- Molecule 55 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SB	211	Total	C	N	O	S	0	0
			1655	1052	300	292	11		

- Molecule 56 is a protein called Putative 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SC	212	Total	C	N	O	S	1	0
			1646	1040	302	291	13		

- Molecule 57 is a protein called Putative 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SD	183	Total	C	N	O	S	0	0
			1508	949	305	246	8		

- Molecule 58 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SE	260	Total	C	N	O	S	0	0
			2054	1301	393	351	9		

- Molecule 59 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SF	222	Total	C	N	O	S	0	0
			1708	1088	301	309	10		

- Molecule 60 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SG	229	Total	C	N	O	S	0	0
			1829	1140	375	311	3		

- Molecule 61 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SH	183	Total	C	N	O	S	0	0
			1447	899	279	262	7		

- Molecule 62 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SI	200	Total	C	N	O	S	0	0
			1649	1050	320	271	8		

- Molecule 63 is a protein called Putative 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SJ	129	Total	C	N	O	S	0	0
			1021	646	188	179	8		

- Molecule 64 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SK	192	Total	C	N	O	S	0	0
			1546	964	319	261	2		

- Molecule 65 is a protein called Putative 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SL	144	Total	C	N	O	S	0	0
			1140	731	210	196	3		

- Molecule 66 is a protein called Putative ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SM	101	Total	C	N	O	S	0	0
			792	496	144	150	2		

- Molecule 67 is a protein called Putative 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SN	99	Total	C	N	O	S	0	0
			813	522	142	142	7		

- Molecule 68 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SO	137	Total	C	N	O	S	0	0
			1024	633	200	183	8		

- Molecule 69 is a protein called Putative 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SP	141	Total	C	N	O	S	0	0
			1100	694	217	186	3		

- Molecule 70 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SQ	99	Total	C	N	O	S	0	0
			662	407	120	130	5		

- Molecule 71 is a protein called Putative 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SR	134	Total	C	N	O	S	0	0
			1077	681	211	181	4		

- Molecule 72 is a protein called Putative ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SS	56	Total	C	N	O	S	0	0
			450	279	94	73	4		

- Molecule 73 is a protein called Putative 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	ST	143	Total	C	N	O	S	0	0
			1167	736	231	191	9		

- Molecule 74 is a protein called Ribosomal protein S17 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SU	144	Total	C	N	O	S	0	0
			1165	737	230	193	5		

- Molecule 75 is a protein called Putative 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SV	122	Total	C	N	O	S	0	0
			992	619	193	175	5		

- Molecule 76 is a protein called Putative 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SW	115	Total	C	N	O	S	0	0
			928	591	176	157	4		

- Molecule 77 is a protein called 40S ribosomal protein S19-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SX	152	Total	C	N	O	S	0	0
			1206	766	237	199	4		

- Molecule 78 is a protein called Putative 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	88	Total	C	N	O	S	0	0
			663	409	121	129	4		

- Molecule 79 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SZ	130	Total	C	N	O	S	0	0
			1051	675	204	169	3		

- Molecule 80 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sa	82	Total	C	N	O	S	0	0
			645	408	117	117	3		

- Molecule 81 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sb	104	Total	C	N	O	S	0	0
			825	511	177	130	7		

- Molecule 82 is a protein called Putative 40S ribosomal protein S27-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sc	85	Total	C	N	O	S	0	0
			674	416	131	119	8		

- Molecule 83 is a protein called Putative 40S ribosomal protein S33.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Sd	66	Total	C	N	O	S	0	0
			492	299	99	90	4		

- Molecule 84 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Se	61	Total	C	N	O	S	0	0
			487	307	102	77	1		

- Molecule 85 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Sf	44	Total	C	N	O	S	0	0
			359	229	67	62	1		

- Molecule 86 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Sg	302	Total	C	N	O	S	0	0
			2331	1462	415	441	13		

- Molecule 87 is a protein called Putative RNA binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	Sh	96	Total	C	N	O	S	0	0
			768	486	146	133	3		

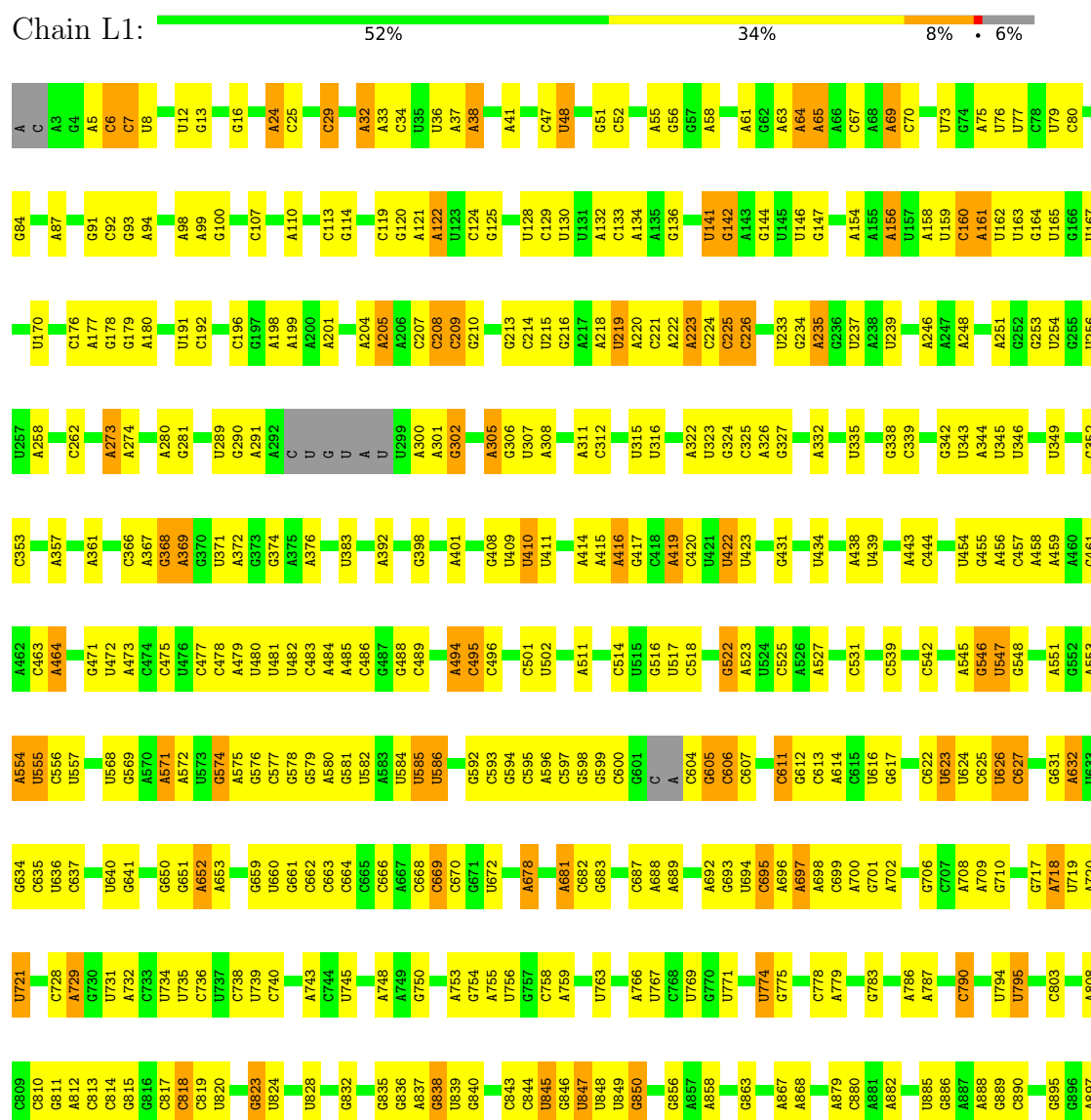
- Molecule 88 is a RNA chain called SSU_rRNA.

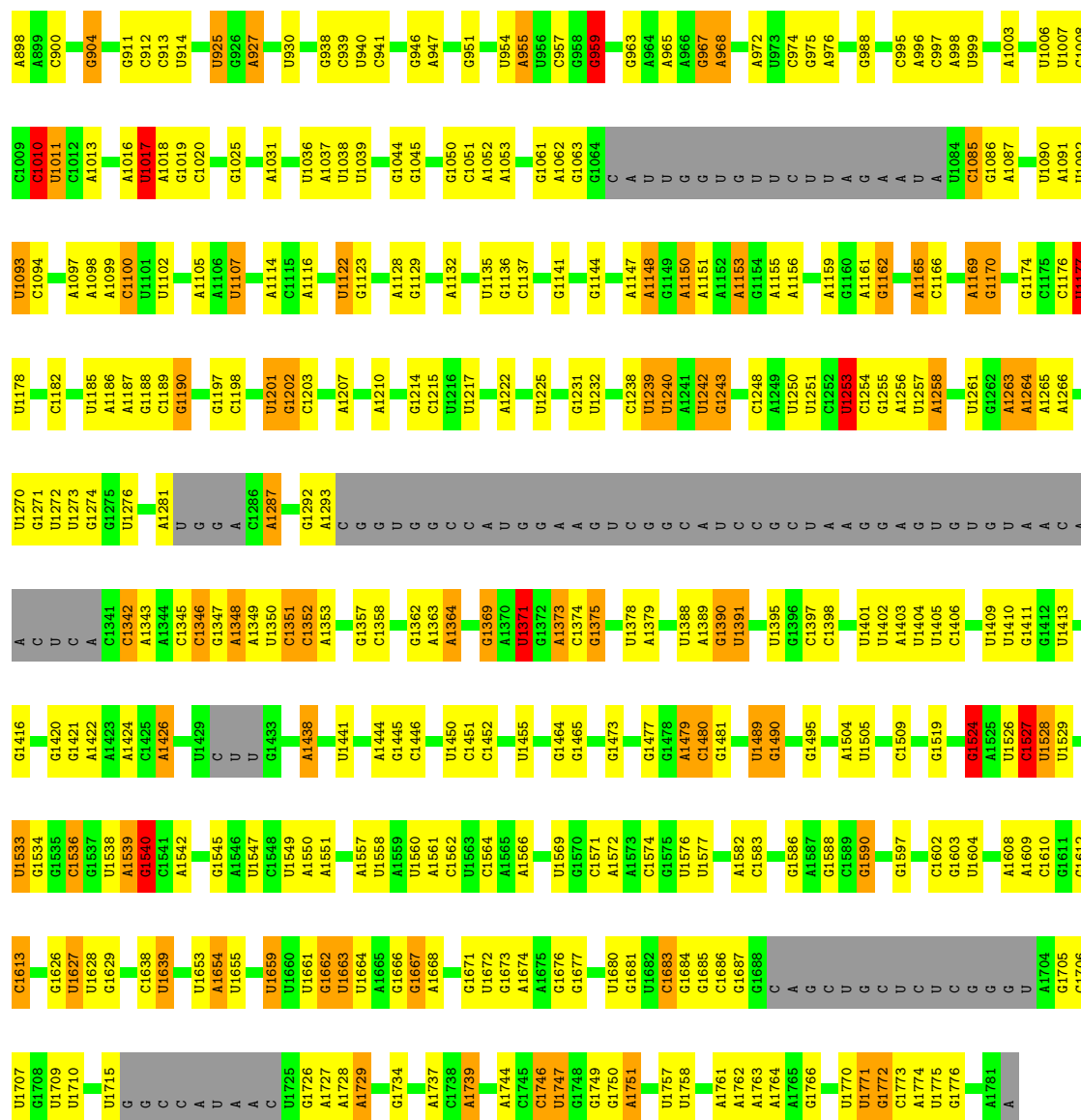
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
88	S1	1216	26009	11628	4725	8440	1216	0	0

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.

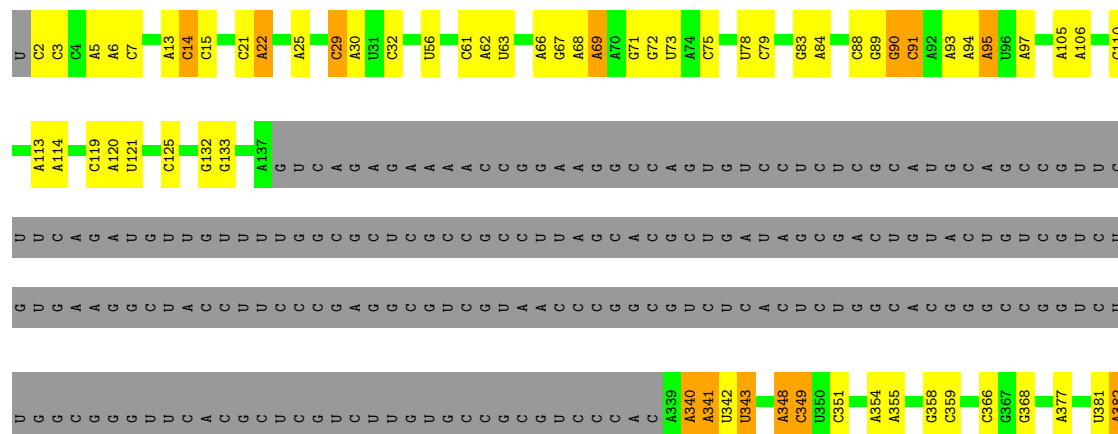
• Molecule 1: LSUa_rRNA

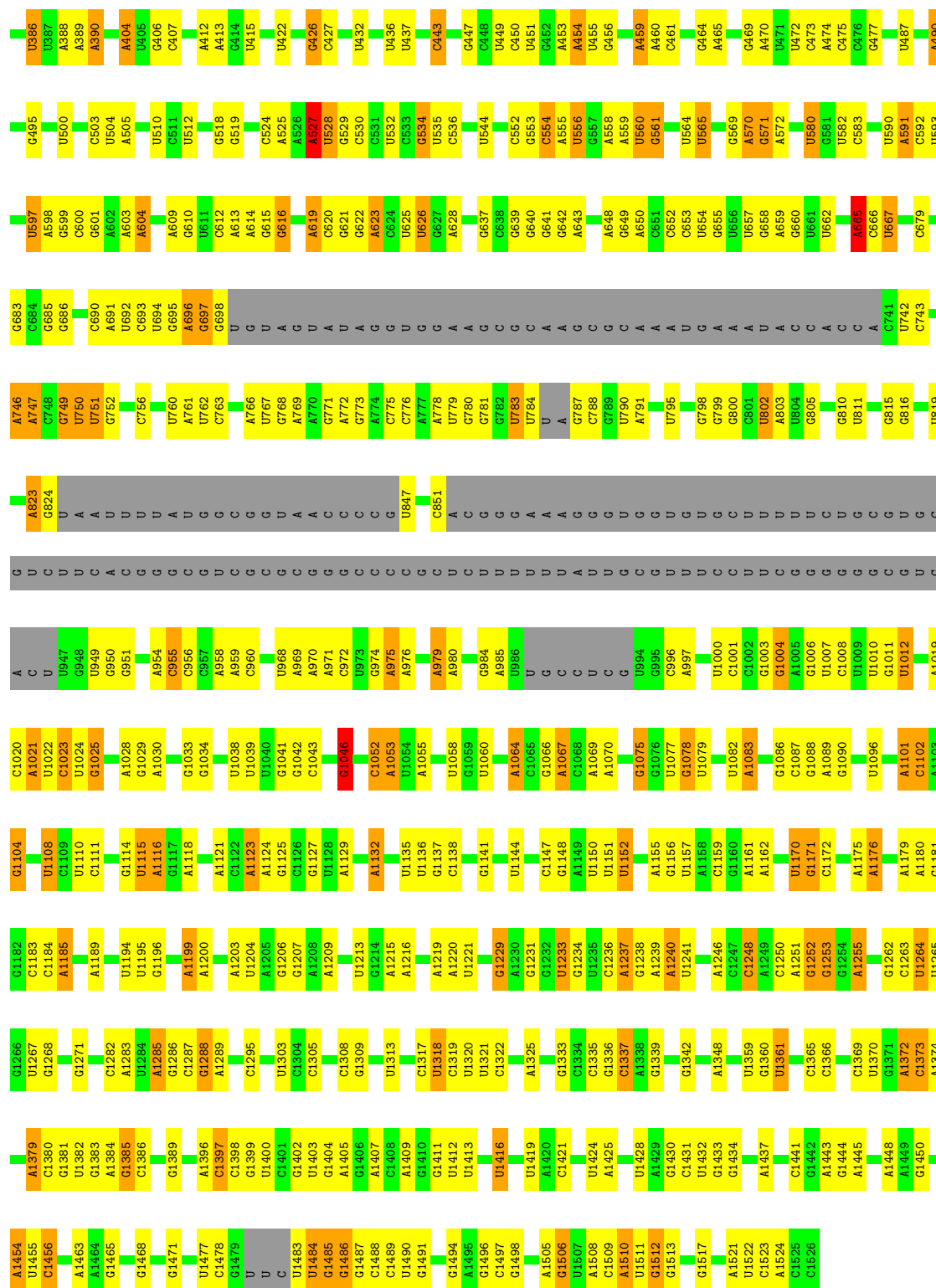




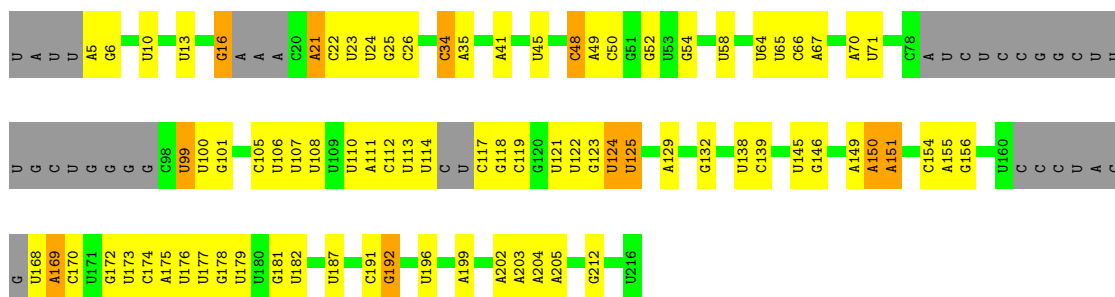
• Molecule 2: LSub_rRNA

Chain L2:

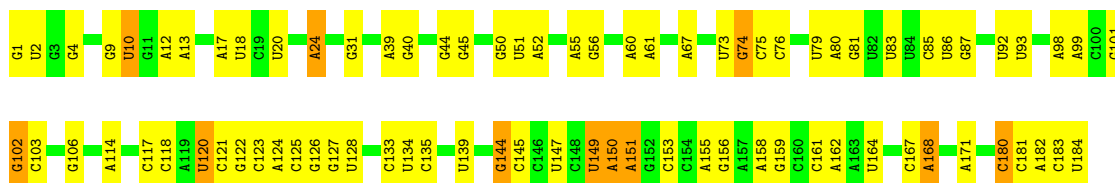




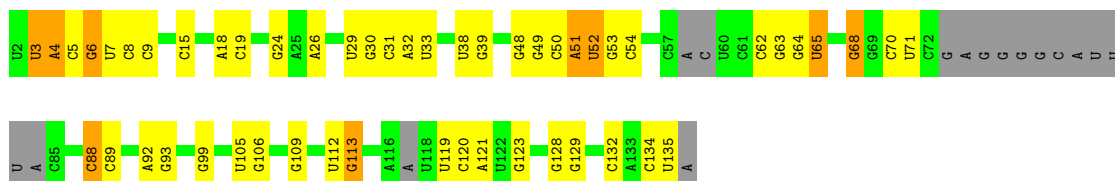
• Molecule 3: SR1_rRNA



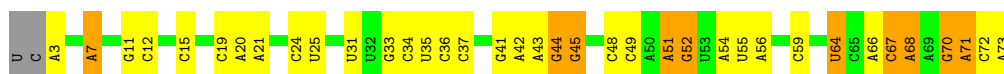
• Molecule 4: SR2_rRNA



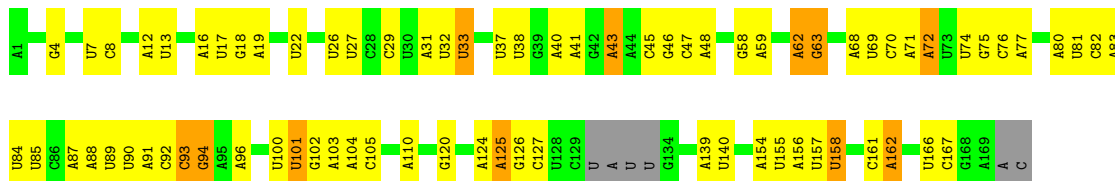
• Molecule 5: SR4_rRNA



• Molecule 6: SR6_rRNA

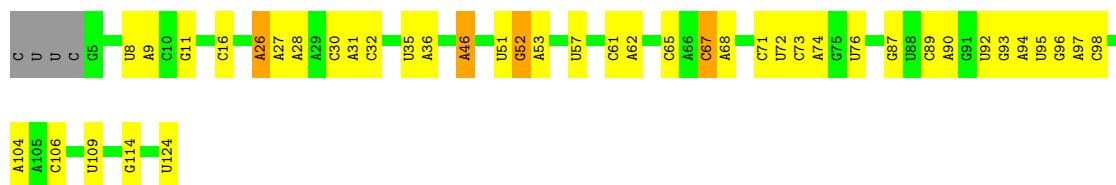


• Molecule 7: 5.8S_rRNA



• Molecule 8: 5S_rRNA





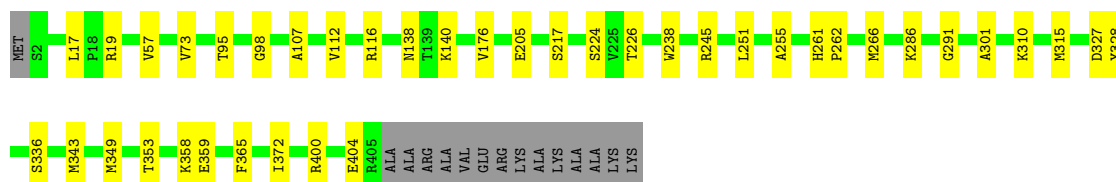
- Molecule 9: Putative 60S ribosomal protein L2

Chain LA: 89% 10% .



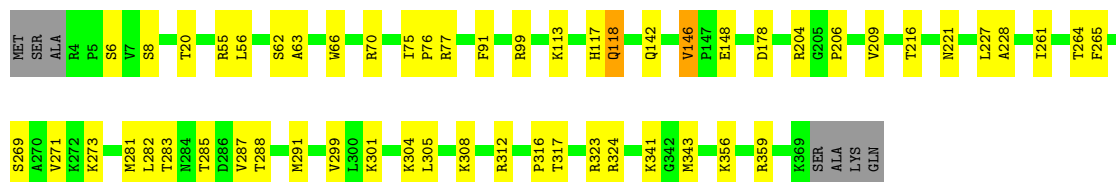
- Molecule 10: Putative ribosomal protein L3

Chain LB: 87% 10% .



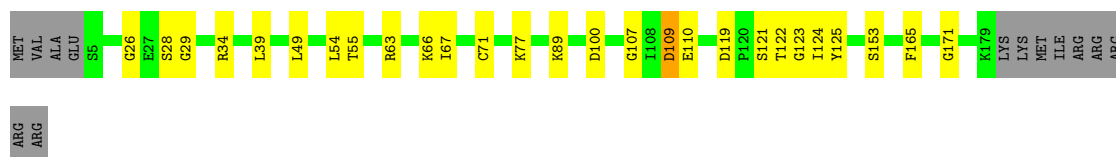
- Molecule 11: Putative ribosomal protein L1a

Chain LC: 83% 14% .



- Molecule 12: 60S ribosomal protein L11

Chain LD: 79% 14% 7% .



- Molecule 13: Putative 60S ribosomal protein L9

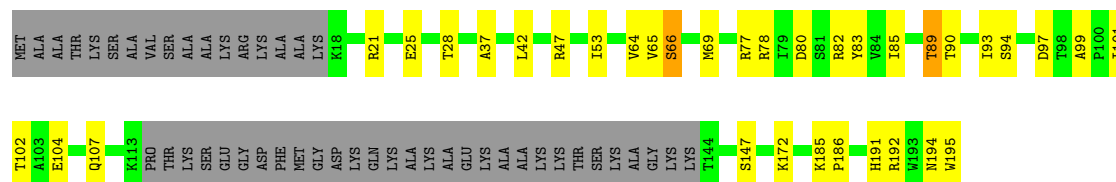
Chain LE: 78% 19% .





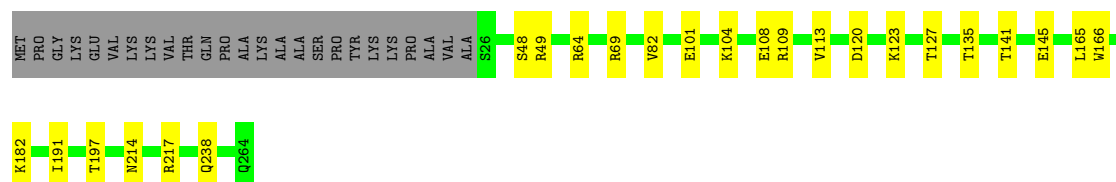
• Molecule 14: Putative 60S ribosomal protein L6

Chain LF: 58% 17% 24%



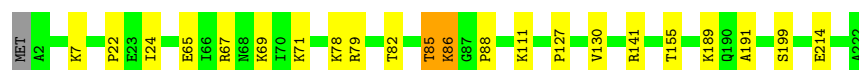
• Molecule 15: 60S ribosomal protein L7a

Chain LG: 81% 9% 9%



• Molecule 16: Putative 60S ribosomal protein L13a

Chain LH: 90% 9%



• Molecule 17: Putative 60S ribosomal protein L13

Chain LI: 88% 9%



• Molecule 18: Putative 60S ribosomal protein L23

Chain LJ: 86% 11%



• Molecule 19: Putative 40S ribosomal protein L14

Chain LK: 79% 17%



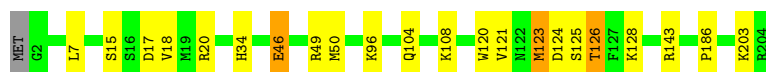
- Molecule 20: Putative 60S ribosomal protein L27A/L29

Chain LL: 86% 14% .



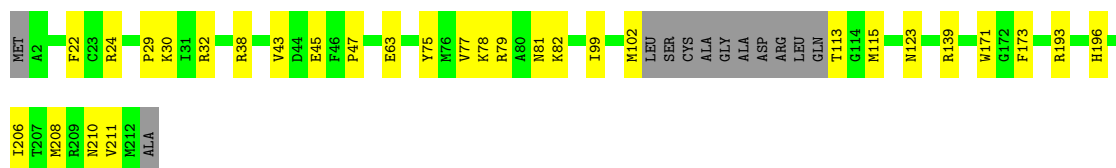
- Molecule 21: Ribosomal protein L15

Chain LM: 89% 9% .



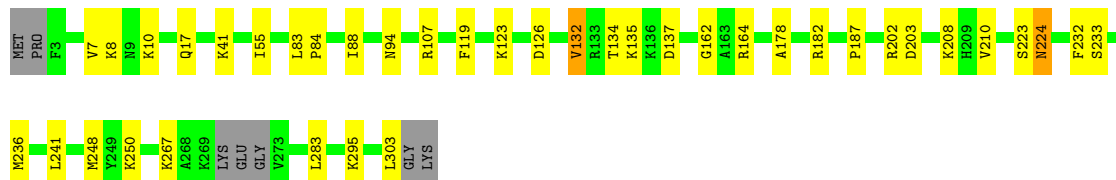
- Molecule 22: Putative 60S ribosomal protein L10

Chain LN: 80% 14% 6%



- Molecule 23: Putative 60S ribosomal protein L5

Chain LO: 85% 12% ..



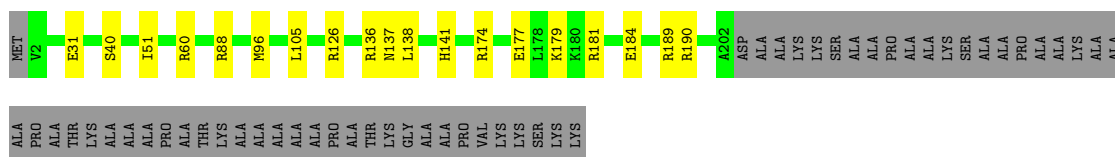
- Molecule 24: 60S ribosomal protein L18

Chain LP: 90% 9% ..



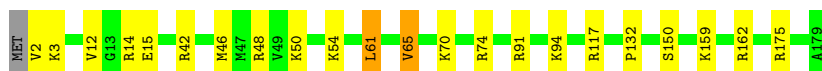
- Molecule 25: Putative 60S ribosomal protein L19

Chain LQ: 72% 7% 21%



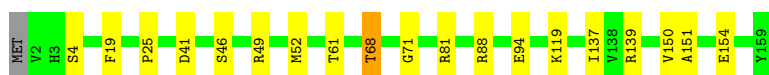
- Molecule 26: 60S ribosomal protein L18a

Chain LR: 87% 11% ..



- Molecule 27: Putative 60S ribosomal protein L21

Chain LS: 87% 11% ..



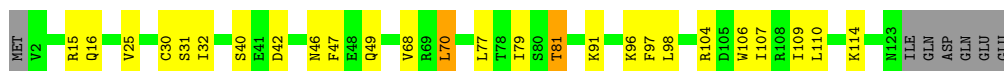
- Molecule 28: Putative 60S ribosomal protein L17

Chain LT: 78% 12% 9%



- Molecule 29: Putative 60S ribosomal protein L22

Chain LU: 74% 19% 5%



- Molecule 30: Putative 60S ribosomal protein L23a

Chain LV: 74% 8% 18%



- Molecule 31: Putative 60S ribosomal protein L26

Chain LW: 64% 21% 15%




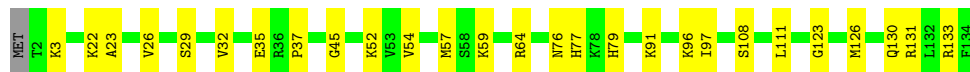
- Molecule 32: Putative ribosomal protein L24

Chain LX:  64% 5% 31%




- Molecule 33: 60S ribosomal protein L27

Chain LY:  79% 20%




- Molecule 34: Putative 60S ribosomal protein L28

Chain LZ:  86% 12%



- Molecule 35: Putative 60S ribosomal protein L35

Chain La:  86% 11%




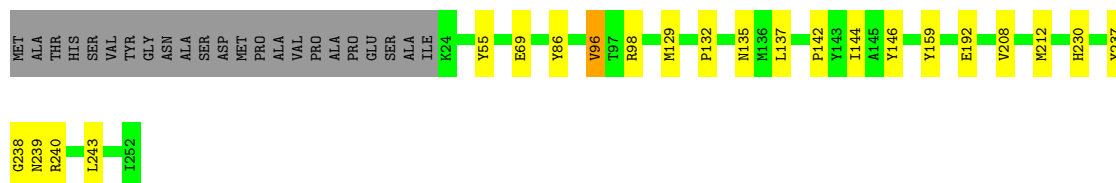
- Molecule 36: 60S ribosomal protein L29

Chain Lb:  91% 6%




- Molecule 37: Putative 60S ribosomal protein L7

Chain Lc:  82% 8% 9%



- Molecule 38: 60S ribosomal protein L30

Chain Ld:  79% 11% 10%



- Molecule 39: Putative 60S ribosomal subunit protein L31

Chain Le: 92% 7%



- Molecule 40: 60S ribosomal protein L32

Chain Lf: 81% 14%



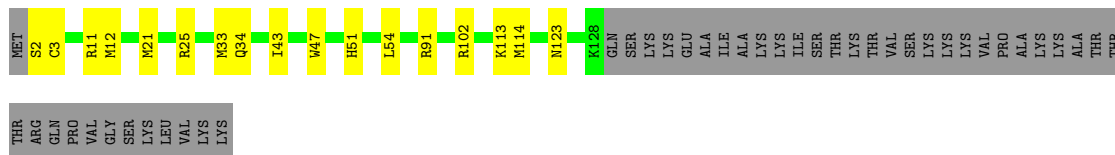
- Molecule 41: Putative ribosomal protein l35a

Chain Lg: 83% 16%



- Molecule 42: Putative 60S ribosomal protein L34

Chain Lh: 65% 10% 24%



- Molecule 43: Putative 60S Ribosomal protein L36

Chain Li: 85% 11%




- Molecule 44: Ribosomal protein L37

Chain Lj: 82% 16%




- Molecule 45: Putative ribosomal protein L38

Chain Lk:  81% 11% 8%



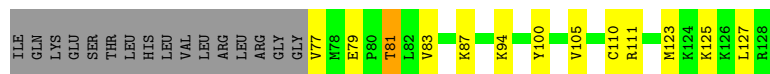
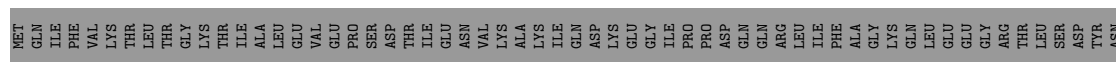
- Molecule 46: Putative 60S ribosomal protein L39

Chain Ll:  82% 16% .




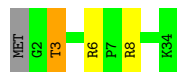
- Molecule 47: Ubiquitin-60S ribosomal protein L40

Chain Lm:  30% 9% . 59%




- Molecule 48: Putative 60S ribosomal protein L41

Chain Ln:  88% 6% . .




- Molecule 49: 60S ribosomal protein L37a

Chain Lo:  85% 11% . .



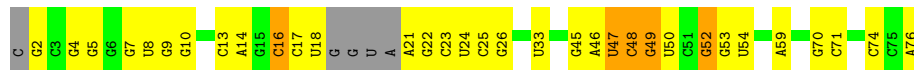
- Molecule 50: Putative 60S ribosomal protein L44

Chain Lp:  74% 17% . 8%



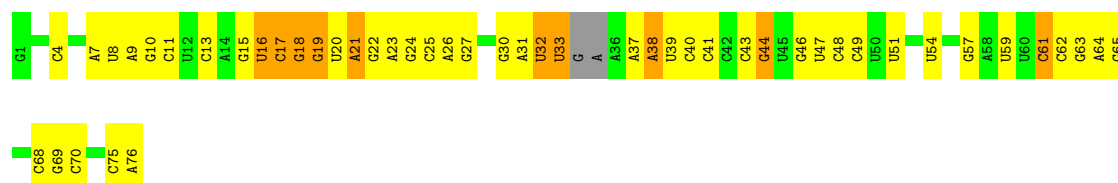
- Molecule 51: P-site_tRNA

Chain S3:  51% 36% 6% 6%



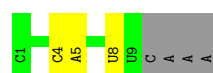
- Molecule 52: E-site_tRNA

Chain S4:  33% 51% 13%



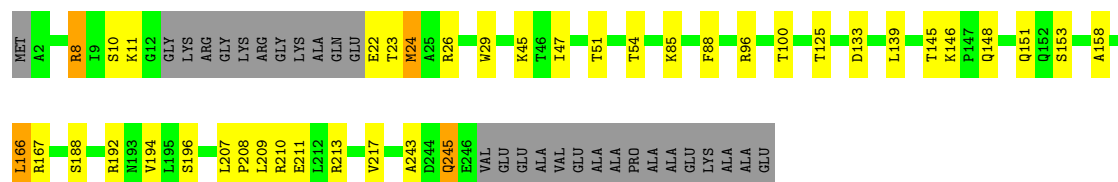
- Molecule 53: mRNA

Chain S5:  46% 23% 31%



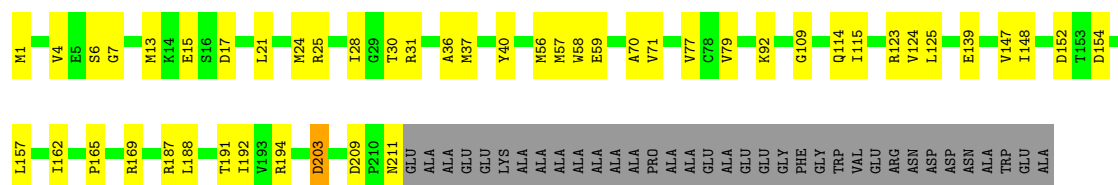
- Molecule 54: Small ribosomal subunit protein eS1

Chain SA:  74% 14% 11%




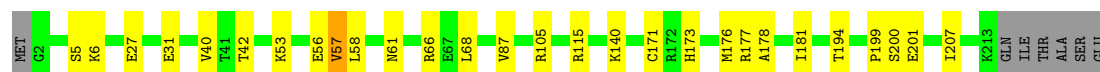
- Molecule 55: 40S ribosomal protein SA

Chain SB:  66% 19% 14%




- Molecule 56: Putative 40S ribosomal protein S3


Chain SC:  84% 12%

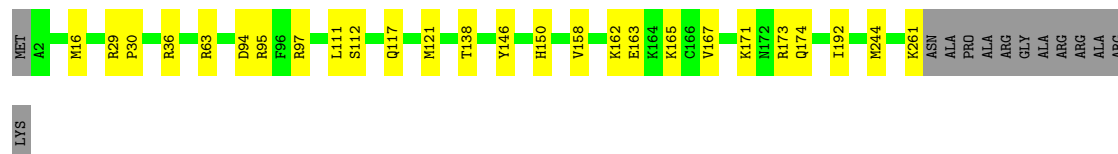


- Molecule 57: Putative 40S ribosomal protein S9

Chain SD:  76% 20%

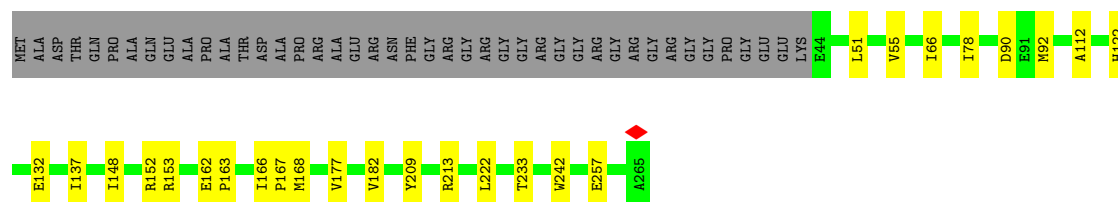
- Molecule 58: 40S ribosomal protein S4

Chain SE:  86% 10% 5%



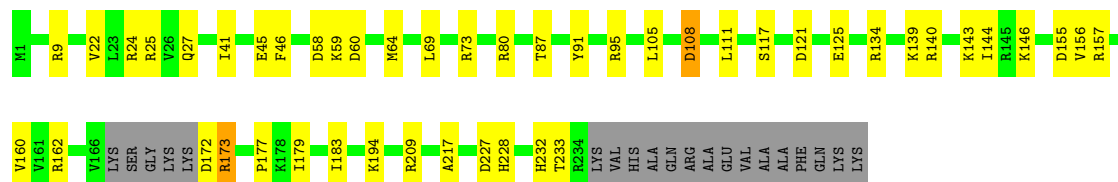
- Molecule 59: 40S ribosomal protein S2

Chain SF: 




- Molecule 60: 40S ribosomal protein S6

Chain SG:  73% 18% 8%



- Molecule 61: 40S ribosomal protein S5

Chain SH:  84% 12% .



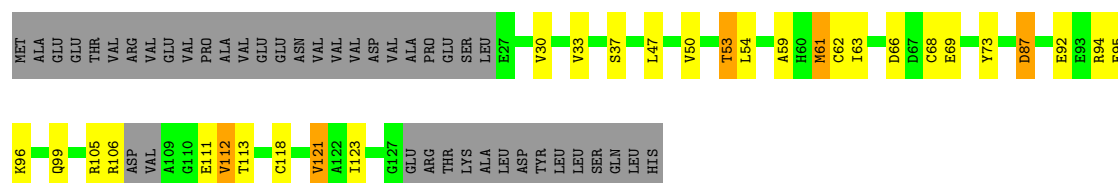
- Molecule 62: 40S ribosomal protein S7

Chain SI:  86% 14%

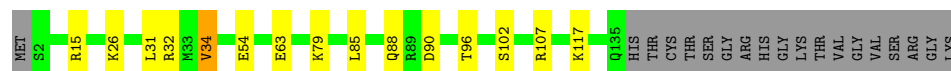


ME1	T2	K3	T32	F33	S34	A35	R36	K48	K54	K60	Q61	P62	N63	I66	R67	K68	L91	I94	F105	D114	I115	P116	R142	ASN
-----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	-----

- Chain SQ:  50% 17% . 30%




- Chain SR: 78% 9% • 12%



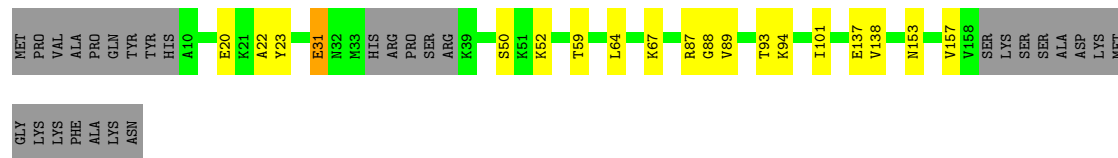
- Chain SS: 91% 7% .



- Chain ST:  77% 17% 5%



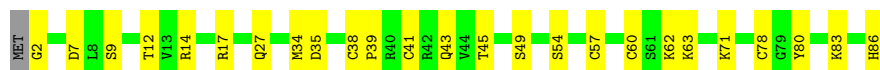
- Chain SU:  72% 10% 17%



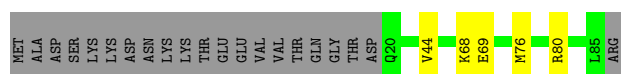
- Chain SV: 74% 10% • 15%



- Molecule 82: Putative 40S ribosomal protein S27-1



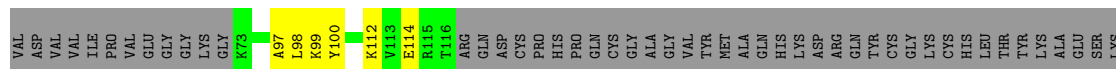
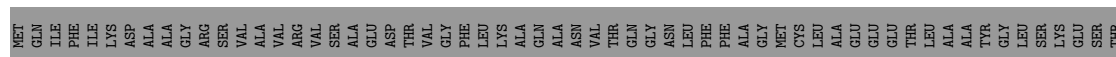
- Molecule 83: Putative 40S ribosomal protein S33



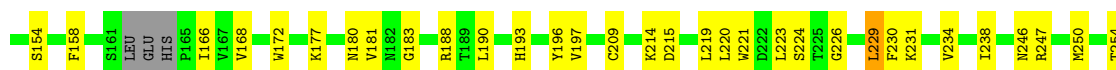
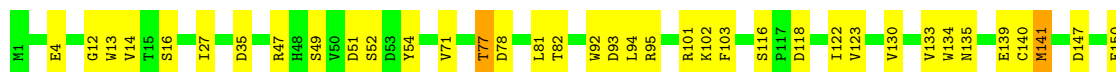
- Molecule 84: 40S ribosomal protein S30



- Molecule 85: Ubiquitin-60S ribosomal protein L40



- Molecule 86: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 87: Putative RNA binding protein





[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	138498	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0018	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.198	Depositor
Minimum map value	-0.055	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	527.68, 527.68, 527.68	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82449996, 0.82449996, 0.82449996	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, OMG, A2M, OMU, 5MC, PSU

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	L1	0.22	0/39257	0.32	0/61207
2	L2	0.24	3/26022 (0.0%)	0.32	0/40555
3	L3	0.19	0/4253	0.30	0/6611
4	L4	0.20	0/4376	0.31	0/6822
5	L5	0.19	0/2826	0.35	0/4395
6	L6	0.17	0/1683	0.34	0/2618
7	L7	0.22	0/3757	0.31	0/5850
8	L8	0.18	0/2851	0.29	0/4439
9	LA	0.15	0/2007	0.30	0/2696
10	LB	0.14	0/3283	0.27	0/4412
11	LC	0.14	0/2870	0.25	0/3861
12	LD	0.11	0/1410	0.23	0/1884
13	LE	0.14	0/1497	0.32	0/2017
14	LF	0.15	0/1165	0.33	0/1574
15	LG	0.17	0/1933	0.32	0/2599
16	LH	0.13	0/1803	0.25	0/2422
17	LI	0.14	0/1728	0.25	0/2313
18	LJ	0.15	0/1029	0.29	0/1388
19	LK	0.11	0/1355	0.22	0/1816
20	LL	0.14	0/1151	0.28	0/1538
21	LM	0.16	0/1751	0.27	0/2338
22	LN	0.14	0/1666	0.28	0/2227
23	LO	0.13	0/2370	0.27	0/3172
24	LP	0.14	0/1564	0.25	0/2092
25	LQ	0.12	0/1701	0.20	0/2250
26	LR	0.14	0/1489	0.24	0/2008
27	LS	0.15	0/1290	0.28	0/1736
28	LT	0.16	0/1235	0.29	0/1656
29	LU	0.12	0/976	0.27	0/1303
30	LV	0.13	0/968	0.24	0/1302
31	LW	0.13	0/981	0.24	0/1310
32	LX	0.13	0/735	0.25	0/989

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LY	0.12	0/1088	0.23	0/1455
34	LZ	0.15	0/1133	0.23	0/1516
35	La	0.12	0/1042	0.24	0/1383
36	Lb	0.14	0/557	0.24	0/743
37	Lc	0.15	0/1896	0.28	0/2540
38	Ld	0.12	0/730	0.23	0/989
39	Le	0.12	0/1488	0.25	0/1979
40	Lf	0.14	0/1066	0.29	0/1424
41	Lg	0.15	0/1172	0.25	0/1573
42	Lh	0.13	0/1045	0.25	0/1390
43	Li	0.12	0/814	0.22	0/1089
44	Lj	0.16	0/686	0.28	0/915
45	Lk	0.12	0/604	0.23	0/810
46	Ll	0.13	0/459	0.23	0/613
47	Lm	0.13	0/424	0.30	0/564
48	Ln	0.24	0/300	0.32	0/390
49	Lo	0.16	0/705	0.36	0/940
50	Lp	0.16	0/797	0.28	0/1053
51	S3	0.15	0/1737	0.28	0/2703
52	S4	0.17	0/1757	0.34	0/2735
53	S5	0.18	0/207	0.32	0/319
54	SA	0.29	0/1922	0.40	0/2582
55	SB	0.14	0/1689	0.29	0/2285
56	SC	0.10	0/1674	0.21	0/2240
57	SD	0.12	0/1536	0.24	0/2059
58	SE	0.12	0/2092	0.26	0/2819
59	SF	0.14	0/1744	0.26	0/2362
60	SG	0.14	0/1851	0.28	0/2474
61	SH	0.12	0/1469	0.25	0/1970
62	SI	0.12	0/1679	0.25	0/2255
63	SJ	0.12	0/1038	0.23	0/1391
64	SK	0.12	0/1569	0.25	0/2103
65	SL	0.15	0/1161	0.26	0/1559
66	SM	0.12	0/802	0.23	0/1088
67	SN	0.60	2/837 (0.2%)	0.86	4/1134 (0.4%)
68	SO	0.35	0/1039	0.51	0/1395
69	SP	0.13	0/1120	0.26	0/1500
70	SQ	0.13	0/663	0.37	0/900
71	SR	0.12	0/1095	0.24	0/1468
72	SS	0.12	0/456	0.25	0/605
73	ST	0.16	0/1190	0.29	0/1594
74	SU	0.14	0/1188	0.27	0/1594
75	SV	0.10	0/1002	0.21	0/1334

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SW	0.14	0/948	0.31	0/1275
77	SX	0.13	0/1237	0.26	0/1661
78	SY	0.21	0/673	0.52	2/913 (0.2%)
79	SZ	0.11	0/1071	0.28	0/1425
80	Sa	0.13	0/652	0.27	0/876
81	Sb	0.20	0/842	0.29	0/1127
82	Sc	0.14	0/688	0.33	0/921
83	Sd	0.11	0/494	0.26	0/663
84	Se	0.16	0/496	0.31	0/658
85	Sf	0.13	0/366	0.30	0/487
86	Sg	0.15	0/2389	0.30	0/3247
87	Sh	0.10	0/783	0.26	0/1053
88	S1	0.15	0/28688	0.22	0/44689
All	All	0.18	5/210832 (0.0%)	0.29	6/308229 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	SN	100	PRO	CG-CD	-15.37	0.98	1.50
2	L2	527	A2M	O3'-P	5.25	1.61	1.56
67	SN	100	PRO	CA-CB	-5.22	1.43	1.53
2	L2	1384	A2M	O3'-P	5.07	1.61	1.56
2	L2	570	A2M	O3'-P	5.02	1.61	1.56

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	SN	100	PRO	N-CD-CG	-19.66	73.70	103.20
67	SN	100	PRO	CA-CB-CG	-15.52	75.02	104.50
78	SY	46	PRO	CA-N-CD	-11.81	95.46	112.00
67	SN	100	PRO	N-CA-CB	-9.83	92.19	103.00
78	SY	46	PRO	N-CD-CG	-5.47	94.99	103.20

There are no chirality outliers.

There are no planarity outliers.

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	L1	35924	0	18118	440	0
2	L2	24694	0	12520	286	0
3	L3	3834	0	1944	50	0
4	L4	3937	0	1989	43	0
5	L5	2533	0	1288	43	0
6	L6	1506	0	768	24	0
7	L7	3511	0	1780	38	0
8	L8	2551	0	1293	27	0
9	LA	1962	0	2011	19	0
10	LB	3216	0	3334	29	0
11	LC	2820	0	2926	40	0
12	LD	1387	0	1425	17	0
13	LE	1477	0	1558	20	0
14	LF	1144	0	1209	26	0
15	LG	1903	0	2039	15	0
16	LH	1767	0	1872	15	0
17	LI	1695	0	1764	15	0
18	LJ	1012	0	1057	9	0
19	LK	1336	0	1403	22	0
20	LL	1124	0	1151	17	0
21	LM	1711	0	1791	18	0
22	LN	1634	0	1705	18	0
23	LO	2329	0	2418	29	0
24	LP	1539	0	1648	14	0
25	LQ	1682	0	1801	16	0
26	LR	1455	0	1492	18	0
27	LS	1261	0	1311	13	0
28	LT	1211	0	1247	17	0
29	LU	960	0	987	13	0
30	LV	953	0	1016	8	0
31	LW	967	0	1040	18	0
32	LX	714	0	727	3	0
33	LY	1067	0	1140	19	0
34	LZ	1117	0	1165	13	0
35	La	1032	0	1132	11	0
36	Lb	546	0	575	3	0
37	Lc	1862	0	1959	15	0
38	Ld	720	0	739	7	0
39	Le	1469	0	1599	10	0
40	Lf	1046	0	1106	14	0
41	Lg	1149	0	1203	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	Lh	1029	0	1084	13	0
43	Li	799	0	853	7	0
44	Lj	672	0	688	9	0
45	Lk	595	0	630	6	0
46	Ll	446	0	472	6	0
47	Lm	418	0	453	9	0
48	Ln	296	0	342	3	0
49	Lo	693	0	716	10	0
50	Lp	784	0	845	12	0
51	S3	1556	0	794	19	0
52	S4	1574	0	801	41	0
53	S5	187	0	97	0	0
54	SA	1898	0	1987	23	0
55	SB	1655	0	1678	31	0
56	SC	1646	0	1716	15	0
57	SD	1508	0	1582	26	0
58	SE	2054	0	2148	17	0
59	SF	1708	0	1754	16	0
60	SG	1829	0	1942	35	0
61	SH	1447	0	1480	14	0
62	SI	1649	0	1752	22	0
63	SJ	1021	0	1050	5	0
64	SK	1546	0	1618	21	0
65	SL	1140	0	1197	9	0
66	SM	792	0	835	9	0
67	SN	813	0	802	9	0
68	SO	1024	0	1052	15	0
69	SP	1100	0	1146	12	0
70	SQ	662	0	597	18	0
71	SR	1077	0	1132	10	0
72	SS	450	0	457	3	0
73	ST	1167	0	1243	21	0
74	SU	1165	0	1209	10	0
75	SV	992	0	1065	10	0
76	SW	928	0	955	14	0
77	SX	1206	0	1231	10	0
78	SY	663	0	658	10	0
79	SZ	1051	0	1130	18	0
80	Sa	645	0	681	6	0
81	Sb	825	0	861	7	0
82	Sc	674	0	674	21	0
83	Sd	492	0	505	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	Se	487	0	542	7	0
85	Sf	359	0	362	5	0
86	Sg	2331	0	2242	52	0
87	Sh	768	0	780	17	0
88	S1	26009	0	13129	176	0
All	All	199587	0	150217	1943	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 1943 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)
78:SY:79:ASP:OD2	88:S1:1358:A:N6	1.99	0.95
1:L1:1683:C:H3'	1:L1:1684:G:H21	1.30	0.95
42:Lh:21:MET:HG3	42:Lh:33:MET:HE3	1.50	0.92
2:L2:1510:A:H61	10:LB:327:ASP:H	1.21	0.86
17:LI:67:THR:HG21	20:LL:66:ASN:HB3	1.58	0.86

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	
9	LA	256/260 (98%)	249 (97%)	7 (3%)	0	100	100
10	LB	402/419 (96%)	396 (98%)	6 (2%)	0	100	100
11	LC	364/373 (98%)	352 (97%)	12 (3%)	0	100	100
12	LD	173/188 (92%)	171 (99%)	2 (1%)	0	100	100
13	LE	184/190 (97%)	176 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	LF	144/195 (74%)	139 (96%)	5 (4%)	0	100	100
15	LG	238/264 (90%)	235 (99%)	3 (1%)	0	100	100
16	LH	219/222 (99%)	216 (99%)	3 (1%)	0	100	100
17	LI	212/220 (96%)	206 (97%)	6 (3%)	0	100	100
18	LJ	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
19	LK	167/175 (95%)	162 (97%)	5 (3%)	0	100	100
20	LL	142/145 (98%)	138 (97%)	4 (3%)	0	100	100
21	LM	201/204 (98%)	200 (100%)	1 (0%)	0	100	100
22	LN	197/213 (92%)	191 (97%)	6 (3%)	0	100	100
23	LO	294/305 (96%)	286 (97%)	8 (3%)	0	100	100
24	LP	195/198 (98%)	191 (98%)	3 (2%)	1 (0%)	25	44
25	LQ	199/254 (78%)	199 (100%)	0	0	100	100
26	LR	176/179 (98%)	175 (99%)	1 (1%)	0	100	100
27	LS	156/159 (98%)	149 (96%)	7 (4%)	0	100	100
28	LT	149/166 (90%)	145 (97%)	4 (3%)	0	100	100
29	LU	120/129 (93%)	118 (98%)	2 (2%)	0	100	100
30	LV	117/145 (81%)	115 (98%)	2 (2%)	0	100	100
31	LW	119/143 (83%)	116 (98%)	2 (2%)	1 (1%)	16	31
32	LX	81/124 (65%)	79 (98%)	2 (2%)	0	100	100
33	LY	131/134 (98%)	130 (99%)	1 (1%)	0	100	100
34	LZ	143/147 (97%)	143 (100%)	0	0	100	100
35	La	122/127 (96%)	120 (98%)	2 (2%)	0	100	100
36	Lb	66/70 (94%)	65 (98%)	1 (2%)	0	100	100
37	Lc	227/252 (90%)	221 (97%)	6 (3%)	0	100	100
38	Ld	92/104 (88%)	92 (100%)	0	0	100	100
39	Le	184/188 (98%)	184 (100%)	0	0	100	100
40	Lf	126/133 (95%)	121 (96%)	5 (4%)	0	100	100
41	Lg	141/144 (98%)	141 (100%)	0	0	100	100
42	Lh	125/168 (74%)	122 (98%)	3 (2%)	0	100	100
43	Li	99/105 (94%)	98 (99%)	1 (1%)	0	100	100
44	Lj	79/83 (95%)	78 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	Lk	74/83 (89%)	74 (100%)	0	0	100	100
46	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
47	Lm	50/128 (39%)	50 (100%)	0	0	100	100
48	Ln	31/34 (91%)	28 (90%)	3 (10%)	0	100	100
49	Lo	87/92 (95%)	81 (93%)	6 (7%)	0	100	100
50	Lp	95/106 (90%)	93 (98%)	2 (2%)	0	100	100
54	SA	232/264 (88%)	228 (98%)	4 (2%)	0	100	100
55	SB	209/246 (85%)	202 (97%)	7 (3%)	0	100	100
56	SC	211/219 (96%)	208 (99%)	3 (1%)	0	100	100
57	SD	181/190 (95%)	181 (100%)	0	0	100	100
58	SE	258/273 (94%)	251 (97%)	7 (3%)	0	100	100
59	SF	220/265 (83%)	213 (97%)	7 (3%)	0	100	100
60	SG	225/249 (90%)	222 (99%)	3 (1%)	0	100	100
61	SH	179/190 (94%)	172 (96%)	7 (4%)	0	100	100
62	SI	198/200 (99%)	194 (98%)	4 (2%)	0	100	100
63	SJ	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
64	SK	188/220 (86%)	187 (100%)	1 (0%)	0	100	100
65	SL	142/149 (95%)	139 (98%)	3 (2%)	0	100	100
66	SM	99/116 (85%)	98 (99%)	1 (1%)	0	100	100
67	SN	97/168 (58%)	95 (98%)	2 (2%)	0	100	100
68	SO	135/144 (94%)	131 (97%)	4 (3%)	0	100	100
69	SP	139/143 (97%)	137 (99%)	2 (1%)	0	100	100
70	SQ	95/141 (67%)	85 (90%)	9 (10%)	1 (1%)	12	23
71	SR	132/153 (86%)	131 (99%)	1 (1%)	0	100	100
72	SS	54/57 (95%)	54 (100%)	0	0	100	100
73	ST	141/151 (93%)	135 (96%)	6 (4%)	0	100	100
74	SU	140/173 (81%)	136 (97%)	4 (3%)	0	100	100
75	SV	120/143 (84%)	119 (99%)	1 (1%)	0	100	100
76	SW	113/152 (74%)	112 (99%)	1 (1%)	0	100	100
77	SX	150/161 (93%)	143 (95%)	7 (5%)	0	100	100
78	SY	86/164 (52%)	83 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
79	SZ	128/137 (93%)	125 (98%)	3 (2%)	0	100	100
80	Sa	80/120 (67%)	77 (96%)	3 (4%)	0	100	100
81	Sb	102/112 (91%)	101 (99%)	1 (1%)	0	100	100
82	Sc	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
83	Sd	64/87 (74%)	62 (97%)	1 (2%)	1 (2%)	8	15
84	Se	59/66 (89%)	56 (95%)	3 (5%)	0	100	100
85	Sf	42/152 (28%)	41 (98%)	1 (2%)	0	100	100
86	Sg	296/312 (95%)	288 (97%)	8 (3%)	0	100	100
87	Sh	94/235 (40%)	93 (99%)	1 (1%)	0	100	100
All	All	11377/12926 (88%)	11128 (98%)	245 (2%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
70	SQ	112	VAL
24	LP	189	SER
31	LW	4	ILE
83	Sd	76	MET

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	
9	LA	200/204 (98%)	196 (98%)	4 (2%)	50	75
10	LB	337/351 (96%)	334 (99%)	3 (1%)	75	90
11	LC	291/301 (97%)	283 (97%)	8 (3%)	40	67
12	LD	147/162 (91%)	143 (97%)	4 (3%)	40	67
13	LE	166/172 (96%)	159 (96%)	7 (4%)	25	49
14	LF	121/153 (79%)	115 (95%)	6 (5%)	20	41
15	LG	199/221 (90%)	198 (100%)	1 (0%)	86	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	LH	182/188 (97%)	179 (98%)	3 (2%)	58	80
17	LI	178/183 (97%)	174 (98%)	4 (2%)	47	73
18	LJ	106/111 (96%)	104 (98%)	2 (2%)	52	77
19	LK	138/145 (95%)	134 (97%)	4 (3%)	37	64
20	LL	113/114 (99%)	113 (100%)	0	100	100
21	LM	178/180 (99%)	174 (98%)	4 (2%)	47	73
22	LN	171/179 (96%)	167 (98%)	4 (2%)	45	72
23	LO	232/242 (96%)	226 (97%)	6 (3%)	41	68
24	LP	163/164 (99%)	162 (99%)	1 (1%)	84	94
25	LQ	170/198 (86%)	168 (99%)	2 (1%)	67	86
26	LR	157/159 (99%)	155 (99%)	2 (1%)	65	85
27	LS	132/134 (98%)	129 (98%)	3 (2%)	45	72
28	LT	127/143 (89%)	125 (98%)	2 (2%)	58	80
29	LU	93/114 (82%)	86 (92%)	7 (8%)	11	23
30	LV	102/124 (82%)	100 (98%)	2 (2%)	50	75
31	LW	104/122 (85%)	100 (96%)	4 (4%)	28	53
32	LX	74/104 (71%)	73 (99%)	1 (1%)	62	83
33	LY	111/116 (96%)	108 (97%)	3 (3%)	40	67
34	LZ	114/118 (97%)	111 (97%)	3 (3%)	41	68
35	La	112/118 (95%)	109 (97%)	3 (3%)	40	67
36	Lb	56/58 (97%)	56 (100%)	0	100	100
37	Lc	191/209 (91%)	190 (100%)	1 (0%)	86	95
38	Ld	82/89 (92%)	79 (96%)	3 (4%)	29	55
39	Le	154/158 (98%)	153 (99%)	1 (1%)	84	94
40	Lf	111/115 (96%)	107 (96%)	4 (4%)	30	56
41	Lg	120/121 (99%)	116 (97%)	4 (3%)	33	59
42	Lh	107/146 (73%)	105 (98%)	2 (2%)	52	77
43	Li	83/88 (94%)	81 (98%)	2 (2%)	44	70
44	Lj	68/70 (97%)	68 (100%)	0	100	100
45	Lk	64/74 (86%)	64 (100%)	0	100	100
46	Ll	45/47 (96%)	45 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	Lm	44/113 (39%)	42 (96%)	2 (4%)	23	46
48	Ln	31/32 (97%)	30 (97%)	1 (3%)	34	60
49	Lo	69/74 (93%)	67 (97%)	2 (3%)	37	64
50	Lp	83/92 (90%)	80 (96%)	3 (4%)	30	56
54	SA	205/222 (92%)	195 (95%)	10 (5%)	21	42
55	SB	177/202 (88%)	172 (97%)	5 (3%)	38	65
56	SC	176/184 (96%)	169 (96%)	7 (4%)	27	51
57	SD	159/164 (97%)	154 (97%)	5 (3%)	35	62
58	SE	216/225 (96%)	214 (99%)	2 (1%)	75	90
59	SF	182/208 (88%)	181 (100%)	1 (0%)	86	95
60	SG	190/208 (91%)	180 (95%)	10 (5%)	19	38
61	SH	153/159 (96%)	149 (97%)	4 (3%)	41	68
62	SI	181/186 (97%)	179 (99%)	2 (1%)	70	87
63	SJ	110/111 (99%)	110 (100%)	0	100	100
64	SK	156/176 (89%)	155 (99%)	1 (1%)	84	94
65	SL	116/120 (97%)	114 (98%)	2 (2%)	56	79
66	SM	92/104 (88%)	87 (95%)	5 (5%)	18	37
67	SN	88/128 (69%)	86 (98%)	2 (2%)	45	72
68	SO	104/113 (92%)	102 (98%)	2 (2%)	52	77
69	SP	114/117 (97%)	112 (98%)	2 (2%)	54	78
70	SQ	56/120 (47%)	50 (89%)	6 (11%)	5	11
71	SR	113/130 (87%)	109 (96%)	4 (4%)	31	57
72	SS	45/49 (92%)	44 (98%)	1 (2%)	47	73
73	ST	126/132 (96%)	124 (98%)	2 (2%)	58	80
74	SU	125/152 (82%)	120 (96%)	5 (4%)	27	51
75	SV	109/126 (86%)	107 (98%)	2 (2%)	54	78
76	SW	98/130 (75%)	95 (97%)	3 (3%)	35	62
77	SX	122/131 (93%)	119 (98%)	3 (2%)	42	69
78	SY	72/116 (62%)	69 (96%)	3 (4%)	25	49
79	SZ	111/118 (94%)	109 (98%)	2 (2%)	54	78
80	Sa	71/95 (75%)	68 (96%)	3 (4%)	25	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
81	Sb	85/93 (91%)	79 (93%)	6 (7%)	12	25
82	Sc	75/76 (99%)	74 (99%)	1 (1%)	65	85
83	Sd	51/75 (68%)	50 (98%)	1 (2%)	50	75
84	Se	52/54 (96%)	49 (94%)	3 (6%)	17	34
85	Sf	37/126 (29%)	37 (100%)	0	100	100
86	Sg	255/265 (96%)	241 (94%)	14 (6%)	18	37
87	Sh	79/177 (45%)	77 (98%)	2 (2%)	42	69
All	All	9627/10798 (89%)	9388 (98%)	239 (2%)	43	69

5 of 239 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	Lp	2	VAL
84	Se	48	THR
57	SD	170	ARG
83	Sd	44	VAL
86	Sg	301	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
60	SG	92	GLN
72	SS	50	HIS
60	SG	232	HIS
65	SL	104	ASN
74	SU	24	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L1	1664/1782 (93%)	342 (20%)	9 (0%)
2	L2	1144/1526 (74%)	217 (18%)	5 (0%)
3	L3	176/216 (81%)	32 (18%)	0
4	L4	183/184 (99%)	31 (16%)	1 (0%)
5	L5	115/135 (85%)	22 (19%)	1 (0%)
51	S3	71/78 (91%)	13 (18%)	0
52	S4	72/76 (94%)	24 (33%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	S5	8/13 (61%)	3 (37%)	0
6	L6	70/73 (95%)	21 (30%)	1 (1%)
7	L7	163/171 (95%)	26 (15%)	1 (0%)
8	L8	119/124 (95%)	11 (9%)	0
88	S1	1198/2204 (54%)	219 (18%)	9 (0%)
All	All	4983/6582 (75%)	961 (19%)	27 (0%)

5 of 961 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L1	6	C
1	L1	7	C
1	L1	16	G
1	L1	24	A
1	L1	29	C

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	L4	149	U
7	L7	93	C
88	S1	958	G
6	L6	51	A
88	S1	128	C

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

133 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	$\# Z > 2$
88	A2M	S1	479	88	18,25,26	4.23	7 (38%)	18,36,39	2.69	3 (16%)
2	OMC	L2	443	2	19,22,23	2.94	8 (42%)	26,31,34	0.86	0
2	OMG	L2	641	2	18,26,27	2.50	8 (44%)	19,38,41	1.59	5 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMU	L1	1253	1	19,22,23	3.12	8 (42%)	26,31,34	1.77	5 (19%)
1	A2M	L1	681	1	18,25,26	4.18	7 (38%)	18,36,39	2.66	3 (16%)
2	PSU	L2	1361	2	18,21,22	4.49	7 (38%)	22,30,33	1.86	5 (22%)
2	OMG	L2	1229	2	18,26,27	2.52	8 (44%)	19,38,41	1.56	4 (21%)
2	A2M	L2	1067	2	18,25,26	4.25	7 (38%)	18,36,39	2.59	3 (16%)
2	OMC	L2	1317	2	19,22,23	2.94	8 (42%)	26,31,34	0.75	0
2	OMC	L2	1397	2	19,22,23	2.94	8 (42%)	26,31,34	0.73	0
88	A2M	S1	28	88	18,25,26	4.28	7 (38%)	18,36,39	2.59	3 (16%)
88	A2M	S1	897	88	18,25,26	4.26	7 (38%)	18,36,39	2.66	3 (16%)
1	A2M	L1	305	1	18,25,26	4.15	8 (44%)	18,36,39	2.67	3 (16%)
2	PSU	L2	78	2	18,21,22	4.43	7 (38%)	22,30,33	1.90	5 (22%)
2	OMC	L2	583	2	19,22,23	2.96	8 (42%)	26,31,34	0.77	0
2	OMU	L2	667	2	19,22,23	2.98	8 (42%)	26,31,34	1.77	5 (19%)
1	PSU	L1	239	1	18,21,22	4.46	7 (38%)	22,30,33	1.79	5 (22%)
2	OMC	L2	14	1,2	19,22,23	2.96	8 (42%)	26,31,34	0.79	0
2	PSU	L2	472	2	18,21,22	4.47	7 (38%)	22,30,33	1.84	5 (22%)
2	OMU	L2	1359	2	19,22,23	2.97	8 (42%)	26,31,34	1.76	5 (19%)
2	PSU	L2	1264	2	18,21,22	4.42	7 (38%)	22,30,33	1.86	5 (22%)
1	PSU	L1	1664	1	18,21,22	4.50	7 (38%)	22,30,33	1.87	6 (27%)
2	A2M	L2	527	2	18,25,26	4.03	8 (44%)	18,36,39	2.62	3 (16%)
2	PSU	L2	1213	2	18,21,22	4.49	7 (38%)	22,30,33	1.82	5 (22%)
7	PSU	L7	74	7	18,21,22	4.46	7 (38%)	22,30,33	1.89	5 (22%)
1	PSU	L1	1529	1	18,21,22	4.46	7 (38%)	22,30,33	1.88	5 (22%)
2	A2M	L2	628	2	18,25,26	4.24	7 (38%)	18,36,39	2.75	3 (16%)
2	PSU	L2	1152	2	18,21,22	4.44	7 (38%)	22,30,33	1.87	6 (27%)
2	A2M	L2	570	1,2	18,25,26	4.21	6 (33%)	18,36,39	2.70	4 (22%)
2	PSU	L2	1265	2	18,21,22	4.47	7 (38%)	22,30,33	1.77	5 (22%)
7	A2M	L7	162	1,7	18,25,26	4.25	6 (33%)	18,36,39	2.61	3 (16%)
1	PSU	L1	1528	1	18,21,22	4.47	7 (38%)	22,30,33	1.74	5 (22%)
2	OMG	L2	655	2	18,26,27	2.55	8 (44%)	19,38,41	1.60	5 (26%)
1	A2M	L1	697	1	18,25,26	4.26	7 (38%)	18,36,39	2.67	3 (16%)
88	OMC	S1	18	88	19,22,23	3.00	8 (42%)	26,31,34	0.71	0
2	PSU	L2	1403	2	18,21,22	4.46	7 (38%)	22,30,33	1.91	6 (27%)
2	PSU	L2	1318	2	18,21,22	4.40	7 (38%)	22,30,33	1.85	6 (27%)
2	OMU	L2	73	2	19,22,23	2.96	8 (42%)	26,31,34	1.65	5 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	L1	1190	1	18,26,27	2.52	8 (44%)	19,38,41	1.67	4 (21%)
2	5MC	L2	524	2	18,22,23	3.48	7 (38%)	26,32,35	0.99	2 (7%)
2	OMG	L2	1231	2	18,26,27	2.49	8 (44%)	19,38,41	1.56	5 (26%)
88	OMG	S1	600	88	18,26,27	2.58	8 (44%)	19,38,41	1.52	4 (21%)
2	PSU	L2	512	2	18,21,22	4.52	7 (38%)	22,30,33	1.79	5 (22%)
7	A2M	L7	43	7	18,25,26	4.22	6 (33%)	18,36,39	2.80	3 (16%)
2	PSU	L2	510	2	18,21,22	4.48	7 (38%)	22,30,33	1.76	5 (22%)
2	PSU	L2	626	2	18,21,22	4.44	7 (38%)	22,30,33	1.80	5 (22%)
2	OMU	L2	560	2	19,22,23	2.93	8 (42%)	26,31,34	1.98	7 (26%)
1	OMC	L1	1527	1	19,22,23	2.96	8 (42%)	26,31,34	0.99	2 (7%)
2	5MC	L2	1308	2	18,22,23	4.85	12 (66%)	26,32,35	1.44	3 (11%)
1	PSU	L1	1017	1	18,21,22	4.44	7 (38%)	22,30,33	1.94	5 (22%)
2	PSU	L2	500	2	18,21,22	4.47	7 (38%)	22,30,33	1.76	5 (22%)
2	A2M	L2	665	2	18,25,26	4.20	7 (38%)	18,36,39	2.69	3 (16%)
2	A2M	L2	95	2	18,25,26	4.25	7 (38%)	18,36,39	2.64	3 (16%)
7	PSU	L7	69	7	18,21,22	4.48	7 (38%)	22,30,33	1.90	6 (27%)
1	PSU	L1	1533	1,2	18,21,22	4.44	7 (38%)	22,30,33	1.85	5 (22%)
88	OMC	S1	38	88	19,22,23	3.05	8 (42%)	26,31,34	0.72	0
2	OMC	L2	1159	2	19,22,23	2.99	8 (42%)	26,31,34	0.81	0
2	PSU	L2	1058	2	18,21,22	4.43	7 (38%)	22,30,33	1.90	5 (22%)
2	OMG	L2	1253	2	18,26,27	2.33	8 (44%)	19,38,41	1.23	3 (15%)
2	A2M	L2	604	1,2	18,25,26	4.25	7 (38%)	18,36,39	2.63	3 (16%)
1	PSU	L1	672	1	18,21,22	4.41	7 (38%)	22,30,33	1.92	5 (22%)
2	PSU	L2	597	2	18,21,22	4.43	7 (38%)	22,30,33	1.84	5 (22%)
1	OMG	L1	1524	1	18,26,27	2.56	8 (44%)	19,38,41	1.75	5 (26%)
1	OMG	L1	1626	1	18,26,27	2.53	8 (44%)	19,38,41	1.53	4 (21%)
1	A2M	L1	235	1	18,25,26	4.26	8 (44%)	18,36,39	2.71	3 (16%)
1	PSU	L1	422	1	18,21,22	4.41	7 (38%)	22,30,33	1.82	5 (22%)
1	A2M	L1	678	1,2	18,25,26	4.23	7 (38%)	18,36,39	2.69	3 (16%)
2	OMU	L2	1419	2	19,22,23	2.97	8 (42%)	26,31,34	1.67	4 (15%)
1	PSU	L1	1177	1	18,21,22	4.38	7 (38%)	22,30,33	1.67	4 (18%)
2	A2M	L2	1372	2	18,25,26	4.24	6 (33%)	18,36,39	2.66	3 (16%)
2	PSU	L2	437	2	18,21,22	4.43	7 (38%)	22,30,33	1.91	5 (22%)
1	PSU	L1	1526	1	18,21,22	4.47	7 (38%)	22,30,33	1.90	6 (27%)
2	A2M	L2	591	2	18,25,26	4.28	6 (33%)	18,36,39	2.67	3 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	OMG	L4	74	4	18,26,27	2.50	8 (44%)	19,38,41	1.55	5 (26%)
2	PSU	L2	1144	2	18,21,22	4.44	7 (38%)	22,30,33	1.87	5 (22%)
88	A2M	S1	668	88	18,25,26	4.15	7 (38%)	18,36,39	2.79	4 (22%)
1	A2M	L1	955	1	18,25,26	4.26	7 (38%)	18,36,39	2.65	3 (16%)
2	A2M	L2	382	2	18,25,26	4.26	6 (33%)	18,36,39	2.57	3 (16%)
1	A2M	L1	858	1	18,25,26	4.22	7 (38%)	18,36,39	2.68	3 (16%)
2	PSU	L2	1382	2	18,21,22	4.46	7 (38%)	22,30,33	1.83	6 (27%)
7	PSU	L7	101	7	18,21,22	4.45	7 (38%)	22,30,33	1.84	6 (27%)
1	PSU	L1	1011	1,2	18,21,22	4.48	9 (50%)	22,30,33	1.79	5 (22%)
2	A2M	L2	572	2	18,25,26	4.22	7 (38%)	18,36,39	2.70	3 (16%)
1	OMU	L1	48	1	19,22,23	2.95	7 (36%)	26,31,34	2.10	7 (26%)
88	OMU	S1	661	88	19,22,23	3.01	8 (42%)	26,31,34	1.69	5 (19%)
2	OMG	L2	686	2	18,26,27	2.54	8 (44%)	19,38,41	1.55	5 (26%)
88	PSU	S1	1292	88	18,21,22	4.53	7 (38%)	22,30,33	1.78	5 (22%)
7	PSU	L7	166	1,7	18,21,22	4.47	7 (38%)	22,30,33	1.86	5 (22%)
88	OMU	S1	8	88	19,22,23	2.97	8 (42%)	26,31,34	1.79	5 (19%)
88	PSU	S1	1246	88	18,21,22	4.54	7 (38%)	22,30,33	1.77	5 (22%)
2	PSU	L2	1060	2	18,21,22	4.45	7 (38%)	22,30,33	1.87	5 (22%)
2	OMG	L2	1078	2	18,26,27	2.48	8 (44%)	19,38,41	1.64	5 (26%)
88	PSU	S1	33	88	18,21,22	4.56	7 (38%)	22,30,33	1.83	5 (22%)
2	OMC	L2	359	2	19,22,23	3.00	8 (42%)	26,31,34	0.68	0
88	OMG	S1	1478	88	18,26,27	2.51	8 (44%)	19,38,41	1.56	5 (26%)
88	PSU	S1	12	88	18,21,22	4.46	7 (38%)	22,30,33	1.77	5 (22%)
1	A2M	L1	1373	1	18,25,26	4.24	6 (33%)	18,36,39	2.64	3 (16%)
2	A2M	L2	1384	2	18,25,26	4.24	7 (38%)	18,36,39	2.64	3 (16%)
2	OMU	L2	565	2	19,22,23	3.03	8 (42%)	26,31,34	2.01	7 (26%)
2	OMG	L2	1046	51,2	18,26,27	2.49	8 (44%)	19,38,41	1.52	5 (26%)
2	PSU	L2	802	2	18,21,22	4.50	7 (38%)	22,30,33	1.77	5 (22%)
1	OMU	L1	845	1	19,22,23	2.96	8 (42%)	26,31,34	2.19	8 (30%)
1	OMU	L1	1659	1	19,22,23	2.98	8 (42%)	26,31,34	1.71	5 (19%)
1	PSU	L1	774	1	18,21,22	4.47	7 (38%)	22,30,33	1.84	5 (22%)
1	OMU	L1	847	1	19,22,23	2.95	8 (42%)	26,31,34	1.75	5 (19%)
88	A2M	S1	98	88	18,25,26	4.25	7 (38%)	18,36,39	2.60	3 (16%)
2	OMG	L2	534	2	18,26,27	2.53	8 (44%)	19,38,41	1.52	4 (21%)
1	A2M	L1	69	1	18,25,26	4.18	6 (33%)	18,36,39	2.81	4 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	L1	940	1	18,21,22	4.49	7 (38%)	22,30,33	1.83	5 (22%)
2	PSU	L2	662	2	18,21,22	4.44	7 (38%)	22,30,33	1.84	5 (22%)
2	OMG	L2	71	2	18,26,27	2.54	8 (44%)	19,38,41	1.59	4 (21%)
2	OMU	L2	1077	2	19,22,23	2.97	8 (42%)	26,31,34	1.73	5 (19%)
2	PSU	L2	504	2	18,21,22	4.44	7 (38%)	22,30,33	1.81	4 (18%)
3	OMU	L3	13	3	19,22,23	2.98	8 (42%)	26,31,34	1.65	4 (15%)
7	OMG	L7	75	7	18,26,27	2.55	8 (44%)	19,38,41	1.50	4 (21%)
1	OMG	L1	856	1	18,26,27	2.50	8 (44%)	19,38,41	1.51	5 (26%)
2	OMC	L2	1248	2	19,22,23	3.00	8 (42%)	26,31,34	0.81	0
1	A2M	L1	1539	1,2	18,25,26	4.23	8 (44%)	18,36,39	2.66	3 (16%)
88	OMU	S1	29	88	19,22,23	2.98	8 (42%)	26,31,34	1.72	5 (19%)
1	A2M	L1	927	1	18,25,26	4.21	8 (44%)	18,36,39	2.69	3 (16%)
1	OMU	L1	1107	1	19,22,23	2.96	8 (42%)	26,31,34	1.76	5 (19%)
2	PSU	L2	1303	2	18,21,22	4.46	7 (38%)	22,30,33	1.90	6 (27%)
2	A2M	L2	1185	2	18,25,26	4.21	7 (38%)	18,36,39	2.69	3 (16%)
2	OMG	L2	1360	2	18,26,27	2.55	8 (44%)	19,38,41	1.52	4 (21%)
88	A2M	S1	512	88	18,25,26	4.25	8 (44%)	18,36,39	2.64	3 (16%)
1	OMG	L1	1540	1,2	18,26,27	2.45	8 (44%)	19,38,41	1.54	4 (21%)
2	PSU	L2	593	2	18,21,22	4.43	7 (38%)	22,30,33	1.76	6 (27%)
1	OMC	L1	1010	1	19,22,23	2.97	8 (42%)	26,31,34	0.78	0
1	OMC	L1	695	1	19,22,23	2.92	8 (42%)	26,31,34	0.68	0
2	PSU	L2	1194	2	18,21,22	4.48	7 (38%)	22,30,33	1.76	5 (22%)
2	OMU	L2	56	1,2	19,22,23	2.96	8 (42%)	26,31,34	1.72	4 (15%)
1	OMG	L1	959	1	18,26,27	2.55	8 (44%)	19,38,41	1.53	4 (21%)
1	OMU	L1	1371	1	19,22,23	3.04	8 (42%)	26,31,34	1.90	6 (23%)

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
88	A2M	S1	479	88	-	0/5/27/28	0/3/3/3
2	OMC	L2	443	2	-	4/9/27/28	0/2/2/2
2	OMG	L2	641	2	-	0/5/27/28	0/3/3/3
1	OMU	L1	1253	1	-	7/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A2M	L1	681	1	-	3/5/27/28	0/3/3/3
2	PSU	L2	1361	2	-	3/7/25/26	0/2/2/2
2	OMG	L2	1229	2	-	2/5/27/28	0/3/3/3
2	A2M	L2	1067	2	-	1/5/27/28	0/3/3/3
2	OMC	L2	1317	2	-	0/9/27/28	0/2/2/2
2	OMC	L2	1397	2	-	0/9/27/28	0/2/2/2
88	A2M	S1	28	88	-	0/5/27/28	0/3/3/3
88	A2M	S1	897	88	-	0/5/27/28	0/3/3/3
1	A2M	L1	305	1	-	2/5/27/28	0/3/3/3
2	PSU	L2	78	2	-	0/7/25/26	0/2/2/2
2	OMC	L2	583	2	-	0/9/27/28	0/2/2/2
2	OMU	L2	667	2	-	1/9/27/28	0/2/2/2
1	PSU	L1	239	1	-	0/7/25/26	0/2/2/2
2	OMC	L2	14	1,2	-	0/9/27/28	0/2/2/2
2	PSU	L2	472	2	-	0/7/25/26	0/2/2/2
2	OMU	L2	1359	2	-	0/9/27/28	0/2/2/2
2	PSU	L2	1264	2	-	2/7/25/26	0/2/2/2
1	PSU	L1	1664	1	-	0/7/25/26	0/2/2/2
2	A2M	L2	527	2	-	1/5/27/28	0/3/3/3
2	PSU	L2	1213	2	-	0/7/25/26	0/2/2/2
7	PSU	L7	74	7	-	0/7/25/26	0/2/2/2
1	PSU	L1	1529	1	-	0/7/25/26	0/2/2/2
2	A2M	L2	628	2	-	0/5/27/28	0/3/3/3
2	PSU	L2	1152	2	-	0/7/25/26	0/2/2/2
2	A2M	L2	570	1,2	-	0/5/27/28	0/3/3/3
2	PSU	L2	1265	2	-	0/7/25/26	0/2/2/2
7	A2M	L7	162	1,7	-	1/5/27/28	0/3/3/3
1	PSU	L1	1528	1	-	0/7/25/26	0/2/2/2
2	OMG	L2	655	2	-	2/5/27/28	0/3/3/3
1	A2M	L1	697	1	-	0/5/27/28	0/3/3/3
88	OMC	S1	18	88	-	0/9/27/28	0/2/2/2
2	PSU	L2	1403	2	-	0/7/25/26	0/2/2/2
2	PSU	L2	1318	2	-	0/7/25/26	0/2/2/2
2	OMU	L2	73	2	-	0/9/27/28	0/2/2/2
1	OMG	L1	1190	1	-	0/5/27/28	0/3/3/3
2	5MC	L2	524	2	-	0/7/25/26	0/2/2/2
2	OMG	L2	1231	2	-	0/5/27/28	0/3/3/3
88	OMG	S1	600	88	-	2/5/27/28	0/3/3/3
2	PSU	L2	512	2	-	0/7/25/26	0/2/2/2
7	A2M	L7	43	7	-	0/5/27/28	0/3/3/3
2	PSU	L2	510	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	L2	626	2	-	0/7/25/26	0/2/2/2
2	OMU	L2	560	2	-	3/9/27/28	0/2/2/2
1	OMC	L1	1527	1	-	4/9/27/28	0/2/2/2
2	5MC	L2	1308	2	-	4/7/25/26	0/2/2/2
1	PSU	L1	1017	1	-	2/7/25/26	0/2/2/2
2	PSU	L2	500	2	-	0/7/25/26	0/2/2/2
2	A2M	L2	665	2	-	3/5/27/28	0/3/3/3
2	A2M	L2	95	2	-	0/5/27/28	0/3/3/3
7	PSU	L7	69	7	-	0/7/25/26	0/2/2/2
1	PSU	L1	1533	1,2	-	0/7/25/26	0/2/2/2
88	OMC	S1	38	88	-	0/9/27/28	0/2/2/2
2	OMC	L2	1159	2	-	0/9/27/28	0/2/2/2
2	PSU	L2	1058	2	-	0/7/25/26	0/2/2/2
2	OMG	L2	1253	2	-	0/5/27/28	0/3/3/3
2	A2M	L2	604	1,2	-	0/5/27/28	0/3/3/3
1	PSU	L1	672	1	-	0/7/25/26	0/2/2/2
2	PSU	L2	597	2	-	0/7/25/26	0/2/2/2
1	OMG	L1	1524	1	-	1/5/27/28	0/3/3/3
1	OMG	L1	1626	1	-	0/5/27/28	0/3/3/3
1	A2M	L1	235	1	-	0/5/27/28	0/3/3/3
1	PSU	L1	422	1	-	0/7/25/26	0/2/2/2
1	A2M	L1	678	1,2	-	1/5/27/28	0/3/3/3
2	OMU	L2	1419	2	-	0/9/27/28	0/2/2/2
1	PSU	L1	1177	1	-	2/7/25/26	0/2/2/2
2	A2M	L2	1372	2	-	0/5/27/28	0/3/3/3
2	PSU	L2	437	2	-	0/7/25/26	0/2/2/2
1	PSU	L1	1526	1	-	2/7/25/26	0/2/2/2
2	A2M	L2	591	2	-	0/5/27/28	0/3/3/3
4	OMG	L4	74	4	-	1/5/27/28	0/3/3/3
2	PSU	L2	1144	2	-	0/7/25/26	0/2/2/2
88	A2M	S1	668	88	-	2/5/27/28	0/3/3/3
1	A2M	L1	955	1	-	0/5/27/28	0/3/3/3
2	A2M	L2	382	2	-	0/5/27/28	0/3/3/3
1	A2M	L1	858	1	-	0/5/27/28	0/3/3/3
2	PSU	L2	1382	2	-	2/7/25/26	0/2/2/2
7	PSU	L7	101	7	-	0/7/25/26	0/2/2/2
1	PSU	L1	1011	1,2	-	0/7/25/26	0/2/2/2
2	A2M	L2	572	2	-	0/5/27/28	0/3/3/3
1	OMU	L1	48	1	-	2/9/27/28	0/2/2/2
88	OMU	S1	661	88	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMG	L2	686	2	-	0/5/27/28	0/3/3/3
88	PSU	S1	1292	88	-	0/7/25/26	0/2/2/2
7	PSU	L7	166	1,7	-	0/7/25/26	0/2/2/2
88	OMU	S1	8	88	-	5/9/27/28	0/2/2/2
88	PSU	S1	1246	88	-	0/7/25/26	0/2/2/2
2	PSU	L2	1060	2	-	0/7/25/26	0/2/2/2
2	OMG	L2	1078	2	-	0/5/27/28	0/3/3/3
88	PSU	S1	33	88	-	0/7/25/26	0/2/2/2
2	OMC	L2	359	2	-	0/9/27/28	0/2/2/2
88	OMG	S1	1478	88	-	1/5/27/28	0/3/3/3
88	PSU	S1	12	88	-	0/7/25/26	0/2/2/2
1	A2M	L1	1373	1	-	0/5/27/28	0/3/3/3
2	A2M	L2	1384	2	-	1/5/27/28	0/3/3/3
2	OMU	L2	565	2	-	3/9/27/28	0/2/2/2
2	OMG	L2	1046	51,2	-	3/5/27/28	0/3/3/3
2	PSU	L2	802	2	-	2/7/25/26	0/2/2/2
1	OMU	L1	845	1	-	3/9/27/28	0/2/2/2
1	OMU	L1	1659	1	-	0/9/27/28	0/2/2/2
1	PSU	L1	774	1	-	0/7/25/26	0/2/2/2
1	OMU	L1	847	1	-	0/9/27/28	0/2/2/2
88	A2M	S1	98	88	-	2/5/27/28	0/3/3/3
2	OMG	L2	534	2	-	2/5/27/28	0/3/3/3
1	A2M	L1	69	1	-	1/5/27/28	0/3/3/3
1	PSU	L1	940	1	-	0/7/25/26	0/2/2/2
2	PSU	L2	662	2	-	0/7/25/26	0/2/2/2
2	OMG	L2	71	2	-	0/5/27/28	0/3/3/3
2	OMU	L2	1077	2	-	0/9/27/28	0/2/2/2
2	PSU	L2	504	2	-	3/7/25/26	0/2/2/2
3	OMU	L3	13	3	-	1/9/27/28	0/2/2/2
7	OMG	L7	75	7	-	0/5/27/28	0/3/3/3
1	OMG	L1	856	1	-	0/5/27/28	0/3/3/3
2	OMC	L2	1248	2	-	1/9/27/28	0/2/2/2
1	A2M	L1	1539	1,2	-	0/5/27/28	0/3/3/3
88	OMU	S1	29	88	-	0/9/27/28	0/2/2/2
1	A2M	L1	927	1	-	1/5/27/28	0/3/3/3
1	OMU	L1	1107	1	-	2/9/27/28	0/2/2/2
2	PSU	L2	1303	2	-	0/7/25/26	0/2/2/2
2	A2M	L2	1185	2	-	2/5/27/28	0/3/3/3
2	OMG	L2	1360	2	-	0/5/27/28	0/3/3/3
88	A2M	S1	512	88	-	2/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	L1	1540	1,2	-	2/5/27/28	0/3/3/3
2	PSU	L2	593	2	-	0/7/25/26	0/2/2/2
1	OMC	L1	1010	1	-	3/9/27/28	0/2/2/2
1	OMC	L1	695	1	-	1/9/27/28	0/2/2/2
2	PSU	L2	1194	2	-	0/7/25/26	0/2/2/2
2	OMU	L2	56	1,2	-	0/9/27/28	0/2/2/2
1	OMG	L1	959	1	-	1/5/27/28	0/3/3/3
1	OMU	L1	1371	1	-	5/9/27/28	0/2/2/2

The worst 5 of 988 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	S1	28	A2M	O4'-C1'	15.47	1.62	1.41
88	S1	897	A2M	O4'-C1'	15.39	1.62	1.41
88	S1	512	A2M	O4'-C1'	15.34	1.62	1.41
2	L2	591	A2M	O4'-C1'	15.34	1.62	1.41
88	S1	98	A2M	O4'-C1'	15.32	1.62	1.41

The worst 5 of 539 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L7	43	A2M	C5-C6-N6	8.41	133.13	120.35
2	L2	628	A2M	C5-C6-N6	8.24	132.88	120.35
88	S1	668	A2M	C5-C6-N6	8.11	132.67	120.35
2	L2	572	A2M	C5-C6-N6	8.11	132.67	120.35
1	L1	697	A2M	C5-C6-N6	8.01	132.53	120.35

There are no chirality outliers.

5 of 107 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	L7	162	A2M	C1'-C2'-O2'-CM'
1	L1	48	OMU	O4'-C1'-N1-C2
1	L1	48	OMU	O4'-C1'-N1-C6
1	L1	69	A2M	C1'-C2'-O2'-CM'
1	L1	305	A2M	O4'-C4'-C5'-O5'

There are no ring outliers.

60 monomers are involved in 87 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	S1	479	A2M	1	0
2	L2	443	OMC	1	0
1	L1	1253	OMU	3	0
2	L2	1067	A2M	1	0
2	L2	1397	OMC	2	0
2	L2	667	OMU	1	0
2	L2	14	OMC	3	0
2	L2	527	A2M	1	0
2	L2	1152	PSU	1	0
2	L2	570	A2M	2	0
7	L7	162	A2M	1	0
1	L1	1528	PSU	1	0
1	L1	697	A2M	3	0
88	S1	18	OMC	1	0
2	L2	1318	PSU	1	0
1	L1	1190	OMG	2	0
7	L7	43	A2M	1	0
2	L2	626	PSU	1	0
2	L2	560	OMU	4	0
1	L1	1527	OMC	3	0
1	L1	1017	PSU	2	0
2	L2	665	A2M	2	0
2	L2	95	A2M	1	0
1	L1	1533	PSU	1	0
2	L2	1253	OMG	1	0
2	L2	604	A2M	1	0
2	L2	597	PSU	1	0
1	L1	1524	OMG	2	0
1	L1	235	A2M	1	0
1	L1	422	PSU	1	0
1	L1	678	A2M	1	0
1	L1	1177	PSU	3	0
2	L2	1372	A2M	1	0
2	L2	591	A2M	2	0
4	L4	74	OMG	1	0
1	L1	955	A2M	1	0
2	L2	382	A2M	4	0
7	L7	101	PSU	1	0
1	L1	48	OMU	1	0
88	S1	661	OMU	2	0
88	S1	1292	PSU	1	0
2	L2	1078	OMG	1	0
88	S1	12	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L1	1373	A2M	1	0
2	L2	565	OMU	2	0
2	L2	1046	OMG	1	0
1	L1	845	OMU	4	0
1	L1	1659	OMU	1	0
1	L1	774	PSU	1	0
1	L1	847	OMU	1	0
88	S1	98	A2M	2	0
1	L1	69	A2M	1	0
1	L1	1539	A2M	1	0
1	L1	927	A2M	1	0
1	L1	1107	OMU	1	0
1	L1	1540	OMG	1	0
1	L1	1010	OMC	1	0
1	L1	695	OMC	2	0
1	L1	959	OMG	1	0
1	L1	1371	OMU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

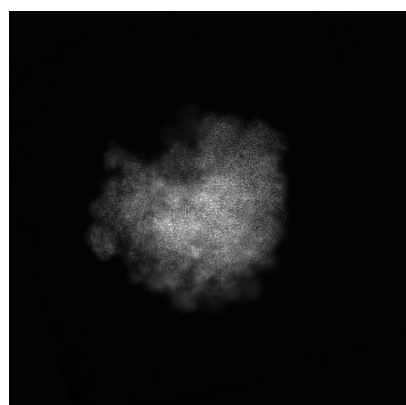
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52247. These allow visual inspection of the internal detail of the map and identification of artifacts.

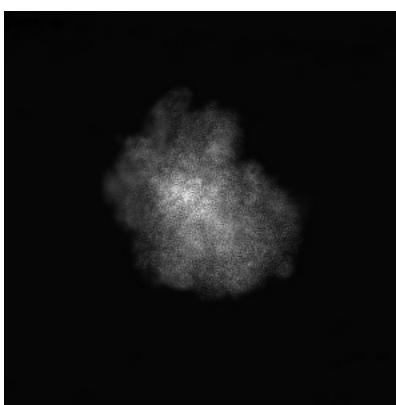
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

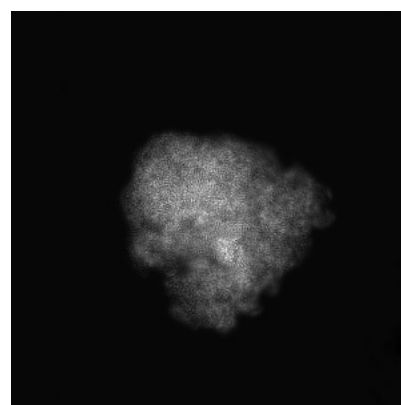
6.1.1 Primary map



X



Y

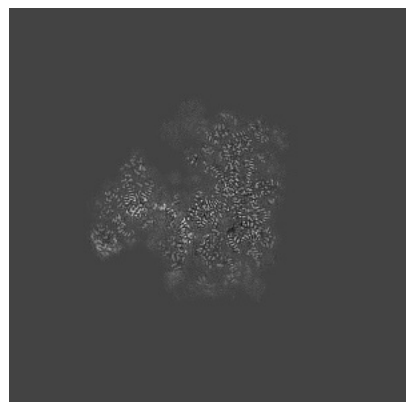


Z

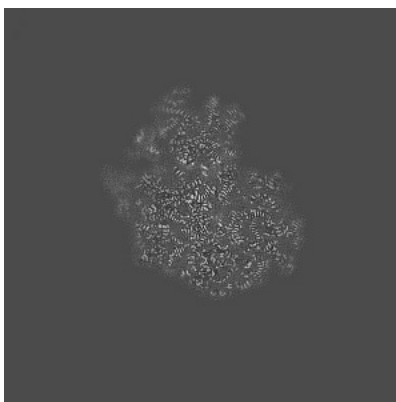
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

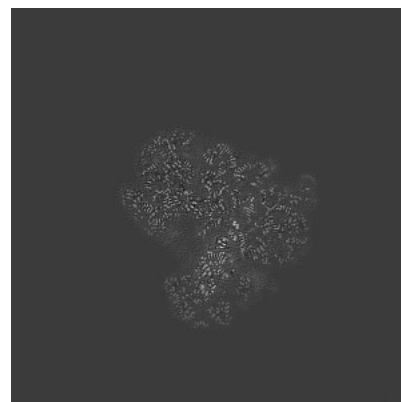
6.2.1 Primary map



X Index: 320



Y Index: 320

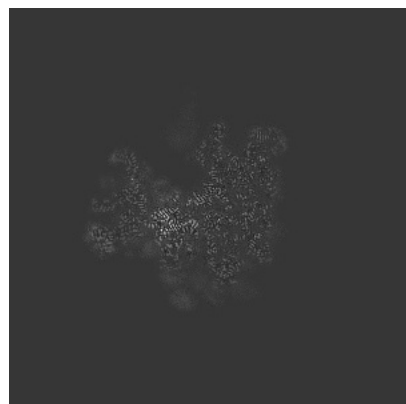


Z Index: 320

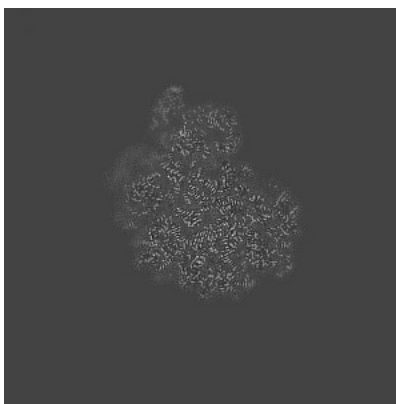
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

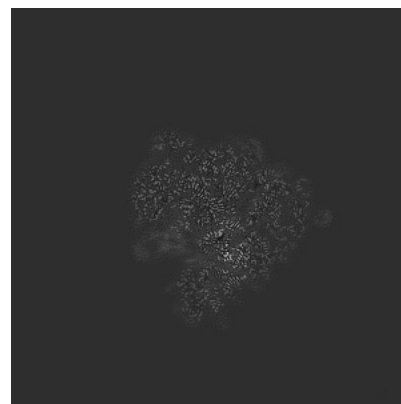
6.3.1 Primary map



X Index: 345



Y Index: 345

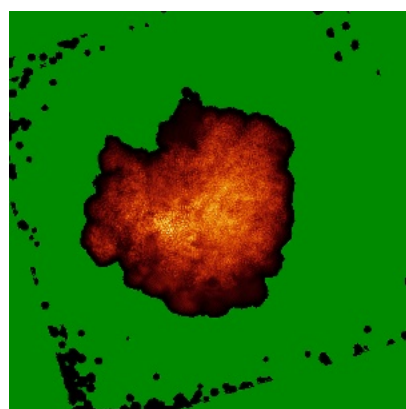


Z Index: 299

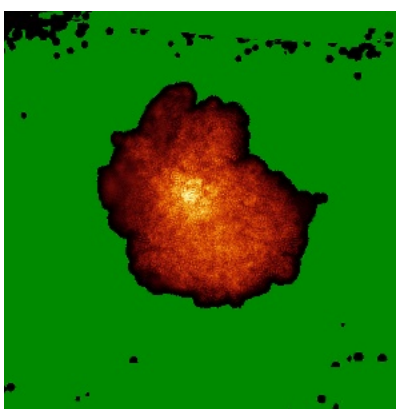
The images above show the largest variance slices of the map in three orthogonal directions.

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

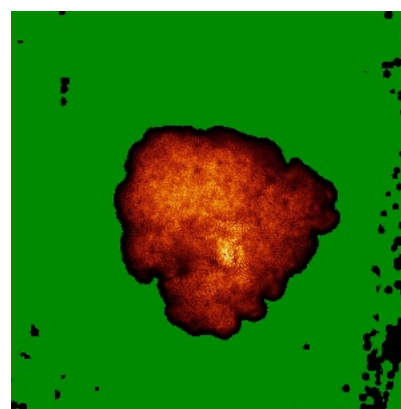
6.4.1 Primary map



X



Y

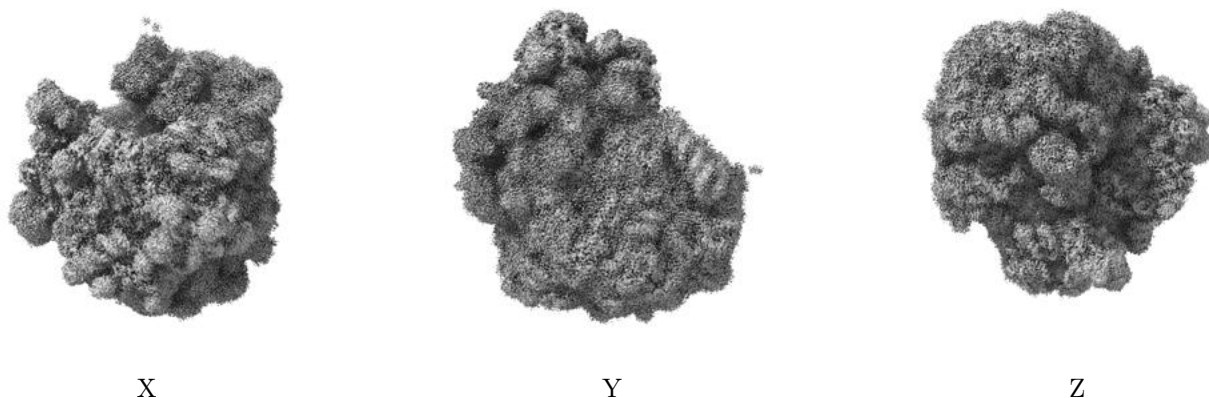


Z

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

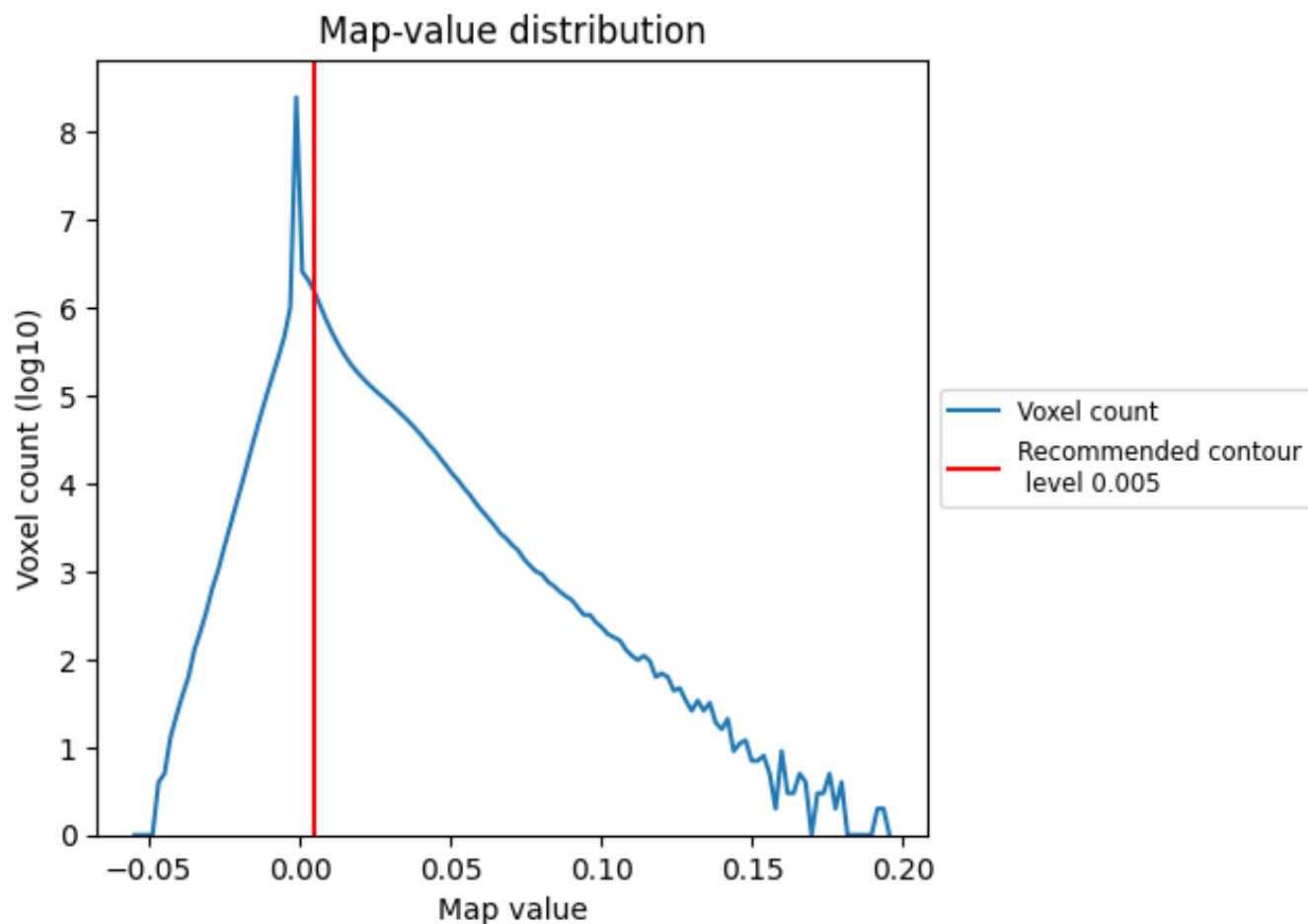
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

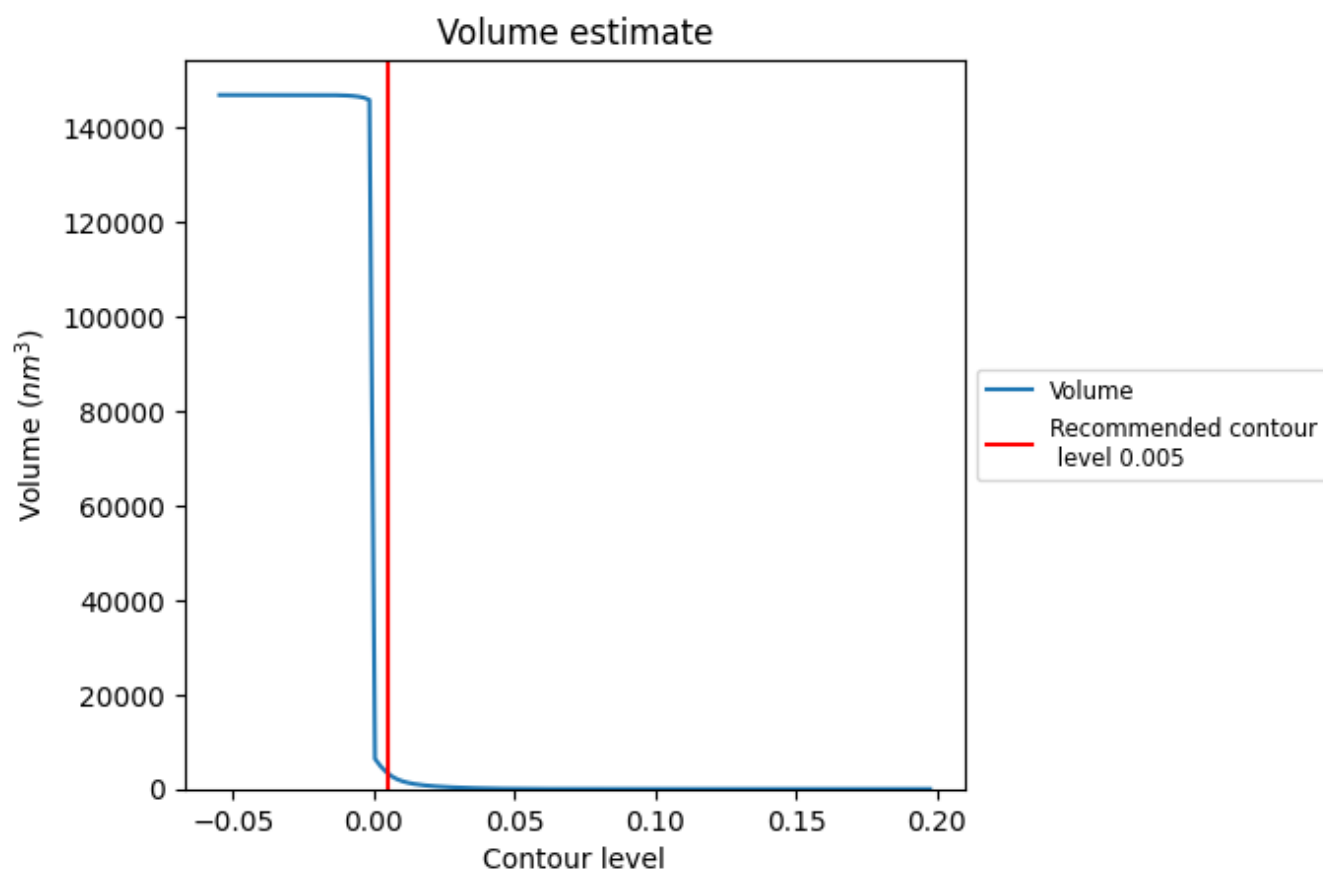
This section contains the results of statistical analysis of the map.

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.

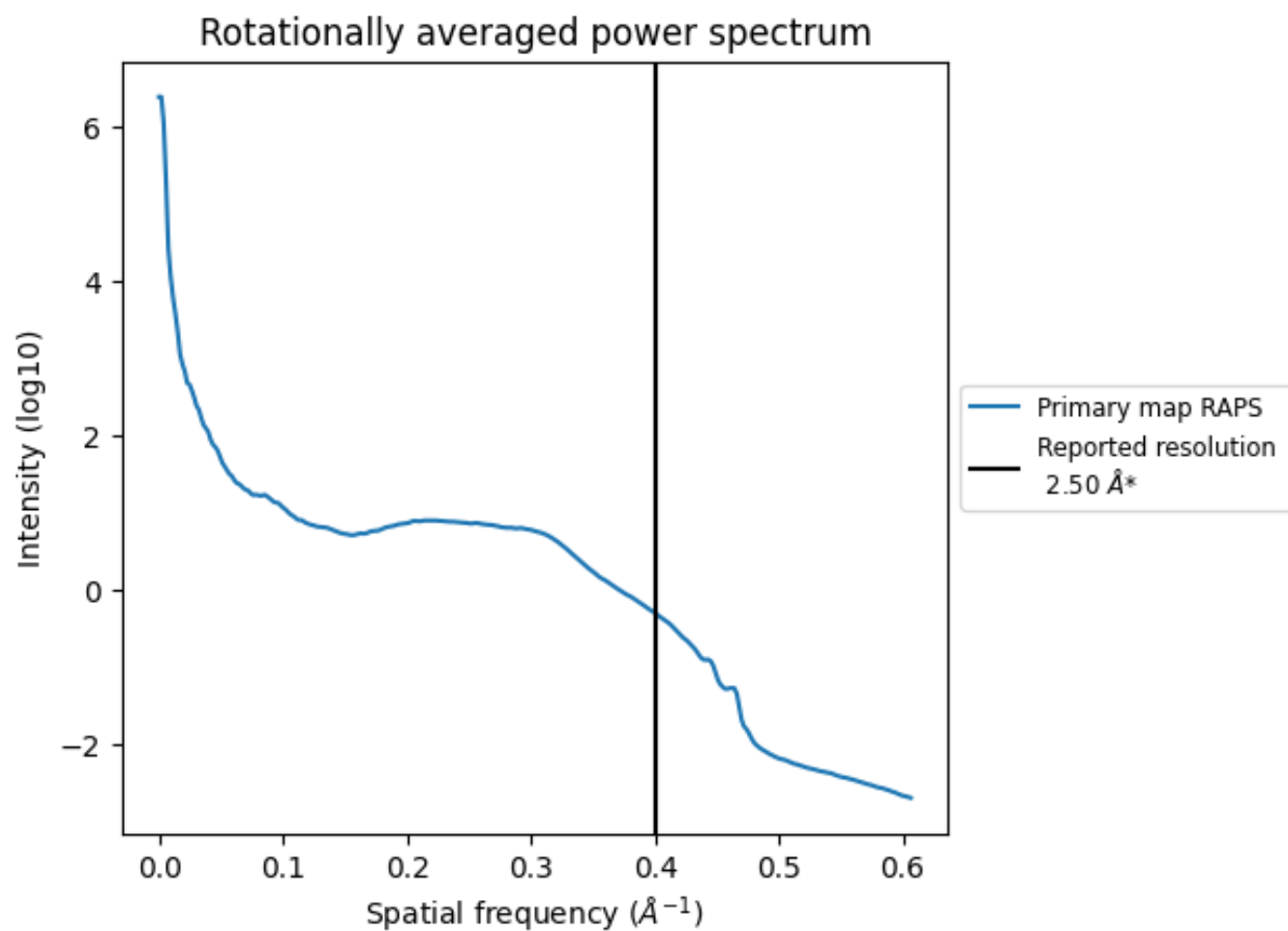
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3337 nm³; this corresponds to an approximate mass of 3014 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 0.400 Å⁻¹

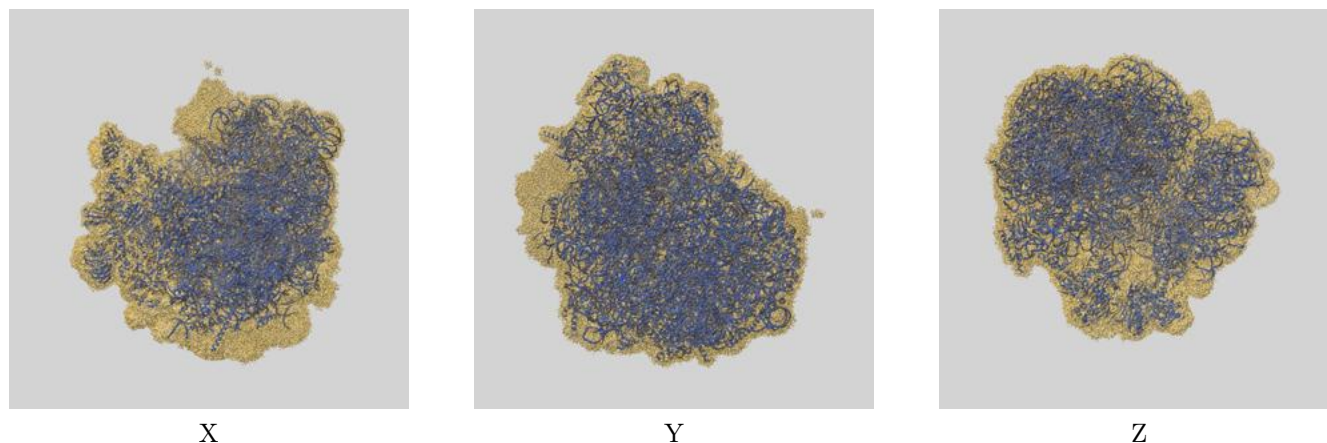
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

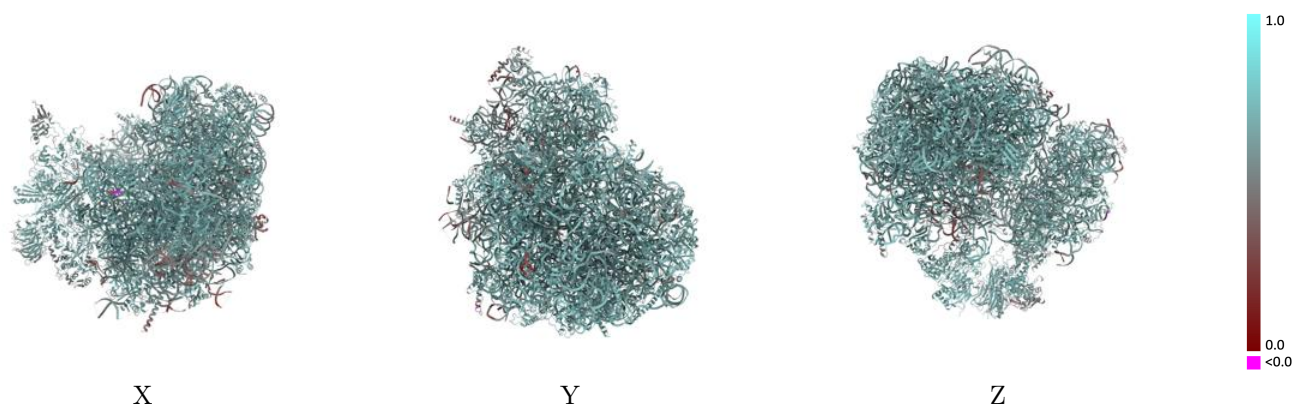
This section contains information regarding the fit between EMDB map EMD-52247 and PDB model 9HL9. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



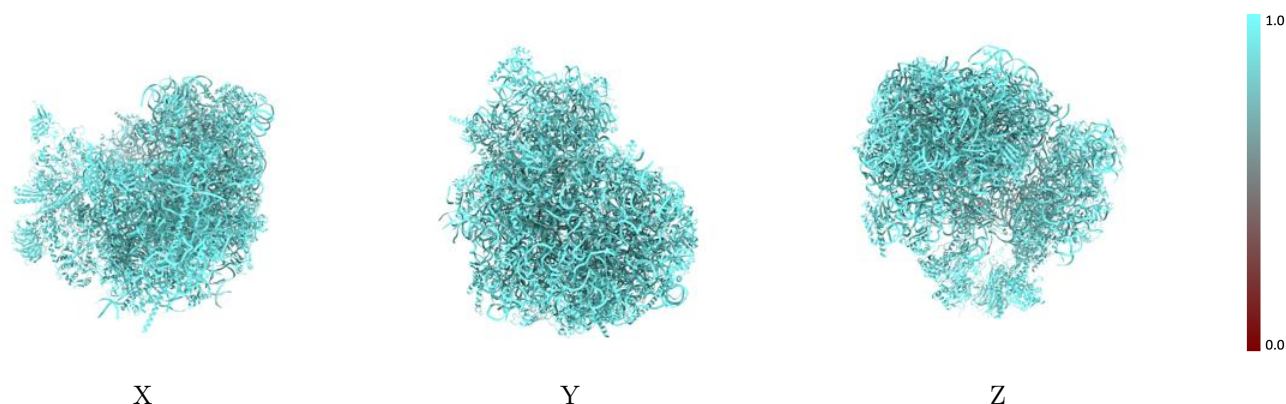
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



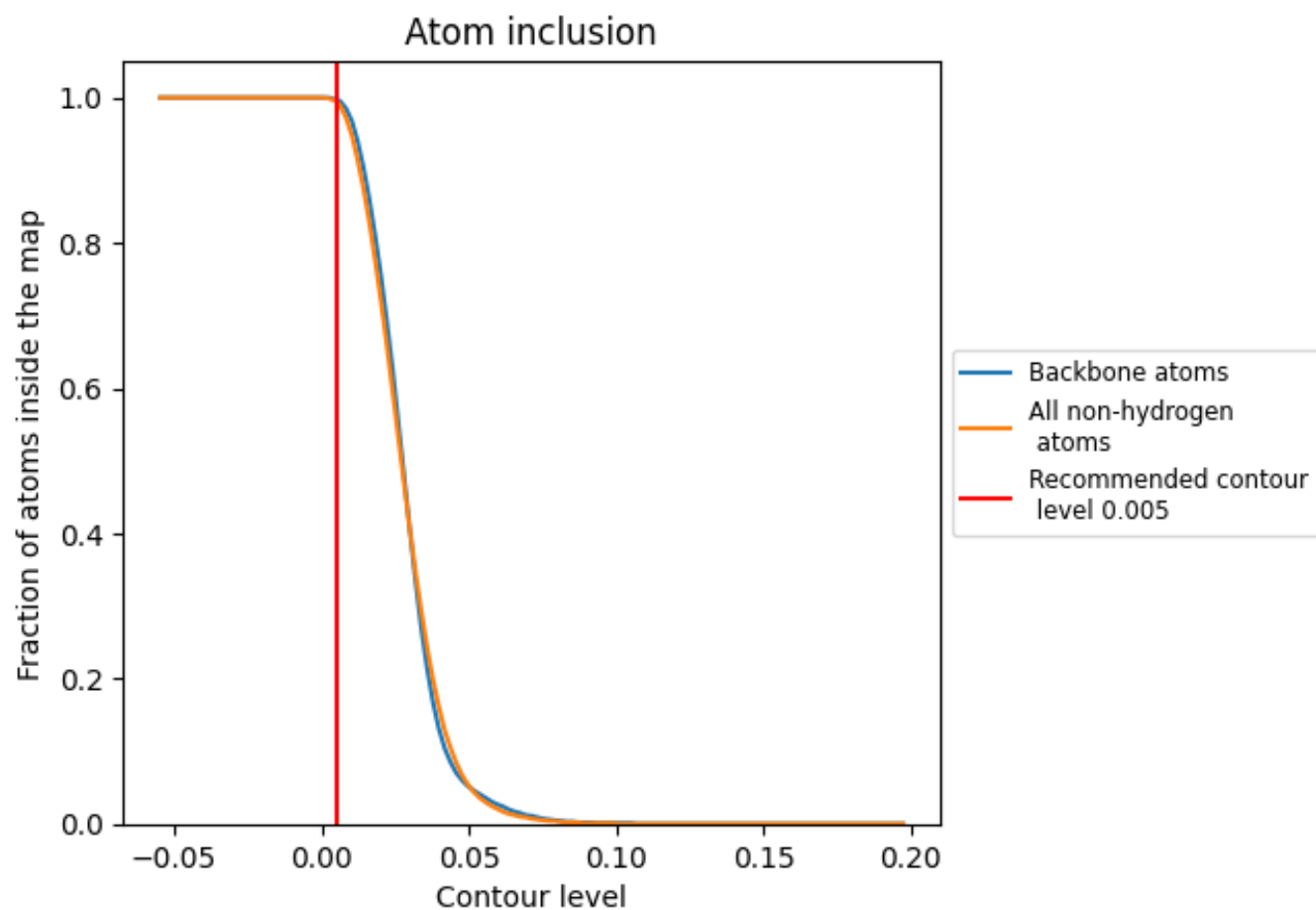
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9950	 0.6530
L1	 0.9950	 0.6540
L2	 0.9970	 0.6560
L3	 0.9910	 0.6350
L4	 0.9990	 0.6730
L5	 0.9960	 0.6530
L6	 0.9910	 0.6350
L7	 0.9890	 0.6480
L8	 0.9990	 0.6680
LA	 1.0000	 0.7040
LB	 0.9940	 0.6960
LC	 0.9990	 0.6860
LD	 0.9940	 0.6310
LE	 0.9940	 0.6750
LF	 0.9930	 0.6560
LG	 0.9870	 0.6580
LH	 0.9970	 0.6960
LI	 0.9900	 0.6680
LJ	 0.9970	 0.6950
LK	 0.9950	 0.6650
LL	 0.9970	 0.6970
LM	 0.9990	 0.7050
LN	 0.9970	 0.6800
LO	 0.9880	 0.6470
LP	 0.9990	 0.6900
LQ	 0.9960	 0.6530
LR	 0.9970	 0.6920
LS	 0.9950	 0.6740
LT	 0.9980	 0.7050
LU	 0.9850	 0.5680
LV	 0.9970	 0.6880
LW	 0.9970	 0.6750
LX	 0.9970	 0.6710
LY	 1.0000	 0.6660
LZ	 0.9990	 0.6750



























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Chain	Atom inclusion	Q-score
La	 0.9960	 0.6660
Lb	 0.9980	 0.6890
Lc	 0.9980	 0.6940
Ld	 0.9970	 0.6780
Le	 0.9910	 0.6540
Lf	 0.9990	 0.6850
Lg	 1.0000	 0.6910
Lh	 0.9980	 0.6750
Li	 0.9950	 0.6580
Lj	 0.9980	 0.7070
Lk	 0.9930	 0.6500
Ll	 0.9980	 0.6970
Lm	 0.9980	 0.6770
Ln	 0.9960	 0.6740
Lo	 0.9940	 0.6980
Lp	 0.9990	 0.6850
S1	 0.9960	 0.6370
S3	 0.9930	 0.4950
S4	 0.9870	 0.3730
S5	 1.0000	 0.5590
SA	 0.9940	 0.6650
SB	 0.9960	 0.6220
SC	 0.9930	 0.6480
SD	 0.9920	 0.6490
SE	 0.9940	 0.6620
SF	 0.9900	 0.6660
SG	 0.9950	 0.6420
SH	 0.9940	 0.6670
SI	 0.9930	 0.6410
SJ	 0.9960	 0.6860
SK	 0.9910	 0.6590
SL	 0.9980	 0.6880
SM	 0.9880	 0.6530
SN	 0.9860	 0.6400
SO	 0.9920	 0.6750
SP	 0.9980	 0.6820
SQ	 0.9950	 0.5050
SR	 0.9970	 0.6540
SS	 1.0000	 0.6830
ST	 0.9960	 0.6820
SU	 0.9940	 0.6790
SV	 0.9840	 0.5930

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Chain	Atom inclusion	Q-score
SW	 0.9860	 0.6410
SX	 0.9950	 0.6740
SY	 0.9860	 0.6290
SZ	 0.9920	 0.6410
Sa	 0.9790	 0.6360
Sb	 1.0000	 0.6780
Sc	 0.9920	 0.6130
Sd	 0.9960	 0.6400
Se	 0.9830	 0.5910
Sf	 0.9860	 0.5340
Sg	 1.0000	 0.6050
Sh	 0.9920	 0.5030