



wwPDB EM Validation Summary Report ⓘ

Sep 19, 2026 – 10:53 pm BST

PDB ID : 9TV2 / pdb_00009tv2
EMDB ID : EMD-56286
Title : 80S ribosomes from primary B-cells infected with delta v-snoRNA1 EBV
Authors : Fedorenko, A.; Bashan, A.; Yonath, A.
Deposited on : 2026-01-11
Resolution : 2.10 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

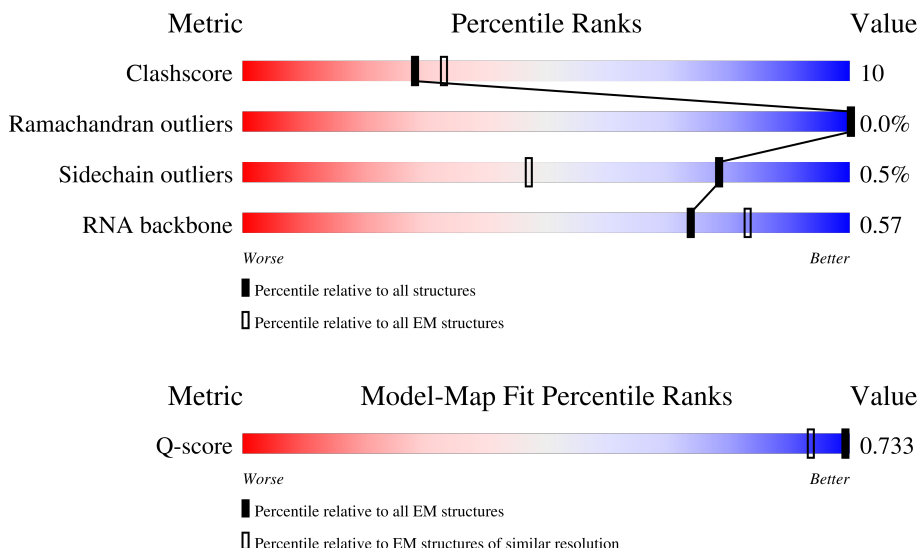
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.10 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.



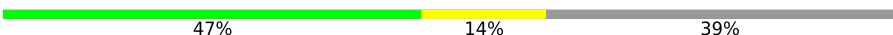
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2317 (1.60 - 2.60)

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	
2	L7	121	
3	L8	156	

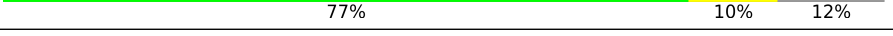
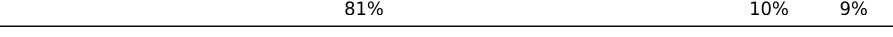
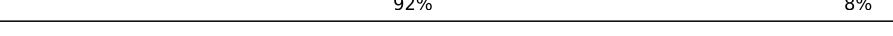
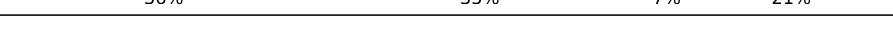
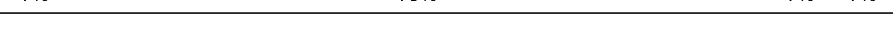
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	S2	1869	
47	S6	14	
48	SA	295	
49	SB	264	
50	SC	293	
51	SD	243	
52	SE	263	
53	SF	204	

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Mol	Chain	Length	Quality of chain
54	SG	249	
55	SH	194	
56	SI	208	
57	SJ	194	
58	SK	165	
59	SL	158	
60	SN	151	
61	SO	151	
62	SP	145	
63	SQ	146	
64	SR	135	
65	SS	152	
66	ST	145	
67	SU	119	
68	SV	83	
69	SW	130	
70	SX	143	
71	SY	133	
72	SZ	125	
73	Sa	115	
74	Sb	84	
75	Sc	69	
76	Sd	56	
77	Se	98	
78	Sg	308	

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
46	A2M	S2	1383	-	-	X	-

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 184489 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	3068	Total	C	N	O	P	0	0
			65889	29386	12068	21367	3068		

- 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	144	Total	C	N	O	P	0	0
			3072	1371	548	1009	144		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LA	245	Total	C	N	O	S	0	0
			1805	1130	365	304	6		

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	391	Total	C	N	O	S	0	0
			2962	1890	559	501	12		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	350	Total	C	N	O	S	0	0
			2721	1717	540	451	13		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	277	Total	C	N	O	S	0	0
			2135	1358	387	378	12		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	188	Total	C	N	O	S	0	0
			1495	967	278	247	3		

- Molecule 9 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	218	Total	C	N	O	S	0	0
			1773	1136	337	291	9		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	202	Total	C	N	O	S	0	0
			1496	962	278	252	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	180	Total	C	N	O	S	0	0
			1320	839	243	232	6		

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	195	Total	C	N	O	S	0	0
			1475	940	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 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	136	Total	C	N	O	S	0	0
			965	616	177	166	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	188	Total	C	N	O	S	0	0
			1406	883	290	229	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	132	Total	C	N	O	S	0	0
			1062	679	205	171	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LN	203	Total	C	N	O	S	0	0
			1695	1069	356	266	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	198	Total	C	N	O	S	0	0
			1579	1018	306	250	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	150	Total	C	N	O	S	0	0
			1182	741	232	200	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

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

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	152	Total	C	N	O	S	0	0
			1190	745	254	182	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

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

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	148	Total	C	N	O	S	0	0
			1164	740	231	188	5		

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	88	Total	C	N	O	S	0	0
			599	390	107	101	1		

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	130	Total	C	N	O	S	0	0
			932	589	173	165	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

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

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	117	Total	C	N	O	S	0	0
			898	579	166	152	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

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

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LZ	135	Total	C	N	O	S	0	0
			1037	670	191	173	3		

- Molecule 29 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 30 is a protein called 60S ribosomal protein L29.

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

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	85	Total	C	N	O	S	0	0
			629	400	109	114	6		

- Molecule 32 is a protein called 60S ribosomal protein L31.

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

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	107	Total	C	N	O	S	0	0
			826	526	163	134	3		

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	101	Total	C	N	O	S	0	0
			772	483	157	126	6		

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	121	Total	C	N	O	S	0	0
			934	589	189	155	1		

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	92	Total	C	N	O	S	0	0
			682	429	138	111	4		

- Molecule 38 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	25	Total	C	N	O	S	0	0
			193	118	48	26	1		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

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

- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lp	87	Total	C	N	O	S	0	0
			645	407	121	110	7		

- Molecule 45 is a protein called 60S ribosomal protein L28.

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

- Molecule 46 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	S2	1481	Total	C	H	N	O	P	0	0
			31703	14174	13	5713	10323	1480		

- Molecule 47 is a RNA chain called E-site tRNA.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SA	205	Total	C	N	O	S	0	0
			1571	1006	279	279	7		

- Molecule 49 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SB	209	Total	C	N	O	S	0	0
			1599	1020	291	275	13		

- Molecule 50 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SC	212	Total	C	N	O	S	0	0
			1546	1006	261	270	9		

- Molecule 51 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SD	206	Total	C	N	O	S	0	0
			1372	887	241	238	6		

- Molecule 52 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SE	257	Total	C	N	O	S	0	0
			1943	1247	361	327	8		

- Molecule 53 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF	178	Total	C	N	O	S	0	0
			1329	841	252	229	7		

- Molecule 54 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SG	179	Total	C	N	O	S	0	0
			1287	811	260	211	5		

- Molecule 55 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	SH	146	Total	C	N	O		
			1021	659	190	172	0	0

- Molecule 56 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	SI	169	Total	C	N	O	S	
			1288	812	247	225	4	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
57	SJ	178	Total	C	N	O	S	
			1328	852	267	207	2	0

- Molecule 58 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	SK	81	Total	C	N	O	S	
			595	392	107	91	5	0

- Molecule 59 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	SL	132	Total	C	N	O	S	
			1017	647	190	174	6	0

- Molecule 60 is a protein called 40S ribosomal protein S13.

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

- Molecule 61 is a protein called 40S ribosomal protein S14.

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

- Molecule 62 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SP	114	Total	C	N	O	S	0	0
			841	542	156	137	6		

- Molecule 63 is a protein called 40S ribosomal protein S16.

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

- Molecule 64 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SR	117	Total	C	N	O	S	0	0
			839	533	159	143	4		

- Molecule 65 is a protein called 40S ribosomal protein S18.

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

- Molecule 66 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 67 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SU	83	Total	C	N	O	S	0	0
			601	376	118	103	4		

- Molecule 68 is a protein called 40S ribosomal protein S21.

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

- Molecule 69 is a protein called 40S ribosomal protein S15a.

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

- Molecule 70 is a protein called 40S ribosomal protein S23.

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

- Molecule 71 is a protein called 40S ribosomal protein S24.

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

- Molecule 72 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 73 is a protein called 40S ribosomal protein S26.

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

- Molecule 74 is a protein called 40S ribosomal protein S27.

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

- Molecule 75 is a protein called 40S ribosomal protein S28.

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

- Molecule 76 is a protein called 40S ribosomal protein S29.

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

- Molecule 77 is a protein called FAU ubiquitin like and ribosomal protein S30 fusion.

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

- Molecule 78 is a protein called RS8_HUMAN Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sg	273	Total	C	N	O	S	0	0
			2031	1298	355	369	9		

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

Mol	Chain	Residues	Atoms		AltConf
79	L5	139	Total	Mg	0
			139	139	
79	L7	3	Total	Mg	0
			3	3	
79	L8	3	Total	Mg	0
			3	3	
79	LP	1	Total	Mg	0
			1	1	
79	LV	1	Total	Mg	0
			1	1	
79	S2	16	Total	Mg	0
			16	16	

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

Mol	Chain	Residues	Atoms		AltConf
80	L5	51	Total	K	0
			51	51	
80	L7	1	Total	K	0
			1	1	
80	LA	2	Total	K	0
			2	2	
80	LH	1	Total	K	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
80	LI	1	Total K 1 1	0
80	LN	1	Total K 1 1	0
80	Lb	1	Total K 1 1	0
80	Le	1	Total K 1 1	0
80	Lf	1	Total K 1 1	0
80	Lo	1	Total K 1 1	0
80	S2	11	Total K 11 11	0
80	SL	1	Total K 1 1	0
80	SO	1	Total K 1 1	0
80	Sd	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

- 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	1500	Total 1500	O 1500	0
83	L7	14	Total 14	O 14	0
83	L8	32	Total 32	O 32	0
83	LA	22	Total 22	O 22	0
83	LB	26	Total 26	O 26	0
83	LC	25	Total 25	O 25	0
83	LD	1	Total 1	O 1	0
83	LF	14	Total 14	O 14	0
83	LG	2	Total 2	O 2	0
83	LH	1	Total 1	O 1	0
83	LL	14	Total 14	O 14	0
83	LM	1	Total 1	O 1	0
83	LN	19	Total 19	O 19	0
83	LO	9	Total 9	O 9	0
83	LP	11	Total 11	O 11	0
83	LQ	18	Total 18	O 18	0
83	LR	3	Total 3	O 3	0
83	LS	2	Total 2	O 2	0

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Mol	Chain	Residues	Atoms		AltConf
83	LT	11	Total 11	O 11	0
83	LV	3	Total 3	O 3	0
83	LW	1	Total 1	O 1	0
83	LX	2	Total 2	O 2	0
83	LY	2	Total 2	O 2	0
83	LZ	1	Total 1	O 1	0
83	La	23	Total 23	O 23	0
83	Lb	5	Total 5	O 5	0
83	Ld	2	Total 2	O 2	0
83	Le	12	Total 12	O 12	0
83	Lf	9	Total 9	O 9	0
83	Lg	9	Total 9	O 9	0
83	Li	1	Total 1	O 1	0
83	Lj	11	Total 11	O 11	0
83	Ll	2	Total 2	O 2	0
83	Ln	3	Total 3	O 3	0
83	Lo	7	Total 7	O 7	0
83	Lp	3	Total 3	O 3	0
83	Lr	4	Total 4	O 4	0
83	S2	202	Total 202	O 202	0
83	S6	2	Total 2	O 2	0

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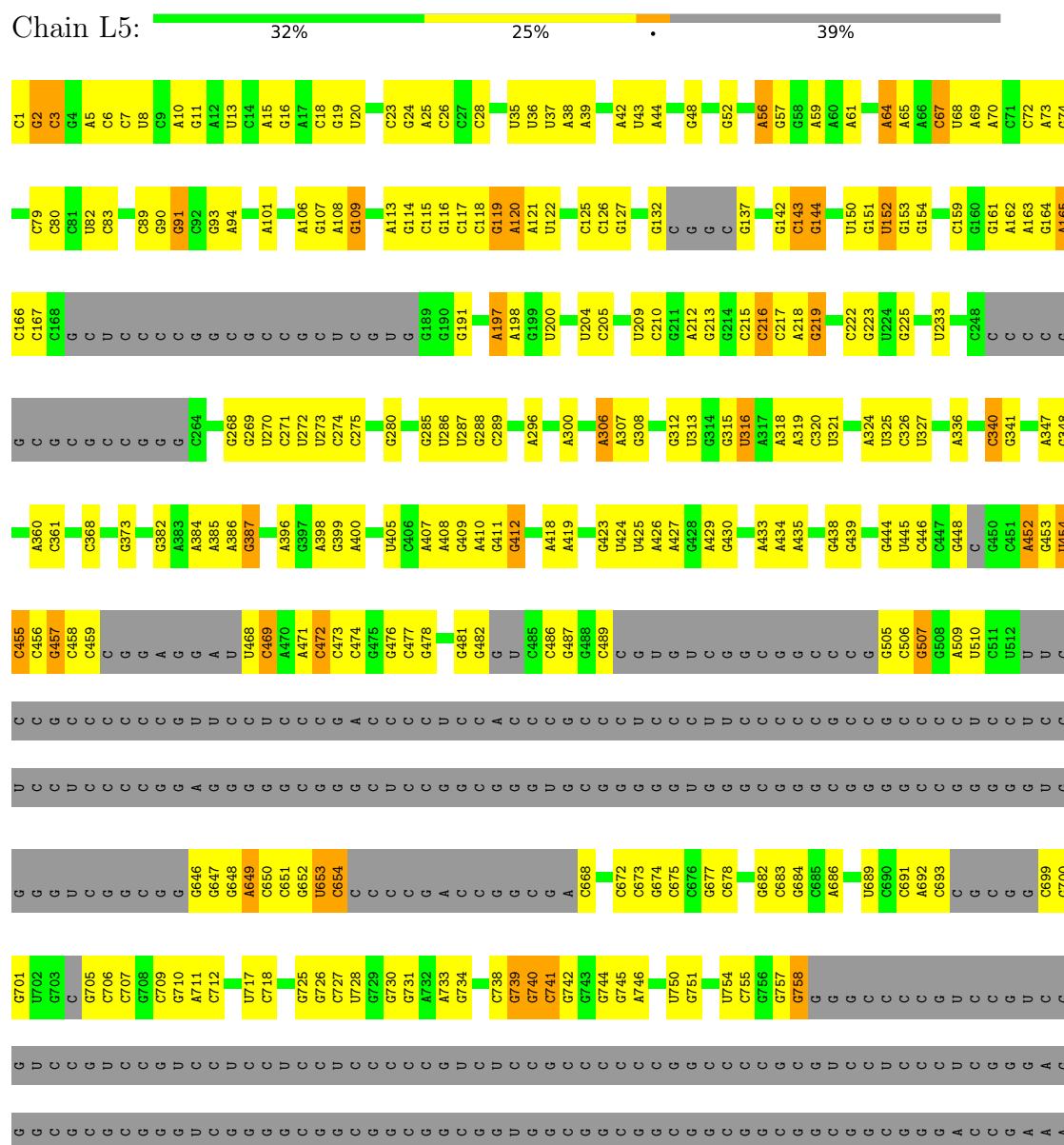
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Mol	Chain	Residues	Atoms		AltConf
83	SI	2	Total 2	O 2	0
83	SL	2	Total 2	O 2	0
83	SN	1	Total 1	O 1	0
83	SO	1	Total 1	O 1	0
83	SQ	1	Total 1	O 1	0
83	SS	2	Total 2	O 2	0
83	SU	1	Total 1	O 1	0
83	SX	1	Total 1	O 1	0
83	Sa	2	Total 2	O 2	0

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

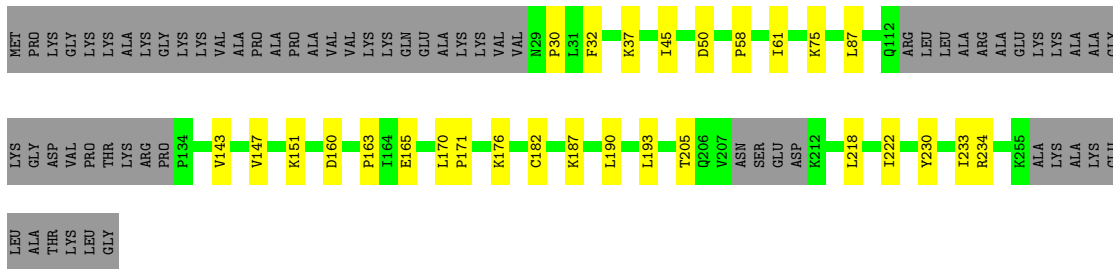






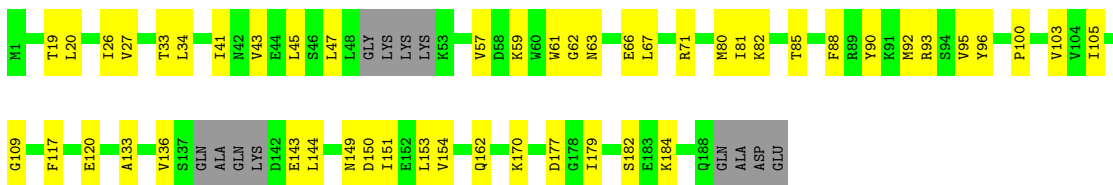


Chain LG:  65% 11% 24%



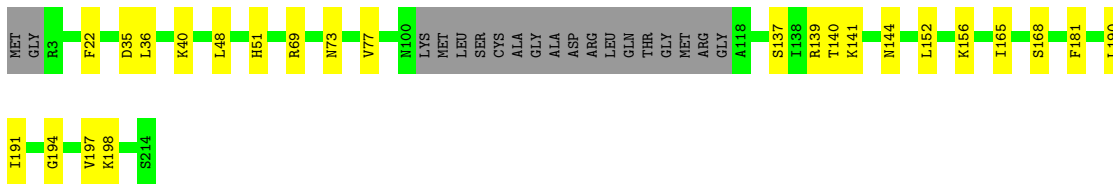
- Molecule 11: 60S ribosomal protein L9

Chain LH:  68% 26% 6%



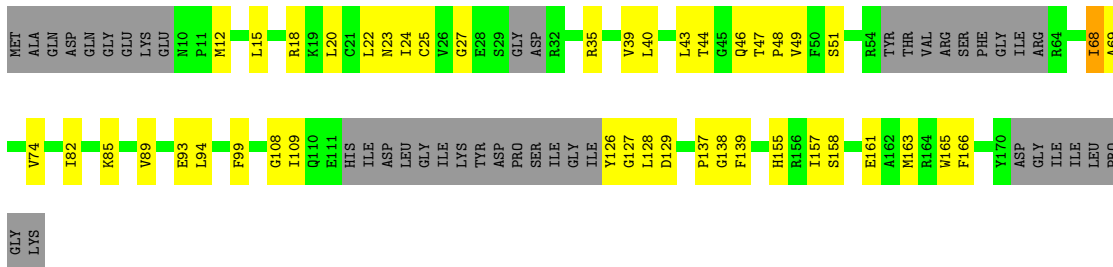
- Molecule 12: 60S ribosomal protein L10-like

Chain LI:  80% 11% 9%



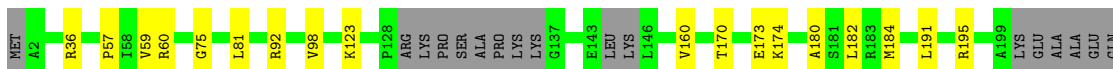
- Molecule 13: 60S ribosomal protein L11

Chain LJ:  52% 24% 24%



- Molecule 14: 60S ribosomal protein L13

Chain LL:  81% 9% 11%



ASP
VAL
GLU
LYS
LYS
LYS

• Molecule 15: 60S ribosomal protein L14

Chain LM:  47% 14% 39%

MET V2 F3 F6 V9 G10 R11 G18 L24 V28 Q33 A36 D39 G40 P41 C42 F52 K53 L62 H66 S67 Q70 W77 I82 K85 W86 T89 R100 M104 D108 V112 M113 M118 E126 A133 LEU

LEU LYS ALA SER PRO LYS ALA PRO GLY THR LYS THR ALA ALA ALA ALA LYS VAL PRO ALA LYS THR ILE THR ALA SER LYS LYS ALA PRO ALA GLN LYS VAL PRO ALA GLN LYS THR GLN LYS ALA PRO LYS ALA GLN

LYS GLY GLN LYS PRO ALA LYS ALA PRO GLY THR LYS THR ALA SER GLY LYS LYS ALA

• Molecule 16: 60S ribosomal protein L15

Chain LN:  84% 16%

MET G2 L10 S16 R20 W28 Q32 R41 P42 A48 Y53 K56 Y59 V60 R67 P84 H87 A95 L113 W120 V121 G122 E131 L134 I135 F138 R143 T165 R169 G177 H178 H181 R193 R204

• Molecule 17: 60S ribosomal protein L13a

Chain LO:  80% 18% .

MET ALA GLU VAL GLN V6 V7 V8 L22 K25 R31 Y48 R49 L52 K53 Y54 F57 M62 N65 P76 S77 R78 W81 L99 R117 M118 V119 V120 P121 L124 L138 L141 V145 Y149 V152 H178 M175 R176 K179 Q180 A181

V185 I189 Y192 L196 K197 T198 L201 V203

• Molecule 18: 60S ribosomal protein L17

Chain LP:  73% 9% 18%

MET V2 P8 ASN P11 K16 S17 R18 L22 Q54 R61 W83 M94 H116 A122 P123 R128 I136 Y139 I146 E147 M148 I149 A153 GLU GLN ILE VAL PRO LYS PRO GLU GLU VAL ALA GLN LYS LYS ILE SER GLN LYS

LEU LYS LYS GLN LYS LEU MET MET ARG GLU

• Molecule 19: 60S ribosomal protein L18

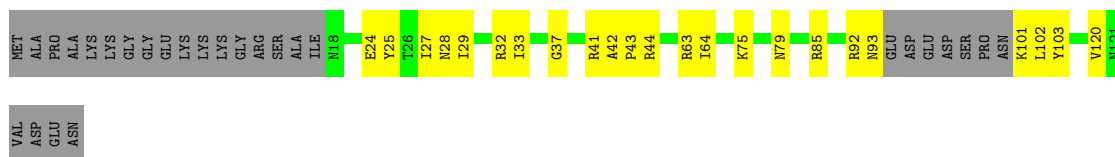
Chain LQ:  85% 15% .

MET G2 K9 R15 R26 L27 L28 V29 K30 F34 R38 T39 N40 S41 T42 F43 R50 L51 F52 M53 S64 T79 D88 D89 Y90 R91 V92 K99 R108 L121 Q125 G133 K144 P159 A177 R184 N188

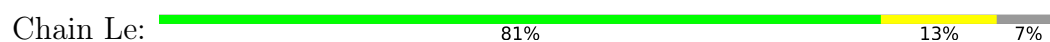
• Molecule 20: 60S ribosomal protein L19



- Molecule 32: 60S ribosomal protein L31



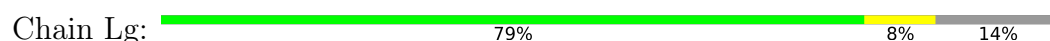
- Molecule 33: 60S ribosomal protein L32



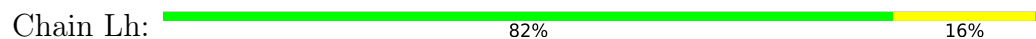
- Molecule 34: 60S ribosomal protein L35a



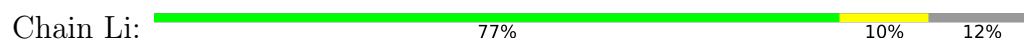
- Molecule 35: 60S ribosomal protein L34



- Molecule 36: 60S ribosomal protein L35



- Molecule 37: 60S ribosomal protein L36



- Molecule 38: Large ribosomal subunit protein eL37

Chain Lj:  73% 15% 11%



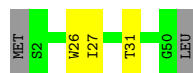
- Molecule 39: 60S ribosomal protein L38

Chain Lk:  81% 10% 9%



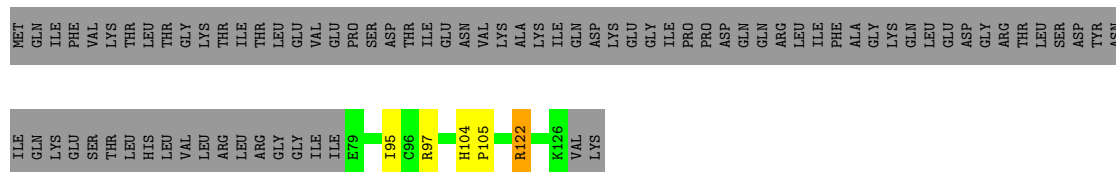
- Molecule 40: 60S ribosomal protein L39

Chain Ll:  90% 6% .

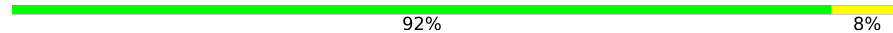


- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm:  34% . . 62%



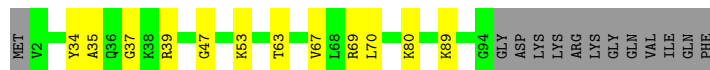
- Molecule 42: 60S ribosomal protein L41

Chain Ln:  92% 8%



- Molecule 43: 60S ribosomal protein L36a

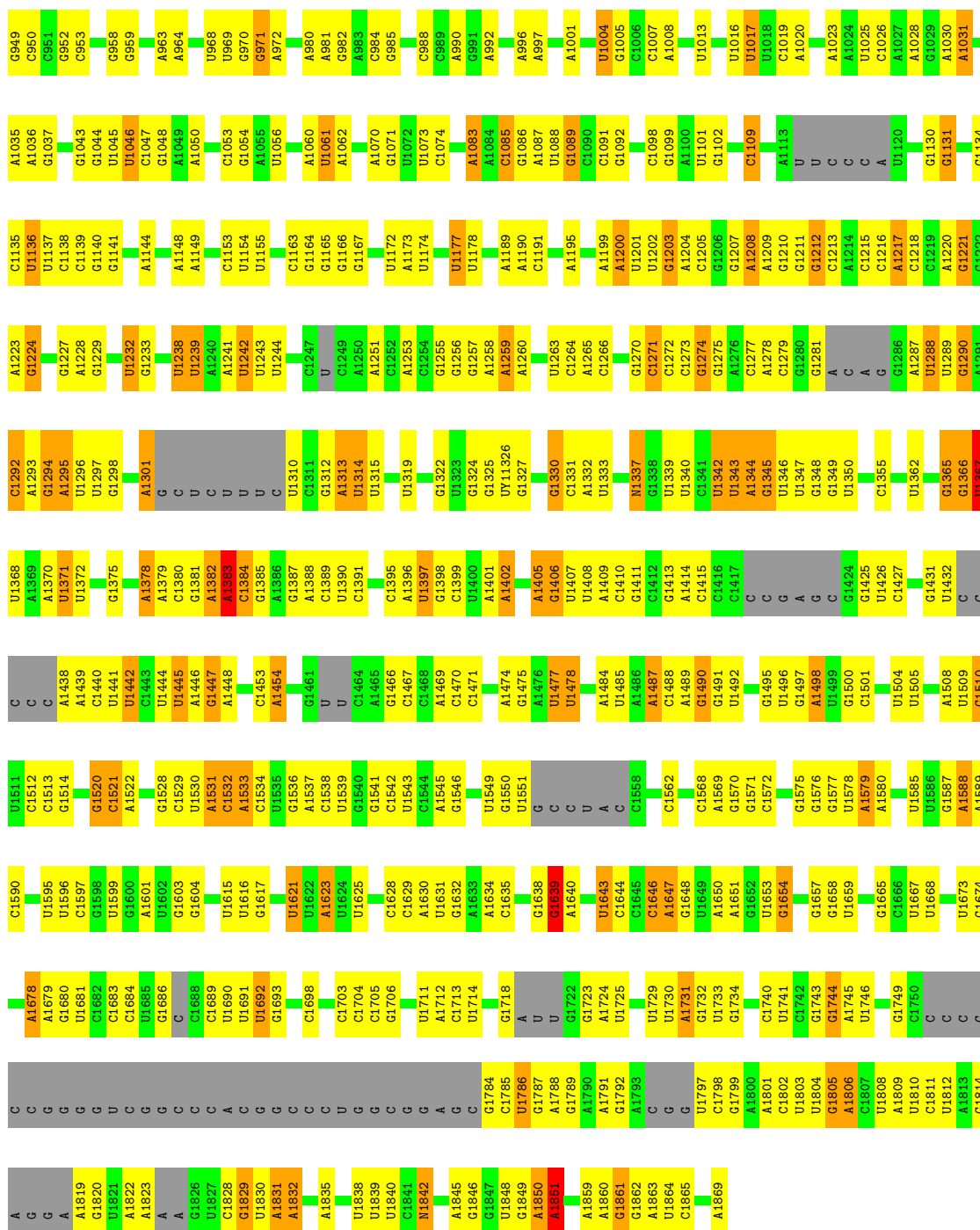
Chain Lo:  76% 11% 12%



- Molecule 44: 60S ribosomal protein L37a

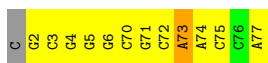
Chain Lp:  82% 13% 5%





• Molecule 47: E-site tRNA

Chain S6:



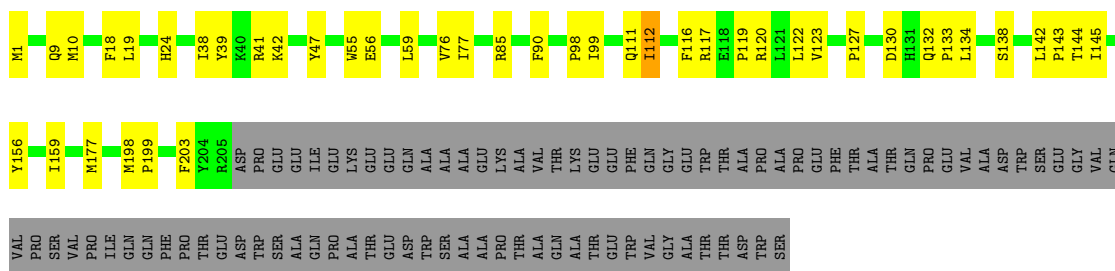
• Molecule 48: 40S ribosomal protein SA

Chain SA:

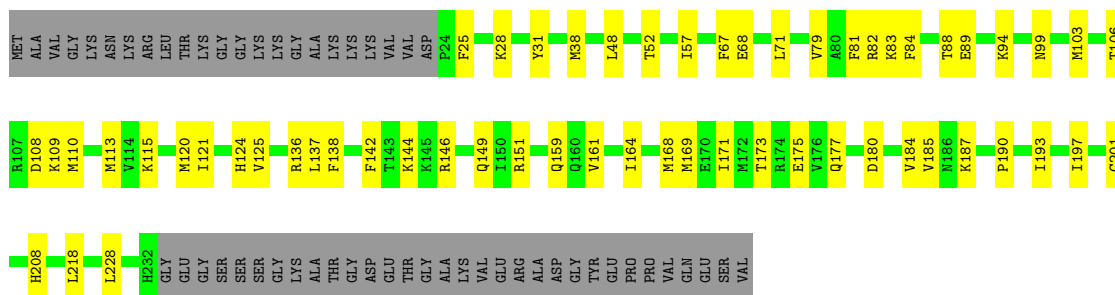
55%

15%

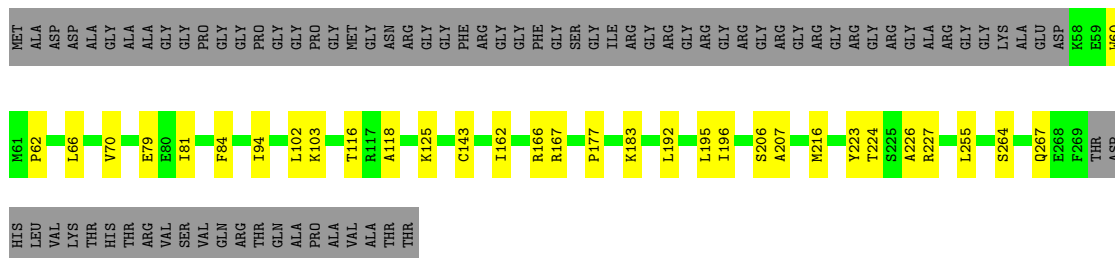
31%



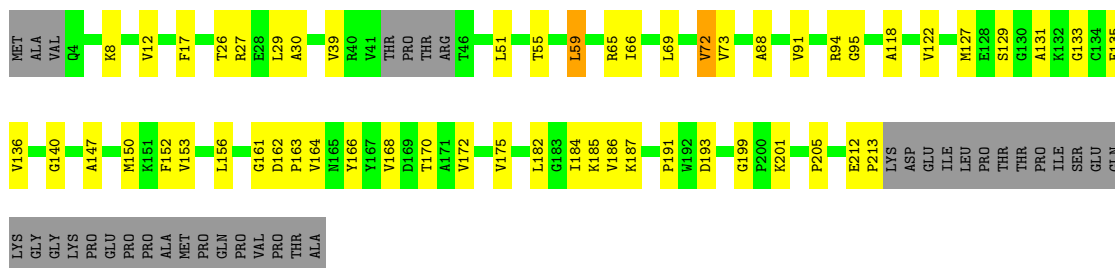
- Molecule 49: 40S ribosomal protein S3a



- Molecule 50: 40S ribosomal protein S2

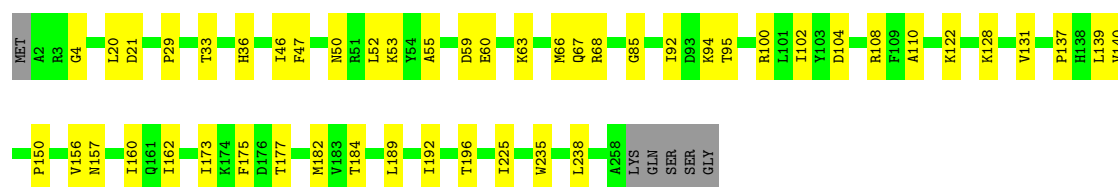


- Molecule 51: 40S ribosomal protein S3



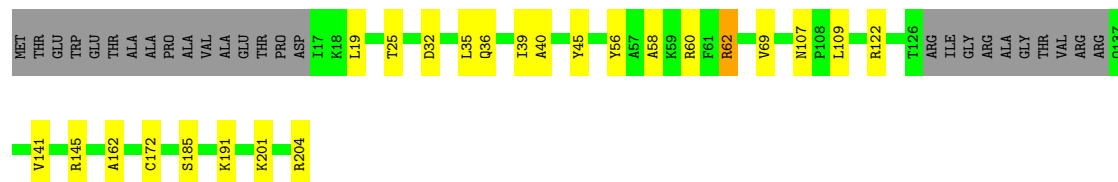
- Molecule 52: Small ribosomal subunit protein eS4, X isoform





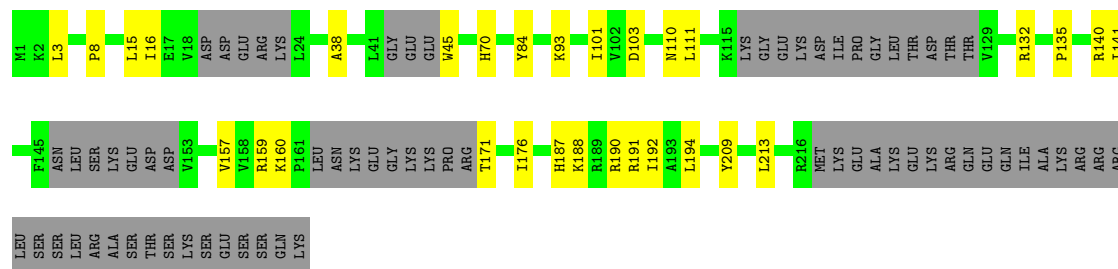
- Molecule 53: 40S ribosomal protein S5

Chain SF: 75% 11% 13%



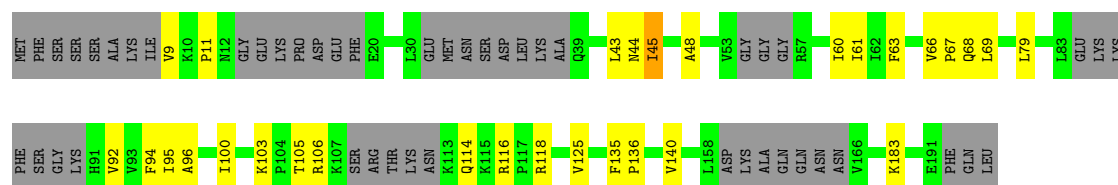
- Molecule 54: 40S ribosomal protein S6

Chain SG: 60% 12% 28%



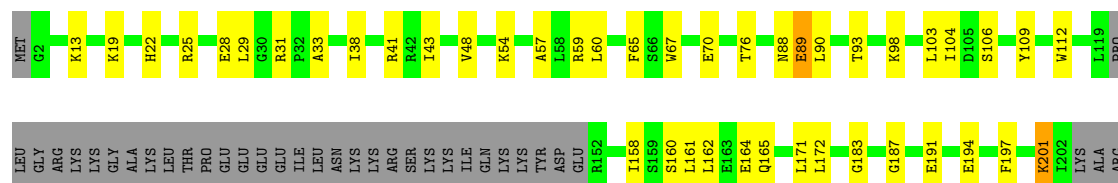
- Molecule 55: 40S ribosomal protein S7

Chain SH: 60% 15% 25%



- Molecule 56: 40S ribosomal protein S8

Chain SI: 60% 20% 19%



LYS
GLY
LYS

- Molecule 57: 40S ribosomal protein S9

Chain SJ:  86% 6% 8%

MET P2 V3 E21 L25 G33 K47 I102 E107 Q111 T112 R127 K179 LYS GLY GLN GLY GLY ALA ALA ALA ASP ASP ASP GLU GLU GLU ASP

- Molecule 58: 40S ribosomal protein S10

Chain SK:  36% 13% 51%

M1 L2 M3 R8 L14 M21 K24 K25 D26 V27 H32 P33 E34 L35 K38 N39 V40 P41 M42 L43 H44 K47 A48 M49 L52 Y68 W69 I76 GLN TYR LEU ARG ASP TYR LEU HIS LEU PRO PRO GLU ILE VAL P91 R95 ARG SER ARG ARG GLU

THR GLY ARG PRO ARG PRO LYS GLY LEU GLY GLY ARG PRO ALA THR ARG LEU THR ARG GLY K38 N39 V40 P41 M42 L43 H44 K47 A48 M49 L52 Y68 W69 I76 GLN TYR LEU ARG ASP TYR LEU HIS LEU PRO PRO GLU ILE VAL P91 R95 ARG SER ARG ARG GLU

GLY GLN PRO PRO GLN

- Molecule 59: Small ribosomal subunit protein uS17

Chain SL:  75% 8% 16%

MET ALA ASP ILE Q5 Y10 K21 ARG VAL LEU LEU GLY GLU THR GLY LYS LYS L33 P61 V66 T78 K79 M80 K81 I86 R89 I96 K136 T137 K144 K147 ALA ALA GLY THR THR LYS GLN PHE GLN LYS PHE

- Molecule 60: 40S ribosomal protein S13

Chain SN:  83% 11% 6%

MET G2 K9 A15 L16 P17 R19 T29 V33 T46 I50 I53 L54 R55 A61 H80 R114 K130 W139 S143 SER THR ALA SER ALA LEU VAL ALA

- Molecule 61: 40S ribosomal protein S14

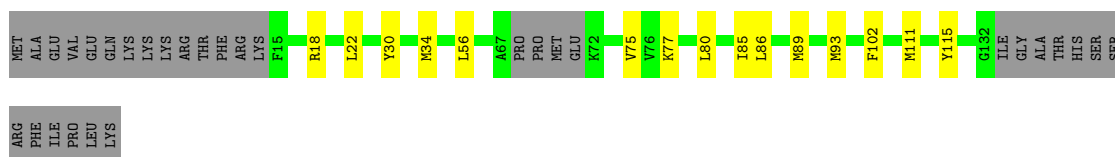
Chain SO:  66% 15% 18%

MET ALA PRO ARG LYS LYS GLU LYS GLU GLU GLN VAL ILE SER LEU LEU GLY PRO VAL V26 V27 F28 T45 S48 G49 K50 E51 G59 M60 K61 E68 Y72 K75 L76 A77 A78 Q79 I95 Q113 R117 A118 K125 I129

T133 P134 I135 P136 S137 S139 R146 R150 LEU

- Molecule 62: 40S ribosomal protein S15

Chain SP:  68% 10% 21%



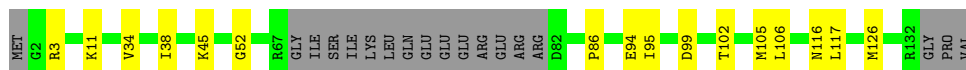
- Molecule 63: 40S ribosomal protein S16

Chain SQ: 80% 15% ..



- Molecule 64: 40S ribosomal protein S17

Chain SR: 75% 12% 13%



- Molecule 65: 40S ribosomal protein S18

Chain SS: 70% 22% 9%



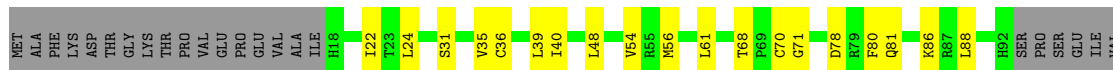
- Molecule 66: Small ribosomal subunit protein eS19

Chain ST: 84% 12% ..



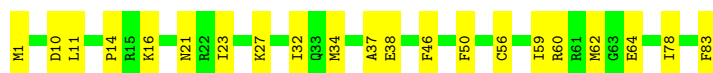
- Molecule 67: 40S ribosomal protein S20

Chain SU: 52% 18% 30%



- Molecule 68: 40S ribosomal protein S21

Chain SV: 75% 25%



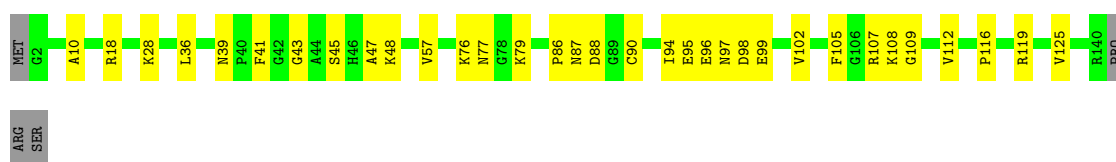
- Molecule 69: 40S ribosomal protein S15a

Chain SW: 79% 20% .



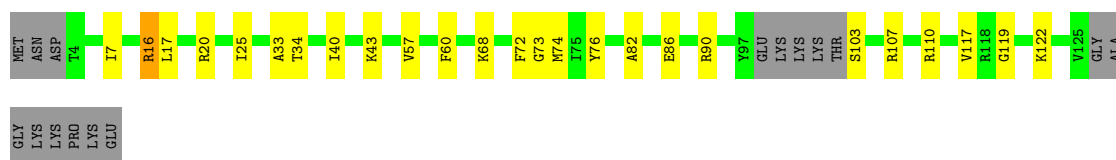
- Molecule 70: 40S ribosomal protein S23

Chain SX: 74% 23% .



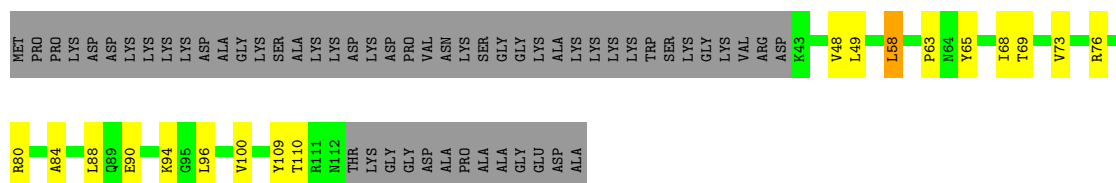
- Molecule 71: 40S ribosomal protein S24

Chain SY: 69% 18% 12% .



- Molecule 72: Small ribosomal subunit protein eS25

Chain SZ: 42% 14% 44% .



- Molecule 73: 40S ribosomal protein S26

Chain Sa: 70% 15% 15% .

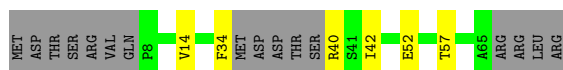


- Molecule 74: 40S ribosomal protein S27

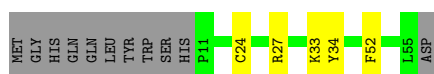
Chain Sb: 61% 12% 27% .



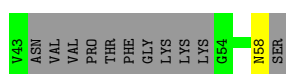
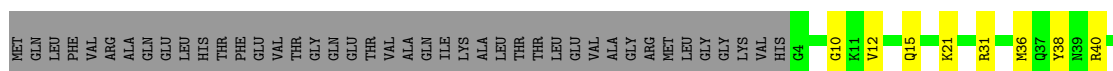
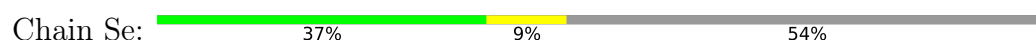
- Molecule 75: 40S ribosomal protein S28



- Molecule 76: 40S ribosomal protein S29



- Molecule 77: FAU ubiquitin like and ribosomal protein S30 fusion



- Molecule 78: RS8_HUMAN Small ribosomal subunit protein eS8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	386469	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 ($e^-/\text{\AA}^2$)	36.8	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	0.176	Depositor
Minimum map value	-0.067	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	395.52, 395.52, 395.52	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: OMU, MA6, NMM, PSU, OMG, 1MA, A2M, MG, 4AC, UY1, NA, 6MZ, UR3, G7M, OMC, HIC, 5MC, V5N, K, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	L5	0.18	2/70851 (0.0%)	0.32	0/110438
2	L7	0.13	0/2836	0.27	0/4421
3	L8	0.15	0/3336	0.27	0/5194
4	LA	0.12	0/1843	0.33	0/2490
5	LB	0.22	0/3015	0.36	0/4070
6	LC	0.11	0/2774	0.27	0/3742
7	LD	0.12	0/2178	0.27	0/2940
8	LE	0.11	0/1525	0.26	0/2054
9	LF	0.11	0/1807	0.28	0/2418
10	LG	0.10	0/1525	0.25	0/2081
11	LH	0.10	0/1337	0.25	0/1815
12	LI	0.10	0/1513	0.25	0/2045
13	LJ	0.10	0/978	0.27	0/1319
14	LL	0.10	0/1433	0.26	0/1941
15	LM	0.11	0/1084	0.24	0/1457
16	LN	0.11	0/1740	0.29	0/2331
17	LO	0.12	0/1611	0.27	0/2166
18	LP	0.11	0/1207	0.29	0/1624
19	LQ	0.12	0/1497	0.31	0/2008
20	LR	0.10	0/1206	0.24	0/1609
21	LS	0.12	0/1413	0.28	0/1901
22	LT	0.11	0/1189	0.30	0/1595
23	LU	0.09	0/606	0.31	0/823
24	LV	0.11	0/946	0.29	0/1279
25	LW	0.10	0/490	0.23	0/662
26	LX	0.11	0/915	0.27	0/1242
27	LY	0.09	0/1015	0.26	0/1364
28	LZ	0.11	0/1060	0.27	0/1430
29	La	0.11	0/1131	0.28	0/1513
30	Lb	0.09	0/622	0.24	0/838
31	Lc	0.09	0/639	0.22	0/867

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Ld	0.11	0/782	0.27	0/1059
33	Le	0.12	0/1006	0.32	0/1354
34	Lf	0.11	0/845	0.29	0/1139
35	Lg	0.11	0/782	0.28	0/1048
36	Lh	0.10	0/942	0.22	0/1259
37	Li	0.09	0/692	0.23	0/929
38	Lj	0.12	0/702	0.29	0/932
39	Lk	0.10	0/451	0.28	0/611
40	Ll	0.11	0/410	0.26	0/548
41	Lm	0.10	0/367	0.27	0/492
42	Ln	0.14	0/194	0.30	0/254
43	Lo	0.11	0/735	0.26	0/978
44	Lp	0.10	0/655	0.27	0/877
45	Lr	0.11	0/946	0.25	0/1273
46	S2	0.19	4/33571 (0.0%)	0.30	0/52275
47	S6	0.13	0/313	0.26	0/484
48	SA	0.09	0/1606	0.25	0/2190
49	SB	0.10	0/1626	0.25	0/2192
50	SC	0.10	0/1581	0.25	0/2154
51	SD	0.10	0/1393	0.23	0/1902
52	SE	0.09	0/1985	0.26	0/2692
53	SF	0.09	0/1349	0.24	0/1824
54	SG	0.10	0/1302	0.24	0/1757
55	SH	0.09	0/1033	0.23	0/1403
56	SI	0.09	0/1313	0.25	0/1773
57	SJ	0.09	0/1353	0.21	0/1835
58	SK	0.10	0/613	0.25	0/834
59	SL	0.10	0/1037	0.24	0/1401
60	SN	0.09	0/1101	0.23	0/1497
61	SO	0.11	0/903	0.27	0/1215
62	SP	0.08	0/857	0.21	0/1159
63	SQ	0.09	0/1082	0.25	0/1455
64	SR	0.08	0/852	0.21	0/1157
65	SS	0.10	0/1075	0.29	1/1455 (0.1%)
66	ST	0.08	0/1061	0.22	0/1431
67	SU	0.08	0/607	0.21	0/822
68	SV	0.09	0/629	0.22	0/844
69	SW	0.10	0/1037	0.25	0/1390
70	SX	0.09	0/1077	0.25	0/1442
71	SY	0.08	0/950	0.23	0/1267
72	SZ	0.08	0/524	0.22	0/715
73	Sa	0.10	0/753	0.23	0/1016
74	Sb	0.09	0/470	0.24	0/629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Sc	0.08	0/371	0.21	0/500
76	Sd	0.10	0/362	0.23	0/480
77	Se	0.07	0/343	0.21	0/451
78	Sg	0.08	0/2080	0.24	0/2838
All	All	0.16	6/191040 (0.0%)	0.29	1/280909 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	1530	A2M	O3'-P	5.26	1.61	1.56
46	S2	576	A2M	O3'-P	5.08	1.61	1.56
46	S2	484	A2M	O3'-P	5.08	1.61	1.56
1	L5	3771	A2M	O3'-P	5.03	1.61	1.56
46	S2	1031	A2M	O3'-P	5.01	1.61	1.56

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	SS	100	ALA	CB-CA-C	-5.69	110.03	116.63

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	65889	0	33349	1112	0
2	L7	2538	0	1286	37	0
3	L8	3072	0	1561	70	0
4	LA	1805	0	1803	24	0
5	LB	2962	0	2899	48	0
6	LC	2721	0	2817	34	0
7	LD	2135	0	2062	34	0
8	LE	1495	0	1586	29	0
9	LF	1773	0	1838	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	LG	1496	0	1464	20	0
11	LH	1320	0	1283	36	0
12	LI	1475	0	1389	24	0
13	LJ	965	0	899	47	0
14	LL	1406	0	1385	14	0
15	LM	1062	0	1084	30	0
16	LN	1695	0	1738	25	0
17	LO	1579	0	1669	33	0
18	LP	1182	0	1184	16	0
19	LQ	1473	0	1543	19	0
20	LR	1190	0	1249	22	0
21	LS	1376	0	1375	26	0
22	LT	1164	0	1194	19	0
23	LU	599	0	518	20	0
24	LV	932	0	945	15	0
25	LW	477	0	440	10	0
26	LX	898	0	922	7	0
27	LY	998	0	1022	18	0
28	LZ	1037	0	1032	27	0
29	La	1116	0	1130	16	0
30	Lb	610	0	558	5	0
31	Lc	629	0	614	9	0
32	Ld	769	0	787	18	0
33	Le	988	0	1020	14	0
34	Lf	826	0	829	6	0
35	Lg	772	0	813	9	0
36	Lh	934	0	983	13	0
37	Li	682	0	667	11	0
38	Lj	687	0	695	12	0
39	Lk	446	0	406	4	0
40	Ll	400	0	404	4	0
41	Lm	361	0	347	3	0
42	Ln	193	0	192	5	0
43	Lo	723	0	741	14	0
44	Lp	645	0	661	13	0
45	Lr	933	0	955	7	0
46	S2	31690	13	16052	659	0
47	S6	281	0	145	17	0
48	SA	1571	0	1565	35	0
49	SB	1599	0	1585	46	0
50	SC	1546	0	1535	33	0
51	SD	1372	0	1271	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	SE	1943	0	1960	34	0
53	SF	1329	0	1317	16	0
54	SG	1287	0	1247	24	0
55	SH	1021	0	949	24	0
56	SI	1288	0	1237	32	0
57	SJ	1328	0	1293	11	0
58	SK	595	0	546	24	0
59	SL	1017	0	984	10	0
60	SN	1077	0	1070	16	0
61	SO	892	0	888	22	0
62	SP	841	0	813	11	0
63	SQ	1065	0	1095	17	0
64	SR	839	0	804	17	0
65	SS	1057	0	1059	25	0
66	ST	1055	0	1034	16	0
67	SU	601	0	596	14	0
68	SV	622	0	609	16	0
69	SW	1020	0	1054	20	0
70	SX	1060	0	1106	26	0
71	SY	934	0	970	20	0
72	SZ	518	0	522	12	0
73	Sa	740	0	764	16	0
74	Sb	463	0	466	8	0
75	Sc	370	0	364	6	0
76	Sd	356	0	344	5	0
77	Se	341	0	360	9	0
78	Sg	2031	0	1911	56	0
79	L5	139	0	0	0	0
79	L7	3	0	0	0	0
79	L8	3	0	0	0	0
79	LP	1	0	0	0	0
79	LV	1	0	0	0	0
79	S2	16	0	0	0	0
80	L5	51	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	LN	1	0	0	0	0
80	Lb	1	0	0	0	0
80	Le	1	0	0	0	0
80	Lf	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	Lo	1	0	0	0	0
80	S2	11	0	0	0	0
80	SL	1	0	0	0	0
80	SO	1	0	0	0	0
80	Sd	1	0	0	0	0
81	L5	12	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	1500	0	0	7	0
83	L7	14	0	0	0	0
83	L8	32	0	0	0	0
83	LA	22	0	0	0	0
83	LB	26	0	0	0	0
83	LC	25	0	0	0	0
83	LD	1	0	0	0	0
83	LF	14	0	0	0	0
83	LG	2	0	0	0	0
83	LH	1	0	0	0	0
83	LL	14	0	0	0	0
83	LM	1	0	0	0	0
83	LN	19	0	0	1	0
83	LO	9	0	0	0	0
83	LP	11	0	0	0	0
83	LQ	18	0	0	0	0
83	LR	3	0	0	0	0
83	LS	2	0	0	0	0
83	LT	11	0	0	0	0
83	LV	3	0	0	0	0
83	LW	1	0	0	0	0
83	LX	2	0	0	0	0
83	LY	2	0	0	0	0
83	LZ	1	0	0	0	0
83	La	23	0	0	1	0
83	Lb	5	0	0	0	0
83	Ld	2	0	0	0	0
83	Le	12	0	0	0	0
83	Lf	9	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	Lg	9	0	0	0	0
83	Li	1	0	0	0	0
83	Lj	11	0	0	0	0
83	Ll	2	0	0	0	0
83	Ln	3	0	0	0	0
83	Lo	7	0	0	0	0
83	Lp	3	0	0	0	0
83	Lr	4	0	0	0	0
83	S2	202	0	0	2	0
83	S6	2	0	0	0	0
83	SI	2	0	0	1	0
83	SL	2	0	0	0	0
83	SN	1	0	0	0	0
83	SO	1	0	0	0	0
83	SQ	1	0	0	0	0
83	SS	2	0	0	0	0
83	SU	1	0	0	0	0
83	SX	1	0	0	0	0
83	Sa	2	0	0	0	0
All	All	184476	13	130853	2984	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 10.

The worst 5 of 2984 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)
15:LM:112:VAL:HG11	17:LO:201:LEU:HD11	1.28	1.12
46:S2:1362:U:H4'	46:S2:1371:U:H3	1.18	1.08
15:LM:112:VAL:CG1	17:LO:201:LEU:HD11	1.92	0.99
17:LO:175:MET:HE3	17:LO:179:LYS:HD3	1.44	0.98
49:SB:110:MET:SD	49:SB:113:MET:CE	2.52	0.98

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	243/257 (95%)	236 (97%)	7 (3%)	0	100	100
5	LB	386/403 (96%)	378 (98%)	8 (2%)	0	100	100
6	LC	348/427 (82%)	342 (98%)	6 (2%)	0	100	100
7	LD	273/297 (92%)	271 (99%)	2 (1%)	0	100	100
8	LE	182/288 (63%)	180 (99%)	2 (1%)	0	100	100
9	LF	216/248 (87%)	211 (98%)	5 (2%)	0	100	100
10	LG	196/266 (74%)	192 (98%)	4 (2%)	0	100	100
11	LH	174/192 (91%)	170 (98%)	4 (2%)	0	100	100
12	LI	191/214 (89%)	185 (97%)	6 (3%)	0	100	100
13	LJ	128/178 (72%)	125 (98%)	3 (2%)	0	100	100
14	LL	182/211 (86%)	179 (98%)	3 (2%)	0	100	100
15	LM	130/215 (60%)	126 (97%)	4 (3%)	0	100	100
16	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
17	LO	196/203 (97%)	193 (98%)	3 (2%)	0	100	100
18	LP	146/184 (79%)	144 (99%)	2 (1%)	0	100	100
19	LQ	185/188 (98%)	183 (99%)	2 (1%)	0	100	100
20	LR	150/196 (76%)	149 (99%)	1 (1%)	0	100	100
21	LS	166/176 (94%)	165 (99%)	1 (1%)	0	100	100
22	LT	144/160 (90%)	143 (99%)	1 (1%)	0	100	100
23	LU	80/128 (62%)	72 (90%)	8 (10%)	0	100	100
24	LV	128/140 (91%)	127 (99%)	1 (1%)	0	100	100
25	LW	59/157 (38%)	59 (100%)	0	0	100	100
26	LX	115/156 (74%)	114 (99%)	1 (1%)	0	100	100
27	LY	126/145 (87%)	123 (98%)	3 (2%)	0	100	100
28	LZ	133/136 (98%)	130 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	140/148 (95%)	135 (96%)	4 (3%)	1 (1%)	18	15
30	Lb	80/159 (50%)	79 (99%)	1 (1%)	0	100	100
31	Lc	83/115 (72%)	83 (100%)	0	0	100	100
32	Ld	93/125 (74%)	93 (100%)	0	0	100	100
33	Le	124/135 (92%)	123 (99%)	1 (1%)	0	100	100
34	Lf	105/110 (96%)	104 (99%)	1 (1%)	0	100	100
35	Lg	99/117 (85%)	99 (100%)	0	0	100	100
36	Lh	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
37	Li	88/105 (84%)	88 (100%)	0	0	100	100
38	Lj	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
39	Lk	60/70 (86%)	59 (98%)	1 (2%)	0	100	100
40	Ll	47/51 (92%)	46 (98%)	1 (2%)	0	100	100
41	Lm	46/128 (36%)	46 (100%)	0	0	100	100
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	91/106 (86%)	89 (98%)	2 (2%)	0	100	100
44	Lp	85/92 (92%)	80 (94%)	5 (6%)	0	100	100
45	Lr	116/137 (85%)	116 (100%)	0	0	100	100
48	SA	203/295 (69%)	197 (97%)	6 (3%)	0	100	100
49	SB	207/264 (78%)	203 (98%)	4 (2%)	0	100	100
50	SC	210/293 (72%)	206 (98%)	4 (2%)	0	100	100
51	SD	202/243 (83%)	199 (98%)	3 (2%)	0	100	100
52	SE	255/263 (97%)	253 (99%)	2 (1%)	0	100	100
53	SF	174/204 (85%)	167 (96%)	7 (4%)	0	100	100
54	SG	167/249 (67%)	164 (98%)	2 (1%)	1 (1%)	21	18
55	SH	132/194 (68%)	131 (99%)	1 (1%)	0	100	100
56	SI	165/208 (79%)	161 (98%)	4 (2%)	0	100	100
57	SJ	176/194 (91%)	173 (98%)	3 (2%)	0	100	100
58	SK	77/165 (47%)	75 (97%)	2 (3%)	0	100	100
59	SL	128/158 (81%)	128 (100%)	0	0	100	100
60	SN	140/151 (93%)	140 (100%)	0	0	100	100
61	SO	120/151 (80%)	119 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	SP	110/145 (76%)	109 (99%)	1 (1%)	0	100	100
63	SQ	138/146 (94%)	135 (98%)	3 (2%)	0	100	100
64	SR	113/135 (84%)	110 (97%)	3 (3%)	0	100	100
65	SS	137/152 (90%)	135 (98%)	2 (2%)	0	100	100
66	ST	139/145 (96%)	137 (99%)	2 (1%)	0	100	100
67	SU	79/119 (66%)	77 (98%)	2 (2%)	0	100	100
68	SV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
69	SW	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
70	SX	137/143 (96%)	135 (98%)	2 (2%)	0	100	100
71	SY	113/133 (85%)	113 (100%)	0	0	100	100
72	SZ	68/125 (54%)	68 (100%)	0	0	100	100
73	Sa	96/115 (84%)	96 (100%)	0	0	100	100
74	Sb	53/84 (63%)	51 (96%)	2 (4%)	0	100	100
75	Sc	49/69 (71%)	48 (98%)	1 (2%)	0	100	100
76	Sd	43/56 (77%)	43 (100%)	0	0	100	100
77	Se	41/98 (42%)	41 (100%)	0	0	100	100
78	Sg	259/308 (84%)	252 (97%)	7 (3%)	0	100	100
All	All	10100/12430 (81%)	9928 (98%)	170 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
54	SG	132	ARG
29	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	LA	170/199 (85%)	170 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	LB	287/348 (82%)	285 (99%)	2 (1%)	76	83
6	LC	277/348 (80%)	277 (100%)	0	100	100
7	LD	204/250 (82%)	203 (100%)	1 (0%)	81	88
8	LE	161/252 (64%)	161 (100%)	0	100	100
9	LF	179/215 (83%)	179 (100%)	0	100	100
10	LG	141/223 (63%)	141 (100%)	0	100	100
11	LH	129/171 (75%)	128 (99%)	1 (1%)	73	81
12	LI	140/182 (77%)	140 (100%)	0	100	100
13	LJ	84/149 (56%)	83 (99%)	1 (1%)	63	72
14	LL	129/177 (73%)	129 (100%)	0	100	100
15	LM	106/161 (66%)	106 (100%)	0	100	100
16	LN	170/172 (99%)	170 (100%)	0	100	100
17	LO	159/174 (91%)	158 (99%)	1 (1%)	78	86
18	LP	122/163 (75%)	122 (100%)	0	100	100
19	LQ	155/165 (94%)	154 (99%)	1 (1%)	78	86
20	LR	116/175 (66%)	116 (100%)	0	100	100
21	LS	143/157 (91%)	143 (100%)	0	100	100
22	LT	119/140 (85%)	118 (99%)	1 (1%)	73	81
23	LU	45/115 (39%)	44 (98%)	1 (2%)	45	53
24	LV	90/107 (84%)	90 (100%)	0	100	100
25	LW	45/126 (36%)	45 (100%)	0	100	100
26	LX	90/133 (68%)	90 (100%)	0	100	100
27	LY	102/135 (76%)	102 (100%)	0	100	100
28	LZ	100/118 (85%)	99 (99%)	1 (1%)	68	76
29	La	109/120 (91%)	109 (100%)	0	100	100
30	Lb	51/126 (40%)	51 (100%)	0	100	100
31	Lc	62/97 (64%)	61 (98%)	1 (2%)	55	64
32	Ld	78/110 (71%)	78 (100%)	0	100	100
33	Le	101/121 (84%)	101 (100%)	0	100	100
34	Lf	78/89 (88%)	78 (100%)	0	100	100
35	Lg	79/100 (79%)	79 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	Lh	90/110 (82%)	90 (100%)	0	100	100
37	Li	62/89 (70%)	62 (100%)	0	100	100
38	Lj	68/80 (85%)	66 (97%)	2 (3%)	37	42
39	Lk	37/65 (57%)	36 (97%)	1 (3%)	39	45
40	Ll	39/48 (81%)	39 (100%)	0	100	100
41	Lm	36/116 (31%)	35 (97%)	1 (3%)	38	43
42	Ln	14/24 (58%)	14 (100%)	0	100	100
43	Lo	73/94 (78%)	73 (100%)	0	100	100
44	Lp	64/75 (85%)	64 (100%)	0	100	100
45	Lr	97/121 (80%)	96 (99%)	1 (1%)	68	76
48	SA	159/243 (65%)	158 (99%)	1 (1%)	78	86
49	SB	162/231 (70%)	161 (99%)	1 (1%)	78	86
50	SC	153/225 (68%)	153 (100%)	0	100	100
51	SD	112/202 (55%)	109 (97%)	3 (3%)	39	45
52	SE	195/225 (87%)	194 (100%)	1 (0%)	81	88
53	SF	127/170 (75%)	126 (99%)	1 (1%)	73	81
54	SG	113/218 (52%)	113 (100%)	0	100	100
55	SH	89/174 (51%)	87 (98%)	2 (2%)	45	53
56	SI	122/180 (68%)	120 (98%)	2 (2%)	55	64
57	SJ	117/168 (70%)	117 (100%)	0	100	100
58	SK	50/136 (37%)	49 (98%)	1 (2%)	48	56
59	SL	102/142 (72%)	101 (99%)	1 (1%)	68	76
60	SN	104/131 (79%)	104 (100%)	0	100	100
61	SO	87/119 (73%)	86 (99%)	1 (1%)	65	74
62	SP	78/130 (60%)	78 (100%)	0	100	100
63	SQ	103/121 (85%)	102 (99%)	1 (1%)	68	76
64	SR	77/122 (63%)	77 (100%)	0	100	100
65	SS	98/132 (74%)	97 (99%)	1 (1%)	68	76
66	ST	97/114 (85%)	96 (99%)	1 (1%)	68	76
67	SU	59/107 (55%)	58 (98%)	1 (2%)	53	62
68	SV	63/67 (94%)	63 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	SW	109/113 (96%)	109 (100%)	0	100	100
70	SX	106/115 (92%)	106 (100%)	0	100	100
71	SY	95/115 (83%)	93 (98%)	2 (2%)	47	54
72	SZ	52/103 (50%)	51 (98%)	1 (2%)	50	58
73	Sa	76/98 (78%)	76 (100%)	0	100	100
74	Sb	49/76 (64%)	49 (100%)	0	100	100
75	Sc	35/62 (56%)	35 (100%)	0	100	100
76	Sd	36/49 (74%)	36 (100%)	0	100	100
77	Se	31/79 (39%)	31 (100%)	0	100	100
78	Sg	206/235 (88%)	206 (100%)	0	100	100
All	All	7663/10542 (73%)	7626 (100%)	37 (0%)	78	88

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	SL	144	LYS
71	SY	68	LYS
61	SO	117	ARG
66	ST	123	LEU
38	Lj	65	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72 such sidechains are listed below:

Mol	Chain	Res	Type
54	SG	110	ASN
77	Se	37	GLN
55	SH	68	GLN
60	SN	90	HIS
23	LU	27	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3015/5054 (59%)	390 (12%)	7 (0%)
2	L7	118/121 (97%)	8 (6%)	0
3	L8	141/156 (90%)	14 (9%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	S2	1454/1869 (77%)	222 (15%)	11 (0%)
47	S6	11/14 (78%)	2 (18%)	0
All	All	4739/7214 (65%)	636 (13%)	18 (0%)

5 of 636 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	3	C
1	L5	13	U
1	L5	39	A
1	L5	42	A

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	S2	1365	G
46	S2	1805	G
46	S2	1646	C
46	S2	671	A
46	S2	1344	A

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

204 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	$\# Z > 2$
46	A2M	S2	1031	46	22,25,26	4.11	12 (54%)	31,36,39	3.31	13 (41%)
46	PSU	S2	1445	46	18,21,22	1.07	1 (5%)	22,30,33	1.78	3 (13%)
1	OMG	L5	1621	1,80	23,26,27	0.52	0	33,38,41	0.47	0
1	OMG	L5	4623	1,80	23,26,27	0.50	0	33,38,41	0.49	0
46	PSU	S2	100	46,79	18,21,22	1.05	1 (5%)	22,30,33	1.87	4 (18%)
1	1MA	L5	1318	79,1	21,25,26	0.47	0	31,37,40	0.76	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	L5	3625	1	18,21,22	1.17	1 (5%)	22,30,33	1.77	5 (22%)
1	OMC	L5	2794	1	19,22,23	0.52	0	26,31,34	0.57	0
46	OMU	S2	121	46	19,22,23	3.21	8 (42%)	26,31,34	1.61	4 (15%)
46	OMG	S2	683	46	23,26,27	0.51	0	33,38,41	0.63	0
46	PSU	S2	36	46	18,21,22	1.08	1 (5%)	22,30,33	1.76	5 (22%)
1	PSU	L5	4409	1	18,21,22	1.08	1 (5%)	22,30,33	1.79	5 (22%)
3	OMU	L8	14	3,1	19,22,23	3.25	8 (42%)	26,31,34	1.68	5 (19%)
1	OMC	L5	2412	79,1	19,22,23	0.55	0	26,31,34	0.50	0
1	OMC	L5	2355	1	19,22,23	0.54	0	26,31,34	0.55	0
46	PSU	S2	918	46	18,21,22	1.13	2 (11%)	22,30,33	1.86	5 (22%)
46	PSU	S2	1174	46	18,21,22	1.10	1 (5%)	22,30,33	1.78	4 (18%)
1	OMG	L5	3613	1	23,26,27	0.50	0	33,38,41	0.65	0
1	A2M	L5	3704	1	22,25,26	4.13	12 (54%)	31,36,39	3.36	12 (38%)
1	A2M	L5	400	1	22,25,26	4.11	12 (54%)	31,36,39	3.30	12 (38%)
1	PSU	L5	4457	1	18,21,22	1.10	1 (5%)	22,30,33	1.75	5 (22%)
46	PSU	S2	866	46	18,21,22	0.88	1 (5%)	22,30,33	0.53	0
1	A2M	L5	3771	1	22,25,26	4.11	12 (54%)	31,36,39	3.38	14 (45%)
1	PSU	L5	3808	1	18,21,22	1.07	1 (5%)	22,30,33	1.81	5 (22%)
46	A2M	S2	166	46	22,25,26	4.13	12 (54%)	31,36,39	3.44	14 (45%)
46	A2M	S2	1678	46	22,25,26	4.14	12 (54%)	31,36,39	3.39	11 (35%)
46	4AC	S2	1842	46	21,24,25	3.38	10 (47%)	29,34,37	0.94	2 (6%)
1	A2M	L5	1319	1	22,25,26	4.13	12 (54%)	31,36,39	3.21	11 (35%)
1	PSU	L5	3837	1	18,21,22	1.06	1 (5%)	22,30,33	1.85	4 (18%)
1	PSU	L5	4339	1	18,21,22	1.05	1 (5%)	22,30,33	1.72	2 (9%)
46	PSU	S2	801	46	18,21,22	1.10	1 (5%)	22,30,33	1.73	5 (22%)
46	OMG	S2	509	46	23,26,27	0.50	0	33,38,41	0.56	0
1	PSU	L5	4958	1	18,21,22	1.09	1 (5%)	22,30,33	1.76	4 (18%)
3	PSU	L8	55	3	18,21,22	1.08	1 (5%)	22,30,33	1.69	2 (9%)
46	PSU	S2	406	46	18,21,22	1.09	1 (5%)	22,30,33	1.77	5 (22%)
46	OMG	S2	601	46	23,26,27	0.49	0	33,38,41	0.44	0
1	OMC	L5	2814	1	19,22,23	0.53	0	26,31,34	0.61	0
1	OMG	L5	4214	1	23,26,27	0.50	0	33,38,41	0.67	0
1	PSU	L5	4622	1	18,21,22	1.03	1 (5%)	22,30,33	1.91	5 (22%)
1	OMC	L5	1336	1	19,22,23	0.54	0	26,31,34	0.62	0
1	OMG	L5	2354	1	23,26,27	0.49	0	33,38,41	0.52	0
29	V5N	La	39	29	9,11,12	0.69	0	9,14,16	1.25	1 (11%)
1	OMC	L5	3873	1	19,22,23	0.58	0	26,31,34	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
46	PSU	S2	1046	46	18,21,22	1.07	1 (5%)	22,30,33	1.73	3 (13%)
1	A2M	L5	3710	1	22,25,26	4.14	12 (54%)	31,36,39	3.35	12 (38%)
1	OMG	L5	4480	1	23,26,27	0.49	0	33,38,41	0.50	0
46	OMC	S2	174	46	19,22,23	0.55	0	26,31,34	0.57	0
1	A2M	L5	2353	79,1	22,25,26	4.14	12 (54%)	31,36,39	3.21	12 (38%)
1	PSU	L5	4614	1	18,21,22	1.11	1 (5%)	22,30,33	1.79	4 (18%)
3	PSU	L8	69	3	18,21,22	1.11	1 (5%)	22,30,33	1.82	6 (27%)
1	PSU	L5	2829	1	18,21,22	1.11	1 (5%)	22,30,33	1.86	5 (22%)
46	OMG	S2	644	46	23,26,27	0.48	0	33,38,41	0.49	0
1	PSU	L5	1679	1	18,21,22	1.09	1 (5%)	22,30,33	1.64	4 (18%)
1	PSU	L5	1777	1	18,21,22	1.05	1 (5%)	22,30,33	1.73	3 (13%)
1	PSU	L5	1788	1,80	18,21,22	1.10	1 (5%)	22,30,33	1.77	5 (22%)
1	6MZ	L5	4206	1	22,25,26	2.53	4 (18%)	30,36,39	2.48	11 (36%)
46	G7M	S2	1639	46	23,26,27	2.87	10 (43%)	35,39,42	2.13	10 (28%)
1	PSU	L5	1856	1	18,21,22	1.06	1 (5%)	22,30,33	1.75	4 (18%)
46	PSU	S2	1232	46	18,21,22	1.05	1 (5%)	22,30,33	1.78	3 (13%)
1	5MC	L5	4433	1,80	18,22,23	0.66	0	26,32,35	0.68	0
1	A2M	L5	1530	79,1	22,25,26	4.10	12 (54%)	31,36,39	3.26	11 (35%)
46	A2M	S2	484	46	22,25,26	4.10	12 (54%)	31,36,39	3.33	11 (35%)
46	PSU	S2	1136	46	18,21,22	1.11	1 (5%)	22,30,33	1.87	5 (22%)
1	OMC	L5	4442	1	19,22,23	0.52	0	26,31,34	0.53	0
1	PSU	L5	4957	1	18,21,22	1.11	1 (5%)	22,30,33	1.81	4 (18%)
46	PSU	S2	1244	46	18,21,22	1.09	1 (5%)	22,30,33	1.77	4 (18%)
46	OMC	S2	1391	46	19,22,23	0.52	0	26,31,34	0.58	0
1	OMG	L5	4182	79,1	23,26,27	0.49	0	33,38,41	0.46	0
1	OMC	L5	3855	1	19,22,23	0.57	0	26,31,34	0.54	0
46	PSU	S2	822	46	18,21,22	1.10	1 (5%)	22,30,33	1.76	5 (22%)
1	PSU	L5	3906	79,1	18,21,22	1.07	1 (5%)	22,30,33	1.81	4 (18%)
46	PSU	S2	572	46	18,21,22	1.07	1 (5%)	22,30,33	1.71	4 (18%)
1	PSU	L5	1775	1	18,21,22	1.07	1 (5%)	22,30,33	1.77	4 (18%)
1	A2M	L5	2805	1	22,25,26	4.08	12 (54%)	31,36,39	3.32	12 (38%)
1	PSU	L5	4282	1	18,21,22	1.08	1 (5%)	22,30,33	1.71	3 (13%)
1	OMG	L5	1518	1	23,26,27	0.55	0	33,38,41	0.59	0
1	PSU	L5	3701	1	18,21,22	1.09	1 (5%)	22,30,33	1.77	5 (22%)
46	PSU	S2	1625	46	18,21,22	1.07	1 (5%)	22,30,33	1.80	5 (22%)
1	PSU	L5	4562	1	18,21,22	1.07	1 (5%)	22,30,33	1.70	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
46	PSU	S2	1643	46	18,21,22	1.08	1 (5%)	22,30,33	1.74	5 (22%)
1	PSU	L5	3870	1	18,21,22	1.08	1 (5%)	22,30,33	1.68	4 (18%)
1	PSU	L5	4285	1	18,21,22	1.06	1 (5%)	22,30,33	1.77	4 (18%)
46	UY1	S2	1326	46	19,22,23	0.35	0	22,31,34	0.82	1 (4%)
3	OMG	L8	75	3	23,26,27	0.47	0	33,38,41	0.51	0
1	PSU	L5	4417	1	18,21,22	1.07	1 (5%)	22,30,33	1.79	4 (18%)
1	PSU	L5	2498	1	18,21,22	0.88	1 (5%)	22,30,33	0.66	0
46	6MZ	S2	1832	46,79,80	22,25,26	2.52	4 (18%)	30,36,39	2.45	11 (36%)
1	A2M	L5	4509	79,1	22,25,26	4.12	11 (50%)	31,36,39	3.34	12 (38%)
46	OMU	S2	116	46	19,22,23	3.24	8 (42%)	26,31,34	1.72	5 (19%)
1	OMG	L5	3730	1	23,26,27	0.50	0	33,38,41	0.49	0
46	PSU	S2	667	46	18,21,22	1.14	1 (5%)	22,30,33	1.77	6 (27%)
1	OMU	L5	4292	1	19,22,23	3.19	8 (42%)	26,31,34	1.66	5 (19%)
1	PSU	L5	3623	1,80	18,21,22	1.05	1 (5%)	22,30,33	1.88	4 (18%)
1	OMG	L5	4609	1	23,26,27	0.50	0	33,38,41	0.59	0
1	PSU	L5	4995	1	18,21,22	1.09	1 (5%)	22,30,33	1.73	4 (18%)
46	A2M	S2	576	46	22,25,26	4.16	12 (54%)	31,36,39	3.37	13 (41%)
1	A2M	L5	1520	1	22,25,26	4.11	11 (50%)	31,36,39	3.33	11 (35%)
46	OMC	S2	517	46	19,22,23	0.53	0	26,31,34	0.62	0
66	NMM	ST	67	66	9,11,12	0.61	0	6,12,14	2.64	2 (33%)
1	OMG	L5	4604	1	23,26,27	0.51	0	33,38,41	0.60	0
46	A2M	S2	27	46	22,25,26	4.12	11 (50%)	31,36,39	3.25	12 (38%)
1	PSU	L5	4538	1	18,21,22	1.06	1 (5%)	22,30,33	1.79	5 (22%)
1	A2M	L5	2777	1	22,25,26	4.08	12 (54%)	31,36,39	3.05	12 (38%)
46	A2M	S2	590	46	22,25,26	4.13	12 (54%)	31,36,39	3.48	12 (38%)
1	OMU	L5	3911	1	19,22,23	3.21	8 (42%)	26,31,34	1.62	4 (15%)
1	PSU	L5	4279	1	18,21,22	1.10	1 (5%)	22,30,33	1.75	3 (13%)
1	PSU	L5	4443	1	18,21,22	1.05	1 (5%)	22,30,33	1.70	3 (13%)
46	PSU	S2	609	46	18,21,22	1.08	1 (5%)	22,30,33	1.73	5 (22%)
46	PSU	S2	34	46	18,21,22	1.07	1 (5%)	22,30,33	1.80	4 (18%)
46	PSU	S2	119	46	18,21,22	1.05	1 (5%)	22,30,33	1.73	4 (18%)
46	PSU	S2	1238	46	18,21,22	1.09	1 (5%)	22,30,33	1.82	4 (18%)
1	OMG	L5	4378	1	23,26,27	0.47	0	33,38,41	0.49	0
1	OMC	L5	1877	79,1	19,22,23	0.56	0	26,31,34	0.64	0
1	OMG	L5	2414	1	23,26,27	0.50	0	33,38,41	0.46	0
1	PSU	L5	1673	1	18,21,22	1.09	2 (11%)	22,30,33	1.91	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	L5	3839	79,1	18,21,22	1.08	1 (5%)	22,30,33	1.86	5 (22%)
46	PSU	S2	1692	46	18,21,22	1.11	1 (5%)	22,30,33	1.72	3 (13%)
1	OMU	L5	2827	1	19,22,23	3.24	8 (42%)	26,31,34	1.67	5 (19%)
46	OMU	S2	354	46	19,22,23	3.21	8 (42%)	26,31,34	1.70	5 (19%)
46	A2M	S2	512	46	22,25,26	4.13	12 (54%)	31,36,39	3.30	13 (41%)
1	PSU	L5	1532	1	18,21,22	1.10	1 (5%)	22,30,33	1.65	2 (9%)
1	OMG	L5	3778	1	23,26,27	0.49	0	33,38,41	0.44	0
1	UY1	L5	3804	1,80	19,22,23	0.46	0	22,31,34	0.54	0
1	A2M	L5	4557	1	22,25,26	4.12	11 (50%)	31,36,39	3.36	10 (32%)
1	PSU	L5	1858	1	18,21,22	1.05	1 (5%)	22,30,33	1.83	5 (22%)
46	OMG	S2	867	46	23,26,27	0.29	0	33,38,41	0.44	0
1	PSU	L5	4428	1	18,21,22	1.07	1 (5%)	22,30,33	1.74	4 (18%)
1	A2M	L5	1322	1	22,25,26	4.13	12 (54%)	31,36,39	3.22	11 (35%)
46	PSU	S2	815	46	18,21,22	1.03	1 (5%)	22,30,33	1.78	4 (18%)
1	PSU	L5	1578	1	18,21,22	1.02	1 (5%)	22,30,33	1.76	3 (13%)
1	PSU	L5	2622	1	18,21,22	1.09	1 (5%)	22,30,33	1.67	5 (22%)
46	A2M	S2	99	46,79	22,25,26	4.10	11 (50%)	31,36,39	3.39	13 (41%)
5	HIC	LB	245	5	10,11,12	0.49	0	8,14,16	0.55	0
46	PSU	S2	1177	46	18,21,22	1.09	1 (5%)	22,30,33	1.75	3 (13%)
1	A2M	L5	398	1	22,25,26	4.09	12 (54%)	31,36,39	3.37	12 (38%)
1	PSU	L5	4347	1	18,21,22	1.06	1 (5%)	22,30,33	1.81	5 (22%)
1	OMG	L5	1312	1	23,26,27	0.52	0	33,38,41	0.57	0
46	OMU	S2	172	46	19,22,23	3.23	8 (42%)	26,31,34	1.72	4 (15%)
1	OMU	L5	2405	1	19,22,23	3.22	8 (42%)	26,31,34	1.60	4 (15%)
46	4AC	S2	1337	46	21,24,25	3.44	9 (42%)	29,34,37	1.37	4 (13%)
1	PSU	L5	2724	1	18,21,22	1.09	1 (5%)	22,30,33	1.83	5 (22%)
46	PSU	S2	109	46	18,21,22	1.06	1 (5%)	22,30,33	1.84	5 (22%)
1	A2M	L5	3853	1	22,25,26	4.14	12 (54%)	31,36,39	3.25	11 (35%)
1	OMU	L5	4213	1	19,22,23	3.26	8 (42%)	26,31,34	1.65	4 (15%)
46	PSU	S2	105	46	18,21,22	1.09	1 (5%)	22,30,33	1.89	5 (22%)
46	A2M	S2	468	46	22,25,26	4.14	12 (54%)	31,36,39	3.39	13 (41%)
1	PSU	L5	3681	1,80	18,21,22	1.10	1 (5%)	22,30,33	1.74	4 (18%)
46	OMU	S2	428	46	19,22,23	3.25	8 (42%)	26,31,34	1.67	4 (15%)
1	A2M	L5	3816	1	22,25,26	4.10	12 (54%)	31,36,39	3.28	12 (38%)
1	PSU	L5	4507	79,1,80	18,21,22	1.10	1 (5%)	22,30,33	1.75	4 (18%)
1	PSU	L5	3830	1	18,21,22	1.04	1 (5%)	22,30,33	1.81	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	L5	3827	1	19,22,23	0.54	0	26,31,34	0.55	0
46	A2M	S2	668	46	22,25,26	4.10	12 (54%)	31,36,39	3.26	13 (41%)
46	OMG	S2	1490	46,79	23,26,27	0.52	0	33,38,41	0.53	0
46	PSU	S2	649	46	18,21,22	1.06	1 (5%)	22,30,33	1.78	5 (22%)
46	A2M	S2	159	46	22,25,26	4.13	12 (54%)	31,36,39	3.40	12 (38%)
1	PSU	L5	4555	1	18,21,22	1.13	1 (5%)	22,30,33	1.81	5 (22%)
1	PSU	L5	4675	1	18,21,22	1.04	1 (5%)	22,30,33	1.80	3 (13%)
1	OMU	L5	4484	1	19,22,23	3.25	8 (42%)	26,31,34	1.70	5 (19%)
1	A2M	L5	4576	1	22,25,26	4.13	11 (50%)	31,36,39	3.22	13 (41%)
46	PSU	S2	863	46	18,21,22	0.86	1 (5%)	22,30,33	0.55	0
46	PSU	S2	1004	46	18,21,22	1.09	1 (5%)	22,30,33	1.68	4 (18%)
1	OMC	L5	2341	1	19,22,23	0.57	0	26,31,34	0.62	0
1	OMG	L5	2866	1	23,26,27	0.52	0	33,38,41	0.48	0
46	PSU	S2	1367	46	18,21,22	1.06	1 (5%)	22,30,33	1.75	3 (13%)
1	A2M	L5	3811	1	22,25,26	4.13	12 (54%)	31,36,39	3.24	12 (38%)
46	OMC	S2	462	46	19,22,23	0.54	0	26,31,34	0.53	0
46	MA6	S2	1851	46	23,26,27	1.51	3 (13%)	34,38,41	3.72	11 (32%)
46	PSU	S2	1045	46	18,21,22	1.09	1 (5%)	22,30,33	1.76	4 (18%)
46	PSU	S2	1056	46	18,21,22	1.07	1 (5%)	22,30,33	1.80	6 (27%)
46	OMG	S2	436	46	23,26,27	0.52	0	33,38,41	0.52	0
1	OMC	L5	2851	1	19,22,23	0.50	0	26,31,34	0.76	1 (3%)
46	PSU	S2	1239	46	18,21,22	1.11	1 (5%)	22,30,33	1.75	4 (18%)
46	PSU	S2	651	46	18,21,22	1.10	1 (5%)	22,30,33	1.78	4 (18%)
46	PSU	S2	93	46	18,21,22	1.09	1 (5%)	22,30,33	1.75	5 (22%)
46	PSU	S2	814	46	18,21,22	1.04	1 (5%)	22,30,33	1.70	3 (13%)
1	OMG	L5	4356	1	23,26,27	0.50	0	33,38,41	0.55	0
46	A2M	S2	1383	46	22,25,26	4.10	13 (59%)	31,36,39	3.40	14 (45%)
46	OMG	S2	1447	46	23,26,27	0.50	0	33,38,41	0.49	0
1	UR3	L5	4516	1	19,22,23	2.84	7 (36%)	26,32,35	1.20	1 (3%)
1	PSU	L5	4517	1	18,21,22	1.05	1 (5%)	22,30,33	1.74	4 (18%)
46	OMU	S2	1442	46	19,22,23	3.26	8 (42%)	26,31,34	1.68	4 (15%)
46	PSU	S2	686	46	18,21,22	0.88	1 (5%)	22,30,33	0.63	0
1	PSU	L5	4298	1	18,21,22	1.02	1 (5%)	22,30,33	1.76	5 (22%)
1	OMG	L5	4485	1	23,26,27	0.49	0	33,38,41	0.63	0
46	MA6	S2	1850	46	23,26,27	1.50	3 (13%)	34,38,41	3.58	11 (32%)
1	OMC	L5	3687	1,80	19,22,23	0.52	0	26,31,34	0.52	0
1	PSU	L5	4518	1	18,21,22	1.08	1 (5%)	22,30,33	1.82	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	L5	1740	1	18,21,22	1.06	1 (5%)	22,30,33	1.76	4 (18%)
1	A2M	L5	1867	79,1	22,25,26	4.12	12 (54%)	31,36,39	3.29	13 (41%)
1	OMC	L5	3794	1	19,22,23	0.56	0	26,31,34	0.63	0
1	OMU	L5	4606	1	19,22,23	3.21	8 (42%)	26,31,34	1.62	4 (15%)
1	PSU	L5	4659	1,80	18,21,22	1.08	1 (5%)	22,30,33	1.74	5 (22%)
1	PSU	L5	4986	1	18,21,22	1.11	1 (5%)	22,30,33	1.77	4 (18%)
1	A2M	L5	2391	1	22,25,26	4.09	12 (54%)	31,36,39	3.28	12 (38%)
1	OMC	L5	4522	1	19,22,23	0.58	0	26,31,34	0.64	0
46	OMG	S2	1328	46,80	23,26,27	0.48	0	33,38,41	0.47	0
1	PSU	L5	1778	1	18,21,22	1.07	1 (5%)	22,30,33	1.73	4 (18%)
46	OMC	S2	1703	46	19,22,23	0.52	0	26,31,34	0.61	0
46	PSU	S2	681	46	18,21,22	1.08	1 (5%)	22,30,33	1.72	3 (13%)
1	PSU	L5	4389	1	18,21,22	1.11	1 (5%)	22,30,33	1.76	5 (22%)
1	OMG	L5	3885	1	23,26,27	0.50	0	33,38,41	0.62	0
1	5MC	L5	3768	1,81	18,22,23	0.59	0	26,32,35	0.50	0
1	PSU	L5	4565	1	18,21,22	1.10	1 (5%)	22,30,33	1.77	4 (18%)

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
46	A2M	S2	1031	46	-	0/9/27/28	0/3/3/3
46	PSU	S2	1445	46	-	0/7/25/26	0/2/2/2
1	OMG	L5	1621	1,80	-	1/9/27/28	0/3/3/3
1	OMG	L5	4623	1,80	-	1/9/27/28	0/3/3/3
46	PSU	S2	100	46,79	-	2/7/25/26	0/2/2/2
1	1MA	L5	1318	79,1	-	2/7/25/26	0/3/3/3
1	PSU	L5	3625	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	2794	1	-	0/9/27/28	0/2/2/2
46	OMU	S2	121	46	-	0/9/27/28	0/2/2/2
46	OMG	S2	683	46	-	2/9/27/28	0/3/3/3
46	PSU	S2	36	46	-	0/7/25/26	0/2/2/2
1	PSU	L5	4409	1	-	0/7/25/26	0/2/2/2
3	OMU	L8	14	3,1	-	0/9/27/28	0/2/2/2
1	OMC	L5	2412	79,1	-	1/9/27/28	0/2/2/2
1	OMC	L5	2355	1	-	0/9/27/28	0/2/2/2
46	PSU	S2	918	46	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
46	PSU	S2	1174	46	-	0/7/25/26	0/2/2/2
1	OMG	L5	3613	1	-	0/9/27/28	0/3/3/3
1	A2M	L5	3704	1	-	1/9/27/28	0/3/3/3
1	A2M	L5	400	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4457	1	-	0/7/25/26	0/2/2/2
46	PSU	S2	866	46	-	3/7/25/26	0/2/2/2
1	A2M	L5	3771	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	3808	1	-	0/7/25/26	0/2/2/2
46	A2M	S2	166	46	-	0/9/27/28	0/3/3/3
46	A2M	S2	1678	46	-	2/9/27/28	0/3/3/3
46	4AC	S2	1842	46	-	0/11/29/30	0/2/2/2
1	A2M	L5	1319	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	3837	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4339	1	-	0/7/25/26	0/2/2/2
46	PSU	S2	801	46	-	0/7/25/26	0/2/2/2
46	OMG	S2	509	46	-	0/9/27/28	0/3/3/3
1	PSU	L5	4958	1	-	0/7/25/26	0/2/2/2
3	PSU	L8	55	3	-	0/7/25/26	0/2/2/2
46	PSU	S2	406	46	-	0/7/25/26	0/2/2/2
46	OMG	S2	601	46	-	1/9/27/28	0/3/3/3
1	OMC	L5	2814	1	-	1/9/27/28	0/2/2/2
1	OMG	L5	4214	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	4622	1	-	4/7/25/26	0/2/2/2
1	OMC	L5	1336	1	-	0/9/27/28	0/2/2/2
1	OMG	L5	2354	1	-	2/9/27/28	0/3/3/3
29	V5N	La	39	29	-	0/9/10/12	0/1/1/1
1	OMC	L5	3873	1	-	0/9/27/28	0/2/2/2
46	PSU	S2	1046	46	-	0/7/25/26	0/2/2/2
1	A2M	L5	3710	1	-	2/9/27/28	0/3/3/3
1	OMG	L5	4480	1	-	2/9/27/28	0/3/3/3
46	OMC	S2	174	46	-	0/9/27/28	0/2/2/2
1	A2M	L5	2353	79,1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4614	1	-	0/7/25/26	0/2/2/2
3	PSU	L8	69	3	-	0/7/25/26	0/2/2/2
1	PSU	L5	2829	1	-	0/7/25/26	0/2/2/2
46	OMG	S2	644	46	-	1/9/27/28	0/3/3/3
1	PSU	L5	1679	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	1777	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	1788	1,80	-	0/7/25/26	0/2/2/2
1	6MZ	L5	4206	1	-	0/9/27/28	0/3/3/3
46	G7M	S2	1639	46	-	2/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	L5	1856	1	-	0/7/25/26	0/2/2/2
46	PSU	S2	1232	46	-	0/7/25/26	0/2/2/2
1	5MC	L5	4433	1,80	-	4/7/25/26	0/2/2/2
1	A2M	L5	1530	79,1	-	2/9/27/28	0/3/3/3
46	A2M	S2	484	46	-	0/9/27/28	0/3/3/3
46	PSU	S2	1136	46	-	0/7/25/26	0/2/2/2
1	OMC	L5	4442	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	4957	1	-	0/7/25/26	0/2/2/2
46	PSU	S2	1244	46	-	0/7/25/26	0/2/2/2
46	OMC	S2	1391	46	-	1/9/27/28	0/2/2/2
1	OMG	L5	4182	79,1	-	1/9/27/28	0/3/3/3
1	OMC	L5	3855	1	-	0/9/27/28	0/2/2/2
46	PSU	S2	822	46	-	1/7/25/26	0/2/2/2
1	PSU	L5	3906	79,1	-	0/7/25/26	0/2/2/2
46	PSU	S2	572	46	-	0/7/25/26	0/2/2/2
1	PSU	L5	1775	1	-	2/7/25/26	0/2/2/2
1	A2M	L5	2805	1	-	3/9/27/28	0/3/3/3
1	PSU	L5	4282	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	1518	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	3701	1	-	0/7/25/26	0/2/2/2
46	PSU	S2	1625	46	-	0/7/25/26	0/2/2/2
1	PSU	L5	4562	1	-	0/7/25/26	0/2/2/2
46	PSU	S2	1643	46	-	0/7/25/26	0/2/2/2
1	PSU	L5	3870	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4285	1	-	0/7/25/26	0/2/2/2
46	UY1	S2	1326	46	-	3/9/27/28	0/2/2/2
3	OMG	L8	75	3	-	0/9/27/28	0/3/3/3
1	PSU	L5	4417	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	2498	1	-	1/7/25/26	0/2/2/2
46	6MZ	S2	1832	46,79,80	-	0/9/27/28	0/3/3/3
1	A2M	L5	4509	79,1	-	1/9/27/28	0/3/3/3
46	OMU	S2	116	46	-	1/9/27/28	0/2/2/2
1	OMG	L5	3730	1	-	0/9/27/28	0/3/3/3
46	PSU	S2	667	46	-	0/7/25/26	0/2/2/2
1	OMU	L5	4292	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	3623	1,80	-	0/7/25/26	0/2/2/2
1	OMG	L5	4609	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4995	1	-	0/7/25/26	0/2/2/2
46	A2M	S2	576	46	-	2/9/27/28	0/3/3/3
1	A2M	L5	1520	1	-	0/9/27/28	0/3/3/3
46	OMC	S2	517	46	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
66	NMM	ST	67	66	-	2/9/11/13	-
1	OMG	L5	4604	1	-	0/9/27/28	0/3/3/3
46	A2M	S2	27	46	-	1/9/27/28	0/3/3/3
1	PSU	L5	4538	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	2777	1	-	4/9/27/28	0/3/3/3
46	A2M	S2	590	46	-	1/9/27/28	0/3/3/3
1	OMU	L5	3911	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	4279	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4443	1	-	0/7/25/26	0/2/2/2
46	PSU	S2	609	46	-	0/7/25/26	0/2/2/2
46	PSU	S2	34	46	-	0/7/25/26	0/2/2/2
46	PSU	S2	119	46	-	0/7/25/26	0/2/2/2
46	PSU	S2	1238	46	-	0/7/25/26	0/2/2/2
1	OMG	L5	4378	1	-	0/9/27/28	0/3/3/3
1	OMC	L5	1877	79,1	-	0/9/27/28	0/2/2/2
1	OMG	L5	2414	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	1673	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	3839	79,1	-	0/7/25/26	0/2/2/2
46	PSU	S2	1692	46	-	0/7/25/26	0/2/2/2
1	OMU	L5	2827	1	-	0/9/27/28	0/2/2/2
46	OMU	S2	354	46	-	0/9/27/28	0/2/2/2
46	A2M	S2	512	46	-	2/9/27/28	0/3/3/3
1	PSU	L5	1532	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	3778	1	-	0/9/27/28	0/3/3/3
1	UY1	L5	3804	1,80	-	2/9/27/28	0/2/2/2
1	A2M	L5	4557	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	1858	1	-	0/7/25/26	0/2/2/2
46	OMG	S2	867	46	-	4/9/27/28	0/3/3/3
1	PSU	L5	4428	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	1322	1	-	2/9/27/28	0/3/3/3
46	PSU	S2	815	46	-	0/7/25/26	0/2/2/2
1	PSU	L5	1578	1	-	2/7/25/26	0/2/2/2
1	PSU	L5	2622	1	-	0/7/25/26	0/2/2/2
46	A2M	S2	99	46,79	-	3/9/27/28	0/3/3/3
5	HIC	LB	245	5	-	0/5/6/8	0/1/1/1
46	PSU	S2	1177	46	-	0/7/25/26	0/2/2/2
1	A2M	L5	398	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	4347	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	1312	1	-	0/9/27/28	0/3/3/3
46	OMU	S2	172	46	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	L5	2405	1	-	0/9/27/28	0/2/2/2
46	4AC	S2	1337	46	-	2/11/29/30	0/2/2/2
1	PSU	L5	2724	1	-	0/7/25/26	0/2/2/2
46	PSU	S2	109	46	-	0/7/25/26	0/2/2/2
1	A2M	L5	3853	1	-	2/9/27/28	0/3/3/3
1	OMU	L5	4213	1	-	0/9/27/28	0/2/2/2
46	PSU	S2	105	46	-	0/7/25/26	0/2/2/2
46	A2M	S2	468	46	-	0/9/27/28	0/3/3/3
1	PSU	L5	3681	1,80	-	2/7/25/26	0/2/2/2
46	OMU	S2	428	46	-	4/9/27/28	0/2/2/2
1	A2M	L5	3816	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	4507	79,1,80	-	1/7/25/26	0/2/2/2
1	PSU	L5	3830	1	-	3/7/25/26	0/2/2/2
1	OMC	L5	3827	1	-	0/9/27/28	0/2/2/2
46	A2M	S2	668	46	-	7/9/27/28	0/3/3/3
46	OMG	S2	1490	46,79	-	3/9/27/28	0/3/3/3
46	PSU	S2	649	46	-	0/7/25/26	0/2/2/2
46	A2M	S2	159	46	-	1/9/27/28	0/3/3/3
1	PSU	L5	4555	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4675	1	-	0/7/25/26	0/2/2/2
1	OMU	L5	4484	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	4576	1	-	1/9/27/28	0/3/3/3
46	PSU	S2	863	46	-	0/7/25/26	0/2/2/2
46	PSU	S2	1004	46	-	0/7/25/26	0/2/2/2
1	OMC	L5	2341	1	-	3/9/27/28	0/2/2/2
1	OMG	L5	2866	1	-	0/9/27/28	0/3/3/3
46	PSU	S2	1367	46	-	2/7/25/26	0/2/2/2
1	A2M	L5	3811	1	-	1/9/27/28	0/3/3/3
46	OMC	S2	462	46	-	1/9/27/28	0/2/2/2
46	MA6	S2	1851	46	-	2/11/29/30	0/3/3/3
46	PSU	S2	1045	46	-	0/7/25/26	0/2/2/2
46	PSU	S2	1056	46	-	0/7/25/26	0/2/2/2
46	OMG	S2	436	46	-	0/9/27/28	0/3/3/3
1	OMC	L5	2851	1	-	1/9/27/28	0/2/2/2
46	PSU	S2	1239	46	-	0/7/25/26	0/2/2/2
46	PSU	S2	651	46	-	0/7/25/26	0/2/2/2
46	PSU	S2	93	46	-	0/7/25/26	0/2/2/2
46	PSU	S2	814	46	-	0/7/25/26	0/2/2/2
1	OMG	L5	4356	1	-	1/9/27/28	0/3/3/3
46	A2M	S2	1383	46	-	3/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
46	OMG	S2	1447	46	-	3/9/27/28	0/3/3/3
1	UR3	L5	4516	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4517	1	-	0/7/25/26	0/2/2/2
46	OMU	S2	1442	46	-	1/9/27/28	0/2/2/2
46	PSU	S2	686	46	-	0/7/25/26	0/2/2/2
1	PSU	L5	4298	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4485	1	-	0/9/27/28	0/3/3/3
46	MA6	S2	1850	46	-	0/11/29/30	0/3/3/3
1	OMC	L5	3687	1,80	-	4/9/27/28	0/2/2/2
1	PSU	L5	4518	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	1740	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	1867	79,1	-	0/9/27/28	0/3/3/3
1	OMC	L5	3794	1	-	0/9/27/28	0/2/2/2
1	OMU	L5	4606	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	4659	1,80	-	0/7/25/26	0/2/2/2
1	PSU	L5	4986	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	2391	1	-	0/9/27/28	0/3/3/3
1	OMC	L5	4522	1	-	0/9/27/28	0/2/2/2
46	OMG	S2	1328	46,80	-	1/9/27/28	0/3/3/3
1	PSU	L5	1778	1	-	0/7/25/26	0/2/2/2
46	OMC	S2	1703	46	-	1/9/27/28	0/2/2/2
46	PSU	S2	681	46	-	0/7/25/26	0/2/2/2
1	PSU	L5	4389	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	3885	1	-	0/9/27/28	0/3/3/3
1	5MC	L5	3768	1,81	-	0/7/25/26	0/2/2/2
1	PSU	L5	4565	1	-	0/7/25/26	0/2/2/2

The worst 5 of 647 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	3853	A2M	C3'-C2'	-13.33	1.23	1.52
46	S2	468	A2M	C3'-C2'	-13.29	1.23	1.52
1	L5	2353	A2M	C3'-C2'	-13.27	1.23	1.52
46	S2	166	A2M	C3'-C2'	-13.23	1.23	1.52
1	L5	4576	A2M	C3'-C2'	-13.23	1.23	1.52

The worst 5 of 898 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	S2	1851	MA6	N1-C6-N6	-15.52	100.12	117.08
46	S2	1850	MA6	N1-C6-N6	-14.86	100.83	117.08
46	S2	590	A2M	C1'-N9-C8	-10.87	102.60	127.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	3704	A2M	C1'-N9-C8	-10.47	103.50	127.14
1	L5	4557	A2M	C1'-N9-C8	-10.46	103.53	127.14

There are no chirality outliers.

5 of 132 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
66	ST	67	NMM	O-C-CA-CB
1	L5	398	A2M	C1'-C2'-O2'-CM'
1	L5	2777	A2M	C1'-C2'-O2'-CM'
1	L5	2805	A2M	O4'-C4'-C5'-O5'
1	L5	2805	A2M	C3'-C4'-C5'-O5'

There are no ring outliers.

100 monomers are involved in 207 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
46	S2	1031	A2M	1	0
46	S2	1445	PSU	1	0
1	L5	4623	OMG	2	0
1	L5	2794	OMC	1	0
46	S2	121	OMU	3	0
3	L8	14	OMU	2	0
46	S2	918	PSU	3	0
1	L5	3613	OMG	1	0
1	L5	3704	A2M	4	0
1	L5	3771	A2M	2	0
46	S2	166	A2M	2	0
46	S2	1678	A2M	1	0
46	S2	1842	4AC	1	0
46	S2	509	OMG	2	0
1	L5	2814	OMC	3	0
1	L5	4214	OMG	5	0
1	L5	4622	PSU	1	0
1	L5	1336	OMC	1	0
46	S2	1046	PSU	1	0
1	L5	3710	A2M	2	0
1	L5	4614	PSU	1	0
3	L8	69	PSU	1	0
1	L5	1679	PSU	1	0
1	L5	1777	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L5	4206	6MZ	1	0
46	S2	1639	G7M	2	0
46	S2	1232	PSU	2	0
1	L5	4433	5MC	2	0
1	L5	1530	A2M	3	0
46	S2	484	A2M	2	0
46	S2	1136	PSU	1	0
46	S2	1391	OMC	2	0
1	L5	1775	PSU	3	0
1	L5	2805	A2M	3	0
1	L5	4282	PSU	1	0
1	L5	3701	PSU	2	0
46	S2	1643	PSU	2	0
3	L8	75	OMG	1	0
46	S2	1832	6MZ	1	0
46	S2	116	OMU	4	0
1	L5	4292	OMU	2	0
1	L5	4995	PSU	1	0
46	S2	576	A2M	5	0
1	L5	1520	A2M	1	0
66	ST	67	NMM	3	0
46	S2	27	A2M	2	0
1	L5	4538	PSU	1	0
1	L5	2777	A2M	1	0
1	L5	4279	PSU	1	0
1	L5	4443	PSU	2	0
46	S2	1238	PSU	1	0
1	L5	4378	OMG	1	0
1	L5	2414	OMG	2	0
1	L5	1673	PSU	1	0
46	S2	1692	PSU	1	0
46	S2	354	OMU	2	0
46	S2	512	A2M	7	0
1	L5	3778	OMG	1	0
1	L5	3804	UY1	1	0
1	L5	4557	A2M	3	0
46	S2	867	OMG	1	0
1	L5	2622	PSU	2	0
46	S2	99	A2M	1	0
46	S2	1177	PSU	1	0
1	L5	2405	OMU	5	0
46	S2	1337	4AC	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L5	2724	PSU	2	0
1	L5	3853	A2M	2	0
1	L5	4213	OMU	4	0
46	S2	105	PSU	1	0
46	S2	468	A2M	6	0
46	S2	428	OMU	3	0
1	L5	3830	PSU	2	0
46	S2	668	A2M	1	0
46	S2	1490	OMG	2	0
46	S2	649	PSU	2	0
46	S2	159	A2M	3	0
1	L5	4576	A2M	2	0
46	S2	1004	PSU	2	0
1	L5	2341	OMC	3	0
1	L5	2866	OMG	1	0
46	S2	1367	PSU	3	0
1	L5	3811	A2M	3	0
46	S2	462	OMC	3	0
46	S2	1851	MA6	3	0
46	S2	1239	PSU	2	0
46	S2	1383	A2M	11	0
46	S2	1447	OMG	4	0
1	L5	4516	UR3	1	0
46	S2	1442	OMU	2	0
46	S2	1850	MA6	5	0
1	L5	4518	PSU	1	0
1	L5	1867	A2M	3	0
1	L5	4606	OMU	2	0
1	L5	4986	PSU	1	0
1	L5	4522	OMC	1	0
46	S2	1703	OMC	2	0
1	L5	4389	PSU	2	0
1	L5	3768	5MC	1	0
1	L5	4565	PSU	3	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 257 ligands modelled in this entry, 257 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	19
47	S6	1

The worst 5 of 20 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L5	266:C	O3'	267:G	P	46.54
1	L5	189:G	O3'	190:G	P	45.41
1	L5	4731:C	O3'	4732:C	P	27.51
1	L5	1211:G	O3'	1212:G	P	23.77
1	L5	1058:C	O3'	1059:G	P	20.75

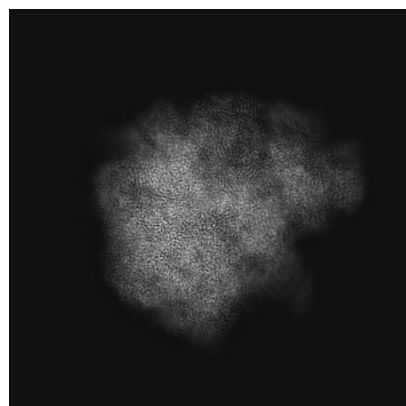
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-56286. These allow visual inspection of the internal detail of the map and identification of artifacts.

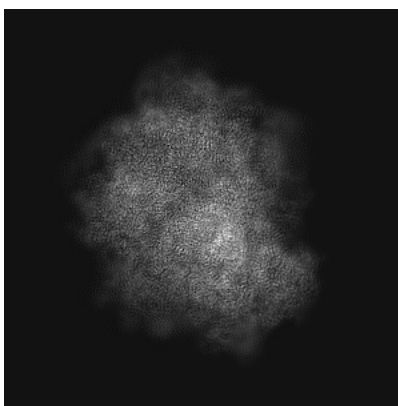
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

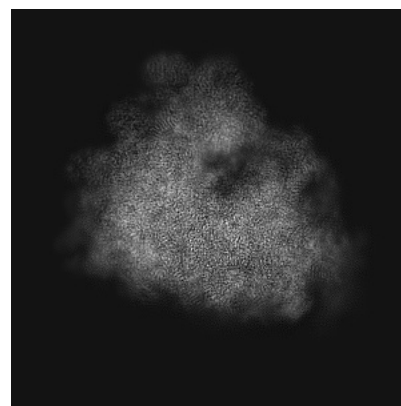
6.1.1 Primary map



X

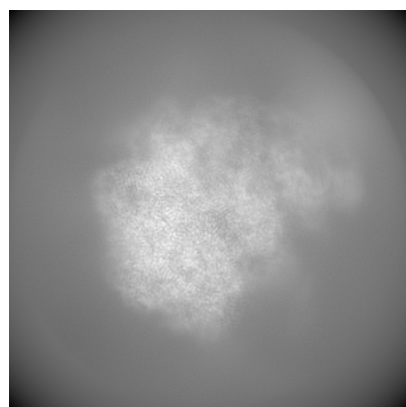


Y

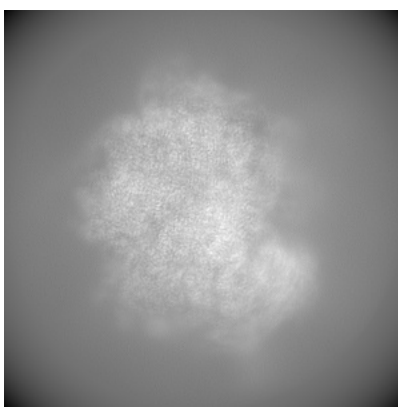


Z

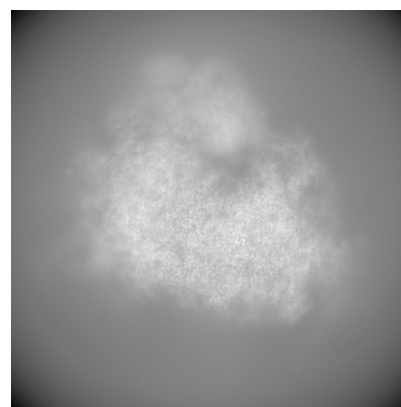
6.1.2 Raw map



X



Y

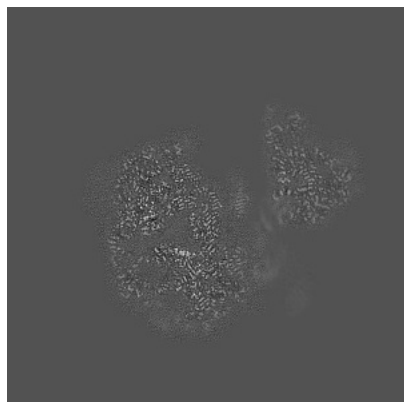


Z

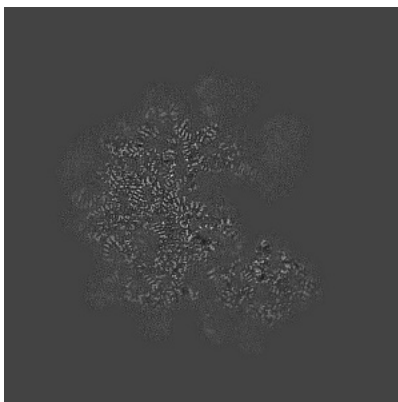
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

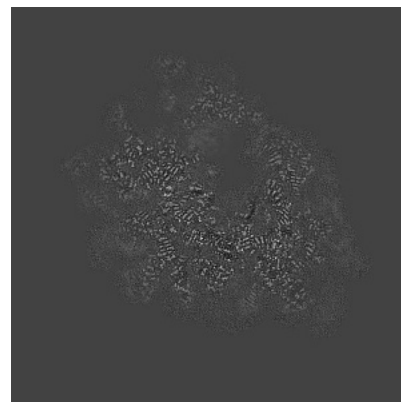
6.2.1 Primary map



X Index: 240

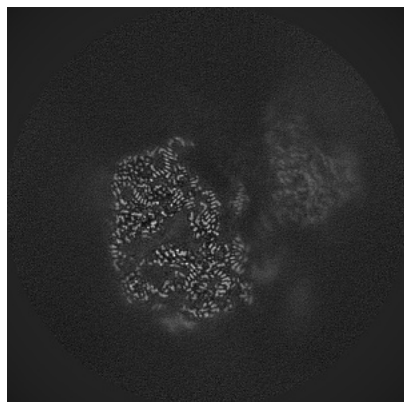


Y Index: 240

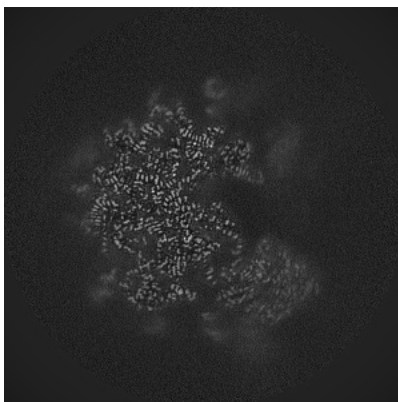


Z Index: 240

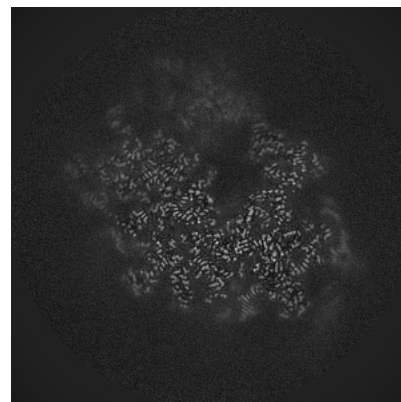
6.2.2 Raw map



X Index: 240



Y Index: 240

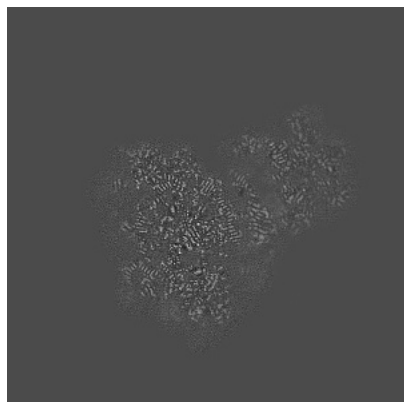


Z Index: 240

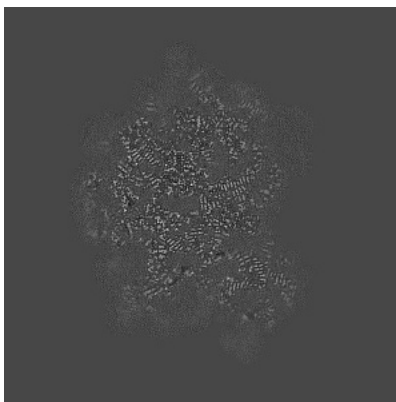
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

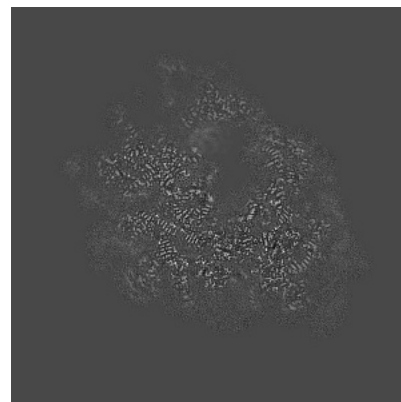
6.3.1 Primary map



X Index: 222

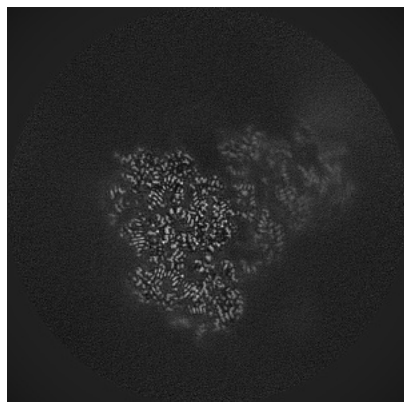


Y Index: 207

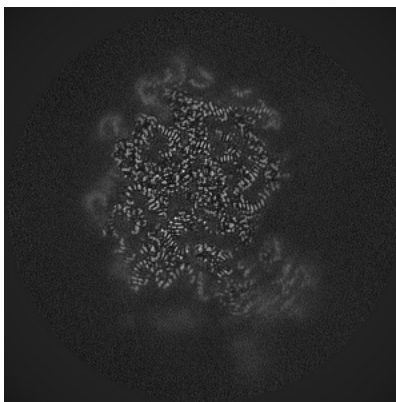


Z Index: 238

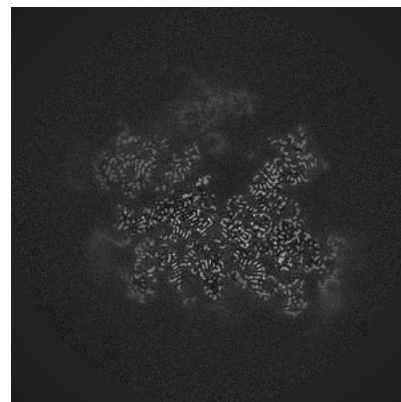
6.3.2 Raw map



X Index: 216



Y Index: 190

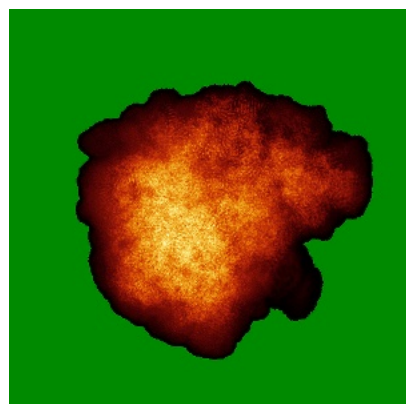


Z Index: 226

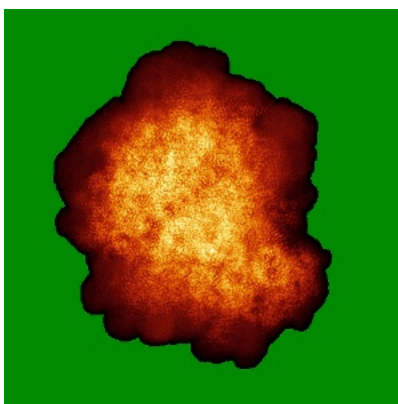
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

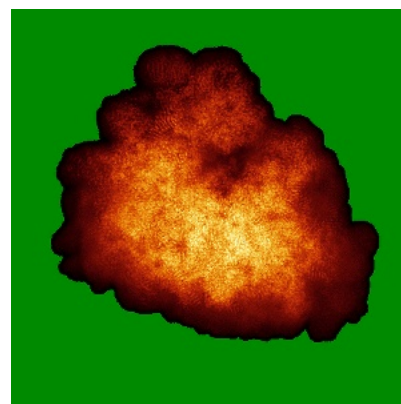
6.4.1 Primary map



X

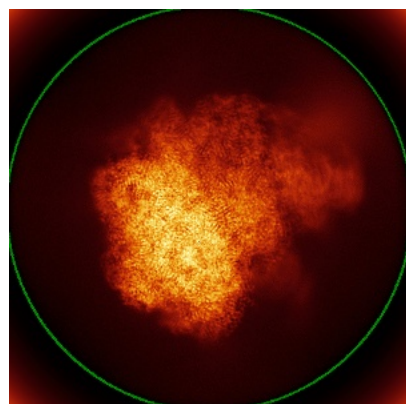


Y

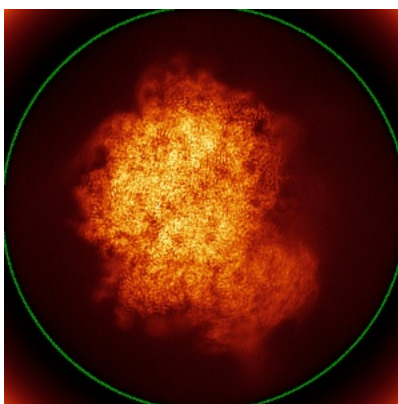


Z

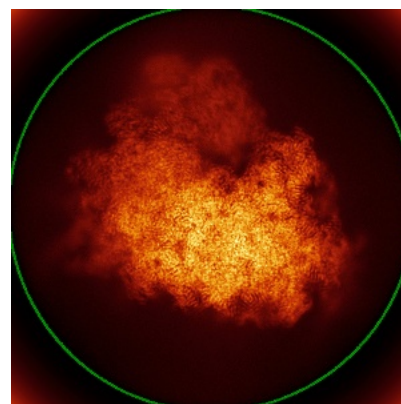
6.4.2 Raw map



X



Y

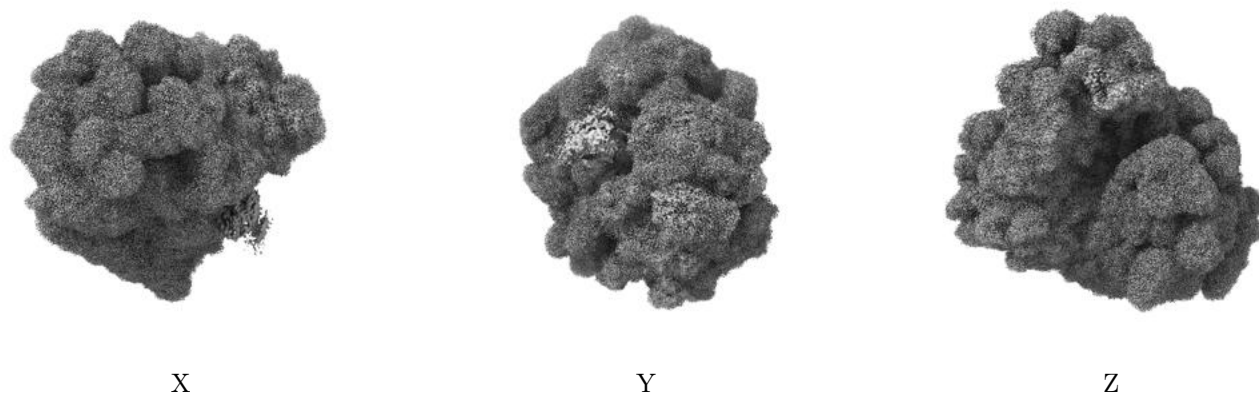


Z

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.

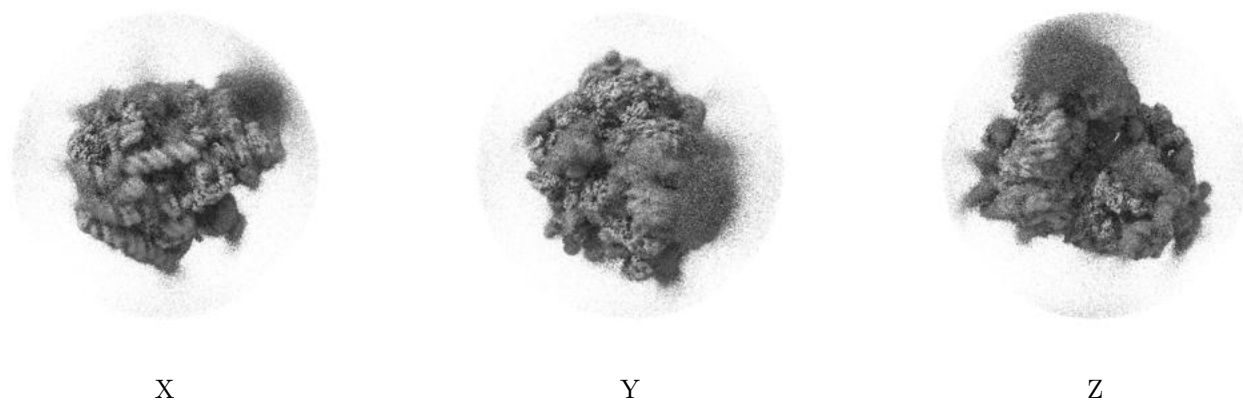
6.5 Orthogonal surface views [i](#)

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.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

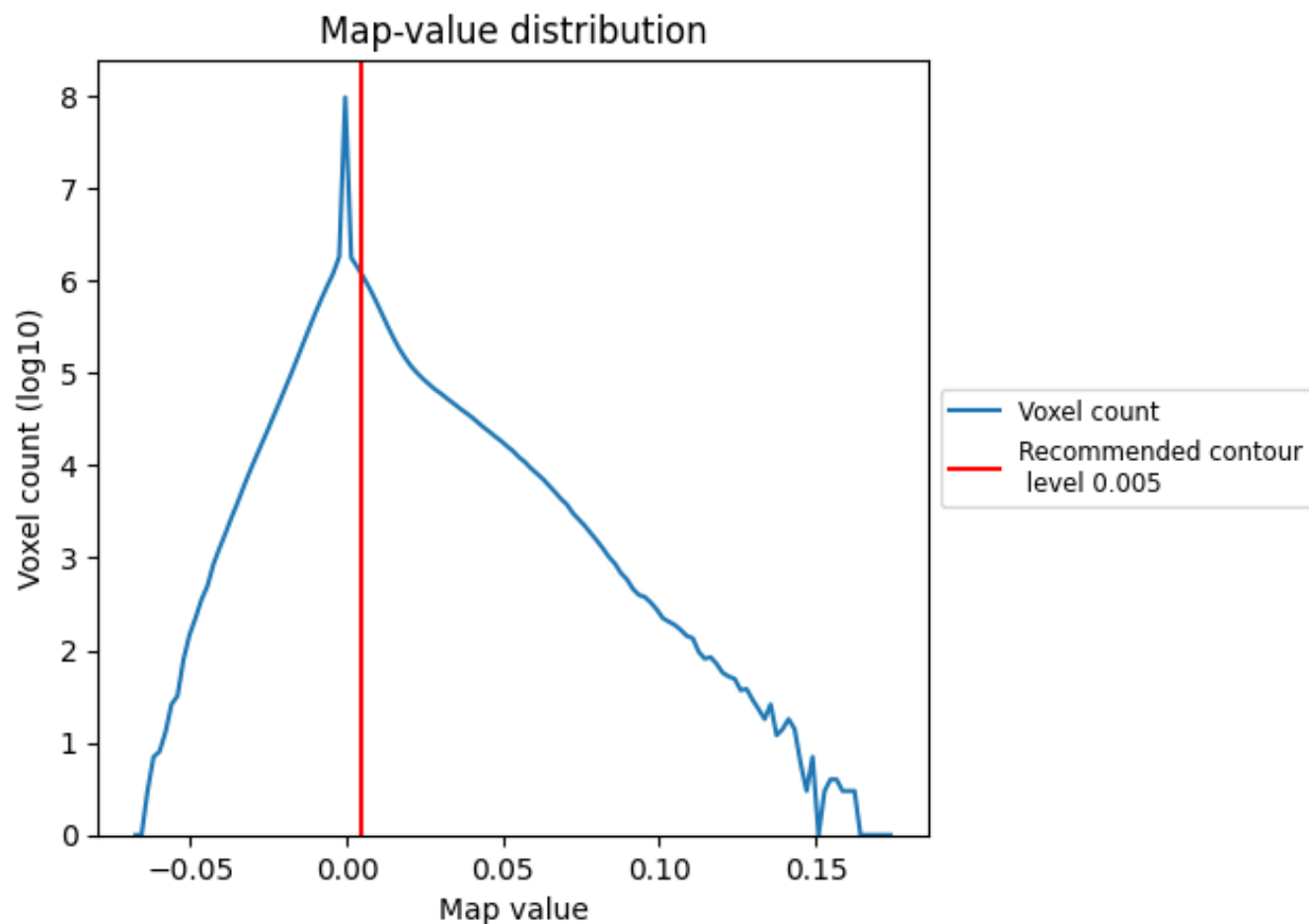
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

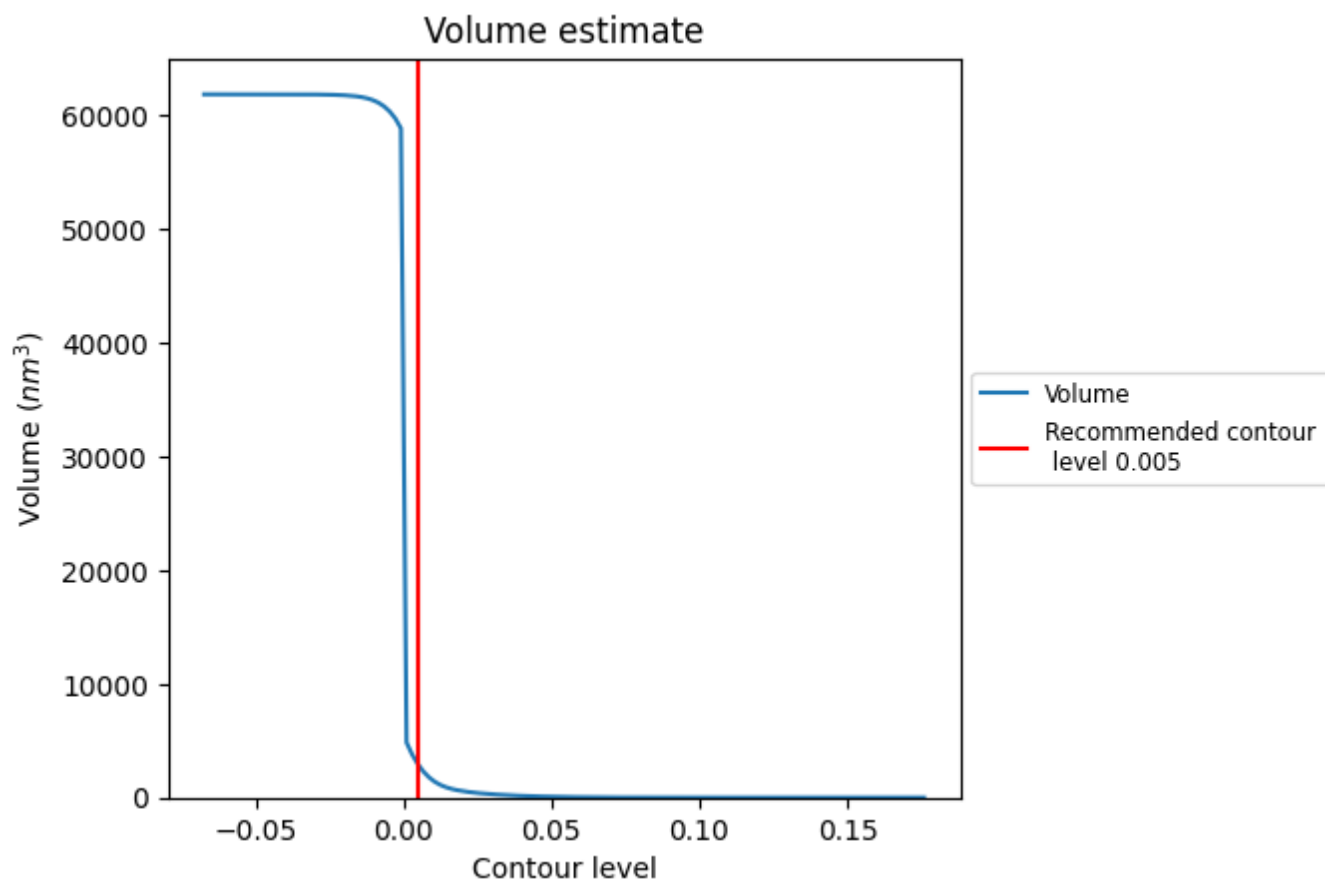
This section contains the results of statistical analysis of the map.

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.

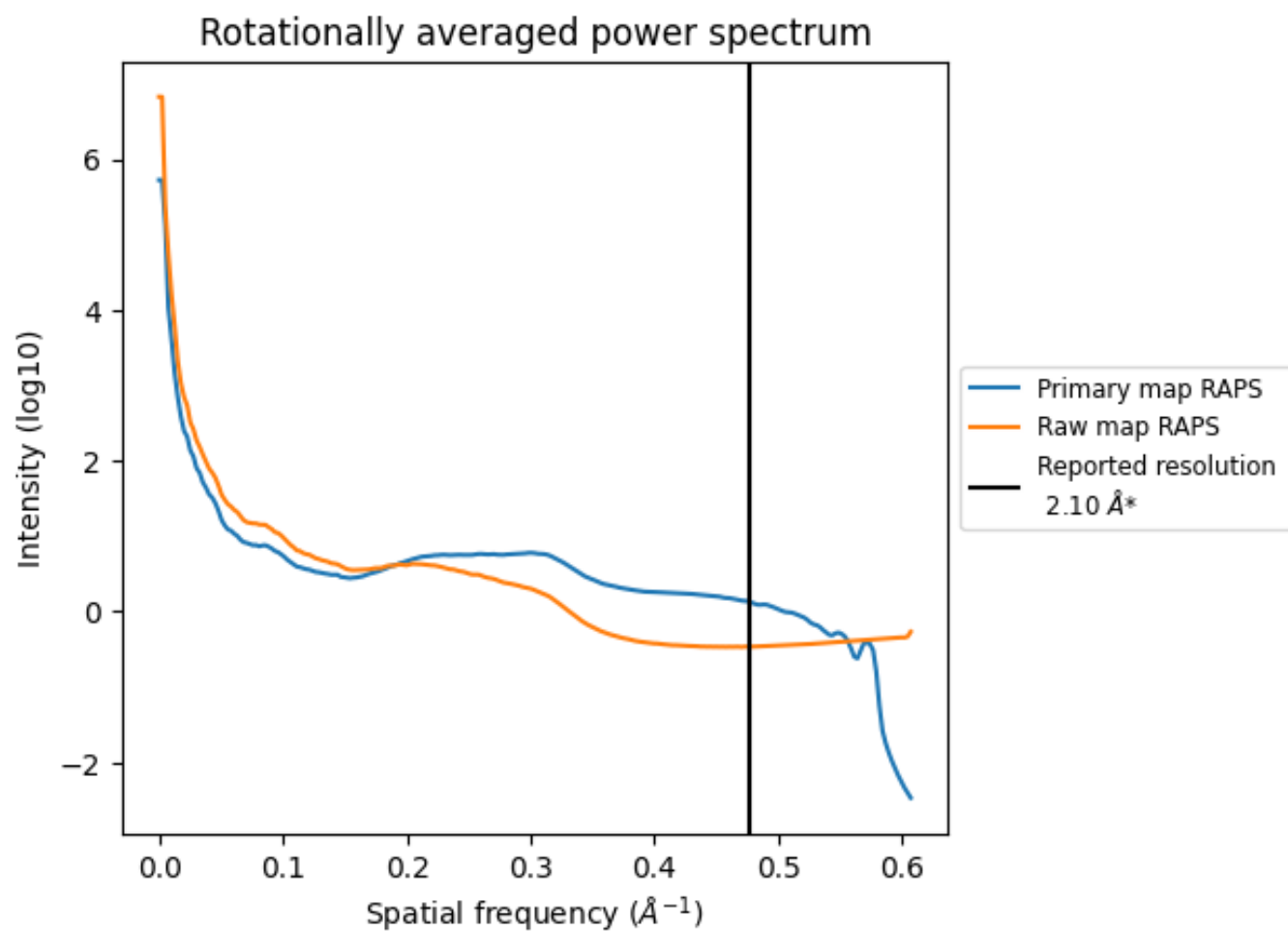
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2878 nm³; this corresponds to an approximate mass of 2600 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 ⓘ

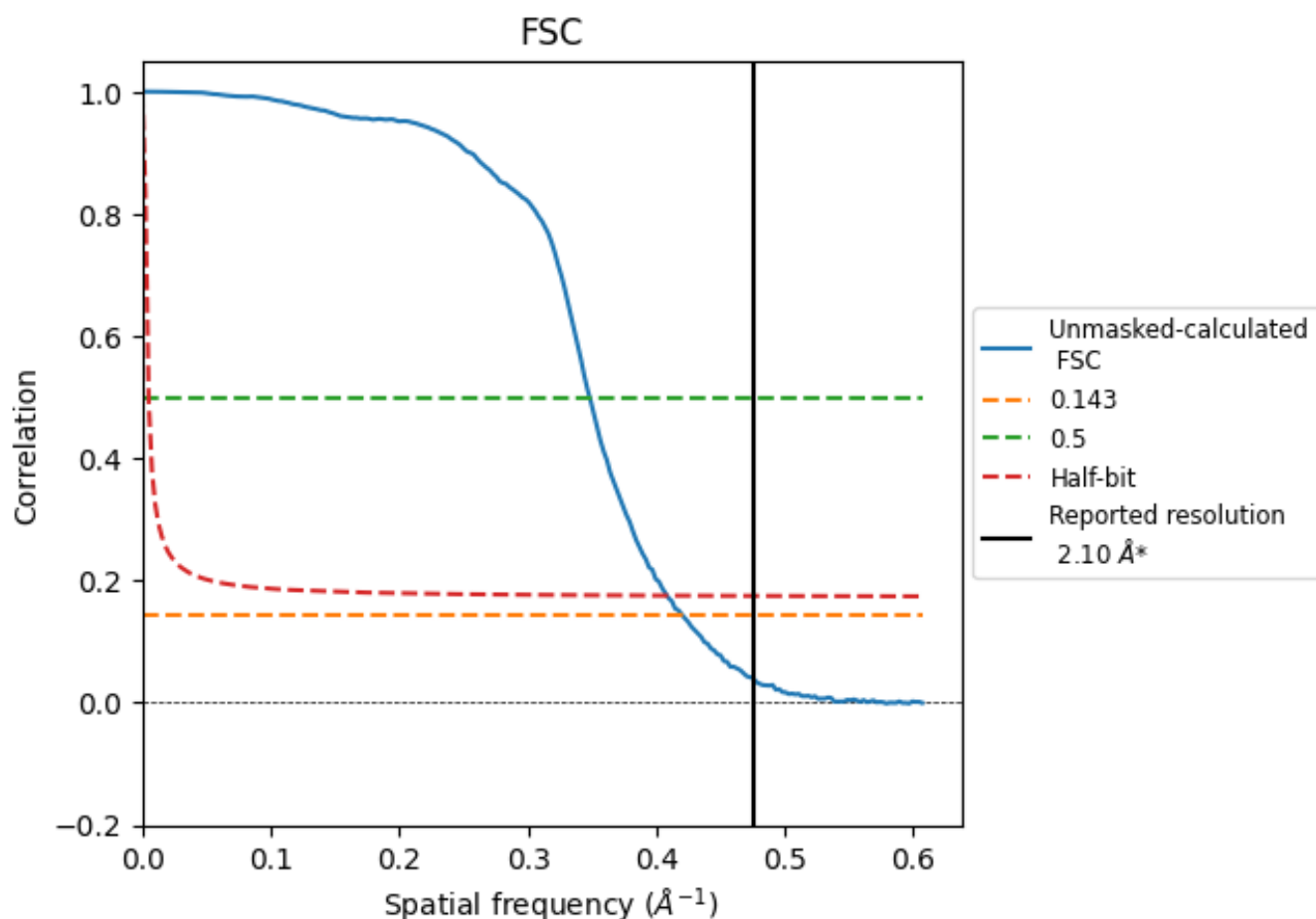


*Reported resolution corresponds to spatial frequency of 0.476 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.476 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

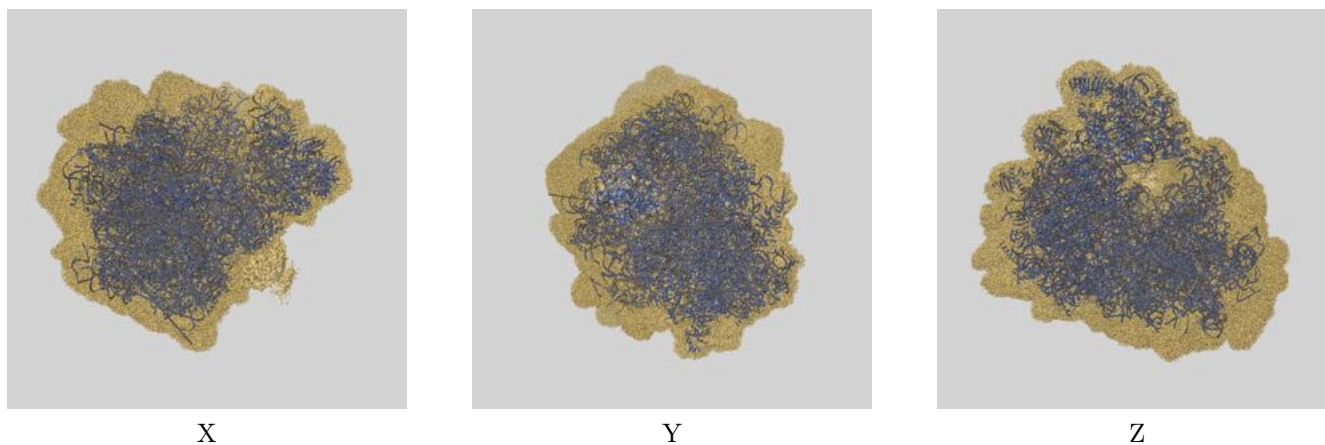
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.38	2.87	2.45

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.38 differs from the reported value 2.1 by more than 10 %

9 Map-model fit [i](#)

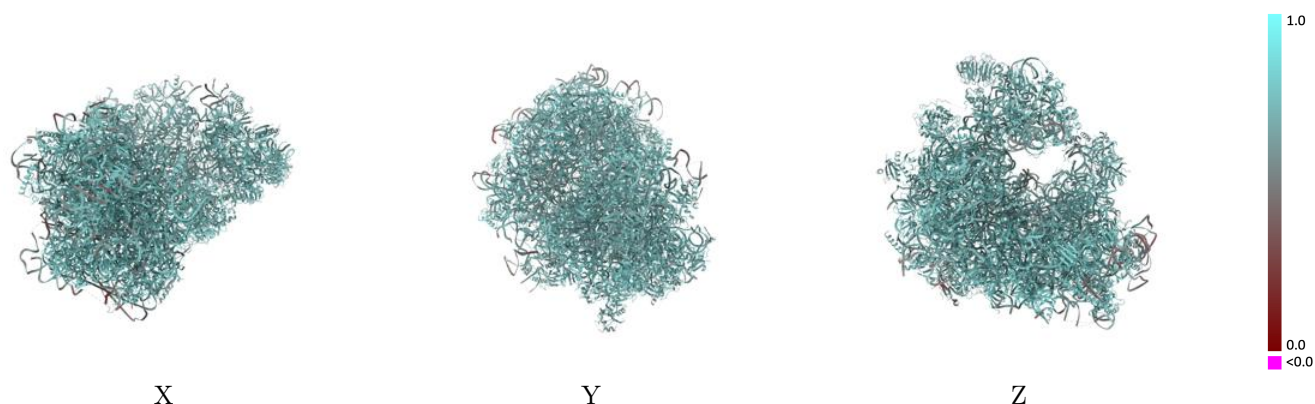
This section contains information regarding the fit between EMDB map EMD-56286 and PDB model 9TV2. Per-residue inclusion information can be found in [section 3](#) on [page 23](#).

9.1 Map-model overlay [i](#)



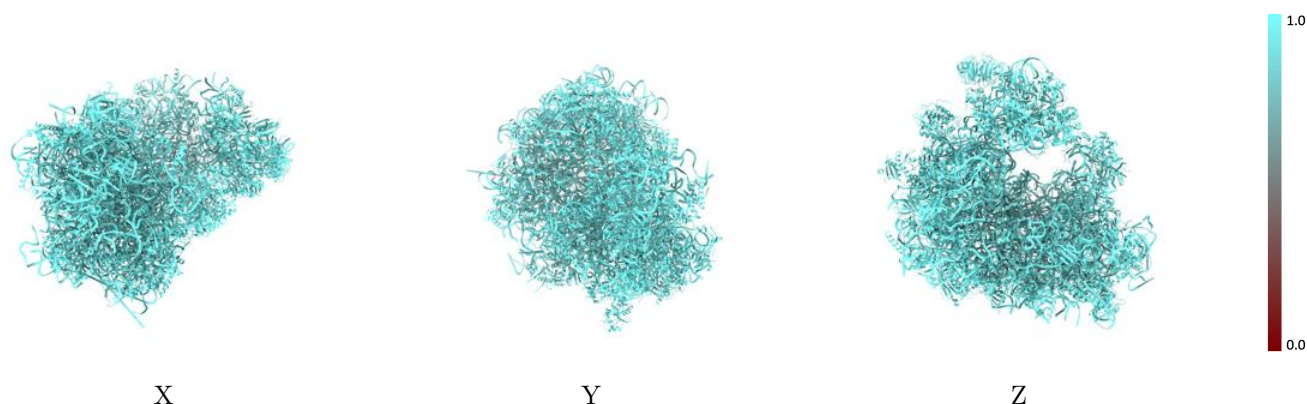
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



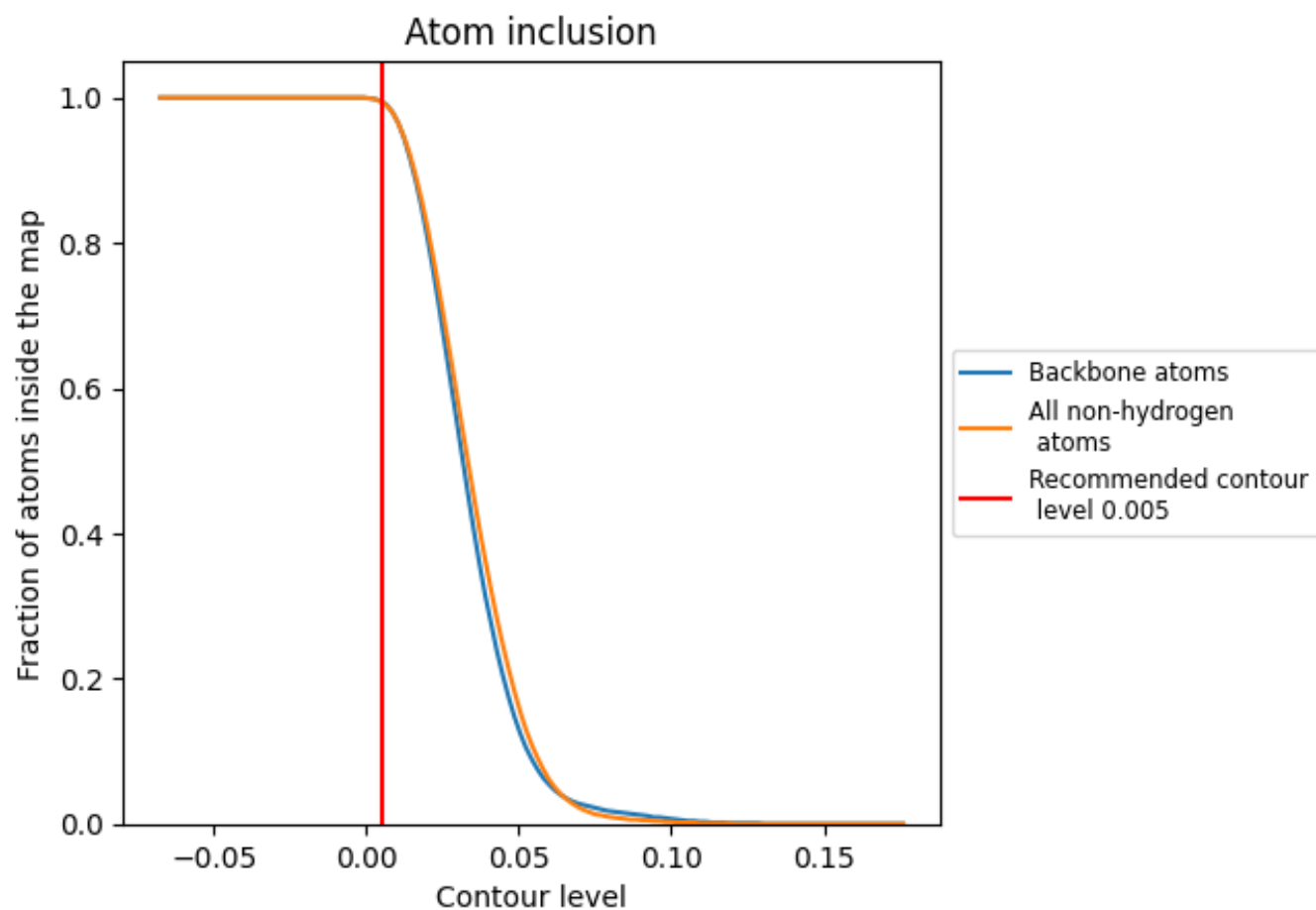
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 99% 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	 0.9940	 0.7330
L5	 0.9920	 0.7280
L7	 1.0000	 0.7310
L8	 0.9970	 0.7390
LA	 0.9990	 0.7990
LB	 0.9990	 0.7880
LC	 1.0000	 0.7920
LD	 0.9980	 0.7270
LE	 0.9980	 0.7430
LF	 0.9980	 0.7890
LG	 0.9990	 0.7420
LH	 0.9990	 0.7390
LI	 0.9950	 0.7350
LJ	 0.9890	 0.6560
LL	 0.9980	 0.7730
LM	 0.9940	 0.7460
LN	 0.9990	 0.7990
LO	 0.9970	 0.7870
LP	 0.9980	 0.7930
LQ	 1.0000	 0.7960
LR	 0.9990	 0.7680
LS	 1.0000	 0.7820
LT	 0.9980	 0.7720
LU	 0.9880	 0.6210
LV	 1.0000	 0.7920
LW	 1.0000	 0.7690
LX	 0.9980	 0.7600
LY	 1.0000	 0.7780
LZ	 0.9980	 0.7260
La	 0.9990	 0.7930
Lb	 1.0000	 0.7480
Lc	 1.0000	 0.7490
Ld	 1.0000	 0.7750
Le	 1.0000	 0.8010
Lf	 1.0000	 0.8010



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Chain	Atom inclusion	Q-score
Lg	 0.9970	 0.7800
Lh	 0.9990	 0.7570
Li	 0.9940	 0.7460
Lj	 1.0000	 0.8010
Lk	 0.9930	 0.6930
Ll	 1.0000	 0.7840
Lm	 0.9970	 0.7460
Ln	 0.9940	 0.7110
Lo	 1.0000	 0.7710
Lp	 1.0000	 0.7860
Lr	 1.0000	 0.7830
S2	 0.9940	 0.7040
S6	 0.9790	 0.5830
SA	 0.9970	 0.7310
SB	 0.9960	 0.7220
SC	 0.9970	 0.7440
SD	 0.9950	 0.6870
SE	 0.9960	 0.7370
SF	 0.9960	 0.7260
SG	 0.9980	 0.6910
SH	 0.9950	 0.6860
SI	 0.9980	 0.7370
SJ	 1.0000	 0.7400
SK	 0.9930	 0.6880
SL	 1.0000	 0.7540
SN	 0.9990	 0.7360
SO	 1.0000	 0.7340
SP	 0.9930	 0.7230
SQ	 1.0000	 0.7290
SR	 0.9840	 0.6760
SS	 0.9960	 0.7190
ST	 0.9970	 0.7260
SU	 0.9880	 0.6920
SV	 0.9950	 0.7260
SW	 0.9980	 0.7590
SX	 0.9980	 0.7600
SY	 0.9950	 0.7230
SZ	 0.9980	 0.7060
Sa	 0.9970	 0.7340
Sb	 0.9960	 0.7150
Sc	 0.9970	 0.7020
Sd	 1.0000	 0.7410

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Chain	Atom inclusion	Q-score
Se	 0.9970	 0.7290
Sg	 0.9850	 0.6620