



wwPDB EM Validation Summary Report ⓘ

Jun 20, 2026 – 12:22 pm BST

PDB ID : 6QZP / pdb_00006qzp
EMDB ID : EMD-3883
Title : High-resolution cryo-EM structure of the human 80S ribosome
Authors : Natchiar, S.K.; Myasnikov, A.G.; Kratzat, H.; Hazemann, I.; Klaholz, B.P.
Deposited on : 2019-03-12
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

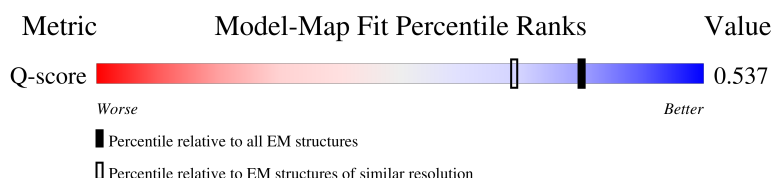
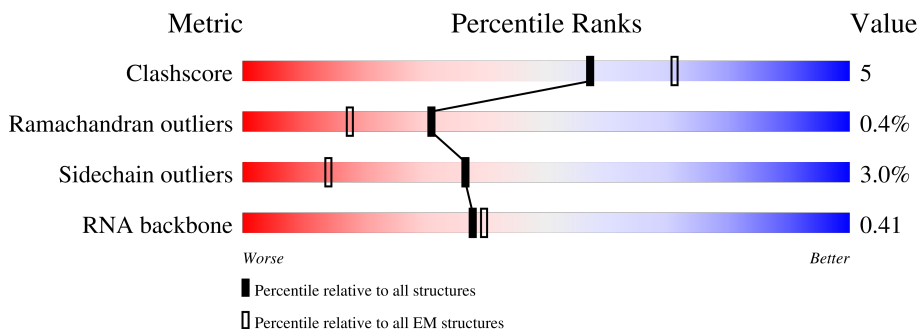
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.



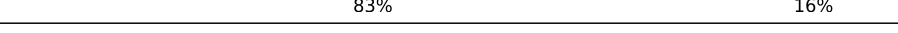
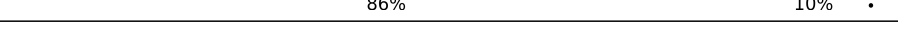
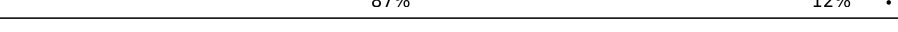
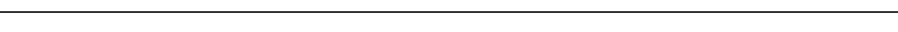
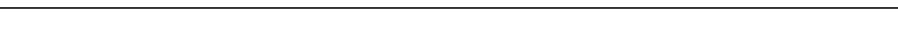
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	3773	 64% 30% 5%
2	L7	120	 78% 20%
3	L8	156	 65% 29% 6%

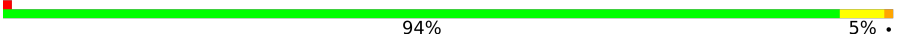
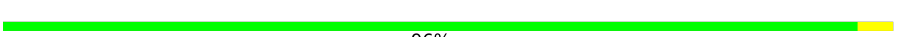
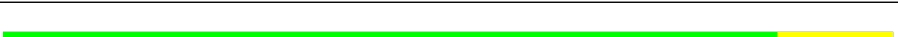
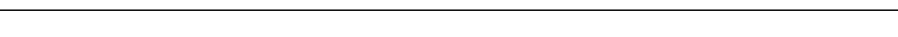
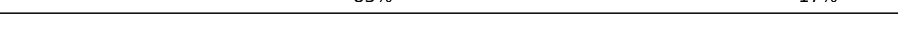
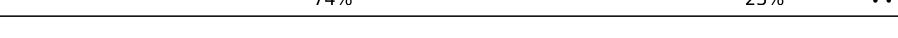
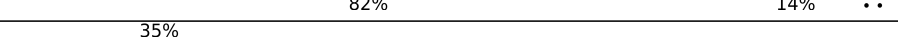
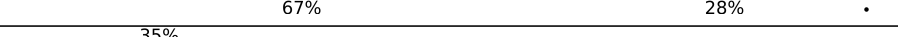
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Mol	Chain	Length	Quality of chain
4	LA	248	 82% 16% .
5	LB	402	 79% 19% .
6	LC	368	 86% 12% .
7	LD	293	 80% 18% .
8	LE	236	 85% 13% .
9	LF	225	 85% 12% .
10	LG	241	 83% 15% .
11	LH	190	 85% 15% .
12	LI	213	 85% 14% .
13	LJ	176	 78% 18% .
14	LL	210	 86% 13% .
15	LM	139	 88% 12%
16	LN	203	 83% 16%
17	LO	201	 86% 10% .
18	LP	153	 76% 22% .
19	LQ	187	 87% 12% .
20	LR	187	 89% 10% ..
21	LS	175	 91% 8% .
22	LT	159	 86% 13% .
23	LU	101	 82% 15% .
24	LV	131	 83% 12% . .
25	LW	124	 86% 11% .
26	LX	120	 89% 9% ..
27	LY	134	 82% 16% ..
28	LZ	135	 85% 15%

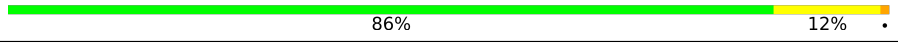
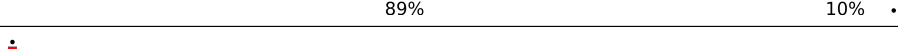
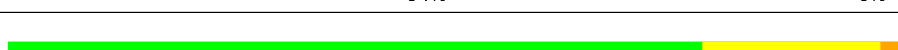
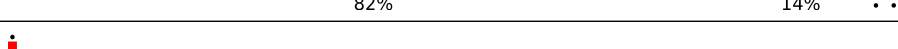
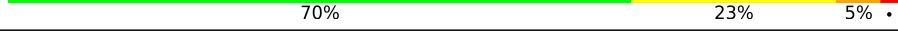
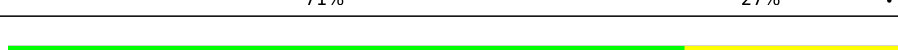
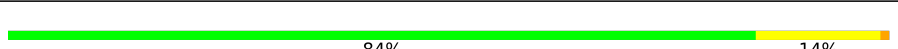
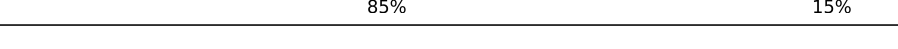
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Mol	Chain	Length	Quality of chain
29	La	147	 86% 13% .
30	Lb	109	 94% 5% .
31	Lc	98	 82% 15% ..
32	Ld	107	 87% 13%
33	Le	128	 78% 20% .
34	Lf	109	 89% 8% .
35	Lg	114	 96% .
36	Lh	122	 89% 10% .
37	Li	102	 90% 10%
38	Lj	86	 88% 10% .
39	Lk	69	 87% 13%
40	Ll	50	 82% 14% .
41	Lm	52	 85% 13% .
42	Ln	24	 83% 17%
43	Lo	105	 74% 23% ..
44	Lp	91	 85% 13% ..
45	Lr	125	 82% 14% ..
46	Lz	217	 35% 84% 14% .
47	S2	1740	 67% 28% .
48	S6	75	 35% 51% 45% .
49	SA	221	 75% 20% 5%
50	SB	214	 90% 10%
51	SD	227	 81% 15% .
52	SE	262	 87% 13%
53	SF	189	 81% 18% .

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Mol	Chain	Length	Quality of chain
54	SH	186	
55	SI	206	
56	SK	98	
57	SL	153	
58	SP	127	
59	SQ	141	
60	SR	135	
61	SS	145	
62	ST	143	
63	SU	103	
64	SV	83	
65	SX	141	
66	Sa	102	
67	Sc	64	
68	Sd	55	
69	Sg	313	
70	SC	222	
71	SG	237	
72	SJ	185	
73	SM	122	
74	SN	150	
75	SO	140	
76	SW	129	
77	SY	131	
78	SZ	75	

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Mol	Chain	Length	Quality of chain
79	Sb	83	78% 19%
80	Se	58	100%
81	Sf	67	93% 7%

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 219527 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S rRNA (3773-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3773	Total	C	N	O	P	0	0
			80201	35717	14590	26122	3772		

- Molecule 2 is a RNA chain called 5S rRNA (120-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S rRNA (156-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	156	Total	C	N	O	P	0	0
			3315	1481	585	1094	155		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	368	Total	C	N	O	S	0	0
			2928	1841	583	489	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	SER	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	VAL	deletion	UNP Q02878
LE	?	-	GLU	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	GLU	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	225	Total	C	N	O	S	1	0
			1878	1207	361	301	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	241	Total	C	N	O	S	1	0
			1935	1233	374	324	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	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
			1701	1072	359	266	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	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
			1513	944	314	250	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	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
			1107	714	208	182	3		

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	109	Total	C	N	O	S	0	0
			882	549	192	137	4		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lb	?	-	LYS	deletion	UNP P47914
Lb	?	-	PRO	deletion	UNP P47914
Lb	?	-	LYS	deletion	UNP P47914
Lb	?	-	GLU	deletion	UNP P47914
Lb	?	-	VAL	deletion	UNP P47914
Lb	?	-	LYS	deletion	UNP P47914
Lb	?	-	PRO	deletion	UNP P47914
Lb	?	-	LYS	deletion	UNP P47914
Lb	?	-	ILE	deletion	UNP P47914
Lb	?	-	PRO	deletion	UNP P47914
Lb	?	-	LYS	deletion	UNP P47914
Lb	?	-	GLY	deletion	UNP P47914

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Chain	Residue	Modelled	Actual	Comment	Reference
Lb	89	ALA	VAL	conflict	UNP P47914

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lj	86	Total	C	N	O	S	1	0
			713	439	158	111	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	105	Total	C	N	O	S	1	0
			870	547	178	139	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 47 is a RNA chain called 18S rRNA (1740-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S2	1740	Total	C	N	O	P	0	0
			36938	16494	6600	12105	1739		

- Molecule 48 is a RNA chain called E site tRNA (75-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 50 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 52 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SH	?	-	SER	deletion	UNP P62081
SH	?	-	ARG	deletion	UNP P62081
SH	?	-	THR	deletion	UNP P62081

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 56 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 57 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 58 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SP	127	Total	C	N	O	S	0	0
			1045	663	198	177	7		

- Molecule 59 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 60 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 61 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 62 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 63 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SU	103	Total	C	N	O	S	0	0
			817	511	155	147	4		

- Molecule 64 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 66 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sa	102	Total	C	N	O	S	1	0
			829	517	174	133	5		

- Molecule 67 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 68 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 69 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 70 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SC	222	Total	C	N	O	S	1	0
			1733	1120	301	302	10		

- Molecule 71 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 72 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SJ	185	Total	C	N	O	S	1	0
			1533	974	309	248	2		

- Molecule 73 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 74 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 75 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 76 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 77 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SY	131	Total	C	N	O	S	1	0
			1073	678	212	178	5		

- Molecule 78 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 79 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 81 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 82 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

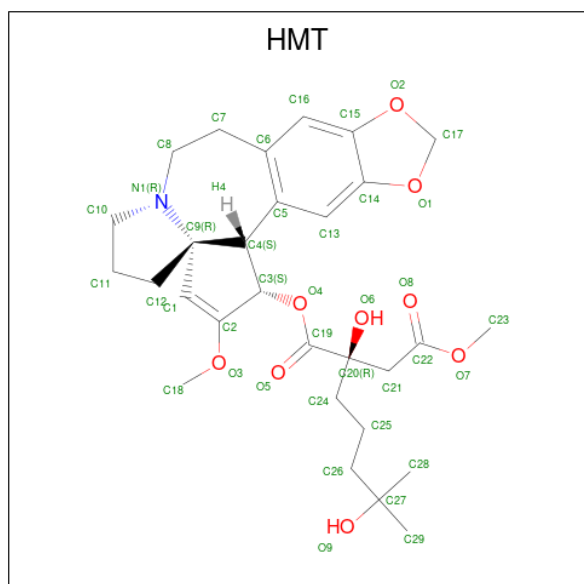
Mol	Chain	Residues	Atoms		AltConf
82	L5	279	Total	Mg	0
			279	279	
82	L7	3	Total	Mg	0
			3	3	
82	L8	6	Total	Mg	0
			6	6	
82	LA	1	Total	Mg	0
			1	1	
82	LI	1	Total	Mg	0
			1	1	
82	LN	1	Total	Mg	0
			1	1	
82	LP	1	Total	Mg	0
			1	1	
82	LS	1	Total	Mg	0
			1	1	
82	LV	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
82	Le	2	Total	Mg	0
			2	2	
82	Lf	1	Total	Mg	0
			1	1	
82	S2	140	Total	Mg	0
			140	140	
82	SF	1	Total	Mg	0
			1	1	

- Molecule 83 is (3beta)-O 3 -[(2R)-2,6-dihydroxy-2-(2-methoxy-2-oxoethyl)-6-methylheptano yl]cephalotaxine (CCD ID: HMT) (formula: C₂₉H₃₉NO₉).



Mol	Chain	Residues	Atoms				AltConf
83	L5	1	Total	C	N	O	0
			39	29	1	9	

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

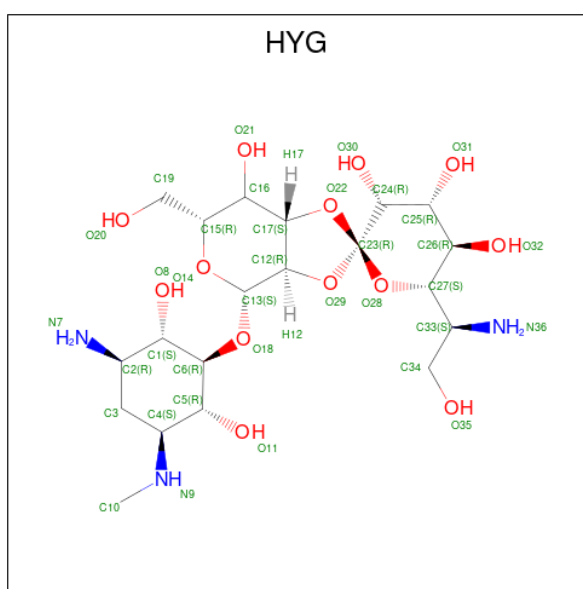
Mol	Chain	Residues	Atoms		AltConf
84	Lg	1	Total	Zn	0
			1	1	
84	Lj	1	Total	Zn	0
			1	1	
84	Lm	1	Total	Zn	0
			1	1	
84	Lo	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
84	Lp	1	Total	Zn	0
			1	1	
84	Sa	1	Total	Zn	0
			1	1	
84	Sd	1	Total	Zn	0
			1	1	
84	Sf	1	Total	Zn	0
			1	1	

- Molecule 85 is HYGROMYCIN B (CCD ID: HYG) (formula: $C_{20}H_{37}N_3O_{13}$).



Mol	Chain	Residues	Atoms				AltConf
85	S2	1	Total	C	N	O	0
			36	20	3	13	

- Molecule 86 is water.

Mol	Chain	Residues	Atoms		AltConf
86	L5	11	Total	O	0
			11	11	
86	LA	1	Total	O	0
			1	1	
86	LB	1	Total	O	0
			1	1	
86	LC	1	Total	O	0
			1	1	

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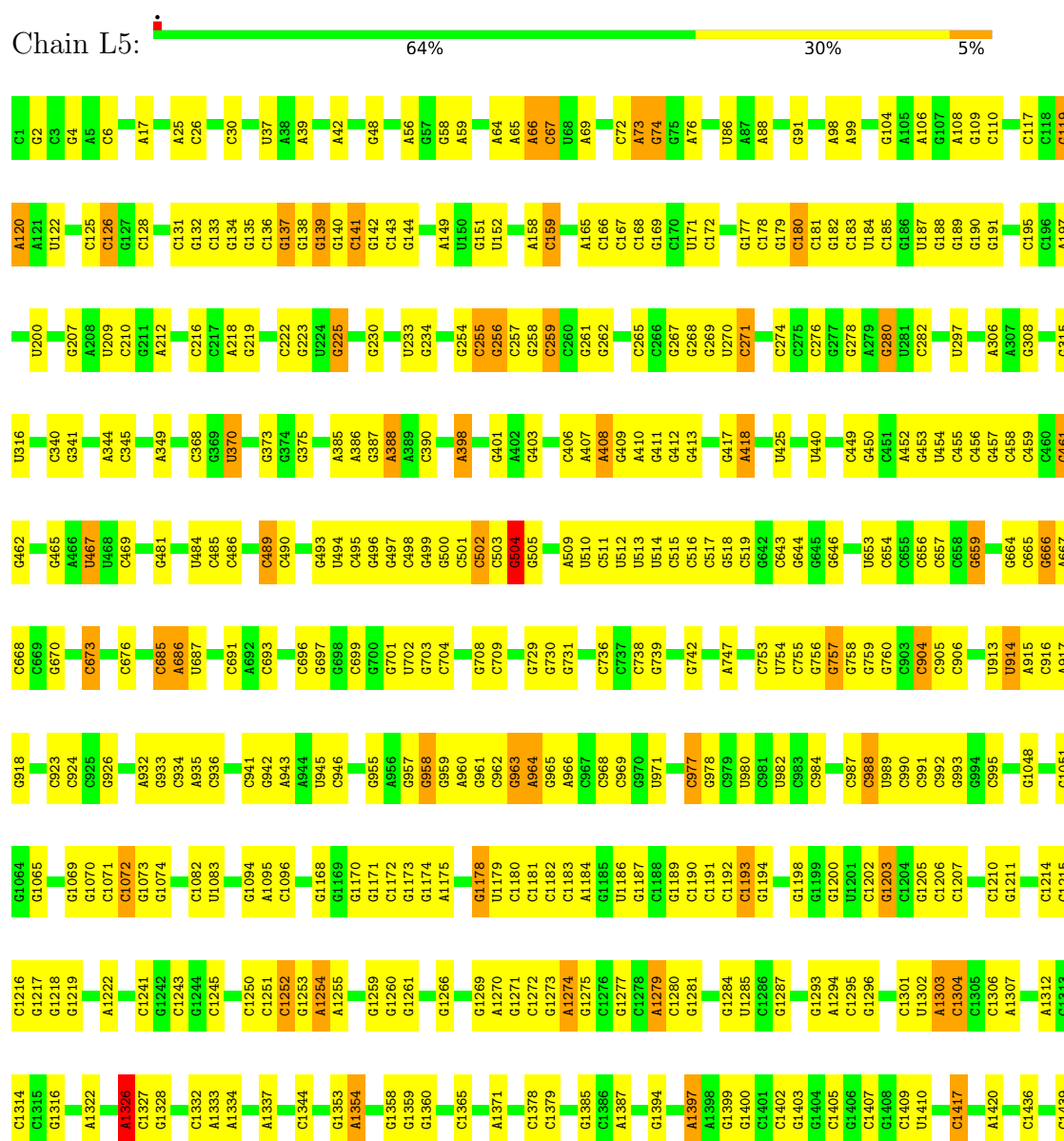
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Mol	Chain	Residues	Atoms		AltConf
86	LF	1	Total 1	O 1	0
86	LG	1	Total 1	O 1	0
86	LH	1	Total 1	O 1	0
86	LI	1	Total 1	O 1	0
86	LY	1	Total 1	O 1	0
86	La	2	Total 2	O 2	0
86	Lb	1	Total 1	O 1	0
86	Lf	1	Total 1	O 1	0
86	Lm	1	Total 1	O 1	0
86	S2	12	Total 12	O 12	0
86	SF	1	Total 1	O 1	0
86	SL	1	Total 1	O 1	0
86	SR	1	Total 1	O 1	0
86	SS	1	Total 1	O 1	0
86	SV	1	Total 1	O 1	0
86	SC	1	Total 1	O 1	0
86	SG	1	Total 1	O 1	0
86	SN	1	Total 1	O 1	0

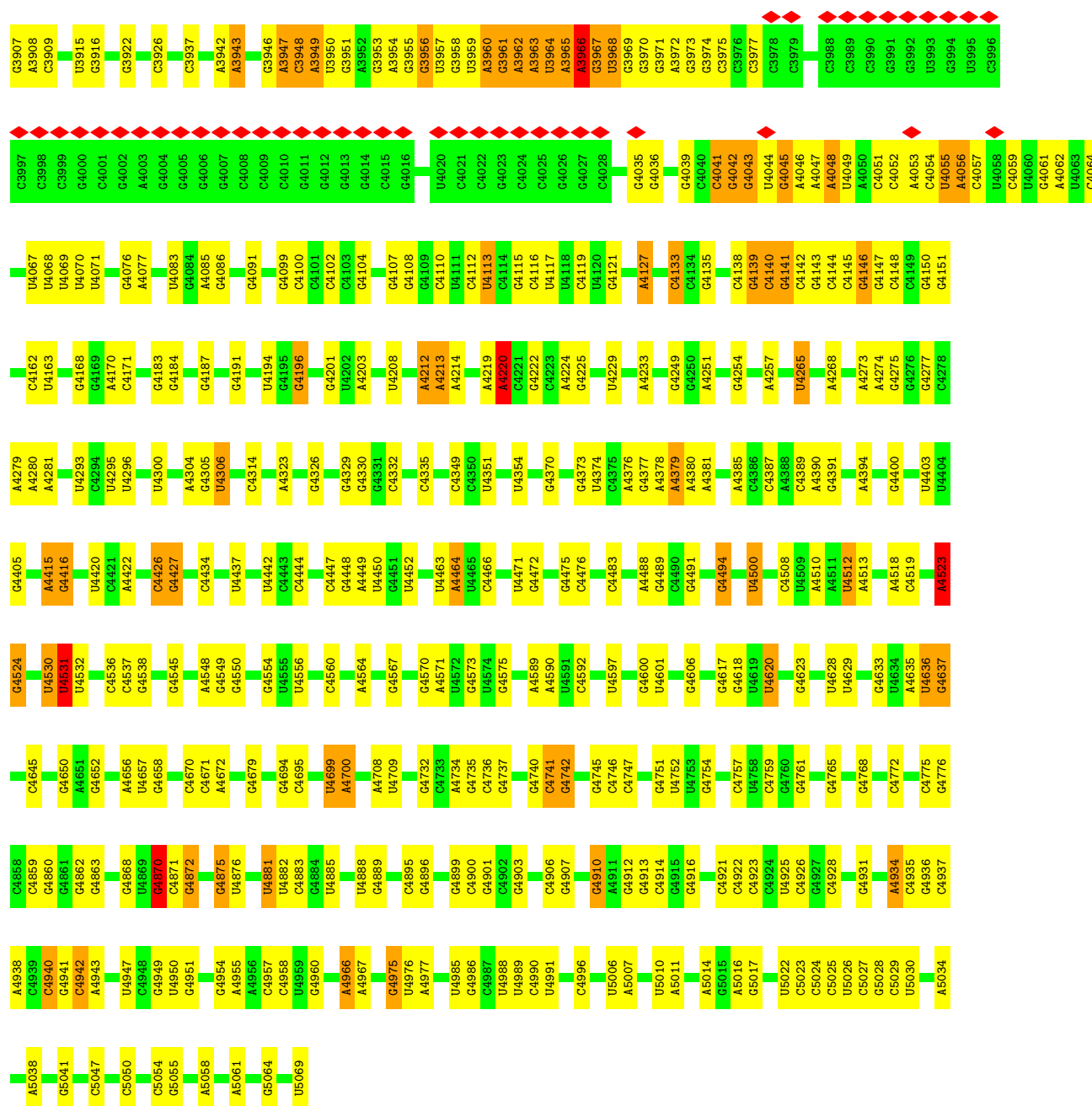
3 Residue-property plots

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

• Molecule 1: 28S rRNA (3773-MER)

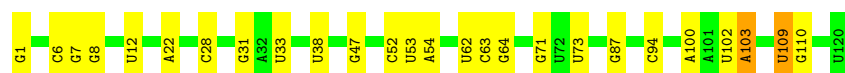


C3782	A3663	G2902	G2754	G2618	G2506	A2395	C2256	C2016	G1946	C1820	C1703	G1581	U1440
A3785	C3667	G2903	A2755	U2626	A2507	A2396	C2257	A2017	U1947	G1821	C1704	G1582	C1441
U3786	G3672	U2904	G2756	C2627	U2508	G2397	C2258	C2019	G1948	U1822	G1705	U1583	C1442
G3787	G3673	G2905	U2761	U2637	A2511	A2401	C2259	C2021	G1952	G1823	G1706	G1586	A1443
C3788	G3674	U2908	G2762	G2652	A2512	G2406	C2260	G2024	U1953	G1824	C1707	G1590	U1444
C3789	U3677	G2909	U2763	C2654	A2513	U2408	G2280	A2025	G1959	U1834	G1716	C1590	U1445
G3792	U3680	G2910	A2764	C2654	U2519	U2409	G2289	A2026	A1960	G1836	A1719	U1591	C1446
A3799	G3681	G3585	C2770	G2662	A2527	G2416	U2293	G2033	G1961	G1837	U1726	U1596	C1447
A3800	A3682	G3586	G2773	C2669	G2528	A2417	G2294	A2034	A1962	G1842	A1729	A1600	G1448
U3801	U3688	C3587	U2768	C2670	A2529	A2418	G2297	C2035	G1965	U1852	G1734	A1601	G1453
U3802	U3688	G3589	A2769	C2673	C2533	G2421	G2297	U2038	C1966	U1855	G1739	C1472	C1456
C3810	A3692	G3590	U2790	G2675	A2537	A2423	A2300	G2039	A1967	G1855	C1740	G1618	G1457
C3811	U3709	C3591	U2801	C2676	A2543	G2426	G2301	U2044	G1968	U1860	G1741	G1624	C1472
C3812	C3708	G3592	C2804	U2687	U2544	U2425	C2302	G2045	G1971	U1866	A1742	G1625	G1482
A3813	U3710	C3593	A2812	C2688	U2545	G2434	C2303	U2046	A1970	C1870	G1753	C1628	C1483
A3814	G3711	C3594	G2813	U2687	U2546	G2434	C2306	G2047	G1974	U1876	G1750	A1631	C1486
U3817	U3712	C3595	C2814	U2687	U2547	U2440	A2313	U2048	G1975	U1882	G1753	A1632	G1493
U3818	A3713	A3596	A2815	C2688	G2547	C2441	G2316	G2050	G1976	U1883	G1754	A1633	A1497
U3819	G3714	G3597	G2815	A2695	U2554	G2441	G2316	G2051	C1977	G1872	C1755	A1634	G1498
A3825	U3715	G3602	C2820	A2696	G2555	G2441	G2316	G2055	U1980	U1876	G1756	A1638	C1502
C3837	A3718	A3604	G2820	G2703	G2556	G2450	C2319	G2056	G1981	U1876	U1757	G1639	G1502
U3838	U3719	C3605	U2826	G2704	G2557	G2450	C2319	G2056	G1982	U1882	G1758	C1640	A1503
G3839	G3720	U3606	G2827	G2705	G2558	A2453	C2325	C2062	A1983	U1883	G1759	G1641	G1504
U3840	A3723	G3614	G2827	G2706	G2559	G2453	G2326	G2068	A1984	U1888	G1760	A1642	U1513
C3726	U3726	G3615	G2838	U2707	G2560	G2464	A2332	A2069	U1985	U1889	G1761	A1646	U1514
A3727	G3616	U3616	G2847	U2708	C2561	G2465	G2333	G2084	U1986	U1890	G1762	G1654	A1515
U3729	C3617	G3618	G2848	C2709	G2562	G2469	G2337	G2085	G1987	U1891	G1763	G1654	G1516
U3734	A3620	U3626	A2849	G2710	G2563	G2470	C2337	G2088	G1988	U1892	A1765	G1661	A1517
G3735	A3630	A3635	G2850	G2711	G2564	G2471	C2338	G2089	U1990	U1897	A1766	A1661	A1518
A3736	C3636	C3636	G2851	G2712	G2565	G2471	C2338	U2090	A1991	C1676	A1767	C1676	C1521
U3738	U3641	U3641	G2855	G2713	G2566	G2475	C2346	U2091	U1992	U1677	G1769	A1522	G1522
C3739	A3642	A3643	G2856	G2714	G2569	G2475	C2347	G2092	G1995	G1680	A1770	A1524	A1524
A3740	A3643	A3644	G2857	G2715	G2578	G2478	C2348	G2093	U1996	G1681	U1771	A1525	A1525
U3741	U3644	U3645	G2858	G2716	G2578	G2482	C2351	G2094	U1997	A1682	A1775	A1534	A1534
U3742	U3645	U3646	G2859	G2717	G2578	G2483	G2357	G2095	A1998	U1683	C1778	A1547	A1547
U3743	U3646	U3647	G2860	G2718	G2578	G2484	G2357	G2096	A1999	G1684	A1787	G1549	G1549
U3744	U3647	U3648	G2861	G2719	G2578	G2485	G2357	G2097	A2002	G1685	G1797	G1559	G1559
U3745	U3648	U3649	G2862	G2720	G2578	G2486	G2357	G2098	G2003	U1693	G1802	C1566	C1566
U3746	U3649	U3650	G2863	G2721	G2578	G2487	G2357	G2099	G2004	C1694	A1803	U1567	U1567
U3747	U3650	U3651	G2864	G2722	G2578	G2488	G2357	A2100	U2005	U1695	A1804	C1696	C1696
U3748	U3651	U3652	G2865	G2723	G2578	G2489	G2357	C2101	U2006	G1697	G1810	U1570	U1570
U3749	U3652	U3653	G2866	G2724	G2578	G2490	G2357	G2106	U2007	C1698	G1811	G1571	G1571
U3750	U3653	U3654	G2867	G2725	G2578	G2491	G2357	G2107	U2008	G1699	C1812	G1700	U1578
U3751	U3654	U3655	G2868	G2726	G2578	G2492	G2357	G2108	U2009	U1699	G1813	G1700	U1578
U3752	U3655	U3656	G2869	G2727	G2578	G2493	G2357	G2109	U2010	C1699	G1814	G1700	U1578
U3753	U3656	U3657	G2870	G2728	G2578	G2494	G2357	G2110	U2011	C1699	G1815	G1700	U1578
U3754	U3657	U3658	G2871	G2729	G2578	G2495	G2357	G2111	U2012	C1699	G1816	G1700	U1578
U3755	U3658	U3659	G2872	G2730	G2578	G2496	G2357	G2112	U2013	C1699	G1817	G1700	U1578
U3756	U3659	U3660	G2873	G2731	G2578	G2497	G2357	G2113	U2014	C1699	G1818	G1700	U1578
U3757	U3660	U3661	G2874	G2732	G2578	G2498	G2357	G2114	U2015	C1699	G1819	G1700	U1578
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U3759	U3662	U3663	G2876	G2734	G2578	G2500	G2357	G2116	U2017	C1699	G1821	G1700	U1578
U3760	U3663	U3664	G2877	G2735	G2578	G2501	G2357	G2117	U2018	C1699	G1822	G1700	U1578
U3761	U3664	U3665	G2878	G2736	G2578	G2502	G2357	G2118	U2019	C1699	G1823	G1700	U1578
U3762	U3665	U3666	G2879	G2737	G2578	G2503	G2357	G2119	U2020	C1699	G1824	G1700	U1578
U3763	U3666	U3667	G2880	G2738	G2578	G2504	G2357	G2120	U2021	C1699	G1825	G1700	U1578
U3764	U3667	U3668	G2881	G2739	G2578	G2505	G2357	G2121	U2022	C1699	G1826	G1700	U1578
U3765	U3668	U3669	G2882	G2740	G2578	G2506	G2357	G2122	U2023	C1699	G1827	G1700	U1578
U3766	U3669	U3670	G2883	G2741	G2578	G2507	G2357	G2123	U2024	C1699	G1828	G1700	U1578
U3767	U3670	U3671	G2884	G2742	G2578	G2508	G2357	G2124	U2025	C1699	G1829	G1700	U1578
U3768	U3671	U3672	G2885	G2743	G2578	G2509	G2357	G2125	U2026	C1699	G1830	G1700	U1578
U3769	U3672	U3673	G2886	G2744	G2578	G2510	G2357	G2126	U2027	C1699	G1831	G1700	U1578
U3770	U3673	U3674	G2887	G2745	G2578	G2511	G2357	G2127	U2028	C1699	G1832	G1700	U1578
U3771	U3674	U3675	G2888	G2746	G2578	G2512	G2357	G2128	U2029	C1699	G1833	G1700	U1578
U3772	U3675	U3676	G2889	G2747	G2578	G2513	G2357	G2129	U2030	C1699	G1834	G1700	U1578
U3773	U3676	U3677	G2890	G2748	G2578	G2514	G2357	G2130	U2031	C1699	G1835	G1700	U1578
U3774	U3677	U3678	G2891	G2749	G2578	G2515	G2357	G2131	U2032	C1699	G1836	G1700	U1578
U3775	U3678	U3679	G2892	G2750	G2578	G2516	G2357	G2132	U2033	C1699	G1837	G1700	U1578
U3776	U3679	U3680	G2893	G2751	G2578	G2517	G2357	G2133	U2034	C1699	G1838	G1700	U1578
U3777	U3680	U3681	G2894	G2752	G2578	G2518	G2357	G2134	U2035	C1699	G1839	G1700	U1578
U3778	U3681	U3682	G2895	G2753	G2578	G2519	G2357	G2135	U2036	C1699	G1840	G1700	U1578
U3779	U3682	U3683	G2896	G2754	G2578	G2520	G2357	G2136	U2037	C1699	G1841	G1700	U1578
U3780	U3683	U3684	G2897	G2755	G2578	G2521	G2357	G2137	U2038	C1699	G1842	G1700	U1578
U3781	U3684	U3685	G2898	G2756	G2578	G2522	G2357	G2138	U2039	C1699	G1843	G1700	U1578
U3782	U3685	U3686	G2899	G2757	G2578	G2523	G2357	G2139	U2040	C1699	G1844	G1700	U1578
U3783	U3686	U3687	G2900	G2758	G2578	G2524	G2357	G2140	U2041	C1699	G1845	G1700	U1578
U3784	U3687	U3688	G2901	G2759	G2578	G2525	G2357	G2141	U2042	C1699	G1846	G1700	U1578
U3785	U3688	U3689	G2902	G2760	G2578	G2526	G2357	G2142	U2043	C1699	G1847	G1700	U1578
U3786	U3689	U3690	G2903	G2761	G2578	G2527	G2357	G2143	U2044	C1699	G1848	G1700	U1578
U3787	U3690	U3691	G2904	G2762	G2578	G2528	G2357	G2144	U2045	C1699	G1849	G1700	U1578
U3788	U3691	U3692	G2905	G2763	G2578	G2529	G2357	G2145	U2046	C1699	G1850	G1700	U1578
U3789	U3692	U3693	G2906	G2764	G2578	G2530	G2357	G2146	U2047	C1699	G1851	G1700	U1578
U3790	U3693	U3694	G2907	G2765	G2578	G2531	G2357	G2147	U2048	C1699	G1852	G1700	U1578
U3791	U3694	U3695	G2908	G2766	G2578	G2532	G2357	G2148	U2049	C1699	G1853	G1700	U1578
U3792	U3695	U3696	G2909	G2767	G2578	G2533	G2357	G2149	U2050	C1699	G1854	G1700	U1578
U3793	U3696	U3697	G2910	G2768	G2578	G2534	G2357	G2150	U2051	C1699	G1855	G1700	U1578
U3794	U3697	U3698	G2911	G2769	G2578	G2535	G2357	G2151	U2052	C1699	G1856	G1700	U1578
U3795	U3698	U3699	G2912	G2770	G2578	G2536	G2357	G2152	U2053	C1699	G1857	G1700	U1578
U3796	U3699	U3700	G2913	G2771	G2578	G2537	G2357	G2153	U2054	C1699	G1858	G1700	U1578
U3797	U3701	U3702	G2914	G2772	G2578	G2538	G2357	G2154	U2055	C1699	G1859	G1700	U1578
U3798	U3702	U3703	G2915	G2773	G2578	G2539	G2357	G2155	U2056	C1699	G1860	G1700	U1578
U3799	U3703	U3704	G29										



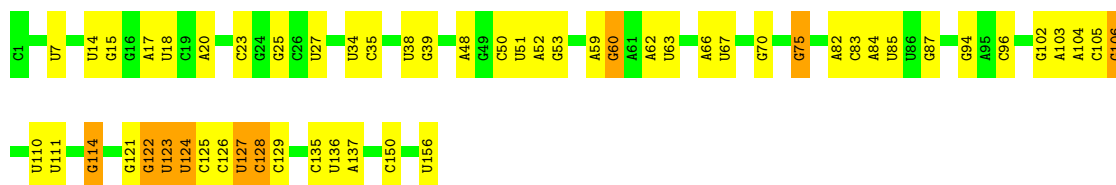
• Molecule 2: 5S rRNA (120-MER)

Chain L7: 78% 20%



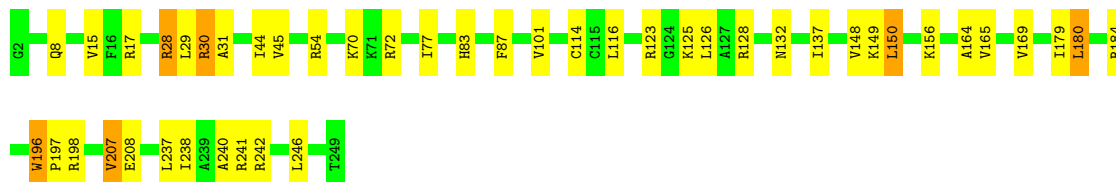
• Molecule 3: 5.8S rRNA (156-MER)

Chain L8: 65% 29% 6%



• Molecule 4: 60S ribosomal protein L8

Chain LA: 82% 16%



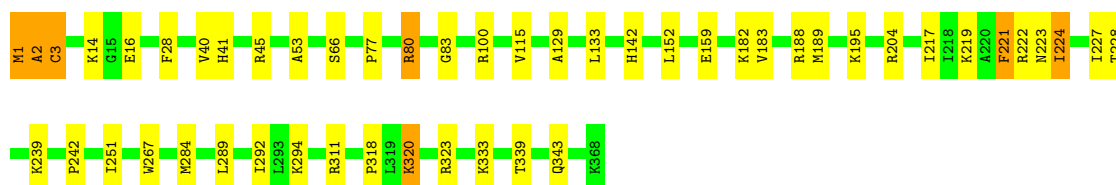
• Molecule 5: 60S ribosomal protein L3

Chain LB: 79% 19%



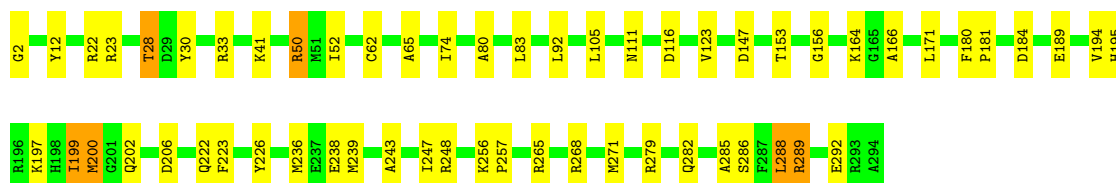
• Molecule 6: 60S ribosomal protein L4

Chain LC: 86% 12%



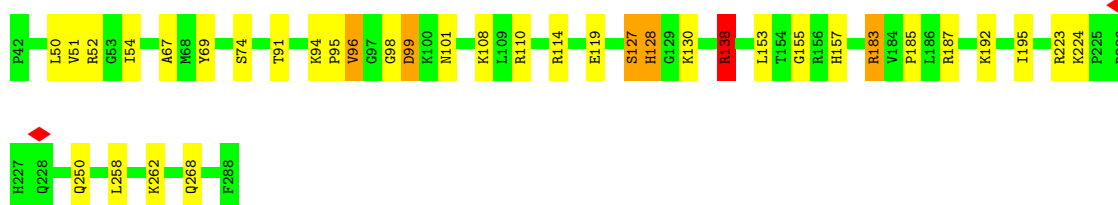
• Molecule 7: 60S ribosomal protein L5

Chain LD: 80% 18%



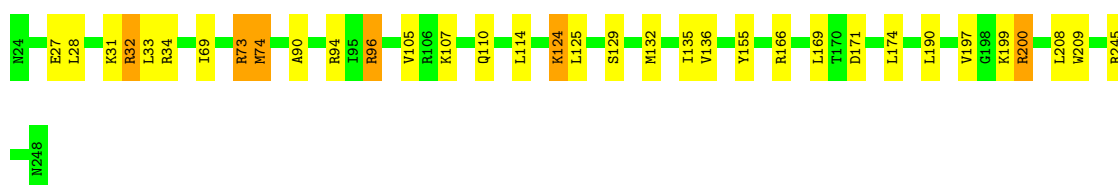
- Molecule 8: 60S ribosomal protein L6

Chain LE:  85% 13%



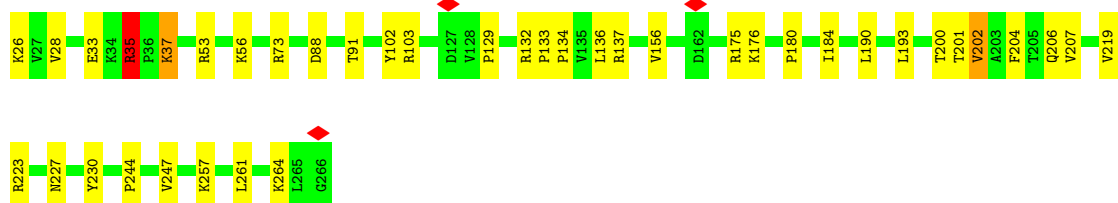
- Molecule 9: 60S ribosomal protein L7

Chain LF:  85% 12%



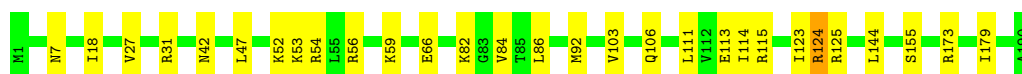
- Molecule 10: 60S ribosomal protein L7a

Chain LG:  83% 15%



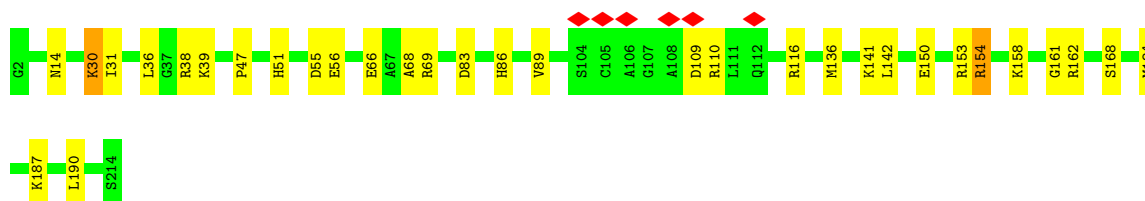
- Molecule 11: 60S ribosomal protein L9

Chain LH:  85% 15%

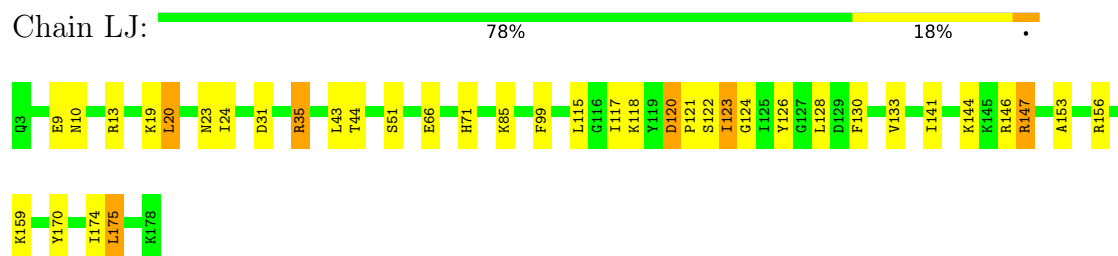


- Molecule 12: 60S ribosomal protein L10-like

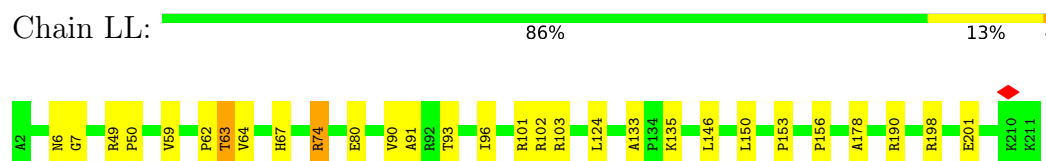
Chain LI:  85% 14%



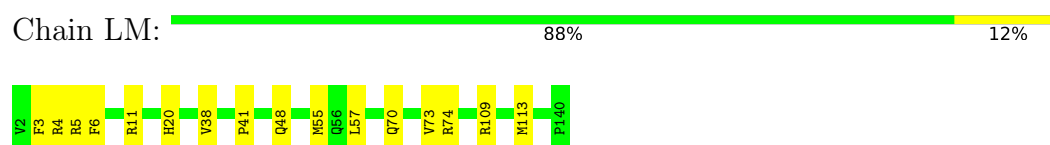
- Molecule 13: 60S ribosomal protein L11



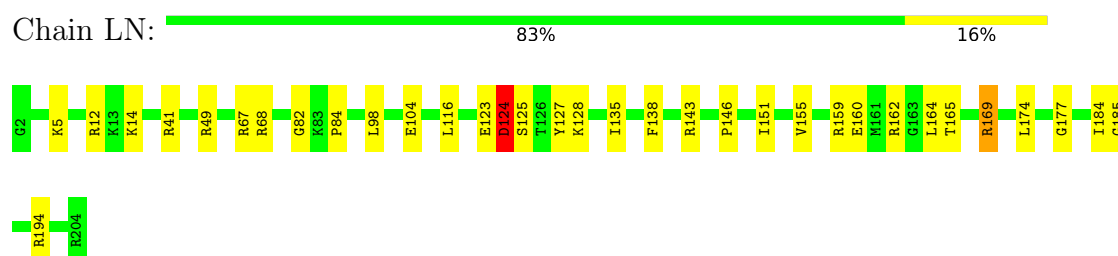
- Molecule 14: 60S ribosomal protein L13



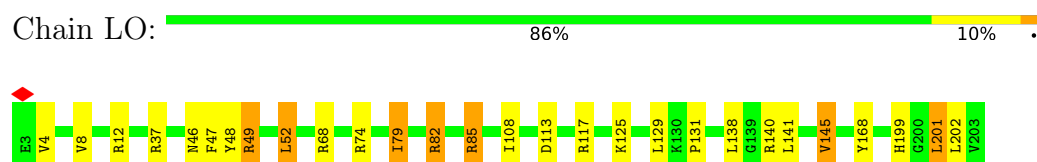
- Molecule 15: 60S ribosomal protein L14



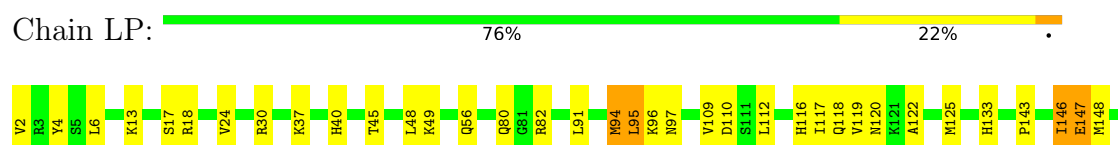
- Molecule 16: 60S ribosomal protein L15



- Molecule 17: 60S ribosomal protein L13a



- Molecule 18: 60S ribosomal protein L17





- Molecule 19: 60S ribosomal protein L18

Chain LQ: 87% 12% .



- Molecule 20: 60S ribosomal protein L19

Chain LR: 89% 10% ..



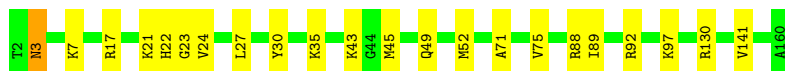
- Molecule 21: 60S ribosomal protein L18a

Chain LS: 91% 8% .



- Molecule 22: 60S ribosomal protein L21

Chain LT: 86% 13% .



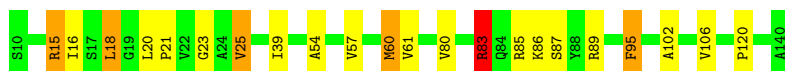
- Molecule 23: 60S ribosomal protein L22

Chain LU: 82% 15% .



- Molecule 24: 60S ribosomal protein L23

Chain LV: 83% 12% ..



- Molecule 25: 60S ribosomal protein L24

Chain LW: 86% 11% .



- Molecule 26: 60S ribosomal protein L23a

Chain LX: 89% 9% ..



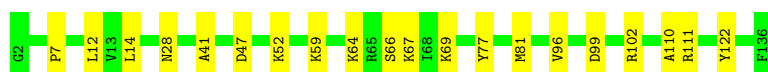
- Molecule 27: 60S ribosomal protein L26

Chain LY: 82% 16% ..



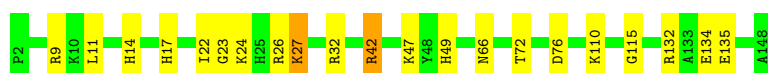
- Molecule 28: 60S ribosomal protein L27

Chain LZ: 85% 15%



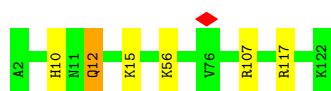
- Molecule 29: 60S ribosomal protein L27a

Chain La: 86% 13%



- Molecule 30: 60S ribosomal protein L29

Chain Lb: 94% 5%



- Molecule 31: 60S ribosomal protein L30

Chain Lc: 82% 15% ..



- Molecule 32: 60S ribosomal protein L31

Chain Ld: 87% 13%



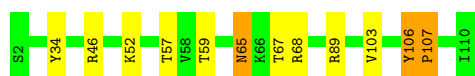
- Molecule 33: 60S ribosomal protein L32

Chain Le: 78% 20% .



- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 89% 8% .



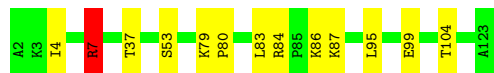
- Molecule 35: 60S ribosomal protein L34

Chain Lg: 96% .



- Molecule 36: 60S ribosomal protein L35

Chain Lh: 89% 10% .



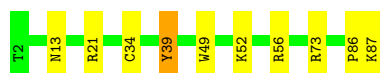
- Molecule 37: 60S ribosomal protein L36

Chain Li: 90% 10% .



- Molecule 38: 60S ribosomal protein L37

Chain Lj: 88% 10% .



- Molecule 39: 60S ribosomal protein L38

Chain Lk: 87% 13% .



- Molecule 40: 60S ribosomal protein L39

Chain Ll: 82% 14% .



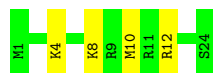
- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm: 85% 13% .



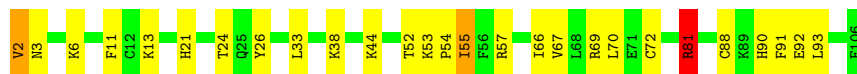
- Molecule 42: 60S ribosomal protein L41

Chain Ln: 83% 17%



- Molecule 43: 60S ribosomal protein L36a

Chain Lo: 74% 23% ..



- Molecule 44: 60S ribosomal protein L37a

Chain Lp: 85% 13% ..



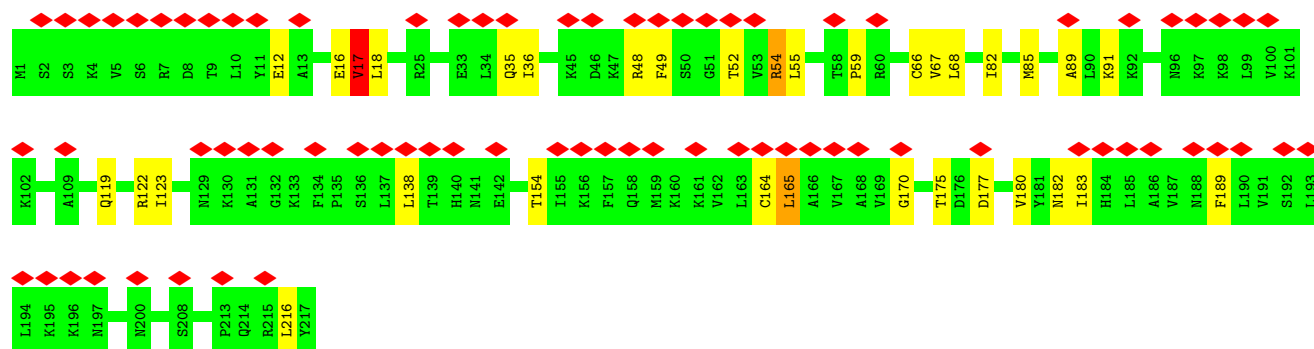
- Molecule 45: 60S ribosomal protein L28

Chain Lr: 82% 14% ..



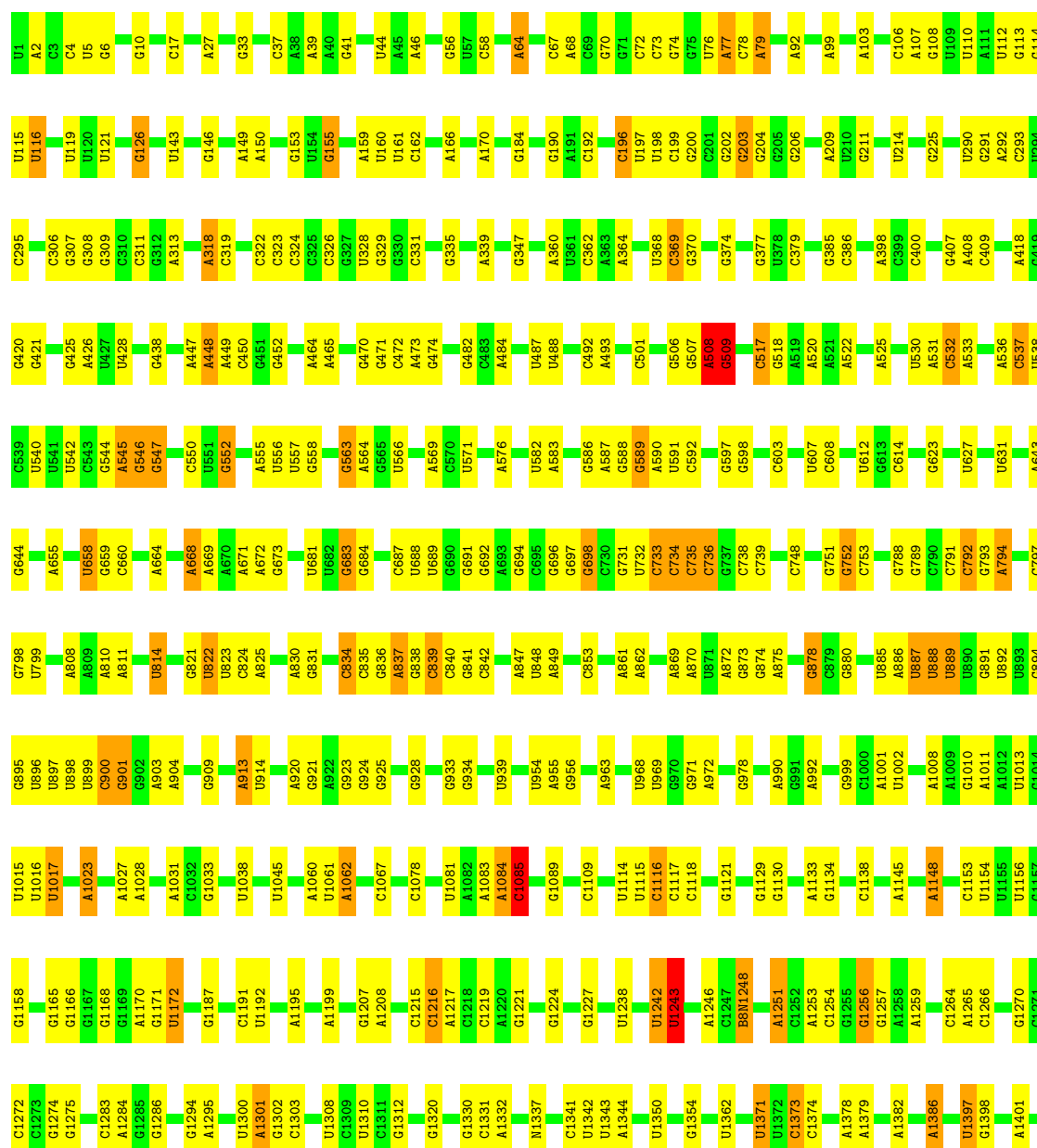
- Molecule 46: 60S ribosomal protein L10a

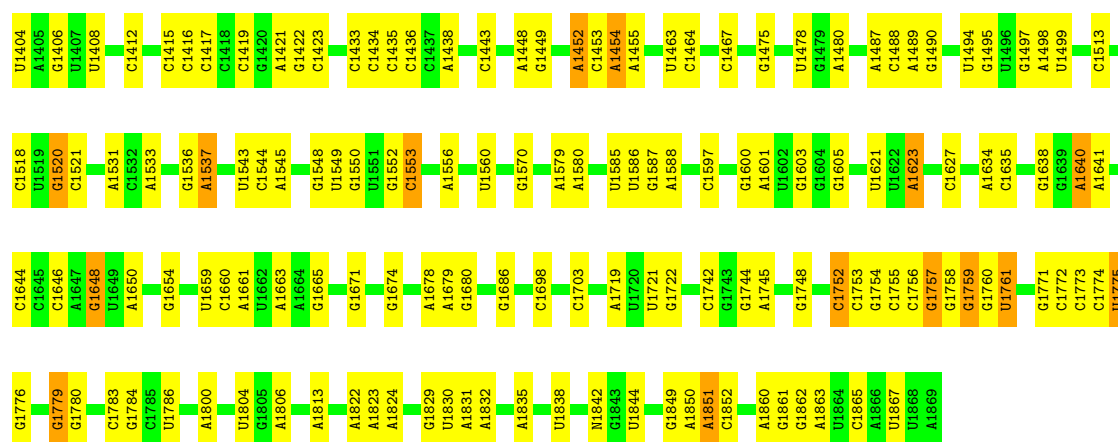
Chain Lz: 35% 84% 14% .



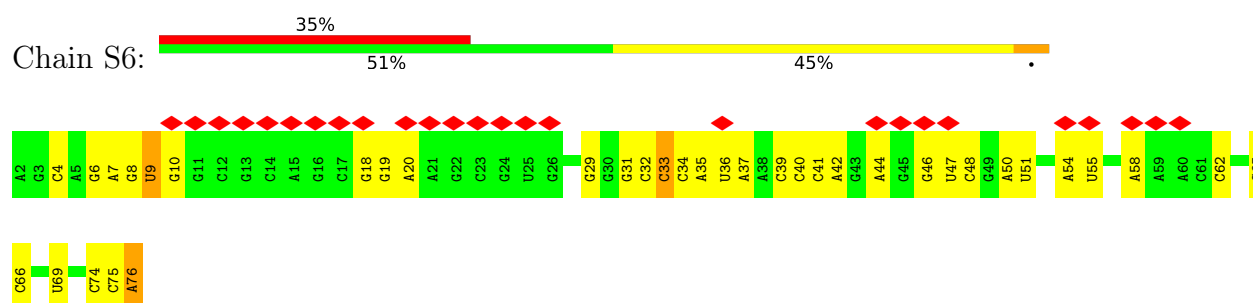
• Molecule 47: 18S rRNA (1740-MER)

Chain S2: 67% 28% .

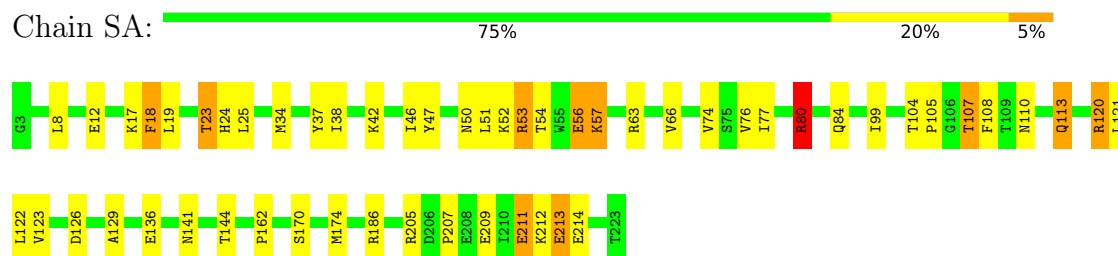




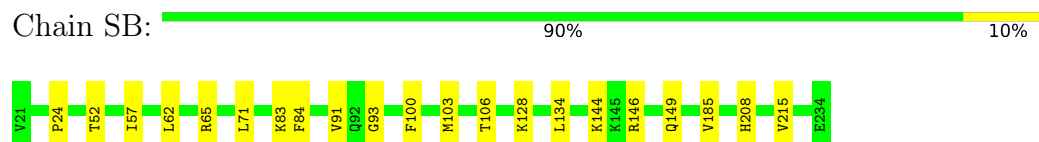
• Molecule 48: E site tRNA (75-MER)



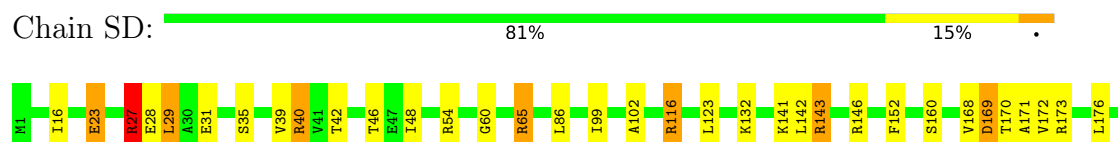
• Molecule 49: 40S ribosomal protein SA



• Molecule 50: 40S ribosomal protein S3a



• Molecule 51: 40S ribosomal protein S3





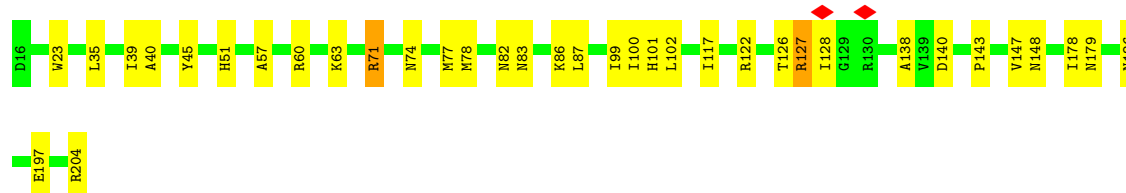
- Molecule 52: 40S ribosomal protein S4, X isoform

Chain SE: 87% 13%



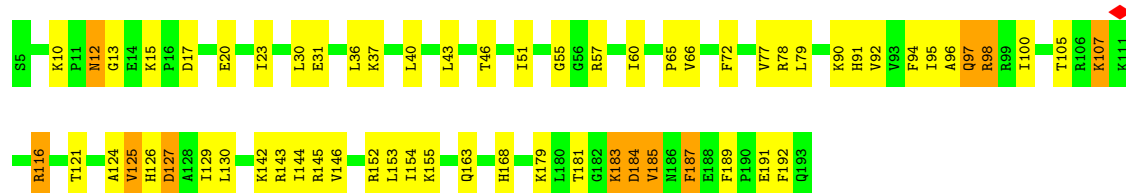
- Molecule 53: 40S ribosomal protein S5

Chain SF: 81% 18%



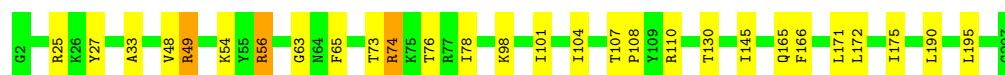
- Molecule 54: 40S ribosomal protein S7

Chain SH: 66% 28% 6%



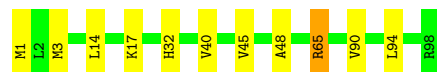
- Molecule 55: 40S ribosomal protein S8

Chain SI: 86% 12%

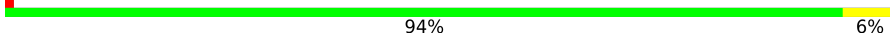


- Molecule 56: 40S ribosomal protein S10

Chain SK: 89% 10%



- Molecule 57: 40S ribosomal protein S11

Chain SL:  94% 6%



- Molecule 58: 40S ribosomal protein S15

Chain SP:  78% 20%



- Molecule 59: 40S ribosomal protein S16

Chain SQ:  81% 16%



- Molecule 60: 40S ribosomal protein S17

Chain SR:  86% 13%



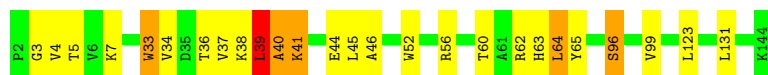
- Molecule 61: 40S ribosomal protein S18

Chain SS:  82% 14%



- Molecule 62: 40S ribosomal protein S19

Chain ST:  82% 14%



- Molecule 63: 40S ribosomal protein S20

Chain SU:  88% 10%



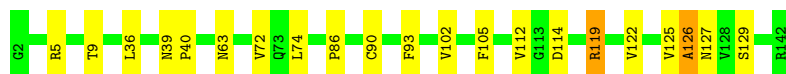
- Molecule 64: 40S ribosomal protein S21

Chain SV:  83% 13% .



- Molecule 65: 40S ribosomal protein S23

Chain SX:  85% 13% .



- Molecule 66: 40S ribosomal protein S26

Chain Sa:  86% 11% ..



- Molecule 67: 40S ribosomal protein S28

Chain Sc:  70% 23% 5% .



- Molecule 68: 40S ribosomal protein S29

Chain Sd:  71% 27% .



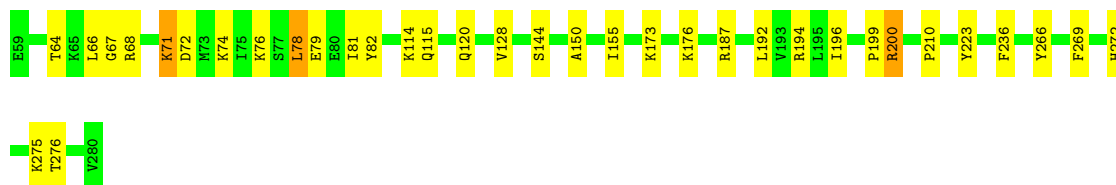
- Molecule 69: Receptor of activated protein C kinase 1

Chain Sg:  76% 24% .



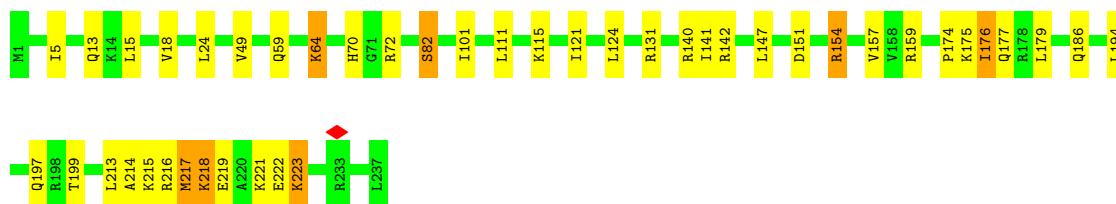
- Molecule 70: 40S ribosomal protein S2

Chain SC:  84% 14% .



- Molecule 71: 40S ribosomal protein S6

Chain SG:  81% 16% .



- Molecule 72: 40S ribosomal protein S9

Chain SJ:  87% 12% .



- Molecule 73: 40S ribosomal protein S12

Chain SM:  85% 15% .



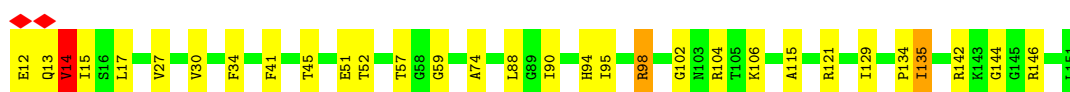
- Molecule 74: 40S ribosomal protein S13

Chain SN:  89% 9% .



- Molecule 75: 40S ribosomal protein S14

Chain SO:  78% 20% ..



- Molecule 76: 40S ribosomal protein S15a

Chain SW:  83% 17%



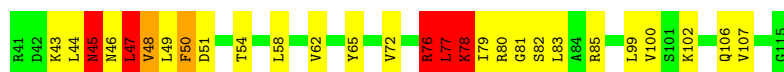
- Molecule 77: 40S ribosomal protein S24

Chain SY:  87% 13%



- Molecule 78: 40S ribosomal protein S25

Chain SZ:  63% 28% 7%



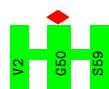
- Molecule 79: 40S ribosomal protein S27

Chain Sb:  78% 19%



- Molecule 80: 40S ribosomal protein S30

Chain Se:  100%



- Molecule 81: Ubiquitin-40S ribosomal protein S27a

Chain Sf:  93% 7%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	138234	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.544	Depositor
Minimum map value	-0.311	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.007	Depositor
Map size ($\text{\AA}$)	544.0, 544.0, 544.0	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UR3, 4AC, 2MG, B8H, MLZ, PSU, HYG, M7A, 5MC, 5MU, A2M, 1MA, JMH, 6MZ, B8T, MA6, OMU, OMG, B8N, HMT, OMC, MG, 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	0.27	1/87760 (0.0%)	0.40	11/136810 (0.0%)
2	L7	0.22	0/2858	0.33	1/4455 (0.0%)
3	L8	0.25	0/3679	0.39	1/5732 (0.0%)
4	LA	0.36	0/1936	0.69	2/2596 (0.1%)
5	LB	0.32	0/3306	0.69	3/4424 (0.1%)
6	LC	0.30	0/2971	0.62	3/3988 (0.1%)
7	LD	0.24	0/2428	0.57	0/3252
8	LE	0.27	0/1942	0.68	2/2606 (0.1%)
9	LF	0.28	0/1916	0.59	0/2553
10	LG	0.27	0/1971	0.62	2/2651 (0.1%)
11	LH	0.29	1/1537 (0.1%)	0.55	0/2066
12	LI	0.21	0/1751	0.52	0/2340
13	LJ	0.25	0/1433	0.66	2/1915 (0.1%)
14	LL	0.27	0/1732	0.59	1/2315 (0.0%)
15	LM	0.26	0/1161	0.56	0/1554
16	LN	0.27	0/1746	0.59	0/2338
17	LO	0.35	0/1682	0.61	2/2250 (0.1%)
18	LP	0.32	0/1268	0.56	0/1701
19	LQ	0.25	0/1537	0.59	0/2052
20	LR	0.27	0/1582	0.56	0/2091
21	LS	0.23	0/1493	0.47	0/2003
22	LT	0.31	0/1326	0.57	0/1770
23	LU	0.24	0/839	0.66	0/1126
24	LV	0.30	0/993	0.64	0/1332
25	LW	0.25	0/1030	0.61	0/1364
26	LX	0.22	0/1002	0.49	1/1345 (0.1%)
27	LY	0.23	0/1132	0.57	0/1504
28	LZ	0.20	0/1130	0.53	0/1507
29	La	0.28	0/1191	0.52	0/1591
30	Lb	0.21	0/895	0.62	2/1182 (0.2%)
31	Lc	0.28	0/774	0.58	1/1038 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Ld	0.21	0/903	0.52	0/1216
33	Le	0.34	0/1071	0.61	0/1429
34	Lf	0.25	0/895	0.54	0/1198
35	Lg	0.21	0/916	0.49	0/1220
36	Lh	0.18	0/1023	0.49	0/1351
37	Li	0.18	0/843	0.50	0/1115
38	Lj	0.25	0/731	0.62	2/966 (0.2%)
39	Lk	0.19	0/575	0.49	0/761
40	Ll	0.34	0/454	0.68	1/599 (0.2%)
41	Lm	0.26	0/425	0.59	0/561
42	Ln	0.41	0/231	0.62	0/294
43	Lo	0.30	0/887	0.61	0/1170
44	Lp	0.26	0/718	0.62	1/953 (0.1%)
45	Lr	0.25	0/1017	0.56	0/1364
46	Lz	0.22	0/1769	0.63	0/2371
47	S2	0.25	0/40466	0.36	3/63037 (0.0%)
48	S6	0.15	0/1795	0.34	0/2798
49	SA	0.30	0/1778	0.64	1/2416 (0.0%)
50	SB	0.20	0/1765	0.47	0/2362
51	SD	0.26	0/1793	0.61	0/2414
52	SE	0.24	0/2118	0.53	1/2849 (0.0%)
53	SF	0.26	0/1516	0.63	1/2037 (0.0%)
54	SH	0.28	0/1519	0.69	2/2033 (0.1%)
55	SI	0.31	0/1715	0.60	0/2287
56	SK	0.22	0/851	0.56	0/1147
57	SL	0.24	0/1268	0.58	0/1696
58	SP	0.25	0/1065	0.65	2/1423 (0.1%)
59	SQ	0.28	0/1142	0.68	2/1528 (0.1%)
60	SR	0.23	0/1105	0.60	0/1484
61	SS	0.25	0/1216	0.58	1/1628 (0.1%)
62	ST	0.30	0/1131	0.62	1/1515 (0.1%)
63	SU	0.22	0/827	0.59	0/1110
64	SV	0.29	0/643	0.59	0/860
65	SX	0.27	0/1116	0.68	1/1490 (0.1%)
66	Sa	0.31	0/847	0.64	0/1135
67	Sc	0.38	0/508	0.88	1/680 (0.1%)
68	Sd	0.29	0/470	0.64	0/623
69	Sg	0.22	0/2493	0.62	2/3394 (0.1%)
70	SC	0.42	4/1773 (0.2%)	0.72	4/2395 (0.2%)
71	SG	0.25	0/1946	0.67	3/2590 (0.1%)
72	SJ	0.24	0/1561	0.63	0/2083
73	SM	0.17	0/950	0.50	0/1275
74	SN	0.22	0/1232	0.45	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	SO	0.30	0/1062	0.72	2/1425 (0.1%)
76	SW	0.25	0/1051	0.56	0/1406
77	SY	0.23	0/1094	0.52	0/1452
78	SZ	0.32	0/604	0.73	1/810 (0.1%)
79	Sb	0.23	0/665	0.59	0/891
80	Se	0.20	0/465	0.51	0/612
81	Sf	0.23	0/560	0.71	0/745
All	All	0.26	6/232569 (0.0%)	0.48	66/341305 (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
4	LA	0	1
5	LB	0	4
6	LC	0	2
8	LE	0	1
9	LF	0	1
10	LG	0	2
12	LI	0	3
13	LJ	0	3
14	LL	0	2
15	LM	0	1
16	LN	0	2
19	LQ	0	2
20	LR	0	1
23	LU	0	1
24	LV	0	1
25	LW	0	1
27	LY	0	1
29	La	0	3
32	Ld	0	1
33	Le	0	1
34	Lf	0	2
36	Lh	0	2
38	Lj	0	1
39	Lk	0	1
40	Ll	0	1
41	Lm	0	1
43	Lo	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
44	Lp	0	1
45	Lr	0	5
46	Lz	0	2
49	SA	0	4
51	SD	0	6
53	SF	0	5
54	SH	0	1
55	SI	0	3
56	SK	0	1
58	SP	0	2
59	SQ	0	2
60	SR	0	2
61	SS	0	1
62	ST	0	1
63	SU	0	1
65	SX	0	5
66	Sa	0	1
69	Sg	0	1
70	SC	0	3
72	SJ	0	3
74	SN	0	1
75	SO	0	1
77	SY	0	1
All	All	0	97

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
70	SC	200[A]	ARG	C-O	7.48	1.32	1.24
70	SC	200[B]	ARG	C-O	7.48	1.32	1.24
70	SC	200[A]	ARG	CA-C	5.70	1.60	1.52
70	SC	200[B]	ARG	CA-C	5.70	1.60	1.52
11	LH	173	ARG	N-CA	5.31	1.52	1.46

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	3884	U	C3'-C2'-O2'	14.04	131.77	110.70
47	S2	508	A	C1'-C2'-O2'	11.78	126.07	108.40
1	L5	504	G	C2'-C3'-O3'	10.24	124.86	109.50
1	L5	914	U	C2'-C3'-O3'	9.79	124.19	109.50
1	L5	2416	G	C2'-C3'-O3'	9.50	123.75	109.50

There are no chirality outliers.

5 of 97 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	30	ARG	Sidechain
5	LB	17	LEU	Peptide
5	LB	174	ARG	Sidechain
5	LB	19	ARG	Sidechain
5	LB	258	HIS	Peptide

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	80201	0	40426	436	0
2	L7	2558	0	1296	11	0
3	L8	3315	0	1685	23	0
4	LA	1898	0	1993	30	0
5	LB	3238	0	3376	60	0
6	LC	2928	0	3105	33	0
7	LD	2382	0	2410	45	0
8	LE	1904	0	2055	35	0
9	LF	1878	0	2009	29	0
10	LG	1935	0	2087	26	0
11	LH	1518	0	1601	26	0
12	LI	1711	0	1749	22	0
13	LJ	1410	0	1441	27	0
14	LL	1701	0	1818	19	0
15	LM	1138	0	1204	11	0
16	LN	1701	0	1749	24	0
17	LO	1650	0	1794	28	0
18	LP	1242	0	1269	32	0
19	LQ	1513	0	1628	14	0
20	LR	1566	0	1729	13	0
21	LS	1453	0	1490	12	0
22	LT	1298	0	1366	17	0
23	LU	825	0	850	12	0
24	LV	979	0	1039	19	0
25	LW	1015	0	1079	13	0
26	LX	985	0	1066	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	LY	1115	0	1205	15	0
28	LZ	1107	0	1182	13	0
29	La	1162	0	1213	15	0
30	Lb	882	0	962	5	0
31	Lc	764	0	804	20	0
32	Ld	888	0	930	7	0
33	Le	1053	0	1147	18	0
34	Lf	876	0	912	9	0
35	Lg	906	0	1002	2	0
36	Lh	1015	0	1148	10	0
37	Li	832	0	917	6	0
38	Lj	713	0	751	8	0
39	Lk	569	0	637	6	0
40	Ll	444	0	483	5	0
41	Lm	430	0	466	8	0
42	Ln	230	0	276	7	0
43	Lo	870	0	945	15	0
44	Lp	708	0	756	17	0
45	Lr	1002	0	1068	16	0
46	Lz	1741	0	1854	17	0
47	S2	36938	0	18623	172	0
48	S6	1604	0	816	13	0
49	SA	1741	0	1746	43	0
50	SB	1738	0	1809	14	0
51	SD	1765	0	1865	42	0
52	SE	2076	0	2177	19	0
53	SF	1495	0	1549	35	0
54	SH	1497	0	1590	52	0
55	SI	1686	0	1772	18	0
56	SK	827	0	854	7	0
57	SL	1247	0	1323	5	0
58	SP	1045	0	1095	20	0
59	SQ	1124	0	1193	20	0
60	SR	1090	0	1149	13	0
61	SS	1198	0	1261	22	0
62	ST	1112	0	1146	23	0
63	SU	817	0	882	10	0
64	SV	636	0	637	15	0
65	SX	1098	0	1167	7	0
66	Sa	829	0	883	13	0
67	Sc	506	0	536	26	0
68	Sd	459	0	448	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	Sg	2436	0	2393	50	0
70	SC	1733	0	1826	22	0
71	SG	1923	0	2089	28	0
72	SJ	1533	0	1653	20	0
73	SM	940	0	965	10	0
74	SN	1208	0	1294	12	0
75	SO	1049	0	1073	22	0
76	SW	1034	0	1080	15	0
77	SY	1073	0	1155	12	0
78	SZ	598	0	656	40	0
79	Sb	651	0	672	11	0
80	Se	459	0	503	0	0
81	Sf	548	0	551	3	0
82	L5	279	0	0	0	0
82	L7	3	0	0	0	0
82	L8	6	0	0	0	0
82	LA	1	0	0	0	0
82	LI	1	0	0	0	0
82	LN	1	0	0	0	0
82	LP	1	0	0	0	0
82	LS	1	0	0	0	0
82	LV	1	0	0	0	0
82	Le	2	0	0	0	0
82	Lf	1	0	0	0	0
82	S2	140	0	0	0	0
82	SF	1	0	0	0	0
83	L5	39	0	39	4	0
84	Lg	1	0	0	0	0
84	Lj	1	0	0	0	0
84	Lm	1	0	0	0	0
84	Lo	1	0	0	0	0
84	Lp	1	0	0	0	0
84	Sa	1	0	0	0	0
84	Sd	1	0	0	0	0
84	Sf	1	0	0	0	0
85	S2	36	0	37	0	0
86	L5	11	0	0	0	0
86	LA	1	0	0	0	0
86	LB	1	0	0	0	0
86	LC	1	0	0	0	0
86	LF	1	0	0	0	0
86	LG	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	LH	1	0	0	0	0
86	LI	1	0	0	0	0
86	LY	1	0	0	0	0
86	La	2	0	0	0	0
86	Lb	1	0	0	0	0
86	Lf	1	0	0	0	0
86	Lm	1	0	0	0	0
86	S2	12	0	0	0	0
86	SC	1	0	0	0	0
86	SF	1	0	0	0	0
86	SG	1	0	0	0	0
86	SL	1	0	0	0	0
86	SN	1	0	0	0	0
86	SR	1	0	0	0	0
86	SS	1	0	0	0	0
86	SV	1	0	0	0	0
All	All	219527	0	162479	1793	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 5.

The worst 5 of 1793 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)
11:LH:115:ARG:NH1	11:LH:123:ILE:HG12	1.47	1.30
31:Lc:20:LEU:CD1	31:Lc:101:ASP:HB3	1.71	1.20
1:L5:3946:G:O2'	1:L5:3947:A:H5''	1.42	1.19
31:Lc:20:LEU:HD12	31:Lc:101:ASP:CB	1.72	1.17
67:Sc:44:ARG:NH2	67:Sc:63:ARG:HB2	1.62	1.12

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	LA	246/248 (99%)	223 (91%)	22 (9%)	1 (0%)	30	59
5	LB	400/402 (100%)	373 (93%)	26 (6%)	1 (0%)	36	65
6	LC	365/368 (99%)	337 (92%)	25 (7%)	3 (1%)	16	44
7	LD	291/293 (99%)	268 (92%)	23 (8%)	0	100	100
8	LE	232/236 (98%)	205 (88%)	26 (11%)	1 (0%)	30	59
9	LF	224/225 (100%)	215 (96%)	8 (4%)	1 (0%)	30	59
10	LG	240/241 (100%)	218 (91%)	22 (9%)	0	100	100
11	LH	188/190 (99%)	173 (92%)	15 (8%)	0	100	100
12	LI	211/213 (99%)	183 (87%)	28 (13%)	0	100	100
13	LJ	174/176 (99%)	154 (88%)	20 (12%)	0	100	100
14	LL	208/210 (99%)	187 (90%)	21 (10%)	0	100	100
15	LM	137/139 (99%)	125 (91%)	11 (8%)	1 (1%)	18	48
16	LN	201/203 (99%)	187 (93%)	12 (6%)	2 (1%)	12	39
17	LO	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
18	LP	151/153 (99%)	139 (92%)	12 (8%)	0	100	100
19	LQ	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
20	LR	185/187 (99%)	180 (97%)	5 (3%)	0	100	100
21	LS	173/175 (99%)	162 (94%)	11 (6%)	0	100	100
22	LT	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
23	LU	99/101 (98%)	85 (86%)	14 (14%)	0	100	100
24	LV	129/131 (98%)	117 (91%)	10 (8%)	2 (2%)	7	27
25	LW	122/124 (98%)	104 (85%)	17 (14%)	1 (1%)	16	44
26	LX	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
27	LY	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
28	LZ	133/135 (98%)	118 (89%)	15 (11%)	0	100	100
29	La	145/147 (99%)	133 (92%)	12 (8%)	0	100	100
30	Lb	105/109 (96%)	91 (87%)	14 (13%)	0	100	100
31	Lc	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
32	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
33	Le	126/128 (98%)	116 (92%)	8 (6%)	2 (2%)	7	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Lf	107/109 (98%)	99 (92%)	7 (6%)	1 (1%)	14	41
35	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
36	Lh	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
37	Li	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
38	Lj	85/86 (99%)	78 (92%)	7 (8%)	0	100	100
39	Lk	67/69 (97%)	64 (96%)	3 (4%)	0	100	100
40	Ll	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
41	Lm	49/52 (94%)	48 (98%)	1 (2%)	0	100	100
42	Ln	22/24 (92%)	22 (100%)	0	0	100	100
43	Lo	104/105 (99%)	100 (96%)	3 (3%)	1 (1%)	12	39
44	Lp	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
45	Lr	123/125 (98%)	113 (92%)	10 (8%)	0	100	100
46	Lz	215/217 (99%)	156 (73%)	59 (27%)	0	100	100
49	SA	219/221 (99%)	194 (89%)	21 (10%)	4 (2%)	6	25
50	SB	212/214 (99%)	201 (95%)	11 (5%)	0	100	100
51	SD	225/227 (99%)	201 (89%)	24 (11%)	0	100	100
52	SE	260/262 (99%)	243 (94%)	17 (6%)	0	100	100
53	SF	187/189 (99%)	165 (88%)	22 (12%)	0	100	100
54	SH	182/186 (98%)	158 (87%)	24 (13%)	0	100	100
55	SI	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
56	SK	96/98 (98%)	85 (88%)	11 (12%)	0	100	100
57	SL	151/153 (99%)	135 (89%)	16 (11%)	0	100	100
58	SP	125/127 (98%)	116 (93%)	8 (6%)	1 (1%)	16	44
59	SQ	139/141 (99%)	125 (90%)	12 (9%)	2 (1%)	9	30
60	SR	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
61	SS	143/145 (99%)	128 (90%)	14 (10%)	1 (1%)	18	48
62	ST	141/143 (99%)	128 (91%)	11 (8%)	2 (1%)	9	30
63	SU	101/103 (98%)	90 (89%)	11 (11%)	0	100	100
64	SV	81/83 (98%)	74 (91%)	5 (6%)	2 (2%)	4	17
65	SX	139/141 (99%)	125 (90%)	12 (9%)	2 (1%)	9	30
66	Sa	101/102 (99%)	91 (90%)	10 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	Sc	62/64 (97%)	51 (82%)	11 (18%)	0	100	100
68	Sd	53/55 (96%)	50 (94%)	2 (4%)	1 (2%)	6	23
69	Sg	311/313 (99%)	268 (86%)	40 (13%)	3 (1%)	12	39
70	SC	221/222 (100%)	202 (91%)	17 (8%)	2 (1%)	14	41
71	SG	235/237 (99%)	217 (92%)	16 (7%)	2 (1%)	14	41
72	SJ	184/185 (100%)	167 (91%)	16 (9%)	1 (0%)	24	54
73	SM	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
74	SN	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
75	SO	138/140 (99%)	120 (87%)	17 (12%)	1 (1%)	18	48
76	SW	127/129 (98%)	115 (91%)	12 (9%)	0	100	100
77	SY	130/131 (99%)	123 (95%)	7 (5%)	0	100	100
78	SZ	73/75 (97%)	58 (80%)	7 (10%)	8 (11%)	0	1
79	Sb	81/83 (98%)	72 (89%)	8 (10%)	1 (1%)	10	34
80	Se	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
81	Sf	65/67 (97%)	51 (78%)	14 (22%)	0	100	100
All	All	11561/11713 (99%)	10531 (91%)	980 (8%)	50 (0%)	31	59

5 of 50 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	LC	3	CYS
16	LN	124	ASP
33	Le	92	ASN
65	SX	127	ASN
70	SC	173	LYS

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	190/190 (100%)	177 (93%)	13 (7%)	14	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	LB	348/348 (100%)	338 (97%)	10 (3%)	37	71
6	LC	305/305 (100%)	296 (97%)	9 (3%)	36	70
7	LD	246/247 (100%)	238 (97%)	8 (3%)	33	67
8	LE	209/209 (100%)	200 (96%)	9 (4%)	26	60
9	LF	195/194 (100%)	188 (96%)	7 (4%)	31	65
10	LG	204/205 (100%)	198 (97%)	6 (3%)	37	71
11	LH	169/169 (100%)	167 (99%)	2 (1%)	63	86
12	LI	180/180 (100%)	179 (99%)	1 (1%)	78	93
13	LJ	148/148 (100%)	142 (96%)	6 (4%)	27	61
14	LL	176/176 (100%)	173 (98%)	3 (2%)	53	82
15	LM	118/118 (100%)	117 (99%)	1 (1%)	73	90
16	LN	171/171 (100%)	169 (99%)	2 (1%)	63	86
17	LO	173/173 (100%)	167 (96%)	6 (4%)	32	66
18	LP	134/134 (100%)	128 (96%)	6 (4%)	24	58
19	LQ	164/164 (100%)	161 (98%)	3 (2%)	51	80
20	LR	166/166 (100%)	161 (97%)	5 (3%)	36	70
21	LS	156/156 (100%)	152 (97%)	4 (3%)	40	73
22	LT	139/139 (100%)	133 (96%)	6 (4%)	26	60
23	LU	91/91 (100%)	89 (98%)	2 (2%)	45	77
24	LV	101/101 (100%)	94 (93%)	7 (7%)	14	41
25	LW	103/103 (100%)	99 (96%)	4 (4%)	28	63
26	LX	108/108 (100%)	105 (97%)	3 (3%)	38	72
27	LY	124/124 (100%)	121 (98%)	3 (2%)	43	75
28	LZ	117/117 (100%)	116 (99%)	1 (1%)	70	90
29	La	120/120 (100%)	118 (98%)	2 (2%)	53	82
30	Lb	89/89 (100%)	88 (99%)	1 (1%)	65	88
31	Lc	83/83 (100%)	79 (95%)	4 (5%)	23	55
32	Ld	98/98 (100%)	98 (100%)	0	100	100
33	Le	114/114 (100%)	109 (96%)	5 (4%)	25	59
34	Lf	88/88 (100%)	86 (98%)	2 (2%)	44	76
35	Lg	98/98 (100%)	96 (98%)	2 (2%)	48	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	Lh	109/109 (100%)	108 (99%)	1 (1%)	70	90
37	Li	86/86 (100%)	86 (100%)	0	100	100
38	Lj	74/73 (101%)	74 (100%)	0	100	100
39	Lk	64/64 (100%)	64 (100%)	0	100	100
40	Ll	47/47 (100%)	43 (92%)	4 (8%)	10	31
41	Lm	47/47 (100%)	47 (100%)	0	100	100
42	Ln	23/23 (100%)	23 (100%)	0	100	100
43	Lo	94/93 (101%)	90 (96%)	4 (4%)	26	60
44	Lp	74/74 (100%)	71 (96%)	3 (4%)	27	61
45	Lr	109/109 (100%)	104 (95%)	5 (5%)	24	57
46	Lz	195/196 (100%)	192 (98%)	3 (2%)	57	84
49	SA	183/183 (100%)	168 (92%)	15 (8%)	10	32
50	SB	195/195 (100%)	195 (100%)	0	100	100
51	SD	190/190 (100%)	179 (94%)	11 (6%)	18	49
52	SE	224/224 (100%)	223 (100%)	1 (0%)	84	94
53	SF	159/159 (100%)	158 (99%)	1 (1%)	78	93
54	SH	166/166 (100%)	150 (90%)	16 (10%)	8	26
55	SI	178/178 (100%)	171 (96%)	7 (4%)	28	63
56	SK	89/89 (100%)	88 (99%)	1 (1%)	65	88
57	SL	137/137 (100%)	136 (99%)	1 (1%)	76	92
58	SP	113/113 (100%)	112 (99%)	1 (1%)	70	90
59	SQ	117/117 (100%)	113 (97%)	4 (3%)	32	66
60	SR	122/122 (100%)	121 (99%)	1 (1%)	73	90
61	SS	126/126 (100%)	120 (95%)	6 (5%)	23	55
62	ST	113/113 (100%)	105 (93%)	8 (7%)	13	40
63	SU	94/94 (100%)	93 (99%)	1 (1%)	65	88
64	SV	67/67 (100%)	63 (94%)	4 (6%)	17	47
65	SX	113/113 (100%)	110 (97%)	3 (3%)	39	73
66	Sa	90/89 (101%)	85 (94%)	5 (6%)	19	50
67	Sc	57/57 (100%)	51 (90%)	6 (10%)	6	22
68	Sd	48/48 (100%)	45 (94%)	3 (6%)	16	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Sg	272/272 (100%)	268 (98%)	4 (2%)	57	84
70	SC	189/188 (100%)	186 (98%)	3 (2%)	55	83
71	SG	207/207 (100%)	196 (95%)	11 (5%)	20	52
72	SJ	162/161 (101%)	160 (99%)	2 (1%)	63	86
73	SM	102/104 (98%)	100 (98%)	2 (2%)	48	78
74	SN	130/130 (100%)	127 (98%)	3 (2%)	44	76
75	SO	110/110 (100%)	105 (96%)	5 (4%)	24	58
76	SW	112/112 (100%)	111 (99%)	1 (1%)	70	90
77	SY	114/113 (101%)	113 (99%)	1 (1%)	70	90
78	SZ	66/66 (100%)	57 (86%)	9 (14%)	3	12
79	Sb	75/75 (100%)	71 (95%)	4 (5%)	20	52
80	Se	47/47 (100%)	47 (100%)	0	100	100
81	Sf	60/60 (100%)	60 (100%)	0	100	100
All	All	10074/10072 (100%)	9771 (97%)	303 (3%)	37	70

5 of 303 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
62	ST	60	THR
75	SO	142	ARG
64	SV	71	ARG
69	Sg	135	LEU
79	Sb	55	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 176 such sidechains are listed below:

Mol	Chain	Res	Type
54	SH	76	GLN
67	Sc	24	GLN
54	SH	162	GLN
58	SP	53	GLN
69	Sg	162	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3705/3773 (98%)	1016 (27%)	35 (0%)
2	L7	119/120 (99%)	15 (12%)	0
3	L8	155/156 (99%)	37 (23%)	1 (0%)
47	S2	1715/1740 (98%)	431 (25%)	11 (0%)
48	S6	74/75 (98%)	29 (39%)	1 (1%)
All	All	5768/5864 (98%)	1528 (26%)	48 (0%)

5 of 1528 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	4	G
1	L5	6	C
1	L5	17	A
1	L5	25	A

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	3961	G
3	L8	83	C
1	L5	4378	A
1	L5	4699	U
47	S2	291	G

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

113 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
1	PSU	L5	3729	1	18,21,22	1.09	1 (5%)	22,30,33	1.68	4 (18%)
1	OMG	L5	1883	1	23,26,27	1.36	4 (17%)	33,38,41	2.12	8 (24%)
1	UR3	L5	1866	1	19,22,23	1.06	2 (10%)	26,32,35	1.52	4 (15%)
1	UR3	L5	4530	1	19,22,23	1.10	1 (5%)	26,32,35	1.58	4 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
47	A2M	S2	166	47	22,25,26	1.47	4 (18%)	31,36,39	2.21	8 (25%)
1	6MZ	L5	4220	1	22,25,26	1.40	4 (18%)	30,36,39	2.16	9 (30%)
47	A2M	S2	668	47,82	22,25,26	1.43	5 (22%)	31,36,39	2.09	9 (29%)
1	OMG	L5	4870	1	23,26,27	1.20	3 (13%)	33,38,41	1.89	6 (18%)
47	A2M	S2	484	47	22,25,26	1.45	4 (18%)	31,36,39	2.06	8 (25%)
1	A2M	L5	1524	1	22,25,26	1.46	4 (18%)	31,36,39	2.12	8 (25%)
47	OMC	S2	1710	47	19,22,23	0.81	0	26,31,34	0.76	0
1	PSU	L5	4500	1	18,21,22	1.08	1 (5%)	22,30,33	1.85	4 (18%)
47	A2M	S2	1031	47	22,25,26	1.44	5 (22%)	31,36,39	2.13	10 (32%)
1	5MC	L5	3782	1,82	18,22,23	0.97	2 (11%)	26,32,35	1.17	2 (7%)
1	A2M	L5	1534	1,82	22,25,26	1.47	5 (22%)	31,36,39	2.04	8 (25%)
47	PSU	S2	612	47	18,21,22	1.07	1 (5%)	22,30,33	1.85	5 (22%)
47	5MU	S2	814	47	19,22,23	1.40	6 (31%)	28,32,35	2.05	7 (25%)
1	OMG	L5	2364	1	23,26,27	1.21	3 (13%)	33,38,41	1.92	6 (18%)
1	2MG	L5	978	1	23,26,27	1.24	3 (13%)	32,38,41	2.18	6 (18%)
1	B8H	L5	3762	1	19,22,23	1.36	3 (15%)	22,32,35	2.00	3 (13%)
1	JMH	L5	1456	1	18,22,23	1.10	1 (5%)	21,32,35	0.95	1 (4%)
1	OMG	L5	4623	1	23,26,27	1.21	3 (13%)	33,38,41	1.97	7 (21%)
47	A2M	S2	159	47	22,25,26	1.46	4 (18%)	31,36,39	2.10	8 (25%)
47	OMC	S2	517	47	19,22,23	0.82	0	26,31,34	0.84	1 (3%)
1	OMC	L5	3701	1,82	19,22,23	0.80	0	26,31,34	0.74	0
47	OMU	S2	121	47	19,22,23	1.22	3 (15%)	26,31,34	1.78	6 (23%)
1	OMG	L5	373	1	23,26,27	1.27	4 (17%)	33,38,41	2.14	8 (24%)
1	B8H	L5	1860	1	19,22,23	1.37	3 (15%)	22,32,35	1.97	4 (18%)
1	OMU	L5	4620	1	19,22,23	1.32	3 (15%)	26,31,34	1.86	6 (23%)
41	MLZ	Lm	98	41	8,9,10	0.77	0	4,9,11	0.62	0
1	OMG	L5	1316	1,82	23,26,27	1.36	4 (17%)	33,38,41	2.16	7 (21%)
1	A2M	L5	3825	1	22,25,26	1.45	5 (22%)	31,36,39	2.08	9 (29%)
1	OMC	L5	3869	1	19,22,23	0.82	0	26,31,34	0.96	1 (3%)
1	A2M	L5	2401	1	22,25,26	1.43	4 (18%)	31,36,39	2.08	9 (29%)
1	OMG	L5	3899	1	23,26,27	1.23	3 (13%)	33,38,41	2.00	5 (15%)
47	PSU	S2	822	47	18,21,22	1.05	1 (5%)	22,30,33	1.80	5 (22%)
6	MLZ	LC	333	6	8,9,10	0.75	0	4,9,11	0.67	0
1	OMC	L5	3909	1	19,22,23	0.81	0	26,31,34	0.94	1 (3%)
1	OMC	L5	3887	1	19,22,23	0.82	0	26,31,34	0.84	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
47	OMU	S2	116	47	19,22,23	1.25	4 (21%)	26,31,34	1.68	6 (23%)
47	OMG	S2	683	47	23,26,27	1.20	3 (13%)	33,38,41	2.02	6 (18%)
47	MA6	S2	1850	47	23,26,27	1.45	4 (17%)	34,38,41	2.18	10 (29%)
1	A2M	L5	1871	1,82	22,25,26	1.44	4 (18%)	31,36,39	2.14	9 (29%)
1	PSU	L5	4636	1	18,21,22	1.08	1 (5%)	22,30,33	1.88	5 (22%)
1	OMG	L5	2773	1	23,26,27	1.21	3 (13%)	33,38,41	1.88	6 (18%)
1	OMG	L5	1522	1	23,26,27	1.22	3 (13%)	33,38,41	1.97	5 (15%)
1	OMC	L5	2365	1,82	19,22,23	0.80	0	26,31,34	0.76	0
1	OMU	L5	4306	1	19,22,23	1.29	4 (21%)	26,31,34	1.72	7 (26%)
1	PSU	L5	1683	1	18,21,22	1.11	1 (5%)	22,30,33	1.73	4 (18%)
47	UR3	S2	1830	47	19,22,23	1.03	2 (10%)	26,32,35	1.74	5 (19%)
1	PSU	L5	4531	1	18,21,22	1.37	2 (11%)	22,30,33	1.97	4 (18%)
47	PSU	S2	1243	47	18,21,22	1.53	5 (27%)	22,30,33	2.12	4 (18%)
47	MA6	S2	1851	47	23,26,27	1.45	4 (17%)	34,38,41	2.16	10 (29%)
1	A2M	L5	2363	1,82	22,25,26	1.43	3 (13%)	31,36,39	2.03	7 (22%)
47	PSU	S2	119	47	18,21,22	1.02	1 (5%)	22,30,33	1.71	4 (18%)
1	UR3	L5	4597	1	19,22,23	0.97	0	26,32,35	1.42	2 (7%)
1	A2M	L5	3785	1	22,25,26	1.38	4 (18%)	31,36,39	2.32	11 (35%)
1	OMG	L5	3792	1	23,26,27	1.22	3 (13%)	33,38,41	1.96	6 (18%)
1	1MA	L5	4415	1	21,25,26	1.36	4 (19%)	31,37,40	1.72	5 (16%)
1	A2M	L5	4523	1,82	22,25,26	1.38	4 (18%)	31,36,39	2.10	8 (25%)
1	B8T	L5	4671	1	19,22,23	0.84	0	26,31,34	1.09	2 (7%)
1	A2M	L5	3718	1	22,25,26	1.43	4 (18%)	31,36,39	2.06	9 (29%)
1	OMG	L5	4196	1	23,26,27	1.21	3 (13%)	33,38,41	1.96	6 (18%)
47	A2M	S2	1678	47	22,25,26	1.43	4 (18%)	31,36,39	2.14	10 (32%)
47	M7A	S2	1806	47	20,25,26	1.52	3 (15%)	28,37,40	2.17	6 (21%)
1	OMC	L5	2804	1	19,22,23	0.83	0	26,31,34	0.83	1 (3%)
1	OMG	L5	4637	1	23,26,27	1.23	3 (13%)	33,38,41	1.98	7 (21%)
1	PSU	L5	2508	1	18,21,22	1.05	1 (5%)	22,30,33	1.71	4 (18%)
1	OMC	L5	2422	1,82	19,22,23	0.84	0	26,31,34	0.98	1 (3%)
47	4AC	S2	1337	47	21,24,25	1.09	2 (9%)	29,34,37	1.03	3 (10%)
47	OMC	S2	1703	47	19,22,23	0.83	0	26,31,34	0.87	1 (3%)
47	OMG	S2	644	47	23,26,27	1.21	3 (13%)	33,38,41	1.92	6 (18%)
1	5MC	L5	4447	1,82	18,22,23	1.04	2 (11%)	26,32,35	1.63	6 (23%)
47	OMC	S2	174	47,82	19,22,23	0.81	0	26,31,34	0.78	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	L5	1625	1	23,26,27	1.23	3 (13%)	33,38,41	1.97	6 (18%)
1	PSU	L5	4450	1,82	18,21,22	1.04	2 (11%)	22,30,33	1.80	5 (22%)
1	2MG	L5	729	1,82	23,26,27	1.24	3 (13%)	32,38,41	2.25	8 (25%)
1	PSU	L5	4442	1	18,21,22	1.04	1 (5%)	22,30,33	1.83	6 (27%)
1	OMC	L5	4536	1	19,22,23	0.83	0	26,31,34	0.93	1 (3%)
47	PSU	S2	823	47	18,21,22	1.14	1 (5%)	22,30,33	1.73	4 (18%)
1	A2M	L5	1326	1	22,25,26	1.35	4 (18%)	31,36,39	2.18	11 (35%)
1	A2M	L5	3867	1	22,25,26	1.42	4 (18%)	31,36,39	2.11	9 (29%)
1	2MG	L5	1517	1	23,26,27	1.22	3 (13%)	32,38,41	2.50	8 (25%)
47	4AC	S2	1842	47	21,24,25	0.96	1 (4%)	29,34,37	1.33	5 (17%)
1	PSU	L5	1677	1	18,21,22	1.55	5 (27%)	22,30,33	2.10	4 (18%)
1	B8H	L5	4296	1	19,22,23	1.36	3 (15%)	22,32,35	2.00	3 (13%)
1	B8T	L5	4483	1	19,22,23	0.77	0	26,31,34	0.88	1 (3%)
1	PSU	L5	4628	1	18,21,22	1.09	1 (5%)	22,30,33	1.81	4 (18%)
1	OMG	L5	2424	1	23,26,27	1.24	3 (13%)	33,38,41	1.88	6 (18%)
47	B8N	S2	1248	47	24,29,30	0.96	1 (4%)	29,42,45	1.47	4 (13%)
47	6MZ	S2	1832	47,82	22,25,26	1.43	3 (13%)	30,36,39	2.13	8 (26%)
1	1MA	L5	1322	1,82	21,25,26	1.38	3 (14%)	31,37,40	1.80	5 (16%)
1	2MG	L5	4872	1	23,26,27	1.22	4 (17%)	32,38,41	2.40	10 (31%)
47	PSU	S2	1081	47	18,21,22	0.97	1 (5%)	22,30,33	1.62	5 (22%)
1	PSU	L5	4293	1	18,21,22	1.01	1 (5%)	22,30,33	1.72	4 (18%)
1	PSU	L5	1582	1	18,21,22	1.50	4 (22%)	22,30,33	2.08	4 (18%)
1	PSU	L5	4403	1	18,21,22	1.01	1 (5%)	22,30,33	1.63	4 (18%)
1	OMC	L5	2861	1	19,22,23	0.80	0	26,31,34	0.78	1 (3%)
1	A2M	L5	3723	1	22,25,26	1.47	4 (18%)	31,36,39	2.11	9 (29%)
1	PSU	L5	3764	1	18,21,22	1.06	1 (5%)	22,30,33	1.68	4 (18%)
1	5MU	L5	4083	1	19,22,23	1.43	4 (21%)	28,32,35	2.30	7 (25%)
1	A2M	L5	4571	1	22,25,26	1.44	4 (18%)	31,36,39	2.03	9 (29%)
47	JMH	S2	1219	47,82	18,22,23	1.11	1 (5%)	21,32,35	1.00	2 (9%)
47	OMG	S2	509	47,82	23,26,27	1.38	4 (17%)	33,38,41	2.02	6 (18%)
1	5MC	L5	4335	1	18,22,23	0.95	2 (11%)	26,32,35	1.18	4 (15%)
1	OMG	L5	2050	1	23,26,27	1.35	4 (17%)	33,38,41	2.06	8 (24%)
47	A2M	S2	27	47,82	22,25,26	1.44	4 (18%)	31,36,39	2.21	9 (29%)
1	PSU	L5	3715	1,82	18,21,22	1.10	1 (5%)	22,30,33	1.64	4 (18%)
3	OMU	L8	14	1,3	19,22,23	1.24	3 (15%)	26,31,34	1.69	4 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	A2M	L5	398	1	22,25,26	1.45	4 (18%)	31,36,39	2.10	10 (32%)
1	OMG	L5	4494	1	23,26,27	1.22	3 (13%)	33,38,41	1.92	5 (15%)
1	OMG	L5	4370	1	23,26,27	1.22	3 (13%)	33,38,41	1.95	7 (21%)
47	5MC	S2	1374	47	18,22,23	0.92	2 (11%)	26,32,35	1.10	3 (11%)

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
1	PSU	L5	3729	1	-	2/7/25/26	0/2/2/2
1	OMG	L5	1883	1	-	3/9/27/28	0/3/3/3
1	UR3	L5	1866	1	-	2/7/25/26	0/2/2/2
1	UR3	L5	4530	1	-	2/7/25/26	0/2/2/2
47	A2M	S2	166	47	-	0/9/27/28	0/3/3/3
1	6MZ	L5	4220	1	-	2/9/27/28	0/3/3/3
47	A2M	S2	668	47,82	-	3/9/27/28	0/3/3/3
1	OMG	L5	4870	1	-	3/9/27/28	0/3/3/3
47	A2M	S2	484	47	-	0/9/27/28	0/3/3/3
1	A2M	L5	1524	1	-	1/9/27/28	0/3/3/3
47	OMC	S2	1710	47	-	0/9/27/28	0/2/2/2
1	PSU	L5	4500	1	-	3/7/25/26	0/2/2/2
47	A2M	S2	1031	47	-	0/9/27/28	0/3/3/3
1	5MC	L5	3782	1,82	-	0/7/25/26	0/2/2/2
1	A2M	L5	1534	1,82	-	2/9/27/28	0/3/3/3
47	PSU	S2	612	47	-	0/7/25/26	0/2/2/2
47	5MU	S2	814	47	-	0/7/25/26	0/2/2/2
1	OMG	L5	2364	1	-	1/9/27/28	0/3/3/3
1	2MG	L5	978	1	-	0/9/27/28	0/3/3/3
1	B8H	L5	3762	1	-	2/7/25/26	0/2/2/2
1	JMH	L5	1456	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4623	1	-	0/9/27/28	0/3/3/3
47	A2M	S2	159	47	-	0/9/27/28	0/3/3/3
47	OMC	S2	517	47	-	0/9/27/28	0/2/2/2
1	OMC	L5	3701	1,82	-	4/9/27/28	0/2/2/2
47	OMU	S2	121	47	-	0/9/27/28	0/2/2/2
1	OMG	L5	373	1	-	0/9/27/28	0/3/3/3
1	B8H	L5	1860	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	L5	4620	1	-	0/9/27/28	0/2/2/2
41	MLZ	Lm	98	41	-	0/7/8/10	-
1	OMG	L5	1316	1,82	-	0/9/27/28	0/3/3/3
1	A2M	L5	3825	1	-	0/9/27/28	0/3/3/3
1	OMC	L5	3869	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	2401	1	-	1/9/27/28	0/3/3/3
1	OMG	L5	3899	1	-	4/9/27/28	0/3/3/3
47	PSU	S2	822	47	-	0/7/25/26	0/2/2/2
6	MLZ	LC	333	6	-	2/7/8/10	-
1	OMC	L5	3909	1	-	0/9/27/28	0/2/2/2
1	OMC	L5	3887	1	-	1/9/27/28	0/2/2/2
47	OMU	S2	116	47	-	3/9/27/28	0/2/2/2
47	OMG	S2	683	47	-	2/9/27/28	0/3/3/3
47	MA6	S2	1850	47	-	0/11/29/30	0/3/3/3
1	A2M	L5	1871	1,82	-	0/9/27/28	0/3/3/3
1	PSU	L5	4636	1	-	4/7/25/26	0/2/2/2
1	OMG	L5	2773	1	-	0/9/27/28	0/3/3/3
1	OMG	L5	1522	1	-	0/9/27/28	0/3/3/3
1	OMC	L5	2365	1,82	-	0/9/27/28	0/2/2/2
1	OMU	L5	4306	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	1683	1	-	0/7/25/26	0/2/2/2
47	UR3	S2	1830	47	-	2/7/25/26	0/2/2/2
1	PSU	L5	4531	1	-	2/7/25/26	0/2/2/2
47	PSU	S2	1243	47	-	2/7/25/26	0/2/2/2
47	MA6	S2	1851	47	-	5/11/29/30	0/3/3/3
1	A2M	L5	2363	1,82	-	0/9/27/28	0/3/3/3
47	PSU	S2	119	47	-	0/7/25/26	0/2/2/2
1	UR3	L5	4597	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	3785	1	-	2/9/27/28	0/3/3/3
1	OMG	L5	3792	1	-	0/9/27/28	0/3/3/3
1	1MA	L5	4415	1	-	2/7/25/26	0/3/3/3
1	A2M	L5	4523	1,82	-	2/9/27/28	0/3/3/3
1	B8T	L5	4671	1	-	0/7/27/28	0/2/2/2
1	A2M	L5	3718	1	-	0/9/27/28	0/3/3/3
1	OMG	L5	4196	1	-	0/9/27/28	0/3/3/3
47	A2M	S2	1678	47	-	0/9/27/28	0/3/3/3
47	M7A	S2	1806	47	-	0/7/37/38	0/3/3/3
1	OMC	L5	2804	1	-	0/9/27/28	0/2/2/2
1	OMG	L5	4637	1	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	L5	2508	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	2422	1,82	-	1/9/27/28	0/2/2/2
47	4AC	S2	1337	47	-	2/11/29/30	0/2/2/2
47	OMC	S2	1703	47	-	2/9/27/28	0/2/2/2
47	OMG	S2	644	47	-	1/9/27/28	0/3/3/3
1	5MC	L5	4447	1,82	-	4/7/25/26	0/2/2/2
47	OMC	S2	174	47,82	-	0/9/27/28	0/2/2/2
1	OMG	L5	1625	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	4450	1,82	-	3/7/25/26	0/2/2/2
1	2MG	L5	729	1,82	-	3/9/27/28	0/3/3/3
1	PSU	L5	4442	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	4536	1	-	0/9/27/28	0/2/2/2
47	PSU	S2	823	47	-	0/7/25/26	0/2/2/2
1	A2M	L5	1326	1	-	1/9/27/28	0/3/3/3
1	A2M	L5	3867	1	-	3/9/27/28	0/3/3/3
1	2MG	L5	1517	1	-	0/9/27/28	0/3/3/3
47	4AC	S2	1842	47	-	0/11/29/30	0/2/2/2
1	PSU	L5	1677	1	-	1/7/25/26	0/2/2/2
1	B8H	L5	4296	1	-	0/7/25/26	0/2/2/2
1	B8T	L5	4483	1	-	0/7/27/28	0/2/2/2
1	PSU	L5	4628	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	2424	1	-	2/9/27/28	0/3/3/3
47	B8N	S2	1248	47	-	4/16/34/35	0/2/2/2
47	6MZ	S2	1832	47,82	-	2/9/27/28	0/3/3/3
1	1MA	L5	1322	1,82	-	4/7/25/26	0/3/3/3
1	2MG	L5	4872	1	-	2/9/27/28	0/3/3/3
47	PSU	S2	1081	47	-	1/7/25/26	0/2/2/2
1	PSU	L5	4293	1	-	2/7/25/26	0/2/2/2
1	PSU	L5	1582	1	-	2/7/25/26	0/2/2/2
1	PSU	L5	4403	1	-	2/7/25/26	0/2/2/2
1	OMC	L5	2861	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	3723	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	3764	1	-	1/7/25/26	0/2/2/2
1	5MU	L5	4083	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	4571	1	-	0/9/27/28	0/3/3/3
47	JMH	S2	1219	47,82	-	0/7/25/26	0/2/2/2
47	OMG	S2	509	47,82	-	2/9/27/28	0/3/3/3
1	5MC	L5	4335	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	2050	1	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	A2M	S2	27	47,82	-	0/9/27/28	0/3/3/3
1	PSU	L5	3715	1,82	-	0/7/25/26	0/2/2/2
3	OMU	L8	14	1,3	-	1/9/27/28	0/2/2/2
1	A2M	L5	398	1	-	2/9/27/28	0/3/3/3
1	OMG	L5	4494	1	-	2/9/27/28	0/3/3/3
1	OMG	L5	4370	1	-	0/9/27/28	0/3/3/3
47	5MC	S2	1374	47	-	0/7/25/26	0/2/2/2

The worst 5 of 279 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	S2	1851	MA6	C5-C4	4.46	1.47	1.39
47	S2	1832	6MZ	C5-C4	4.44	1.47	1.39
1	L5	3723	A2M	C5-C4	4.44	1.47	1.39
47	S2	1806	M7A	C8-N9	-4.43	1.35	1.45
47	S2	159	A2M	C5-C4	4.41	1.47	1.39

The worst 5 of 601 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	1517	2MG	C2-N3-C4	8.50	122.58	112.04
1	L5	4872	2MG	C2-N3-C4	7.91	121.85	112.04
1	L5	729	2MG	C2-N3-C4	7.62	121.48	112.04
1	L5	978	2MG	C2-N3-C4	7.22	120.99	112.04
1	L5	1517	2MG	C5-C4-N3	-7.04	117.03	128.46

There are no chirality outliers.

5 of 117 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	L5	729	2MG	N1-C2-N2-CM2
1	L5	729	2MG	N3-C2-N2-CM2
1	L5	1883	OMG	C1'-C2'-O2'-CM2
1	L5	2424	OMG	O4'-C4'-C5'-O5'
1	L5	2424	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

23 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L5	1883	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L5	1866	UR3	1	0
1	L5	4530	UR3	1	0
1	L5	4220	6MZ	1	0
1	L5	4870	OMG	1	0
47	S2	814	5MU	1	0
47	S2	517	OMC	1	0
1	L5	4620	OMU	1	0
41	Lm	98	MLZ	1	0
6	LC	333	MLZ	2	0
1	L5	1871	A2M	1	0
1	L5	4531	PSU	1	0
47	S2	1243	PSU	1	0
1	L5	2363	A2M	1	0
1	L5	4523	A2M	1	0
1	L5	4196	OMG	1	0
1	L5	1326	A2M	1	0
1	L5	2424	OMG	2	0
1	L5	4872	2MG	1	0
1	L5	1582	PSU	2	0
47	S2	509	OMG	2	0
1	L5	2050	OMG	2	0
1	L5	3715	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 448 ligands modelled in this entry, 446 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
85	HYG	S2	2039	-	35,39,39	0.97	1 (2%)	43,60,60	1.37	5 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
83	HMT	L5	5374	-	40,43,43	1.89	7 (17%)	41,66,66	1.49	6 (14%)

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
85	HYG	S2	2039	-	-	3/12/87/87	0/4/4/4
83	HMT	L5	5374	-	-	6/27/74/74	0/5/5/5

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	L5	5374	HMT	C5-C4	-7.13	1.40	1.51
83	L5	5374	HMT	C7-C6	-5.88	1.38	1.51
85	S2	2039	HYG	O28-C23	3.83	1.45	1.40
83	L5	5374	HMT	C3-C2	-3.80	1.40	1.50
83	L5	5374	HMT	C13-C14	-2.81	1.33	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	S2	2039	HYG	O22-C17-C12	-4.70	96.07	103.58
83	L5	5374	HMT	C25-C24-C20	-3.88	109.71	115.65
83	L5	5374	HMT	C7-C6-C16	-3.71	111.24	119.42
85	S2	2039	HYG	O18-C6-C1	3.55	116.73	107.28
83	L5	5374	HMT	C6-C5-C4	3.30	132.61	121.06

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

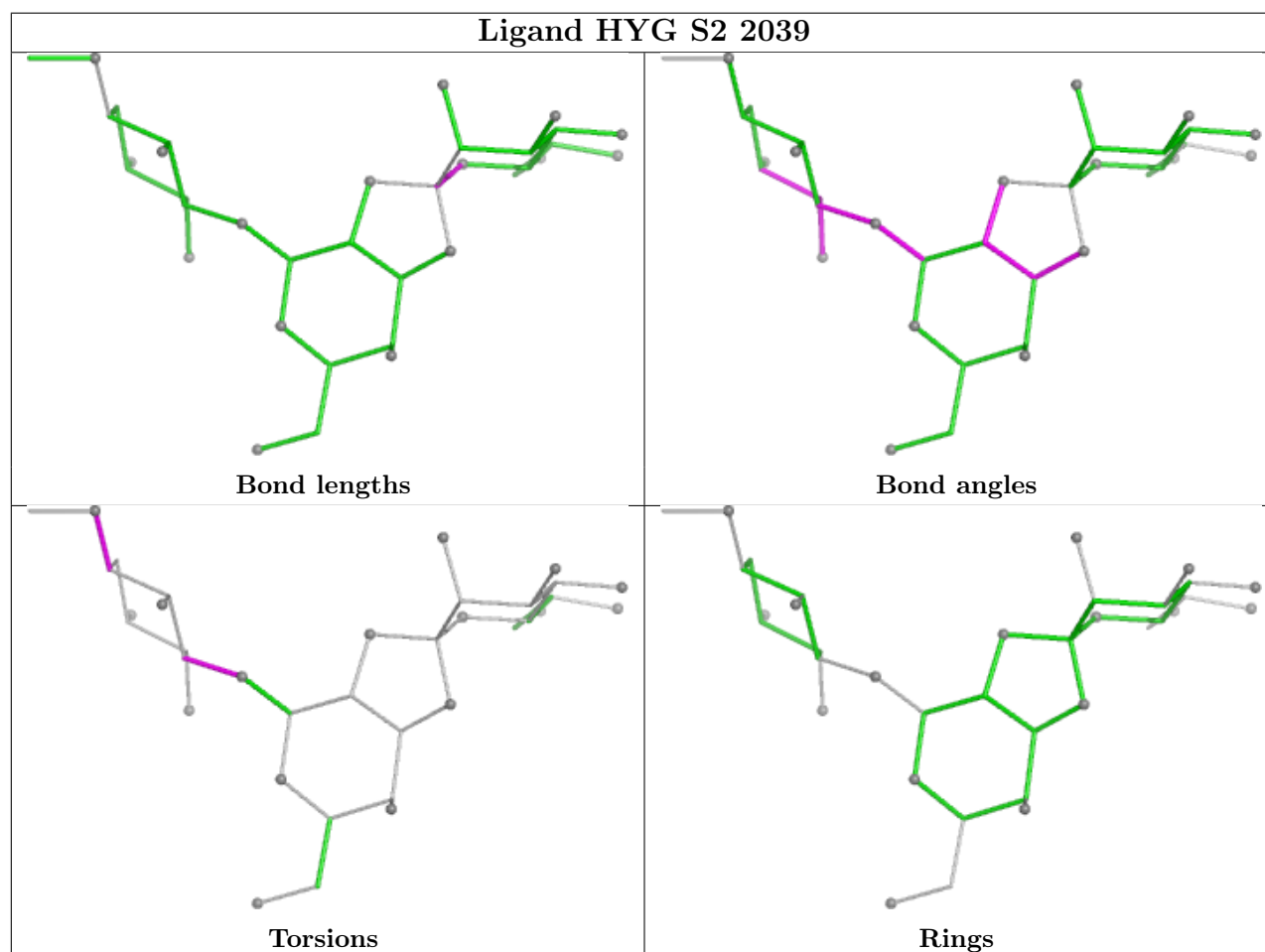
Mol	Chain	Res	Type	Atoms
83	L5	5374	HMT	C1-C2-O3-C18
83	L5	5374	HMT	C3-C2-O3-C18
83	L5	5374	HMT	C19-C20-C21-C22
83	L5	5374	HMT	O6-C20-C21-C22
85	S2	2039	HYG	C5-C4-N9-C10

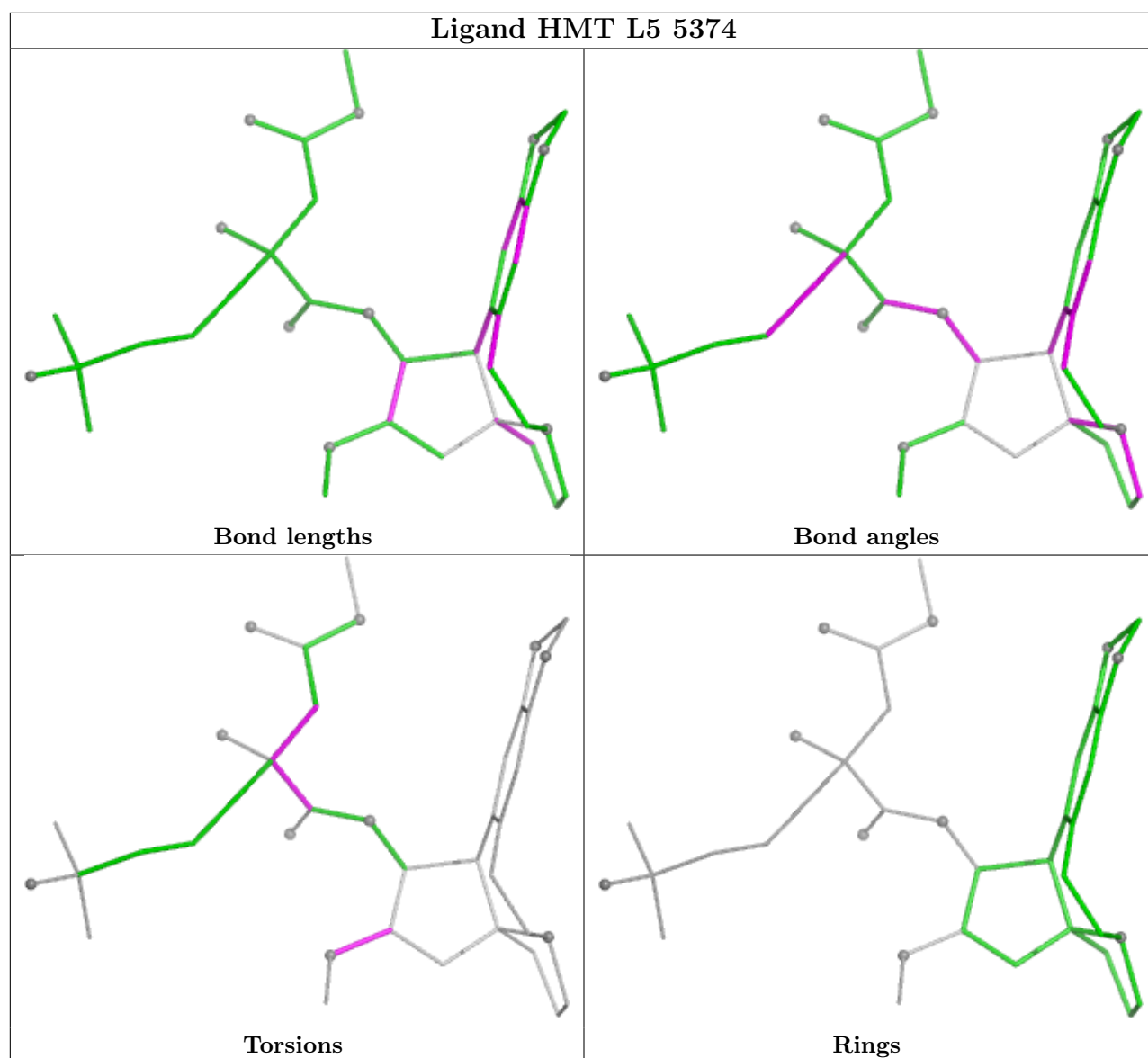
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
83	L5	5374	HMT	4	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	L5	10
47	S2	4
30	Lb	1
8	LE	1

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Mol	Chain	Number of breaks
54	SH	1

The worst 5 of 17 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lb	76:VAL	C	89:ALA	N	34.87
1	LE	76:ALA	C	88:VAL	N	26.61
1	S2	753:C	O3'	785:C	P	24.68
1	L5	2910:G	O3'	3584:C	P	22.67
1	S2	698:G	O3'	730:C	P	17.52

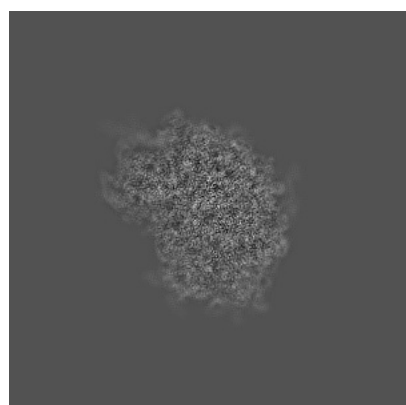
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3883. These allow visual inspection of the internal detail of the map and identification of artifacts.

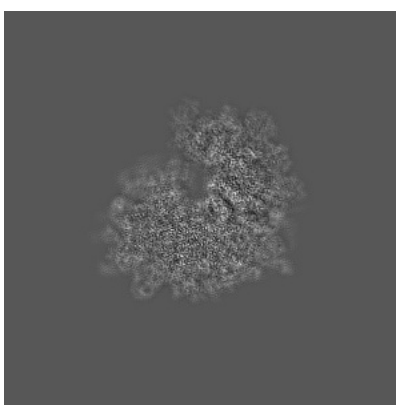
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

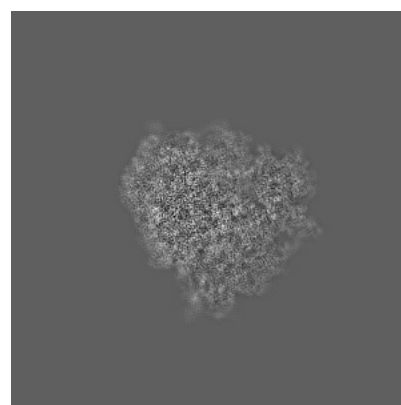
6.1.1 Primary map



X



Y

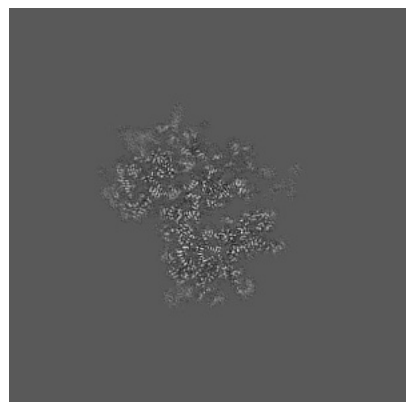


Z

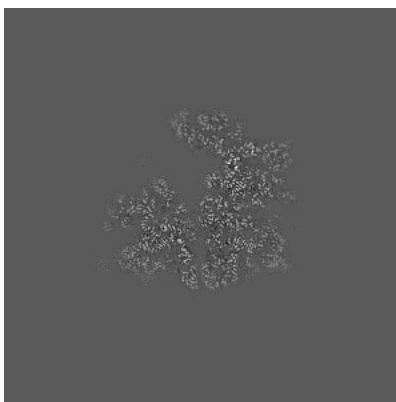
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

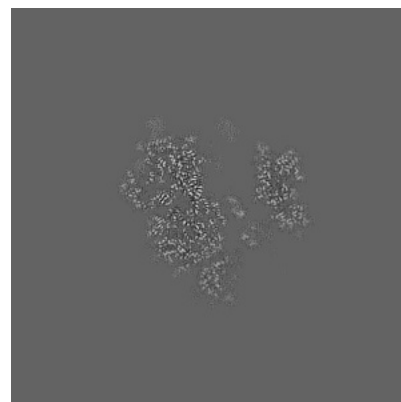
6.2.1 Primary map



X Index: 320



Y Index: 320

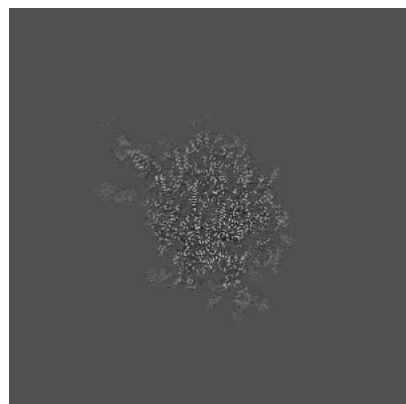


Z Index: 320

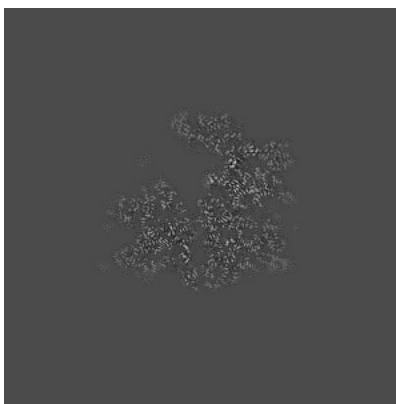
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

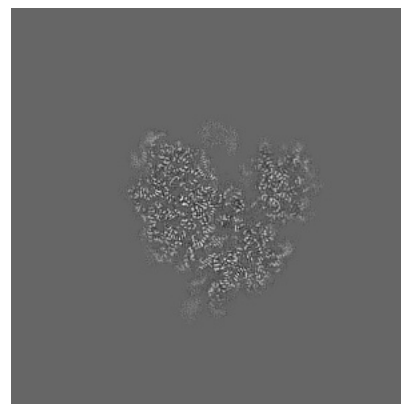
6.3.1 Primary map



X Index: 286



Y Index: 318

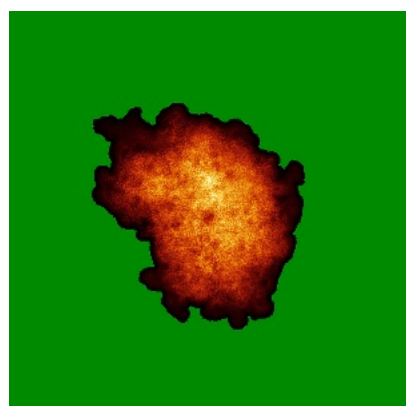


Z Index: 350

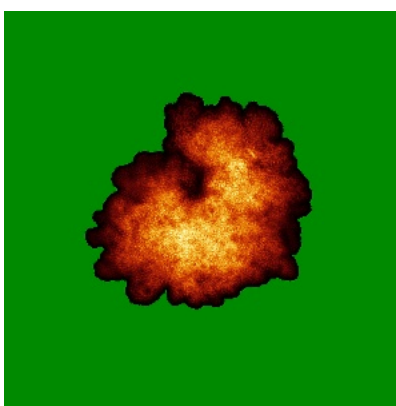
The images above show the largest variance slices of the map in three orthogonal directions.

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

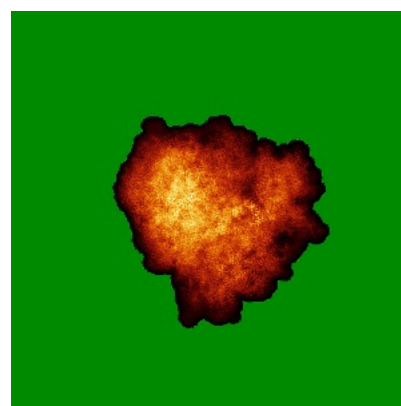
6.4.1 Primary map



X



Y

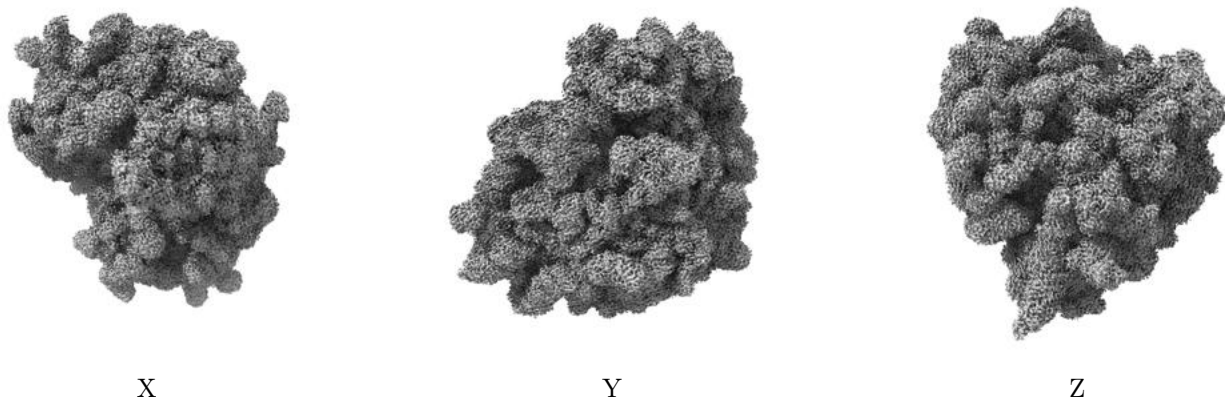


Z

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

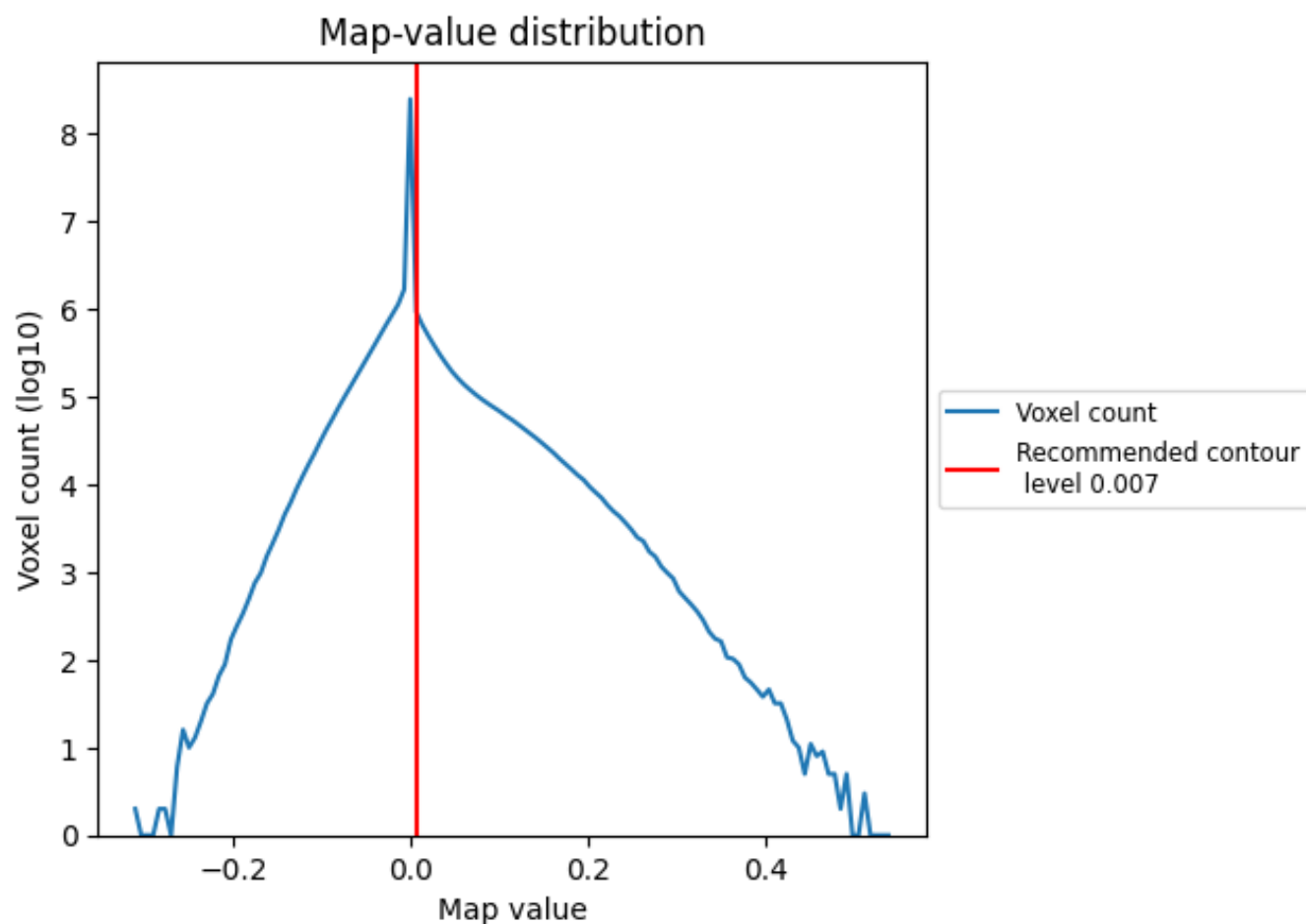
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

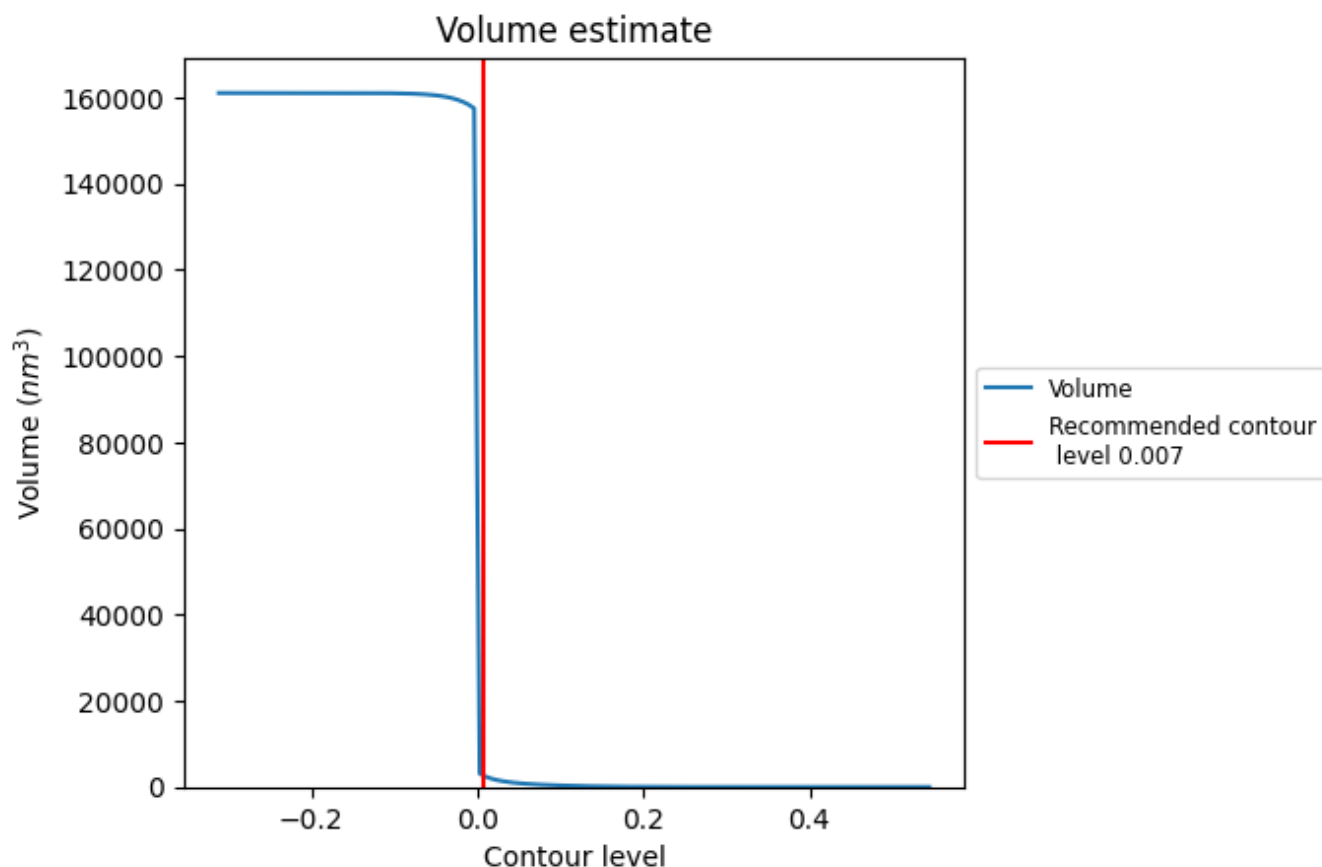
This section contains the results of statistical analysis of the map.

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.

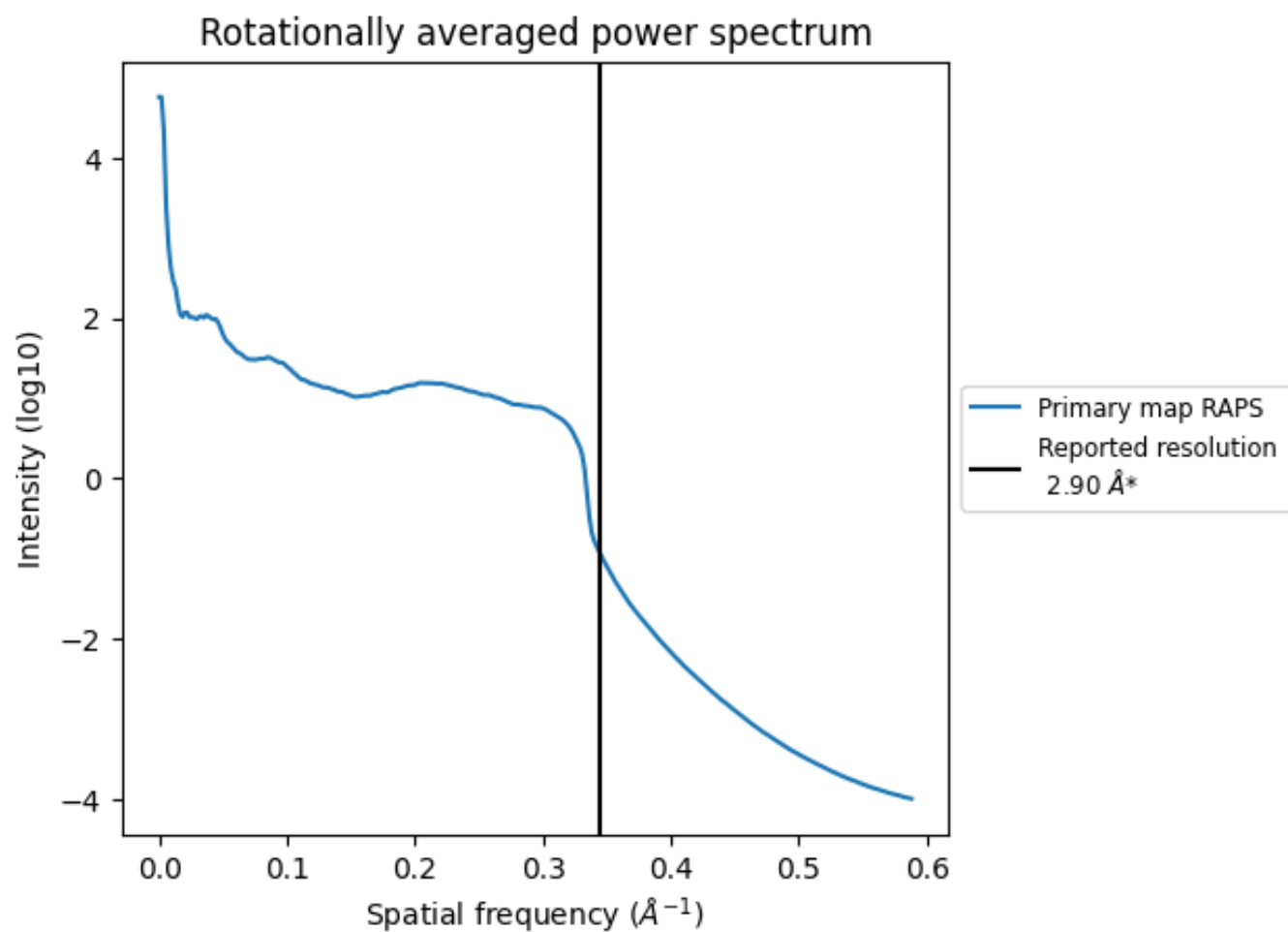
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2699 nm³; this corresponds to an approximate mass of 2438 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 ⓘ

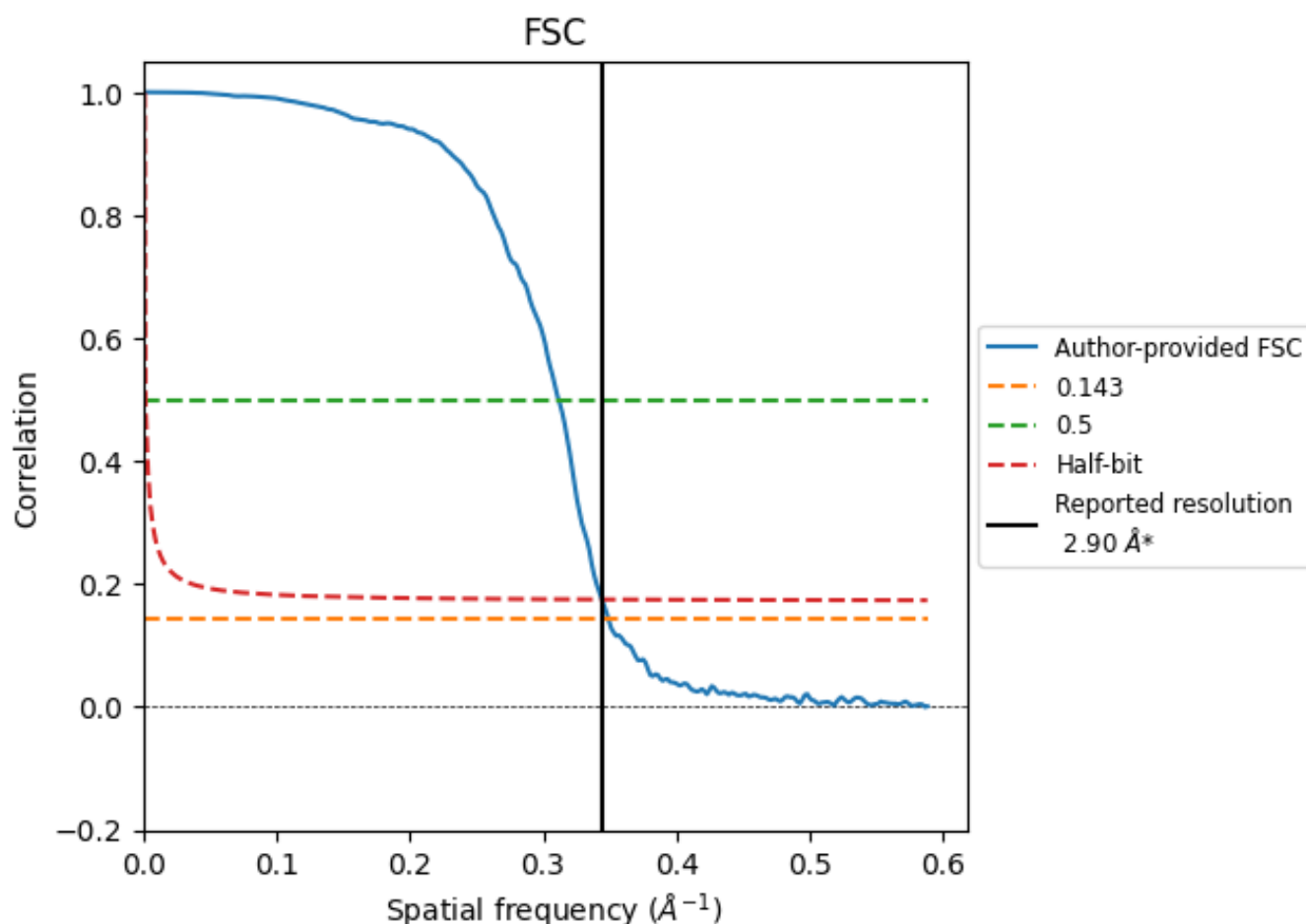


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

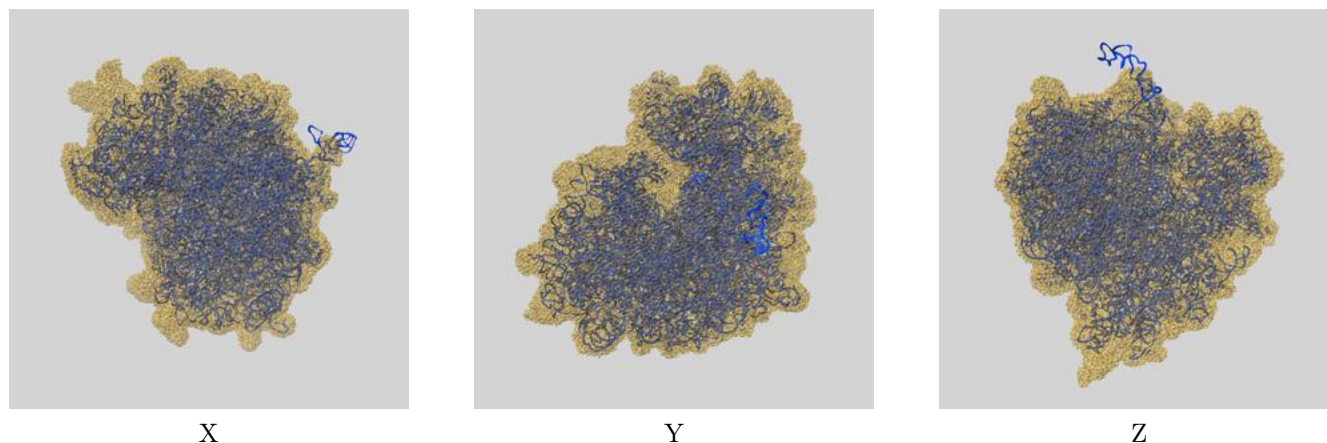
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.87	3.21	2.91
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

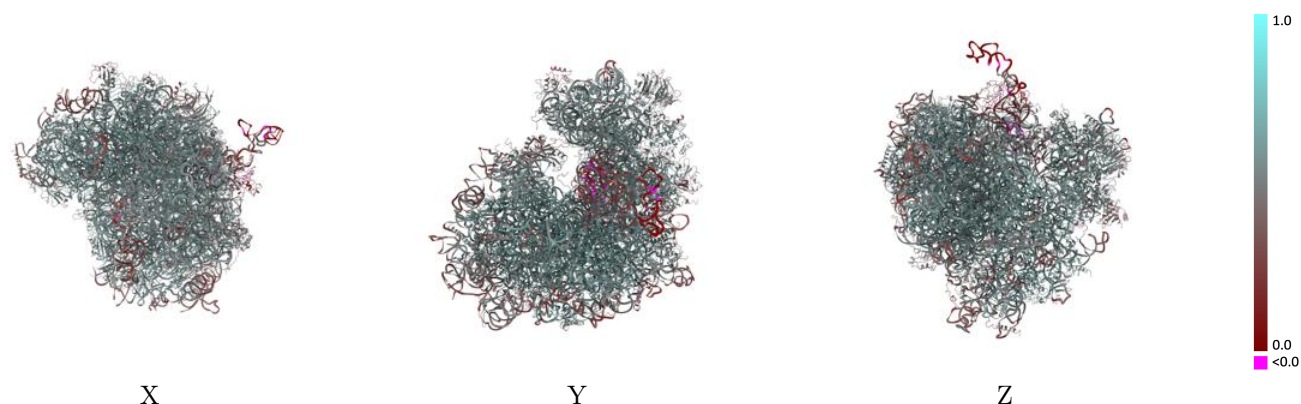
This section contains information regarding the fit between EMDB map EMD-3883 and PDB model 6QZP. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay [i](#)



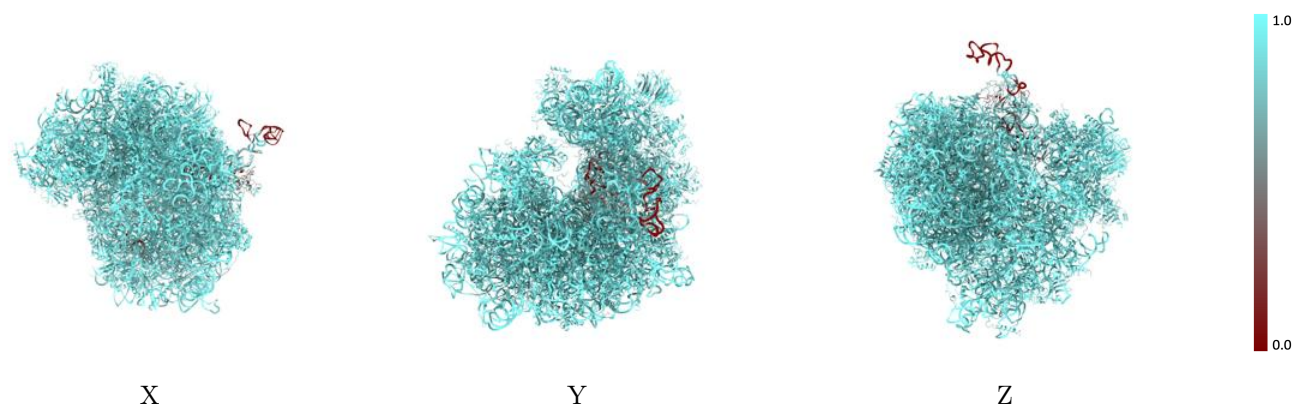
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



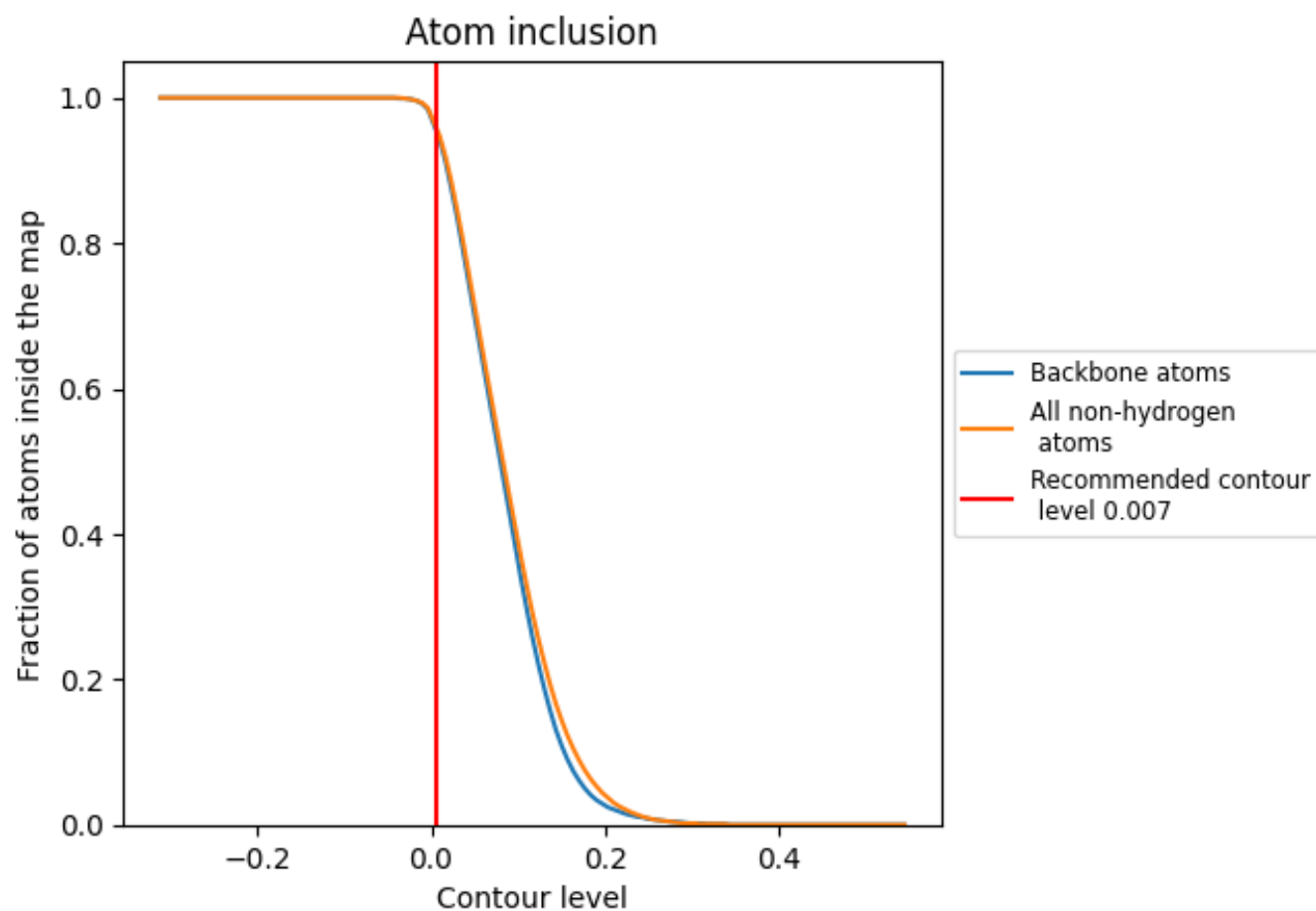
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 96% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9560	 0.5370
L5	 0.9670	 0.5430
L7	 0.9920	 0.5690
L8	 0.9780	 0.5720
LA	 0.9670	 0.5850
LB	 0.9660	 0.5610
LC	 0.9670	 0.5650
LD	 0.9560	 0.5110
LE	 0.9410	 0.5010
LF	 0.9520	 0.5750
LG	 0.9500	 0.5050
LH	 0.9670	 0.5520
LI	 0.9220	 0.5260
LJ	 0.9190	 0.4380
LL	 0.9550	 0.5320
LM	 0.9720	 0.5590
LN	 0.9740	 0.5990
LO	 0.9690	 0.5820
LP	 0.9720	 0.5800
LQ	 0.9610	 0.5770
LR	 0.9540	 0.5310
LS	 0.9810	 0.5840
LT	 0.9660	 0.5590
LU	 0.9420	 0.4470
LV	 0.9690	 0.5640
LW	 0.8980	 0.4490
LX	 0.9530	 0.5540
LY	 0.9580	 0.5470
LZ	 0.9630	 0.5260
La	 0.9750	 0.5890
Lb	 0.9270	 0.5040
Lc	 0.9490	 0.5140
Ld	 0.9560	 0.5430
Le	 0.9620	 0.5860
Lf	 0.9680	 0.5880



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Chain	Atom inclusion	Q-score
Lg	 0.9590	 0.5570
Lh	 0.9600	 0.5420
Li	 0.9650	 0.5340
Lj	 0.9720	 0.5930
Lk	 0.9590	 0.4870
Ll	 0.9600	 0.5650
Lm	 0.9590	 0.5600
Ln	 0.9470	 0.5760
Lo	 0.9640	 0.5550
Lp	 0.9580	 0.5650
Lr	 0.9630	 0.5490
Lz	 0.5030	 0.1930
S2	 0.9820	 0.5540
S6	 0.4870	 0.2120
SA	 0.9690	 0.5320
SB	 0.9600	 0.5330
SC	 0.9620	 0.5510
SD	 0.9410	 0.5010
SE	 0.9670	 0.5650
SF	 0.9180	 0.5040
SG	 0.9540	 0.4980
SH	 0.9390	 0.4620
SI	 0.9540	 0.5330
SJ	 0.9600	 0.5480
SK	 0.9630	 0.5030
SL	 0.9450	 0.5480
SM	 0.8700	 0.3480
SN	 0.9630	 0.5610
SO	 0.9310	 0.5240
SP	 0.9530	 0.5090
SQ	 0.9410	 0.5360
SR	 0.9620	 0.5060
SS	 0.9460	 0.5050
ST	 0.9560	 0.5340
SU	 0.9510	 0.4970
SV	 0.9780	 0.5480
SW	 0.9570	 0.5670
SX	 0.9660	 0.5670
SY	 0.9470	 0.5300
SZ	 0.9360	 0.4770
Sa	 0.9540	 0.5380
Sb	 0.9370	 0.5080

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Chain	Atom inclusion	Q-score
Sc	 0.9200	 0.4630
Sd	 0.9480	 0.5570
Se	 0.9080	 0.4930
Sf	 0.9380	 0.4310
Sg	 0.9440	 0.4810