



wwPDB EM Validation Summary Report ⓘ

Sep 20, 2026 – 11:18 am BST

PDB ID : 9TT7 / pdb_00009tt7
EMDB ID : EMD-56227
Title : 80S ribosome of WT EBV infected human B-cells
Authors : Fedorenko, A.; Bashan, A.; Yonath, A.
Deposited on : 2026-01-06
Resolution : 2.20 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:

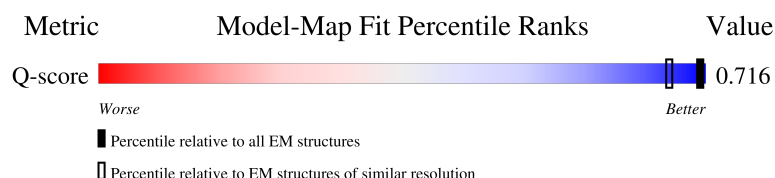
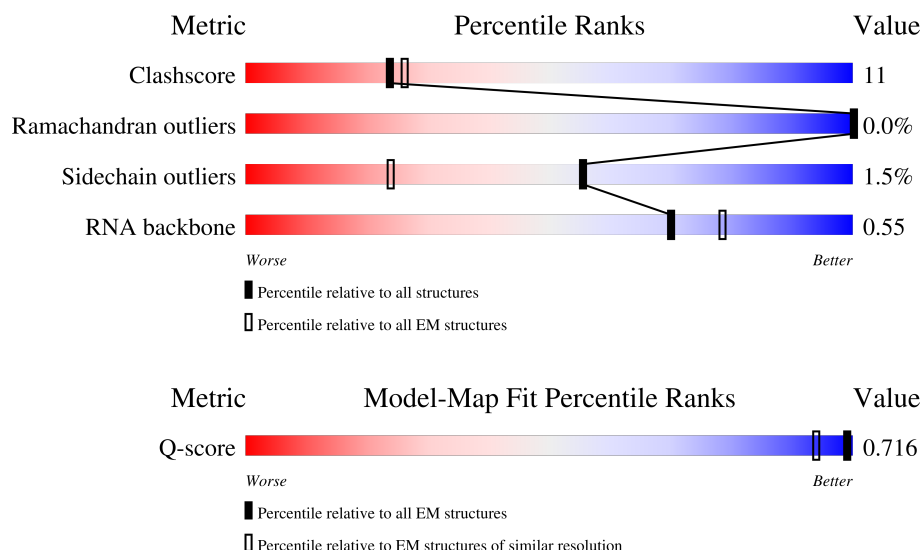
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

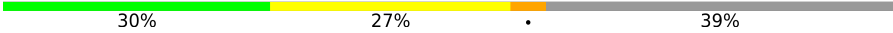
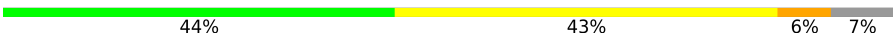
The reported resolution of this entry is 2.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3184 (1.71 - 2.70)

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

Mol	Chain	Length	Quality of chain
1	L5	5054	 30% 27% . 39%
2	L7	121	 64% 28% 6% .
3	L8	156	 44% 43% 6% 7%

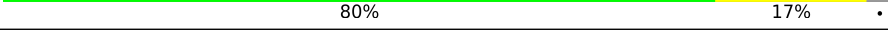
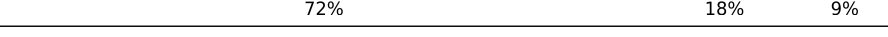
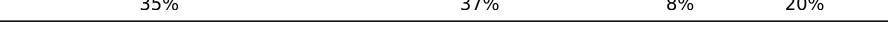
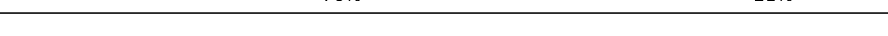
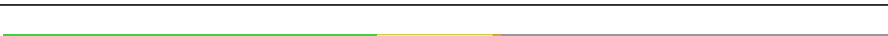
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Mol	Chain	Length	Quality of chain
4	LC	427	
5	LD	297	
6	LE	288	
7	LF	248	
8	LG	266	
9	LJ	178	
10	LM	215	
11	LN	204	
12	LO	203	
13	LP	184	
14	LQ	188	
15	LT	160	
16	LU	128	
17	LX	156	
18	LY	145	
19	LZ	136	
20	La	148	
21	Lb	159	
22	Lc	115	
23	Ld	125	
24	Le	135	
25	Lf	110	
26	Lg	117	
27	Lh	123	
28	Li	105	

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Mol	Chain	Length	Quality of chain
29	Lj	97	
30	Lk	70	
31	Ll	51	
32	Lm	128	
33	Lo	106	
34	Lp	92	
35	Lr	137	
36	LA	257	
37	LB	403	
38	LH	192	
39	LI	214	
40	LL	211	
41	LS	176	
42	S2	1869	
43	SA	295	
44	SB	264	
45	SC	293	
46	SD	243	
47	SE	263	
48	SF	204	
49	SG	249	
50	SH	194	
51	SI	208	
52	SJ	194	
53	SK	165	

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Mol	Chain	Length	Quality of chain
54	SL	158	
55	SN	151	
56	SO	151	
57	SP	145	
58	SQ	146	
59	SR	135	
60	SS	152	
61	ST	145	
62	SU	119	
63	SV	83	
64	SW	130	
65	SX	143	
66	SY	133	
67	SZ	125	
68	Sa	115	
69	Sb	84	
70	Sc	69	
71	Sd	56	
72	Se	98	
73	Sg	310	
74	Ln	25	
75	LR	196	
76	S6	14	
77	LV	140	
78	LW	157	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
42	OMU	S2	1804	-	-	X	-

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 185896 atoms, of which 13 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3066	Total	C	N	O	P	0	0
			65849	29368	12063	21352	3066		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	119	Total	C	N	O	P	0	0
			2538	1132	455	833	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	145	Total	C	N	O	P	0	0
			3094	1381	553	1015	145		

- Molecule 4 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LC	352	Total	C	N	O	S	0	0
			2761	1743	549	455	14		

- Molecule 5 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LD	285	Total	C	N	O	S	0	0
			2281	1443	411	414	13		

- Molecule 6 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LE	210	Total	C	N	O	S	0	0
			1675	1082	314	276	3		

- Molecule 7 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LF	218	Total	C	N	O	S	0	0
			1770	1134	337	291	8		

- Molecule 8 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LG	209	Total	C	N	O	S	0	0
			1527	979	285	259	4		

- Molecule 9 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LJ	43	Total	C	N	O	S	0	0
			321	203	67	48	3		

- Molecule 10 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LM	132	Total	C	N	O	S	0	0
			1074	687	207	173	7		

- Molecule 11 is a protein called 60S ribosomal protein L15.

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

- Molecule 12 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LO	198	Total	C	N	O	S	0	0
			1575	1015	305	250	5		

- Molecule 13 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LP	152	Total	C	N	O	S	0	0
			1211	759	238	205	9		

- Molecule 14 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LQ	187	Total	C	N	O	S	0	0
			1473	919	303	246	5		

- Molecule 15 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LT	148	Total	C	N	O	S	0	0
			1168	743	232	188	5		

- Molecule 16 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LU	95	Total	C	N	O	S	0	0
			619	399	111	108	1		

- Molecule 17 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LX	117	Total	C	N	O	S	0	0
			902	581	166	154	1		

- Molecule 18 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LY	128	Total	C	N	O	S	0	0
			998	632	200	163	3		

- Molecule 19 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LZ	135	Total	C	N	O	S	0	0
			1041	673	192	173	3		

- Molecule 20 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	La	145	Total	C	N	O	S	0	0
			1116	708	229	176	3		

- Molecule 21 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Lb	84	Total	C	N	O	S	0	0
			610	380	127	102	1		

- Molecule 22 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Lc	89	Total	C	N	O	S	0	0
			648	411	113	118	6		

- Molecule 23 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Ld	97	Total	C	N	O	S	0	0
			769	491	151	126	1		

- Molecule 24 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Le	126	Total	C	N	O	S	0	0
			988	625	201	157	5		

- Molecule 25 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Lf	107	Total	C	N	O	S	0	0
			830	529	164	134	3		

- Molecule 26 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Lg	101	Total	C	N	O	S	0	0
			765	477	156	126	6		

- Molecule 27 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Lh	121	Total	C	N	O	S	0	0
			930	586	188	155	1		

- Molecule 28 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Li	94	Total	C	N	O	S	0	0
			692	437	139	112	4		

- Molecule 29 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lj	86	Total	C	N	O	S	0	0
			687	422	152	108	5		

- Molecule 30 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lk	64	Total	C	N	O	S	0	0
			446	284	83	78	1		

- Molecule 31 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ll	49	Total	C	N	O		0	0
			400	256	83	61			

- Molecule 32 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lm	48	Total	C	N	O	S	0	0
			361	221	75	59	6		

- Molecule 33 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lo	93	Total	C	N	O	S	0	0
			723	454	145	118	6		

- Molecule 34 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lp	87	Total	C	N	O	S	0	0
			641	404	120	110	7		

- Molecule 35 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lr	119	Total	C	N	O	S	1	0
			933	578	192	159	4		

- Molecule 36 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LA	245	Total	C	N	O	S	0	0
			1794	1124	362	302	6		

- Molecule 37 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LB	391	Total	C	N	O	S	0	0
			2950	1883	558	497	12		

- Molecule 38 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LH	180	Total	C	N	O	S	0	0
			1312	834	242	230	6		

- Molecule 39 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LI	195	Total	C	N	O	S	0	0
			1472	937	277	247	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	49	CYS	GLY	conflict	UNP Q96L21

- Molecule 40 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LL	190	Total	C	N	O	S	0	0
			1422	895	293	230	4		

- Molecule 41 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LS	170	Total	C	N	O	S	0	0
			1376	879	262	225	10		

- Molecule 42 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	S2	1503	Total	C	H	N	O	P	0	0
			32177	14387	13	5797	10478	1502		

- Molecule 43 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SA	205	Total	C	N	O	S	0	0
			1568	1004	278	278	8		

- Molecule 44 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SB	201	Total	C	N	O	S	0	0
			1525	975	275	262	13		

- Molecule 45 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SC	212	Total	C	N	O	S	0	0
			1545	1006	264	266	9		

- Molecule 46 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SD	206	Total	C	N	O	S	0	0
			1364	881	240	238	5		

- Molecule 47 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SE	257	Total	C	N	O	S	0	0
			1940	1244	361	327	8		

- Molecule 48 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SF	178	Total	C	N	O	S	0	0
			1319	835	248	229	7		

- Molecule 49 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SG	185	Total	C	N	O	S	0	0
			1307	826	259	217	5		

- Molecule 50 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SH	146	Total	C	N	O	S	0	0
			1022	659	191	172			

- Molecule 51 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SI	169	Total	C	N	O	S	0	0
			1284	811	247	223	3		

- Molecule 52 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SJ	178	Total	C	N	O	S	0	0
			1321	849	267	203	2		

- Molecule 53 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SK	92	Total	C	N	O	S	0	0
			652	428	117	102	5		

- Molecule 54 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SL	132	Total	C	N	O	S	0	0
			1010	641	190	173	6		

- Molecule 55 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SN	142	Total	C	N	O	S	0	0
			1077	694	201	181	1		

- Molecule 56 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SO	124	Total	C	N	O	S	0	0
			892	548	177	162	5		

- Molecule 57 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SP	114	Total	C	N	O	S	0	0
			835	539	155	135	6		

- Molecule 58 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SQ	140	Total	C	N	O	S	0	0
			1065	681	200	181	3		

- Molecule 59 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SR	117	Total	C	N	O	S	0	0
			833	530	156	143	4		

- Molecule 60 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SS	139	Total	C	N	O	S	0	0
			1057	676	210	170	1		

- Molecule 61 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	ST	142	Total	C	N	O	S	0	0
			1055	662	205	186	2		

- Molecule 62 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SU	83	Total	C	N	O	S	0	0
			609	380	118	107	4		

- Molecule 63 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SV	83	Total	C	N	O	S	0	0
			622	385	114	118	5		

- Molecule 64 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SW	129	Total	C	N	O	S	0	0
			1020	651	189	174	6		

- Molecule 65 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SX	139	Total	C	N	O	S	0	0
			1060	669	211	177	3		

- Molecule 66 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SY	117	Total	C	N	O	S	0	0
			934	592	184	153	5		

- Molecule 67 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SZ	70	Total	C	N	O	S	0	0
			518	333	92	92	1		

- Molecule 68 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sa	98	Total	C	N	O	S	0	0
			740	465	150	120	5		

- Molecule 69 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sb	61	Total	C	N	O	S	0	0
			463	294	88	79	2		

- Molecule 70 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sc	53	Total	C	N	O	S	0	0
			370	228	76	65	1		

- Molecule 71 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Sd	45	Total	C	N	O	S	0	0
			356	220	74	57	5		

- Molecule 72 is a protein called FAU ubiquitin like and ribosomal protein S30 fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Se	45	Total	C	N	O	S	0	0
			341	208	78	54	1		

- Molecule 73 is a protein called RS8_HUMAN Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sg	278	Total	C	N	O	S	0	0
			2055	1312	360	374	9		

- Molecule 74 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Ln	25	Total	C	N	O	S	0	0
			199	121	51	26	1		

- Molecule 75 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	LR	154	Total	C	N	O	S	0	0
			1200	751	256	184	9		

- Molecule 76 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	S6	13	Total	C	N	O	P	0	0
			281	125	55	88	13		

- Molecule 77 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	LV	130	Total	C	N	O	S	1	0
			943	595	177	166	5		

- Molecule 78 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	LW	61	Total	C	N	O	S	0	0
			477	304	91	80	2		

- Molecule 79 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
79	L5	142	Total	Mg	0
			142	142	
79	L7	2	Total	Mg	0
			2	2	
79	L8	3	Total	Mg	0
			3	3	
79	LN	1	Total	Mg	0
			1	1	
79	LP	1	Total	Mg	0
			1	1	
79	LI	1	Total	Mg	0
			1	1	
79	S2	25	Total	Mg	0
			25	25	
79	LV	1	Total	Mg	0
			1	1	

- Molecule 80 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
80	L5	24	Total	K	0
			24	24	
80	L7	1	Total	K	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
80	Lf	1	Total K 1 1	0
80	Lo	1	Total K 1 1	0
80	LA	2	Total K 2 2	0
80	LH	1	Total K 1 1	0
80	LI	1	Total K 1 1	0
80	S2	3	Total K 3 3	0
80	SF	1	Total K 1 1	0
80	SL	1	Total K 1 1	0
80	SO	1	Total K 1 1	0

- Molecule 81 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	AltConf
81	L5	12	Total Na 12 12	0
81	S2	1	Total Na 1 1	0

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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Mol	Chain	Residues	Atoms		AltConf
82	Sd	1	Total 1	Zn 1	0

- Molecule 83 is water.

Mol	Chain	Residues	Atoms		AltConf
83	L5	2093	Total 2093	O 2093	0
83	L7	51	Total 51	O 51	0
83	L8	135	Total 135	O 135	0
83	LC	85	Total 85	O 85	0
83	LD	15	Total 15	O 15	0
83	LE	10	Total 10	O 10	0
83	LF	42	Total 42	O 42	0
83	LG	10	Total 10	O 10	0
83	LM	2	Total 2	O 2	0
83	LN	69	Total 69	O 69	0
83	LO	34	Total 34	O 34	0
83	LP	33	Total 33	O 33	0
83	LQ	59	Total 59	O 59	0
83	LT	26	Total 26	O 26	0
83	LX	7	Total 7	O 7	0
83	LY	14	Total 14	O 14	0
83	LZ	4	Total 4	O 4	0
83	La	43	Total 43	O 43	0

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Mol	Chain	Residues	Atoms		AltConf
83	Lb	13	Total 13	O 13	0
83	Lc	2	Total 2	O 2	0
83	Ld	9	Total 9	O 9	0
83	Le	41	Total 41	O 41	0
83	Lf	20	Total 20	O 20	0
83	Lg	22	Total 22	O 22	0
83	Lh	5	Total 5	O 5	0
83	Li	7	Total 7	O 7	0
83	Lj	21	Total 21	O 21	0
83	Lk	1	Total 1	O 1	0
83	Ll	8	Total 8	O 8	0
83	Lm	2	Total 2	O 2	0
83	Lo	11	Total 11	O 11	0
83	Lp	12	Total 12	O 12	0
83	Lr	19	Total 19	O 19	0
83	LA	75	Total 75	O 75	0
83	LB	70	Total 70	O 70	0
83	LH	7	Total 7	O 7	0
83	LI	6	Total 6	O 6	0
83	LL	32	Total 32	O 32	0
83	LS	5	Total 5	O 5	0

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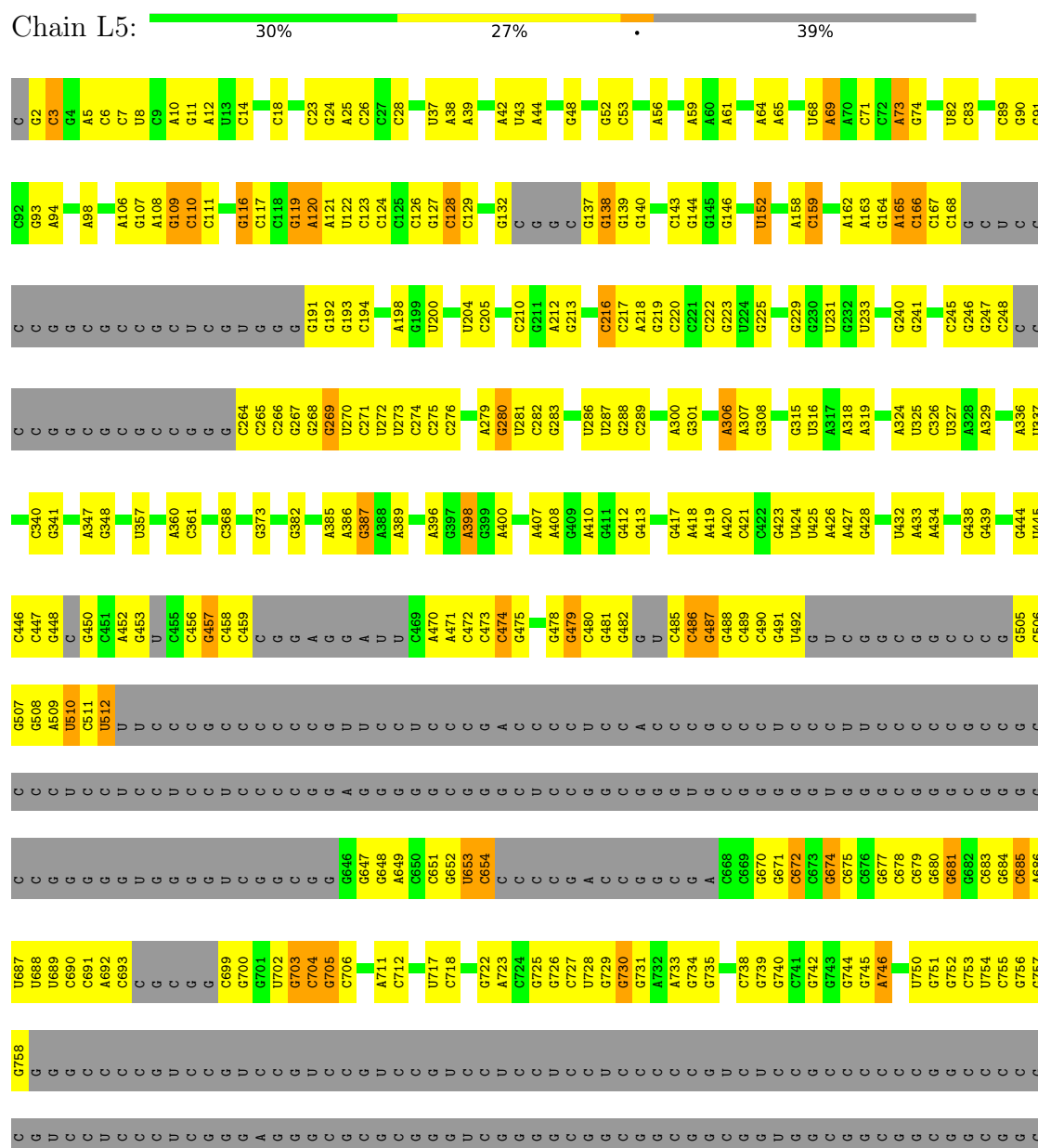
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Mol	Chain	Residues	Atoms		AltConf
83	S2	29	Total 29	O 29	0
83	SS	2	Total 2	O 2	0
83	Sa	2	Total 2	O 2	0
83	Sb	1	Total 1	O 1	0
83	LR	8	Total 8	O 8	0
83	S6	2	Total 2	O 2	0
83	LV	18	Total 18	O 18	0
83	LW	2	Total 2	O 2	0

3 Residue-property plots [i](#)

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.

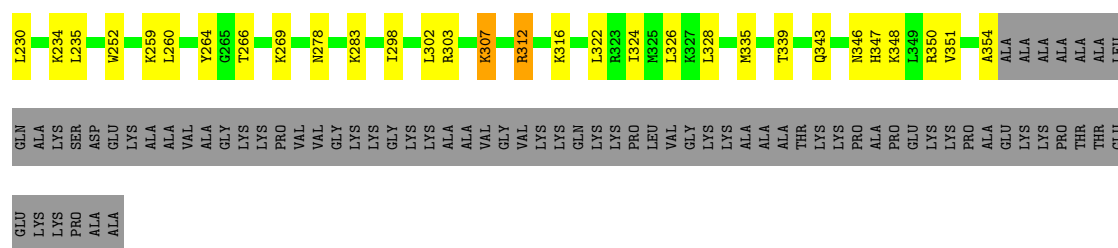
• Molecule 1: 28S rRNA



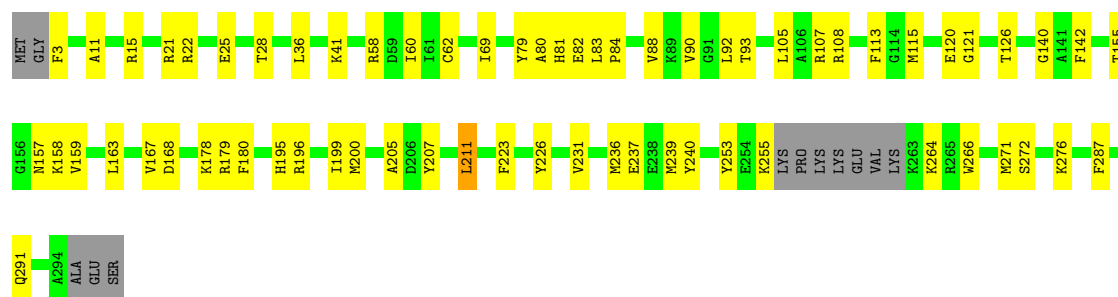
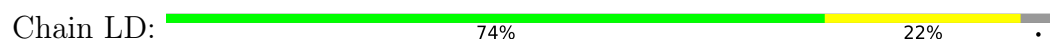




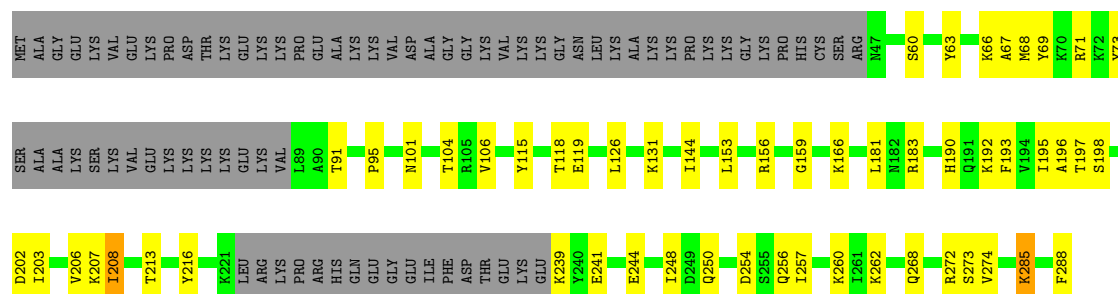
U4467	A4380	U4282	C4116	U	C	G3930	A3862	U3784	A3703	A3615	C	G	U	C	G
U4468	C4387	U4285	G4117	A	C	U	A3863	A3785	A3704	A3621	G	G	C	C	G
C4469	C4388	U4119	C4118	C	G	C	C3864	A3786	A3705	C3622	C	G	C	C	G
U4470	U4389	U4120	C4119	C	U	U	G3865	U3787	G3706	G3623	G	G	C	C	G
C4471	U4390	G4121	G4120	A	U	G	G3866	U3788	U3707	G3624	C	G	C	C	G
A4474	U4391	U4205	G	C	U	C	G3867	C3794	G3708	U3625	C	G	C	C	G
G4475	U4292	A4206	U4056	U	U	C	C3868	G3795	A3709	U3626	C	G	C	C	G
C4399	U4207	G4207	U4057	C	C	A	U3869	C3796	A3710	U3627	G	G	C	C	G
A4400	G4208	C	U4058	C	C	G	U3870	G3797	G3711	U3628	C	G	C	C	G
A4401	U4213	C	A4059	C	C	G	A3876	G3797	A3712	U3629	G	G	C	C	G
U4479	G4214	C	U4061	C	C	U	U3877	U3800	A3713	U3630	G	G	C	C	G
U4483	U4215	A	G4062	G	C	G	U3878	A3803	A3714	U3631	U	U	C	C	G
U4484	A	A	C4065	G	A	A	C3879	U3804	U3715	U3632	C	G	C	C	A
G4485	U4218	C	U4066	A	C	G	A3880	G3805	U3716	A3632	C	G	C	C	G
U4486	A4219	C	G4067	G	G	C	C3881	G3806	A3717	A3633	G	G	C	C	G
U4487	G4132	G	G4132	G	C	G	G3882	G3807	A3718	A3634	C	G	C	C	G
C4488	G4133	C	C4133	G	G	A	C3883	U3808	A3719	A3637	G	G	C	C	G
A4489	C4134	U	C4134	C	C	C	G3884	G3809	A3722	A3638	C	G	C	C	G
C4490	G4135	U	G4135	C	C	C	G3885	A3810	A3723	A3639	G	G	C	C	G
C4491	G4316	C	G4137	C	C	A	A3887	A3811	C3727	A3642	C	G	C	C	G
C4492	G4317	U	G4138	G	U	U	C3888	A3816	G3730	U3643	C	G	C	C	G
A4493	C4318	U	G4139	C	C	G	A3890	C3823	A3734	C3644	C	G	C	C	G
C4494	G4227	G	G4073	G	G	A	A3891	U3824	C3735	A3648	U	G	C	C	G
U4495	U4228	C	G	C	C	G	A3892	G3825	G3739	A3649	C	G	C	C	G
A4496	G4229	U	C	C	C	G	G3893	U3826	G3740	G3650	C	G	C	C	G
A4497	C4235	C	G4146	C	C	A	A3894	C3827	G3741	G3651	C	G	C	C	G
U4498	G4236	U	G4147	C	C	G	C3895	C3828	A3742	C3656	U	G	C	C	G
A4499	A4237	C	U4149	G	C	U	C3896	C3829	G	G3657	C	G	C	C	G
C4505	C	G	G4154	A	U	U	C3897	U3830	G3658	G3658	C	G	C	C	G
G4506	G	A	G4155	G	C	C	U3898	A3831	G	G3659	C	G	C	C	G
U4507	A	G	G4156	G	C	G	G3899	U3832	G	C3669	C	G	C	C	G
G4508	C	C	A4157	C	C	A	U3900	A3833	G	G3670	C	G	C	C	G
A4509	U	U	G4158	C	C	U	C3902	U3834	U	C3671	C	G	C	C	G
G4510	C4244	C	G4159	G	C	U	A3903	A3835	A	G3676	C	G	C	C	G
C4511	G4245	G	U4160	C	C	U	C3904	U3836	A	G3677	C	G	C	C	G
U4512	U4246	G	G	C	C	G	C3905	A3837	C	C3591	C	G	C	C	G
G4513	C4247	U	C4163	G	C	U	U3906	U3838	G	U3592	C	G	C	C	G
U4516	G4252	C	G4164	C	C	U	C3907	U3839	G	A3593	C	G	C	C	G
U4517	A4254	C	U4165	G	C	G	A3908	C3840	C	C3594	C	G	C	C	G
U4518	A4254	C	G4169	G	C	A	C3909	C3841	G	U3594	C	G	C	C	G
C4523	A4259	U	G4170	A	C	C	U3911	A3842	G	C3595	C	G	C	C	G
G4524	U4260	C	A4171	G	C	G	A3914	G3845	U3756	C3685	C	G	C	C	G
U4525	G4261	C	A4172	G	C	C	G3915	A3846	C3757	C3686	C	G	C	C	G
G4531	C4361	U	G4173	C	C	C	U3916	A3847	U3758	U3599	C	G	C	C	G
A4534	A4267	C	U4174	C	C	C	C3917	A3848	U3759	G3600	C	G	C	C	G
G4535	G4270	C	U4175	C	C	C	U3918	A3851	A3761	G3601	G	G	C	C	G
U4536	U4271	C	G4176	G	C	C	G3919	C3852	A3762	C3604	G	G	C	C	G
U4537	A4365	C	A4177	C	C	G	C3920	A3853	G3762	C3694	C	G	C	C	G
U4538	A4367	C	U4178	C	C	G	C3921	G3854	G3763	U3695	U	C	C	C	G
C4546	U4275	U	U4180	C	C	C	C3922	A3857	A3771	U	C	C	C	C	G
G4547	U4276	G	G4181	U	C	C	C3923	A3858	U3772	G	C	C	C	C	G
C4548	G4277	C	A4189	G	C	C	G3924	G3859	A3781	G3700	C	G	C	C	G
U4549	A4278	A	U4190	A	C	C	C3925	G3860	U3782	C3702	C	G	C	C	G
A4550	U4281	A	U4196	A	C	C	A3929	G3861	C3783						



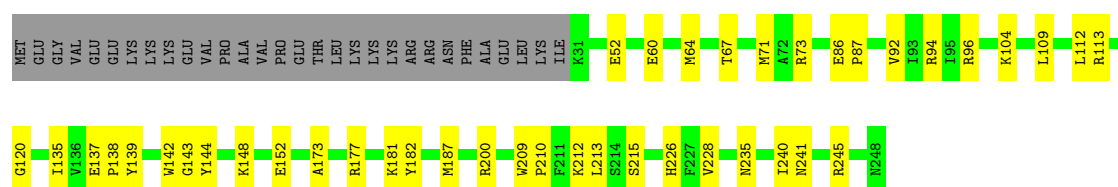
- Molecule 5: 60S ribosomal protein L5



- Molecule 6: Large ribosomal subunit protein eL6

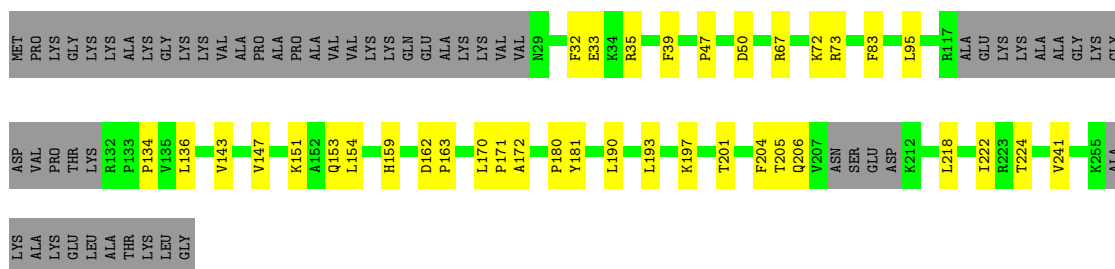


- Molecule 7: Large ribosomal subunit protein uL30



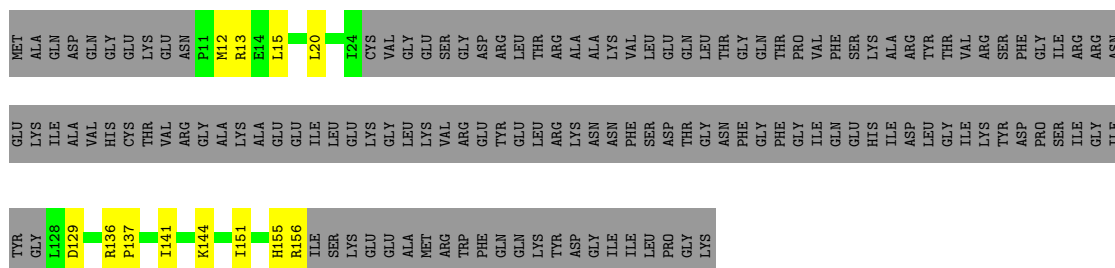
- Molecule 8: 60S ribosomal protein L7a





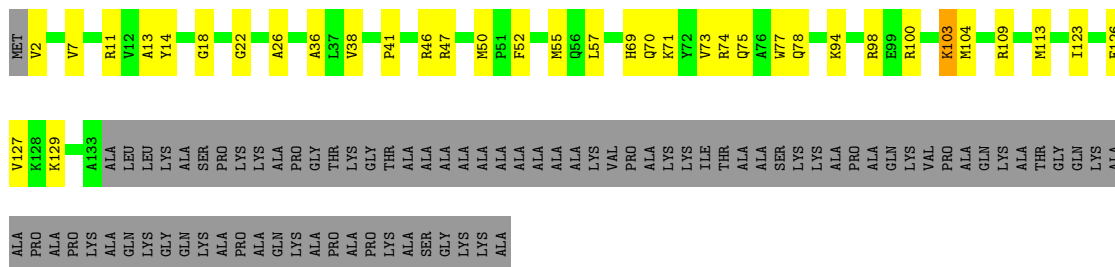
• Molecule 9: Large ribosomal subunit protein uL5

Chain LJ: 17% 7% 76%



• Molecule 10: 60S ribosomal protein L14

Chain LM: 45% 16% 39%



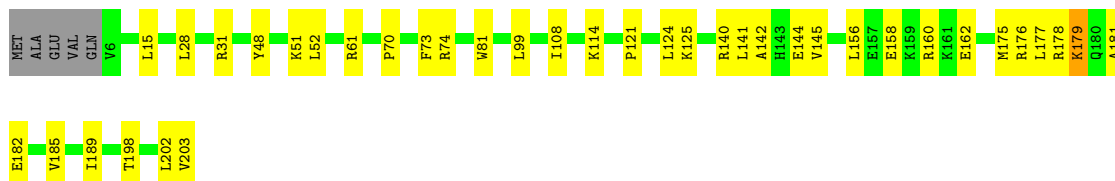
• Molecule 11: 60S ribosomal protein L15

Chain LN: 85% 15%

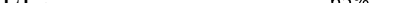


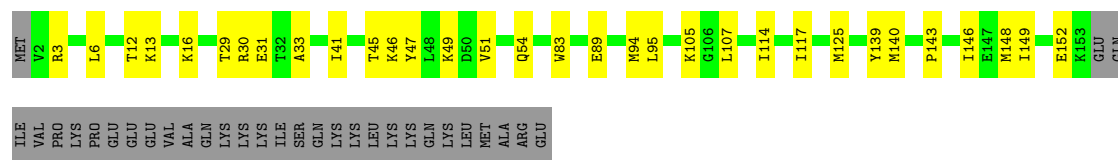
• Molecule 12: 60S ribosomal protein L13a

Chain LO: 79% 18%



- Molecule 13: 60S ribosomal protein L17

Chain LP:  65% 17% 17%



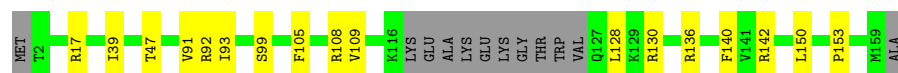
- Molecule 14: 60S ribosomal protein L18

Chain LQ:  84% 15%



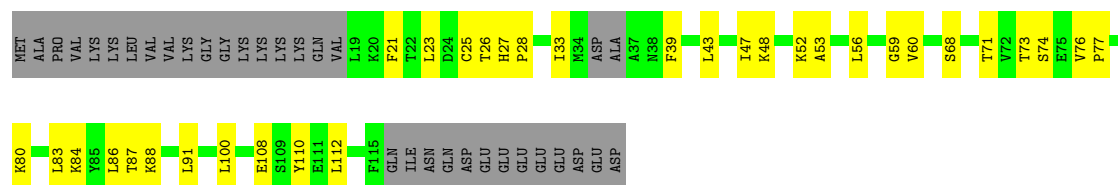
- Molecule 15: 60S ribosomal protein L21

Chain LT:  82% 11% 8%

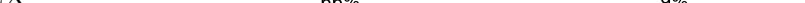


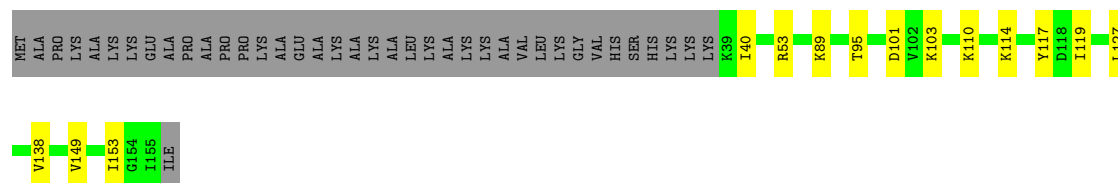
- Molecule 16: 60S ribosomal protein L22

Chain LU: 

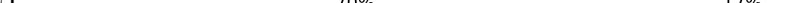


- Molecule 17: 60S ribosomal protein L23a

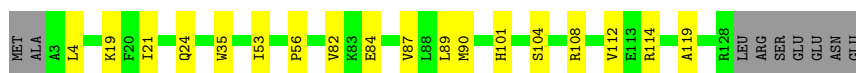
Chain LX:  66% 9% 25%



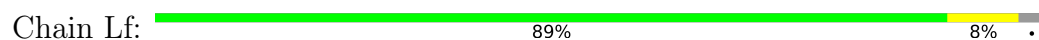
- Molecule 18: 60S ribosomal protein L26

Chain LY: 

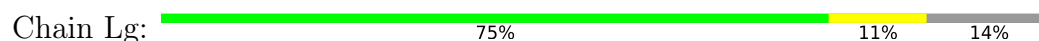




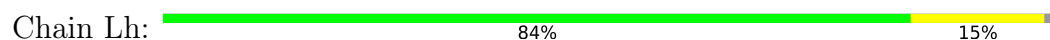
- Molecule 25: Large ribosomal subunit protein eL33



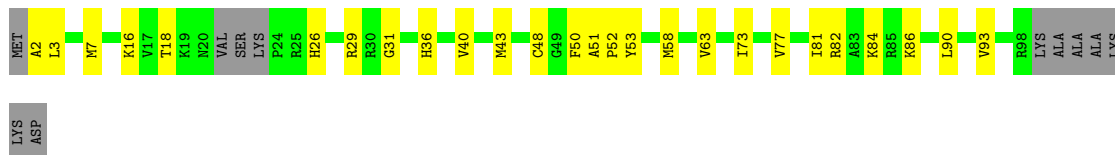
- Molecule 26: 60S ribosomal protein L34



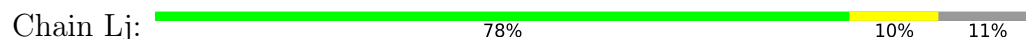
- Molecule 27: 60S ribosomal protein L35



- Molecule 28: 60S ribosomal protein L36



- Molecule 29: Large ribosomal subunit protein eL37



- Molecule 30: 60S ribosomal protein L38



- Molecule 31: 60S ribosomal protein L39

MET	S2	T6	I9	K10	R11	F12	L13	K16	Q17	I23	T31	H43	W44	R45	L49	G50	LEU
-----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- [illegible]

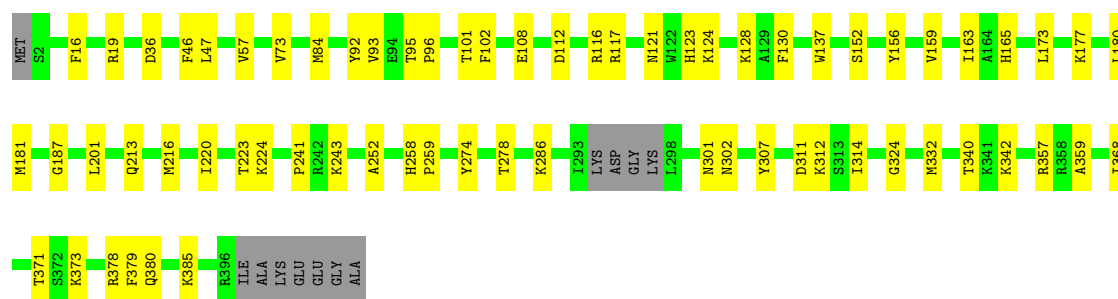
- | MET |
|-----|
| V2 |
| K6 |
| K14 |
| V23 |
| A35 |
| G36 |
| G37 |
| K38 |
| R39 |
| I66 |
| V67 |
| L68 |
| R69 |
| L70 |
| M82 |
| L83 |
| A84 |
| R87 |
| C98 |
| G94 |
| GLY |
| ASP |
| LYS |
| LYS |
| ARG |
| LYS |
| GLY |
| GLN |
| VAL |
| TLE |
| PHE |
| PHF |

- | | | | |
|-----|----|----|-----|
| MET | A2 | V8 | V11 | Y18 | R23 | K24 | W26 | I29 | E30 | T38 | T45 | V64 | W69 | T78 | V79 | K80 | S81 | A82 | I83 | R84 | R85 | E88 | LEU | LVS | ASP | GLN |
|-----|----|----|-----|

- | | | | | | | | | | | | | | | | | |
|-----|----|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | S2 | S14 | L17 | S26 | K33 | S37 | Y40 | K47 | A54 | ALA | ASP | G57 | V60 | I64 | R65 | R66 | R67 | T75 | S76 | Y77 | R78 | R79 | Y102 | I117 | K122 | PRO | VAL | MET | VAL | LYS | ARG | ARG | THR | PRO | THR | LYS | SER |
|-----|----|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

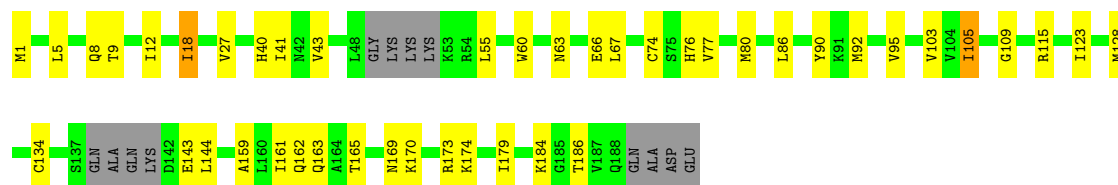
- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| A240 | R241 | R242 | L246 | ARG | GLY | THR | LYS | THR | VAL | GLN | GLU | LYS | GLU | ASN | MET | G2 | R9 | V20 | K21 | K22 | R23 | K24 | R28 | L29 | R30 | L49 | P52 | E74 | H83 | Q86 | V101 | L102 | E117 | G124 | A129 | N132 | T135 | V136 | I137 | P141 | K149 | V165 | I175 | L180 | G183 | R204 | R205 | P206 | K221 | R233 |
|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|

- 



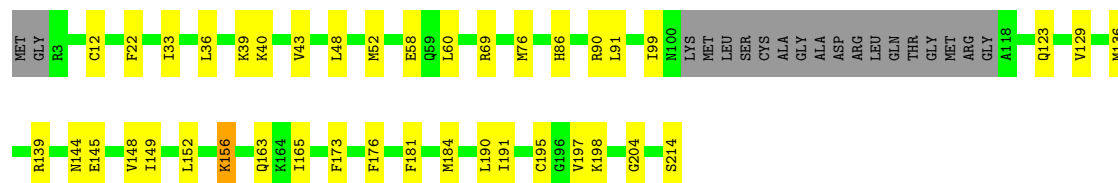
- Molecule 38: 60S ribosomal protein L9

Chain LH: 71% 22% 6%



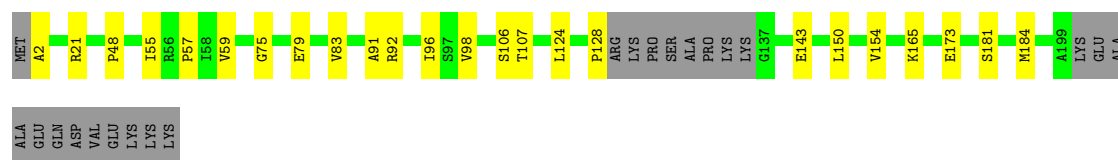
- Molecule 39: 60S ribosomal protein L10-like

Chain LI: 72% 18% 9%



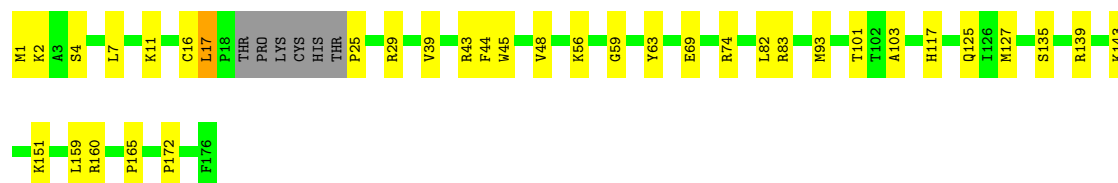
- Molecule 40: Large ribosomal subunit protein eL13

Chain LL: 79% 11% 10%



- Molecule 41: 60S ribosomal protein L18a

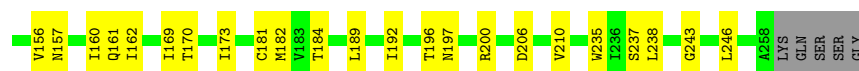
Chain LS: 77% 19% 2%



- Molecule 42: 18S rRNA

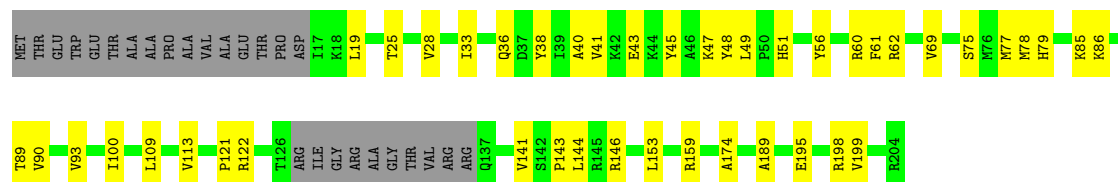
Response	Percentage
Yes, the U.S. should take action to address climate change	35%
No, the U.S. should focus on other issues	37%
Don't know	8%
Other	20%





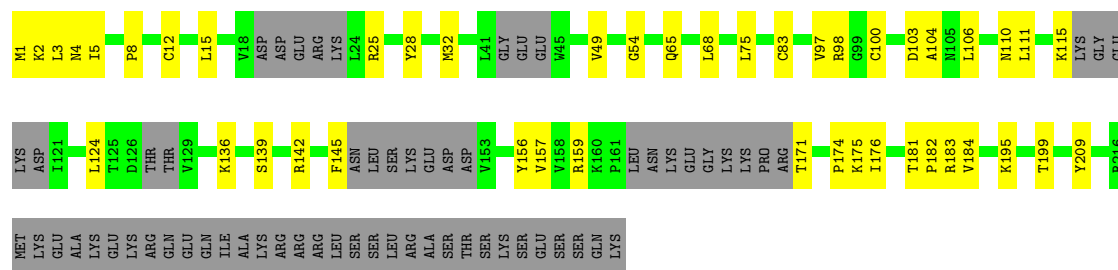
- Molecule 48: 40S ribosomal protein S5

Chain SF: 66% 22% 13%



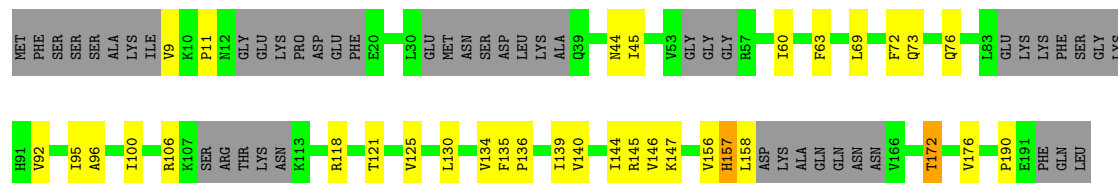
- Molecule 49: 40S ribosomal protein S6

Chain SG: 56% 18% 26%



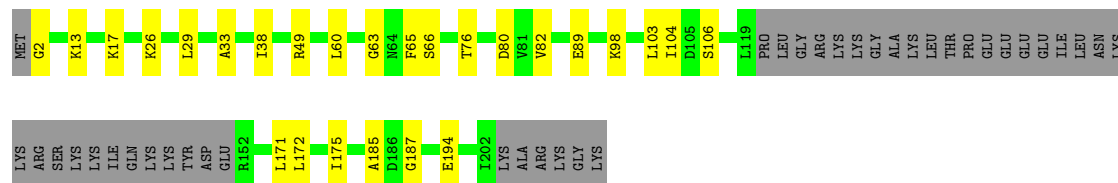
- Molecule 50: 40S ribosomal protein S7

Chain SH: 58% 16% 25%



- Molecule 51: 40S ribosomal protein S8

Chain SI: 69% 12% 19%



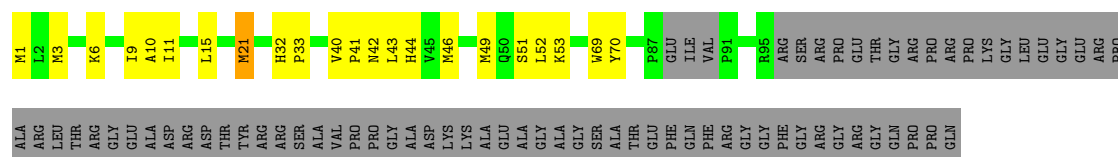
- Molecule 52: 40S ribosomal protein S9

Chain SJ: 77% 15% 8%



- Molecule 53: 40S ribosomal protein S10

Chain SK: 42% 13% 44%



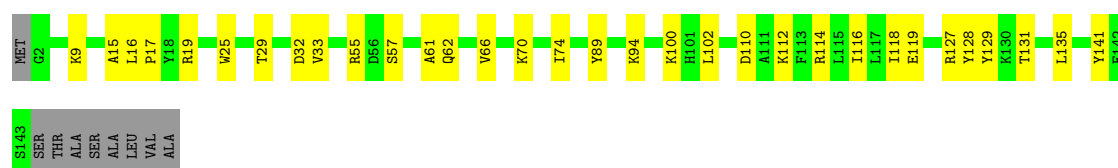
- Molecule 54: Small ribosomal subunit protein uS17

Chain SL: 69% 15% 16%



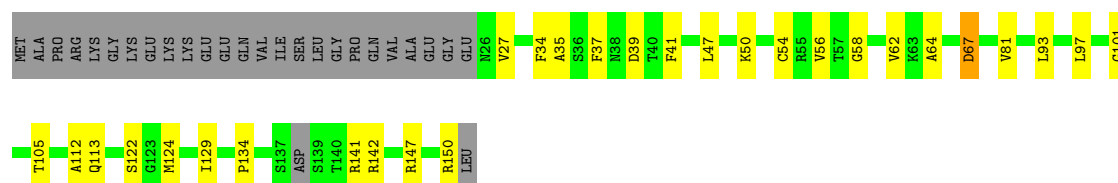
- Molecule 55: 40S ribosomal protein S13

Chain SN: 73% 21% 6%



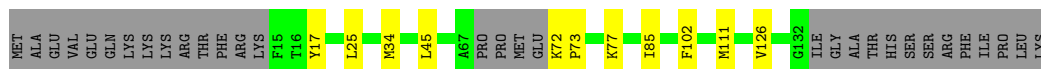
- Molecule 56: 40S ribosomal protein S14

Chain SO: 63% 19% 18%



- Molecule 57: 40S ribosomal protein S15

Chain SP: 71% 8% 21%



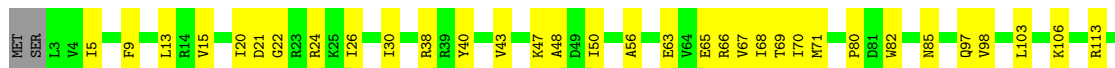
- Molecule 58: 40S ribosomal protein S16



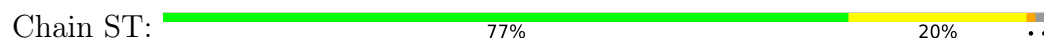
- Molecule 59: 40S ribosomal protein S17



- Molecule 60: 40S ribosomal protein S18



- Molecule 61: Small ribosomal subunit protein eS19



- Molecule 62: 40S ribosomal protein S20



- Molecule 63: 40S ribosomal protein S21

Chain SV:  65% 35%



- Molecule 64: 40S ribosomal protein S15a

Chain SW:  75% 24%



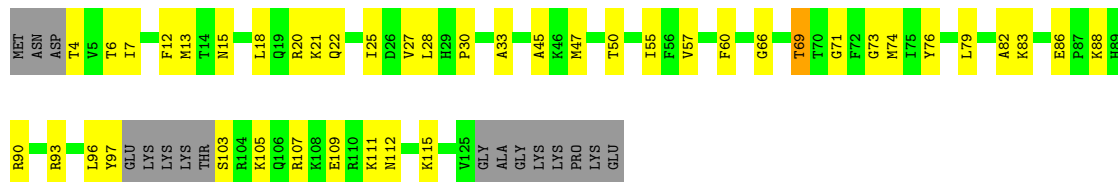
- Molecule 65: 40S ribosomal protein S23

Chain SX:  78% 20%

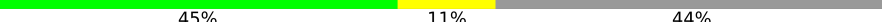


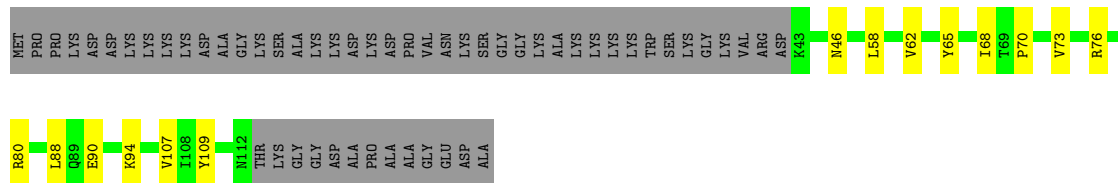
- Molecule 66: 40S ribosomal protein S24

Chain SY:  56% 32% 12%



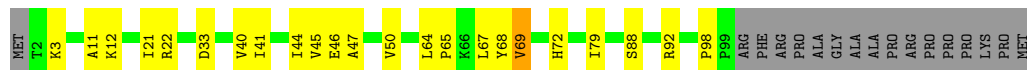
- Molecule 67: Small ribosomal subunit protein eS25

Chain SZ:  45% 11% 44%



- Molecule 68: 40S ribosomal protein S26

Chain Sa:  65% 19% 15%



- Molecule 69: 40S ribosomal protein S27

- Molecule 70: 40S ribosomal protein S28

Chain Sc: 

- Molecule 71: 40S ribosomal protein S29

Chain Sd:  64% 16% 20%

Amino Acid	Chain Sd
MET	0.00
GLY	0.00
HIS	0.00
GLN	0.00
GLU	0.00
LEU	0.00
TTR	0.00
TRP	0.00
SER	0.00
HIS	0.00
P11	0.00
R22	0.00
V23	0.00
C24	0.00
S25	0.00
N26	0.00
L30	0.00
L36	0.00
M37	0.00
M38	0.00
F43	0.00
I50	0.00
G51	0.00
F52	0.00
L55	0.00
ASP	0.00

- Molecule 72: FAU ubiquitin like and ribosomal protein S30 fusion

Chain Se: 

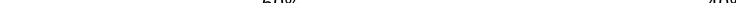


Amino Acid	Count	Category
THR	1	Green
PHE	1	Green
GLY	1	Green
LYS	1	Green
LYS	1	Green
LYS	1	Green
G54	1	Green
N58	1	Yellow
SER	1	Yellow
MET	1	Grey
GLN	1	Grey
LEU	1	Grey
PHE	1	Grey
VAL	1	Grey
ARG	1	Grey
ALA	1	Grey
GLU	1	Grey
LEU	1	Grey
HIS	1	Grey
THR	1	Grey
PHE	1	Grey
GLU	1	Grey
VAL	1	Grey
THR	1	Grey
GLY	1	Grey
GLN	1	Grey
THR	1	Grey
GLU	1	Grey
VAL	1	Grey
ALA	1	Grey
GLN	1	Grey
ILE	1	Grey
LYS	1	Grey
ALA	1	Grey
LEU	1	Grey
THR	1	Grey
THR	1	Grey
LEU	1	Grey
GLU	1	Grey
VAL	1	Grey
ALA	1	Grey
GLY	1	Grey
ARG	1	Grey
MET	1	Grey
LEU	1	Grey
GLY	1	Grey
GLY	1	Grey
LYS	1	Grey
VAL	1	Grey
HIS	1	Grey
G4	1	Yellow
R8	1	Yellow
V12	1	Yellow
Q15	1	Yellow
K26	1	Orange
K27	1	Orange
M36	1	Yellow
V43	1	Green
ASN	1	Grey
VAL	1	Grey
VAL	1	Grey
VAL	1	Grey
THR	1	Grey

- Molecule 73: RS8 HUMAN Small ribosomal subunit protein eS8

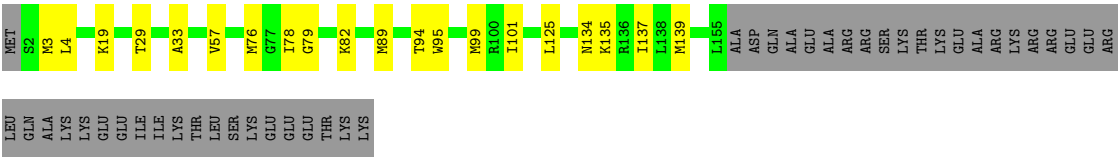
[illegible]

- Molecule 74: 60S ribosomal protein L41

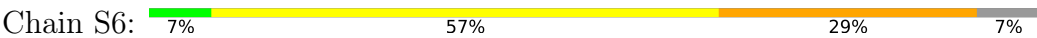
Chain Ln: 



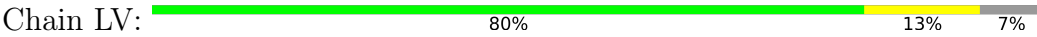
● Molecule 75: 60S ribosomal protein L19



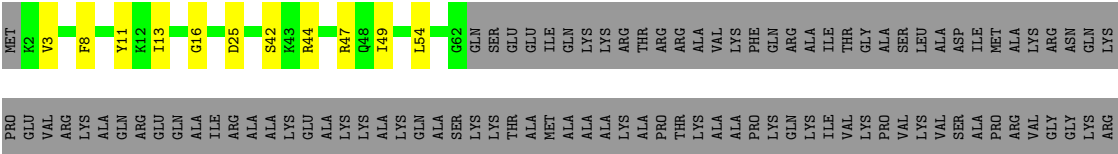
● Molecule 76: E-site tRNA



● Molecule 77: 60S ribosomal protein L23



● Molecule 78: 60S ribosomal protein L24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	178121	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 ($e^-/\text{\AA}^2$)	37.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.190	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.005	Depositor
Map size ($\text{\AA}$)	395.52, 395.52, 395.52	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.824, 0.824, 0.824	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 4AC, OMC, 6MZ, PSU, OMG, A2M, MA6, 1MA, 5MC, K, UR3, NA, UY1, ZN, V5N, HIC, G7M, NMM, MG, OMU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	L5	0.17	2/70852 (0.0%)	0.31	0/110442
2	L7	0.13	0/2836	0.27	0/4421
3	L8	0.16	0/3361	0.28	0/5233
4	LC	0.12	0/2815	0.30	0/3790
5	LD	0.12	0/2325	0.27	0/3124
6	LE	0.11	0/1707	0.26	0/2293
7	LF	0.13	0/1804	0.31	0/2415
8	LG	0.12	0/1557	0.29	0/2128
9	LJ	0.12	0/325	0.32	0/430
10	LM	0.14	0/1096	0.30	0/1470
11	LN	0.13	0/1746	0.32	0/2338
12	LO	0.14	0/1607	0.31	0/2162
13	LP	0.12	0/1237	0.33	0/1663
14	LQ	0.13	0/1497	0.31	0/2008
15	LT	0.11	0/1193	0.28	0/1599
16	LU	0.12	0/627	0.37	1/856 (0.1%)
17	LX	0.10	0/919	0.28	0/1247
18	LY	0.11	0/1015	0.28	0/1364
19	LZ	0.11	0/1064	0.23	0/1434
20	La	0.14	0/1131	0.29	0/1513
21	Lb	0.12	0/622	0.28	0/838
22	Lc	0.12	0/658	0.29	0/893
23	Ld	0.13	0/782	0.31	0/1059
24	Le	0.12	0/1006	0.28	0/1354
25	Lf	0.12	0/849	0.29	0/1143
26	Lg	0.13	0/775	0.30	0/1040
27	Lh	0.11	0/938	0.26	0/1255
28	Li	0.11	0/702	0.27	0/943
29	Lj	0.13	0/702	0.31	0/932
30	Lk	0.14	0/451	0.31	0/611
31	Ll	0.13	0/410	0.29	0/548

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Lm	0.11	0/367	0.28	0/492
33	Lo	0.12	0/735	0.29	0/978
34	Lp	0.13	0/651	0.31	0/873
35	Lr	0.12	0/946	0.30	0/1273
36	LA	0.13	0/1831	0.34	0/2474
37	LB	0.12	0/3003	0.31	0/4056
38	LH	0.12	0/1329	0.28	0/1806
39	LI	0.11	0/1510	0.29	0/2041
40	LL	0.11	0/1449	0.29	0/1963
41	LS	0.13	0/1413	0.29	0/1901
42	S2	0.17	2/34033 (0.0%)	0.28	0/52999
43	SA	0.10	0/1603	0.26	0/2186
44	SB	0.10	0/1550	0.28	0/2090
45	SC	0.12	0/1580	0.30	0/2152
46	SD	0.09	0/1385	0.26	0/1893
47	SE	0.10	0/1982	0.27	0/2688
48	SF	0.10	0/1339	0.29	1/1813 (0.1%)
49	SG	0.10	0/1322	0.26	0/1787
50	SH	0.11	0/1034	0.26	0/1403
51	SI	0.11	0/1309	0.29	0/1768
52	SJ	0.10	0/1346	0.25	0/1826
53	SK	0.10	0/672	0.27	0/919
54	SL	0.11	0/1029	0.29	0/1390
55	SN	0.13	0/1101	0.29	0/1497
56	SO	0.24	0/903	0.39	0/1215
57	SP	0.08	0/851	0.23	0/1151
58	SQ	0.11	0/1082	0.29	0/1455
59	SR	0.11	0/846	0.28	0/1150
60	SS	0.09	0/1075	0.25	0/1455
61	ST	0.08	0/1061	0.22	0/1431
62	SU	0.09	0/615	0.27	0/832
63	SV	0.10	0/629	0.29	0/844
64	SW	0.12	0/1037	0.28	0/1390
65	SX	0.10	0/1077	0.26	0/1442
66	SY	0.10	0/950	0.26	0/1267
67	SZ	0.09	0/524	0.24	0/715
68	Sa	0.10	0/753	0.24	0/1016
69	Sb	0.10	0/470	0.26	0/629
70	Sc	0.09	0/371	0.22	0/500
71	Sd	0.09	0/362	0.22	0/480
72	Se	0.09	0/343	0.34	0/451
73	Sg	0.10	0/2105	0.29	0/2874
74	Ln	0.15	0/200	0.31	0/261

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	LR	0.12	0/1216	0.26	0/1623
76	S6	0.13	0/313	0.30	0/484
77	LV	0.11	0/957	0.30	0/1293
78	LW	0.11	0/490	0.26	0/662
All	All	0.15	4/191358 (0.0%)	0.30	2/281434 (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
56	SO	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S2	576	A2M	O3'-P	5.22	1.61	1.56
1	L5	1322	A2M	O3'-P	5.13	1.61	1.56
42	S2	484	A2M	O3'-P	5.04	1.61	1.56
1	L5	3771	A2M	O3'-P	5.04	1.61	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	SF	43	GLU	CB-CA-C	-5.28	110.05	117.23
16	LU	33	ILE	N-CA-C	-5.09	108.33	113.47

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
56	SO	141	ARG	Sidechain
56	SO	142	ARG	Sidechain

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	L5	65849	0	33336	1217	0
2	L7	2538	0	1286	33	0
3	L8	3094	0	1572	62	0
4	LC	2761	0	2891	48	0
5	LD	2281	0	2251	57	0
6	LE	1675	0	1807	51	0
7	LF	1770	0	1831	29	0
8	LG	1527	0	1467	28	0
9	LJ	321	0	323	10	0
10	LM	1074	0	1110	30	0
11	LN	1701	0	1749	27	0
12	LO	1575	0	1658	32	0
13	LP	1211	0	1229	23	0
14	LQ	1473	0	1543	23	0
15	LT	1168	0	1205	15	0
16	LU	619	0	522	37	0
17	LX	902	0	926	11	0
18	LY	998	0	1022	21	0
19	LZ	1041	0	1043	23	0
20	La	1116	0	1130	7	0
21	Lb	610	0	558	14	0
22	Lc	648	0	623	14	0
23	Ld	769	0	787	18	0
24	Le	988	0	1020	13	0
25	Lf	830	0	842	7	0
26	Lg	765	0	793	11	0
27	Lh	930	0	972	14	0
28	Li	692	0	679	25	0
29	Lj	687	0	695	10	0
30	Lk	446	0	406	12	0
31	Ll	400	0	404	17	0
32	Lm	361	0	347	5	0
33	Lo	723	0	741	11	0
34	Lp	641	0	650	20	0
35	Lr	933	0	955	10	0
36	LA	1794	0	1784	30	0
37	LB	2950	0	2880	51	0
38	LH	1312	0	1268	32	0
39	LI	1472	0	1380	42	0
40	LL	1422	0	1402	18	0
41	LS	1376	0	1375	27	0
42	S2	32164	13	16296	721	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	SA	1568	0	1562	47	0
44	SB	1525	0	1498	47	0
45	SC	1545	0	1540	28	0
46	SD	1364	0	1248	46	0
47	SE	1940	0	1951	41	0
48	SF	1319	0	1295	37	0
49	SG	1307	0	1250	43	0
50	SH	1022	0	951	36	0
51	SI	1284	0	1232	22	0
52	SJ	1321	0	1287	19	0
53	SK	652	0	574	18	0
54	SL	1010	0	977	19	0
55	SN	1077	0	1070	25	0
56	SO	892	0	888	19	0
57	SP	835	0	802	6	0
58	SQ	1065	0	1095	40	0
59	SR	833	0	793	30	0
60	SS	1057	0	1059	26	0
61	ST	1055	0	1034	24	0
62	SU	609	0	604	17	0
63	SV	622	0	609	28	0
64	SW	1020	0	1054	28	0
65	SX	1060	0	1106	22	0
66	SY	934	0	970	33	0
67	SZ	518	0	522	11	0
68	Sa	740	0	764	22	0
69	Sb	463	0	466	14	0
70	Sc	370	0	364	5	0
71	Sd	356	0	344	6	0
72	Se	341	0	360	9	0
73	Sg	2055	0	1923	63	0
74	Ln	199	0	203	15	0
75	LR	1200	0	1253	17	0
76	S6	281	0	145	17	0
77	LV	943	0	957	16	0
78	LW	477	0	440	10	0
79	L5	142	0	0	0	0
79	L7	2	0	0	0	0
79	L8	3	0	0	0	0
79	LI	1	0	0	0	0
79	LN	1	0	0	0	0
79	LP	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	LV	1	0	0	0	0
79	S2	25	0	0	0	0
80	L5	24	0	0	0	0
80	L7	1	0	0	0	0
80	LA	2	0	0	0	0
80	LH	1	0	0	0	0
80	LI	1	0	0	0	0
80	Lf	1	0	0	0	0
80	Lo	1	0	0	0	0
80	S2	3	0	0	0	0
80	SF	1	0	0	0	0
80	SL	1	0	0	0	0
80	SO	1	0	0	0	0
81	L5	12	0	0	0	0
81	S2	1	0	0	0	0
82	Lg	1	0	0	0	0
82	Lj	1	0	0	0	0
82	Lm	1	0	0	0	0
82	Lo	1	0	0	0	0
82	Lp	1	0	0	0	0
82	Sa	1	0	0	0	0
82	Sd	1	0	0	0	0
83	L5	2093	0	0	13	0
83	L7	51	0	0	0	0
83	L8	135	0	0	1	0
83	LA	75	0	0	0	0
83	LB	70	0	0	0	0
83	LC	85	0	0	0	0
83	LD	15	0	0	0	0
83	LE	10	0	0	0	0
83	LF	42	0	0	0	0
83	LG	10	0	0	1	0
83	LH	7	0	0	0	0
83	LI	6	0	0	0	0
83	LL	32	0	0	0	0
83	LM	2	0	0	0	0
83	LN	69	0	0	3	0
83	LO	34	0	0	0	0
83	LP	33	0	0	0	0
83	LQ	59	0	0	1	0
83	LR	8	0	0	0	0
83	LS	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	LT	26	0	0	0	0
83	LV	18	0	0	1	0
83	LW	2	0	0	0	0
83	LX	7	0	0	0	0
83	LY	14	0	0	0	0
83	LZ	4	0	0	1	0
83	La	43	0	0	2	0
83	Lb	13	0	0	0	0
83	Lc	2	0	0	0	0
83	Ld	9	0	0	0	0
83	Le	41	0	0	2	0
83	Lf	20	0	0	0	0
83	Lg	22	0	0	0	0
83	Lh	5	0	0	0	0
83	Li	7	0	0	0	0
83	Lj	21	0	0	0	0
83	Lk	1	0	0	0	0
83	Ll	8	0	0	2	0
83	Lm	2	0	0	0	0
83	Lo	11	0	0	0	0
83	Lp	12	0	0	0	0
83	Lr	19	0	0	1	0
83	S2	29	0	0	0	0
83	S6	2	0	0	0	0
83	SS	2	0	0	0	0
83	Sa	2	0	0	0	0
83	Sb	1	0	0	0	0
All	All	185883	13	130948	3415	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 11.

The worst 5 of 3415 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)
76:S6:74:A:H2'	76:S6:75:C:H5''	1.39	1.02
42:S2:1816:G:H2'	42:S2:1817:G:H5''	1.38	1.01
73:Sg:212:LYS:HA	73:Sg:235:ILE:HG23	1.42	0.97
6:LE:68:MET:HA	6:LE:68:MET:HE3	1.46	0.97
42:S2:1816:G:C2'	42:S2:1817:G:H5''	1.97	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LC	350/427 (82%)	345 (99%)	5 (1%)	0	100	100
5	LD	281/297 (95%)	276 (98%)	5 (2%)	0	100	100
6	LE	204/288 (71%)	199 (98%)	5 (2%)	0	100	100
7	LF	216/248 (87%)	209 (97%)	7 (3%)	0	100	100
8	LG	203/266 (76%)	197 (97%)	6 (3%)	0	100	100
9	LJ	39/178 (22%)	39 (100%)	0	0	100	100
10	LM	130/215 (60%)	127 (98%)	3 (2%)	0	100	100
11	LN	201/204 (98%)	198 (98%)	3 (2%)	0	100	100
12	LO	196/203 (97%)	195 (100%)	1 (0%)	0	100	100
13	LP	150/184 (82%)	148 (99%)	2 (1%)	0	100	100
14	LQ	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
15	LT	144/160 (90%)	142 (99%)	2 (1%)	0	100	100
16	LU	91/128 (71%)	83 (91%)	8 (9%)	0	100	100
17	LX	115/156 (74%)	113 (98%)	2 (2%)	0	100	100
18	LY	126/145 (87%)	122 (97%)	4 (3%)	0	100	100
19	LZ	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
20	La	140/148 (95%)	132 (94%)	7 (5%)	1 (1%)	18	19
21	Lb	80/159 (50%)	79 (99%)	1 (1%)	0	100	100
22	Lc	87/115 (76%)	83 (95%)	4 (5%)	0	100	100
23	Ld	93/125 (74%)	92 (99%)	1 (1%)	0	100	100
24	Le	124/135 (92%)	122 (98%)	2 (2%)	0	100	100
25	Lf	105/110 (96%)	105 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Lg	99/117 (85%)	96 (97%)	3 (3%)	0	100	100
27	Lh	119/123 (97%)	118 (99%)	1 (1%)	0	100	100
28	Li	90/105 (86%)	88 (98%)	2 (2%)	0	100	100
29	Lj	84/97 (87%)	84 (100%)	0	0	100	100
30	Lk	60/70 (86%)	56 (93%)	4 (7%)	0	100	100
31	Ll	47/51 (92%)	46 (98%)	1 (2%)	0	100	100
32	Lm	46/128 (36%)	46 (100%)	0	0	100	100
33	Lo	91/106 (86%)	87 (96%)	4 (4%)	0	100	100
34	Lp	85/92 (92%)	80 (94%)	5 (6%)	0	100	100
35	Lr	116/137 (85%)	116 (100%)	0	0	100	100
36	LA	243/257 (95%)	228 (94%)	15 (6%)	0	100	100
37	LB	386/403 (96%)	372 (96%)	14 (4%)	0	100	100
38	LH	174/192 (91%)	173 (99%)	1 (1%)	0	100	100
39	LI	191/214 (89%)	186 (97%)	5 (3%)	0	100	100
40	LL	186/211 (88%)	181 (97%)	5 (3%)	0	100	100
41	LS	166/176 (94%)	164 (99%)	2 (1%)	0	100	100
43	SA	203/295 (69%)	198 (98%)	5 (2%)	0	100	100
44	SB	197/264 (75%)	192 (98%)	5 (2%)	0	100	100
45	SC	210/293 (72%)	202 (96%)	8 (4%)	0	100	100
46	SD	202/243 (83%)	198 (98%)	4 (2%)	0	100	100
47	SE	255/263 (97%)	250 (98%)	5 (2%)	0	100	100
48	SF	174/204 (85%)	168 (97%)	6 (3%)	0	100	100
49	SG	171/249 (69%)	168 (98%)	3 (2%)	0	100	100
50	SH	132/194 (68%)	129 (98%)	3 (2%)	0	100	100
51	SI	165/208 (79%)	158 (96%)	7 (4%)	0	100	100
52	SJ	176/194 (91%)	171 (97%)	5 (3%)	0	100	100
53	SK	88/165 (53%)	84 (96%)	4 (4%)	0	100	100
54	SL	128/158 (81%)	124 (97%)	4 (3%)	0	100	100
55	SN	140/151 (93%)	132 (94%)	8 (6%)	0	100	100
56	SO	120/151 (80%)	117 (98%)	3 (2%)	0	100	100
57	SP	110/145 (76%)	110 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	SQ	138/146 (94%)	132 (96%)	6 (4%)	0	100	100
59	SR	113/135 (84%)	109 (96%)	4 (4%)	0	100	100
60	SS	137/152 (90%)	134 (98%)	3 (2%)	0	100	100
61	ST	139/145 (96%)	136 (98%)	3 (2%)	0	100	100
62	SU	79/119 (66%)	77 (98%)	2 (2%)	0	100	100
63	SV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
64	SW	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
65	SX	137/143 (96%)	135 (98%)	2 (2%)	0	100	100
66	SY	113/133 (85%)	113 (100%)	0	0	100	100
67	SZ	68/125 (54%)	67 (98%)	1 (2%)	0	100	100
68	Sa	96/115 (84%)	93 (97%)	3 (3%)	0	100	100
69	Sb	53/84 (63%)	52 (98%)	1 (2%)	0	100	100
70	Sc	49/69 (71%)	49 (100%)	0	0	100	100
71	Sd	43/56 (77%)	42 (98%)	1 (2%)	0	100	100
72	Se	41/98 (42%)	40 (98%)	1 (2%)	0	100	100
73	Sg	266/310 (86%)	253 (95%)	13 (5%)	0	100	100
74	Ln	23/25 (92%)	23 (100%)	0	0	100	100
75	LR	152/196 (78%)	150 (99%)	2 (1%)	0	100	100
77	LV	129/140 (92%)	128 (99%)	1 (1%)	0	100	100
78	LW	59/157 (38%)	57 (97%)	2 (3%)	0	100	100
All	All	10090/12432 (81%)	9836 (98%)	253 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	La	15	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LC	285/348 (82%)	280 (98%)	5 (2%)	51	68
5	LD	230/250 (92%)	225 (98%)	5 (2%)	45	61
6	LE	182/252 (72%)	179 (98%)	3 (2%)	55	71
7	LF	178/215 (83%)	176 (99%)	2 (1%)	65	79
8	LG	140/223 (63%)	137 (98%)	3 (2%)	47	63
9	LJ	29/149 (20%)	29 (100%)	0	100	100
10	LM	109/161 (68%)	106 (97%)	3 (3%)	38	52
11	LN	171/172 (99%)	170 (99%)	1 (1%)	78	89
12	LO	158/174 (91%)	154 (98%)	4 (2%)	42	56
13	LP	127/163 (78%)	126 (99%)	1 (1%)	73	85
14	LQ	155/165 (94%)	154 (99%)	1 (1%)	78	89
15	LT	120/140 (86%)	119 (99%)	1 (1%)	73	85
16	LU	44/115 (38%)	42 (96%)	2 (4%)	24	33
17	LX	91/133 (68%)	91 (100%)	0	100	100
18	LY	102/135 (76%)	98 (96%)	4 (4%)	28	39
19	LZ	101/118 (86%)	99 (98%)	2 (2%)	48	64
20	La	109/120 (91%)	109 (100%)	0	100	100
21	Lb	51/126 (40%)	50 (98%)	1 (2%)	48	64
22	Lc	62/97 (64%)	61 (98%)	1 (2%)	55	71
23	Ld	78/110 (71%)	78 (100%)	0	100	100
24	Le	101/121 (84%)	101 (100%)	0	100	100
25	Lf	79/89 (89%)	79 (100%)	0	100	100
26	Lg	77/100 (77%)	77 (100%)	0	100	100
27	Lh	89/110 (81%)	88 (99%)	1 (1%)	65	79
28	Li	62/89 (70%)	61 (98%)	1 (2%)	55	71
29	Lj	68/80 (85%)	68 (100%)	0	100	100
30	Lk	37/65 (57%)	37 (100%)	0	100	100
31	Ll	39/48 (81%)	39 (100%)	0	100	100
32	Lm	36/116 (31%)	36 (100%)	0	100	100
33	Lo	73/94 (78%)	70 (96%)	3 (4%)	27	37
34	Lp	63/75 (84%)	63 (100%)	0	100	100
35	Lr	97/121 (80%)	95 (98%)	2 (2%)	47	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	LA	167/199 (84%)	166 (99%)	1 (1%)	78	89
37	LB	284/348 (82%)	283 (100%)	1 (0%)	84	92
38	LH	127/171 (74%)	124 (98%)	3 (2%)	43	58
39	LI	139/182 (76%)	136 (98%)	3 (2%)	45	61
40	LL	129/177 (73%)	129 (100%)	0	100	100
41	LS	143/157 (91%)	141 (99%)	2 (1%)	59	75
43	SA	159/243 (65%)	156 (98%)	3 (2%)	50	66
44	SB	153/231 (66%)	150 (98%)	3 (2%)	48	64
45	SC	152/225 (68%)	152 (100%)	0	100	100
46	SD	109/202 (54%)	107 (98%)	2 (2%)	51	68
47	SE	194/225 (86%)	190 (98%)	4 (2%)	47	63
48	SF	125/170 (74%)	124 (99%)	1 (1%)	73	85
49	SG	113/218 (52%)	113 (100%)	0	100	100
50	SH	89/174 (51%)	86 (97%)	3 (3%)	32	44
51	SI	120/180 (67%)	118 (98%)	2 (2%)	53	69
52	SJ	115/168 (68%)	115 (100%)	0	100	100
53	SK	51/136 (38%)	49 (96%)	2 (4%)	28	39
54	SL	101/142 (71%)	100 (99%)	1 (1%)	68	81
55	SN	104/131 (79%)	102 (98%)	2 (2%)	50	66
56	SO	87/119 (73%)	83 (95%)	4 (5%)	24	32
57	SP	76/130 (58%)	76 (100%)	0	100	100
58	SQ	103/121 (85%)	101 (98%)	2 (2%)	50	66
59	SR	76/122 (62%)	71 (93%)	5 (7%)	15	18
60	SS	98/132 (74%)	96 (98%)	2 (2%)	48	64
61	ST	97/114 (85%)	93 (96%)	4 (4%)	27	37
62	SU	61/107 (57%)	60 (98%)	1 (2%)	55	71
63	SV	63/67 (94%)	61 (97%)	2 (3%)	34	47
64	SW	109/113 (96%)	108 (99%)	1 (1%)	70	84
65	SX	106/115 (92%)	105 (99%)	1 (1%)	70	84
66	SY	95/115 (83%)	93 (98%)	2 (2%)	47	63
67	SZ	52/103 (50%)	52 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	Sa	76/98 (78%)	75 (99%)	1 (1%)	61	76
69	Sb	49/76 (64%)	47 (96%)	2 (4%)	27	37
70	Sc	35/62 (56%)	35 (100%)	0	100	100
71	Sd	36/49 (74%)	36 (100%)	0	100	100
72	Se	31/79 (39%)	30 (97%)	1 (3%)	34	47
73	Sg	206/239 (86%)	202 (98%)	4 (2%)	50	66
74	Ln	15/24 (62%)	15 (100%)	0	100	100
75	LR	116/175 (66%)	113 (97%)	3 (3%)	40	55
77	LV	91/107 (85%)	91 (100%)	0	100	100
78	LW	45/126 (36%)	44 (98%)	1 (2%)	45	61
All	All	7640/10546 (72%)	7525 (98%)	115 (2%)	55	73

5 of 115 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	SA	152	SER
73	Sg	287	THR
50	SH	172	THR
73	Sg	148	SER
64	SW	74	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
65	SX	16	HIS
65	SX	92	ASN
73	Sg	117	ASN
22	Lc	73	HIS
21	Lb	101	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3014/5054 (59%)	438 (14%)	9 (0%)
2	L7	118/121 (97%)	10 (8%)	0
3	L8	142/156 (91%)	16 (11%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
42	S2	1480/1869 (79%)	221 (14%)	2 (0%)
76	S6	11/14 (78%)	5 (45%)	0
All	All	4765/7214 (66%)	690 (14%)	11 (0%)

5 of 690 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	3	C
1	L5	39	A
1	L5	42	A
1	L5	48	G
1	L5	56	A

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	4364	A
1	L5	4685	U
42	S2	1520	G
42	S2	1344	A
1	L5	2665	G

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

205 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	$\# Z > 2$
42	OMG	S2	1447	42	23,26,27	0.48	0	33,38,41	0.48	0
1	5MC	L5	3768	1,81	18,22,23	0.62	0	26,32,35	0.52	0
42	OMU	S2	1288	42	19,22,23	3.30	8 (42%)	26,31,34	1.67	4 (15%)
1	PSU	L5	4428	1	18,21,22	1.09	1 (5%)	22,30,33	1.84	6 (27%)
42	PSU	S2	1136	42	18,21,22	1.11	1 (5%)	22,30,33	1.78	4 (18%)
1	A2M	L5	1322	1	22,25,26	4.13	12 (54%)	31,36,39	3.24	12 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
42	MA6	S2	1851	42	23,26,27	1.52	3 (13%)	34,38,41	3.72	12 (35%)
1	PSU	L5	1777	1	18,21,22	1.08	1 (5%)	22,30,33	1.77	5 (22%)
42	OMU	S2	121	42	19,22,23	3.21	8 (42%)	26,31,34	1.62	5 (19%)
1	OMG	L5	2866	1	23,26,27	0.53	0	33,38,41	0.50	0
1	OMC	L5	2851	1	19,22,23	0.27	0	26,31,34	0.35	0
1	OMC	L5	3794	1	19,22,23	0.32	0	26,31,34	0.37	0
1	PSU	L5	3830	1	18,21,22	1.05	1 (5%)	22,30,33	1.79	4 (18%)
37	HIC	LB	245	37	10,11,12	0.47	0	8,14,16	0.69	0
3	PSU	L8	69	3	18,21,22	1.10	1 (5%)	22,30,33	1.76	5 (22%)
1	PSU	L5	3906	79,1	18,21,22	1.12	1 (5%)	22,30,33	1.61	3 (13%)
42	OMC	S2	1391	42	19,22,23	0.28	0	26,31,34	0.45	0
1	PSU	L5	4507	79,1,80	18,21,22	1.13	1 (5%)	22,30,33	1.71	4 (18%)
42	PSU	S2	109	42	18,21,22	1.09	1 (5%)	22,30,33	1.77	4 (18%)
42	PSU	S2	822	42	18,21,22	1.09	1 (5%)	22,30,33	1.74	5 (22%)
42	OMG	S2	1328	42	23,26,27	0.50	0	33,38,41	0.47	0
42	PSU	S2	681	42	18,21,22	1.08	1 (5%)	22,30,33	1.71	5 (22%)
42	OMG	S2	867	42	23,26,27	0.48	0	33,38,41	0.49	0
1	OMU	L5	4292	1	19,22,23	3.24	8 (42%)	26,31,34	1.63	5 (19%)
1	A2M	L5	2391	1	22,25,26	4.08	12 (54%)	31,36,39	3.26	13 (41%)
42	A2M	S2	166	42	22,25,26	4.16	12 (54%)	31,36,39	3.46	14 (45%)
42	PSU	S2	801	42	18,21,22	1.10	1 (5%)	22,30,33	1.77	5 (22%)
1	PSU	L5	4565	1	18,21,22	1.06	1 (5%)	22,30,33	1.75	5 (22%)
42	PSU	S2	863	42	18,21,22	1.07	1 (5%)	22,30,33	1.77	4 (18%)
1	OMG	L5	3730	1	23,26,27	0.51	0	33,38,41	0.53	0
42	PSU	S2	667	42	18,21,22	1.09	1 (5%)	22,30,33	1.68	3 (13%)
1	A2M	L5	1319	1	22,25,26	4.10	12 (54%)	31,36,39	3.23	11 (35%)
1	A2M	L5	1520	1	22,25,26	4.11	12 (54%)	31,36,39	3.37	10 (32%)
1	OMG	L5	3885	1	23,26,27	0.53	0	33,38,41	0.60	0
1	PSU	L5	4347	1	18,21,22	1.08	1 (5%)	22,30,33	1.75	4 (18%)
1	PSU	L5	4659	1	18,21,22	1.08	1 (5%)	22,30,33	1.70	4 (18%)
1	OMC	L5	4522	1	19,22,23	0.29	0	26,31,34	0.51	0
1	A2M	L5	3816	1	22,25,26	4.12	12 (54%)	31,36,39	3.30	12 (38%)
42	A2M	S2	1678	42	22,25,26	4.12	12 (54%)	31,36,39	3.44	14 (45%)
1	PSU	L5	4995	1	18,21,22	1.08	1 (5%)	22,30,33	1.75	4 (18%)
42	OMC	S2	174	42	19,22,23	0.28	0	26,31,34	0.49	0
42	PSU	S2	1056	42	18,21,22	1.10	1 (5%)	22,30,33	1.72	4 (18%)
42	OMG	S2	509	42	23,26,27	0.50	0	33,38,41	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
42	A2M	S2	1383	42	22,25,26	4.16	12 (54%)	31,36,39	3.43	14 (45%)
1	OMC	L5	2355	1	19,22,23	0.29	0	26,31,34	0.44	0
1	PSU	L5	3808	1	18,21,22	1.10	1 (5%)	22,30,33	1.77	4 (18%)
1	A2M	L5	1530	79,1	22,25,26	4.12	12 (54%)	31,36,39	3.25	12 (38%)
20	V5N	La	39	20	9,11,12	0.72	0	9,14,16	1.09	0
42	A2M	S2	512	42	22,25,26	4.14	12 (54%)	31,36,39	3.40	13 (41%)
42	PSU	S2	1692	42	18,21,22	1.05	1 (5%)	22,30,33	1.74	4 (18%)
42	PSU	S2	1244	42	18,21,22	1.06	1 (5%)	22,30,33	1.77	5 (22%)
1	A2M	L5	3771	1	22,25,26	4.09	11 (50%)	31,36,39	3.32	14 (45%)
42	OMU	S2	172	42	19,22,23	3.23	8 (42%)	26,31,34	1.70	5 (19%)
1	OMC	L5	3855	1	19,22,23	0.30	0	26,31,34	0.47	0
42	4AC	S2	1337	42	21,24,25	3.45	9 (42%)	29,34,37	1.34	4 (13%)
1	A2M	L5	3853	1	22,25,26	4.13	12 (54%)	31,36,39	3.33	11 (35%)
1	PSU	L5	4622	1	18,21,22	1.06	1 (5%)	22,30,33	1.85	5 (22%)
42	A2M	S2	576	42	22,25,26	4.14	12 (54%)	31,36,39	3.32	12 (38%)
1	OMU	L5	4213	1	19,22,23	3.27	8 (42%)	26,31,34	1.74	5 (19%)
1	PSU	L5	4538	1	18,21,22	1.06	1 (5%)	22,30,33	1.78	4 (18%)
42	A2M	S2	590	42	22,25,26	4.13	11 (50%)	31,36,39	3.51	13 (41%)
1	PSU	L5	4285	1	18,21,22	1.06	1 (5%)	22,30,33	1.76	4 (18%)
42	G7M	S2	1639	42	23,26,27	2.87	10 (43%)	35,39,42	2.15	10 (28%)
42	PSU	S2	1004	42	18,21,22	1.10	1 (5%)	22,30,33	1.68	4 (18%)
42	PSU	S2	1347	42	18,21,22	1.06	1 (5%)	22,30,33	1.78	5 (22%)
1	PSU	L5	3701	1	18,21,22	1.04	1 (5%)	22,30,33	1.75	5 (22%)
42	PSU	S2	649	42	18,21,22	1.09	1 (5%)	22,30,33	1.74	4 (18%)
1	A2M	L5	4509	79,1	22,25,26	4.10	12 (54%)	31,36,39	3.33	13 (41%)
1	PSU	L5	4614	1	18,21,22	1.12	1 (5%)	22,30,33	1.76	4 (18%)
42	PSU	S2	609	42	18,21,22	1.07	1 (5%)	22,30,33	1.74	4 (18%)
1	PSU	L5	1778	1	18,21,22	1.08	1 (5%)	22,30,33	1.70	4 (18%)
1	A2M	L5	2777	1	22,25,26	4.10	12 (54%)	31,36,39	3.07	11 (35%)
1	PSU	L5	3870	1	18,21,22	1.13	1 (5%)	22,30,33	1.70	4 (18%)
42	PSU	S2	572	42	18,21,22	1.07	1 (5%)	22,30,33	1.73	5 (22%)
1	A2M	L5	4557	1	22,25,26	4.12	12 (54%)	31,36,39	3.39	12 (38%)
42	PSU	S2	1177	42	18,21,22	1.06	1 (5%)	22,30,33	1.74	3 (13%)
1	PSU	L5	3623	1	18,21,22	1.04	1 (5%)	22,30,33	1.72	4 (18%)
42	OMU	S2	116	42	19,22,23	3.23	8 (42%)	26,31,34	1.73	5 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	A2M	L5	400	1	22,25,26	4.14	12 (54%)	31,36,39	3.32	12 (38%)
1	PSU	L5	1856	1	18,21,22	1.06	1 (5%)	22,30,33	1.77	5 (22%)
1	5MC	L5	4433	1	18,22,23	0.68	0	26,32,35	0.66	0
1	PSU	L5	4675	1	18,21,22	1.09	1 (5%)	22,30,33	1.78	5 (22%)
42	PSU	S2	105	42	18,21,22	1.08	1 (5%)	22,30,33	1.77	4 (18%)
1	A2M	L5	1867	79,1	22,25,26	4.12	12 (54%)	31,36,39	3.24	13 (41%)
42	PSU	S2	1596	42	18,21,22	1.09	1 (5%)	22,30,33	1.73	5 (22%)
1	A2M	L5	398	1	22,25,26	4.08	11 (50%)	31,36,39	3.33	11 (35%)
1	PSU	L5	4389	1	18,21,22	1.11	1 (5%)	22,30,33	1.67	5 (22%)
42	PSU	S2	218	42	18,21,22	1.05	1 (5%)	22,30,33	1.73	4 (18%)
1	PSU	L5	4339	1	18,21,22	1.04	1 (5%)	22,30,33	1.76	4 (18%)
1	PSU	L5	4518	1	18,21,22	1.06	1 (5%)	22,30,33	1.74	4 (18%)
42	OMC	S2	621	42	19,22,23	0.29	0	26,31,34	0.38	0
1	PSU	L5	1740	1	18,21,22	1.02	1 (5%)	22,30,33	1.76	4 (18%)
42	OMG	S2	601	42	23,26,27	0.50	0	33,38,41	0.45	0
1	UR3	L5	4516	1	19,22,23	2.87	7 (36%)	26,32,35	1.28	2 (7%)
3	PSU	L8	55	3	18,21,22	1.06	1 (5%)	22,30,33	1.72	4 (18%)
1	PSU	L5	4957	1	18,21,22	1.11	1 (5%)	22,30,33	1.78	4 (18%)
42	PSU	S2	1238	42	18,21,22	1.11	1 (5%)	22,30,33	1.84	5 (22%)
1	PSU	L5	1673	1	18,21,22	1.11	2 (11%)	22,30,33	1.82	6 (27%)
42	PSU	S2	119	42	18,21,22	1.09	1 (5%)	22,30,33	1.76	4 (18%)
42	A2M	S2	668	79,42	22,25,26	4.11	12 (54%)	31,36,39	3.22	13 (41%)
1	OMG	L5	4356	1	23,26,27	0.49	0	33,38,41	0.50	0
1	PSU	L5	4555	1	18,21,22	1.11	1 (5%)	22,30,33	1.73	4 (18%)
1	PSU	L5	4298	1	18,21,22	1.04	1 (5%)	22,30,33	1.69	3 (13%)
1	OMC	L5	2814	1	19,22,23	0.29	0	26,31,34	0.37	0
1	PSU	L5	1788	1,80	18,21,22	1.05	1 (5%)	22,30,33	1.70	3 (13%)
1	PSU	L5	4517	1	18,21,22	1.03	1 (5%)	22,30,33	1.83	5 (22%)
1	PSU	L5	4409	1	18,21,22	1.05	1 (5%)	22,30,33	1.79	5 (22%)
42	PSU	S2	34	42	18,21,22	1.07	1 (5%)	22,30,33	1.78	5 (22%)
42	OMC	S2	462	42	19,22,23	0.29	0	26,31,34	0.48	0
42	PSU	S2	651	42	18,21,22	1.07	1 (5%)	22,30,33	1.80	5 (22%)
1	PSU	L5	1578	1	18,21,22	1.07	1 (5%)	22,30,33	1.63	4 (18%)
42	PSU	S2	406	42	18,21,22	1.09	1 (5%)	22,30,33	1.76	4 (18%)
1	OMG	L5	2354	1	23,26,27	0.49	0	33,38,41	0.53	0
42	A2M	S2	99	42	22,25,26	4.11	12 (54%)	31,36,39	3.37	13 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
42	PSU	S2	1045	42	18,21,22	1.06	1 (5%)	22,30,33	1.78	3 (13%)
42	A2M	S2	468	42	22,25,26	4.13	12 (54%)	31,36,39	3.39	13 (41%)
1	PSU	L5	2829	1	18,21,22	1.11	1 (5%)	22,30,33	1.69	4 (18%)
1	OMG	L5	3613	1	23,26,27	0.51	0	33,38,41	0.70	0
1	OMG	L5	1312	1	23,26,27	0.55	0	33,38,41	0.64	0
42	OMU	S2	1804	42	19,22,23	3.26	8 (42%)	26,31,34	1.64	4 (15%)
61	NMM	ST	67	61	9,11,12	0.59	0	6,12,14	2.80	2 (33%)
1	UY1	L5	3804	79,1,80	19,22,23	0.45	0	22,31,34	0.55	0
42	PSU	S2	918	42	18,21,22	1.12	1 (5%)	22,30,33	1.83	6 (27%)
1	6MZ	L5	4206	1	22,25,26	2.54	4 (18%)	30,36,39	2.46	10 (33%)
42	A2M	S2	159	42	22,25,26	4.14	12 (54%)	31,36,39	3.40	12 (38%)
42	OMU	S2	354	42	19,22,23	3.25	8 (42%)	26,31,34	1.72	5 (19%)
1	PSU	L5	4986	1	18,21,22	1.09	1 (5%)	22,30,33	1.77	4 (18%)
1	OMU	L5	4606	1	19,22,23	3.22	8 (42%)	26,31,34	1.57	5 (19%)
1	A2M	L5	3704	1	22,25,26	4.14	11 (50%)	31,36,39	3.29	12 (38%)
42	MA6	S2	1850	42	23,26,27	1.52	4 (17%)	34,38,41	3.61	11 (32%)
1	PSU	L5	3681	1	18,21,22	1.05	1 (5%)	22,30,33	1.73	4 (18%)
1	A2M	L5	2805	1	22,25,26	4.11	12 (54%)	31,36,39	3.28	12 (38%)
42	OMG	S2	644	42	23,26,27	0.50	0	33,38,41	0.48	0
1	PSU	L5	1532	1	18,21,22	1.09	1 (5%)	22,30,33	1.67	4 (18%)
42	PSU	S2	36	42	18,21,22	1.09	1 (5%)	22,30,33	1.73	4 (18%)
1	A2M	L5	4576	1	22,25,26	4.14	11 (50%)	31,36,39	3.28	13 (41%)
1	OMG	L5	1518	1	23,26,27	0.52	0	33,38,41	0.62	0
42	A2M	S2	27	42	22,25,26	4.13	12 (54%)	31,36,39	3.31	13 (41%)
42	OMC	S2	517	42	19,22,23	0.28	0	26,31,34	0.46	0
1	OMC	L5	2341	1	19,22,23	0.28	0	26,31,34	0.38	0
42	PSU	S2	100	42	18,21,22	1.07	1 (5%)	22,30,33	1.76	3 (13%)
42	PSU	S2	1232	42	18,21,22	1.07	1 (5%)	22,30,33	1.80	5 (22%)
42	OMU	S2	1442	79,42	19,22,23	3.28	8 (42%)	26,31,34	1.68	4 (15%)
1	OMU	L5	3911	1	19,22,23	3.22	8 (42%)	26,31,34	1.61	5 (19%)
1	OMU	L5	4484	1	19,22,23	3.21	8 (42%)	26,31,34	1.67	5 (19%)
1	PSU	L5	4457	1	18,21,22	1.13	1 (5%)	22,30,33	1.74	5 (22%)
1	PSU	L5	4486	1	18,21,22	1.08	1 (5%)	22,30,33	1.81	5 (22%)
1	OMG	L5	4609	1	23,26,27	0.52	0	33,38,41	0.62	0
3	OMU	L8	14	3,1	19,22,23	3.24	8 (42%)	26,31,34	1.70	5 (19%)
1	OMG	L5	4182	79,1	23,26,27	0.51	0	33,38,41	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
42	PSU	S2	814	42	18,21,22	1.04	1 (5%)	22,30,33	1.77	4 (18%)
1	PSU	L5	3837	1	18,21,22	1.08	1 (5%)	22,30,33	1.77	4 (18%)
1	1MA	L5	1318	79,1	21,25,26	0.47	0	31,37,40	0.75	0
1	OMG	L5	4604	1	23,26,27	0.52	0	33,38,41	0.55	0
1	OMG	L5	4623	1	23,26,27	0.50	0	33,38,41	0.51	0
1	OMC	L5	3687	1,80	19,22,23	0.25	0	26,31,34	0.47	0
42	PSU	S2	1046	42	18,21,22	1.10	1 (5%)	22,30,33	1.74	4 (18%)
1	OMG	L5	4485	1	23,26,27	0.49	0	33,38,41	0.57	0
42	OMU	S2	428	42	19,22,23	3.27	8 (42%)	26,31,34	1.68	5 (19%)
1	OMU	L5	2405	1	19,22,23	3.22	8 (42%)	26,31,34	1.57	5 (19%)
42	6MZ	S2	1832	79,42,80	22,25,26	2.55	4 (18%)	30,36,39	2.45	10 (33%)
1	PSU	L5	4562	1	18,21,22	1.07	1 (5%)	22,30,33	1.73	4 (18%)
1	PSU	L5	4417	1	18,21,22	1.09	1 (5%)	22,30,33	1.77	4 (18%)
1	OMG	L5	4378	1	23,26,27	0.49	0	33,38,41	0.48	0
3	OMG	L8	75	3	23,26,27	0.49	0	33,38,41	0.52	0
42	OMG	S2	436	42	23,26,27	0.50	0	33,38,41	0.52	0
1	OMC	L5	4442	1	19,22,23	0.27	0	26,31,34	0.39	0
1	PSU	L5	1679	1	18,21,22	1.04	1 (5%)	22,30,33	1.72	3 (13%)
1	OMG	L5	2414	1	23,26,27	0.49	0	33,38,41	0.47	0
1	OMC	L5	3827	1	19,22,23	0.28	0	26,31,34	0.42	0
1	PSU	L5	3839	79,1	18,21,22	1.09	1 (5%)	22,30,33	1.75	4 (18%)
42	UY1	S2	1326	42	19,22,23	0.33	0	22,31,34	0.87	2 (9%)
1	OMC	L5	1336	1	19,22,23	0.29	0	26,31,34	0.44	0
42	PSU	S2	686	42	18,21,22	1.07	1 (5%)	22,30,33	1.75	4 (18%)
1	A2M	L5	3811	1	22,25,26	4.13	12 (54%)	31,36,39	3.29	12 (38%)
1	OMG	L5	4480	1	23,26,27	0.50	0	33,38,41	0.49	0
1	OMG	L5	1621	1,80	23,26,27	0.53	0	33,38,41	0.47	0
1	OMC	L5	2412	79,1	19,22,23	0.30	0	26,31,34	0.40	0
1	OMC	L5	2794	1	19,22,23	0.30	0	26,31,34	0.36	0
42	PSU	S2	93	42	18,21,22	1.09	1 (5%)	22,30,33	1.76	3 (13%)
42	PSU	S2	1625	42	18,21,22	1.10	1 (5%)	22,30,33	1.73	4 (18%)
42	A2M	S2	484	42	22,25,26	4.11	11 (50%)	31,36,39	3.31	11 (35%)
42	A2M	S2	1031	42	22,25,26	4.13	12 (54%)	31,36,39	3.33	13 (41%)
42	4AC	S2	1842	42	21,24,25	3.37	10 (47%)	29,34,37	0.91	2 (6%)
1	A2M	L5	2353	79,1	22,25,26	4.13	12 (54%)	31,36,39	3.21	12 (38%)
1	PSU	L5	3625	1	18,21,22	1.06	1 (5%)	22,30,33	1.63	5 (22%)
42	OMG	S2	1490	42	23,26,27	0.51	0	33,38,41	0.50	0
1	PSU	L5	2622	1	18,21,22	1.08	1 (5%)	22,30,33	1.74	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	L5	4282	1	18,21,22	1.04	1 (5%)	22,30,33	1.68	4 (18%)
1	PSU	L5	4279	1	18,21,22	1.09	1 (5%)	22,30,33	1.69	4 (18%)
1	OMU	L5	2827	1	19,22,23	3.24	8 (42%)	26,31,34	1.68	5 (19%)
1	PSU	L5	1858	1	18,21,22	1.06	1 (5%)	22,30,33	1.85	4 (18%)
1	OMC	L5	1877	79,1	19,22,23	0.25	0	26,31,34	0.62	0
1	A2M	L5	3710	1	22,25,26	4.14	11 (50%)	31,36,39	3.37	12 (38%)
1	OMG	L5	4214	1	23,26,27	0.49	0	33,38,41	0.65	0
42	PSU	S2	1643	42	18,21,22	1.08	1 (5%)	22,30,33	1.71	4 (18%)
1	OMC	L5	3873	1	19,22,23	0.29	0	26,31,34	0.52	0
42	PSU	S2	1445	42	18,21,22	1.07	1 (5%)	22,30,33	1.74	5 (22%)
42	PSU	S2	1174	42	18,21,22	1.08	1 (5%)	22,30,33	1.75	4 (18%)
1	OMG	L5	3778	1	23,26,27	0.50	0	33,38,41	0.48	0
1	PSU	L5	4443	1	18,21,22	1.12	1 (5%)	22,30,33	1.68	5 (22%)
42	OMG	S2	683	42	23,26,27	0.49	0	33,38,41	0.58	0
1	PSU	L5	4958	1	18,21,22	1.08	1 (5%)	22,30,33	1.76	6 (27%)
42	PSU	S2	815	42	18,21,22	1.06	1 (5%)	22,30,33	1.76	3 (13%)
42	OMC	S2	1703	42	19,22,23	0.27	0	26,31,34	0.46	0

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
42	OMG	S2	1447	42	-	3/9/27/28	0/3/3/3
1	5MC	L5	3768	1,81	-	0/7/25/26	0/2/2/2
42	OMU	S2	1288	42	-	1/9/27/28	0/2/2/2
1	PSU	L5	4428	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	1136	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	1322	1	-	1/9/27/28	0/3/3/3
42	MA6	S2	1851	42	-	3/11/29/30	0/3/3/3
1	PSU	L5	1777	1	-	0/7/25/26	0/2/2/2
42	OMU	S2	121	42	-	0/9/27/28	0/2/2/2
1	OMG	L5	2866	1	-	0/9/27/28	0/3/3/3
1	OMC	L5	2851	1	-	0/9/27/28	0/2/2/2
1	OMC	L5	3794	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	3830	1	-	3/7/25/26	0/2/2/2
37	HIC	LB	245	37	-	1/5/6/8	0/1/1/1
3	PSU	L8	69	3	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	L5	3906	79,1	-	0/7/25/26	0/2/2/2
42	OMC	S2	1391	42	-	0/9/27/28	0/2/2/2
1	PSU	L5	4507	79,1,80	-	1/7/25/26	0/2/2/2
42	PSU	S2	109	42	-	0/7/25/26	0/2/2/2
42	PSU	S2	822	42	-	0/7/25/26	0/2/2/2
42	OMG	S2	1328	42	-	2/9/27/28	0/3/3/3
42	PSU	S2	681	42	-	0/7/25/26	0/2/2/2
42	OMG	S2	867	42	-	4/9/27/28	0/3/3/3
1	OMU	L5	4292	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	2391	1	-	0/9/27/28	0/3/3/3
42	A2M	S2	166	42	-	2/9/27/28	0/3/3/3
42	PSU	S2	801	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	4565	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	863	42	-	0/7/25/26	0/2/2/2
1	OMG	L5	3730	1	-	1/9/27/28	0/3/3/3
42	PSU	S2	667	42	-	2/7/25/26	0/2/2/2
1	A2M	L5	1319	1	-	1/9/27/28	0/3/3/3
1	A2M	L5	1520	1	-	1/9/27/28	0/3/3/3
1	OMG	L5	3885	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4347	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4659	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	4522	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	3816	1	-	1/9/27/28	0/3/3/3
42	A2M	S2	1678	42	-	2/9/27/28	0/3/3/3
1	PSU	L5	4995	1	-	0/7/25/26	0/2/2/2
42	OMC	S2	174	42	-	0/9/27/28	0/2/2/2
42	PSU	S2	1056	42	-	0/7/25/26	0/2/2/2
42	OMG	S2	509	42	-	0/9/27/28	0/3/3/3
42	A2M	S2	1383	42	-	2/9/27/28	0/3/3/3
1	OMC	L5	2355	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	3808	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	1530	79,1	-	2/9/27/28	0/3/3/3
20	V5N	La	39	20	-	0/9/10/12	0/1/1/1
42	A2M	S2	512	42	-	3/9/27/28	0/3/3/3
42	PSU	S2	1692	42	-	0/7/25/26	0/2/2/2
42	PSU	S2	1244	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	3771	1	-	1/9/27/28	0/3/3/3
42	OMU	S2	172	42	-	0/9/27/28	0/2/2/2
1	OMC	L5	3855	1	-	0/9/27/28	0/2/2/2
42	4AC	S2	1337	42	-	2/11/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A2M	L5	3853	1	-	4/9/27/28	0/3/3/3
1	PSU	L5	4622	1	-	3/7/25/26	0/2/2/2
42	A2M	S2	576	42	-	2/9/27/28	0/3/3/3
1	OMU	L5	4213	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	4538	1	-	0/7/25/26	0/2/2/2
42	A2M	S2	590	42	-	5/9/27/28	0/3/3/3
1	PSU	L5	4285	1	-	0/7/25/26	0/2/2/2
42	G7M	S2	1639	42	-	2/7/25/26	0/3/3/3
42	PSU	S2	1004	42	-	0/7/25/26	0/2/2/2
42	PSU	S2	1347	42	-	2/7/25/26	0/2/2/2
1	PSU	L5	3701	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	649	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	4509	79,1	-	1/9/27/28	0/3/3/3
1	PSU	L5	4614	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	609	42	-	1/7/25/26	0/2/2/2
1	PSU	L5	1778	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	2777	1	-	3/9/27/28	0/3/3/3
1	PSU	L5	3870	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	572	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	4557	1	-	0/9/27/28	0/3/3/3
42	PSU	S2	1177	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	3623	1	-	0/7/25/26	0/2/2/2
42	OMU	S2	116	42	-	0/9/27/28	0/2/2/2
1	A2M	L5	400	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	1856	1	-	0/7/25/26	0/2/2/2
1	5MC	L5	4433	1	-	3/7/25/26	0/2/2/2
1	PSU	L5	4675	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	105	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	1867	79,1	-	1/9/27/28	0/3/3/3
42	PSU	S2	1596	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	398	1	-	2/9/27/28	0/3/3/3
1	PSU	L5	4389	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	218	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	4339	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4518	1	-	0/7/25/26	0/2/2/2
42	OMC	S2	621	42	-	0/9/27/28	0/2/2/2
1	PSU	L5	1740	1	-	0/7/25/26	0/2/2/2
42	OMG	S2	601	42	-	0/9/27/28	0/3/3/3
1	UR3	L5	4516	1	-	0/7/25/26	0/2/2/2
3	PSU	L8	55	3	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	L5	4957	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	1238	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	1673	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	119	42	-	0/7/25/26	0/2/2/2
42	A2M	S2	668	79,42	-	4/9/27/28	0/3/3/3
1	OMG	L5	4356	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4555	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4298	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	2814	1	-	1/9/27/28	0/2/2/2
1	PSU	L5	1788	1,80	-	0/7/25/26	0/2/2/2
1	PSU	L5	4517	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4409	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	34	42	-	0/7/25/26	0/2/2/2
42	OMC	S2	462	42	-	0/9/27/28	0/2/2/2
42	PSU	S2	651	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	1578	1	-	2/7/25/26	0/2/2/2
42	PSU	S2	406	42	-	0/7/25/26	0/2/2/2
1	OMG	L5	2354	1	-	0/9/27/28	0/3/3/3
42	A2M	S2	99	42	-	3/9/27/28	0/3/3/3
42	PSU	S2	1045	42	-	0/7/25/26	0/2/2/2
42	A2M	S2	468	42	-	1/9/27/28	0/3/3/3
1	PSU	L5	2829	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	3613	1	-	0/9/27/28	0/3/3/3
1	OMG	L5	1312	1	-	0/9/27/28	0/3/3/3
42	OMU	S2	1804	42	-	1/9/27/28	0/2/2/2
61	NMM	ST	67	61	-	3/9/11/13	-
1	UY1	L5	3804	79,1,80	-	1/9/27/28	0/2/2/2
42	PSU	S2	918	42	-	1/7/25/26	0/2/2/2
1	6MZ	L5	4206	1	-	0/9/27/28	0/3/3/3
42	A2M	S2	159	42	-	3/9/27/28	0/3/3/3
42	OMU	S2	354	42	-	0/9/27/28	0/2/2/2
1	PSU	L5	4986	1	-	0/7/25/26	0/2/2/2
1	OMU	L5	4606	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	3704	1	-	1/9/27/28	0/3/3/3
42	MA6	S2	1850	42	-	0/11/29/30	0/3/3/3
1	PSU	L5	3681	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	2805	1	-	4/9/27/28	0/3/3/3
42	OMG	S2	644	42	-	2/9/27/28	0/3/3/3
1	PSU	L5	1532	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	36	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	4576	1	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	L5	1518	1	-	0/9/27/28	0/3/3/3
42	A2M	S2	27	42	-	1/9/27/28	0/3/3/3
42	OMC	S2	517	42	-	0/9/27/28	0/2/2/2
1	OMC	L5	2341	1	-	3/9/27/28	0/2/2/2
42	PSU	S2	100	42	-	2/7/25/26	0/2/2/2
42	PSU	S2	1232	42	-	0/7/25/26	0/2/2/2
42	OMU	S2	1442	79,42	-	0/9/27/28	0/2/2/2
1	OMU	L5	3911	1	-	1/9/27/28	0/2/2/2
1	OMU	L5	4484	1	-	1/9/27/28	0/2/2/2
1	PSU	L5	4457	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4486	1	-	3/7/25/26	0/2/2/2
1	OMG	L5	4609	1	-	0/9/27/28	0/3/3/3
3	OMU	L8	14	3,1	-	1/9/27/28	0/2/2/2
1	OMG	L5	4182	79,1	-	3/9/27/28	0/3/3/3
42	PSU	S2	814	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	3837	1	-	0/7/25/26	0/2/2/2
1	1MA	L5	1318	79,1	-	2/7/25/26	0/3/3/3
1	OMG	L5	4604	1	-	0/9/27/28	0/3/3/3
1	OMG	L5	4623	1	-	1/9/27/28	0/3/3/3
1	OMC	L5	3687	1,80	-	4/9/27/28	0/2/2/2
42	PSU	S2	1046	42	-	0/7/25/26	0/2/2/2
1	OMG	L5	4485	1	-	0/9/27/28	0/3/3/3
42	OMU	S2	428	42	-	4/9/27/28	0/2/2/2
1	OMU	L5	2405	1	-	0/9/27/28	0/2/2/2
42	6MZ	S2	1832	79,42,80	-	0/9/27/28	0/3/3/3
1	PSU	L5	4562	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4417	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4378	1	-	0/9/27/28	0/3/3/3
3	OMG	L8	75	3	-	0/9/27/28	0/3/3/3
42	OMG	S2	436	42	-	0/9/27/28	0/3/3/3
1	OMC	L5	4442	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	1679	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	2414	1	-	1/9/27/28	0/3/3/3
1	OMC	L5	3827	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	3839	79,1	-	0/7/25/26	0/2/2/2
42	UY1	S2	1326	42	-	3/9/27/28	0/2/2/2
1	OMC	L5	1336	1	-	0/9/27/28	0/2/2/2
42	PSU	S2	686	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	3811	1	-	1/9/27/28	0/3/3/3
1	OMG	L5	4480	1	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	L5	1621	1,80	-	1/9/27/28	0/3/3/3
1	OMC	L5	2412	79,1	-	1/9/27/28	0/2/2/2
1	OMC	L5	2794	1	-	0/9/27/28	0/2/2/2
42	PSU	S2	93	42	-	0/7/25/26	0/2/2/2
42	PSU	S2	1625	42	-	0/7/25/26	0/2/2/2
42	A2M	S2	484	42	-	1/9/27/28	0/3/3/3
42	A2M	S2	1031	42	-	1/9/27/28	0/3/3/3
42	4AC	S2	1842	42	-	0/11/29/30	0/2/2/2
1	A2M	L5	2353	79,1	-	0/9/27/28	0/3/3/3
1	PSU	L5	3625	1	-	0/7/25/26	0/2/2/2
42	OMG	S2	1490	42	-	3/9/27/28	0/3/3/3
1	PSU	L5	2622	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4282	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4279	1	-	0/7/25/26	0/2/2/2
1	OMU	L5	2827	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	1858	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	1877	79,1	-	0/9/27/28	0/2/2/2
1	A2M	L5	3710	1	-	3/9/27/28	0/3/3/3
1	OMG	L5	4214	1	-	0/9/27/28	0/3/3/3
42	PSU	S2	1643	42	-	0/7/25/26	0/2/2/2
1	OMC	L5	3873	1	-	1/9/27/28	0/2/2/2
42	PSU	S2	1445	42	-	0/7/25/26	0/2/2/2
42	PSU	S2	1174	42	-	0/7/25/26	0/2/2/2
1	OMG	L5	3778	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4443	1	-	0/7/25/26	0/2/2/2
42	OMG	S2	683	42	-	2/9/27/28	0/3/3/3
1	PSU	L5	4958	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	815	42	-	0/7/25/26	0/2/2/2
42	OMC	S2	1703	42	-	0/9/27/28	0/2/2/2

The worst 5 of 659 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S2	166	A2M	C3'-C2'	-13.29	1.23	1.52
1	L5	3710	A2M	C3'-C2'	-13.22	1.23	1.52
1	L5	4576	A2M	C3'-C2'	-13.21	1.23	1.52
1	L5	3853	A2M	C3'-C2'	-13.21	1.23	1.52
42	S2	27	A2M	C3'-C2'	-13.20	1.23	1.52

The worst 5 of 935 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	S2	1851	MA6	N1-C6-N6	-15.45	100.19	117.08
42	S2	1850	MA6	N1-C6-N6	-14.94	100.75	117.08
1	L5	1520	A2M	C1'-N9-C8	-10.78	102.79	127.14
42	S2	590	A2M	C1'-N9-C8	-10.76	102.83	127.14
1	L5	4557	A2M	C1'-N9-C8	-10.59	103.21	127.14

There are no chirality outliers.

5 of 140 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L8	14	OMU	C1'-C2'-O2'-CM2
37	LB	245	HIC	O-C-CA-CB
61	ST	67	NMM	O-C-CA-CB
1	L5	398	A2M	C1'-C2'-O2'-CM'
1	L5	1578	PSU	O4'-C1'-C5-C4

There are no ring outliers.

104 monomers are involved in 205 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
42	S2	1447	OMG	4	0
42	S2	1288	OMU	4	0
42	S2	1136	PSU	1	0
1	L5	1322	A2M	1	0
42	S2	1851	MA6	4	0
1	L5	1777	PSU	1	0
42	S2	121	OMU	4	0
1	L5	2866	OMG	1	0
1	L5	2851	OMC	1	0
1	L5	3794	OMC	2	0
1	L5	3830	PSU	1	0
1	L5	3906	PSU	2	0
42	S2	1391	OMC	3	0
42	S2	1328	OMG	3	0
42	S2	681	PSU	2	0
42	S2	867	OMG	1	0
42	S2	166	A2M	1	0
42	S2	863	PSU	1	0
1	L5	3730	OMG	1	0
42	S2	667	PSU	1	0
42	S2	1678	A2M	1	0
42	S2	509	OMG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
42	S2	1383	A2M	1	0
42	S2	512	A2M	5	0
1	L5	3771	A2M	1	0
42	S2	172	OMU	1	0
42	S2	1337	4AC	4	0
1	L5	3853	A2M	2	0
42	S2	576	A2M	4	0
1	L5	4213	OMU	1	0
1	L5	4538	PSU	1	0
42	S2	590	A2M	1	0
42	S2	1639	G7M	2	0
1	L5	3701	PSU	1	0
42	S2	649	PSU	1	0
1	L5	4614	PSU	1	0
1	L5	2777	A2M	2	0
1	L5	3870	PSU	1	0
42	S2	572	PSU	1	0
1	L5	4557	A2M	5	0
42	S2	1177	PSU	2	0
42	S2	116	OMU	3	0
1	L5	4433	5MC	1	0
1	L5	1867	A2M	3	0
42	S2	1596	PSU	1	0
1	L5	398	A2M	2	0
42	S2	218	PSU	2	0
1	L5	4339	PSU	1	0
42	S2	621	OMC	2	0
42	S2	601	OMG	1	0
42	S2	1238	PSU	2	0
1	L5	1673	PSU	1	0
42	S2	668	A2M	2	0
1	L5	2814	OMC	2	0
42	S2	462	OMC	2	0
1	L5	1578	PSU	1	0
1	L5	2354	OMG	1	0
42	S2	99	A2M	1	0
42	S2	468	A2M	3	0
1	L5	3613	OMG	1	0
42	S2	1804	OMU	8	0
61	ST	67	NMM	3	0
42	S2	918	PSU	3	0
42	S2	159	A2M	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
42	S2	354	OMU	4	0
1	L5	4986	PSU	1	0
1	L5	4606	OMU	2	0
1	L5	3704	A2M	4	0
42	S2	1850	MA6	8	0
1	L5	3681	PSU	1	0
1	L5	2805	A2M	4	0
1	L5	1532	PSU	1	0
1	L5	4576	A2M	2	0
42	S2	27	A2M	2	0
42	S2	517	OMC	1	0
1	L5	2341	OMC	4	0
42	S2	1232	PSU	2	0
42	S2	1442	OMU	1	0
1	L5	4484	OMU	1	0
3	L8	14	OMU	1	0
1	L5	4623	OMG	1	0
42	S2	1046	PSU	2	0
42	S2	428	OMU	1	0
1	L5	2405	OMU	4	0
42	S2	1832	6MZ	1	0
1	L5	4378	OMG	1	0
1	L5	4442	OMC	1	0
1	L5	2414	OMG	5	0
1	L5	3827	OMC	1	0
1	L5	1336	OMC	1	0
1	L5	3811	A2M	1	0
1	L5	1621	OMG	1	0
1	L5	2794	OMC	2	0
42	S2	484	A2M	3	0
42	S2	1031	A2M	4	0
1	L5	2353	A2M	1	0
42	S2	1490	OMG	3	0
1	L5	2622	PSU	6	0
1	L5	3710	A2M	1	0
1	L5	4214	OMG	1	0
42	S2	1643	PSU	1	0
42	S2	1445	PSU	3	0
1	L5	4443	PSU	1	0
42	S2	1703	OMC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 233 ligands modelled in this entry, 233 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	L5	17
42	S2	4
76	S6	1

The worst 5 of 22 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L5	191:G	O3'	192:G	P	55.88
1	L5	266:C	O3'	267:G	P	46.82
1	L5	4731:C	O3'	4732:C	P	27.22
1	L5	1211:G	O3'	1212:G	P	24.08
1	S2	128:U	O3'	141:A	P	20.46

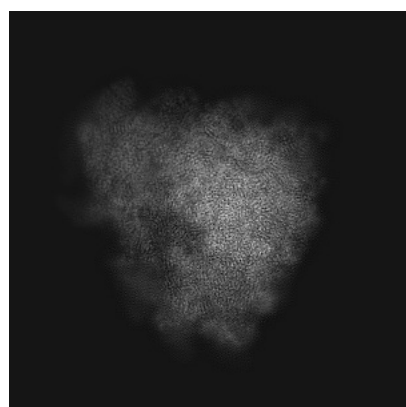
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-56227. These allow visual inspection of the internal detail of the map and identification of artifacts.

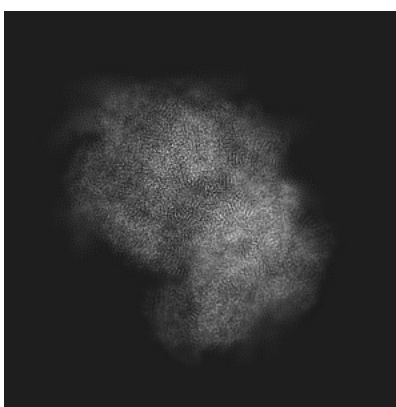
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

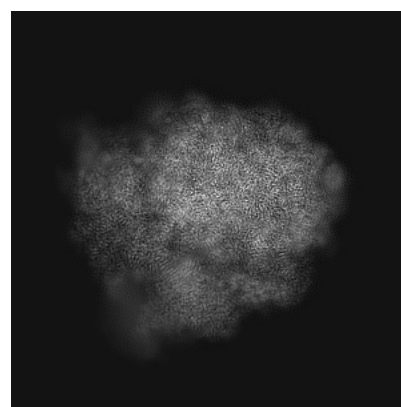
6.1.1 Primary map



X



Y

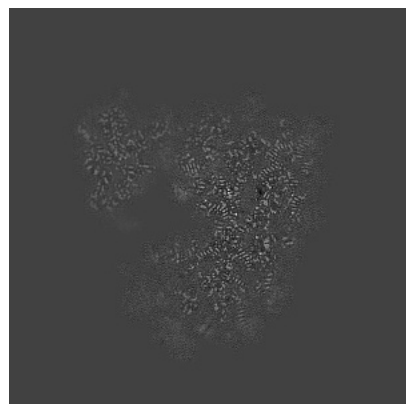


Z

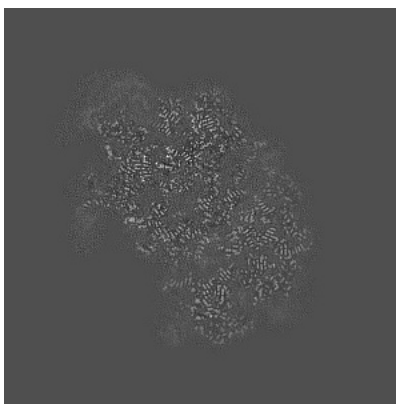
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

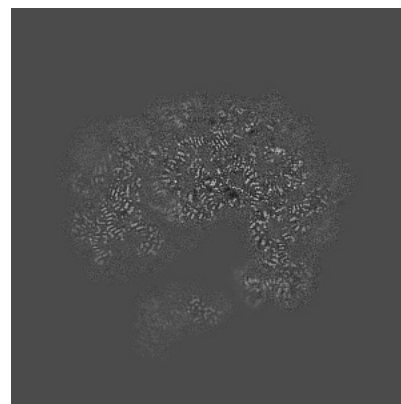
6.2.1 Primary map



X Index: 240



Y Index: 240

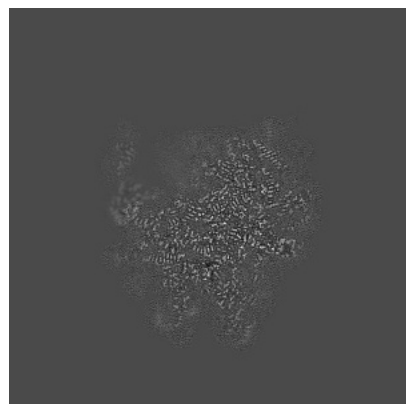


Z Index: 240

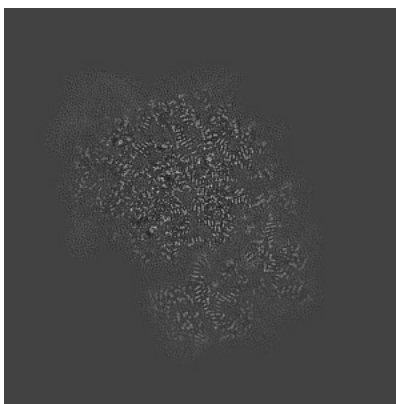
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

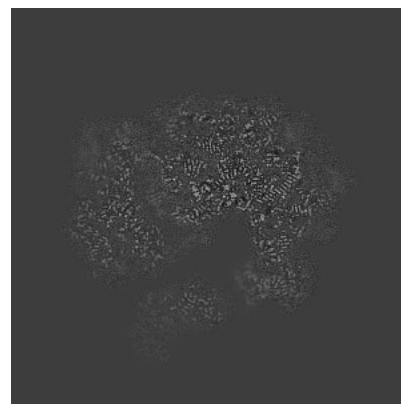
6.3.1 Primary map



X Index: 292



Y Index: 261

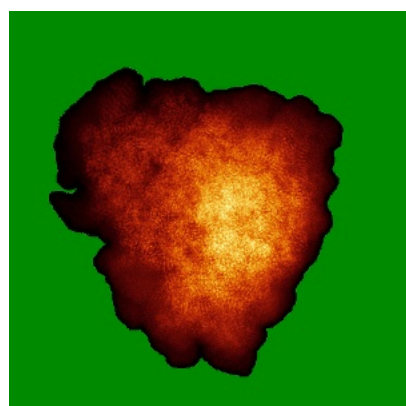


Z Index: 246

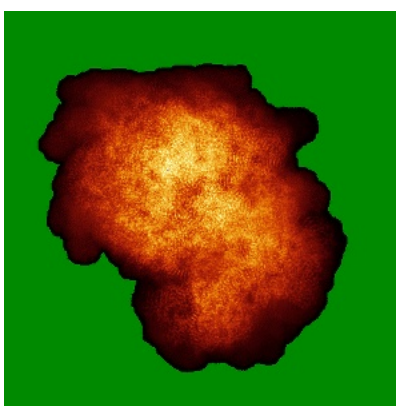
The images above show the largest variance slices of the map in three orthogonal directions.

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

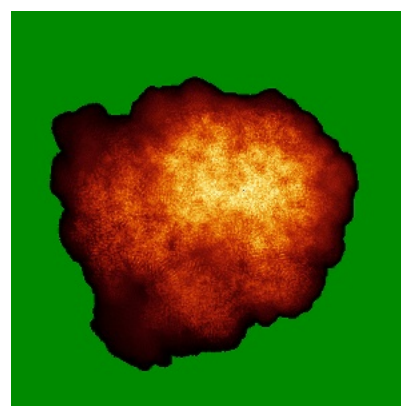
6.4.1 Primary map



X



Y

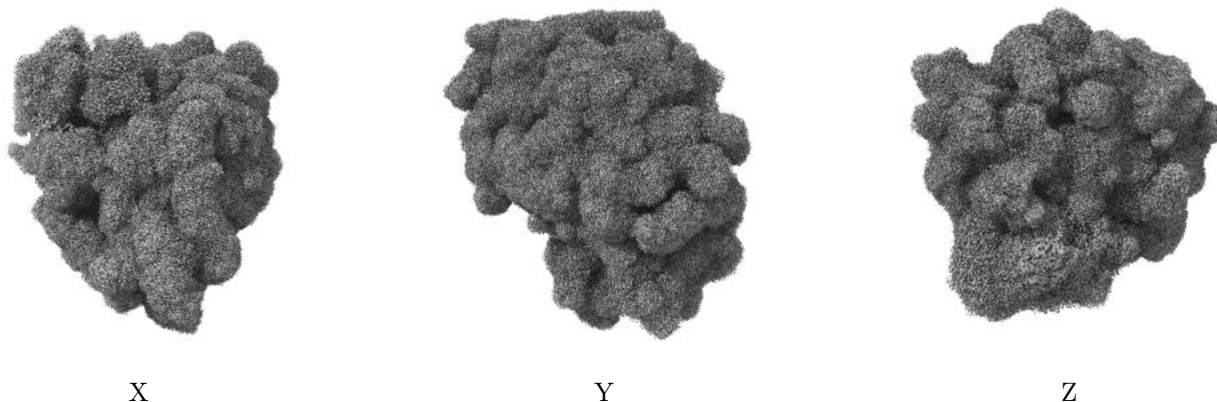


Z

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.

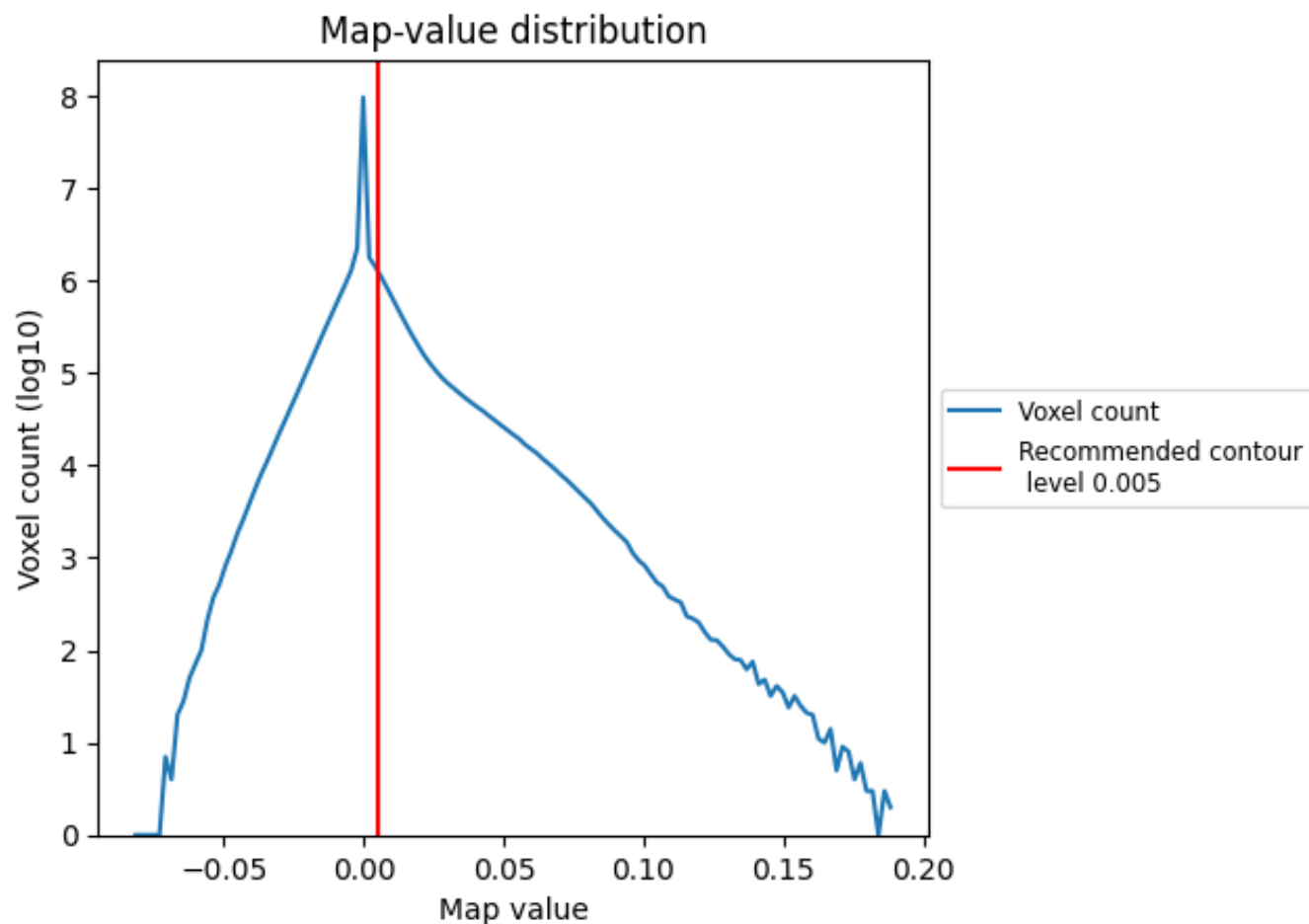
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

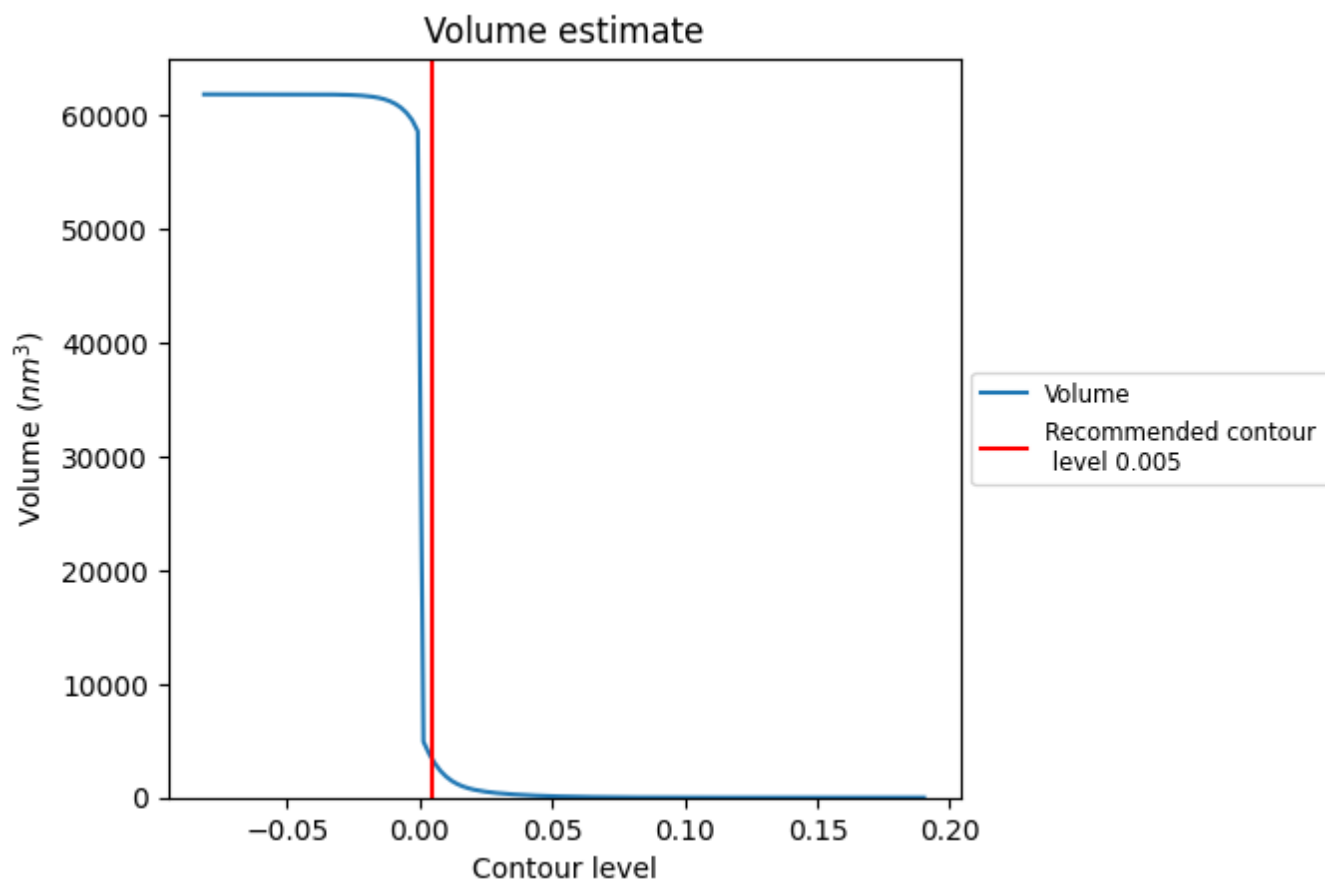
This section contains the results of statistical analysis of the map.

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.

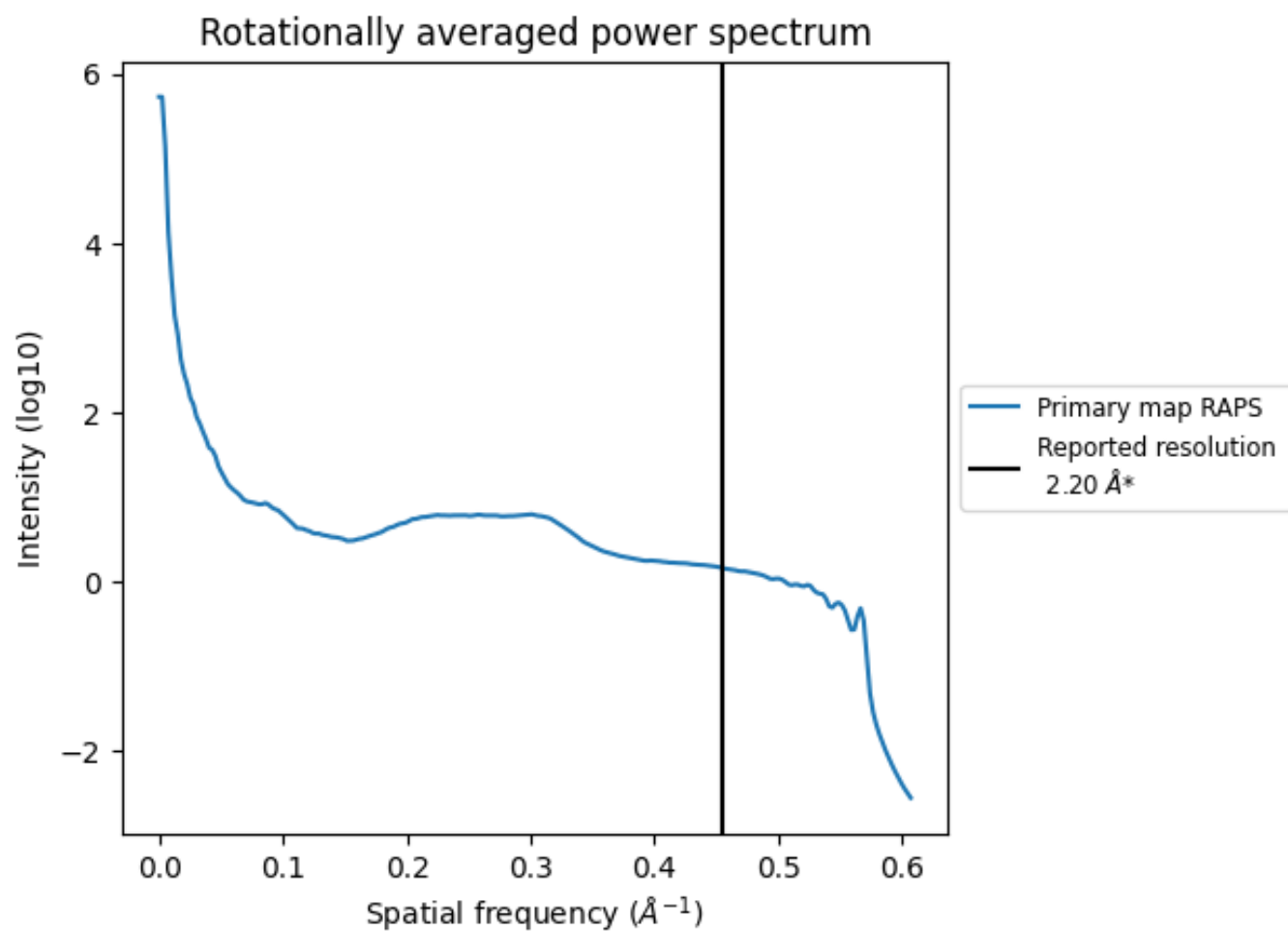
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3283 nm³; this corresponds to an approximate mass of 2965 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 0.455 Å⁻¹

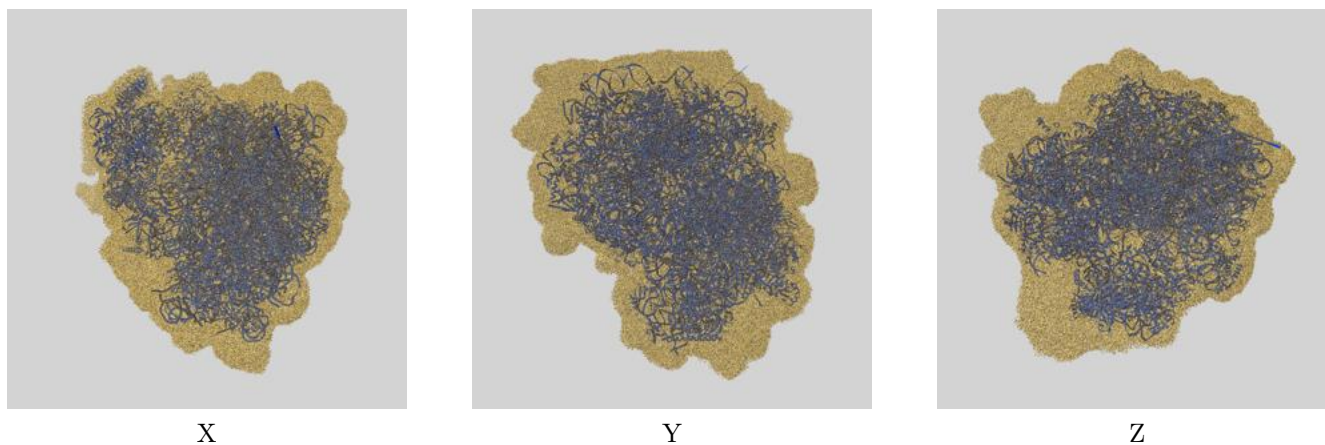
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

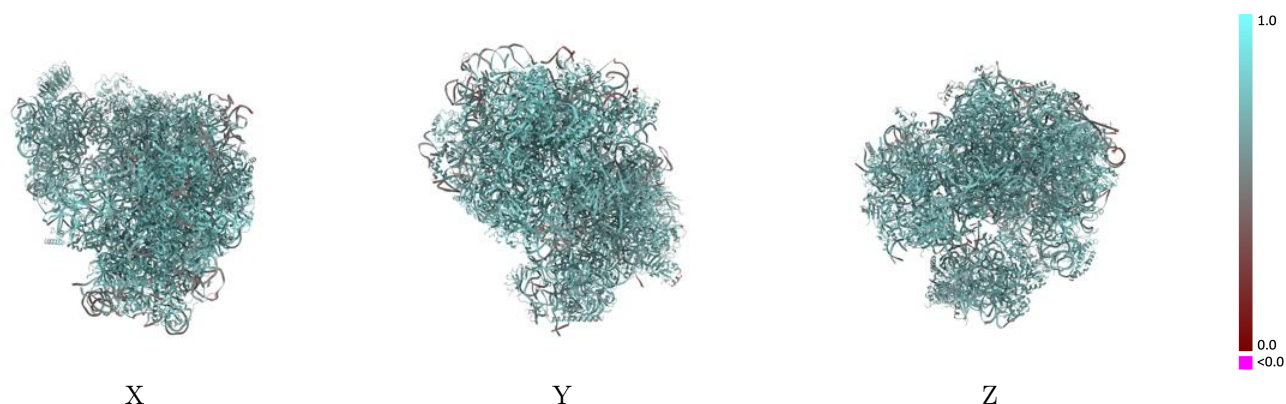
This section contains information regarding the fit between EMDB map EMD-56227 and PDB model 9TT7. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



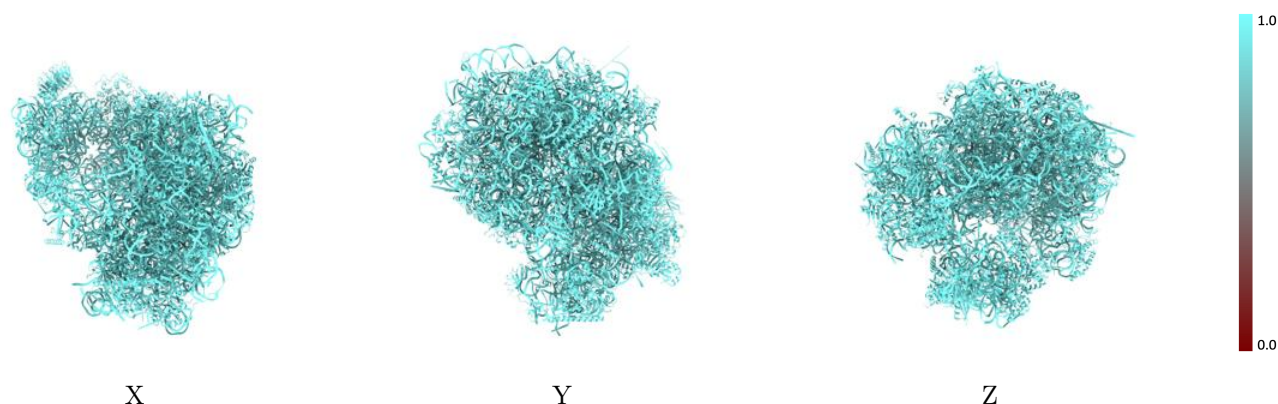
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



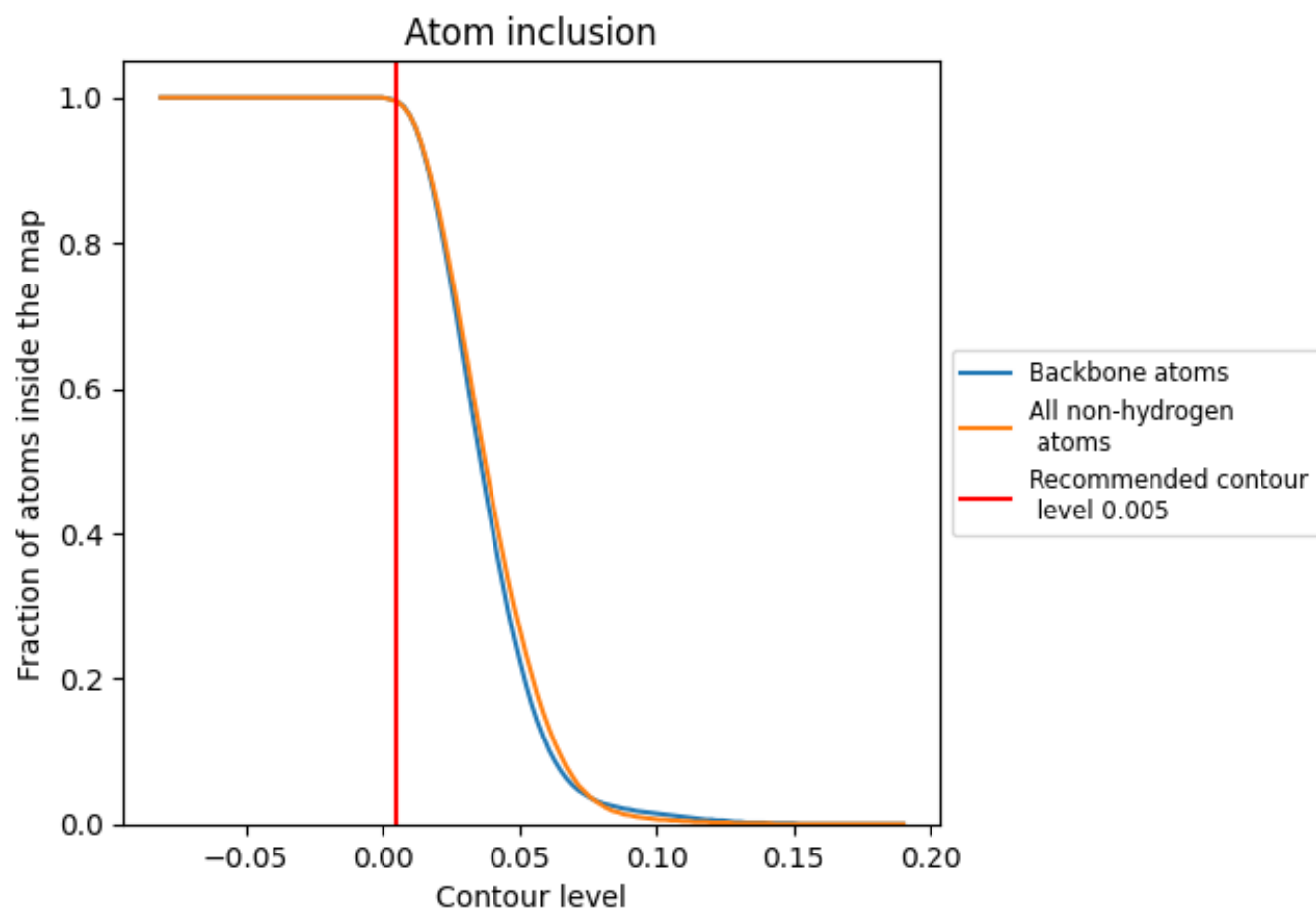
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.7160
L5	 0.9930	 0.7150
L7	 1.0000	 0.7200
L8	 0.9980	 0.7290
LA	 0.9990	 0.7850
LB	 0.9990	 0.7750
LC	 1.0000	 0.7740
LD	 0.9950	 0.7000
LE	 0.9930	 0.7030
LF	 0.9980	 0.7770
LG	 0.9950	 0.7120
LH	 0.9990	 0.7210
LI	 0.9970	 0.7260
LJ	 0.9940	 0.6700
LL	 0.9980	 0.7500
LM	 1.0000	 0.7330
LN	 0.9990	 0.7850
LO	 0.9990	 0.7730
LP	 1.0000	 0.7830
LQ	 1.0000	 0.7860
LR	 1.0000	 0.7440
LS	 1.0000	 0.7700
LT	 0.9990	 0.7650
LU	 0.9760	 0.5630
LV	 1.0000	 0.7760
LW	 1.0000	 0.7460
LX	 0.9990	 0.7480
LY	 1.0000	 0.7570
LZ	 0.9990	 0.7070
La	 0.9990	 0.7810
Lb	 1.0000	 0.7230
Lc	 0.9970	 0.7130
Ld	 1.0000	 0.7640
Le	 1.0000	 0.7870
Lf	 1.0000	 0.7930



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Chain	Atom inclusion	Q-score
Lg	 1.0000	 0.7700
Lh	 1.0000	 0.7340
Li	 0.9970	 0.7160
Lj	 1.0000	 0.7840
Lk	 0.9980	 0.6800
Ll	 0.9970	 0.7710
Lm	 1.0000	 0.7190
Ln	 1.0000	 0.6720
Lo	 0.9990	 0.7630
Lp	 1.0000	 0.7720
Lr	 1.0000	 0.7710
S2	 0.9950	 0.6830
S6	 0.9890	 0.5840
SA	 0.9970	 0.7110
SB	 0.9960	 0.7000
SC	 0.9980	 0.7270
SD	 0.9940	 0.6650
SE	 1.0000	 0.7180
SF	 0.9950	 0.6950
SG	 0.9950	 0.6610
SH	 0.9960	 0.6580
SI	 0.9980	 0.7200
SJ	 1.0000	 0.7250
SK	 0.9940	 0.6380
SL	 0.9990	 0.7430
SN	 0.9960	 0.7160
SO	 0.9990	 0.7050
SP	 0.9980	 0.7040
SQ	 0.9970	 0.6990
SR	 0.9900	 0.6330
SS	 0.9980	 0.6980
ST	 0.9980	 0.7020
SU	 0.9900	 0.6740
SV	 0.9950	 0.6980
SW	 1.0000	 0.7480
SX	 0.9970	 0.7410
SY	 0.9980	 0.6970
SZ	 0.9980	 0.6690
Sa	 1.0000	 0.7210
Sb	 0.9960	 0.7050
Sc	 0.9970	 0.6610
Sd	 1.0000	 0.7110

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Chain	Atom inclusion	Q-score
Se	 0.9910	 0.7070
Sg	 0.9910	 0.6400