



wwPDB EM Validation Summary Report ⓘ

Jun 27, 2026 – 11:57 AM EDT

PDB ID : 9P9J / pdb_00009p9j
EMDB ID : EMD-71413
Title : In situ human 60S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2025-06-24
Resolution : 2.87 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

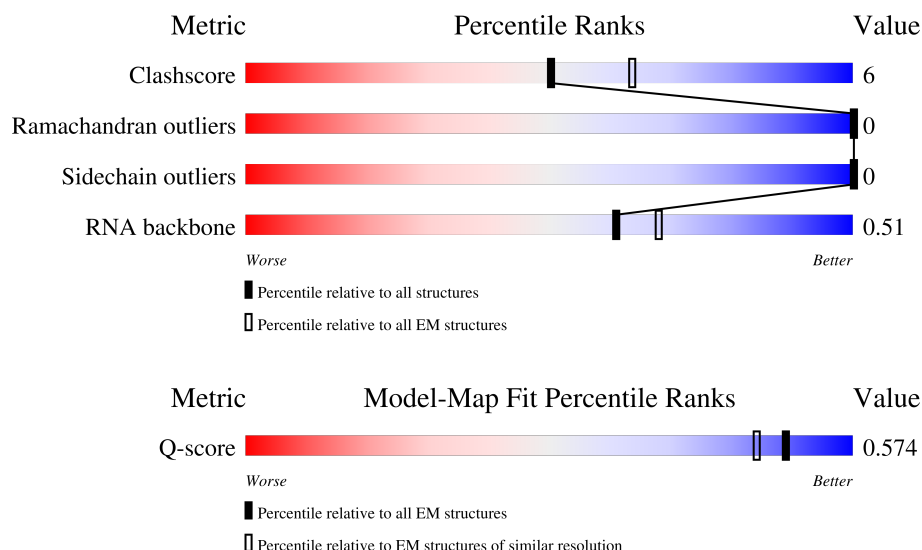
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 2.87 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.



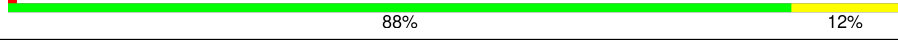
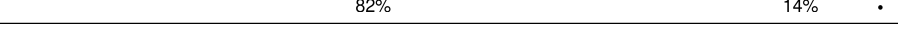
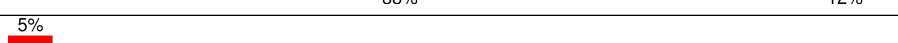
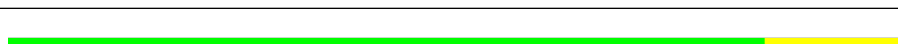
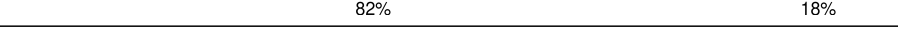
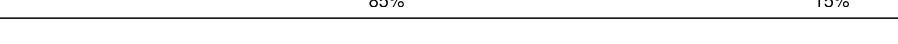
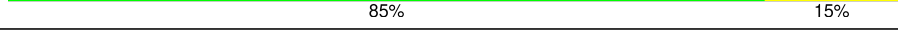
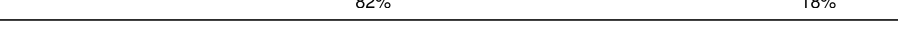
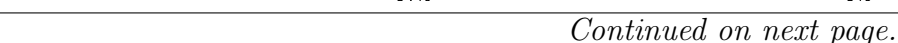
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12062 (2.37 - 3.37)

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	3675	
2	L7	120	
3	L8	156	

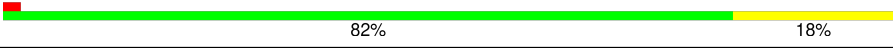
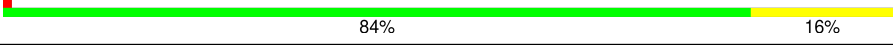
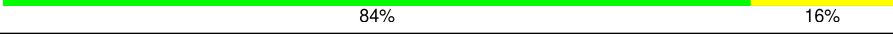
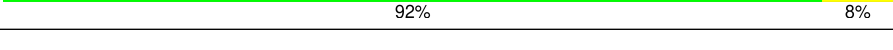
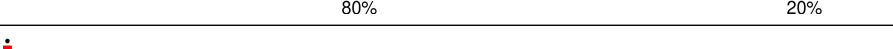
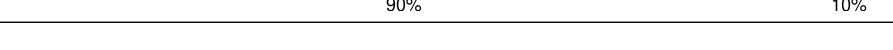
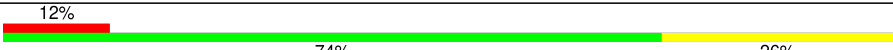
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Mol	Chain	Length	Quality of chain
4	LA	248	 81% 19%
5	LB	402	 78% 21%
6	LC	368	 88% 12%
7	LD	293	 86% 14%
8	LE	250	 82% 14%
9	LF	225	 88% 12%
10	LG	241	 5% 90% 10%
11	LH	190	 85% 15%
12	LI	213	 83% 17%
13	LJ	176	 87% 10%
14	LL	210	 88% 12%
15	LM	139	 82% 18%
16	LN	203	 88% 12%
17	LO	201	 82% 18%
18	LP	153	 85% 15%
19	LQ	187	 87% 13%
20	LR	187	 71% 11% 19%
21	LS	175	 89% 11%
22	LT	159	 84% 16%
23	LU	101	 83% 17%
24	LV	131	 91% 9%
25	LX	120	 84% 16%
26	LY	134	 85% 15%
27	LZ	135	 82% 18%
28	La	147	 91% 9%

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Mol	Chain	Length	Quality of chain
29	Lb	121	
30	Lc	98	
31	Ld	107	
32	Le	128	
33	Lf	109	
34	Lg	114	
35	Lh	122	
36	Li	102	
37	Lj	86	
38	Lk	69	
39	Ll	50	
40	Lm	52	
41	Lo	105	
42	Lp	91	
43	Lr	125	
44	CA	356	

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 139317 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3655	Total	C	N	O	P	1	0
			78444	34968	14346	25475	3655		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

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

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 Large ribosomal subunit protein uL3.

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
			2927	1840	583	489	15		

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

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 Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	240	Total	C	N	O	S	0	0
			1935	1242	368	321	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	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	0	0
			1927	1228	371	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 Ribosomal protein uL16-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	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.

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	152	Total	C	N	O	S	0	0
			1273	793	275	196	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 Heparin-binding protein HBp15.

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 L23a.

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

- Molecule 26 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 27 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 28 is a protein called 60S ribosomal protein L27a.

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

- Molecule 29 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 30 is a protein called 60S ribosomal protein L30.

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

- Molecule 31 is a protein called 60S ribosomal protein L31.

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

- Molecule 32 is a protein called 60S ribosomal protein L32.

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

- Molecule 33 is a protein called 60S ribosomal protein L35a.

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

- Molecule 34 is a protein called 60S ribosomal protein L34.

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

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

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

- Molecule 36 is a protein called 60S ribosomal protein L36.

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

- Molecule 37 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

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

- Molecule 39 is a protein called 60S ribosomal protein L39.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 41 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 42 is a protein called 60S ribosomal protein L37a.

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

- Molecule 43 is a protein called 60S ribosomal protein L28.

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

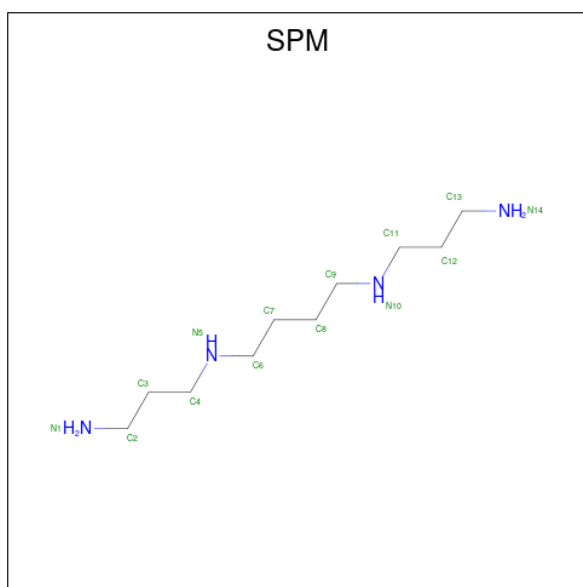
- Molecule 44 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	17		

- Molecule 45 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

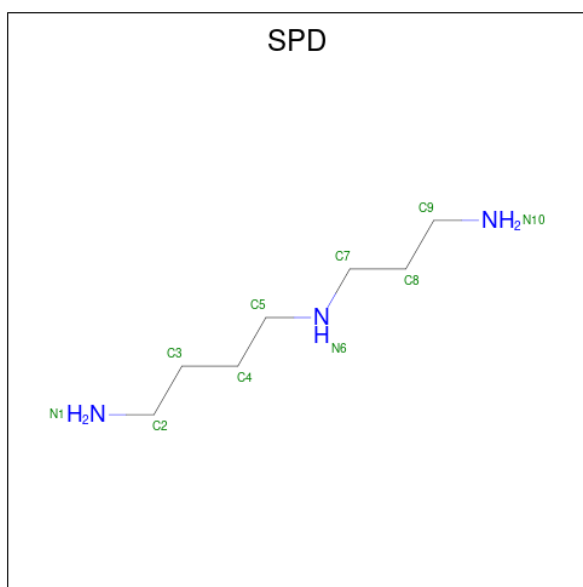
Mol	Chain	Residues	Atoms		AltConf
45	L5	178	Total	Mg	0
			178	178	
45	L7	3	Total	Mg	0
			3	3	
45	L8	5	Total	Mg	0
			5	5	
45	LA	1	Total	Mg	0
			1	1	
45	LI	1	Total	Mg	0
			1	1	
45	LP	1	Total	Mg	0
			1	1	
45	LV	1	Total	Mg	0
			1	1	
45	Le	1	Total	Mg	0
			1	1	

- Molecule 46 is SPERMINE (CCD ID: SPM) (formula: C₁₀H₂₆N₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
46	L5	1	Total	C	N	0
			14	10	4	
46	L5	1	Total	C	N	0
			14	10	4	
46	L5	1	Total	C	N	0
			14	10	4	
46	L5	1	Total	C	N	0
			14	10	4	
46	L5	1	Total	C	N	0
			14	10	4	
46	L5	1	Total	C	N	0
			14	10	4	

- Molecule 47 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
47	L5	1	Total	C	N	0
			10	7	3	
47	L5	1	Total	C	N	0
			10	7	3	
47	L5	1	Total	C	N	0
			10	7	3	
47	L5	1	Total	C	N	0
			10	7	3	
47	L5	1	Total	C	N	0
			10	7	3	
47	L5	1	Total	C	N	0
			10	7	3	
47	L5	1	Total	C	N	0
			10	7	3	
47	LN	1	Total	C	N	0
			10	7	3	

- Molecule 48 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
48	Lg	1	Total	Zn	0
			1	1	

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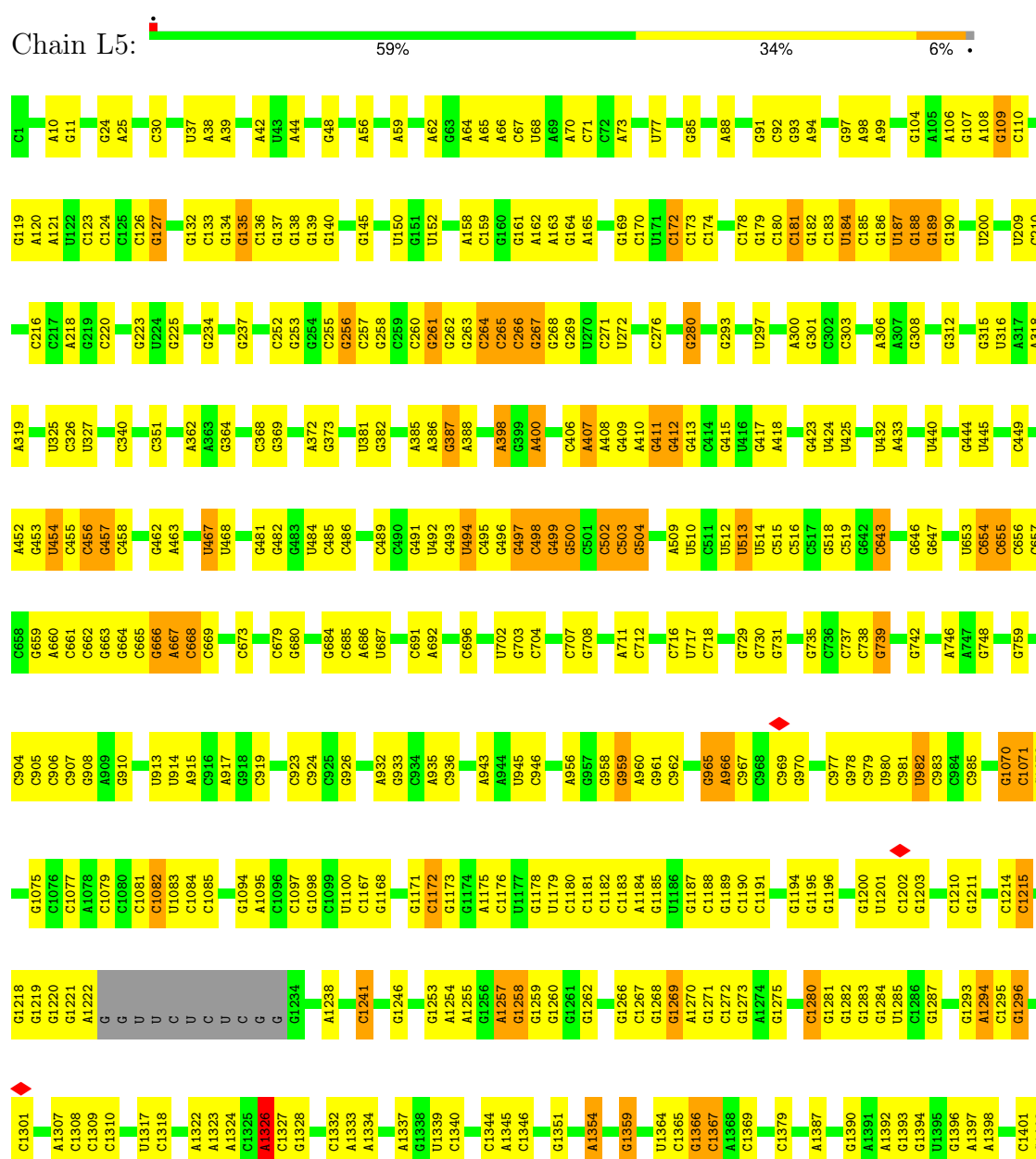
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Mol	Chain	Residues	Atoms		AltConf
48	Lj	1	Total 1	Zn 1	0
48	Lm	1	Total 1	Zn 1	0
48	Lo	1	Total 1	Zn 1	0
48	Lp	1	Total 1	Zn 1	0

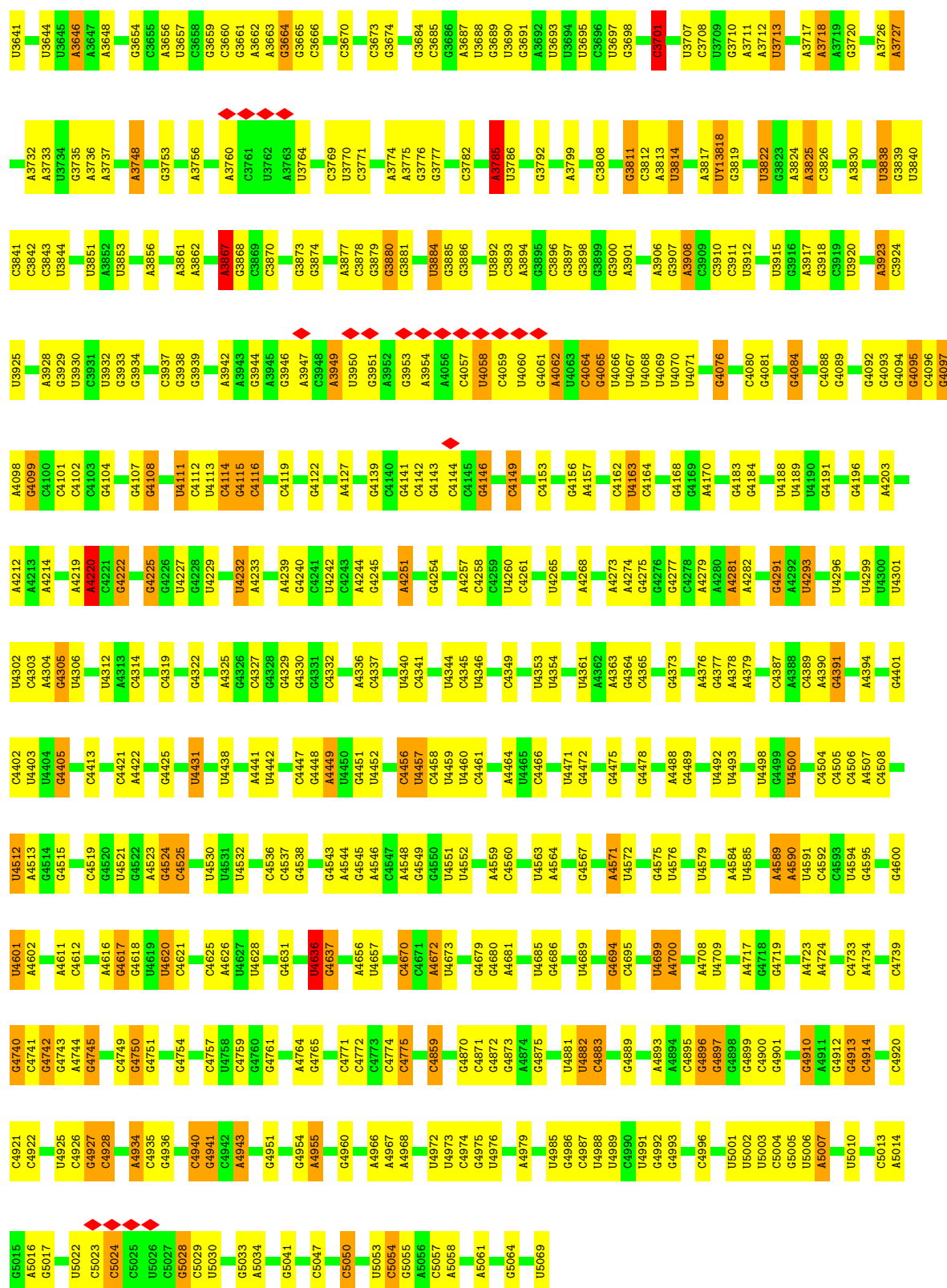
3 Residue-property plots

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

• Molecule 1: 28S rRNA







• Molecule 2: 5S rRNA

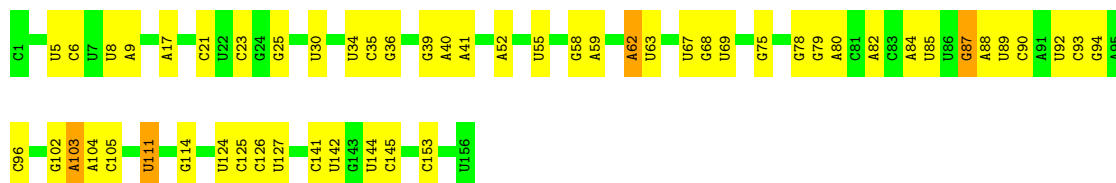
Chain L7:

82%

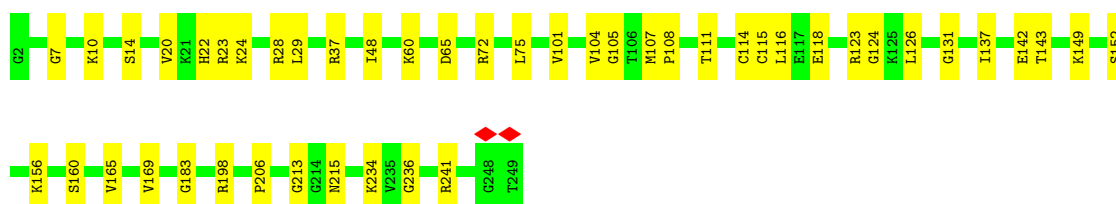
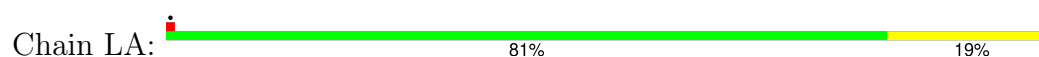
17%



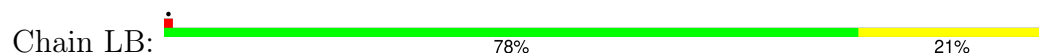
- Molecule 3: 5.8S rRNA



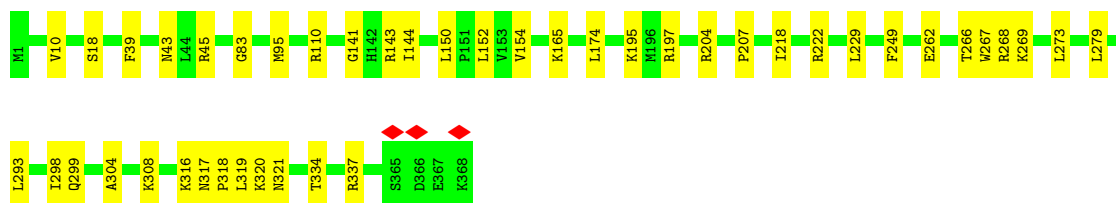
- Molecule 4: 60S ribosomal protein L8



- Molecule 5: Large ribosomal subunit protein uL3

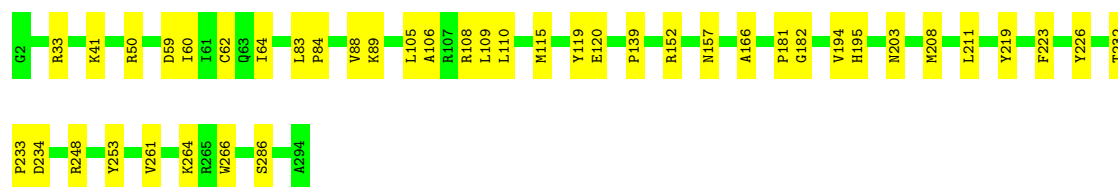


- Molecule 6: 60S ribosomal protein L4



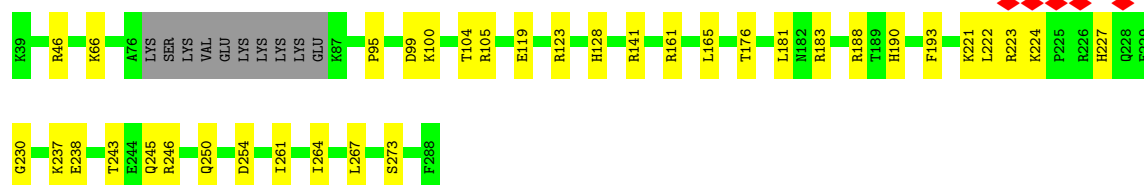
- Molecule 7: Large ribosomal subunit protein uL18

Chain LD:  86% 14%



- Molecule 8: Large ribosomal subunit protein eL6

Chain LE:  82% 14%



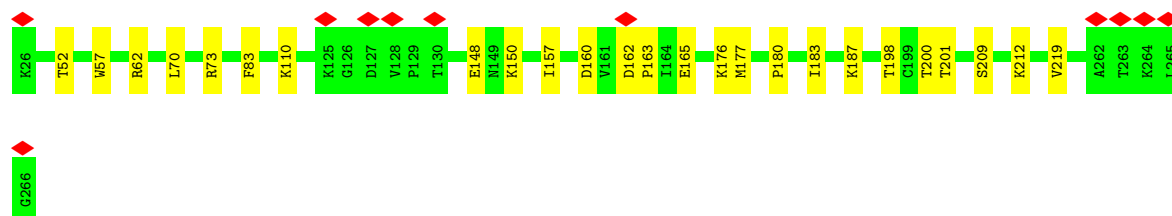
- Molecule 9: 60S ribosomal protein L7

Chain LF:  88% 12%



- Molecule 10: 60S ribosomal protein L7a

Chain LG:  5% 90% 10%



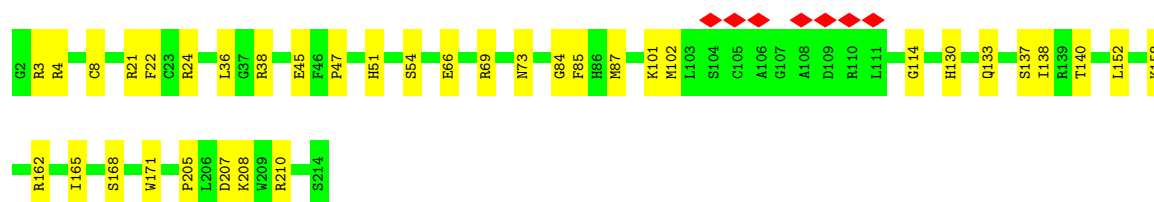
- Molecule 11: 60S ribosomal protein L9

Chain LH:  85% 15%



- Molecule 12: Ribosomal protein uL16-like

Chain LI:  83% 17%



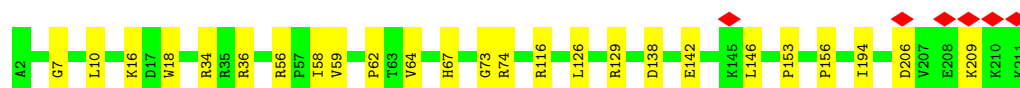
- Molecule 13: 60S ribosomal protein L11

Chain LJ: 87% 10%



- Molecule 14: Large ribosomal subunit protein eL13

Chain LL: 88% 12%



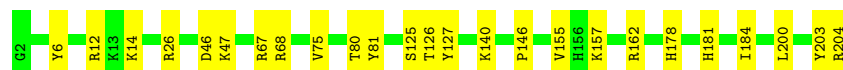
- Molecule 15: 60S ribosomal protein L14

Chain LM: 82% 18%



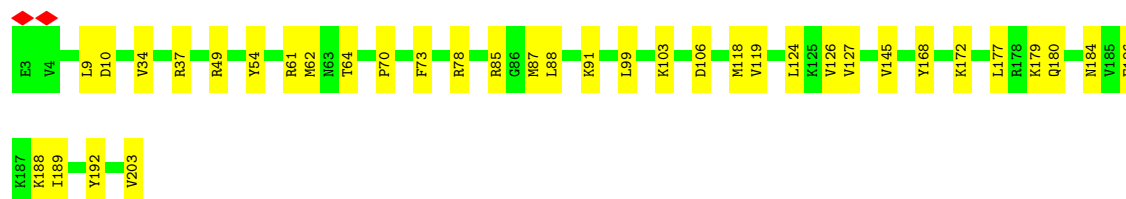
- Molecule 16: 60S ribosomal protein L15

Chain LN: 88% 12%



- Molecule 17: 60S ribosomal protein L13a

Chain LO: 82% 18%



- Molecule 18: 60S ribosomal protein L17

Chain LP: 85% 15%



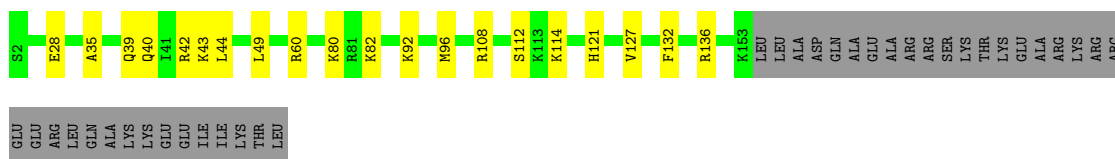
- Molecule 19: 60S ribosomal protein L18

Chain LQ: 87% 13%



- Molecule 20: 60S ribosomal protein L19

Chain LR: 71% 11% 19%



- Molecule 21: 60S ribosomal protein L18a

Chain LS: 89% 11%



- Molecule 22: 60S ribosomal protein L21

Chain LT: 84% 16%



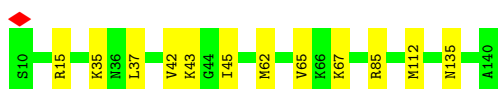
- Molecule 23: Heparin-binding protein HBp15

Chain LU: 83% 17%



- Molecule 24: 60S ribosomal protein L23

Chain LV: 91% 9%



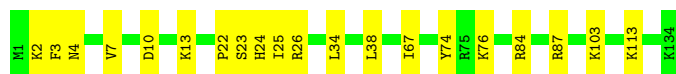
- Molecule 25: 60S ribosomal protein L23a

Chain LX:  84% 16%



- Molecule 26: 60S ribosomal protein L26

Chain LY:  85% 15%



- Molecule 27: 60S ribosomal protein L27

Chain LZ:  82% 18%



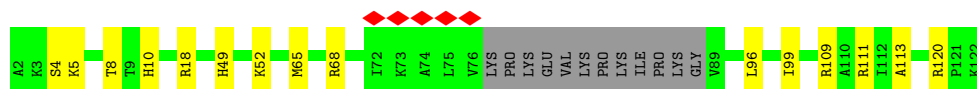
- Molecule 28: 60S ribosomal protein L27a

Chain La:  91% 9%



- Molecule 29: Large ribosomal subunit protein eL29

Chain Lb:  78% 12% 10%



- Molecule 30: 60S ribosomal protein L30

Chain Lc:  87% 13%

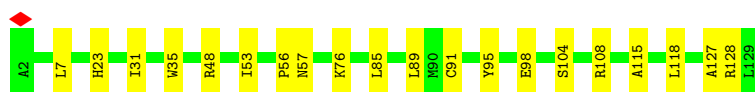
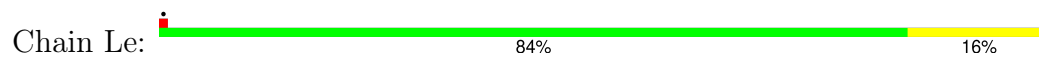


- Molecule 31: 60S ribosomal protein L31

Chain Ld:  82% 18%



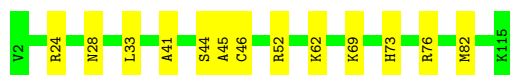
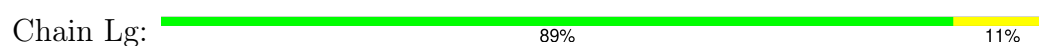
- Molecule 32: 60S ribosomal protein L32



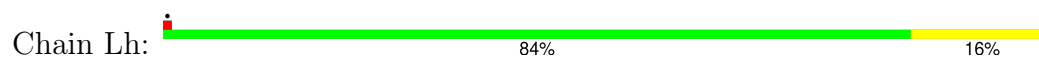
- Molecule 33: 60S ribosomal protein L35a



- Molecule 34: 60S ribosomal protein L34



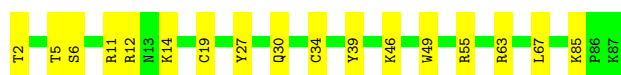
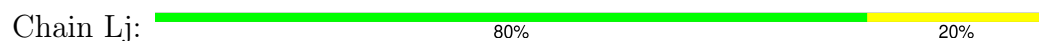
- Molecule 35: 60S ribosomal protein L35



- Molecule 36: 60S ribosomal protein L36



- Molecule 37: 60S ribosomal protein L37



- Molecule 38: 60S ribosomal protein L38



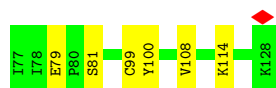
- Molecule 39: 60S ribosomal protein L39

Chain Ll:  78% 22%



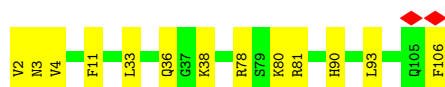
- Molecule 40: Large ribosomal subunit protein eL40

Chain Lm:  88% 12%



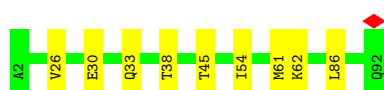
- Molecule 41: 60S ribosomal protein L36a

Chain Lo:  88% 12%



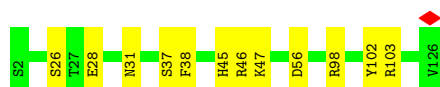
- Molecule 42: 60S ribosomal protein L37a

Chain Lp:  90% 10%



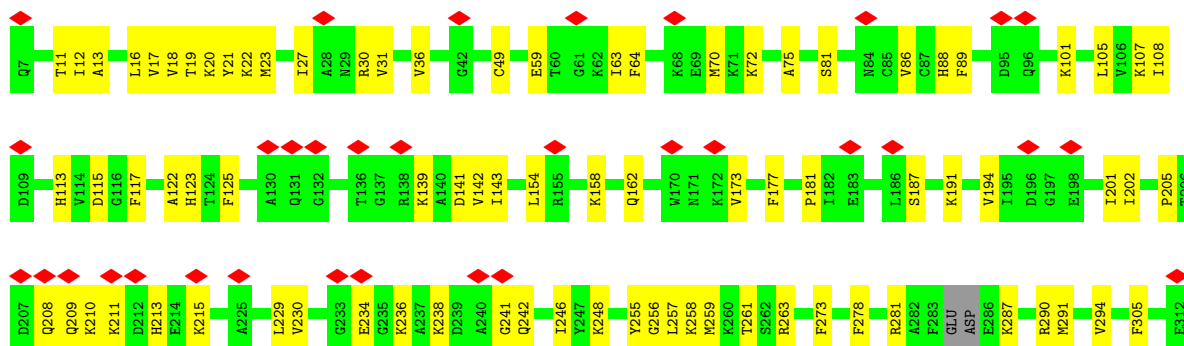
- Molecule 43: 60S ribosomal protein L28

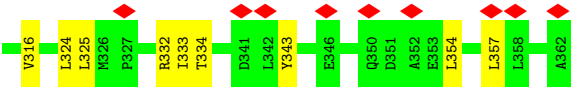
Chain Lr:  90% 10%



- Molecule 44: Proliferation-associated protein 2G4

Chain CA:  12% 74% 26%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	220618	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.298	Depositor
Minimum map value	-0.097	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0134	Depositor
Map size ($\text{\AA}$)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: A2M, SPD, 6MZ, UR3, ZN, MG, OMC, 5MC, OMU, UY1, PSU, SPM, OMG, 1MA

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	0.32	0/85098	0.31	0/132762
2	L7	0.30	0/2861	0.27	0/4459
3	L8	0.32	0/3631	0.29	0/5657
4	LA	0.32	0/1936	0.44	0/2596
5	LB	0.29	0/3306	0.38	0/4424
6	LC	0.30	0/2981	0.41	0/4002
7	LD	0.25	0/2428	0.34	0/3252
8	LE	0.24	0/1973	0.42	0/2645
9	LF	0.29	0/1905	0.30	0/2539
10	LG	0.25	0/1960	0.38	0/2637
11	LH	0.26	0/1537	0.35	0/2066
12	LI	0.25	0/1751	0.33	0/2340
13	LJ	0.20	0/1385	0.34	0/1852
14	LL	0.27	0/1732	0.33	0/2315
15	LM	0.28	0/1161	0.36	0/1554
16	LN	0.31	0/1746	0.35	0/2338
17	LO	0.30	0/1682	0.37	0/2250
18	LP	0.30	0/1268	0.40	0/1701
19	LQ	0.31	0/1537	0.37	0/2052
20	LR	0.26	0/1289	0.31	0/1705
21	LS	0.30	0/1493	0.35	0/2003
22	LT	0.27	0/1326	0.32	0/1770
23	LU	0.22	0/839	0.46	0/1126
24	LV	0.26	0/993	0.38	0/1332
25	LX	0.25	0/1002	0.31	0/1345
26	LY	0.28	0/1132	0.37	0/1504
27	LZ	0.25	0/1130	0.35	0/1507
28	La	0.29	0/1191	0.32	0/1591
29	Lb	0.23	0/889	0.38	0/1175
30	Lc	0.26	0/774	0.35	0/1038
31	Ld	0.27	0/903	0.35	0/1216
32	Le	0.30	0/1071	0.33	0/1429

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lf	0.31	0/895	0.38	0/1198
34	Lg	0.27	0/916	0.33	0/1220
35	Lh	0.25	0/1023	0.31	0/1351
36	Li	0.23	0/843	0.31	0/1115
37	Lj	0.31	0/720	0.41	0/952
38	Lk	0.21	0/575	0.32	0/761
39	Ll	0.28	0/454	0.31	0/599
40	Lm	0.25	0/435	0.39	1/575 (0.2%)
41	Lo	0.27	0/876	0.35	0/1156
42	Lp	0.27	0/718	0.33	0/953
43	Lr	0.28	0/1017	0.35	0/1364
44	CA	0.18	0/2810	0.40	0/3780
All	All	0.30	0/147192	0.33	1/217206 (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
5	LB	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	Lm	108	VAL	N-CA-C	-5.10	107.84	112.12

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	LB	174	ARG	Sidechain

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	78444	0	39717	756	0
2	L7	2561	0	1295	10	0
3	L8	3315	0	1685	31	0
4	LA	1898	0	1993	35	0
5	LB	3238	0	3376	63	0
6	LC	2927	0	3104	34	0
7	LD	2382	0	2410	28	0
8	LE	1935	0	2096	29	0
9	LF	1870	0	1996	18	0
10	LG	1927	0	2074	18	0
11	LH	1518	0	1601	19	0
12	LI	1711	0	1749	25	0
13	LJ	1362	0	1399	11	0
14	LL	1701	0	1818	20	0
15	LM	1138	0	1204	20	0
16	LN	1701	0	1749	24	0
17	LO	1650	0	1794	27	0
18	LP	1242	0	1269	18	0
19	LQ	1513	0	1628	18	0
20	LR	1273	0	1407	16	0
21	LS	1453	0	1490	12	0
22	LT	1298	0	1366	21	0
23	LU	825	0	850	11	0
24	LV	979	0	1039	8	0
25	LX	985	0	1066	49	0
26	LY	1115	0	1205	14	0
27	LZ	1107	0	1182	16	0
28	La	1162	0	1213	10	0
29	Lb	876	0	948	13	0
30	Lc	764	0	804	7	0
31	Ld	888	0	930	12	0
32	Le	1053	0	1147	14	0
33	Lf	876	0	912	8	0
34	Lg	906	0	998	12	0
35	Lh	1015	0	1148	19	0
36	Li	832	0	917	7	0
37	Lj	705	0	737	16	0
38	Lk	569	0	637	5	0
39	Ll	444	0	483	11	0
40	Lm	429	0	465	4	0
41	Lo	862	0	929	8	0
42	Lp	708	0	756	7	0
43	Lr	1002	0	1068	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	CA	2764	0	2778	113	0
45	L5	178	0	0	0	0
45	L7	3	0	0	0	0
45	L8	5	0	0	0	0
45	LA	1	0	0	0	0
45	LI	1	0	0	0	0
45	LP	1	0	0	0	0
45	LV	1	0	0	0	0
45	Le	1	0	0	0	0
46	L5	98	0	182	4	0
47	L5	90	0	171	5	0
47	LN	10	0	19	0	0
48	Lg	1	0	0	0	0
48	Lj	1	0	0	0	0
48	Lm	1	0	0	0	0
48	Lo	1	0	0	0	0
48	Lp	1	0	0	0	0
All	All	139317	0	100804	1310	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 1310 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)
1:L5:2709:C:O2'	44:CA:263:ARG:CD	1.96	1.12
25:LX:156:ILE:HG12	44:CA:290:ARG:HB3	1.33	1.05
25:LX:156:ILE:HD11	44:CA:291:MET:HB2	1.38	1.01
25:LX:156:ILE:HG13	44:CA:290:ARG:O	1.62	0.97
1:L5:2709:C:H2'	44:CA:263:ARG:HD3	1.47	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	246/248 (99%)	229 (93%)	17 (7%)	0	100	100
5	LB	400/402 (100%)	385 (96%)	15 (4%)	0	100	100
6	LC	366/368 (100%)	353 (96%)	13 (4%)	0	100	100
7	LD	291/293 (99%)	282 (97%)	9 (3%)	0	100	100
8	LE	236/250 (94%)	226 (96%)	10 (4%)	0	100	100
9	LF	223/225 (99%)	216 (97%)	7 (3%)	0	100	100
10	LG	239/241 (99%)	226 (95%)	13 (5%)	0	100	100
11	LH	188/190 (99%)	183 (97%)	5 (3%)	0	100	100
12	LI	211/213 (99%)	207 (98%)	4 (2%)	0	100	100
13	LJ	168/176 (96%)	162 (96%)	6 (4%)	0	100	100
14	LL	208/210 (99%)	201 (97%)	7 (3%)	0	100	100
15	LM	137/139 (99%)	130 (95%)	7 (5%)	0	100	100
16	LN	201/203 (99%)	198 (98%)	3 (2%)	0	100	100
17	LO	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
18	LP	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
19	LQ	185/187 (99%)	182 (98%)	3 (2%)	0	100	100
20	LR	150/187 (80%)	146 (97%)	4 (3%)	0	100	100
21	LS	173/175 (99%)	165 (95%)	8 (5%)	0	100	100
22	LT	157/159 (99%)	154 (98%)	3 (2%)	0	100	100
23	LU	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
24	LV	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
25	LX	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
26	LY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
27	LZ	133/135 (98%)	126 (95%)	7 (5%)	0	100	100
28	La	145/147 (99%)	140 (97%)	5 (3%)	0	100	100
29	Lb	105/121 (87%)	100 (95%)	5 (5%)	0	100	100
30	Lc	96/98 (98%)	92 (96%)	4 (4%)	0	100	100
31	Ld	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
32	Le	126/128 (98%)	125 (99%)	1 (1%)	0	100	100
33	Lf	107/109 (98%)	105 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
35	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
36	Li	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
37	Lj	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
38	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
39	Ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
40	Lm	50/52 (96%)	50 (100%)	0	0	100	100
41	Lo	103/105 (98%)	98 (95%)	5 (5%)	0	100	100
42	Lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
43	Lr	123/125 (98%)	121 (98%)	2 (2%)	0	100	100
44	CA	350/356 (98%)	334 (95%)	16 (5%)	0	100	100
All	All	6670/6823 (98%)	6448 (97%)	222 (3%)	0	100	100

There are no Ramachandran outliers to report.

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%)	190 (100%)	0	100	100
5	LB	348/348 (100%)	348 (100%)	0	100	100
6	LC	306/306 (100%)	306 (100%)	0	100	100
7	LD	246/247 (100%)	246 (100%)	0	100	100
8	LE	212/222 (96%)	212 (100%)	0	100	100
9	LF	194/194 (100%)	194 (100%)	0	100	100
10	LG	203/205 (99%)	203 (100%)	0	100	100
11	LH	169/169 (100%)	169 (100%)	0	100	100
12	LI	180/180 (100%)	180 (100%)	0	100	100
13	LJ	143/148 (97%)	143 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	LL	176/176 (100%)	176 (100%)	0	100	100
15	LM	118/118 (100%)	118 (100%)	0	100	100
16	LN	171/171 (100%)	171 (100%)	0	100	100
17	LO	173/173 (100%)	173 (100%)	0	100	100
18	LP	134/134 (100%)	134 (100%)	0	100	100
19	LQ	164/164 (100%)	164 (100%)	0	100	100
20	LR	136/166 (82%)	136 (100%)	0	100	100
21	LS	156/156 (100%)	156 (100%)	0	100	100
22	LT	139/139 (100%)	139 (100%)	0	100	100
23	LU	91/91 (100%)	91 (100%)	0	100	100
24	LV	101/101 (100%)	101 (100%)	0	100	100
25	LX	108/108 (100%)	108 (100%)	0	100	100
26	LY	124/124 (100%)	124 (100%)	0	100	100
27	LZ	117/117 (100%)	117 (100%)	0	100	100
28	La	120/120 (100%)	120 (100%)	0	100	100
29	Lb	88/101 (87%)	88 (100%)	0	100	100
30	Lc	83/83 (100%)	83 (100%)	0	100	100
31	Ld	98/98 (100%)	98 (100%)	0	100	100
32	Le	114/114 (100%)	114 (100%)	0	100	100
33	Lf	88/88 (100%)	88 (100%)	0	100	100
34	Lg	98/98 (100%)	98 (100%)	0	100	100
35	Lh	109/109 (100%)	109 (100%)	0	100	100
36	Li	86/86 (100%)	86 (100%)	0	100	100
37	Lj	73/73 (100%)	73 (100%)	0	100	100
38	Lk	64/64 (100%)	64 (100%)	0	100	100
39	Ll	47/47 (100%)	47 (100%)	0	100	100
40	Lm	48/48 (100%)	48 (100%)	0	100	100
41	Lo	93/93 (100%)	93 (100%)	0	100	100
42	Lp	74/74 (100%)	74 (100%)	0	100	100
43	Lr	109/109 (100%)	109 (100%)	0	100	100
44	CA	303/305 (99%)	303 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	5794/5857 (99%)	5794 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
19	LQ	21	GLN
28	La	34	ASN
20	LR	134	ASN
24	LV	77	HIS
28	La	120	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3643/3675 (99%)	714 (19%)	16 (0%)
2	L7	119/120 (99%)	11 (9%)	0
3	L8	155/156 (99%)	22 (14%)	0
All	All	3917/3951 (99%)	747 (19%)	16 (0%)

5 of 747 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	25	A
1	L5	30	C
1	L5	39	A
1	L5	42	A
1	L5	48	G

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	4699	U
1	L5	4600	G
1	L5	2416	G
1	L5	3673	C
1	L5	1977	C

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

114 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	OMC	L5	2365	45,1	19,22,23	0.63	0	25,31,34	0.59	0
1	OMG	L5	1625	1	23,26,27	0.58	0	32,38,41	0.50	0
1	PSU	L5	3920	45,1	18,21,22	1.07	1 (5%)	21,30,33	1.97	4 (19%)
1	PSU	L5	4431	1	18,21,22	1.06	1 (5%)	21,30,33	1.88	4 (19%)
1	PSU	L5	4628	1	18,21,22	1.01	1 (5%)	21,30,33	1.86	4 (19%)
1	PSU	L5	4636	1	18,21,22	1.13	2 (11%)	21,30,33	2.08	6 (28%)
1	PSU	L5	3639	1	18,21,22	1.10	2 (11%)	21,30,33	1.97	5 (23%)
1	OMG	L5	4637	1	23,26,27	0.59	0	32,38,41	0.50	0
1	PSU	L5	4312	1	18,21,22	1.07	1 (5%)	21,30,33	1.91	4 (19%)
1	OMG	L5	4618	1	23,26,27	0.59	0	32,38,41	0.53	0
1	OMG	L5	4623	1	23,26,27	0.60	0	32,38,41	0.62	0
1	PSU	L5	1683	1	18,21,22	1.09	2 (11%)	21,30,33	2.06	5 (23%)
1	PSU	L5	3822	1	18,21,22	1.08	1 (5%)	21,30,33	1.99	6 (28%)
1	OMG	L5	3899	1	23,26,27	0.65	0	32,38,41	0.53	0
1	OMC	L5	4456	1	19,22,23	0.71	1 (5%)	25,31,34	0.79	0
1	PSU	L5	4500	1	18,21,22	1.13	2 (11%)	21,30,33	2.06	5 (23%)
1	OMG	L5	1522	1	23,26,27	0.60	0	32,38,41	0.69	1 (3%)
1	A2M	L5	4590	1	22,25,26	1.19	1 (4%)	30,36,39	1.51	5 (16%)
1	OMC	L5	2824	1	19,22,23	0.64	0	25,31,34	0.65	0
1	OMU	L5	4498	1	19,22,23	3.23	7 (36%)	25,31,34	1.90	5 (20%)
1	A2M	L5	1326	1	22,25,26	1.24	2 (9%)	30,36,39	1.44	8 (26%)
1	OMU	L5	3925	1	19,22,23	3.22	7 (36%)	25,31,34	1.95	5 (20%)
1	OMG	L5	1316	1	23,26,27	0.65	0	32,38,41	0.56	0
1	OMC	L5	3869	1	19,22,23	0.64	0	25,31,34	0.79	0
1	A2M	L5	2363	45,1	22,25,26	1.22	2 (9%)	30,36,39	1.55	9 (30%)
1	A2M	L5	3867	1	22,25,26	1.28	2 (9%)	30,36,39	1.48	6 (20%)
1	A2M	L5	1524	1	22,25,26	1.32	2 (9%)	30,36,39	1.51	6 (20%)
1	PSU	L5	1792	1	18,21,22	1.03	1 (5%)	21,30,33	1.92	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	L5	3782	45,1	19,22,23	0.72	0	26,32,35	0.81	1 (3%)
1	PSU	L5	3853	45,1	18,21,22	1.05	1 (5%)	21,30,33	1.89	4 (19%)
1	OMC	L5	1340	1	19,22,23	0.69	0	25,31,34	0.80	0
1	OMG	L5	4370	1	23,26,27	0.57	0	32,38,41	0.53	0
1	PSU	L5	4521	45,1	18,21,22	1.09	2 (11%)	21,30,33	2.02	6 (28%)
1	OMG	L5	3627	1	23,26,27	0.57	0	32,38,41	0.58	0
1	OMG	L5	3744	1	23,26,27	0.57	0	32,38,41	0.51	0
1	PSU	L5	1677	1	18,21,22	1.06	3 (16%)	21,30,33	1.95	5 (23%)
1	OMU	L5	2837	1	19,22,23	3.25	7 (36%)	25,31,34	1.86	4 (16%)
1	A2M	L5	4523	45,1	22,25,26	1.22	3 (13%)	30,36,39	1.53	6 (20%)
3	PSU	L8	55	3	18,21,22	1.08	1 (5%)	21,30,33	1.88	4 (19%)
1	PSU	L5	4442	1	18,21,22	1.09	2 (11%)	21,30,33	2.04	6 (28%)
1	OMC	L5	4536	1	19,22,23	0.67	0	25,31,34	0.75	0
1	OMG	L5	2876	1	23,26,27	0.58	0	32,38,41	0.52	0
1	OMU	L5	4306	1	19,22,23	3.21	7 (36%)	25,31,34	1.91	4 (16%)
1	PSU	L5	3695	1	18,21,22	1.07	2 (11%)	21,30,33	1.95	4 (19%)
3	OMG	L8	75	3	23,26,27	0.55	0	32,38,41	0.54	0
1	PSU	L5	1781	1	18,21,22	1.07	1 (5%)	21,30,33	1.79	4 (19%)
1	6MZ	L5	4220	1	22,25,26	3.96	11 (50%)	29,36,39	2.49	11 (37%)
1	OMG	L5	4196	1	23,26,27	0.55	0	32,38,41	0.46	0
1	PSU	L5	4972	1	18,21,22	1.04	1 (5%)	21,30,33	1.95	4 (19%)
1	PSU	L5	4471	1	18,21,22	1.06	1 (5%)	21,30,33	1.90	4 (19%)
1	PSU	L5	5010	1	18,21,22	1.08	1 (5%)	21,30,33	1.93	4 (19%)
1	PSU	L5	3637	1	18,21,22	1.09	1 (5%)	21,30,33	1.97	3 (14%)
1	OMC	L5	3808	45,1	19,22,23	0.69	0	25,31,34	0.85	1 (4%)
1	OMC	L5	3701	1	19,22,23	0.72	1 (5%)	25,31,34	1.82	4 (16%)
1	PSU	L5	4689	1	18,21,22	1.11	2 (11%)	21,30,33	2.07	4 (19%)
1	PSU	L5	4576	1	18,21,22	1.06	2 (11%)	21,30,33	1.86	4 (19%)
1	OMG	L5	2424	1	23,26,27	0.60	0	32,38,41	0.43	0
1	PSU	L5	4457	1	18,21,22	1.05	2 (11%)	21,30,33	1.99	5 (23%)
1	PSU	L5	4293	1	18,21,22	1.08	2 (11%)	21,30,33	2.01	4 (19%)
1	PSU	L5	4673	45,1	18,21,22	1.07	2 (11%)	21,30,33	1.90	4 (19%)
1	PSU	L5	4403	1	18,21,22	1.07	2 (11%)	21,30,33	2.06	6 (28%)
1	A2M	L5	400	1	22,25,26	1.28	3 (13%)	30,36,39	1.57	9 (30%)
1	PSU	L5	3851	1	18,21,22	1.08	1 (5%)	21,30,33	1.94	4 (19%)
1	OMC	L5	3887	1	19,22,23	0.65	0	25,31,34	0.67	0
1	PSU	L5	1536	1	18,21,22	1.05	1 (5%)	21,30,33	1.89	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMU	L5	4227	1	19,22,23	3.26	7 (36%)	25,31,34	1.91	4 (16%)
1	OMC	L5	2861	1	19,22,23	0.63	0	25,31,34	0.82	1 (4%)
1	A2M	L5	398	1	22,25,26	1.17	1 (4%)	30,36,39	1.62	7 (23%)
1	PSU	L5	1862	1	18,21,22	1.05	1 (5%)	21,30,33	2.00	4 (19%)
1	OMC	L5	3841	1	19,22,23	0.67	0	25,31,34	0.73	0
1	PSU	L5	4353	1	18,21,22	1.09	2 (11%)	21,30,33	1.99	6 (28%)
1	A2M	L5	2787	1	22,25,26	1.16	1 (4%)	30,36,39	1.49	7 (23%)
1	A2M	L5	3785	45,1	22,25,26	1.17	2 (9%)	30,36,39	1.59	10 (33%)
1	PSU	L5	4361	1	18,21,22	1.06	2 (11%)	21,30,33	1.88	4 (19%)
1	A2M	L5	3825	1	22,25,26	1.17	2 (9%)	30,36,39	1.55	7 (23%)
1	PSU	L5	4973	1	18,21,22	1.03	1 (5%)	21,30,33	1.92	4 (19%)
1	PSU	L5	1782	1	18,21,22	1.05	1 (5%)	21,30,33	1.86	4 (19%)
3	PSU	L8	69	3	18,21,22	1.06	2 (11%)	21,30,33	1.96	5 (23%)
1	OMG	L5	4499	1	23,26,27	0.53	0	32,38,41	0.48	0
1	PSU	L5	4532	1	18,21,22	1.09	1 (5%)	21,30,33	1.86	4 (19%)
1	OMG	L5	4494	1	23,26,27	0.59	0	32,38,41	0.49	0
1	PSU	L5	3844	1	18,21,22	1.11	1 (5%)	21,30,33	1.91	4 (19%)
1	PSU	L5	1744	45,1	18,21,22	1.09	1 (5%)	21,30,33	1.96	4 (19%)
1	PSU	L5	5001	1	18,21,22	1.08	1 (5%)	21,30,33	1.88	4 (19%)
1	OMG	L5	4392	1	23,26,27	0.61	0	32,38,41	0.50	0
1	OMC	L5	2804	1	19,22,23	0.66	0	25,31,34	0.91	1 (4%)
1	A2M	L5	1871	45,1	22,25,26	1.30	3 (13%)	30,36,39	1.63	7 (23%)
1	PSU	L5	4552	1	18,21,22	1.10	2 (11%)	21,30,33	2.03	4 (19%)
1	5MC	L5	4447	1	19,22,23	0.93	1 (5%)	26,32,35	0.67	0
1	A2M	L5	4571	1	22,25,26	1.24	2 (9%)	30,36,39	1.58	9 (30%)
1	PSU	L5	1582	1	18,21,22	1.08	1 (5%)	21,30,33	1.90	4 (19%)
1	A2M	L5	1534	45,1	22,25,26	1.26	3 (13%)	30,36,39	1.46	7 (23%)
1	PSU	L5	4296	1	18,21,22	1.06	1 (5%)	21,30,33	1.93	4 (19%)
1	UR3	L5	4530	1	19,22,23	2.66	6 (31%)	26,32,35	1.59	3 (11%)
1	A2M	L5	3718	1	22,25,26	1.16	1 (4%)	30,36,39	1.52	6 (20%)
1	PSU	L5	4493	1	18,21,22	1.05	1 (5%)	21,30,33	1.85	4 (19%)
1	OMG	L5	3792	1	23,26,27	0.57	0	32,38,41	0.54	0
1	PSU	L5	2632	1	18,21,22	1.06	1 (5%)	21,30,33	1.92	4 (19%)
1	A2M	L5	3830	1	22,25,26	1.19	1 (4%)	30,36,39	1.57	6 (20%)
1	OMU	L5	4620	1	19,22,23	3.16	7 (36%)	25,31,34	1.71	4 (16%)
1	PSU	L5	1860	1	18,21,22	1.07	1 (5%)	21,30,33	1.94	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	A2M	L5	2815	1	22,25,26	1.21	2 (9%)	30,36,39	1.51	7 (23%)
1	1MA	L5	1322	45,1	21,25,26	0.65	0	30,37,40	0.80	2 (6%)
1	PSU	L5	4299	1	18,21,22	1.01	1 (5%)	21,30,33	1.90	4 (19%)
1	OMG	L5	2364	45,1	23,26,27	0.60	0	32,38,41	0.44	0
1	PSU	L5	4579	1	18,21,22	1.08	1 (5%)	21,30,33	1.95	4 (19%)
1	OMC	L5	2422	45,1	19,22,23	0.65	0	25,31,34	0.74	1 (4%)
1	OMG	L5	4228	1	23,26,27	0.58	0	32,38,41	0.67	0
1	PSU	L5	2839	1	18,21,22	1.02	1 (5%)	21,30,33	1.93	4 (19%)
1	OMC	L5	2351	45,1	19,22,23	0.71	1 (5%)	25,31,34	1.10	2 (8%)
1	PSU	L5	3884	1	18,21,22	1.09	2 (11%)	21,30,33	1.97	4 (19%)
1	A2M	L5	2401	1	22,25,26	1.23	1 (4%)	30,36,39	1.61	5 (16%)
1	UY1	L5	3818	1	19,22,23	4.79	9 (47%)	21,31,34	2.04	5 (23%)
1	A2M	L5	1323	1	22,25,26	1.23	2 (9%)	30,36,39	1.58	7 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	L5	2365	45,1	-	0/9/27/28	0/2/2/2
1	OMG	L5	1625	1	-	2/9/27/28	0/3/3/3
1	PSU	L5	3920	45,1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4431	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4628	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4636	1	-	1/7/25/26	0/2/2/2
1	PSU	L5	3639	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4637	1	-	3/9/27/28	0/3/3/3
1	PSU	L5	4312	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4618	1	-	2/9/27/28	0/3/3/3
1	OMG	L5	4623	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	1683	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	3822	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	3899	1	-	2/9/27/28	0/3/3/3
1	OMC	L5	4456	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	4500	1	-	3/7/25/26	0/2/2/2
1	OMG	L5	1522	1	-	0/9/27/28	0/3/3/3
1	A2M	L5	4590	1	-	3/9/27/28	0/3/3/3
1	OMC	L5	2824	1	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	L5	4498	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	1326	1	-	3/9/27/28	0/3/3/3
1	OMU	L5	3925	1	-	0/9/27/28	0/2/2/2
1	OMG	L5	1316	1	-	0/9/27/28	0/3/3/3
1	OMC	L5	3869	1	-	1/9/27/28	0/2/2/2
1	A2M	L5	2363	45,1	-	0/9/27/28	0/3/3/3
1	A2M	L5	3867	1	-	2/9/27/28	0/3/3/3
1	A2M	L5	1524	1	-	3/9/27/28	0/3/3/3
1	PSU	L5	1792	1	-	0/7/25/26	0/2/2/2
1	5MC	L5	3782	45,1	-	0/7/25/26	0/2/2/2
1	PSU	L5	3853	45,1	-	0/7/25/26	0/2/2/2
1	OMC	L5	1340	1	-	1/9/27/28	0/2/2/2
1	OMG	L5	4370	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4521	45,1	-	0/7/25/26	0/2/2/2
1	OMG	L5	3627	1	-	1/9/27/28	0/3/3/3
1	OMG	L5	3744	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	1677	1	-	2/7/25/26	0/2/2/2
1	OMU	L5	2837	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	4523	45,1	-	0/9/27/28	0/3/3/3
3	PSU	L8	55	3	-	0/7/25/26	0/2/2/2
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
1	OMG	L5	2876	1	-	0/9/27/28	0/3/3/3
1	OMU	L5	4306	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	3695	1	-	0/7/25/26	0/2/2/2
3	OMG	L8	75	3	-	1/9/27/28	0/3/3/3
1	PSU	L5	1781	1	-	1/7/25/26	0/2/2/2
1	6MZ	L5	4220	1	-	2/9/27/28	0/3/3/3
1	OMG	L5	4196	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	4972	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4471	1	-	1/7/25/26	0/2/2/2
1	PSU	L5	5010	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	3637	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	3808	45,1	-	0/9/27/28	0/2/2/2
1	OMC	L5	3701	1	-	5/9/27/28	0/2/2/2
1	PSU	L5	4689	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4576	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	2424	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4457	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4293	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4673	45,1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	L5	4403	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	400	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	3851	1	-	1/7/25/26	0/2/2/2
1	OMC	L5	3887	1	-	1/9/27/28	0/2/2/2
1	PSU	L5	1536	1	-	2/7/25/26	0/2/2/2
1	OMU	L5	4227	1	-	0/9/27/28	0/2/2/2
1	OMC	L5	2861	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	398	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	1862	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	3841	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	4353	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	2787	1	-	5/9/27/28	0/3/3/3
1	A2M	L5	3785	45,1	-	2/9/27/28	0/3/3/3
1	PSU	L5	4361	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	3825	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4973	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	1782	1	-	0/7/25/26	0/2/2/2
3	PSU	L8	69	3	-	0/7/25/26	0/2/2/2
1	OMG	L5	4499	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4532	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4494	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	3844	1	-	1/7/25/26	0/2/2/2
1	PSU	L5	1744	45,1	-	0/7/25/26	0/2/2/2
1	PSU	L5	5001	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4392	1	-	0/9/27/28	0/3/3/3
1	OMC	L5	2804	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	1871	45,1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4552	1	-	0/7/25/26	0/2/2/2
1	5MC	L5	4447	1	-	4/7/25/26	0/2/2/2
1	A2M	L5	4571	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	1582	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	1534	45,1	-	1/9/27/28	0/3/3/3
1	PSU	L5	4296	1	-	2/7/25/26	0/2/2/2
1	UR3	L5	4530	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	3718	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4493	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	3792	1	-	2/9/27/28	0/3/3/3
1	PSU	L5	2632	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	3830	1	-	0/9/27/28	0/3/3/3
1	OMU	L5	4620	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	1860	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A2M	L5	2815	1	-	2/9/27/28	0/3/3/3
1	1MA	L5	1322	45,1	-	2/7/25/26	0/3/3/3
1	PSU	L5	4299	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	2364	45,1	-	2/9/27/28	0/3/3/3
1	PSU	L5	4579	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	2422	45,1	-	2/9/27/28	0/2/2/2
1	OMG	L5	4228	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	2839	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	2351	45,1	-	3/9/27/28	0/2/2/2
1	PSU	L5	3884	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	2401	1	-	0/9/27/28	0/3/3/3
1	UY1	L5	3818	1	-	2/9/27/28	0/2/2/2
1	A2M	L5	1323	1	-	2/9/27/28	0/3/3/3

The worst 5 of 177 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	3818	UY1	C6-C5	12.48	1.49	1.35
1	L5	4220	6MZ	C6-N6	12.04	1.48	1.34
1	L5	3818	UY1	C2-N1	11.46	1.51	1.36
1	L5	4220	6MZ	C3'-C2'	-8.41	1.30	1.53
1	L5	4227	OMU	C2-N1	8.03	1.51	1.38

The worst 5 of 406 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	3925	OMU	C4-N3-C2	-6.15	118.98	126.61
1	L5	4227	OMU	C4-N3-C2	-6.02	119.13	126.61
1	L5	4498	OMU	C4-N3-C2	-5.91	119.28	126.61
1	L5	4306	OMU	C4-N3-C2	-5.81	119.40	126.61
1	L5	4220	6MZ	N1-C2-N3	-5.81	119.79	128.58

There are no chirality outliers.

5 of 80 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L8	75	OMG	C1'-C2'-O2'-CM2
1	L5	400	A2M	C1'-C2'-O2'-CM'
1	L5	1326	A2M	O4'-C4'-C5'-O5'
1	L5	1340	OMC	C1'-C2'-O2'-CM2

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Mol	Chain	Res	Type	Atoms
1	L5	1625	OMG	O4'-C4'-C5'-O5'

There are no ring outliers.

37 monomers are involved in 47 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L5	1625	OMG	1	0
1	L5	4431	PSU	1	0
1	L5	4636	PSU	1	0
1	L5	4637	OMG	1	0
1	L5	4618	OMG	1	0
1	L5	1683	PSU	1	0
1	L5	3822	PSU	1	0
1	L5	4456	OMC	1	0
1	L5	2824	OMC	1	0
1	L5	1326	A2M	2	0
1	L5	2363	A2M	1	0
1	L5	3867	A2M	4	0
1	L5	1340	OMC	2	0
1	L5	1677	PSU	1	0
1	L5	4536	OMC	1	0
3	L8	75	OMG	2	0
1	L5	4220	6MZ	1	0
1	L5	4196	OMG	1	0
1	L5	3701	OMC	1	0
1	L5	4457	PSU	1	0
1	L5	4293	PSU	1	0
1	L5	400	A2M	1	0
1	L5	398	A2M	1	0
1	L5	3841	OMC	1	0
1	L5	3785	A2M	1	0
1	L5	3825	A2M	1	0
1	L5	2804	OMC	1	0
1	L5	1871	A2M	1	0
1	L5	4571	A2M	1	0
1	L5	1534	A2M	1	0
1	L5	3718	A2M	3	0
1	L5	2632	PSU	1	0
1	L5	4620	OMU	2	0
1	L5	2422	OMC	1	0
1	L5	2351	OMC	2	0
1	L5	3884	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L5	3818	UY1	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 213 ligands modelled in this entry, 196 are monoatomic - leaving 17 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	$\# Z > 2$
46	SPM	L5	5267	-	13,13,13	0.36	0	12,12,12	1.12	0
47	SPD	L5	5284	-	9,9,9	0.31	0	8,8,8	0.81	0
46	SPM	L5	5264	-	13,13,13	0.36	0	12,12,12	0.97	0
47	SPD	L5	5261	-	9,9,9	0.31	0	8,8,8	0.97	0
46	SPM	L5	5292	-	13,13,13	0.37	0	12,12,12	0.97	0
46	SPM	L5	5293	-	13,13,13	0.36	0	12,12,12	0.89	0
46	SPM	L5	5259	-	13,13,13	0.36	0	12,12,12	0.98	0
47	SPD	L5	5288	-	9,9,9	0.31	0	8,8,8	0.87	0
47	SPD	L5	5290	-	9,9,9	0.31	0	8,8,8	0.81	0
47	SPD	L5	5291	-	9,9,9	0.33	0	8,8,8	0.81	0
46	SPM	L5	5289	-	13,13,13	0.38	0	12,12,12	1.01	0
46	SPM	L5	5263	-	13,13,13	0.36	0	12,12,12	0.92	0
47	SPD	L5	5287	-	9,9,9	0.31	0	8,8,8	0.89	0
47	SPD	LN	301	-	9,9,9	0.34	0	8,8,8	0.85	0
47	SPD	L5	5285	-	9,9,9	0.32	0	8,8,8	0.90	0
47	SPD	L5	5283	-	9,9,9	0.33	0	8,8,8	0.82	0
47	SPD	L5	5286	-	9,9,9	0.32	0	8,8,8	0.82	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
46	SPM	L5	5267	-	-	4/11/11/11	-
47	SPD	L5	5284	-	-	3/7/7/7	-
46	SPM	L5	5264	-	-	3/11/11/11	-
47	SPD	L5	5261	-	-	0/7/7/7	-
46	SPM	L5	5292	-	-	4/11/11/11	-
46	SPM	L5	5293	-	-	4/11/11/11	-
46	SPM	L5	5259	-	-	3/11/11/11	-
47	SPD	L5	5288	-	-	1/7/7/7	-
47	SPD	L5	5290	-	-	2/7/7/7	-
47	SPD	L5	5291	-	-	3/7/7/7	-
46	SPM	L5	5289	-	-	5/11/11/11	-
46	SPM	L5	5263	-	-	7/11/11/11	-
47	SPD	L5	5287	-	-	3/7/7/7	-
47	SPD	LN	301	-	-	1/7/7/7	-
47	SPD	L5	5285	-	-	5/7/7/7	-
47	SPD	L5	5283	-	-	2/7/7/7	-
47	SPD	L5	5286	-	-	0/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
47	L5	5285	SPD	N6-C7-C8-C9
46	L5	5292	SPM	C7-C8-C9-N10
47	L5	5285	SPD	C3-C4-C5-N6
47	L5	5287	SPD	C3-C4-C5-N6
46	L5	5264	SPM	C2-C3-C4-N5

There are no ring outliers.

8 monomers are involved in 9 short contacts:

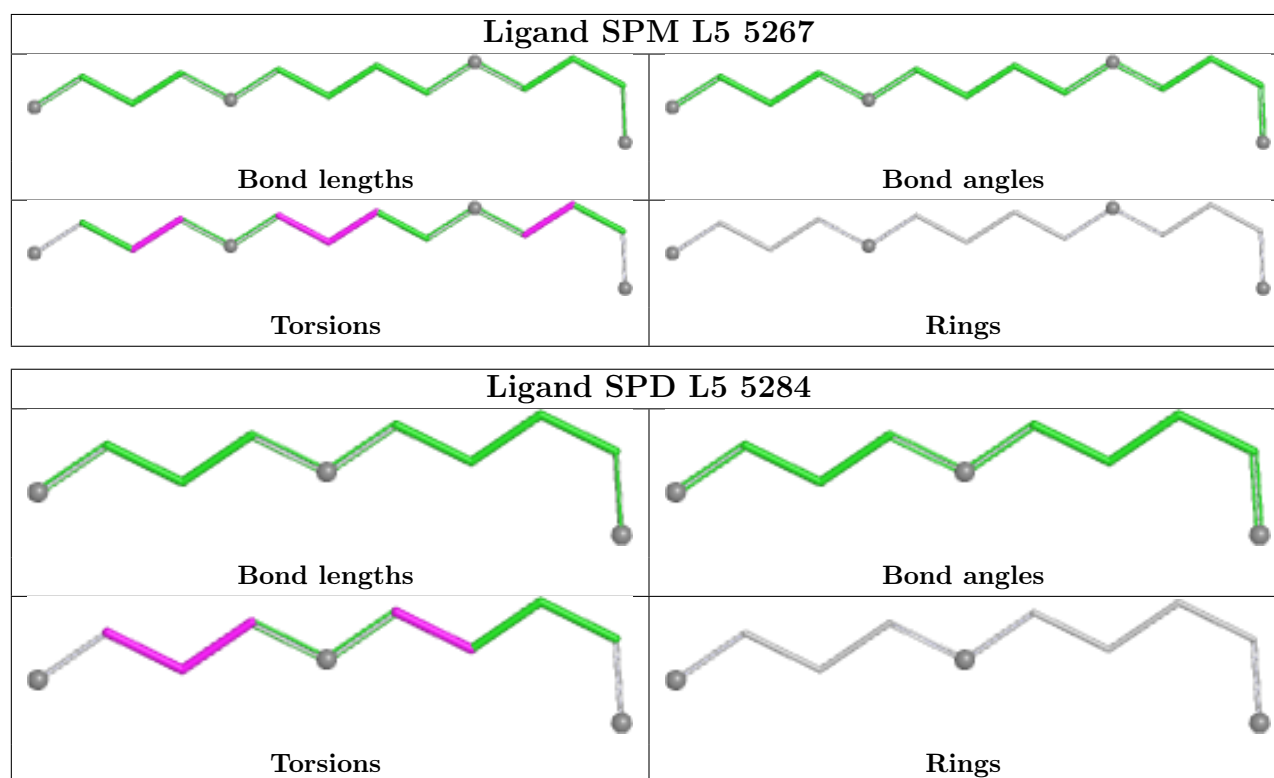
Mol	Chain	Res	Type	Clashes	Symm-Clashes
47	L5	5284	SPD	1	0
46	L5	5264	SPM	2	0
47	L5	5261	SPD	1	0
46	L5	5292	SPM	1	0

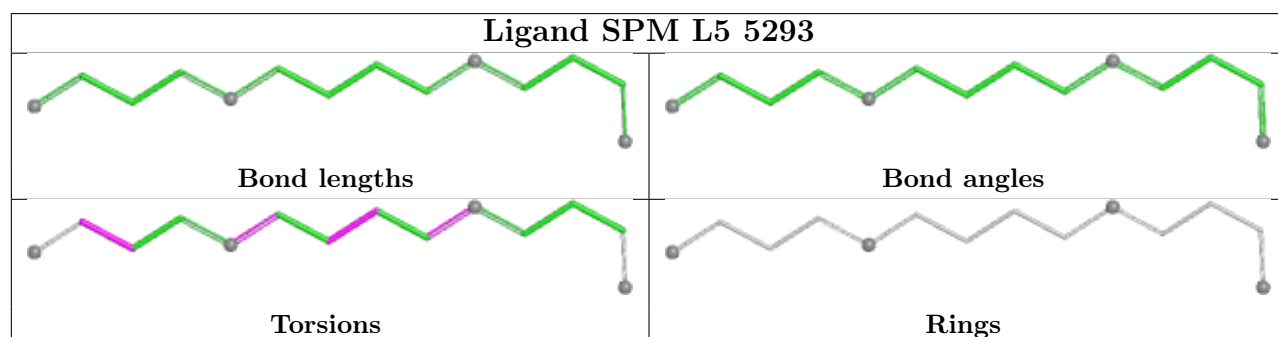
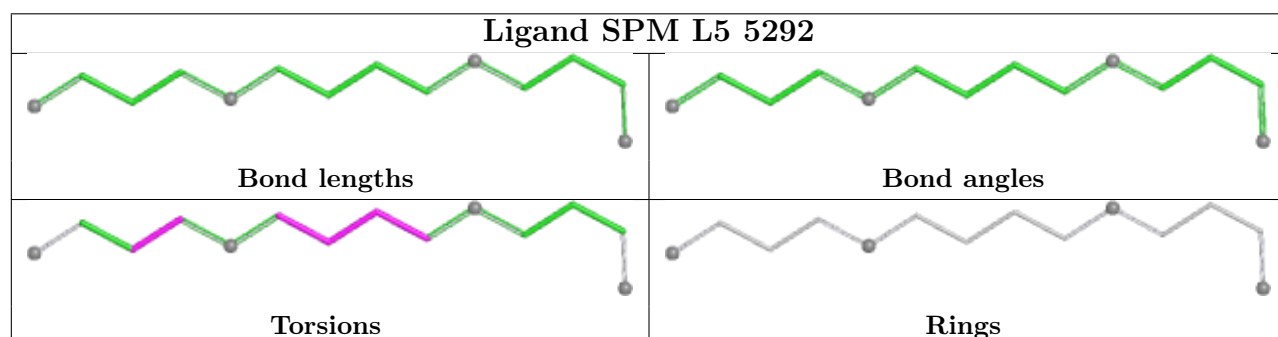
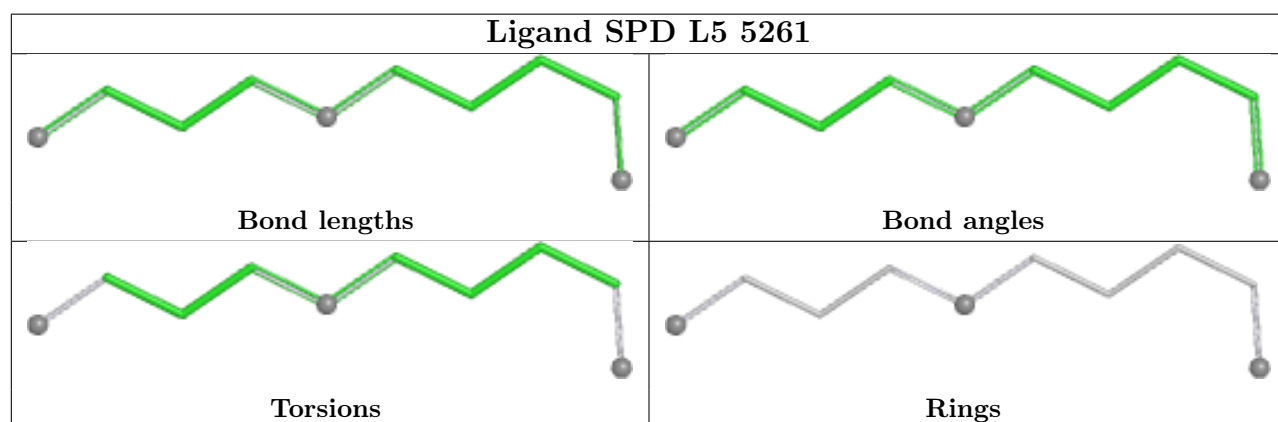
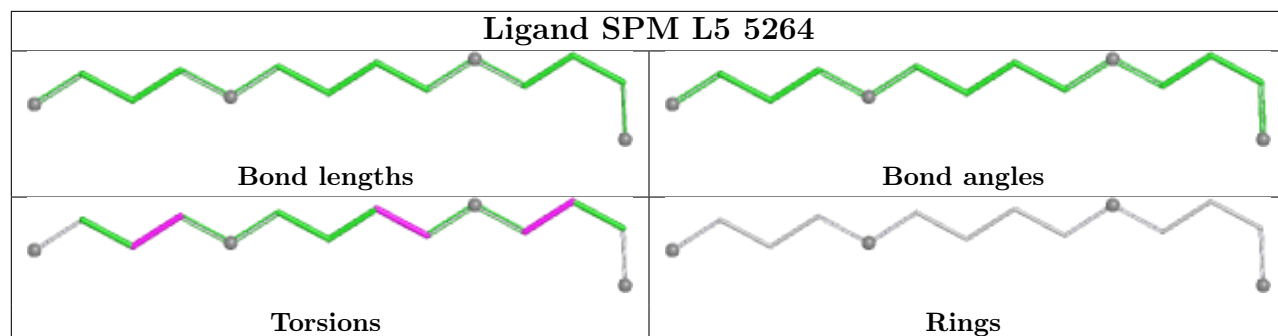
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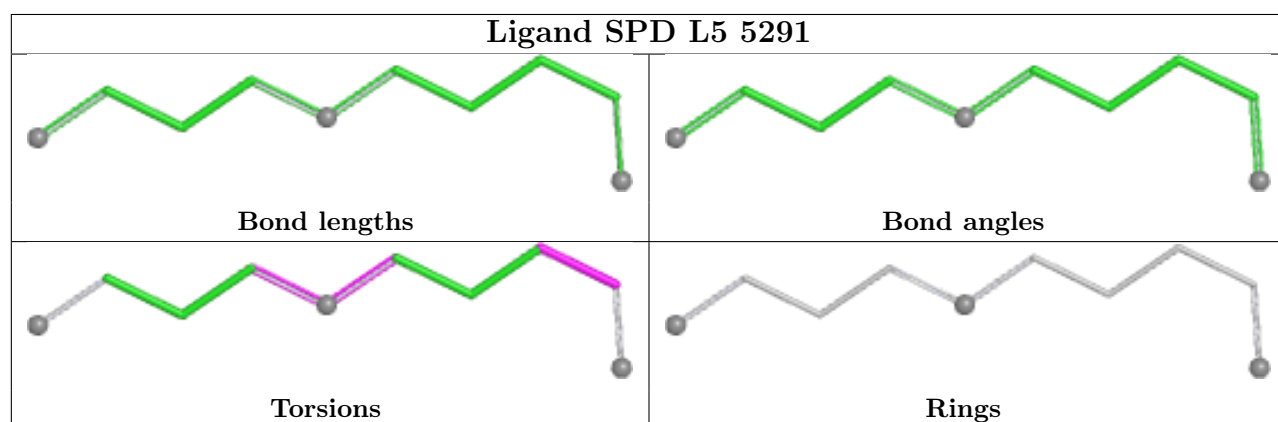
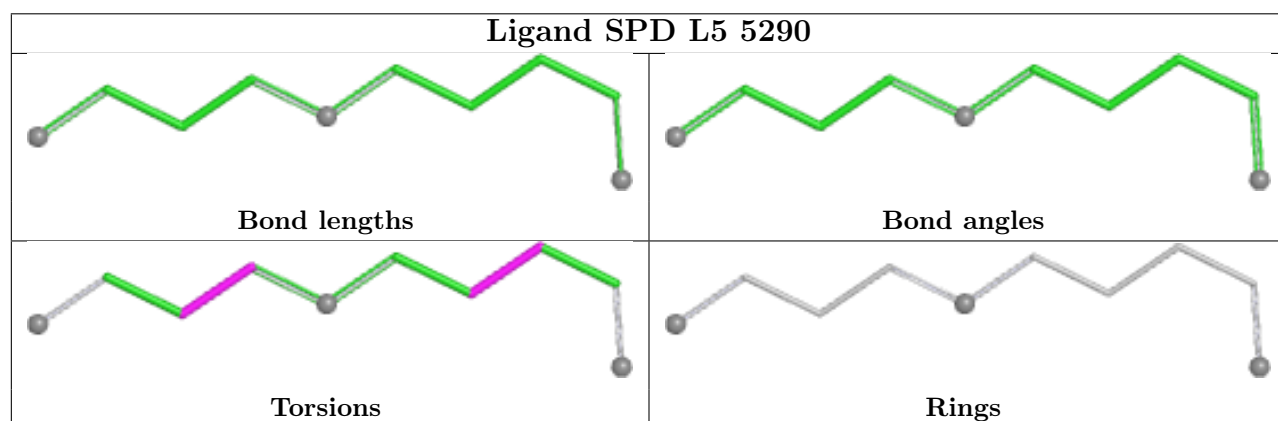
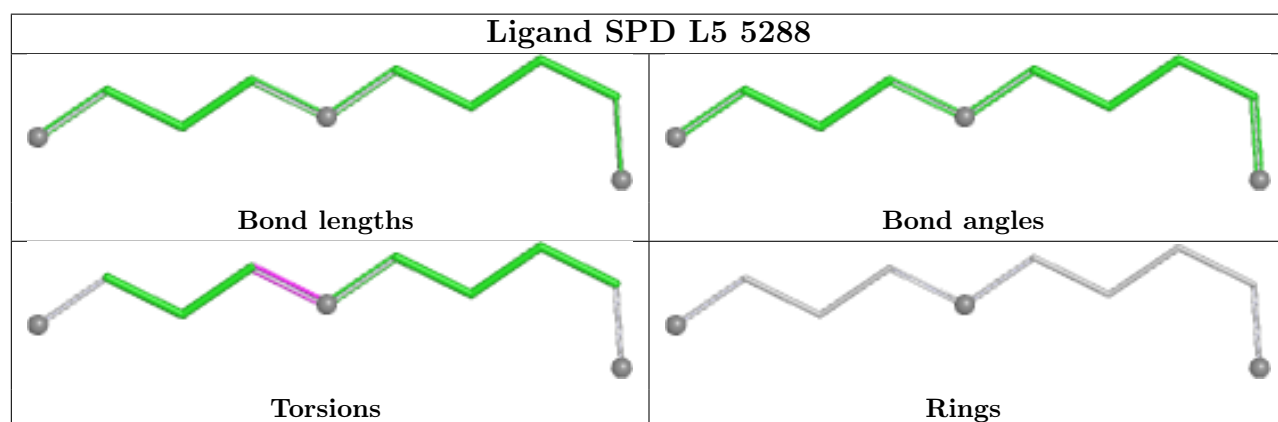
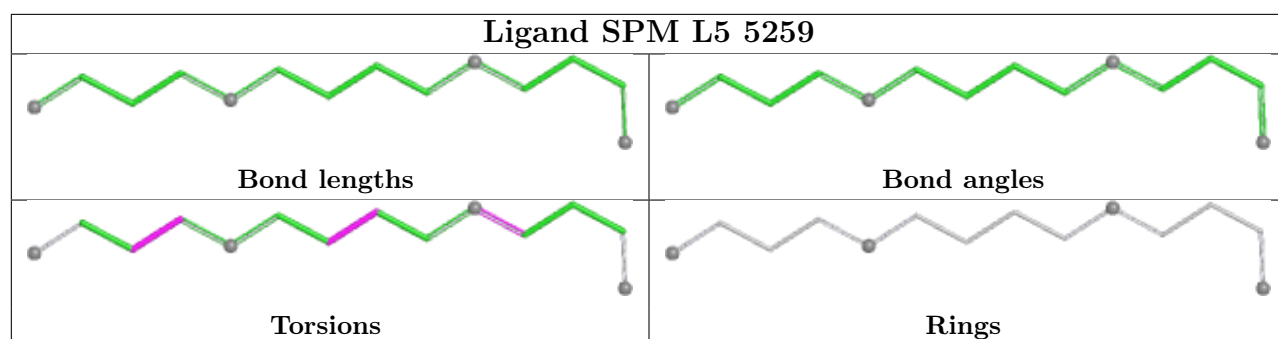
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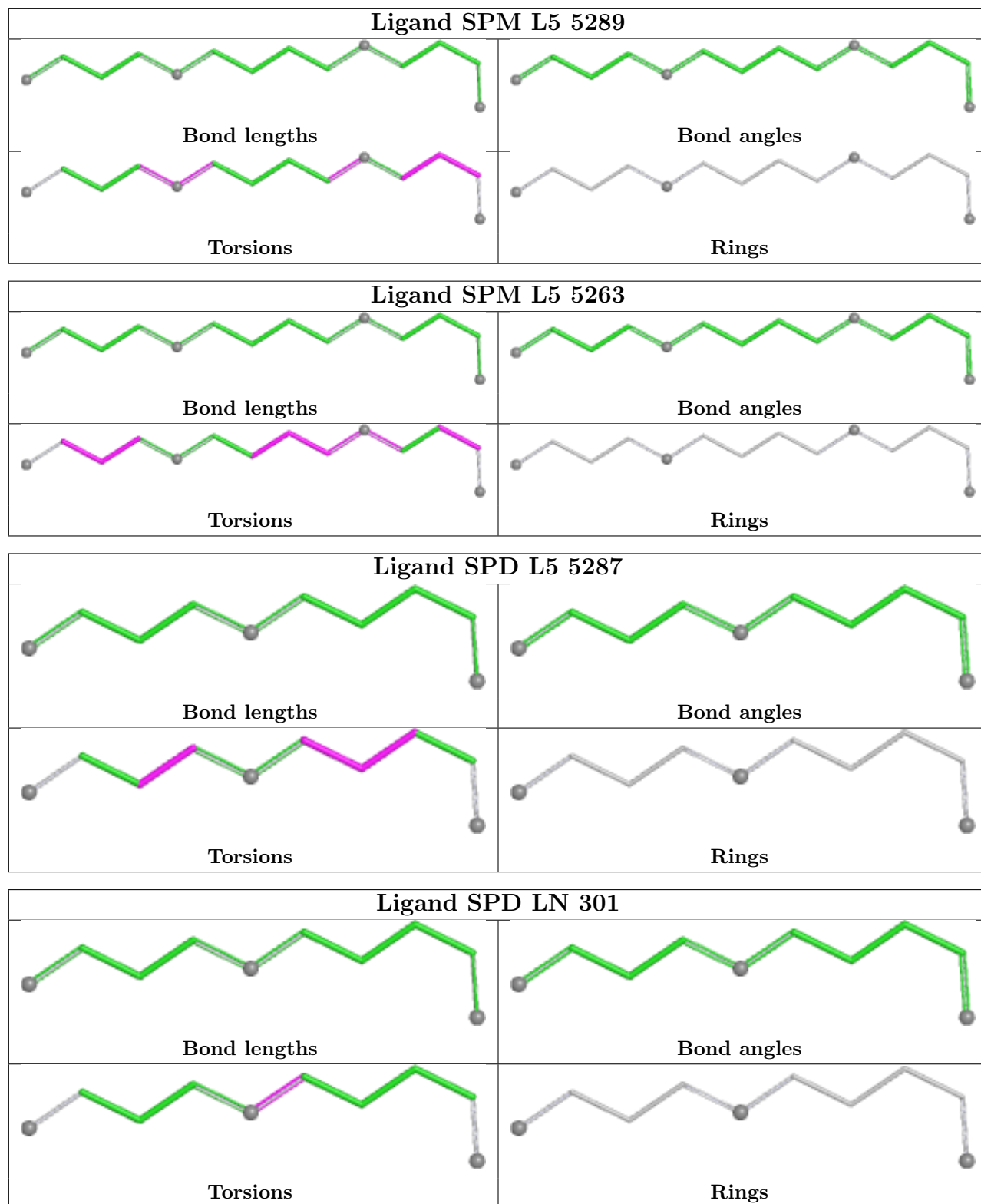
Mol	Chain	Res	Type	Clashes	Symm-Clashes
46	L5	5293	SPM	1	0
47	L5	5290	SPD	1	0
47	L5	5291	SPD	1	0
47	L5	5286	SPD	1	0

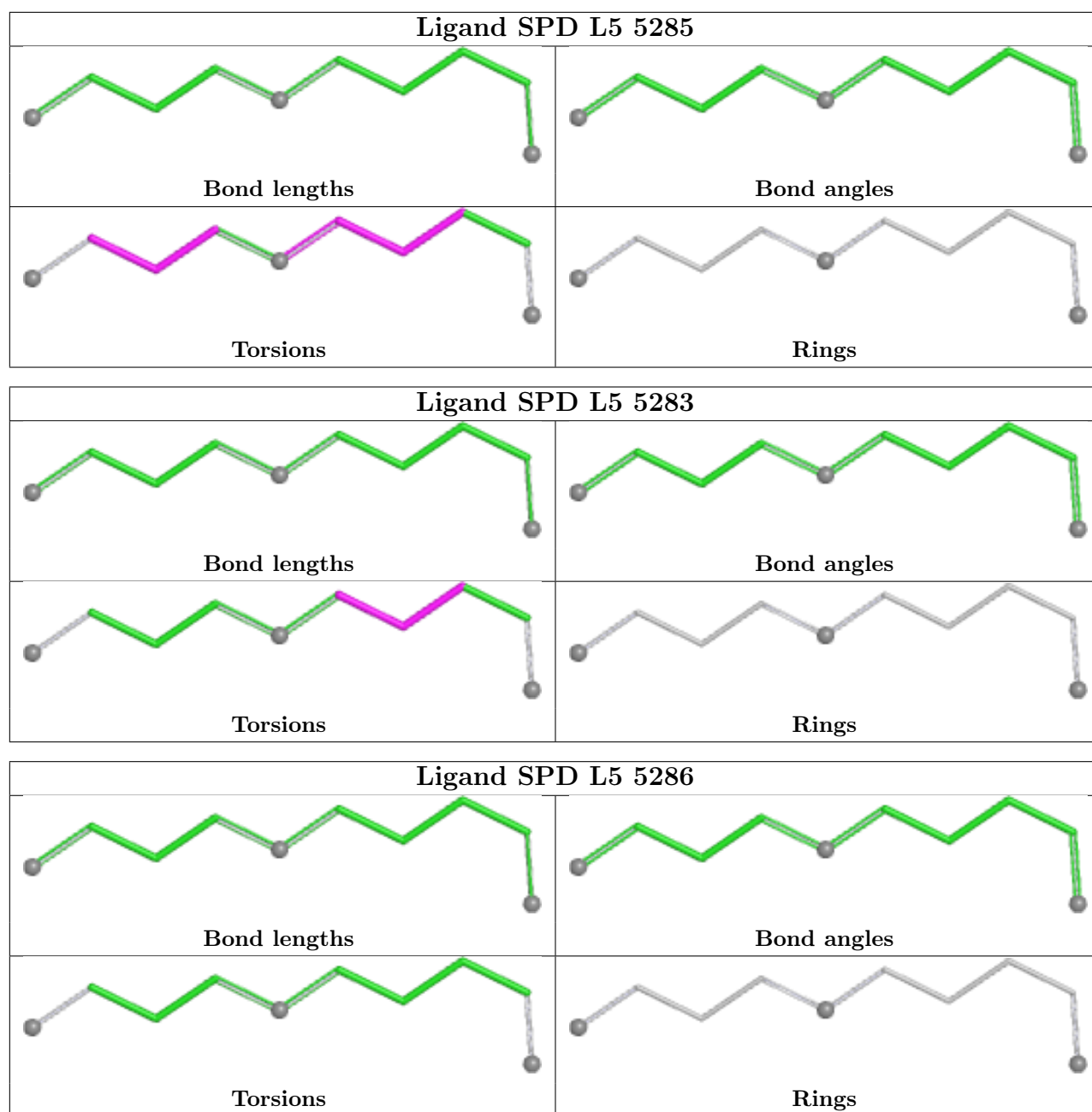
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	8

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L5	2910:G	O3'	3584:C	P	21.32
1	L5	760:G	O3'	903:C	P	16.88
1	L5	519:C	O3'	642:G	P	15.66
1	L5	4776:G	O3'	4858:C	P	15.18
1	L5	2112:G	O3'	2249:C	P	14.87

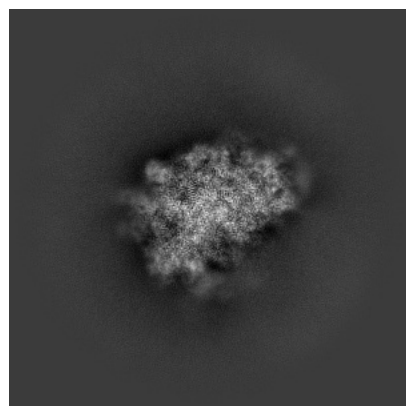
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71413. These allow visual inspection of the internal detail of the map and identification of artifacts.

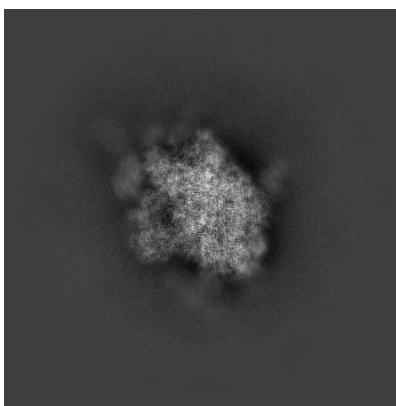
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

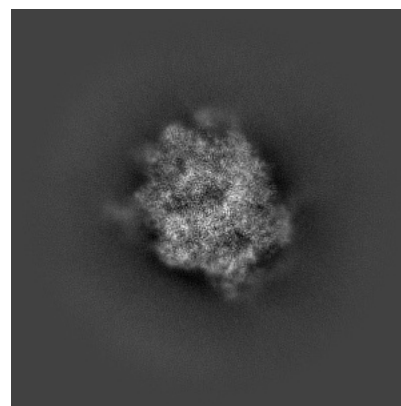
6.1.1 Primary map



X

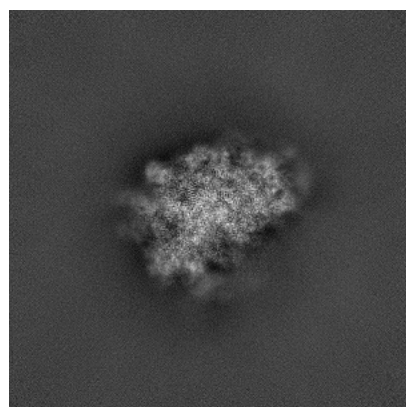


Y

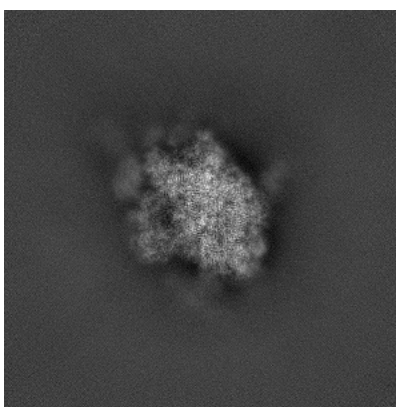


Z

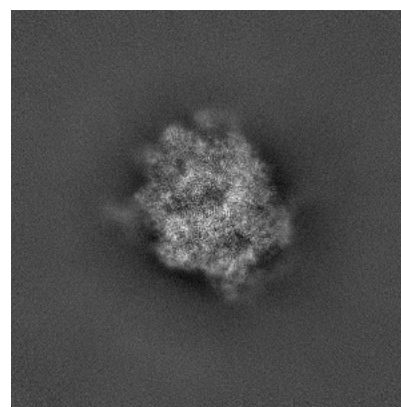
6.1.2 Raw map



X



Y

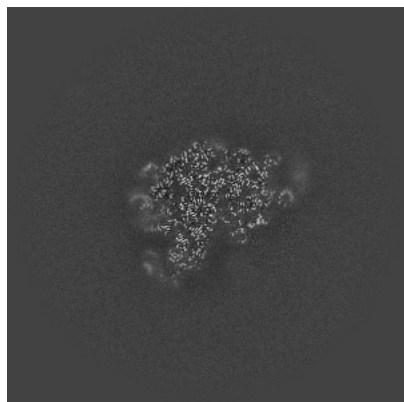


Z

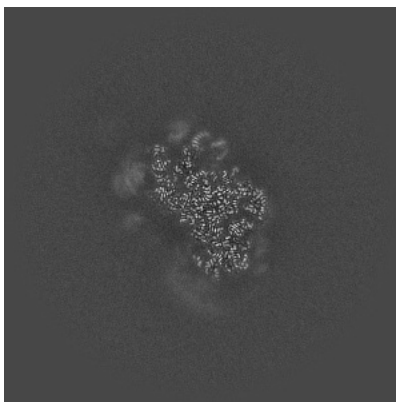
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

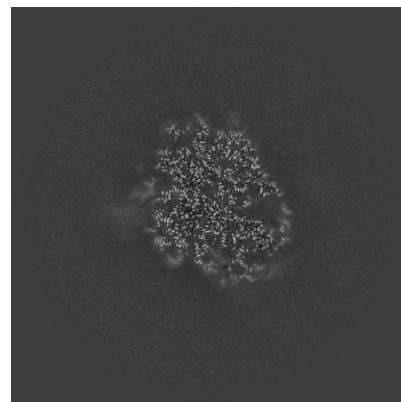
6.2.1 Primary map



X Index: 256

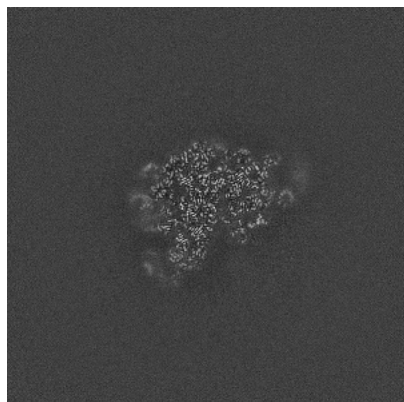


Y Index: 256

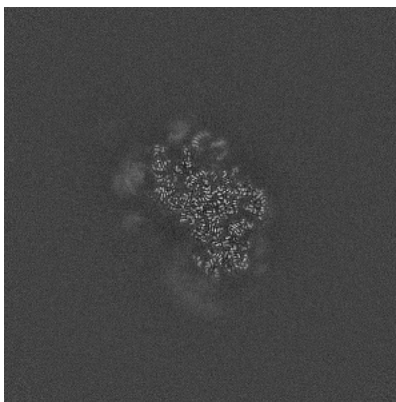


Z Index: 256

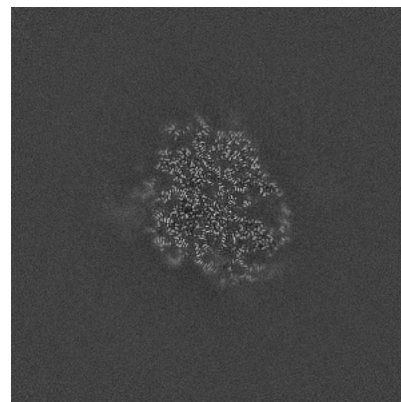
6.2.2 Raw map



X Index: 256



Y Index: 256

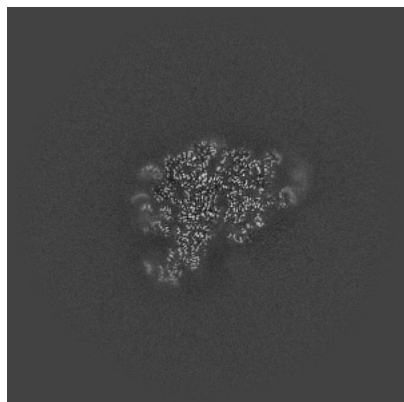


Z Index: 256

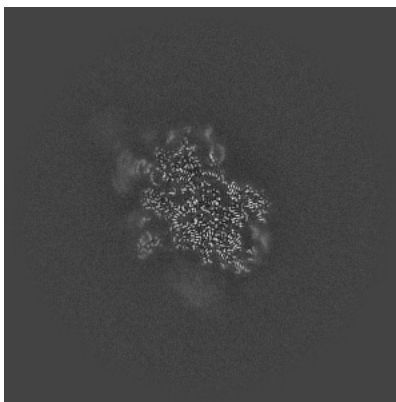
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

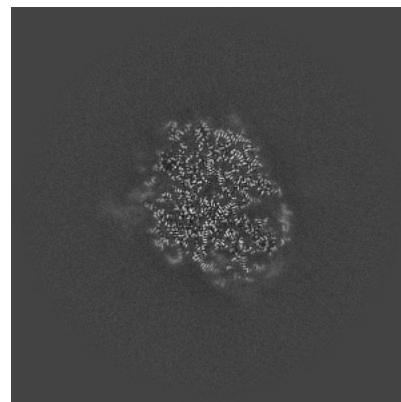
6.3.1 Primary map



X Index: 253

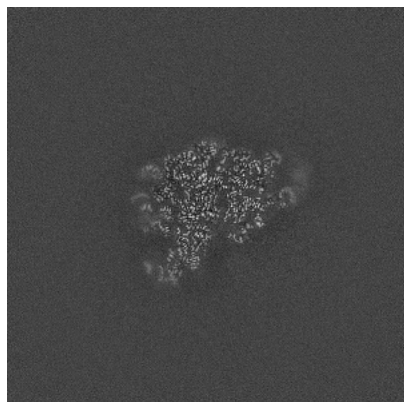


Y Index: 243

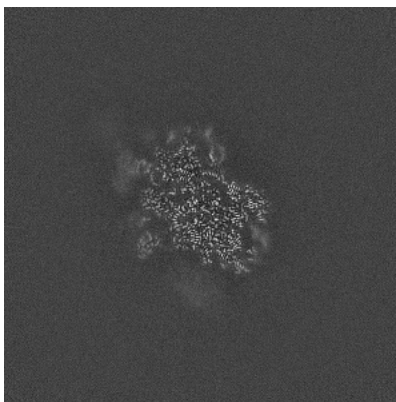


Z Index: 258

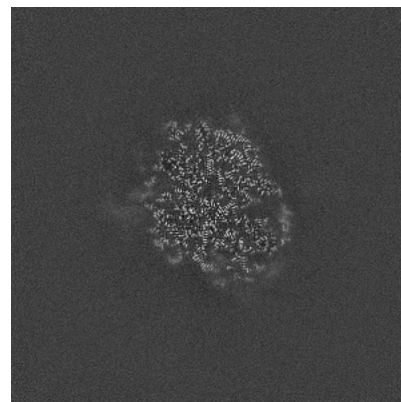
6.3.2 Raw map



X Index: 253



Y Index: 243

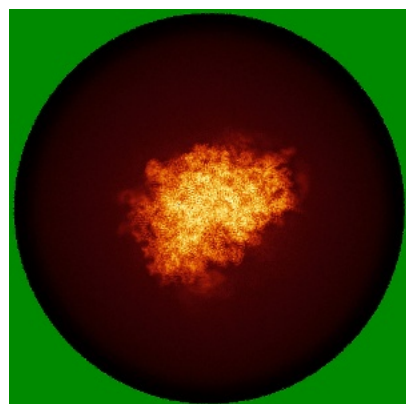


Z Index: 258

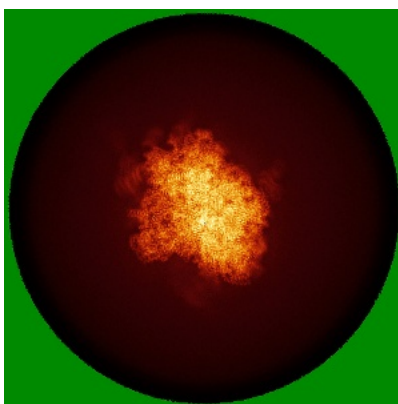
The images above show the largest variance slices of the map in three orthogonal directions.

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

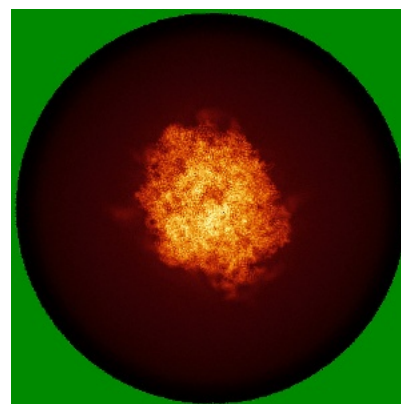
6.4.1 Primary map



X

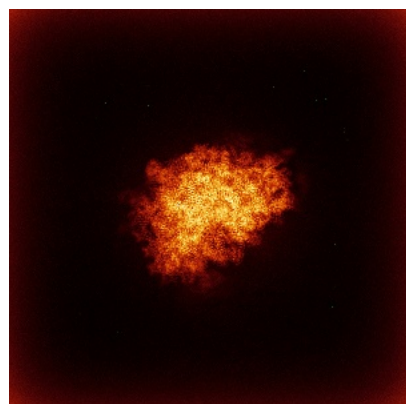


Y

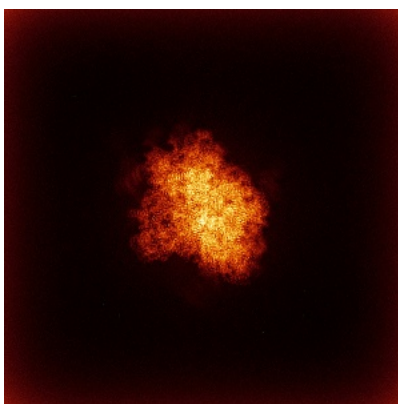


Z

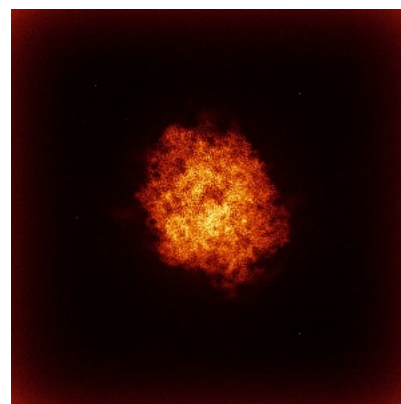
6.4.2 Raw map



X



Y

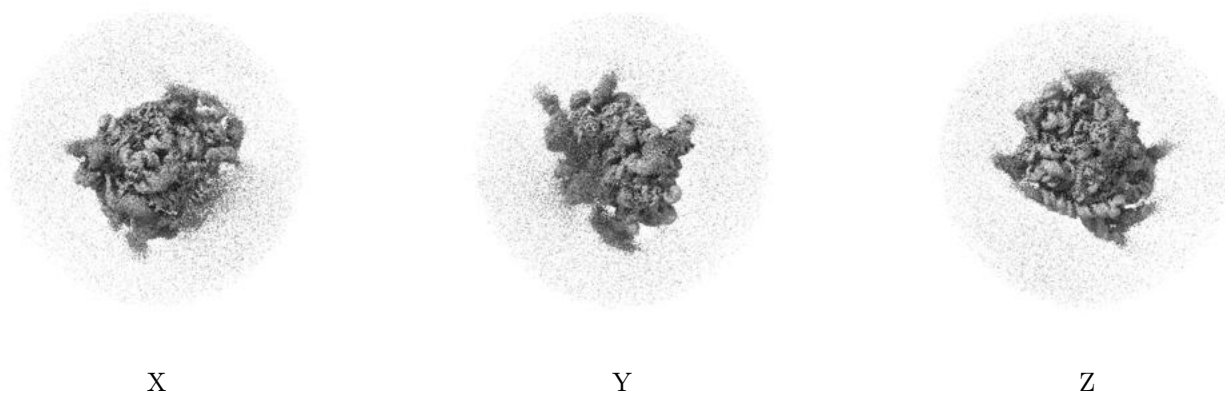


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

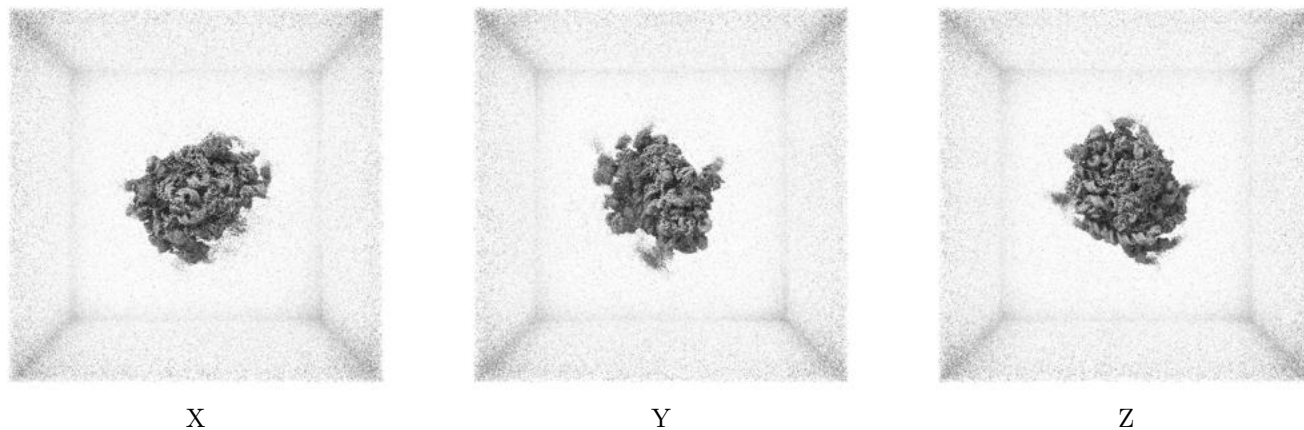
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0134. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

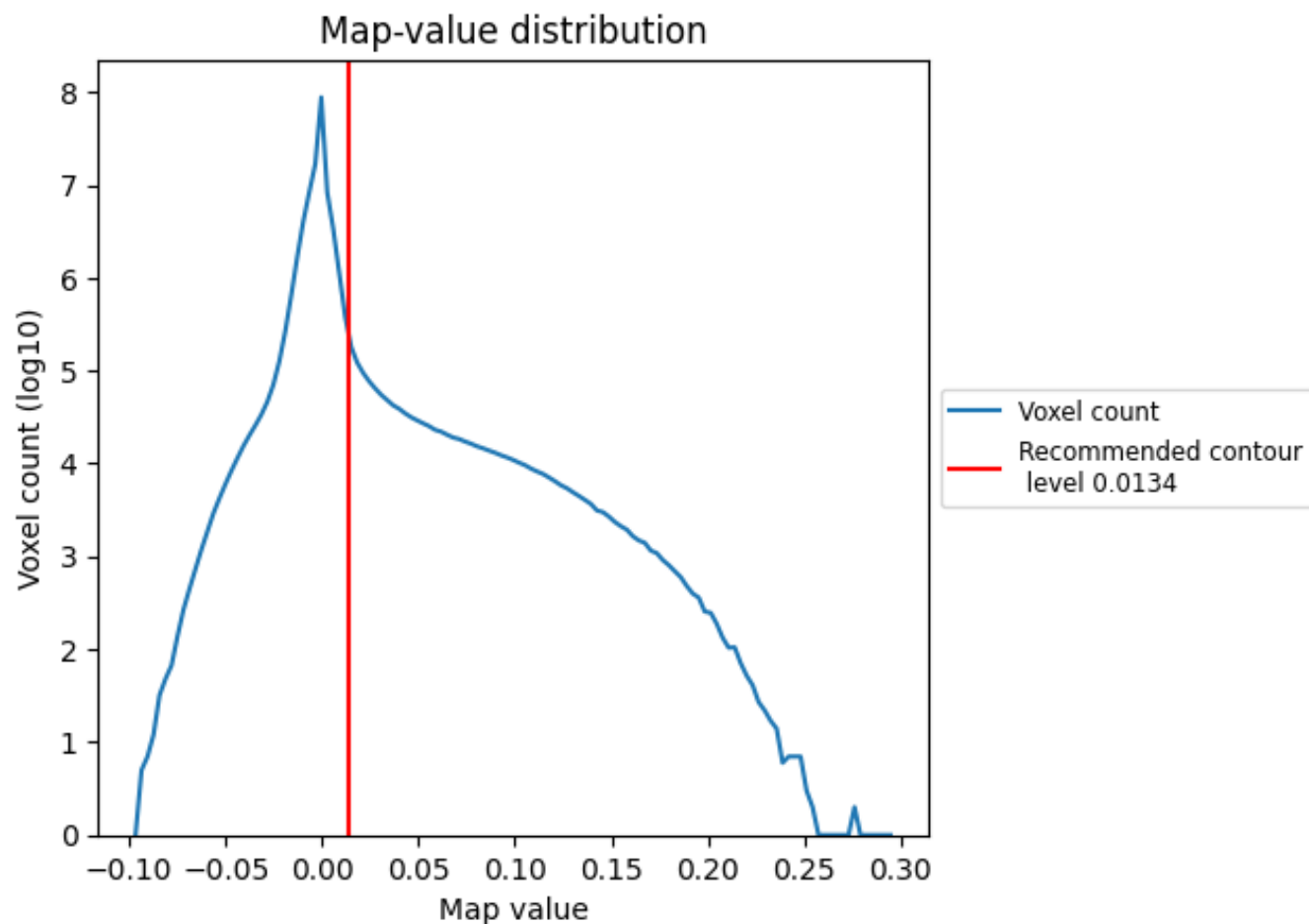
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

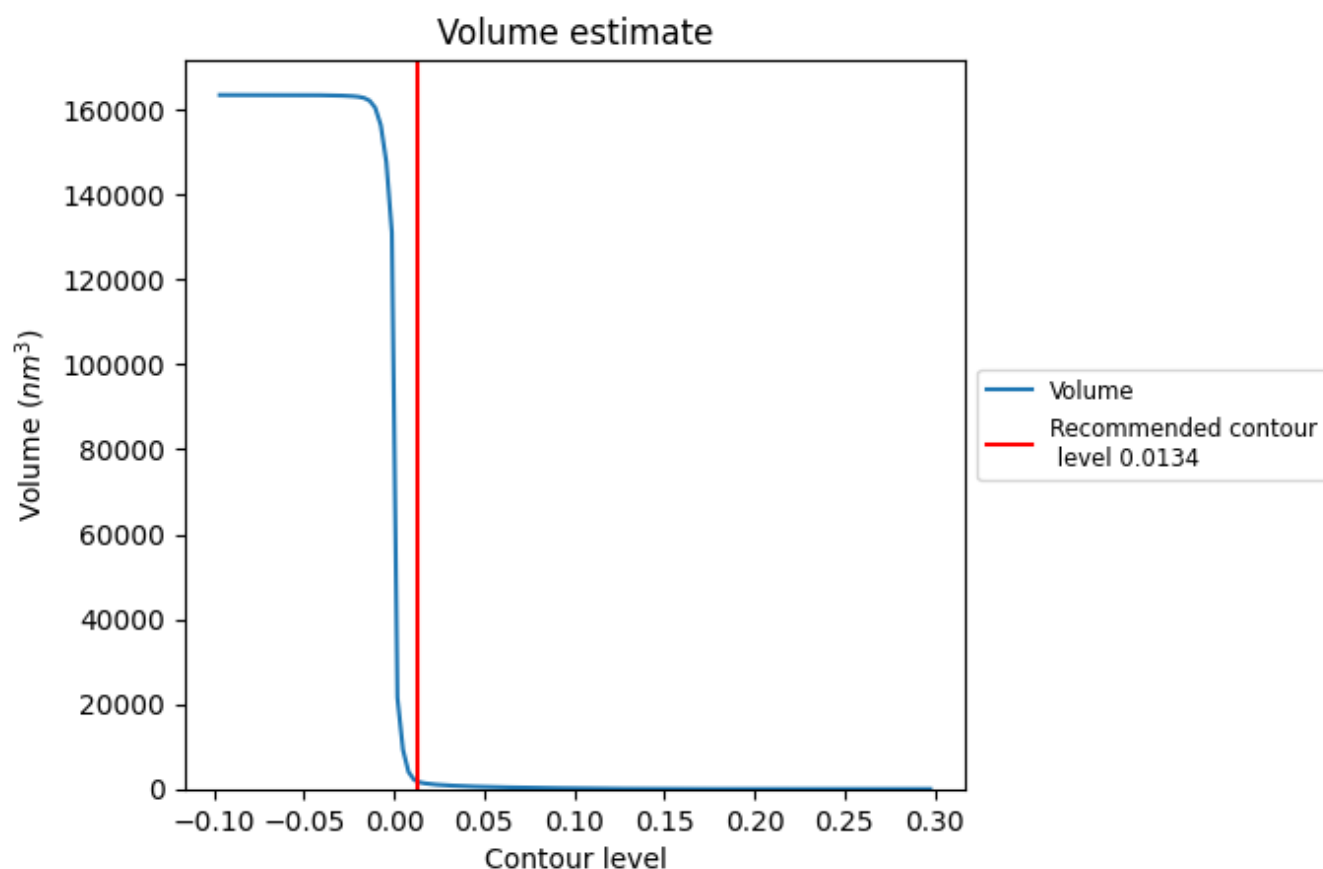
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

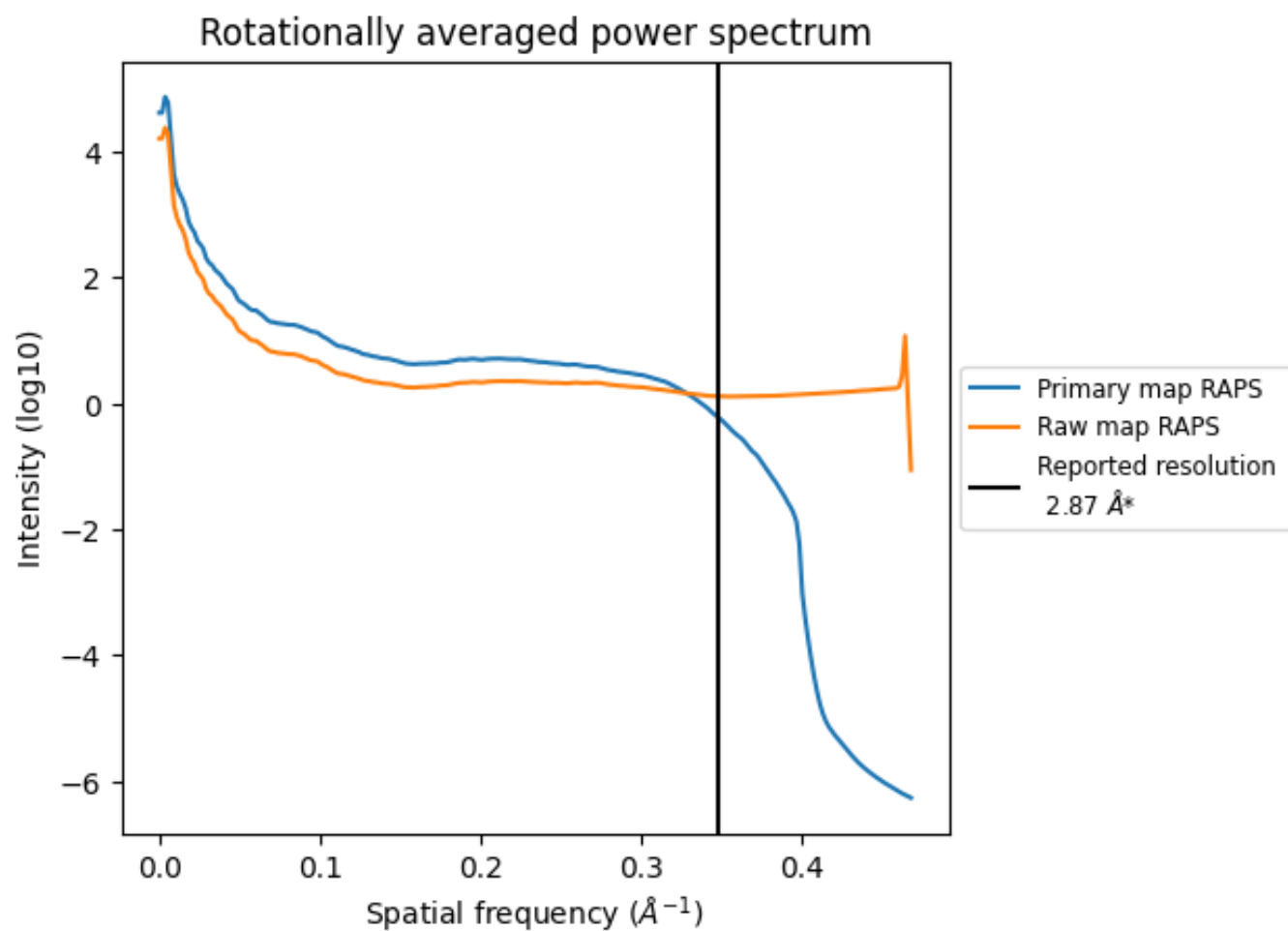
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1739 nm^3 ; this corresponds to an approximate mass of 1571 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 ⓘ

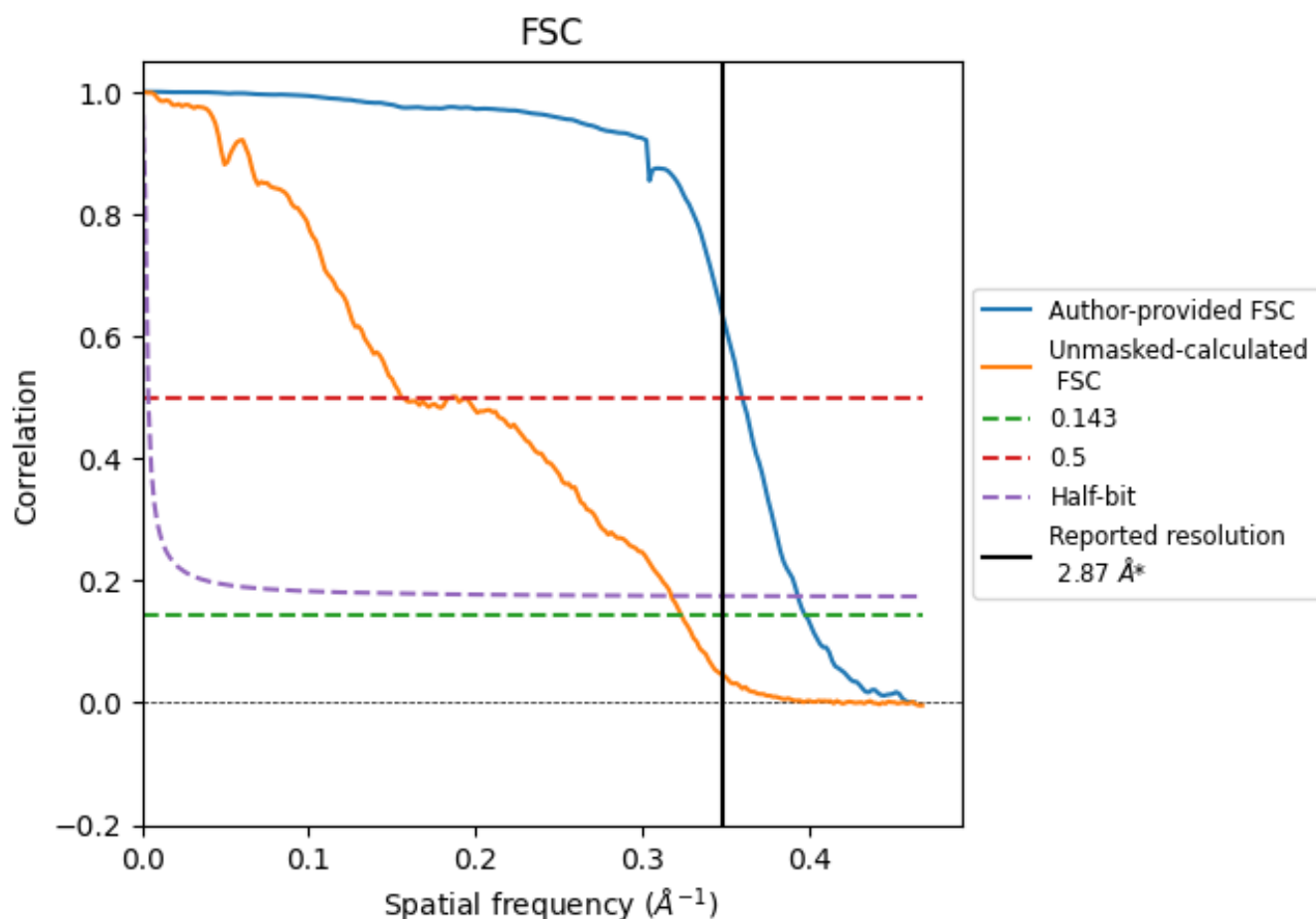


*Reported resolution corresponds to spatial frequency of 0.348 Å⁻¹

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 $0.348 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

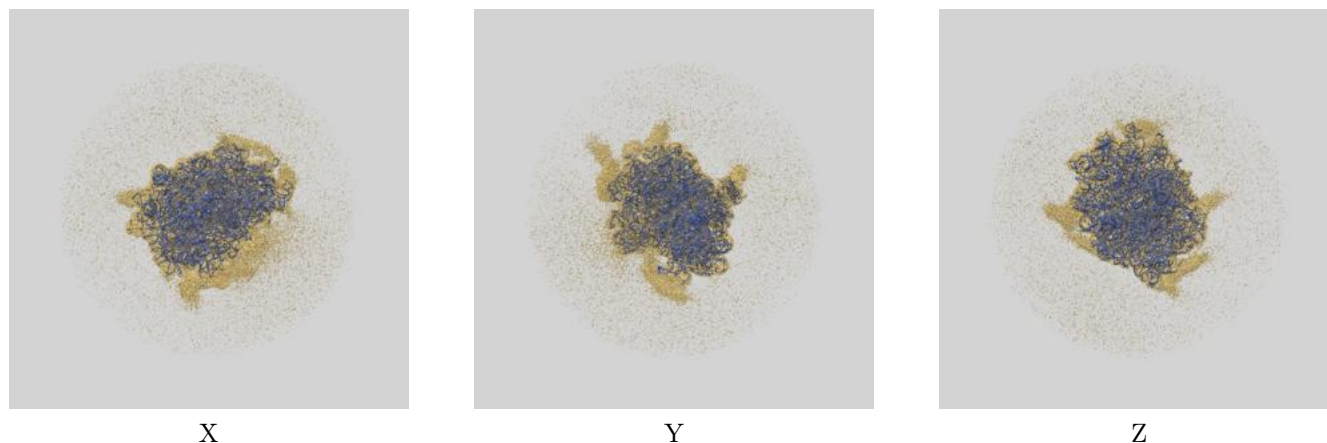
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.87	-	-
Author-provided FSC curve	2.51	2.78	2.54
Unmasked-calculated*	3.09	6.44	3.15

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.51 differs from the reported value 2.87 by more than 10 %

9 Map-model fit [i](#)

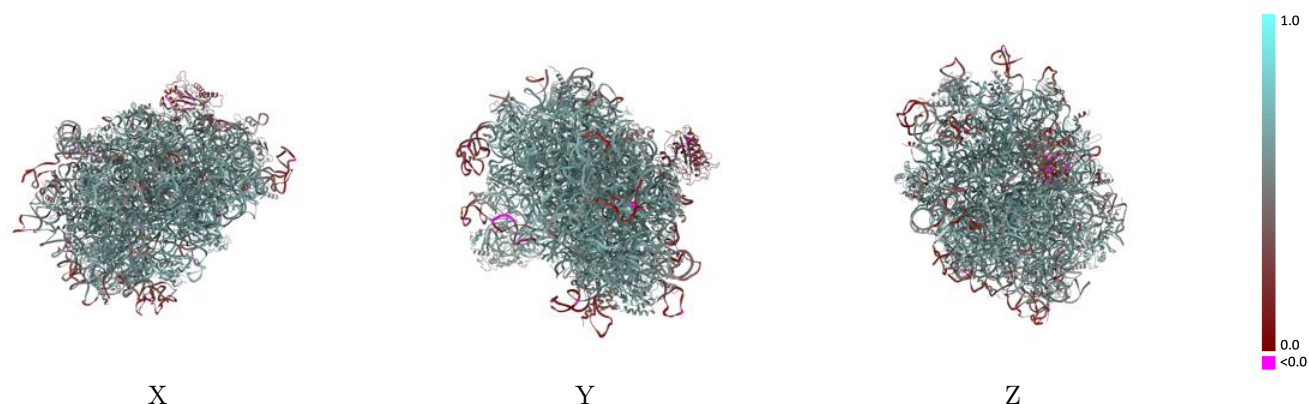
This section contains information regarding the fit between EMDB map EMD-71413 and PDB model 9P9J. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



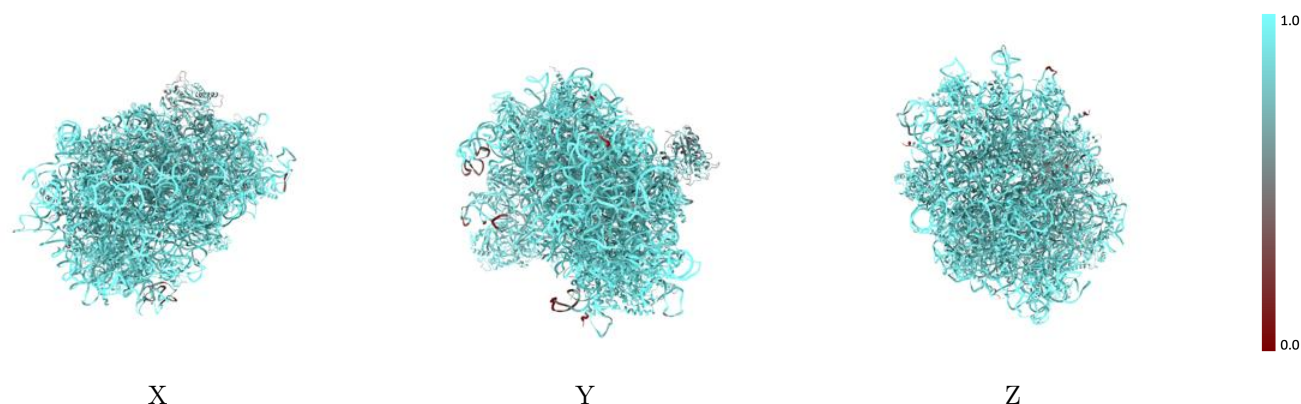
The images above show the 3D surface view of the map at the recommended contour level 0.0134 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



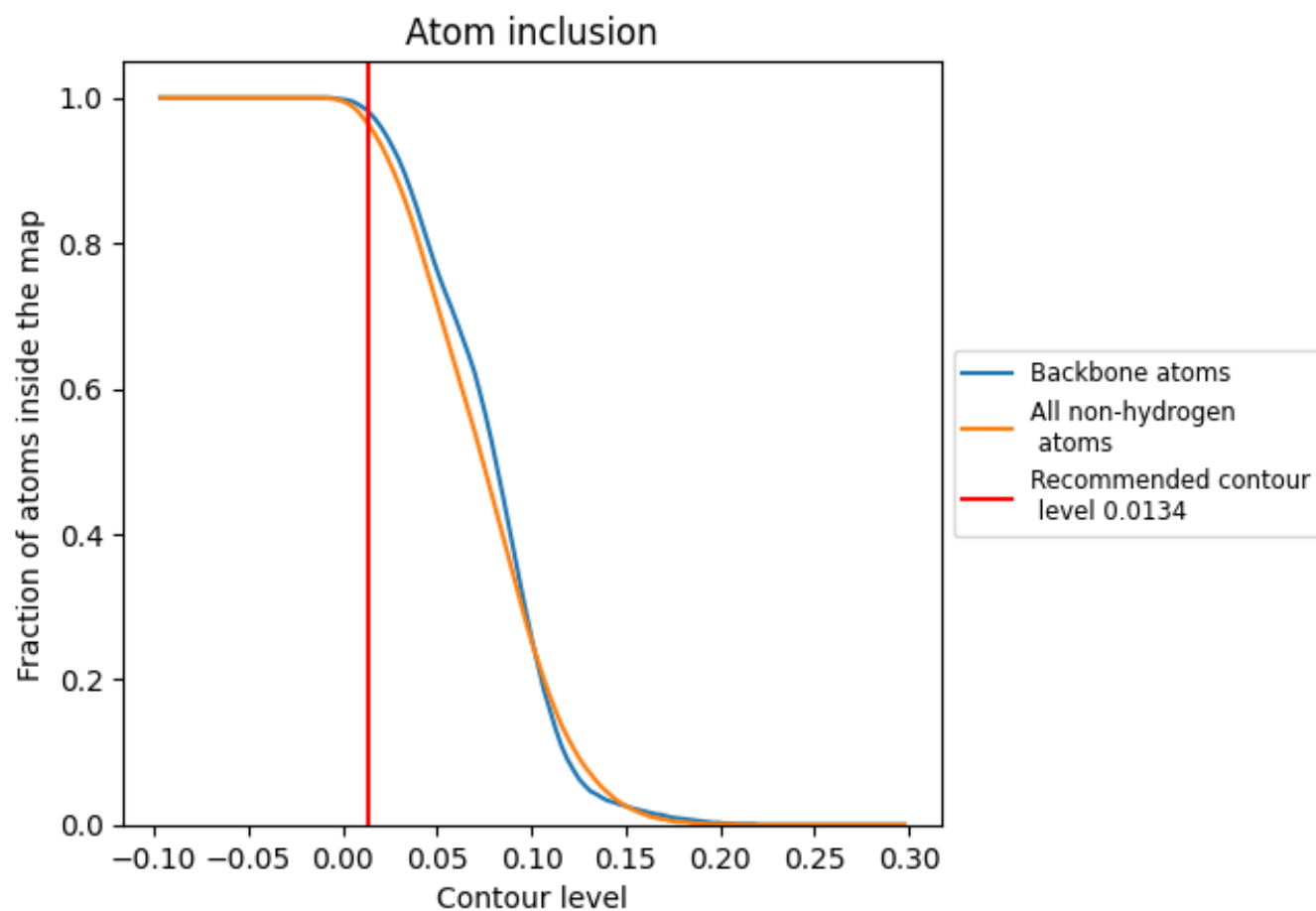
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0134).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% 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 (0.0134) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.5740
CA	 0.6940	 0.2890
L5	 0.9760	 0.5650
L7	 0.9980	 0.6190
L8	 0.9860	 0.5950
LA	 0.9800	 0.6280
LB	 0.9600	 0.6090
LC	 0.9600	 0.6110
LD	 0.9650	 0.5720
LE	 0.9290	 0.5480
LF	 0.9720	 0.6210
LG	 0.9210	 0.5500
LH	 0.9670	 0.6020
LI	 0.9320	 0.6010
LJ	 0.9430	 0.5260
LL	 0.9350	 0.5860
LM	 0.9680	 0.5960
LN	 0.9880	 0.6460
LO	 0.9660	 0.6150
LP	 0.9590	 0.6250
LQ	 0.9720	 0.6360
LR	 0.9680	 0.6080
LS	 0.9840	 0.6350
LT	 0.9480	 0.5960
LU	 0.9290	 0.4910
LV	 0.9680	 0.6160
LX	 0.9380	 0.5950
LY	 0.9580	 0.5980
LZ	 0.9750	 0.5840
La	 0.9780	 0.6320
Lb	 0.9000	 0.5440
Lc	 0.9470	 0.5640
Ld	 0.9480	 0.5930
Le	 0.9750	 0.6330
Lf	 0.9770	 0.6390



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Chain	Atom inclusion	Q-score
Lg	 0.9630	 0.6030
Lh	 0.9410	 0.5920
Li	 0.9500	 0.5890
Lj	 0.9760	 0.6370
Lk	 0.9050	 0.5290
Ll	 0.9620	 0.6160
Lm	 0.9450	 0.6090
Lo	 0.9400	 0.6090
Lp	 0.9610	 0.6150
Lr	 0.9740	 0.6170