



wwPDB EM Validation Summary Report ⓘ

Jun 26, 2026 – 03:04 AM EDT

PDB ID : 9P73 / pdb_00009p73
EMDB ID : EMD-71332
Title : In situ human eEF2-A/P-P/E state 80S ribosome
Authors : Wei, Z.; Yong, Z.
Deposited on : 2025-06-20
Resolution : 2.66 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 : 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) : 2.49

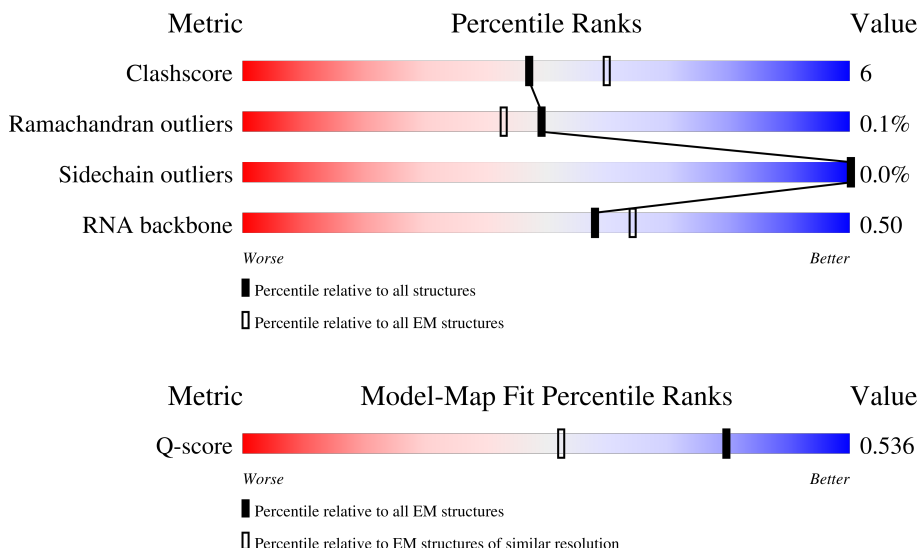
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.66 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.



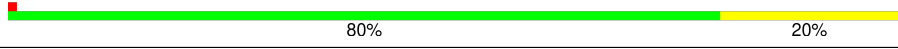
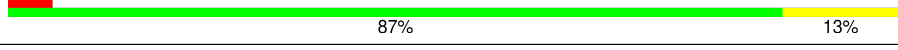
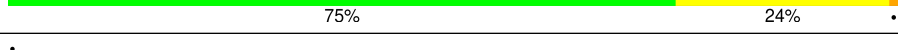
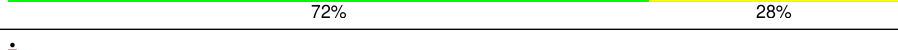
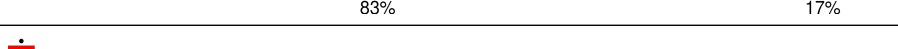
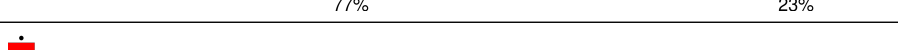
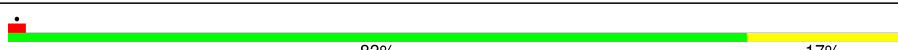
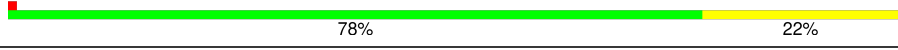
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9119 (2.16 - 3.16)

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	AP	71	
2	CB	856	
3	PE	75	

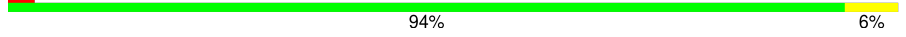
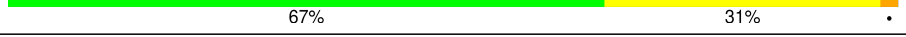
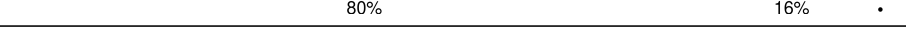
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Mol	Chain	Length	Quality of chain
4	SD	227	
5	SF	189	
6	SK	98	
7	SM	122	
8	SP	127	
9	SQ	144	
10	SR	135	
11	SS	145	
12	ST	143	
13	SU	104	
14	SZ	75	
15	Sc	64	
16	Sd	55	
17	Sf	67	
18	Sg	313	
19	SA	221	
20	SB	214	
21	SC	222	
22	SE	262	
23	SG	237	
24	SH	189	
25	SI	206	
26	SJ	185	
27	SL	153	
28	SN	150	

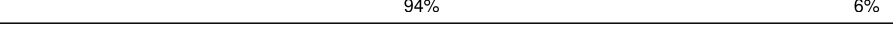
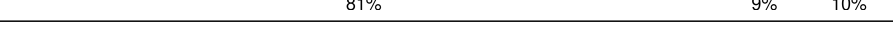
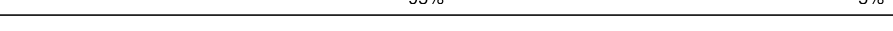
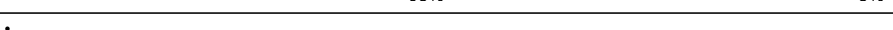
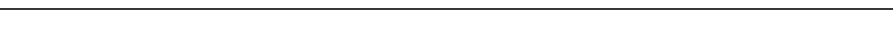
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Mol	Chain	Length	Quality of chain
29	SO	140	
30	SV	83	
31	SW	129	
32	SX	141	
33	SY	131	
34	Sa	102	
35	Sb	83	
36	S2	1740	
37	LR	187	
38	LW	124	
39	CI	31	
40	L5	3655	
41	L7	120	
42	L8	156	
43	LA	248	
44	LB	402	
45	LC	368	
46	LD	293	
47	LE	250	
48	LF	225	
49	LG	241	
50	LH	190	
51	LI	213	
52	LJ	176	
53	LL	210	

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Mol	Chain	Length	Quality of chain
54	LM	139	 88%12%
55	LN	203	 89%11%
56	LO	201	 82%18%
57	LP	153	 86%14%
58	LQ	187	 91%9%
59	LS	175	 91%9%
60	LT	159	 90%10%
61	LU	101	 82%18%
62	LV	131	 91%9%
63	LX	120	 89%11%
64	LY	134	 85%15%
65	LZ	135	 87%13%
66	La	147	 94%6%
67	Lb	121	 81%9%10%
68	Lc	98	 79%21%
69	Ld	107	 85%15%
70	Le	128	 91%9%
71	Lf	109	 95%5%
72	Lg	114	 95%5%
73	Lh	122	 89%11%
74	Li	102	 95%5%
75	Lj	86	 86%14%
76	Lk	69	 86%14%
77	Ll	50	 80%20%
78	Lm	52	 90%10%

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Mol	Chain	Length	Quality of chain
79	Ln	24	 79%21%
80	Lo	105	 83%17%
81	Lp	91	 90%10%
82	Lr	125	 88%12%
83	Ls	196	 25%79%21%
84	Lt	157	 10%64%21%15%
85	CH	132	 5%80%20%

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 227131 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 A/P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AP	71	Total	C	N	O	P	0	0
			1514	677	275	492	70		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AP	3	C	U	conflict	GB 2583636049
AP	?	-	U	deletion	GB 2583636049
AP	?	-	U	deletion	GB 2583636049

- Molecule 2 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

- Molecule 3 is a RNA chain called P/E site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	PE	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 4 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 5 is a protein called 40S ribosomal protein S5.

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

- Molecule 6 is a protein called 40S ribosomal protein S10.

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

- Molecule 7 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 8 is a protein called 40S ribosomal protein S15.

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

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 10 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 11 is a protein called 40S ribosomal protein S18.

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

- Molecule 12 is a protein called 40S ribosomal protein S19.

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

- Molecule 13 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 14 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 15 is a protein called 40S ribosomal protein S28.

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

- Molecule 16 is a protein called 40S ribosomal protein S29.

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

- Molecule 17 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 18 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 19 is a protein called 40S ribosomal protein SA.

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

- Molecule 20 is a protein called 40S ribosomal protein S3a.

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

- Molecule 21 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SC	220	Total	C	N	O	S	0	0
			1707	1104	293	300	10		

- Molecule 22 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 23 is a protein called 40S ribosomal protein S6.

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

- Molecule 24 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 25 is a protein called 40S ribosomal protein S8.

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

- Molecule 26 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 27 is a protein called 40S ribosomal protein S11.

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

- Molecule 28 is a protein called 40S ribosomal protein S13.

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

- Molecule 29 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SO	137	Total	C	N	O	S	0	0
			1024	627	200	191	6		

- Molecule 30 is a protein called Small ribosomal subunit protein eS21.

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

- Molecule 31 is a protein called 40S ribosomal protein S15a.

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

- Molecule 32 is a protein called 40S ribosomal protein S23.

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

- Molecule 33 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 34 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 35 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 36 is a RNA chain called 18S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
36	S2	1740	Total	C	N	O	P	0	0
			36952	16508	6600	12105	1739		

- Molecule 37 is a protein called 60S ribosomal protein L19.

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

- Molecule 38 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LW	116	Total	C	N	O	S	0	0
			945	592	193	156	4		

- Molecule 39 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	CI	31	Total	C	N	O	S	0	0
			247	153	55	38	1		

- Molecule 40 is a RNA chain called 28S rRNA.

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

- Molecule 41 is a RNA chain called 5S rRNA.

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

- Molecule 42 is a RNA chain called 5.8S rRNA.

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

- Molecule 43 is a protein called 60S ribosomal protein L8.

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

- Molecule 44 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 45 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 46 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 47 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 48 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 49 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 50 is a protein called 60S ribosomal protein L9.

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

- Molecule 51 is a protein called Ribosomal protein uL16-like.

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

- Molecule 52 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LJ	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 53 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 54 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 55 is a protein called 60S ribosomal protein L15.

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

- Molecule 56 is a protein called 60S ribosomal protein L13a.

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

- Molecule 57 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 58 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 59 is a protein called 60S ribosomal protein L18a.

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

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

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

- Molecule 61 is a protein called Heparin-binding protein HBp15.

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

- Molecule 62 is a protein called 60S ribosomal protein L23.

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

- Molecule 63 is a protein called 60S ribosomal protein L23a.

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

- Molecule 64 is a protein called 60S ribosomal protein L26.

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

- Molecule 65 is a protein called 60S ribosomal protein L27.

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

- Molecule 66 is a protein called 60S ribosomal protein L27a.

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

- Molecule 67 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 68 is a protein called 60S ribosomal protein L30.

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

- Molecule 69 is a protein called 60S ribosomal protein L31.

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

- Molecule 70 is a protein called 60S ribosomal protein L32.

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

- Molecule 71 is a protein called 60S ribosomal protein L35a.

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

- Molecule 72 is a protein called 60S ribosomal protein L34.

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

- Molecule 73 is a protein called 60S ribosomal protein L35.

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

- Molecule 74 is a protein called 60S ribosomal protein L36.

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

- Molecule 75 is a protein called 60S ribosomal protein L37.

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

- Molecule 76 is a protein called 60S ribosomal protein L38.

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

- Molecule 77 is a protein called 60S ribosomal protein L39.

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

- Molecule 78 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 79 is a protein called 60S ribosomal protein L41.

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

- Molecule 80 is a protein called 60S ribosomal protein L36a.

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

- Molecule 81 is a protein called 60S ribosomal protein L37a.

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

- Molecule 82 is a protein called 60S ribosomal protein L28.

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

- Molecule 83 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 84 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Lt	134	Total	C	N	O	S	0	0
			998	626	180	189	3		

- Molecule 85 is a protein called Endothelial differentiation-related factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	CH	132	Total	C	N	O		0	0
			1018	625	199	194			

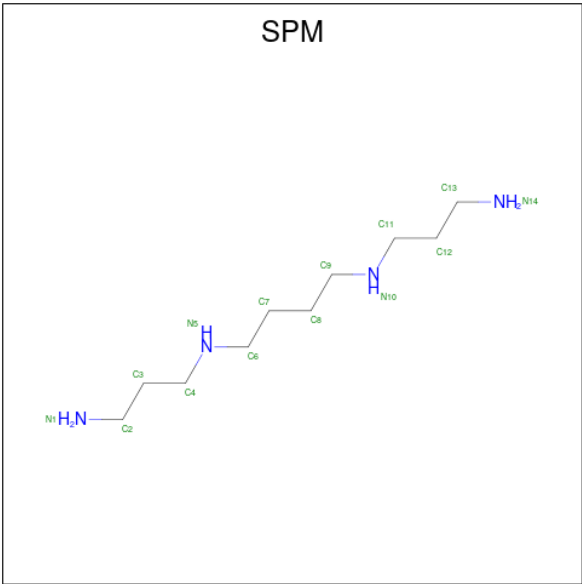
- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
86	SS	1	Total	Mg	0
			1	1	
86	SG	1	Total	Mg	0
			1	1	
86	S2	25	Total	Mg	0
			25	25	
86	L5	178	Total	Mg	0
			178	178	
86	L7	3	Total	Mg	0
			3	3	
86	L8	4	Total	Mg	0
			4	4	
86	LA	1	Total	Mg	0
			1	1	
86	LB	1	Total	Mg	0
			1	1	
86	LI	1	Total	Mg	0
			1	1	
86	LP	1	Total	Mg	0
			1	1	
86	LV	1	Total	Mg	0
			1	1	
86	Le	1	Total	Mg	0
			1	1	

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 88 is SPERMINE (CCD ID: SPM) (formula: C₁₀H₂₆N₄) (labeled as "Ligand of Interest" by depositor).



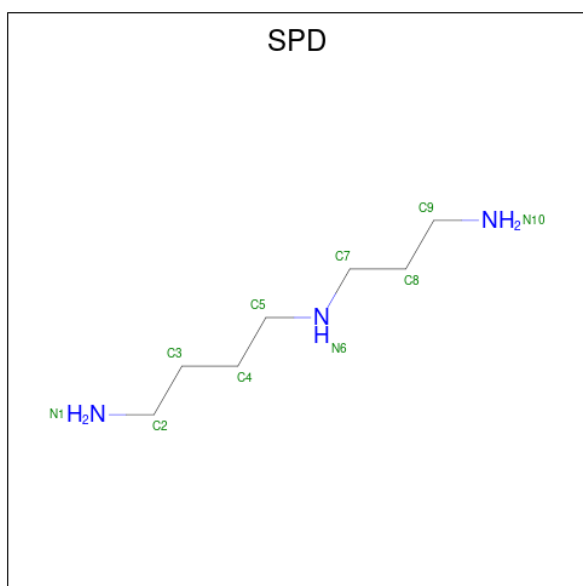
Mol	Chain	Residues	Atoms			AltConf
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	

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

- Molecule 89 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$) (labeled as "Ligand of Interest" by depositor).



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

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Mol	Chain	Residues	Atoms			AltConf
89	L8	1	Total	C	N	0
			10	7	3	
89	LN	1	Total	C	N	0
			10	7	3	

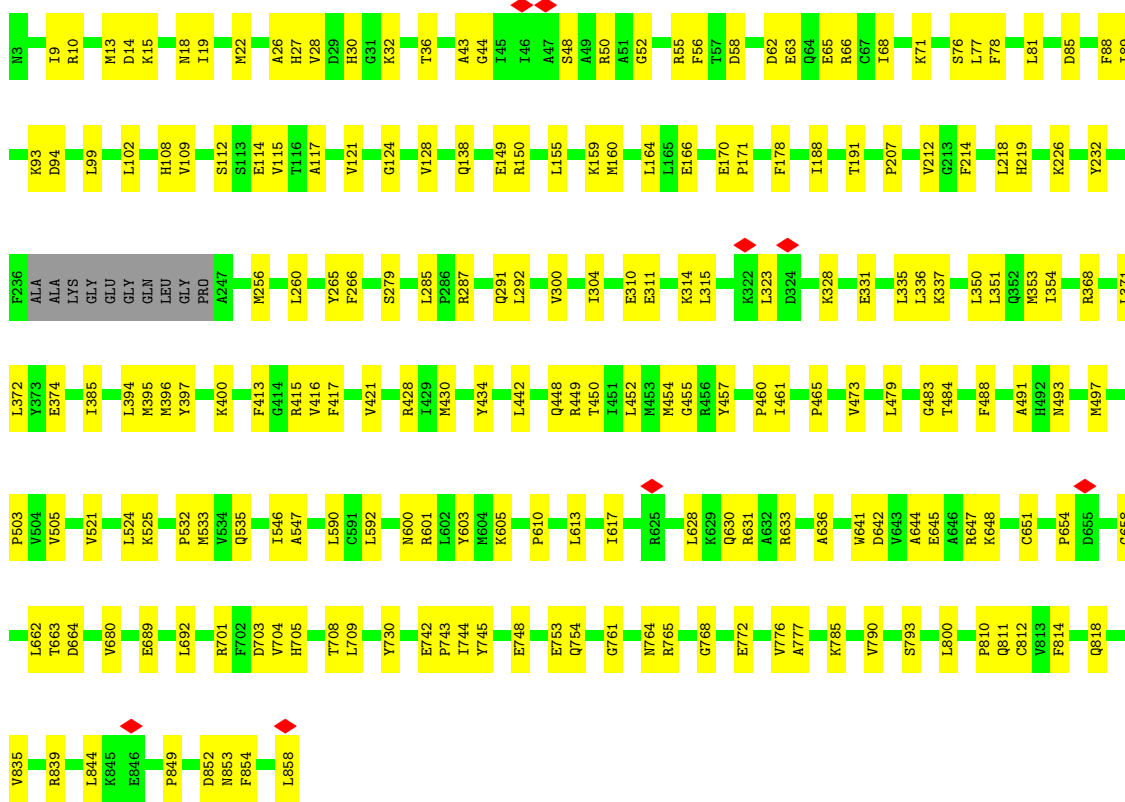
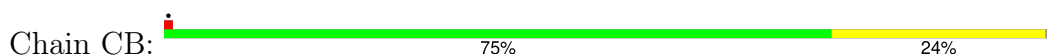
3 Residue-property plots

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: A/P site tRNA

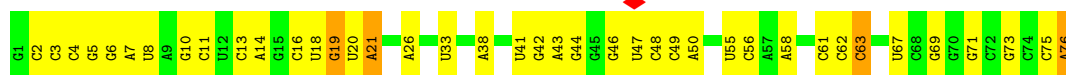


- Molecule 2: Elongation factor 2



- Molecule 3: P/E site tRNA

Chain PE:  47% 48% 5%



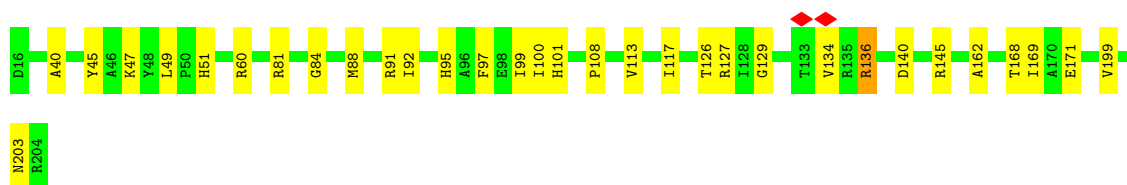
- Molecule 4: Small ribosomal subunit protein uS3

Chain SD:  82% 18%



- Molecule 5: 40S ribosomal protein S5

Chain SF:  83% 16%



- Molecule 6: 40S ribosomal protein S10

Chain SK:  80% 20%



- Molecule 7: Small ribosomal subunit protein eS12

Chain SM:  5% 87% 13%

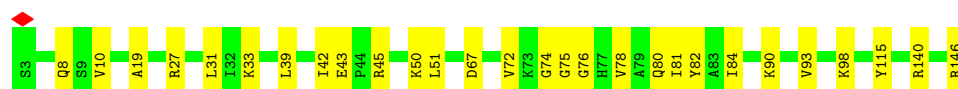
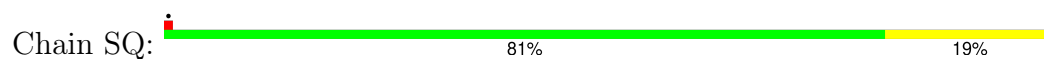


- Molecule 8: 40S ribosomal protein S15

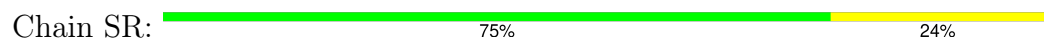
Chain SP:  81% 19%



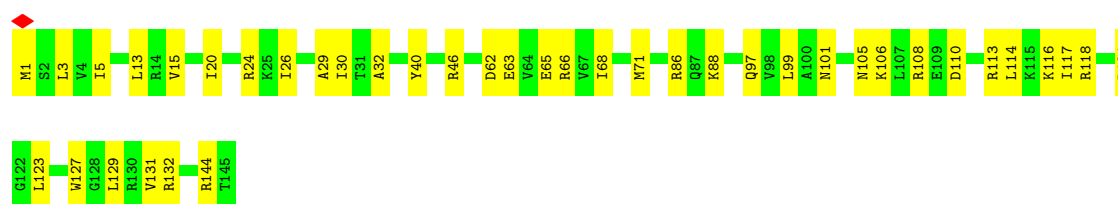
- Molecule 9: Small ribosomal subunit protein uS9



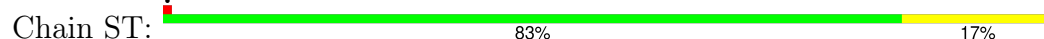
- Molecule 10: Small ribosomal subunit protein eS17



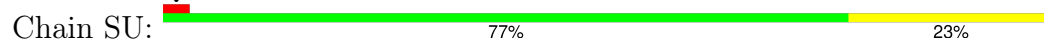
- Molecule 11: 40S ribosomal protein S18



- Molecule 12: 40S ribosomal protein S19



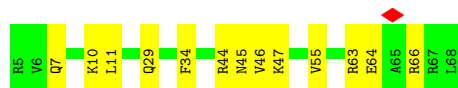
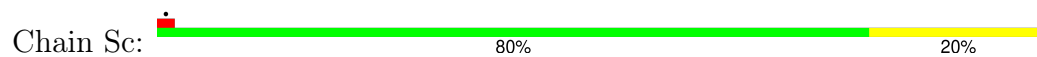
- Molecule 13: 40S ribosomal protein S20



- Molecule 14: Small ribosomal subunit protein eS25



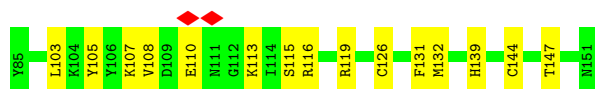
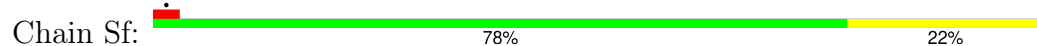
- Molecule 15: 40S ribosomal protein S28



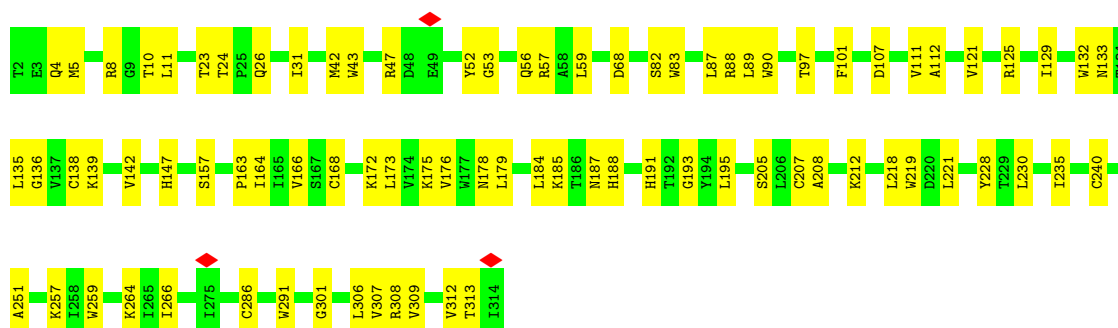
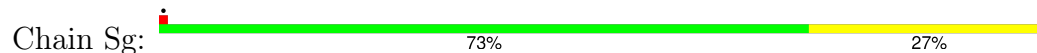
- Molecule 16: 40S ribosomal protein S29



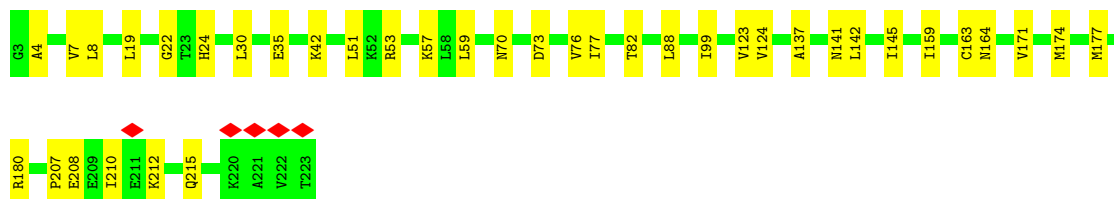
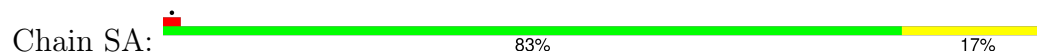
- Molecule 17: Ubiquitin-40S ribosomal protein S27a



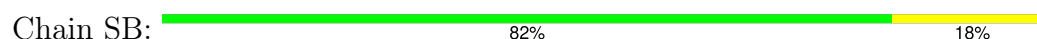
- Molecule 18: Receptor of activated protein C kinase 1



- Molecule 19: 40S ribosomal protein SA

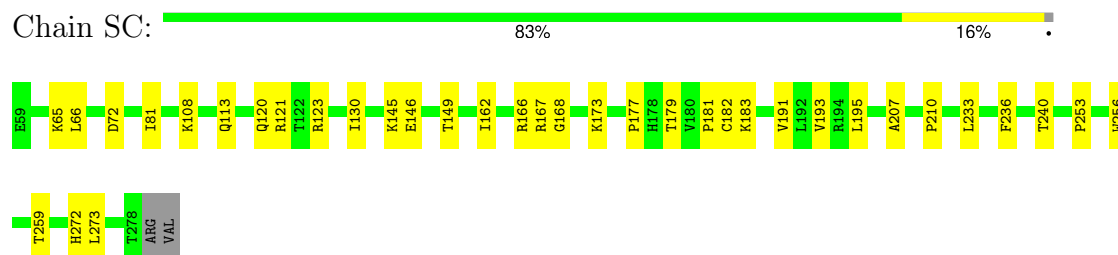


- Molecule 20: 40S ribosomal protein S3a

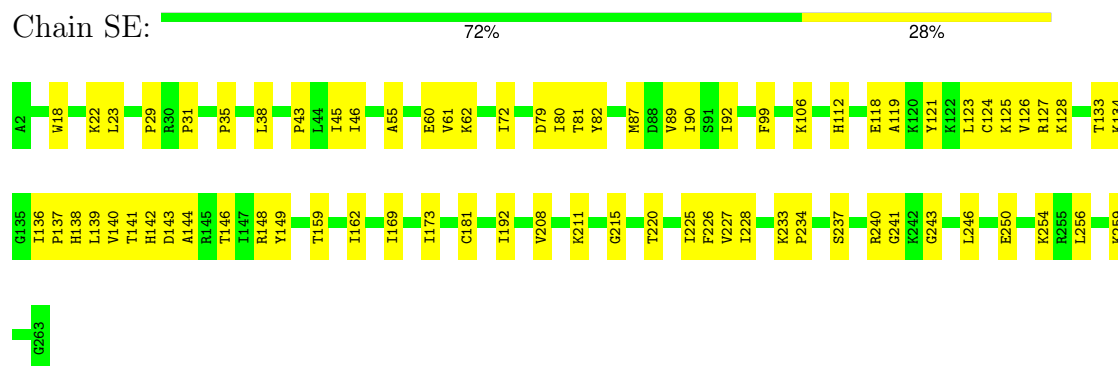




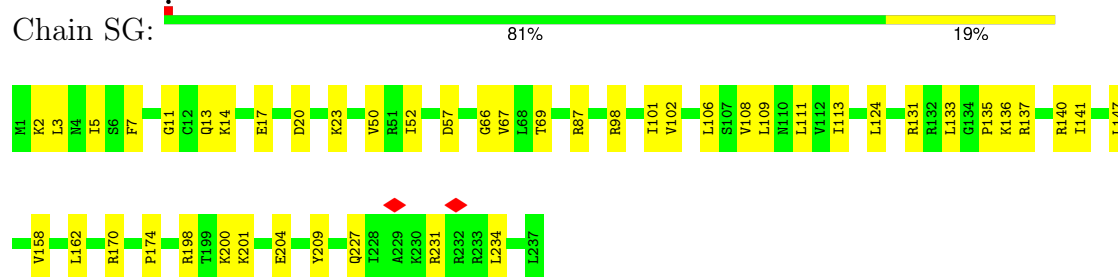
- Molecule 21: 40S ribosomal protein S2



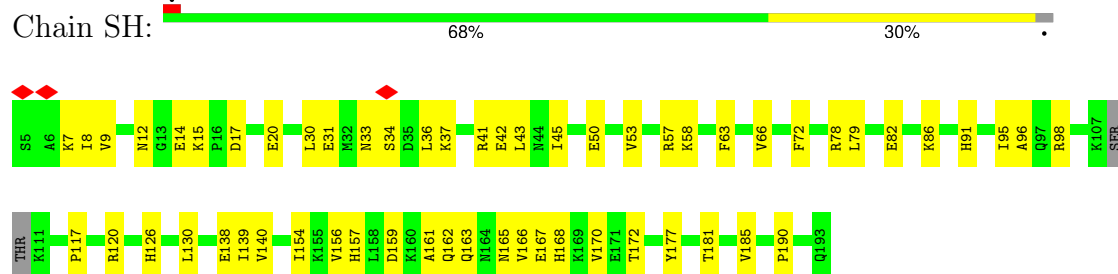
- Molecule 22: Small ribosomal subunit protein eS4, X isoform



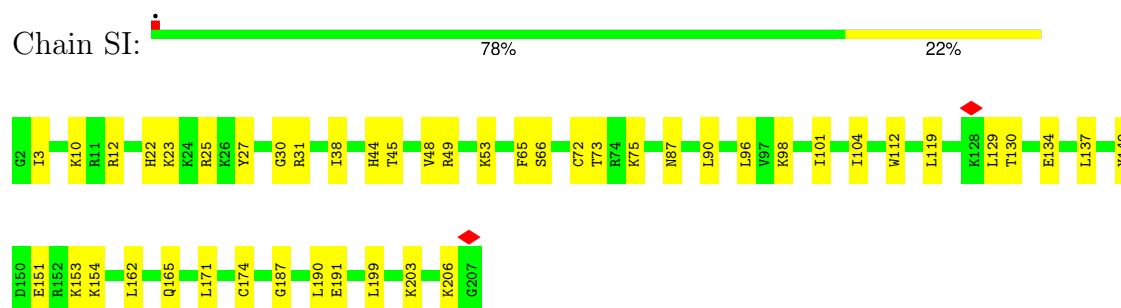
- Molecule 23: 40S ribosomal protein S6



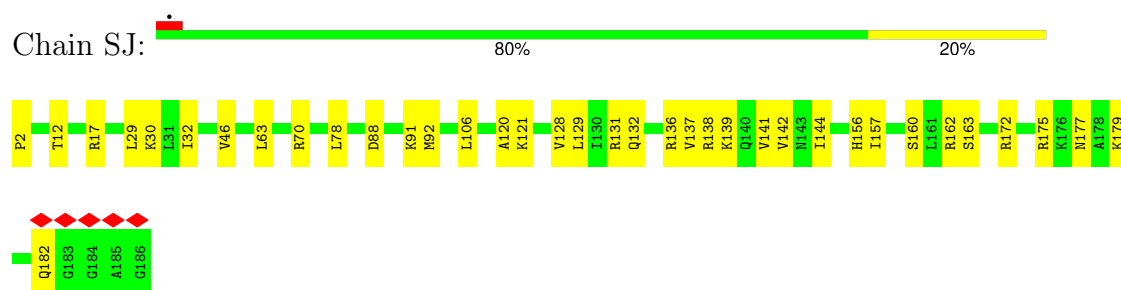
- Molecule 24: Small ribosomal subunit protein eS7



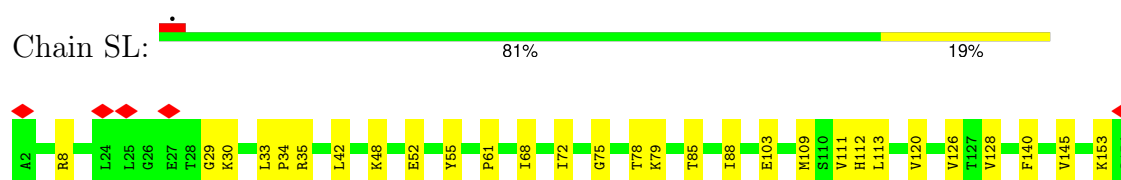
- Molecule 25: 40S ribosomal protein S8



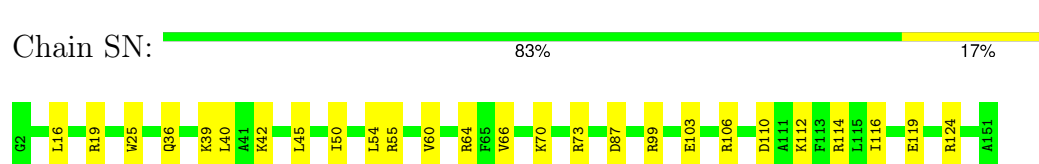
- Molecule 26: 40S ribosomal protein S9



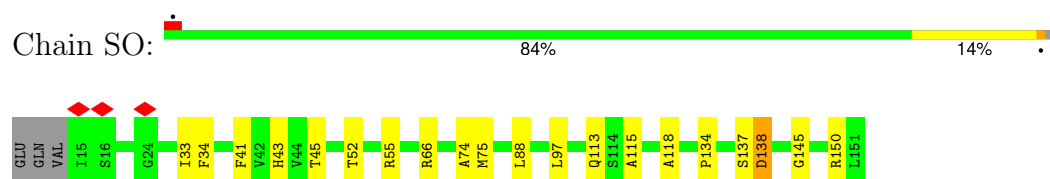
- Molecule 27: 40S ribosomal protein S11



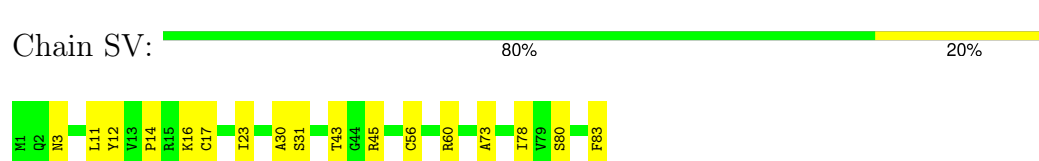
- Molecule 28: 40S ribosomal protein S13



- Molecule 29: Small ribosomal subunit protein uS11



- Molecule 30: Small ribosomal subunit protein eS21



- Molecule 31: 40S ribosomal protein S15a

Chain SW:  81% 19%



- Molecule 32: 40S ribosomal protein S23

Chain SX:  88% 12%



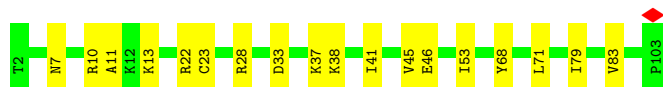
- Molecule 33: 40S ribosomal protein S24

Chain SY:  78% 22%



- Molecule 34: 40S ribosomal protein S26

Chain Sa:  82% 18%



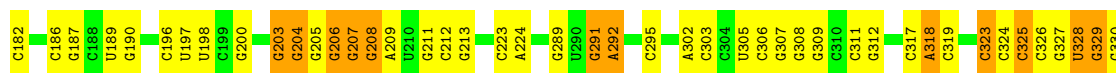
- Molecule 35: Small ribosomal subunit protein eS27

Chain Sb:  78% 22%

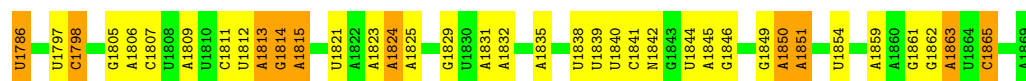


- Molecule 36: 18S rRNA [Homo sapiens]

Chain S2:  55% 37% 7%



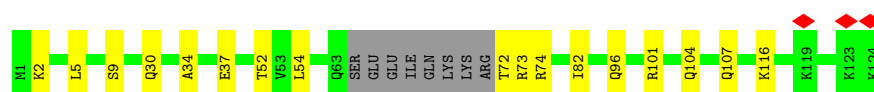
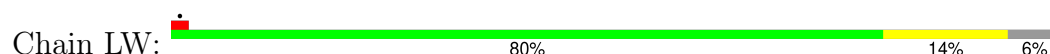
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U1714	C1629	G1528	G1320	U1238	G1129	C1019	A919	C835	G677	G601	A520	A439	G332
A1715	G1423	A1531	G1321	U1239	G1130	A1020	A920	G836	U681	A604	A525	A399	A339
G1718	G1632	C1532	U1326	U1242	A1133	A1023	G925	G837	G663	U607	A526	C340	C341
U1721	A1633	A1533	G1327	U1243	G1134	A1024	G928	G838	U666	U608	C527	C342	C343
G1722	A1634	G1536	G1328	U1244	G1135	A1027	G929	C839	U667	U609	A528	A448	C346
G1723	A1637	A1537	U1333	B81248	C1138	A1028	G930	G840	U668	U610	A529	A449	C347
A1724	G1638	C1542	U1334	U1248	C1139	G1029	C930	C841	U688	G611	A530	A450	A348
U1725	G1639	U1543	C1337	B81249	C1140	A1030	G933	G842	U689	U612	A531	A349	A349
G1726	U1643	U1544	M1337	U1251	G1141	A1031	G934	G843	G690	U613	A532	G451	A348
G1727	C1644	A1545	G1338	C1252	A1144	C1032	G942	A847	G691	C614	A533	G452	A349
U1728	C1644	A1545	U1342	A1253	A1145	G1033	G943	A848	G692	C615	A534	C453	C350
U1729	C1645	G1546	U1343	C1254	A1146	G1034	U944	C851	A693	U616	A535	U454	U354
U1730	U1648	U1547	G1348	G1255	A1147	G1035	U945	G852	G694	G617	A536	A455	U354
A1731	G1648	G1550	U1349	G1256	A1148	U1045	U946	G853	G695	U618	A537	C456	A360
G1736	A1651	A1556	G1354	A1257	C1153	U1046	C953	U857	G696	G623	A538	U461	U361
G1737	G1652	C1557	C1355	A1258	U1154	A1055	A962	A858	G697	U627	A539	C462	C362
C1740	U1653	G1558	G1356	A1259	U1155	U1056	A963	G860	U732	A628	A540	C463	A363
U1741	G1654	C1559	A1357	C1261	G1171	C1057	A964	U861	U733	U629	A541	A465	A364
G1744	U1655	U1560	U1358	C1262	U1172	A1058	U965	U862	C736	U631	A542	G466	U367
A1745	G1656	A1561	G1365	C1263	U1173	G1059	U966	A864	G737	A634	A543	G467	U368
U1746	C1657	C1562	G1366	U1264	U1174	A1060	U967	A865	G738	G635	A544	C369	C369
G1748	G1658	G1563	U1367	C1265	U1175	U1061	U968	U866	C739	U636	A545	G470	G370
C1752	U1659	A1569	C1368	G1266	G1187	A1062	G970	G867	C740	U637	A546	A471	A371
G1753	C1660	U1570	U1371	G1267	U1188	C1063	G971	A870	C741	U638	A547	C472	G377
C1754	U1661	U1571	U1372	G1268	A1195	G1064	A972	U871	U749	C639	A548	G473	G377
G1755	G1662	C1572	C1373	A1269	U1196	A1065	A973	U872	G750	A640	A549	G474	G377
C1756	U1663	A1573	A1374	C1270	U1197	U1066	A974	U873	C751	A641	A550	G482	C382
G1757	U1664	C1574	G1375	U1271	A1198	A1067	A975	U874	G752	U642	A551	C483	G383
U1758	C1665	U1575	U1376	G1272	A1200	U1068	A976	A875	C753	U643	A552	A484	U384
G1759	U1666	C1576	A1377	C1273	U1201	A1069	A977	U876	G754	U644	A553	G485	G385
U1760	U1667	U1577	U1378	G1274	U1202	A1070	A978	U877	G755	G645	A554	A486	C386
G1761	C1668	C1578	A1379	G1275	U1203	A1071	A979	U878	G756	U646	A555	U487	U387
U1762	U1669	A1579	G1380	A1276	A1204	U1072	A980	U879	G757	U647	A556	U488	U388
C1763	G1670	C1580	A1381	C1277	U1205	U1073	A981	U880	G758	U648	A557	A489	A389
G1764	U1671	U1581	U1382	U1278	U1206	A1074	A982	U881	C759	U649	A558	C390	C390
C1765	C1672	A1582	A1383	G1279	U1207	A1075	A983	U882	C760	U650	A559	C391	A392
U1766	U1673	C1583	A1384	C1280	U1208	U1076	A984	U883	G761	U651	A560	C491	A392
G1767	G1674	U1584	A1385	U1281	U1209	U1077	A985	U884	G762	U652	A561	A492	A393
C1768	U1675	C1585	U1386	G1282	U1210	U1078	A986	U885	G763	U653	A562	C493	A394
G1769	U1676	A1586	G1387	C1283	U1211	U1079	A987	U886	G764	U654	A563	U494	A395
U1770	C1677	C1587	A1388	U1284	U1212	U1080	A988	U887	G765	U655	A564	C495	A396
C1771	G1678	U1588	U1389	G1285	U1213	U1081	A989	U888	G766	U656	A565	U496	U406
G1772	U1679	C1589	A1390	C1286	U1214	U1082	A990	U889	G767	U657	A566	C497	C409
U1773	C1680	A1590	U1391	U1287	U1215	A1083	A991	U890	G768	U658	A567	U502	A426
C1774	U1681	U1591	G1392	G1288	U1216	U1084	A992	U891	C769	U659	A568	U503	U427
G1775	C1682	C1592	A1393	U1289	U1217	U1085	A993	U892	G770	U660	A569	U504	U428
U1776	U1683	U1593	U1394	C1290	U1218	U1086	A994	U893	G771	U661	A570	G507	G431
G1777	C1684	C1594	A1395	U1291	U1219	U1087	A995	U894	G772	U662	A571	A508	G432
C1778	U1685	U1595	U1396	G1292	U1220	U1088	A996	U895	G773	U663	A572	G509	A433
G1779	C1686	A1596	A1397	U1293	U1221	U1089	A997	U896	G774	U664	A573	G510	A434
U1780	U1687	C1597	U1398	C1294	U1222	U1090	A998	U897	G775	U665	A574	U511	G435
G1781	C1688	U1598	A1399	U1295	U1223	U1091	A999	U898	G776	U666	A575	A512	A435
U1782	U1689	C1599	U1400	G1296	U1224	U1092	A999	U899	G777	U667	A576	G513	A436
C1783	C1690	A1600	A1401	U1297	U1225	U1093	A999	U900	G778	U668	A577	U514	A437
G1784	U1691	G1601	U1402	C1298	U1226	U1094	A999	U901	G779	U669	A578	G515	A438
U1785	C1692	C1602	A1403	U1299	U1227	U1095	A999	U902	G780	U670	A579	U516	A439
G1786	U1693	U1603	U1404	U1300	U1228	U1096	A999	U903	G781	U671	A580	G517	A440
U1787	C1694	G1604	A1405	A1301	U1229	U1097	A999	U904	G782	U672	A581	U518	A441
G1788	U1695	U1605	U1406	C1302	U1230	U1098	A999	U905	G783	U673	A582	G519	A442
C1789	C1696	C1606	U1407	C1303	U1231	U1099	A999	U906	G784	U674	A583	U520	A443
U1790	U1697	A1607	U1408	U1304	U1232	U1100	A999	U907	G785	U675	A584	G521	A444
G1791	C1698	G1608	U1409	C1305	U1233	U1101	A999	U908	G786	U676	A585	U522	A445
U1792	C1699	U1609	A1410	U1306	U1234	U1102	A999	U909	G787	U677	A586	G523	A446
C1793	U1700	C1610	U1411	U1307	U1235	U1103	A999	U910	G788	U678	A587	U524	A447
G1794	U1701	U1611	A1412	U1308	U1236	U1104	A999	U911	G789	U679	A588	G525	A448
U1795	C1700	A1612	U1413	U1309	U1237	U1105	A999	U912	G790	U680	A589	U526	A449
G1796	U1701	U1613	U1414	C1310	U1238	U1106	A999	U913	G791	U681	A590	G527	A450
C1797	C1702	C1614	A1415	U1311	U1239	U1107	A999	U914	G792	U682	A591	U528	A451
U1798	U1703	U1615	U1416	C1312	U1240	U1108	A999	U915	G793	U683	A592	G529	A452
G1799	C1704	A1616	A1417	U1313	U1241	U1109	A999	U916	G794	U684	A593	U530	A453
U1800	U1705	U1617	U1418	U1314	U1242	U1110	A999	U917	G795	U685	A594	G531	A454
C1801	C1706	C1618	C1419	C1315	U1243	U1111	A999	U918	G796	U686	A595	U532	A455
U1802	U1707	U1619	U1420	U1316	U1244	U1112	A999	U919	G797	U687	A596	G533	A456
G1803	C1708	A1620	U1421	C1317	U1245	U1113	A999	U920	G798	U688	A597	U534	A457
U1804	U1709	U1621	U1422	U1318	U1246	U1114	A999	U921	G799	U689	A598	G535	A458
C1805	C1710	C1622	U1423	U1319	U1247	U1115	A999	U922	G800	U690	A599	U536	A459
U1806	U1711	U1623	U1424	C1320	U1248	U1116	A999	U923	G801	U691	A600	G537	A460
G1807	C1712	A1624	U1425	U1321	U1249	U1117	A999	U924	G802	U692	A601	U538	A461
U1808	U1713	U1625	G1426	G1322	U1250	U1118	A999	U925	G803	U693	A602	G539	A462
C1809	C1714	C1626	U1427	U1323	U1251	U1119	A999	U926	G804	U694	A603	U540	A463
U1810	U1715	U1627	U1428	C1324	U1252	U1120	A999	U927	G805	U695	A604	G541	A464
G1811	C1716	A1628	U1429	U1325	U1253	U1121	A999	U928	G806	U696	A605	U542	A465
U1812	U1717	U1629	U1430	U1326	U1254	U1122	A999	U929	G807	U697	A606	G543	A466
C1813	C1718	C1630	U1431	G1327	U1255	U1123	A999	U930	G808	U698	A607	U544	A467
U1814	U1719	U1631	U1432	U1328	U1256	U1124	A999	U931	G809	U699	A608	G545	A468
G1815	C1720	A1632	U1433	U1329	U1257	U1125	A999	U932	G810	U700	A609	U546	A469
U1816	U1721	U1633	U1434	C1330	U1258	U1126	A999	U933	G811	U701	A610	G547	A470
C1817	C1722	C1634	U1435	U1331	U1259	U1127	A999	U934	G812	U702	A611	U548	A471
U1818	U1723	U1635	U1436	U1332	U1260	U1128	A999	U935	G813	U703	A612	G549	A472
G1819	C1724	A1636	U1437	B81248	C1261	U1129	A999	U936	G814	U704	A613	U550	A473
U1820	U1725	U1637	U1438	U1248	U1262	U1130	A999	U937	G815	U705	A614	G551	A474
C1821	C1726	C1638	U1439	U1249	U1263	U1131	A999	U938	G816	U706	A615	U552	A475
U1822	U1727	U1639	A1440	U1250	U1264	U1132	A999	U939	G817	U707	A616	G553	A476
G1823	G1728	A1640	U1441	C1265	U1265	U1133	A999	U940	G818	U708	A617	U554	A477
U182													



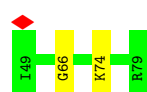
- Molecule 37: 60S ribosomal protein L19



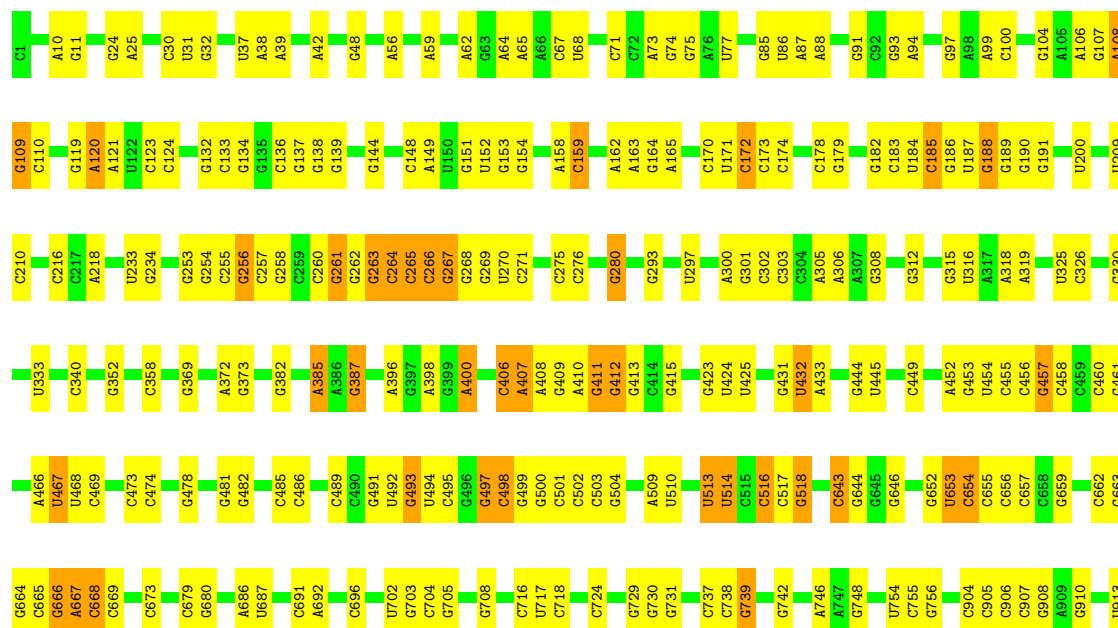
- Molecule 38: Ribosomal protein L24



- Molecule 39: Transcription factor BTF3

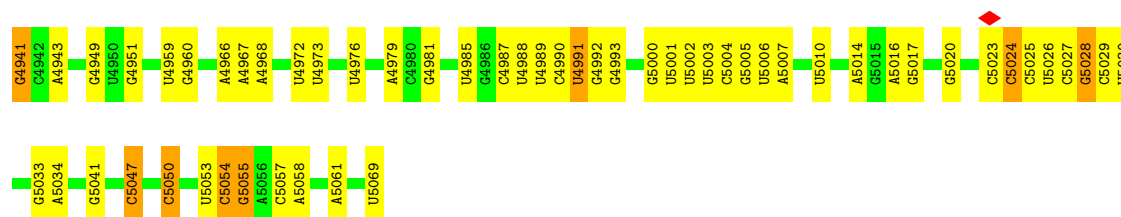


- Molecule 40: 28S rRNA

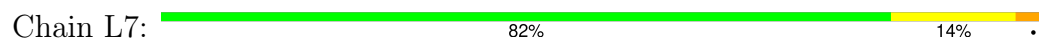




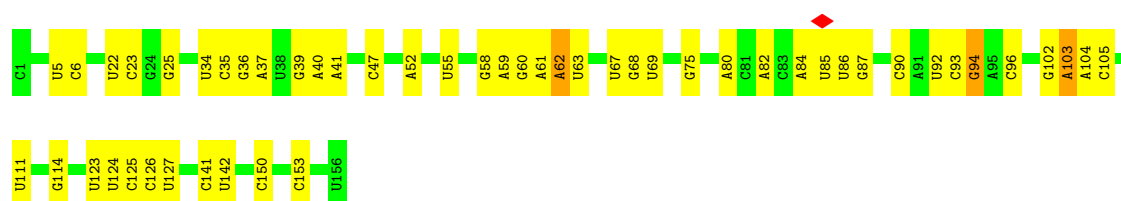




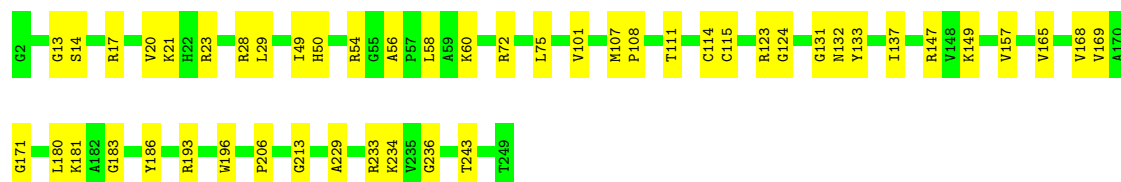
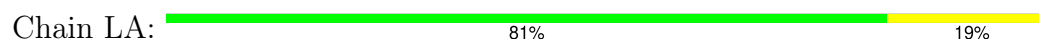
• Molecule 41: 5S rRNA



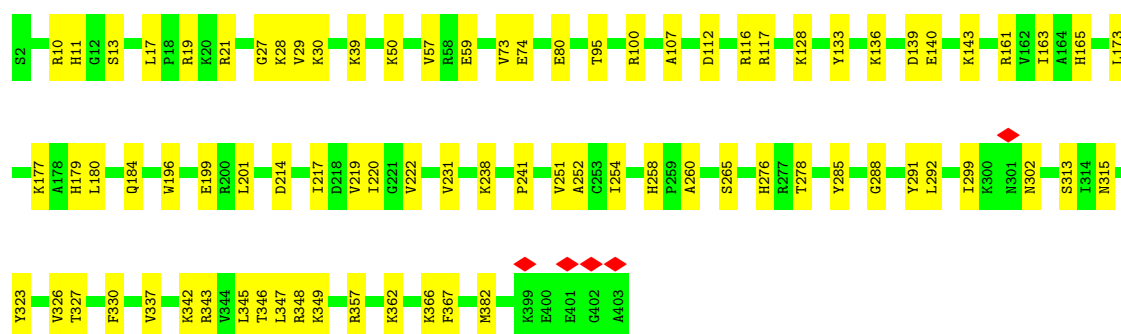
• Molecule 42: 5.8S rRNA



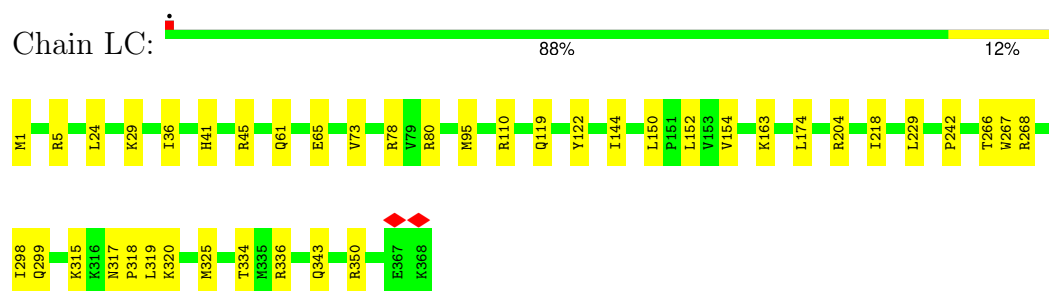
• Molecule 43: 60S ribosomal protein L8



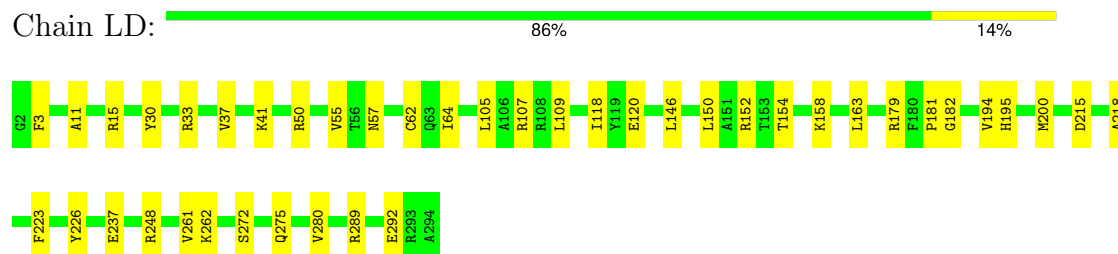
• Molecule 44: Large ribosomal subunit protein uL3



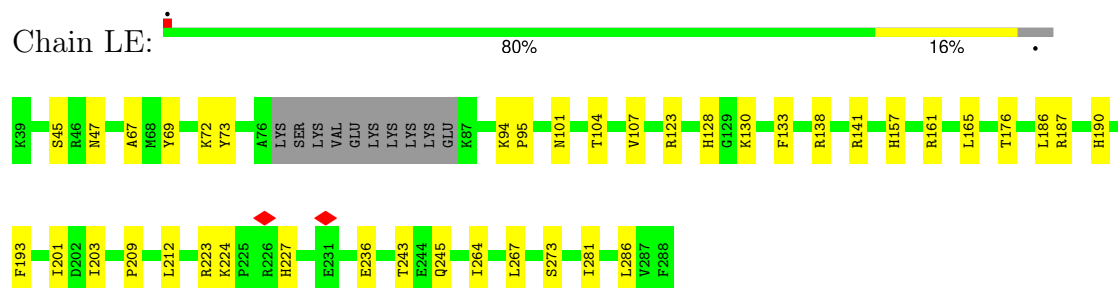
• Molecule 45: 60S ribosomal protein L4



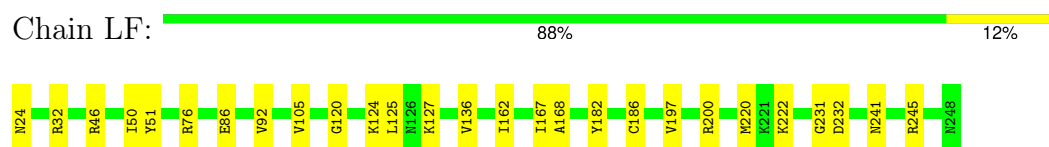
- Molecule 46: Large ribosomal subunit protein uL18



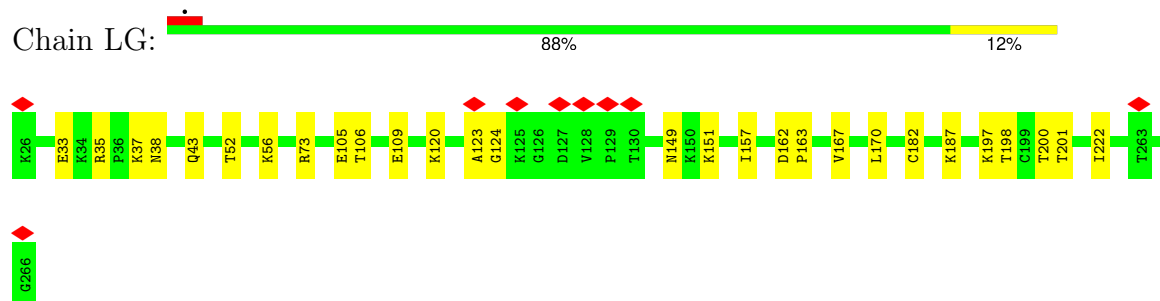
- Molecule 47: Large ribosomal subunit protein eL6



- Molecule 48: 60S ribosomal protein L7

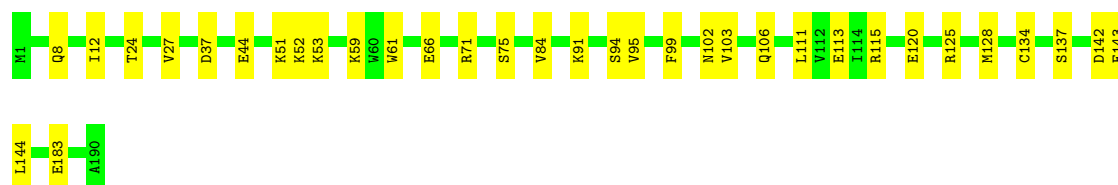


- Molecule 49: 60S ribosomal protein L7a



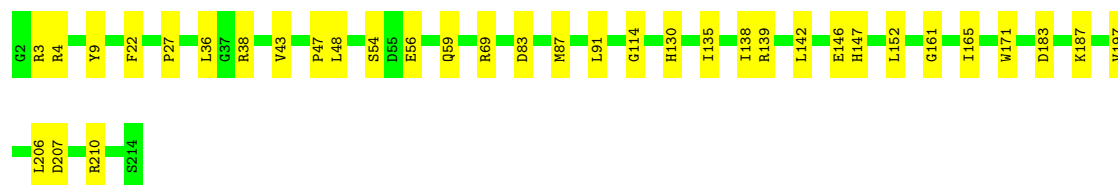
- Molecule 50: 60S ribosomal protein L9

Chain LH:  82% 18%



- Molecule 51: Ribosomal protein uL16-like

Chain LI:  84% 16%



- Molecule 52: 60S ribosomal protein L11

Chain LJ:  82% 15%



- Molecule 53: Large ribosomal subunit protein eL13

Chain LL:  89% 11%



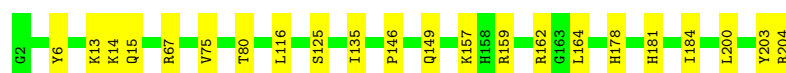
- Molecule 54: 60S ribosomal protein L14

Chain LM:  88% 12%



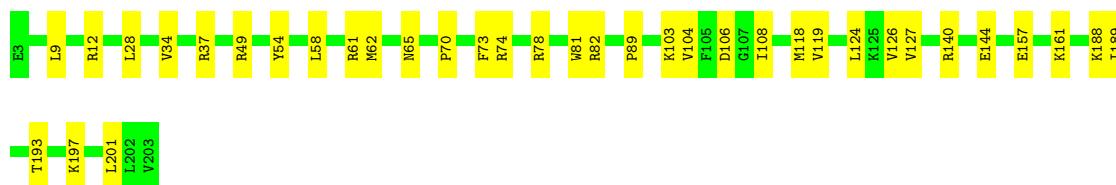
- Molecule 55: 60S ribosomal protein L15

Chain LN:  89% 11%



- Molecule 56: 60S ribosomal protein L13a

Chain LO:  82% 18%



- Molecule 57: 60S ribosomal protein L17

Chain LP: 86% 14%



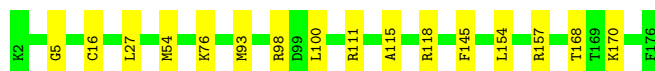
- Molecule 58: 60S ribosomal protein L18

Chain LQ: 91% 9%



- Molecule 59: 60S ribosomal protein L18a

Chain LS: 91% 9%



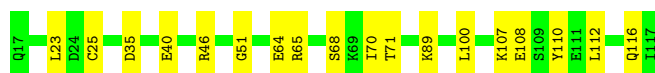
- Molecule 60: 60S ribosomal protein L21

Chain LT: 90% 10%



- Molecule 61: Heparin-binding protein HBp15

Chain LU: 82% 18%



- Molecule 62: 60S ribosomal protein L23

Chain LV: 91% 9%



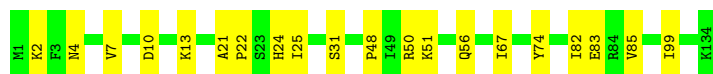
- Molecule 63: 60S ribosomal protein L23a

Chain LX:  89% 11%



- Molecule 64: 60S ribosomal protein L26

Chain LY:  85% 15%



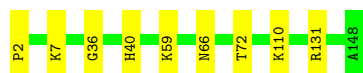
- Molecule 65: 60S ribosomal protein L27

Chain LZ:  87% 13%



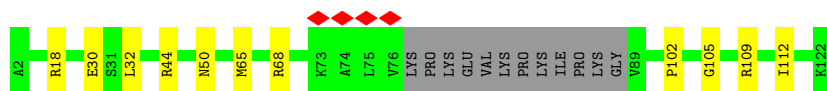
- Molecule 66: 60S ribosomal protein L27a

Chain La:  94% 6%



- Molecule 67: Large ribosomal subunit protein eL29

Chain Lb:  81% 9% 10%



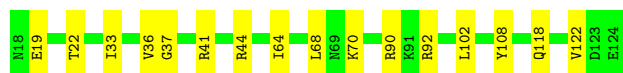
- Molecule 68: 60S ribosomal protein L30

Chain Lc:  79% 21%



- Molecule 69: 60S ribosomal protein L31

Chain Ld:  85% 15%



- Molecule 70: 60S ribosomal protein L32

Chain Le:  91% 9%

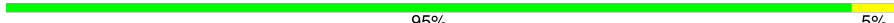


- Molecule 71: 60S ribosomal protein L35a

Chain Lf:  95% 5%



- Molecule 72: 60S ribosomal protein L34

Chain Lg:  95% 5%



- Molecule 73: 60S ribosomal protein L35

Chain Lh:  89% 11%



- Molecule 74: 60S ribosomal protein L36

Chain Li:  95% 5%



- Molecule 75: 60S ribosomal protein L37

Chain Lj:  86% 14%



- Molecule 76: 60S ribosomal protein L38

Chain Lk:  86% 14%



- Molecule 77: 60S ribosomal protein L39

Chain Ll:  80% 20%



- Molecule 78: Large ribosomal subunit protein eL40

Chain Lm:  90% 10%



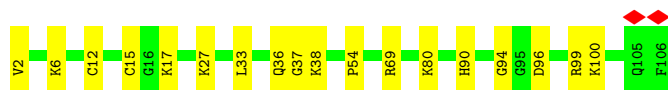
- Molecule 79: 60S ribosomal protein L41

Chain Ln:  79% 21%



- Molecule 80: 60S ribosomal protein L36a

Chain Lo:  83% 17%



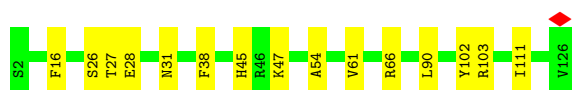
- Molecule 81: 60S ribosomal protein L37a

Chain Lp:  90% 10%



- Molecule 82: 60S ribosomal protein L28

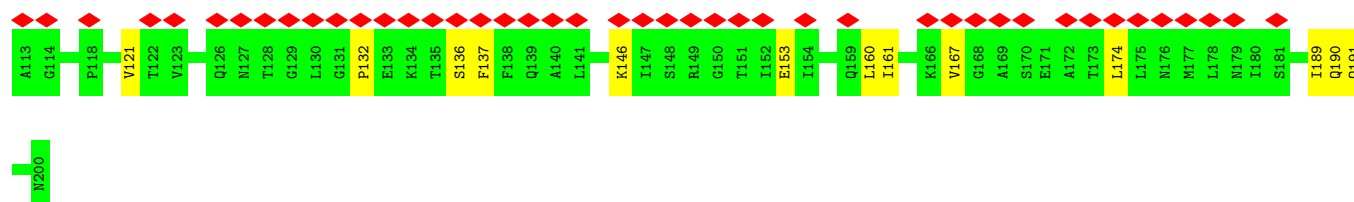
Chain Lr:  88% 12%



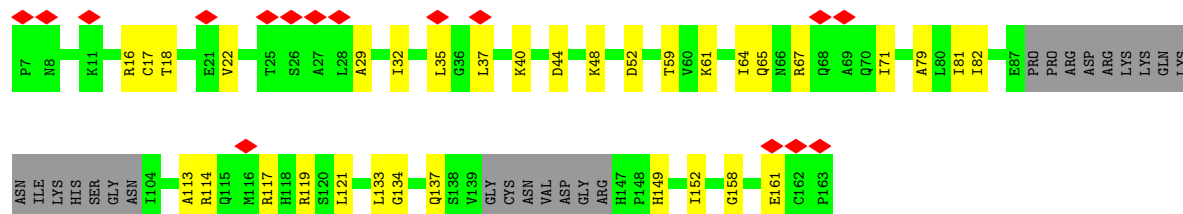
- Molecule 83: 60S acidic ribosomal protein P0

Chain Ls:  25% 79% 21%

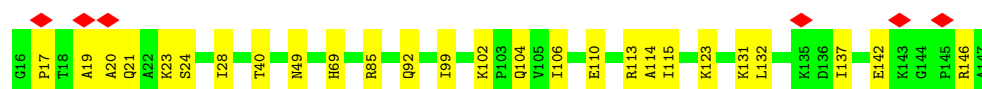
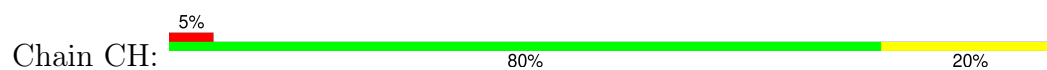




- Molecule 84: Large ribosomal subunit protein uL11



- Molecule 85: Endothelial differentiation-related factor 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	130154	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)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.252	Depositor
Minimum map value	-0.070	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0159	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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 6MZ, SPM, 5MC, UY1, A2M, OMG, B8N, MG, G7M, ZN, OMC, 1MA, SPD, MA6, 4AC, PSU, UR3, OMU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AP	0.15	0/1692	0.24	0/2634
2	CB	0.18	0/6734	0.39	0/9094
3	PE	0.20	0/1778	0.31	0/2767
4	SD	0.19	0/1793	0.31	0/2414
5	SF	0.18	0/1516	0.38	0/2037
6	SK	0.20	0/851	0.42	0/1147
7	SM	0.14	0/950	0.39	0/1275
8	SP	0.18	0/1065	0.31	0/1423
9	SQ	0.18	0/1160	0.37	0/1553
10	SR	0.25	0/1105	0.50	0/1484
11	SS	0.19	0/1216	0.36	0/1628
12	ST	0.18	0/1131	0.32	0/1515
13	SU	0.19	0/831	0.40	0/1115
14	SZ	0.19	0/604	0.38	0/810
15	Sc	0.18	0/508	0.34	0/680
16	Sd	0.21	0/470	0.32	0/623
17	Sf	0.19	0/560	0.44	0/745
18	Sg	0.16	0/2493	0.40	0/3394
19	SA	0.22	0/1778	0.36	0/2416
20	SB	0.21	0/1765	0.38	0/2362
21	SC	0.23	0/1744	0.39	0/2357
22	SE	0.18	0/2118	0.36	0/2849
23	SG	0.16	0/1946	0.32	0/2590
24	SH	0.17	0/1519	0.37	0/2033
25	SI	0.18	0/1715	0.36	0/2287
26	SJ	0.16	0/1550	0.32	0/2069
27	SL	0.20	0/1268	0.30	0/1696
28	SN	0.21	0/1232	0.31	0/1656
29	SO	0.23	0/1037	0.41	0/1391
30	SV	0.18	0/643	0.30	0/860
31	SW	0.23	0/1051	0.37	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	SX	0.21	0/1116	0.38	0/1490
33	SY	0.16	0/1083	0.36	0/1438
34	Sa	0.25	0/836	0.39	0/1121
35	Sb	0.19	0/665	0.32	0/891
36	S2	0.25	0/39756	0.28	0/61939
37	LR	0.29	0/1582	0.40	0/2091
38	LW	0.23	0/959	0.30	0/1270
39	CI	0.15	0/247	0.27	0/323
40	L5	0.34	0/85098	0.32	0/132762
41	L7	0.33	0/2861	0.27	0/4459
42	L8	0.34	0/3631	0.29	0/5657
43	LA	0.34	0/1936	0.44	0/2596
44	LB	0.31	0/3306	0.40	0/4424
45	LC	0.32	0/2981	0.38	0/4002
46	LD	0.26	0/2428	0.35	0/3252
47	LE	0.25	0/1973	0.40	0/2645
48	LF	0.32	0/1905	0.33	0/2539
49	LG	0.26	0/1960	0.37	0/2637
50	LH	0.27	0/1537	0.37	0/2066
51	LI	0.28	0/1751	0.32	0/2340
52	LJ	0.24	0/1385	0.39	0/1852
53	LL	0.27	0/1732	0.34	0/2315
54	LM	0.29	0/1161	0.39	0/1554
55	LN	0.33	0/1746	0.36	0/2338
56	LO	0.32	0/1682	0.37	0/2250
57	LP	0.33	0/1268	0.43	0/1701
58	LQ	0.32	0/1537	0.37	0/2052
59	LS	0.31	0/1493	0.36	0/2003
60	LT	0.29	0/1326	0.33	0/1770
61	LU	0.24	0/839	0.49	0/1126
62	LV	0.30	0/993	0.39	0/1332
63	LX	0.28	0/1002	0.34	0/1345
64	LY	0.28	0/1132	0.36	0/1504
65	LZ	0.26	0/1130	0.34	0/1507
66	La	0.31	0/1191	0.34	0/1591
67	Lb	0.24	0/889	0.41	0/1175
68	Lc	0.27	0/774	0.39	0/1038
69	Ld	0.30	0/903	0.38	0/1216
70	Le	0.34	0/1071	0.35	0/1429
71	Lf	0.33	0/895	0.37	0/1198
72	Lg	0.30	0/916	0.35	0/1220
73	Lh	0.27	0/1023	0.37	0/1351
74	Li	0.24	0/843	0.32	0/1115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Lj	0.34	0/720	0.42	0/952
76	Lk	0.24	0/575	0.34	0/761
77	Ll	0.30	0/454	0.28	0/599
78	Lm	0.27	0/435	0.35	0/575
79	Ln	0.23	0/231	0.32	0/294
80	Lo	0.29	0/876	0.34	0/1156
81	Lp	0.29	0/718	0.38	0/953
82	Lr	0.31	0/1017	0.36	0/1364
83	Ls	0.14	0/1519	0.38	0/2052
84	Lt	0.15	0/1009	0.45	0/1363
85	CH	0.16	0/1028	0.40	0/1376
All	All	0.29	0/238947	0.33	0/349679

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
10	SR	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	SR	81	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	AP	1514	0	770	22	0
2	CB	6605	0	6679	133	0
3	PE	1593	0	810	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	SD	1765	0	1865	28	0
5	SF	1495	0	1549	26	0
6	SK	827	0	854	14	0
7	SM	940	0	965	11	0
8	SP	1045	0	1095	19	0
9	SQ	1142	0	1213	21	0
10	SR	1090	0	1149	21	0
11	SS	1198	0	1261	29	0
12	ST	1112	0	1146	18	0
13	SU	821	0	883	18	0
14	SZ	598	0	656	17	0
15	Sc	506	0	536	8	0
16	Sd	459	0	452	5	0
17	Sf	548	0	551	9	0
18	Sg	2436	0	2393	55	0
19	SA	1741	0	1746	25	0
20	SB	1738	0	1809	26	0
21	SC	1707	0	1791	23	0
22	SE	2076	0	2177	52	0
23	SG	1923	0	2089	40	0
24	SH	1497	0	1590	37	0
25	SI	1686	0	1772	31	0
26	SJ	1525	0	1640	26	0
27	SL	1247	0	1323	18	0
28	SN	1208	0	1294	18	0
29	SO	1024	0	1050	16	0
30	SV	636	0	637	11	0
31	SW	1034	0	1080	20	0
32	SX	1098	0	1167	16	0
33	SY	1065	0	1142	21	0
34	Sa	821	0	870	14	0
35	Sb	651	0	672	14	0
36	S2	36952	0	18678	409	0
37	LR	1566	0	1729	13	0
38	LW	945	0	1003	15	0
39	CI	247	0	283	2	0
40	L5	78444	0	39719	673	0
41	L7	2561	0	1295	12	0
42	L8	3315	0	1685	23	0
43	LA	1898	0	1993	41	0
44	LB	3238	0	3376	61	0
45	LC	2927	0	3104	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	LD	2382	0	2410	33	0
47	LE	1935	0	2096	27	0
48	LF	1870	0	1996	19	0
49	LG	1927	0	2074	19	0
50	LH	1518	0	1601	22	0
51	LI	1711	0	1749	22	0
52	LJ	1362	0	1399	15	0
53	LL	1701	0	1818	20	0
54	LM	1138	0	1204	16	0
55	LN	1701	0	1749	19	0
56	LO	1650	0	1794	29	0
57	LP	1242	0	1269	15	0
58	LQ	1513	0	1628	14	0
59	LS	1453	0	1490	12	0
60	LT	1298	0	1366	15	0
61	LU	825	0	850	13	0
62	LV	979	0	1039	9	0
63	LX	985	0	1066	8	0
64	LY	1115	0	1205	14	0
65	LZ	1107	0	1182	11	0
66	La	1162	0	1213	9	0
67	Lb	876	0	948	9	0
68	Lc	764	0	804	13	0
69	Ld	888	0	930	11	0
70	Le	1053	0	1147	9	0
71	Lf	876	0	912	3	0
72	Lg	906	0	998	5	0
73	Lh	1015	0	1148	14	0
74	Li	832	0	917	5	0
75	Lj	705	0	737	9	0
76	Lk	569	0	637	8	0
77	Ll	444	0	483	7	0
78	Lm	429	0	465	4	0
79	Ln	230	0	276	3	0
80	Lo	862	0	929	12	0
81	Lp	708	0	756	7	0
82	Lr	1002	0	1068	9	0
83	Ls	1496	0	1540	28	0
84	Lt	998	0	1032	25	0
85	CH	1018	0	1064	19	0
86	L5	178	0	0	0	0
86	L7	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	L8	4	0	0	0	0
86	LA	1	0	0	0	0
86	LB	1	0	0	0	0
86	LI	1	0	0	0	0
86	LP	1	0	0	0	0
86	LV	1	0	0	0	0
86	Le	1	0	0	0	0
86	S2	25	0	0	0	0
86	SG	1	0	0	0	0
86	SS	1	0	0	0	0
87	Lg	1	0	0	0	0
87	Lj	1	0	0	0	0
87	Lm	1	0	0	0	0
87	Lo	1	0	0	0	0
87	Lp	1	0	0	0	0
87	Sa	1	0	0	0	0
88	L5	98	0	182	5	0
89	L5	80	0	152	3	0
89	L8	10	0	19	0	0
89	LN	10	0	19	0	0
All	All	227131	0	170902	2350	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 2350 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)
40:L5:1095:A:H2	40:L5:1200:G:N1	1.45	1.15
40:L5:1095:A:C2	40:L5:1200:G:N1	2.19	1.05
3:PE:26:A:H61	3:PE:44:G:H1	1.06	0.91
40:L5:1100:U:H3	40:L5:1194:G:H1	1.23	0.87
36:S2:1815:A:H8	40:L5:3806:G:H21	1.20	0.83

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	CB	842/856 (98%)	786 (93%)	55 (6%)	1 (0%)	48	66
4	SD	225/227 (99%)	219 (97%)	5 (2%)	1 (0%)	30	45
5	SF	187/189 (99%)	168 (90%)	18 (10%)	1 (0%)	24	39
6	SK	96/98 (98%)	87 (91%)	9 (9%)	0	100	100
7	SM	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
8	SP	125/127 (98%)	123 (98%)	2 (2%)	0	100	100
9	SQ	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
10	SR	133/135 (98%)	126 (95%)	5 (4%)	2 (2%)	8	13
11	SS	143/145 (99%)	136 (95%)	7 (5%)	0	100	100
12	ST	141/143 (99%)	139 (99%)	2 (1%)	0	100	100
13	SU	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
14	SZ	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
15	Sc	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
16	Sd	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
17	Sf	65/67 (97%)	59 (91%)	6 (9%)	0	100	100
18	Sg	311/313 (99%)	287 (92%)	24 (8%)	0	100	100
19	SA	219/221 (99%)	210 (96%)	9 (4%)	0	100	100
20	SB	212/214 (99%)	208 (98%)	4 (2%)	0	100	100
21	SC	218/222 (98%)	204 (94%)	14 (6%)	0	100	100
22	SE	260/262 (99%)	245 (94%)	15 (6%)	0	100	100
23	SG	235/237 (99%)	225 (96%)	10 (4%)	0	100	100
24	SH	182/189 (96%)	168 (92%)	14 (8%)	0	100	100
25	SI	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
26	SJ	183/185 (99%)	178 (97%)	5 (3%)	0	100	100
27	SL	151/153 (99%)	146 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	SN	148/150 (99%)	146 (99%)	2 (1%)	0	100	100
29	SO	135/140 (96%)	128 (95%)	6 (4%)	1 (1%)	18	30
30	SV	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
31	SW	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
32	SX	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
33	SY	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
34	Sa	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
35	Sb	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
37	LR	185/187 (99%)	181 (98%)	4 (2%)	0	100	100
38	LW	112/124 (90%)	109 (97%)	3 (3%)	0	100	100
39	CI	29/31 (94%)	29 (100%)	0	0	100	100
43	LA	246/248 (99%)	228 (93%)	18 (7%)	0	100	100
44	LB	400/402 (100%)	382 (96%)	18 (4%)	0	100	100
45	LC	366/368 (100%)	350 (96%)	16 (4%)	0	100	100
46	LD	291/293 (99%)	279 (96%)	12 (4%)	0	100	100
47	LE	236/250 (94%)	221 (94%)	15 (6%)	0	100	100
48	LF	223/225 (99%)	216 (97%)	7 (3%)	0	100	100
49	LG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
50	LH	188/190 (99%)	178 (95%)	10 (5%)	0	100	100
51	LI	211/213 (99%)	207 (98%)	4 (2%)	0	100	100
52	LJ	168/176 (96%)	159 (95%)	8 (5%)	1 (1%)	21	34
53	LL	208/210 (99%)	202 (97%)	6 (3%)	0	100	100
54	LM	137/139 (99%)	132 (96%)	5 (4%)	0	100	100
55	LN	201/203 (99%)	199 (99%)	2 (1%)	0	100	100
56	LO	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
57	LP	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
58	LQ	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
59	LS	173/175 (99%)	165 (95%)	8 (5%)	0	100	100
60	LT	157/159 (99%)	152 (97%)	5 (3%)	0	100	100
61	LU	99/101 (98%)	94 (95%)	5 (5%)	0	100	100
62	LV	129/131 (98%)	125 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	LX	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
64	LY	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
65	LZ	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
66	La	145/147 (99%)	140 (97%)	5 (3%)	0	100	100
67	Lb	105/121 (87%)	99 (94%)	6 (6%)	0	100	100
68	Lc	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
69	Ld	105/107 (98%)	103 (98%)	2 (2%)	0	100	100
70	Le	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
71	Lf	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
72	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
73	Lh	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
74	Li	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
75	Lj	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
76	Lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
77	Ll	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
78	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
79	Ln	22/24 (92%)	22 (100%)	0	0	100	100
80	Lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
81	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
82	Lr	123/125 (98%)	119 (97%)	4 (3%)	0	100	100
83	Ls	194/196 (99%)	181 (93%)	13 (7%)	0	100	100
84	Lt	128/157 (82%)	110 (86%)	18 (14%)	0	100	100
85	CH	130/132 (98%)	108 (83%)	21 (16%)	1 (1%)	16	27
All	All	12594/12843 (98%)	12007 (95%)	579 (5%)	8 (0%)	49	66

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	SF	136	ARG
85	CH	114	ALA
10	SR	84	TYR
52	LJ	31	ASP
10	SR	129	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	
2	CB	722/728 (99%)	722 (100%)	0	100	100
4	SD	190/190 (100%)	190 (100%)	0	100	100
5	SF	159/159 (100%)	159 (100%)	0	100	100
6	SK	89/89 (100%)	89 (100%)	0	100	100
7	SM	102/104 (98%)	102 (100%)	0	100	100
8	SP	113/113 (100%)	113 (100%)	0	100	100
9	SQ	119/119 (100%)	119 (100%)	0	100	100
10	SR	122/122 (100%)	121 (99%)	1 (1%)	73	85
11	SS	126/126 (100%)	126 (100%)	0	100	100
12	ST	113/113 (100%)	113 (100%)	0	100	100
13	SU	94/94 (100%)	94 (100%)	0	100	100
14	SZ	66/66 (100%)	66 (100%)	0	100	100
15	Sc	57/57 (100%)	57 (100%)	0	100	100
16	Sd	48/48 (100%)	48 (100%)	0	100	100
17	Sf	60/60 (100%)	60 (100%)	0	100	100
18	Sg	272/272 (100%)	272 (100%)	0	100	100
19	SA	183/183 (100%)	183 (100%)	0	100	100
20	SB	195/195 (100%)	195 (100%)	0	100	100
21	SC	186/188 (99%)	186 (100%)	0	100	100
22	SE	224/224 (100%)	224 (100%)	0	100	100
23	SG	207/207 (100%)	207 (100%)	0	100	100
24	SH	166/169 (98%)	166 (100%)	0	100	100
25	SI	178/178 (100%)	178 (100%)	0	100	100
26	SJ	161/161 (100%)	161 (100%)	0	100	100
27	SL	137/137 (100%)	137 (100%)	0	100	100
28	SN	130/130 (100%)	130 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	SO	107/110 (97%)	107 (100%)	0	100	100
30	SV	67/67 (100%)	67 (100%)	0	100	100
31	SW	112/112 (100%)	112 (100%)	0	100	100
32	SX	113/113 (100%)	113 (100%)	0	100	100
33	SY	113/113 (100%)	113 (100%)	0	100	100
34	Sa	89/89 (100%)	89 (100%)	0	100	100
35	Sb	75/75 (100%)	75 (100%)	0	100	100
37	LR	166/166 (100%)	166 (100%)	0	100	100
38	LW	95/103 (92%)	95 (100%)	0	100	100
39	CI	25/25 (100%)	25 (100%)	0	100	100
43	LA	190/190 (100%)	190 (100%)	0	100	100
44	LB	348/348 (100%)	348 (100%)	0	100	100
45	LC	306/306 (100%)	306 (100%)	0	100	100
46	LD	246/247 (100%)	246 (100%)	0	100	100
47	LE	212/222 (96%)	212 (100%)	0	100	100
48	LF	194/194 (100%)	194 (100%)	0	100	100
49	LG	203/205 (99%)	203 (100%)	0	100	100
50	LH	169/169 (100%)	169 (100%)	0	100	100
51	LI	180/180 (100%)	180 (100%)	0	100	100
52	LJ	143/148 (97%)	143 (100%)	0	100	100
53	LL	176/176 (100%)	176 (100%)	0	100	100
54	LM	118/118 (100%)	118 (100%)	0	100	100
55	LN	171/171 (100%)	171 (100%)	0	100	100
56	LO	173/173 (100%)	173 (100%)	0	100	100
57	LP	134/134 (100%)	134 (100%)	0	100	100
58	LQ	164/164 (100%)	164 (100%)	0	100	100
59	LS	156/156 (100%)	156 (100%)	0	100	100
60	LT	139/139 (100%)	139 (100%)	0	100	100
61	LU	91/91 (100%)	91 (100%)	0	100	100
62	LV	101/101 (100%)	101 (100%)	0	100	100
63	LX	108/108 (100%)	108 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
64	LY	124/124 (100%)	124 (100%)	0	100	100
65	LZ	117/117 (100%)	117 (100%)	0	100	100
66	La	120/120 (100%)	120 (100%)	0	100	100
67	Lb	88/101 (87%)	88 (100%)	0	100	100
68	Lc	83/83 (100%)	83 (100%)	0	100	100
69	Ld	98/98 (100%)	98 (100%)	0	100	100
70	Le	114/114 (100%)	114 (100%)	0	100	100
71	Lf	88/88 (100%)	88 (100%)	0	100	100
72	Lg	98/98 (100%)	98 (100%)	0	100	100
73	Lh	109/109 (100%)	109 (100%)	0	100	100
74	Li	86/86 (100%)	86 (100%)	0	100	100
75	Lj	73/73 (100%)	73 (100%)	0	100	100
76	Lk	64/64 (100%)	64 (100%)	0	100	100
77	Ll	47/47 (100%)	47 (100%)	0	100	100
78	Lm	48/48 (100%)	48 (100%)	0	100	100
79	Ln	23/23 (100%)	23 (100%)	0	100	100
80	Lo	93/93 (100%)	93 (100%)	0	100	100
81	Lp	74/74 (100%)	74 (100%)	0	100	100
82	Lr	109/109 (100%)	109 (100%)	0	100	100
83	Ls	162/164 (99%)	162 (100%)	0	100	100
84	Lt	107/130 (82%)	107 (100%)	0	100	100
85	CH	106/106 (100%)	106 (100%)	0	100	100
All	All	10934/11014 (99%)	10933 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	SR	82	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 100 such sidechains are listed below:

Mol	Chain	Res	Type
46	LD	131	ASN

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Mol	Chain	Res	Type
56	LO	50	ASN
85	CH	100	ASN
46	LD	282	GLN
50	LH	189	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AP	69/71 (97%)	11 (15%)	0
3	PE	74/75 (98%)	21 (28%)	1 (1%)
36	S2	1715/1740 (98%)	374 (21%)	3 (0%)
40	L5	3643/3655 (99%)	729 (20%)	15 (0%)
41	L7	119/120 (99%)	11 (9%)	0
42	L8	155/156 (99%)	24 (15%)	0
All	All	5775/5817 (99%)	1170 (20%)	19 (0%)

5 of 1170 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AP	8	U
1	AP	9	A
1	AP	11	U
1	AP	13	U
1	AP	14	A

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
40	L5	2760	G
40	L5	4699	U
40	L5	4913	G
40	L5	4600	G
40	L5	1633	G

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

178 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
40	PSU	L5	1862	40	18,21,22	1.06	1 (5%)	21,30,33	2.01	4 (19%)
40	PSU	L5	4532	40	18,21,22	1.09	2 (11%)	21,30,33	1.95	4 (19%)
40	A2M	L5	4571	40	22,25,26	1.32	3 (13%)	30,36,39	1.61	8 (26%)
40	OMU	L5	4620	40	19,22,23	3.13	7 (36%)	25,31,34	1.72	5 (20%)
40	1MA	L5	1322	40,86	21,25,26	0.68	0	30,37,40	0.83	2 (6%)
42	PSU	L8	55	42	18,21,22	1.03	1 (5%)	21,30,33	1.87	4 (19%)
36	PSU	S2	686	36	18,21,22	1.06	1 (5%)	21,30,33	1.99	5 (23%)
40	A2M	L5	3718	40	22,25,26	1.17	2 (9%)	30,36,39	1.56	8 (26%)
36	PSU	S2	1367	36	18,21,22	1.05	1 (5%)	21,30,33	1.90	4 (19%)
36	PSU	S2	651	36	18,21,22	1.08	1 (5%)	21,30,33	1.91	4 (19%)
40	OMC	L5	2824	40	19,22,23	0.63	0	25,31,34	0.66	0
36	PSU	S2	649	36	18,21,22	1.09	1 (5%)	21,30,33	1.96	4 (19%)
40	PSU	L5	2839	40	18,21,22	1.07	2 (11%)	21,30,33	2.01	4 (19%)
40	PSU	L5	3884	40	18,21,22	1.08	2 (11%)	21,30,33	1.97	4 (19%)
40	PSU	L5	4361	40	18,21,22	1.02	1 (5%)	21,30,33	1.81	4 (19%)
40	PSU	L5	1683	40	18,21,22	1.06	2 (11%)	21,30,33	2.00	4 (19%)
40	PSU	L5	1677	40	18,21,22	1.13	3 (16%)	21,30,33	2.12	5 (23%)
40	OMU	L5	4498	40	19,22,23	3.20	7 (36%)	25,31,34	1.92	5 (20%)
40	OMG	L5	2424	40	23,26,27	0.61	0	32,38,41	0.41	0
40	OMG	L5	1316	40	23,26,27	0.69	0	32,38,41	0.56	0
36	PSU	S2	966	86,36	18,21,22	1.08	1 (5%)	21,30,33	1.98	4 (19%)
36	PSU	S2	1045	36	18,21,22	1.06	1 (5%)	21,30,33	1.94	4 (19%)
36	PSU	S2	1046	36	18,21,22	1.08	2 (11%)	21,30,33	1.87	4 (19%)
36	OMC	S2	174	36	19,22,23	0.57	0	25,31,34	0.80	1 (4%)
36	PSU	S2	93	36	18,21,22	1.06	1 (5%)	21,30,33	1.77	4 (19%)
40	PSU	L5	4500	40	18,21,22	1.08	2 (11%)	21,30,33	2.05	6 (28%)
36	A2M	S2	99	86,36	22,25,26	1.17	1 (4%)	30,36,39	1.58	7 (23%)
40	PSU	L5	4636	40	18,21,22	1.09	2 (11%)	21,30,33	2.10	6 (28%)
40	OMG	L5	4499	40	23,26,27	0.58	0	32,38,41	0.47	0
36	A2M	S2	27	36	22,25,26	1.21	1 (4%)	30,36,39	1.52	8 (26%)
40	PSU	L5	3639	40	18,21,22	1.13	2 (11%)	21,30,33	2.04	4 (19%)
40	PSU	L5	4552	40	18,21,22	1.08	2 (11%)	21,30,33	2.00	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
40	A2M	L5	4523	40,86	22,25,26	1.27	3 (13%)	30,36,39	1.57	8 (26%)
40	OMC	L5	3701	40	19,22,23	0.74	1 (5%)	25,31,34	1.83	4 (16%)
36	A2M	S2	468	36	22,25,26	1.25	1 (4%)	30,36,39	1.58	7 (23%)
36	PSU	S2	1004	36	18,21,22	1.09	2 (11%)	21,30,33	1.94	5 (23%)
40	PSU	L5	4673	40,86	18,21,22	1.09	2 (11%)	21,30,33	1.97	4 (19%)
40	PSU	L5	3853	40,86	18,21,22	1.02	1 (5%)	21,30,33	1.90	4 (19%)
36	A2M	S2	1383	36	22,25,26	1.15	1 (4%)	30,36,39	1.64	7 (23%)
40	PSU	L5	4442	40	18,21,22	1.05	2 (11%)	21,30,33	2.06	6 (28%)
40	OMC	L5	2422	40,86	19,22,23	0.66	0	25,31,34	0.74	1 (4%)
40	PSU	L5	3844	40	18,21,22	1.07	2 (11%)	21,30,33	1.90	4 (19%)
40	PSU	L5	5010	40	18,21,22	1.10	1 (5%)	21,30,33	1.90	4 (19%)
40	OMG	L5	4623	40	23,26,27	0.61	0	32,38,41	0.60	0
40	OMG	L5	4494	40	23,26,27	0.61	0	32,38,41	0.48	0
40	PSU	L5	4576	40	18,21,22	1.03	1 (5%)	21,30,33	1.93	4 (19%)
40	A2M	L5	1323	40	22,25,26	1.27	2 (9%)	30,36,39	1.60	9 (30%)
36	A2M	S2	159	36	22,25,26	1.18	1 (4%)	30,36,39	1.51	8 (26%)
36	PSU	S2	1081	36	18,21,22	1.03	1 (5%)	21,30,33	1.81	5 (23%)
40	A2M	L5	3867	40	22,25,26	1.37	3 (13%)	30,36,39	1.53	9 (30%)
36	PSU	S2	109	36	18,21,22	1.11	1 (5%)	21,30,33	2.02	6 (28%)
36	OMG	S2	601	36	23,26,27	0.52	0	32,38,41	0.41	0
36	OMU	S2	627	36	19,22,23	3.36	7 (36%)	25,31,34	1.79	4 (16%)
40	5MC	L5	4447	40	19,22,23	0.96	2 (10%)	26,32,35	0.70	0
40	A2M	L5	4590	40	22,25,26	1.24	2 (9%)	30,36,39	1.58	5 (16%)
40	OMC	L5	2861	40	19,22,23	0.68	0	25,31,34	0.80	1 (4%)
36	OMC	S2	1703	36	19,22,23	0.65	0	25,31,34	0.68	0
36	PSU	S2	1244	36	18,21,22	1.08	1 (5%)	21,30,33	1.99	5 (23%)
40	OMG	L5	4392	40	23,26,27	0.64	0	32,38,41	0.48	0
40	PSU	L5	4521	40,86	18,21,22	1.08	2 (11%)	21,30,33	1.99	4 (19%)
36	OMC	S2	462	36	19,22,23	0.59	0	25,31,34	0.78	0
40	OMG	L5	4618	40	23,26,27	0.61	0	32,38,41	0.52	0
36	OMC	S2	517	36	19,22,23	0.56	0	25,31,34	0.67	0
36	PSU	S2	1232	36	18,21,22	1.08	1 (5%)	21,30,33	1.93	4 (19%)
40	6MZ	L5	4220	40	22,25,26	2.89	6 (27%)	29,36,39	2.47	10 (34%)
36	A2M	S2	1031	36	22,25,26	1.15	1 (4%)	30,36,39	1.56	7 (23%)
36	A2M	S2	166	36	22,25,26	1.24	1 (4%)	30,36,39	1.62	7 (23%)
36	4AC	S2	1842	36	21,24,25	0.40	0	28,34,37	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
40	PSU	L5	3637	40	18,21,22	1.07	2 (11%)	21,30,33	2.00	5 (23%)
40	OMU	L5	2837	40	19,22,23	3.24	7 (36%)	25,31,34	1.91	5 (20%)
40	OMU	L5	4227	40	19,22,23	3.20	7 (36%)	25,31,34	1.86	4 (16%)
40	A2M	L5	400	40	22,25,26	1.29	3 (13%)	30,36,39	1.55	8 (26%)
40	PSU	L5	4493	40	18,21,22	1.02	1 (5%)	21,30,33	1.91	4 (19%)
36	PSU	S2	863	36	18,21,22	1.13	1 (5%)	21,30,33	1.89	4 (19%)
40	PSU	L5	1582	40	18,21,22	1.04	1 (5%)	21,30,33	1.81	4 (19%)
40	A2M	L5	3825	40	22,25,26	1.21	2 (9%)	30,36,39	1.58	8 (26%)
36	OMU	S2	799	36	19,22,23	3.39	7 (36%)	25,31,34	1.83	5 (20%)
40	A2M	L5	3785	40,86	22,25,26	1.23	1 (4%)	30,36,39	1.65	10 (33%)
36	PSU	S2	406	36	18,21,22	1.09	2 (11%)	21,30,33	2.02	4 (19%)
40	OMC	L5	3841	40	19,22,23	0.66	0	25,31,34	0.67	0
36	OMG	S2	436	36	23,26,27	0.52	0	32,38,41	0.54	0
36	OMU	S2	1442	36	19,22,23	3.31	7 (36%)	25,31,34	1.80	5 (20%)
40	UY1	L5	3818	40	19,22,23	4.79	9 (47%)	21,31,34	2.00	5 (23%)
36	OMG	S2	509	36	23,26,27	0.51	0	32,38,41	0.51	0
40	PSU	L5	1782	40	18,21,22	1.07	1 (5%)	21,30,33	1.96	5 (23%)
36	OMU	S2	428	36	19,22,23	3.31	7 (36%)	25,31,34	1.84	5 (20%)
40	OMC	L5	3869	40	19,22,23	0.67	0	25,31,34	0.71	0
36	OMU	S2	354	36	19,22,23	3.26	7 (36%)	25,31,34	1.92	5 (20%)
36	PSU	S2	1056	36	18,21,22	1.05	2 (11%)	21,30,33	2.01	6 (28%)
36	G7M	S2	1639	3,36	23,26,27	2.63	9 (39%)	34,39,42	2.58	11 (32%)
36	MA6	S2	1850	36	23,26,27	2.69	9 (39%)	33,38,41	3.35	13 (39%)
40	UR3	L5	4530	40	19,22,23	2.61	7 (36%)	26,32,35	1.64	3 (11%)
40	PSU	L5	4431	40	18,21,22	1.04	2 (11%)	21,30,33	1.95	4 (19%)
40	OMG	L5	1522	40	23,26,27	0.63	0	32,38,41	0.65	1 (3%)
40	PSU	L5	1744	40,86	18,21,22	1.07	2 (11%)	21,30,33	1.96	4 (19%)
36	A2M	S2	668	86,36	22,25,26	1.31	2 (9%)	30,36,39	1.66	8 (26%)
36	A2M	S2	576	36	22,25,26	1.19	1 (4%)	30,36,39	1.54	5 (16%)
36	4AC	S2	1337	36	21,24,25	0.41	0	28,34,37	0.79	2 (7%)
40	OMG	L5	2364	40,86	23,26,27	0.62	0	32,38,41	0.45	0
36	OMG	S2	867	36	23,26,27	0.51	0	32,38,41	0.46	0
40	OMG	L5	3792	40	23,26,27	0.60	0	32,38,41	0.49	0
40	OMU	L5	4306	40	19,22,23	3.21	7 (36%)	25,31,34	1.90	5 (20%)
40	PSU	L5	4689	40	18,21,22	1.04	2 (11%)	21,30,33	1.98	4 (19%)
36	OMC	S2	1391	36	19,22,23	0.58	0	25,31,34	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
40	A2M	L5	2401	40	22,25,26	1.24	2 (9%)	30,36,39	1.61	8 (26%)
36	6MZ	S2	1832	86,36	22,25,26	4.04	11 (50%)	29,36,39	2.33	9 (31%)
40	OMG	L5	3899	40	23,26,27	0.65	0	32,38,41	0.54	0
40	OMC	L5	3887	40	19,22,23	0.67	0	25,31,34	0.67	0
36	PSU	S2	1174	36	18,21,22	1.07	2 (11%)	21,30,33	1.89	4 (19%)
40	A2M	L5	1524	40	22,25,26	1.32	3 (13%)	30,36,39	1.52	6 (20%)
40	OMG	L5	1625	40	23,26,27	0.59	0	32,38,41	0.46	0
36	PSU	S2	801	36	18,21,22	1.11	1 (5%)	21,30,33	1.78	4 (19%)
40	A2M	L5	2815	40	22,25,26	1.19	2 (9%)	30,36,39	1.53	9 (30%)
40	OMC	L5	4536	40	19,22,23	0.68	0	25,31,34	0.71	0
40	OMC	L5	3808	40	19,22,23	0.72	0	25,31,34	0.89	2 (8%)
40	OMG	L5	3744	40	23,26,27	0.60	0	32,38,41	0.47	0
40	PSU	L5	4293	40	18,21,22	1.07	2 (11%)	21,30,33	2.05	4 (19%)
40	PSU	L5	1860	40	18,21,22	1.07	2 (11%)	21,30,33	1.96	4 (19%)
40	PSU	L5	1792	40	18,21,22	1.05	1 (5%)	21,30,33	1.91	4 (19%)
40	5MC	L5	3782	40,86	19,22,23	0.76	0	26,32,35	0.77	1 (3%)
36	OMC	S2	1272	36	19,22,23	0.62	0	25,31,34	0.84	1 (4%)
40	A2M	L5	398	40	22,25,26	1.18	1 (4%)	30,36,39	1.67	7 (23%)
40	PSU	L5	4471	40	18,21,22	1.05	2 (11%)	21,30,33	1.95	4 (19%)
40	PSU	L5	1781	40	18,21,22	1.05	1 (5%)	21,30,33	1.84	4 (19%)
36	OMG	S2	1490	36	23,26,27	0.57	0	32,38,41	0.47	0
42	PSU	L8	69	42	18,21,22	1.09	2 (11%)	21,30,33	2.04	6 (28%)
40	OMC	L5	4456	40	19,22,23	0.76	1 (5%)	25,31,34	0.77	0
36	PSU	S2	814	36	18,21,22	1.07	1 (5%)	21,30,33	1.83	4 (19%)
40	OMC	L5	2365	40,86	19,22,23	0.66	0	25,31,34	0.59	0
40	OMC	L5	2351	40,86	19,22,23	0.74	1 (5%)	25,31,34	0.88	1 (4%)
36	PSU	S2	105	36	18,21,22	1.06	1 (5%)	21,30,33	1.86	4 (19%)
40	OMG	L5	4196	40	23,26,27	0.60	0	32,38,41	0.42	0
36	PSU	S2	1177	36	18,21,22	1.04	2 (11%)	21,30,33	1.98	4 (19%)
36	OMG	S2	1328	36	23,26,27	0.51	0	32,38,41	0.44	0
36	A2M	S2	484	36	22,25,26	1.17	1 (4%)	30,36,39	1.47	8 (26%)
40	PSU	L5	3695	40	18,21,22	1.03	2 (11%)	21,30,33	1.97	4 (19%)
40	A2M	L5	1534	40,86	22,25,26	1.20	2 (9%)	30,36,39	1.42	7 (23%)
40	OMG	L5	3627	40	23,26,27	0.60	0	32,38,41	0.59	0
40	OMG	L5	2876	40	23,26,27	0.58	0	32,38,41	0.52	0
40	PSU	L5	1536	40	18,21,22	1.06	2 (11%)	21,30,33	1.94	4 (19%)
40	PSU	L5	4457	40	18,21,22	1.03	2 (11%)	21,30,33	2.02	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	OMU	S2	116	36	19,22,23	3.29	7 (36%)	25,31,34	1.69	4 (16%)
40	PSU	L5	4296	40	18,21,22	1.10	2 (11%)	21,30,33	1.97	4 (19%)
40	A2M	L5	1871	40,86	22,25,26	1.35	3 (13%)	30,36,39	1.64	7 (23%)
40	PSU	L5	4312	40	18,21,22	1.07	2 (11%)	21,30,33	1.92	4 (19%)
40	PSU	L5	4403	40	18,21,22	1.05	2 (11%)	21,30,33	2.08	6 (28%)
36	OMG	S2	644	36	23,26,27	0.50	0	32,38,41	0.46	0
36	OMU	S2	121	36	19,22,23	3.33	7 (36%)	25,31,34	1.85	5 (20%)
40	PSU	L5	4353	40	18,21,22	1.07	2 (11%)	21,30,33	2.04	6 (28%)
40	PSU	L5	4972	40	18,21,22	1.06	2 (11%)	21,30,33	1.92	4 (19%)
40	OMU	L5	3925	40	19,22,23	3.19	7 (36%)	25,31,34	1.92	5 (20%)
36	OMU	S2	172	36	19,22,23	3.31	7 (36%)	25,31,34	1.83	5 (20%)
40	OMG	L5	4370	40	23,26,27	0.61	0	32,38,41	0.55	0
42	OMG	L8	75	42	23,26,27	0.57	0	32,38,41	0.53	0
40	PSU	L5	3851	40	18,21,22	1.06	1 (5%)	21,30,33	1.98	4 (19%)
36	PSU	S2	681	36	18,21,22	1.03	1 (5%)	21,30,33	1.95	4 (19%)
40	PSU	L5	3822	40	18,21,22	1.03	1 (5%)	21,30,33	1.98	5 (23%)
40	A2M	L5	1326	40	22,25,26	1.26	2 (9%)	30,36,39	1.53	9 (30%)
36	MA6	S2	1851	36	23,26,27	1.30	2 (8%)	33,38,41	3.41	12 (36%)
40	A2M	L5	3830	40	22,25,26	1.22	2 (9%)	30,36,39	1.58	6 (20%)
36	OMU	S2	1288	36	19,22,23	3.35	7 (36%)	25,31,34	1.77	5 (20%)
40	A2M	L5	2787	40	22,25,26	1.19	1 (4%)	30,36,39	1.53	8 (26%)
40	PSU	L5	2632	40	18,21,22	1.04	2 (11%)	21,30,33	2.02	5 (23%)
40	PSU	L5	4973	40	18,21,22	1.03	2 (11%)	21,30,33	1.99	5 (23%)
40	OMC	L5	1340	40	19,22,23	0.71	0	25,31,34	0.78	0
40	OMC	L5	2804	40	19,22,23	0.68	0	25,31,34	0.64	0
36	PSU	S2	866	36	18,21,22	1.07	2 (11%)	21,30,33	2.01	6 (28%)
40	A2M	L5	2363	40,86	22,25,26	1.25	2 (9%)	30,36,39	1.55	9 (30%)
40	PSU	L5	5001	40	18,21,22	1.06	1 (5%)	21,30,33	1.91	4 (19%)
40	PSU	L5	4628	40	18,21,22	1.06	2 (11%)	21,30,33	2.02	4 (19%)
40	PSU	L5	4299	40	18,21,22	1.04	1 (5%)	21,30,33	1.94	4 (19%)
36	B8N	S2	1248	36	25,29,30	3.25	7 (28%)	28,42,45	2.01	8 (28%)
36	OMU	S2	1326	36	19,22,23	3.29	7 (36%)	25,31,34	1.88	5 (20%)
40	PSU	L5	4579	40	18,21,22	1.05	2 (11%)	21,30,33	1.92	4 (19%)
40	OMG	L5	4637	40	23,26,27	0.60	0	32,38,41	0.47	0
40	OMG	L5	4228	40	23,26,27	0.58	0	32,38,41	0.60	0
36	OMG	S2	683	36	23,26,27	0.55	0	32,38,41	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
40	PSU	L5	3920	40,86	18,21,22	1.07	2 (11%)	21,30,33	1.96	4 (19%)

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
40	PSU	L5	1862	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	4532	40	-	0/7/25/26	0/2/2/2
40	A2M	L5	4571	40	-	0/9/27/28	0/3/3/3
40	OMU	L5	4620	40	-	0/9/27/28	0/2/2/2
40	1MA	L5	1322	40,86	-	2/7/25/26	0/3/3/3
42	PSU	L8	55	42	-	0/7/25/26	0/2/2/2
36	PSU	S2	686	36	-	0/7/25/26	0/2/2/2
40	A2M	L5	3718	40	-	0/9/27/28	0/3/3/3
36	PSU	S2	1367	36	-	0/7/25/26	0/2/2/2
36	PSU	S2	651	36	-	0/7/25/26	0/2/2/2
40	OMC	L5	2824	40	-	1/9/27/28	0/2/2/2
36	PSU	S2	649	36	-	0/7/25/26	0/2/2/2
40	PSU	L5	2839	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	3884	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	4361	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	1683	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	1677	40	-	1/7/25/26	0/2/2/2
40	OMU	L5	4498	40	-	0/9/27/28	0/2/2/2
40	OMG	L5	2424	40	-	0/9/27/28	0/3/3/3
40	OMG	L5	1316	40	-	0/9/27/28	0/3/3/3
36	PSU	S2	966	86,36	-	0/7/25/26	0/2/2/2
36	PSU	S2	1045	36	-	2/7/25/26	0/2/2/2
36	PSU	S2	1046	36	-	0/7/25/26	0/2/2/2
36	OMC	S2	174	36	-	0/9/27/28	0/2/2/2
36	PSU	S2	93	36	-	0/7/25/26	0/2/2/2
40	PSU	L5	4500	40	-	3/7/25/26	0/2/2/2
36	A2M	S2	99	86,36	-	2/9/27/28	0/3/3/3
40	PSU	L5	4636	40	-	2/7/25/26	0/2/2/2
40	OMG	L5	4499	40	-	0/9/27/28	0/3/3/3
36	A2M	S2	27	36	-	1/9/27/28	0/3/3/3
40	PSU	L5	3639	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	4552	40	-	0/7/25/26	0/2/2/2
40	A2M	L5	4523	40,86	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
40	OMC	L5	3701	40	-	5/9/27/28	0/2/2/2
36	A2M	S2	468	36	-	0/9/27/28	0/3/3/3
36	PSU	S2	1004	36	-	0/7/25/26	0/2/2/2
40	PSU	L5	4673	40,86	-	0/7/25/26	0/2/2/2
40	PSU	L5	3853	40,86	-	0/7/25/26	0/2/2/2
36	A2M	S2	1383	36	-	3/9/27/28	0/3/3/3
40	PSU	L5	4442	40	-	0/7/25/26	0/2/2/2
40	OMC	L5	2422	40,86	-	2/9/27/28	0/2/2/2
40	PSU	L5	3844	40	-	1/7/25/26	0/2/2/2
40	PSU	L5	5010	40	-	0/7/25/26	0/2/2/2
40	OMG	L5	4623	40	-	0/9/27/28	0/3/3/3
40	OMG	L5	4494	40	-	1/9/27/28	0/3/3/3
40	PSU	L5	4576	40	-	0/7/25/26	0/2/2/2
40	A2M	L5	1323	40	-	2/9/27/28	0/3/3/3
36	A2M	S2	159	36	-	1/9/27/28	0/3/3/3
36	PSU	S2	1081	36	-	1/7/25/26	0/2/2/2
40	A2M	L5	3867	40	-	2/9/27/28	0/3/3/3
36	PSU	S2	109	36	-	0/7/25/26	0/2/2/2
36	OMG	S2	601	36	-	1/9/27/28	0/3/3/3
36	OMU	S2	627	36	-	6/9/27/28	0/2/2/2
40	5MC	L5	4447	40	-	4/7/25/26	0/2/2/2
40	A2M	L5	4590	40	-	3/9/27/28	0/3/3/3
40	OMC	L5	2861	40	-	0/9/27/28	0/2/2/2
36	OMC	S2	1703	36	-	1/9/27/28	0/2/2/2
36	PSU	S2	1244	36	-	0/7/25/26	0/2/2/2
40	OMG	L5	4392	40	-	0/9/27/28	0/3/3/3
40	PSU	L5	4521	40,86	-	0/7/25/26	0/2/2/2
36	OMC	S2	462	36	-	1/9/27/28	0/2/2/2
40	OMG	L5	4618	40	-	1/9/27/28	0/3/3/3
36	OMC	S2	517	36	-	0/9/27/28	0/2/2/2
36	PSU	S2	1232	36	-	0/7/25/26	0/2/2/2
40	6MZ	L5	4220	40	-	2/9/27/28	0/3/3/3
36	A2M	S2	1031	36	-	1/9/27/28	0/3/3/3
36	A2M	S2	166	36	-	0/9/27/28	0/3/3/3
36	4AC	S2	1842	36	-	0/11/29/30	0/2/2/2
40	PSU	L5	3637	40	-	0/7/25/26	0/2/2/2
40	OMU	L5	2837	40	-	0/9/27/28	0/2/2/2
40	OMU	L5	4227	40	-	0/9/27/28	0/2/2/2
40	A2M	L5	400	40	-	1/9/27/28	0/3/3/3
40	PSU	L5	4493	40	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	PSU	S2	863	36	-	0/7/25/26	0/2/2/2
40	PSU	L5	1582	40	-	0/7/25/26	0/2/2/2
40	A2M	L5	3825	40	-	0/9/27/28	0/3/3/3
36	OMU	S2	799	36	-	2/9/27/28	0/2/2/2
40	A2M	L5	3785	40,86	-	2/9/27/28	0/3/3/3
36	PSU	S2	406	36	-	0/7/25/26	0/2/2/2
40	OMC	L5	3841	40	-	0/9/27/28	0/2/2/2
36	OMG	S2	436	36	-	0/9/27/28	0/3/3/3
36	OMU	S2	1442	36	-	2/9/27/28	0/2/2/2
40	UY1	L5	3818	40	-	3/9/27/28	0/2/2/2
36	OMG	S2	509	36	-	0/9/27/28	0/3/3/3
40	PSU	L5	1782	40	-	0/7/25/26	0/2/2/2
36	OMU	S2	428	36	-	4/9/27/28	0/2/2/2
40	OMC	L5	3869	40	-	0/9/27/28	0/2/2/2
36	OMU	S2	354	36	-	0/9/27/28	0/2/2/2
36	PSU	S2	1056	36	-	0/7/25/26	0/2/2/2
36	G7M	S2	1639	3,36	-	1/7/25/26	0/3/3/3
36	MA6	S2	1850	36	-	0/11/29/30	0/3/3/3
40	UR3	L5	4530	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	4431	40	-	0/7/25/26	0/2/2/2
40	OMG	L5	1522	40	-	0/9/27/28	0/3/3/3
40	PSU	L5	1744	40,86	-	0/7/25/26	0/2/2/2
36	A2M	S2	668	86,36	-	3/9/27/28	0/3/3/3
36	A2M	S2	576	36	-	3/9/27/28	0/3/3/3
36	4AC	S2	1337	36	-	1/11/29/30	0/2/2/2
40	OMG	L5	2364	40,86	-	3/9/27/28	0/3/3/3
36	OMG	S2	867	36	-	2/9/27/28	0/3/3/3
40	OMG	L5	3792	40	-	2/9/27/28	0/3/3/3
40	OMU	L5	4306	40	-	0/9/27/28	0/2/2/2
40	PSU	L5	4689	40	-	0/7/25/26	0/2/2/2
36	OMC	S2	1391	36	-	0/9/27/28	0/2/2/2
40	A2M	L5	2401	40	-	1/9/27/28	0/3/3/3
36	6MZ	S2	1832	86,36	-	2/9/27/28	0/3/3/3
40	OMG	L5	3899	40	-	3/9/27/28	0/3/3/3
40	OMC	L5	3887	40	-	1/9/27/28	0/2/2/2
36	PSU	S2	1174	36	-	0/7/25/26	0/2/2/2
40	A2M	L5	1524	40	-	3/9/27/28	0/3/3/3
40	OMG	L5	1625	40	-	2/9/27/28	0/3/3/3
36	PSU	S2	801	36	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
40	A2M	L5	2815	40	-	2/9/27/28	0/3/3/3
40	OMC	L5	4536	40	-	0/9/27/28	0/2/2/2
40	OMC	L5	3808	40	-	1/9/27/28	0/2/2/2
40	OMG	L5	3744	40	-	0/9/27/28	0/3/3/3
40	PSU	L5	4293	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	1860	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	1792	40	-	0/7/25/26	0/2/2/2
40	5MC	L5	3782	40,86	-	1/7/25/26	0/2/2/2
36	OMC	S2	1272	36	-	2/9/27/28	0/2/2/2
40	A2M	L5	398	40	-	0/9/27/28	0/3/3/3
40	PSU	L5	4471	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	1781	40	-	1/7/25/26	0/2/2/2
36	OMG	S2	1490	36	-	1/9/27/28	0/3/3/3
42	PSU	L8	69	42	-	0/7/25/26	0/2/2/2
40	OMC	L5	4456	40	-	0/9/27/28	0/2/2/2
36	PSU	S2	814	36	-	0/7/25/26	0/2/2/2
40	OMC	L5	2365	40,86	-	0/9/27/28	0/2/2/2
40	OMC	L5	2351	40,86	-	1/9/27/28	0/2/2/2
36	PSU	S2	105	36	-	0/7/25/26	0/2/2/2
40	OMG	L5	4196	40	-	1/9/27/28	0/3/3/3
36	PSU	S2	1177	36	-	0/7/25/26	0/2/2/2
36	OMG	S2	1328	36	-	0/9/27/28	0/3/3/3
36	A2M	S2	484	36	-	0/9/27/28	0/3/3/3
40	PSU	L5	3695	40	-	0/7/25/26	0/2/2/2
40	A2M	L5	1534	40,86	-	1/9/27/28	0/3/3/3
40	OMG	L5	3627	40	-	0/9/27/28	0/3/3/3
40	OMG	L5	2876	40	-	0/9/27/28	0/3/3/3
40	PSU	L5	1536	40	-	2/7/25/26	0/2/2/2
40	PSU	L5	4457	40	-	0/7/25/26	0/2/2/2
36	OMU	S2	116	36	-	0/9/27/28	0/2/2/2
40	PSU	L5	4296	40	-	2/7/25/26	0/2/2/2
40	A2M	L5	1871	40,86	-	0/9/27/28	0/3/3/3
40	PSU	L5	4312	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	4403	40	-	0/7/25/26	0/2/2/2
36	OMG	S2	644	36	-	3/9/27/28	0/3/3/3
36	OMU	S2	121	36	-	0/9/27/28	0/2/2/2
40	PSU	L5	4353	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	4972	40	-	0/7/25/26	0/2/2/2
40	OMU	L5	3925	40	-	1/9/27/28	0/2/2/2
36	OMU	S2	172	36	-	0/9/27/28	0/2/2/2
40	OMG	L5	4370	40	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
42	OMG	L8	75	42	-	1/9/27/28	0/3/3/3
40	PSU	L5	3851	40	-	1/7/25/26	0/2/2/2
36	PSU	S2	681	36	-	0/7/25/26	0/2/2/2
40	PSU	L5	3822	40	-	0/7/25/26	0/2/2/2
40	A2M	L5	1326	40	-	4/9/27/28	0/3/3/3
36	MA6	S2	1851	36	-	1/11/29/30	0/3/3/3
40	A2M	L5	3830	40	-	0/9/27/28	0/3/3/3
36	OMU	S2	1288	36	-	2/9/27/28	0/2/2/2
40	A2M	L5	2787	40	-	5/9/27/28	0/3/3/3
40	PSU	L5	2632	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	4973	40	-	0/7/25/26	0/2/2/2
40	OMC	L5	1340	40	-	1/9/27/28	0/2/2/2
40	OMC	L5	2804	40	-	0/9/27/28	0/2/2/2
36	PSU	S2	866	36	-	0/7/25/26	0/2/2/2
40	A2M	L5	2363	40,86	-	0/9/27/28	0/3/3/3
40	PSU	L5	5001	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	4628	40	-	0/7/25/26	0/2/2/2
40	PSU	L5	4299	40	-	0/7/25/26	0/2/2/2
36	B8N	S2	1248	36	-	1/16/34/35	0/2/2/2
36	OMU	S2	1326	36	-	0/9/27/28	0/2/2/2
40	PSU	L5	4579	40	-	0/7/25/26	0/2/2/2
40	OMG	L5	4637	40	-	2/9/27/28	0/3/3/3
40	OMG	L5	4228	40	-	2/9/27/28	0/3/3/3
36	OMG	S2	683	36	-	2/9/27/28	0/3/3/3
40	PSU	L5	3920	40,86	-	0/7/25/26	0/2/2/2

The worst 5 of 343 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	S2	1832	6MZ	C6-N6	12.83	1.48	1.34
40	L5	3818	UY1	C6-C5	12.43	1.49	1.35
40	L5	4220	6MZ	C6-N6	11.49	1.47	1.34
40	L5	3818	UY1	C2-N1	11.45	1.51	1.36
36	S2	799	OMU	C2-N1	8.55	1.51	1.38

The worst 5 of 703 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	S2	1851	MA6	N1-C6-N6	-12.23	101.95	116.86
36	S2	1850	MA6	N1-C6-N6	-11.47	102.89	116.86
36	S2	1851	MA6	C5-C6-N6	8.09	138.14	125.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	S2	1850	MA6	C5-C6-N6	7.75	137.59	125.33
36	S2	1639	G7M	C1'-N9-C4	7.42	148.41	126.49

There are no chirality outliers.

5 of 136 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
42	L8	75	OMG	C1'-C2'-O2'-CM2
36	S2	27	A2M	C1'-C2'-O2'-CM'
36	S2	159	A2M	C1'-C2'-O2'-CM'
36	S2	462	OMC	C1'-C2'-O2'-CM2
36	S2	601	OMG	C1'-C2'-O2'-CM2

There are no ring outliers.

61 monomers are involved in 84 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
40	L5	4571	A2M	1	0
40	L5	4620	OMU	2	0
40	L5	3718	A2M	2	0
40	L5	2824	OMC	1	0
36	S2	649	PSU	1	0
40	L5	1683	PSU	1	0
36	S2	93	PSU	1	0
36	S2	99	A2M	2	0
36	S2	27	A2M	2	0
40	L5	4523	A2M	1	0
40	L5	3701	OMC	1	0
36	S2	1383	A2M	1	0
40	L5	2422	OMC	1	0
40	L5	4623	OMG	1	0
36	S2	159	A2M	2	0
40	L5	3867	A2M	3	0
36	S2	601	OMG	1	0
40	L5	4392	OMG	1	0
40	L5	4521	PSU	1	0
36	S2	462	OMC	2	0
36	S2	1232	PSU	2	0
36	S2	1031	A2M	2	0
36	S2	166	A2M	1	0
36	S2	1842	4AC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
40	L5	400	A2M	1	0
40	L5	3818	UY1	1	0
36	S2	509	OMG	1	0
36	S2	428	OMU	2	0
36	S2	1639	G7M	1	0
36	S2	1850	MA6	2	0
40	L5	4431	PSU	1	0
36	S2	576	A2M	2	0
36	S2	1337	4AC	3	0
40	L5	2364	OMG	1	0
36	S2	867	OMG	1	0
40	L5	4536	OMC	1	0
40	L5	3808	OMC	1	0
40	L5	3782	5MC	1	0
40	L5	1781	PSU	1	0
40	L5	4456	OMC	1	0
40	L5	2351	OMC	2	0
40	L5	4196	OMG	1	0
36	S2	1328	OMG	1	0
36	S2	484	A2M	1	0
40	L5	1534	A2M	1	0
40	L5	4457	PSU	1	0
36	S2	116	OMU	3	0
40	L5	1871	A2M	1	0
36	S2	644	OMG	1	0
36	S2	121	OMU	1	0
40	L5	4353	PSU	1	0
42	L8	75	OMG	2	0
36	S2	681	PSU	1	0
40	L5	3822	PSU	2	0
40	L5	1326	A2M	3	0
40	L5	3830	A2M	1	0
36	S2	1288	OMU	1	0
40	L5	2632	PSU	1	0
40	L5	1340	OMC	2	0
40	L5	2363	A2M	1	0
40	L5	3920	PSU	1	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 241 ligands modelled in this entry, 224 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
89	SPD	L5	5289	-	9,9,9	0.32	0	8,8,8	0.85	0
89	SPD	L5	5285	-	9,9,9	0.33	0	8,8,8	0.94	0
88	SPM	L5	5258	-	13,13,13	0.36	0	12,12,12	0.93	0
88	SPM	L5	5291	-	13,13,13	0.35	0	12,12,12	0.84	0
88	SPM	L5	5292	-	13,13,13	0.35	0	12,12,12	0.85	0
89	SPD	L5	5283	-	9,9,9	0.32	0	8,8,8	0.90	0
89	SPD	L5	5284	-	9,9,9	0.31	0	8,8,8	0.78	0
89	SPD	L5	5290	-	9,9,9	0.32	0	8,8,8	0.83	0
88	SPM	L5	5263	-	13,13,13	0.34	0	12,12,12	0.96	0
89	SPD	L8	201	-	9,9,9	0.32	0	8,8,8	0.90	0
89	SPD	LN	301	-	9,9,9	0.35	0	8,8,8	0.92	0
89	SPD	L5	5261	-	9,9,9	0.32	0	8,8,8	0.96	0
88	SPM	L5	5288	-	13,13,13	0.35	0	12,12,12	0.98	0
88	SPM	L5	5267	-	13,13,13	0.36	0	12,12,12	0.94	0
88	SPM	L5	5264	-	13,13,13	0.37	0	12,12,12	1.07	0
89	SPD	L5	5286	-	9,9,9	0.32	0	8,8,8	0.85	0
89	SPD	L5	5287	-	9,9,9	0.32	0	8,8,8	0.81	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
89	SPD	L5	5289	-	-	3/7/7/7	-
89	SPD	L5	5285	-	-	4/7/7/7	-
88	SPM	L5	5258	-	-	4/11/11/11	-
88	SPM	L5	5291	-	-	4/11/11/11	-
88	SPM	L5	5292	-	-	4/11/11/11	-
89	SPD	L5	5283	-	-	1/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
89	SPD	L5	5284	-	-	3/7/7/7	-
89	SPD	L5	5290	-	-	4/7/7/7	-
88	SPM	L5	5263	-	-	4/11/11/11	-
89	SPD	L8	201	-	-	4/7/7/7	-
89	SPD	LN	301	-	-	2/7/7/7	-
89	SPD	L5	5261	-	-	0/7/7/7	-
88	SPM	L5	5288	-	-	4/11/11/11	-
88	SPM	L5	5267	-	-	4/11/11/11	-
88	SPM	L5	5264	-	-	7/11/11/11	-
89	SPD	L5	5286	-	-	2/7/7/7	-
89	SPD	L5	5287	-	-	2/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 56 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
88	L5	5264	SPM	N5-C6-C7-C8
89	L5	5284	SPD	C3-C4-C5-N6
88	L5	5263	SPM	N10-C11-C12-C13
88	L5	5292	SPM	N10-C11-C12-C13
89	L5	5285	SPD	N6-C7-C8-C9

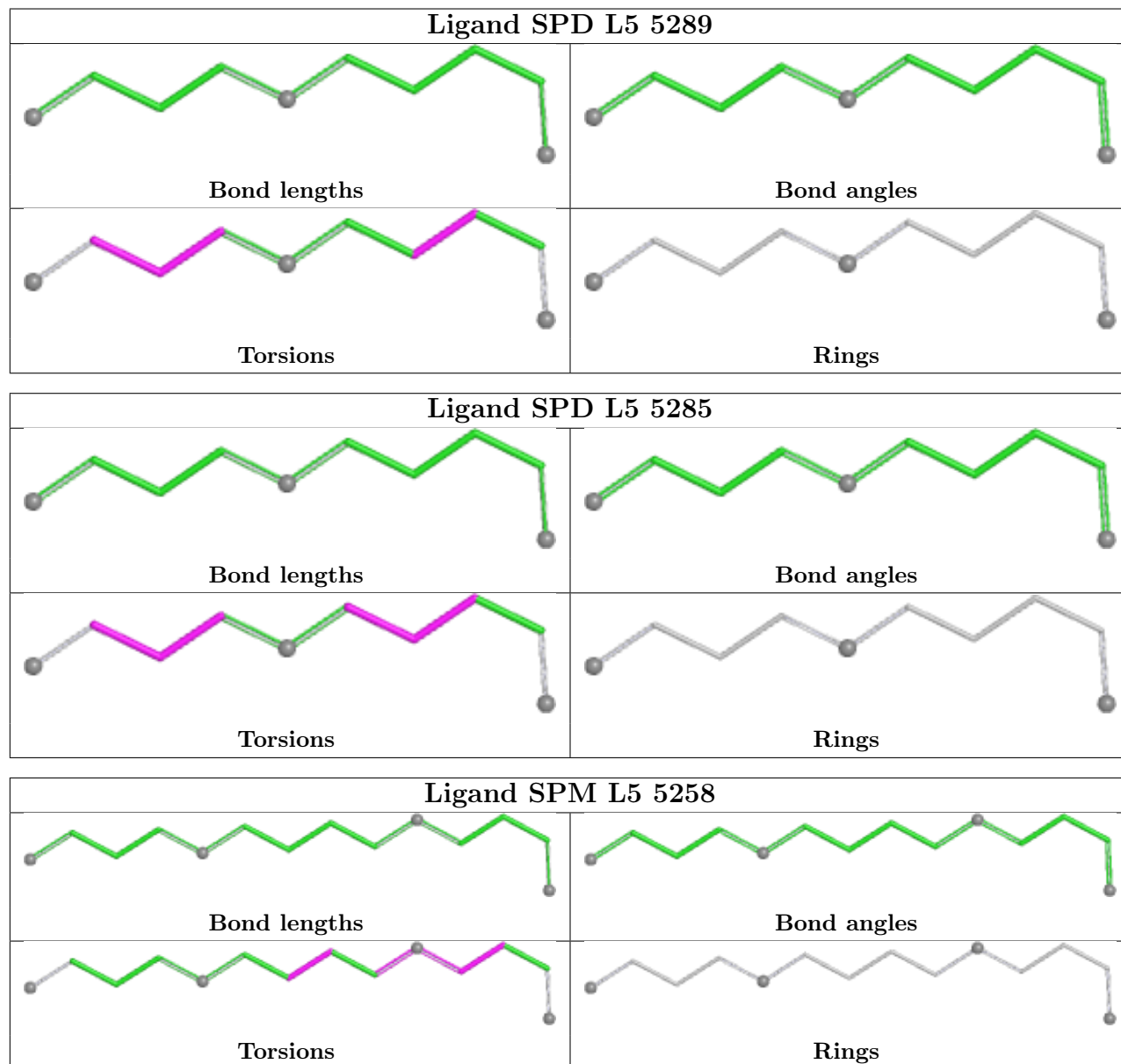
There are no ring outliers.

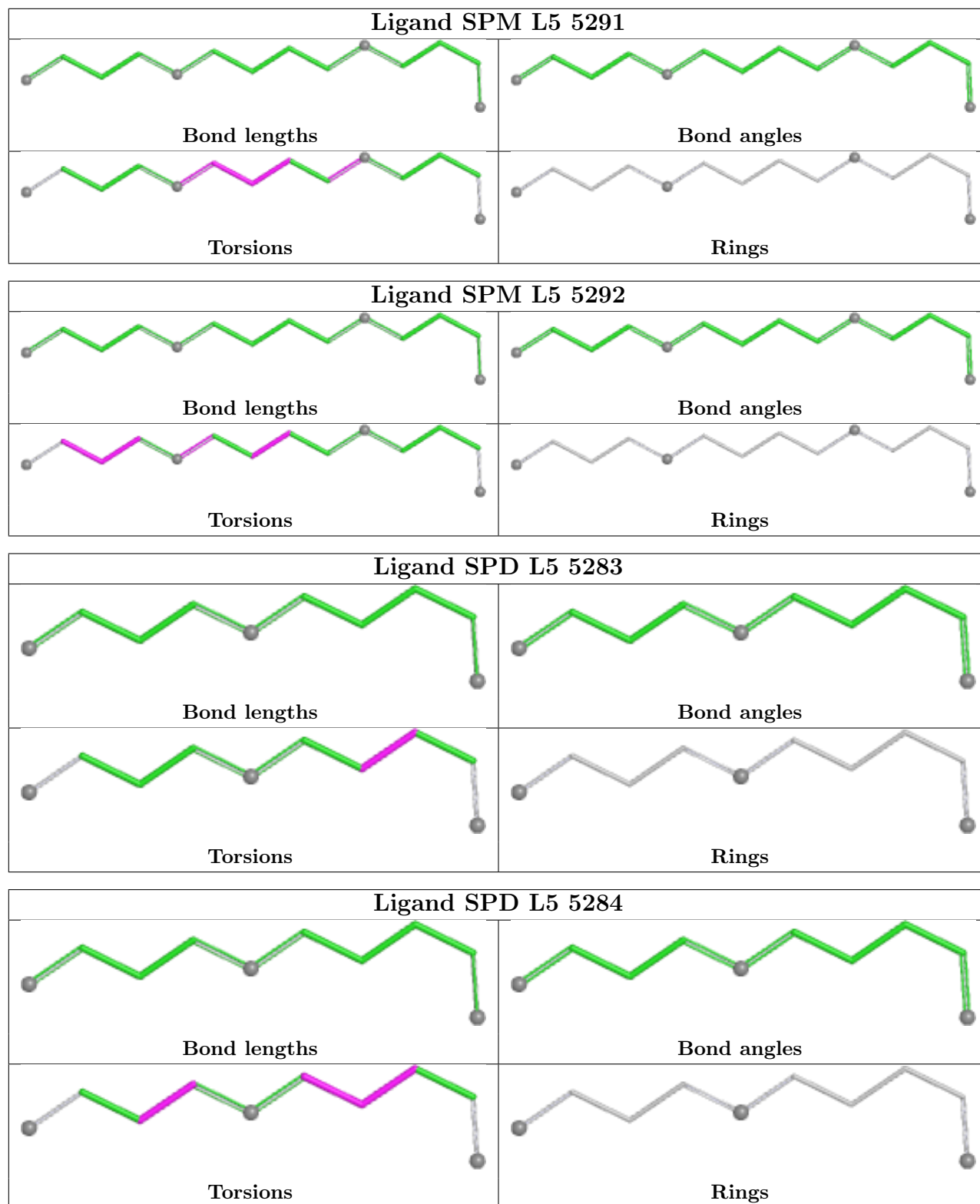
7 monomers are involved in 8 short contacts:

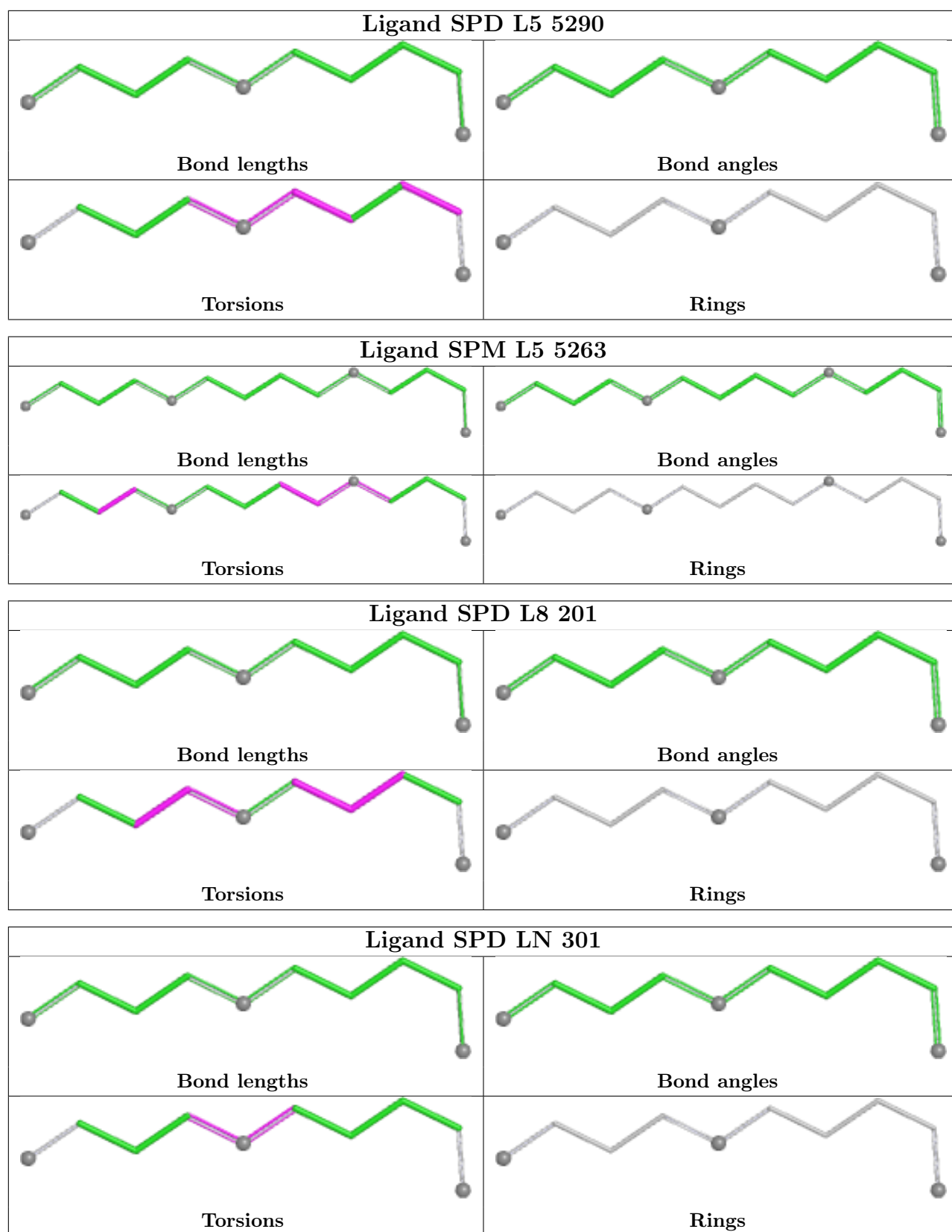
Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	L5	5291	SPM	2	0
88	L5	5292	SPM	1	0
89	L5	5284	SPD	1	0
88	L5	5263	SPM	1	0
89	L5	5261	SPD	1	0
88	L5	5264	SPM	1	0
89	L5	5286	SPD	1	0

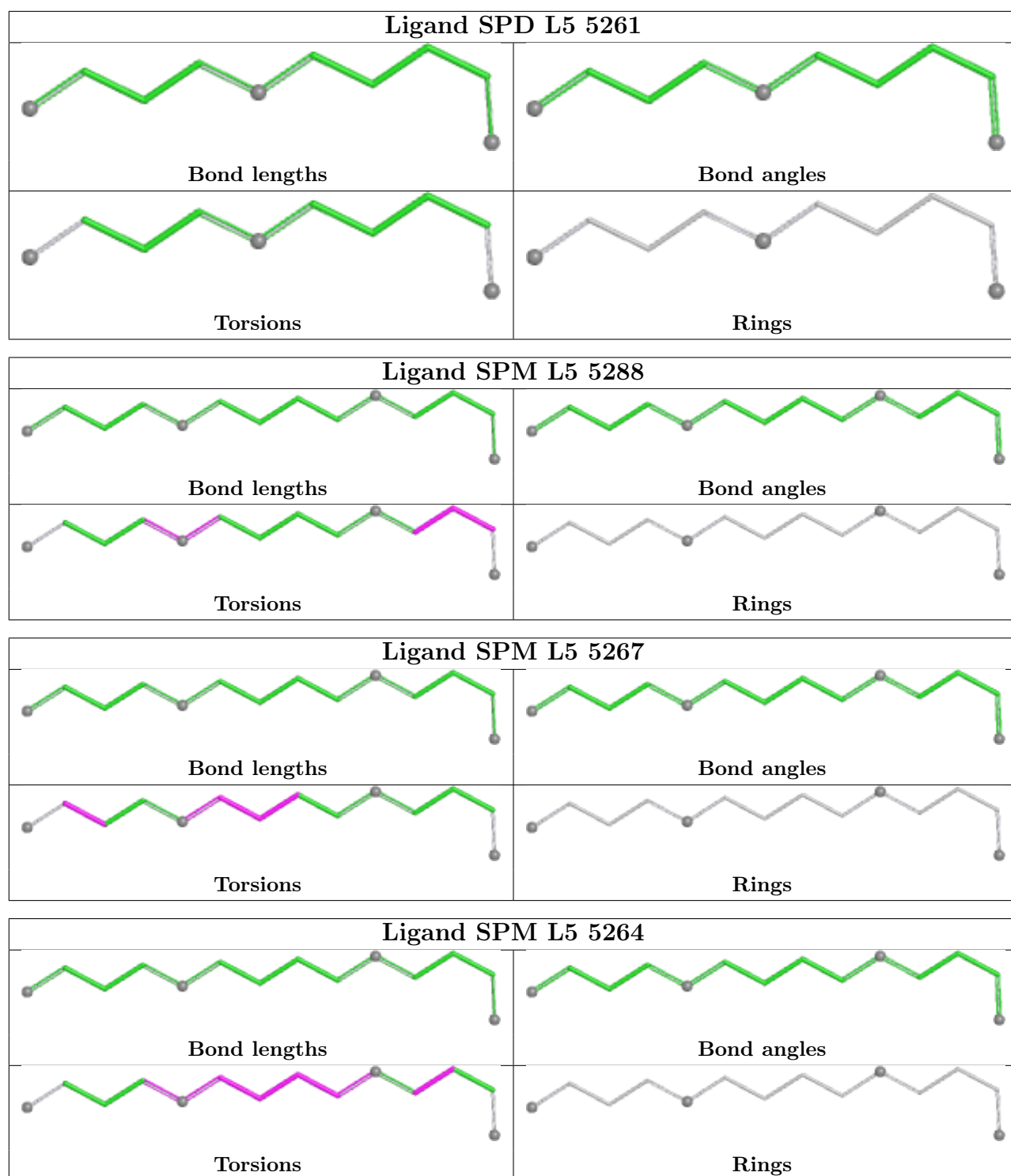
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

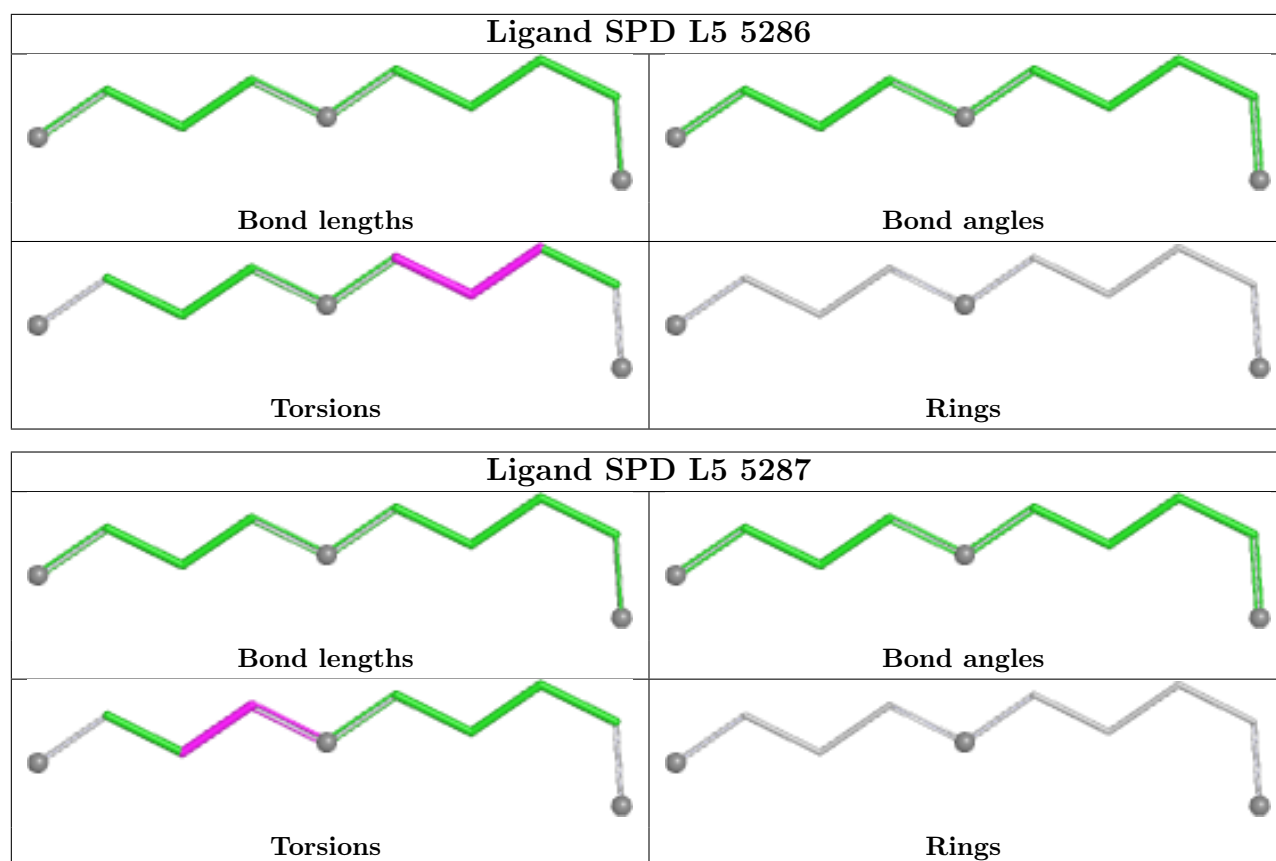
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. 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
40	L5	10
36	S2	4
1	AP	1
3	PE	1

The worst 5 of 16 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	753:C	O3'	785:C	P	28.44
1	L5	2910:G	O3'	3584:C	P	20.91
1	L5	1706:A	O3'	1716:G	P	20.70
1	L5	760:G	O3'	903:C	P	17.17

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L5	3954:A	O3'	4056:A	P	16.36

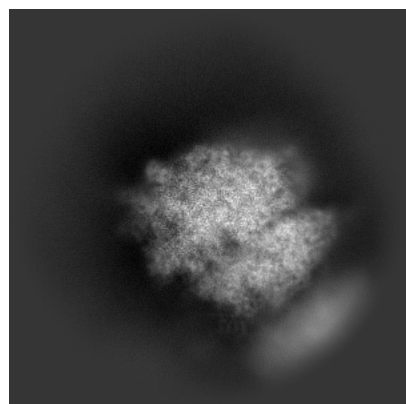
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71332. These allow visual inspection of the internal detail of the map and identification of artifacts.

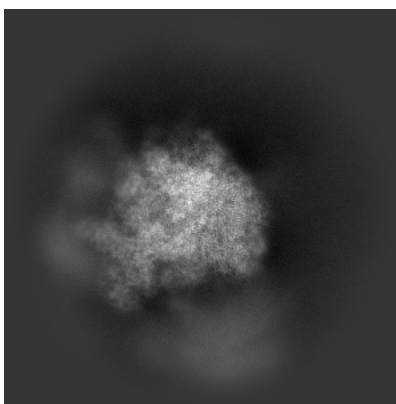
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

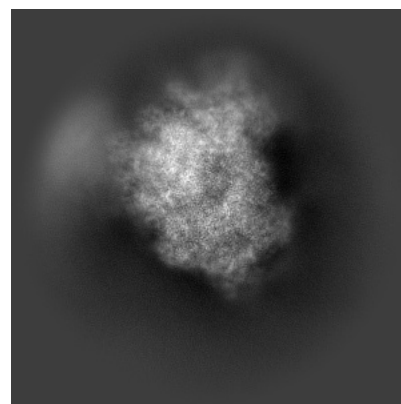
6.1.1 Primary map



X

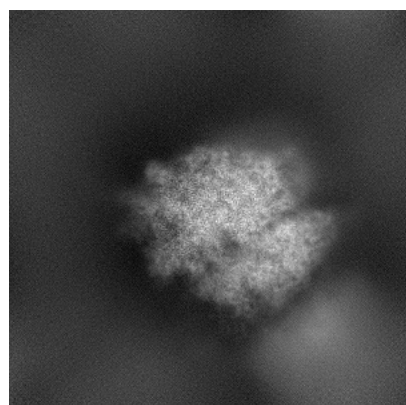


Y

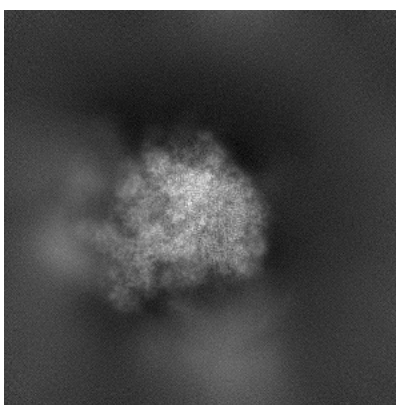


Z

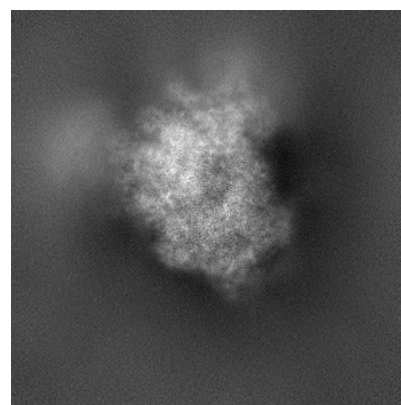
6.1.2 Raw map



X



Y

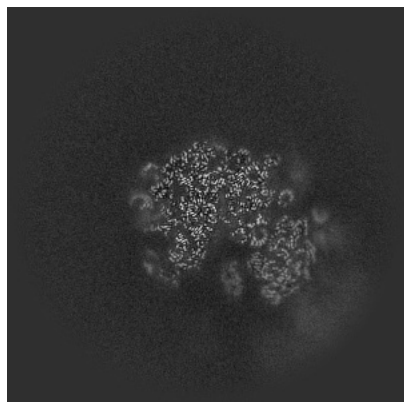


Z

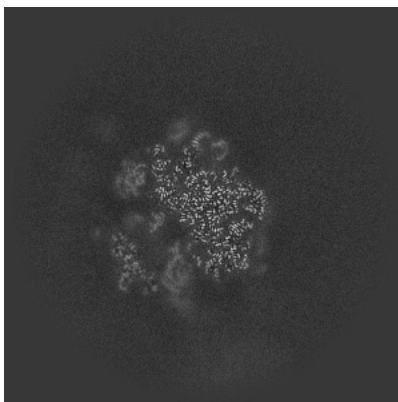
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

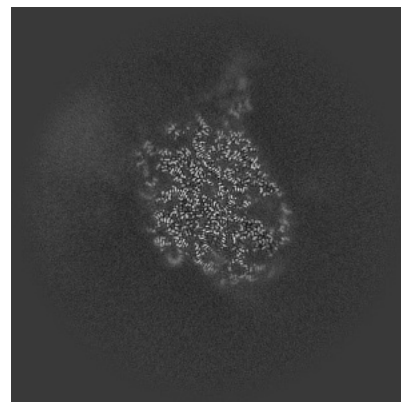
6.2.1 Primary map



X Index: 256

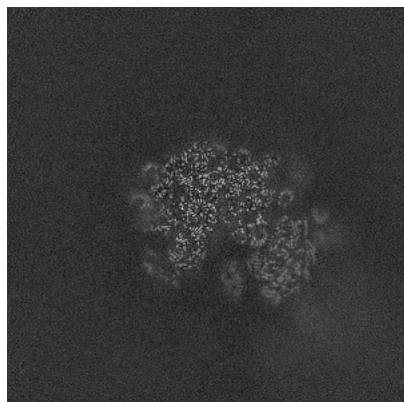


Y Index: 256

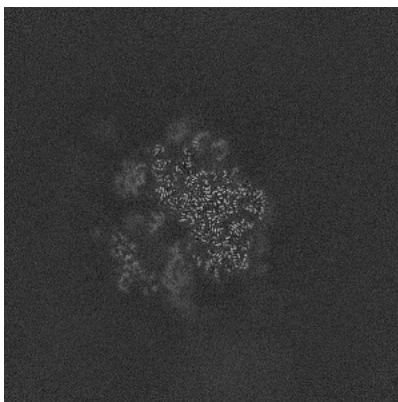


Z Index: 256

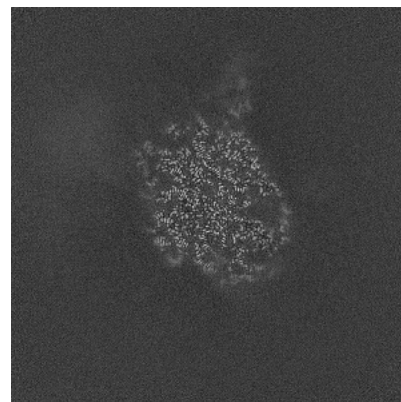
6.2.2 Raw map



X Index: 256



Y Index: 256

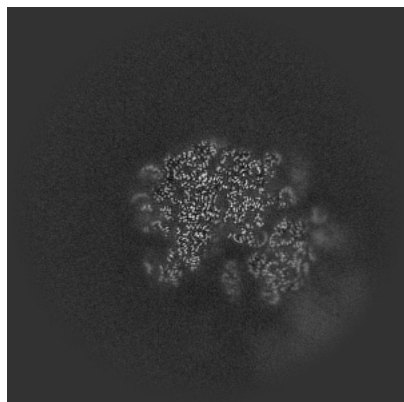


Z Index: 256

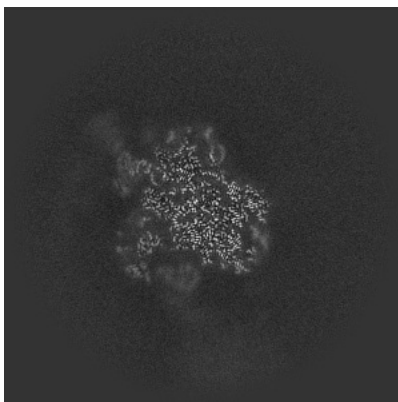
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

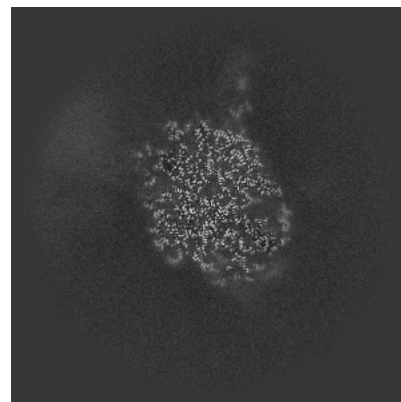
6.3.1 Primary map



X Index: 253

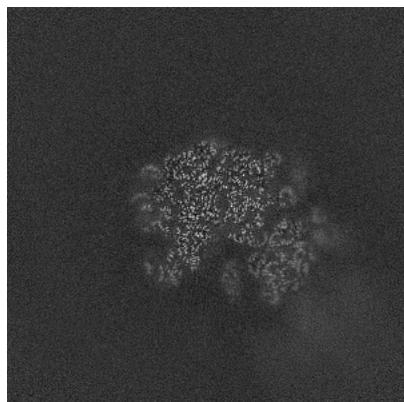


Y Index: 243

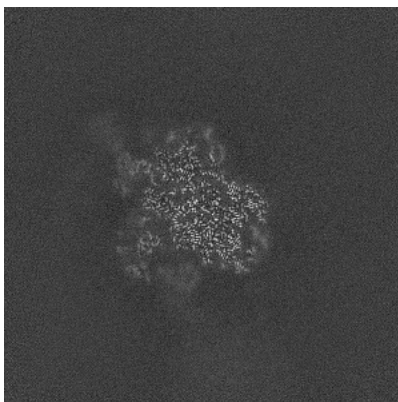


Z Index: 258

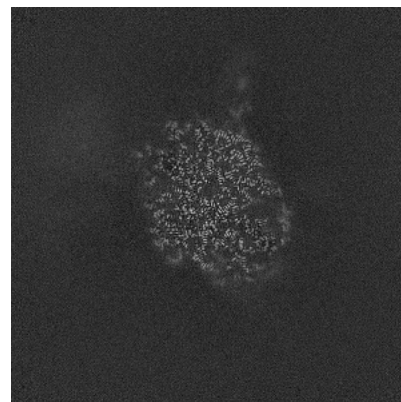
6.3.2 Raw map



X Index: 253



Y Index: 243

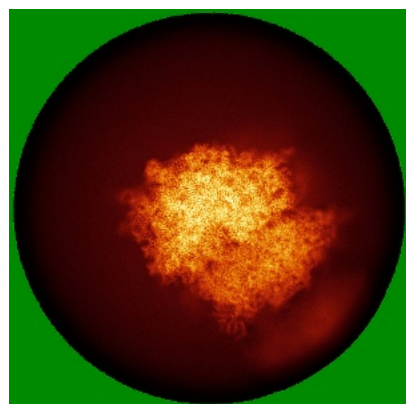


Z Index: 258

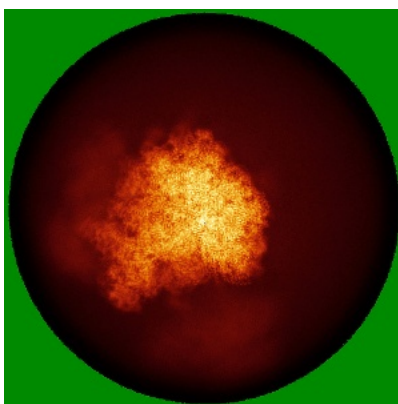
The images above show the largest variance slices of the map in three orthogonal directions.

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

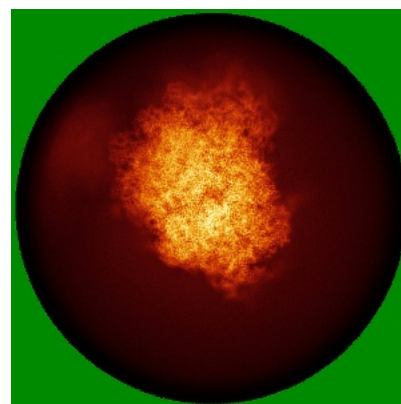
6.4.1 Primary map



X

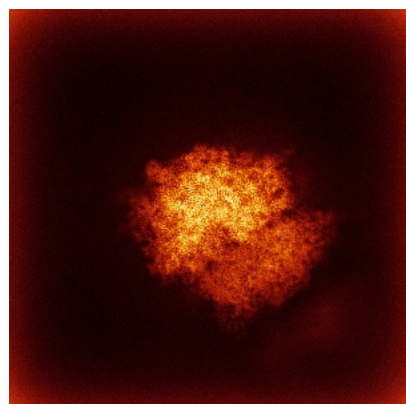


Y

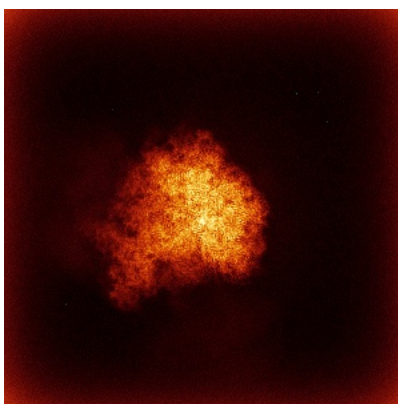


Z

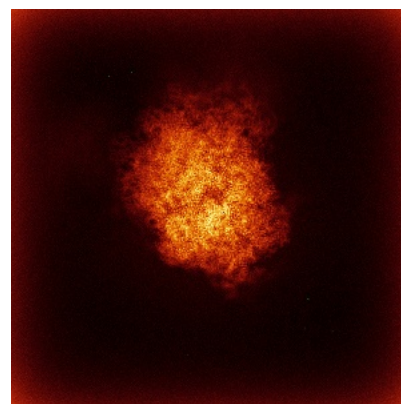
6.4.2 Raw map



X



Y

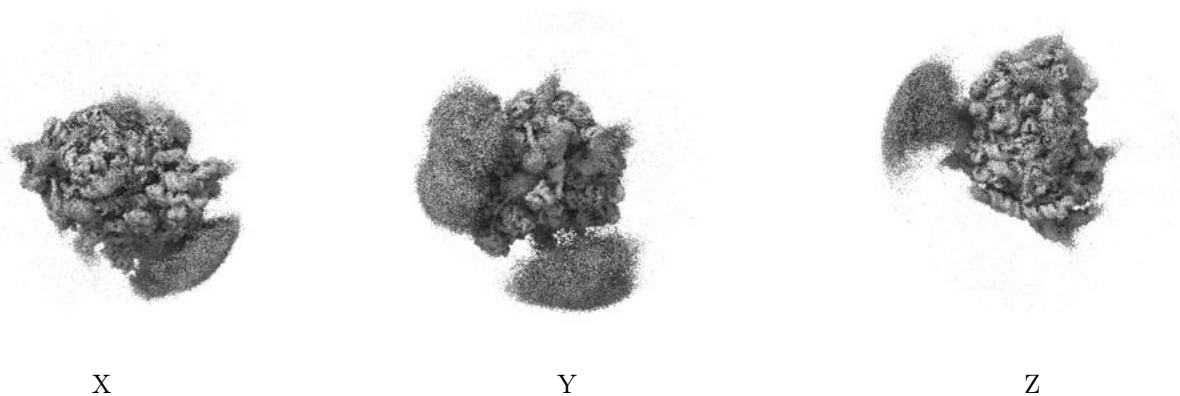


Z

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.

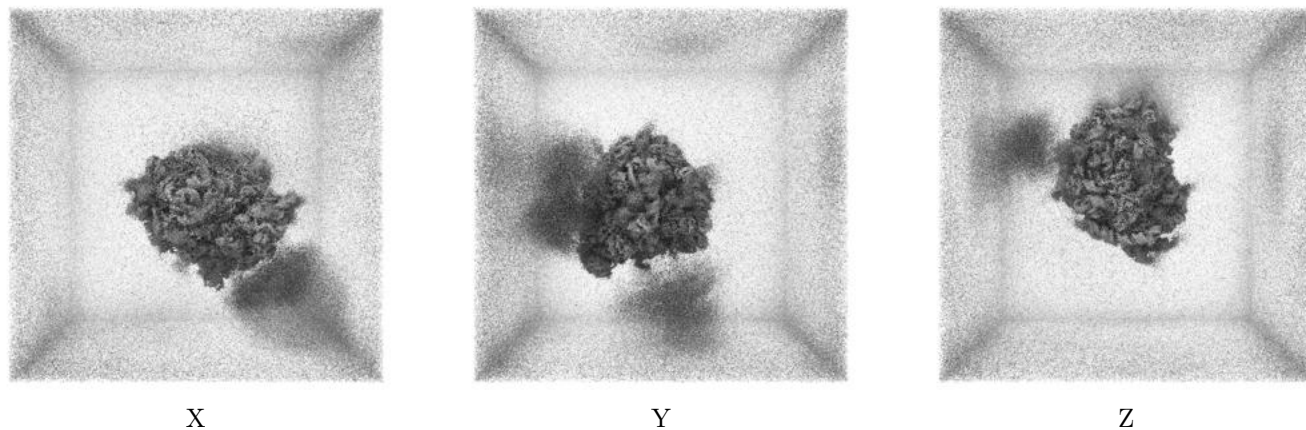
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0159. 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.

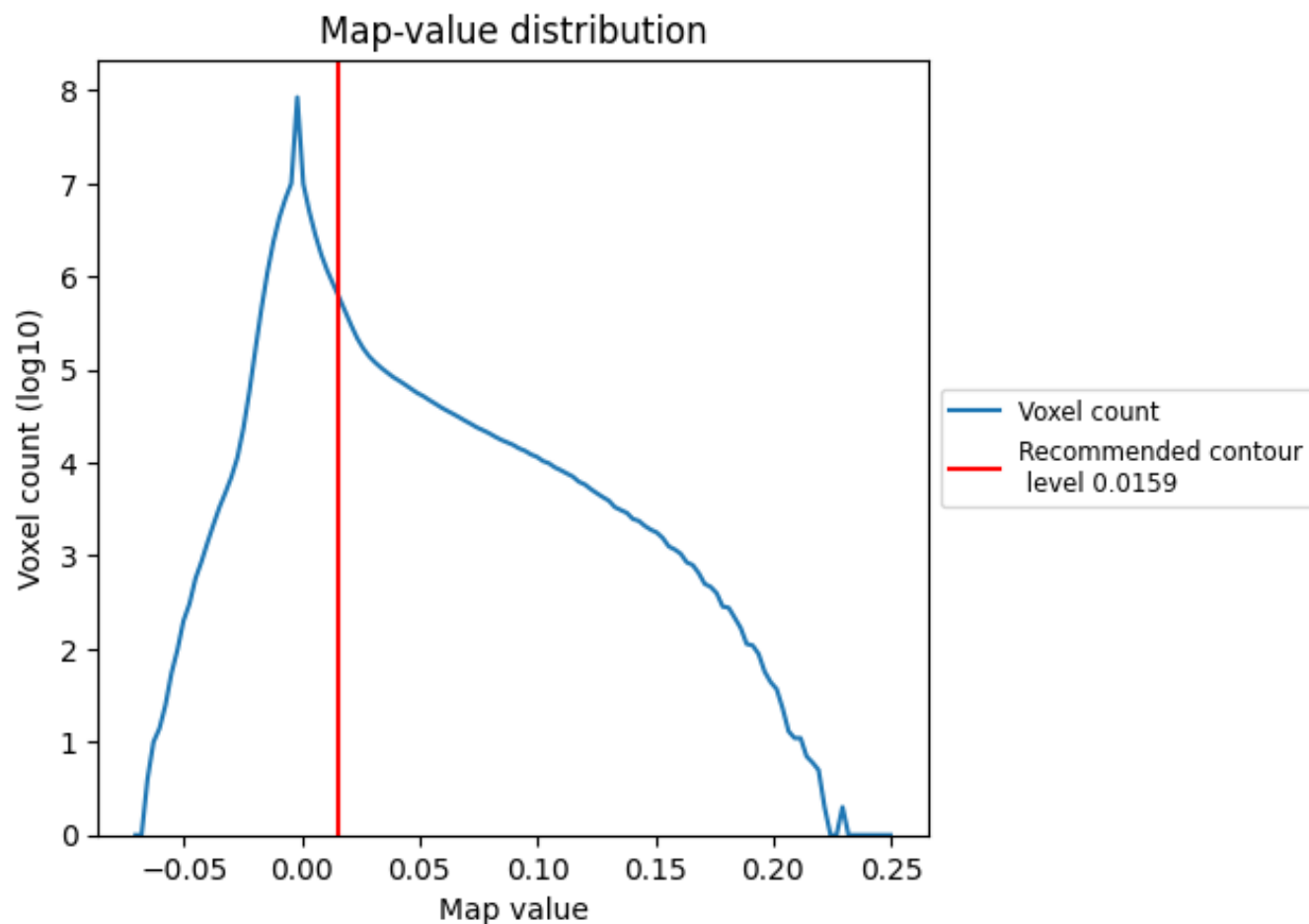
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

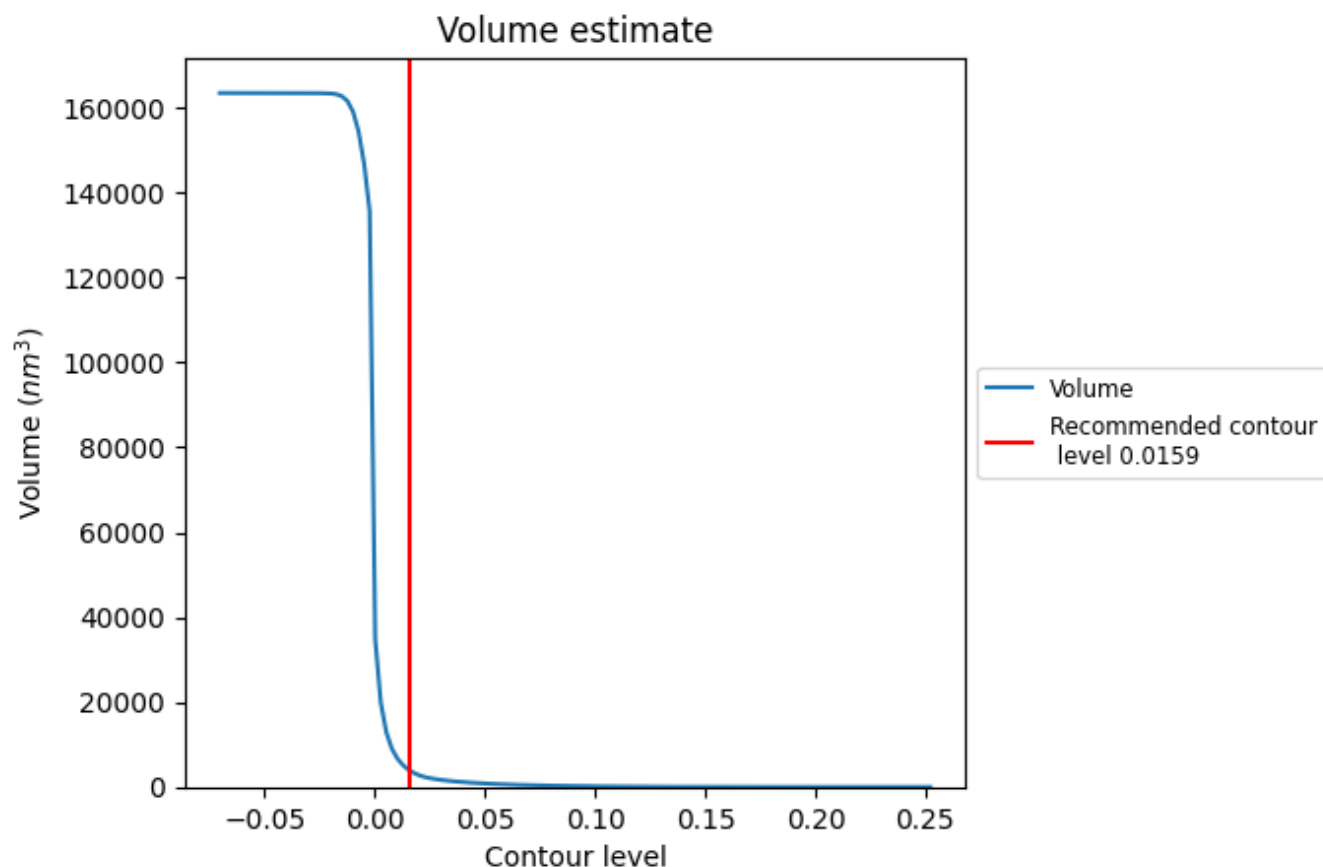
This section contains the results of statistical analysis of the map.

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.

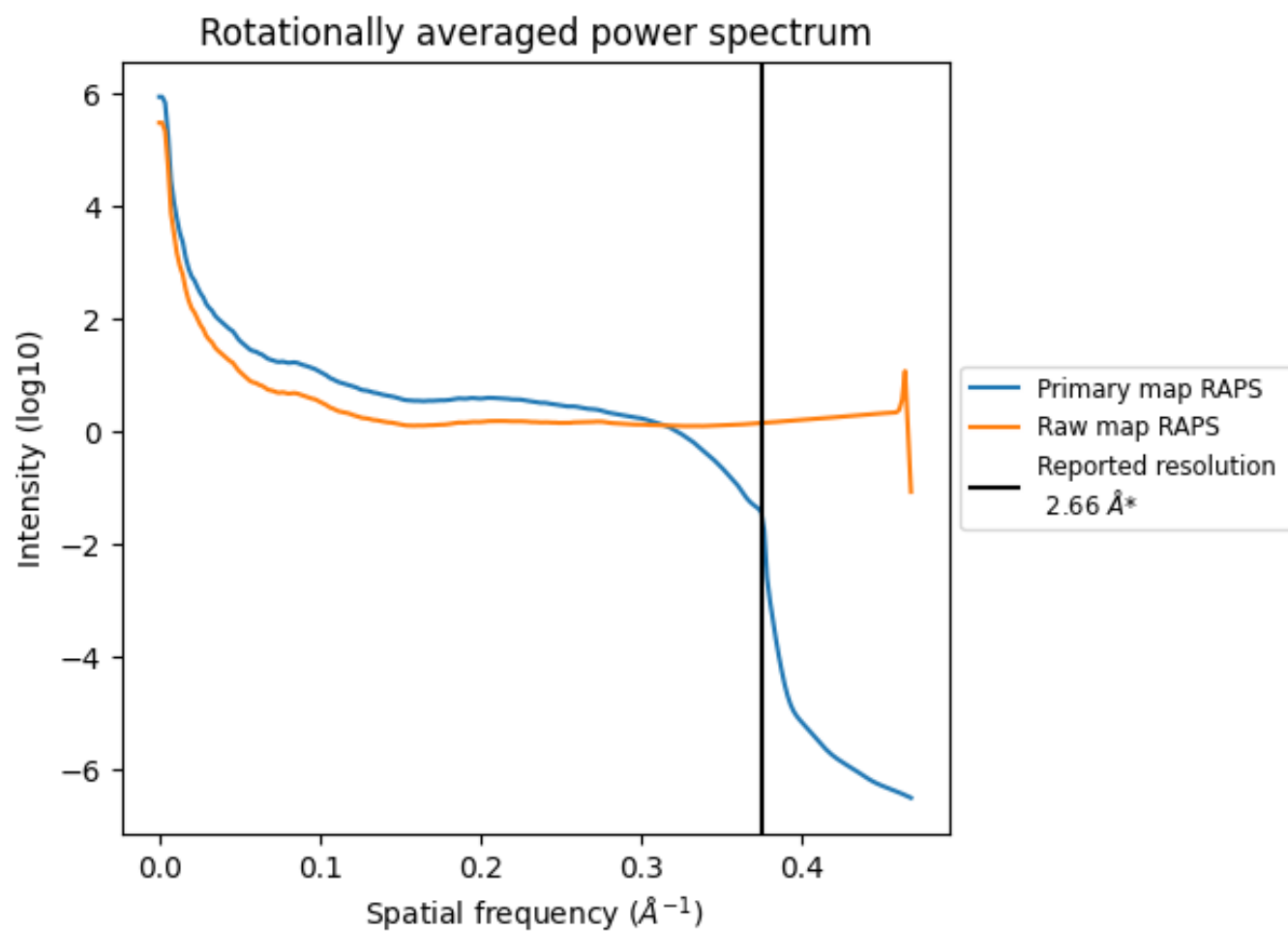
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3867 nm³; this corresponds to an approximate mass of 3493 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 ⓘ

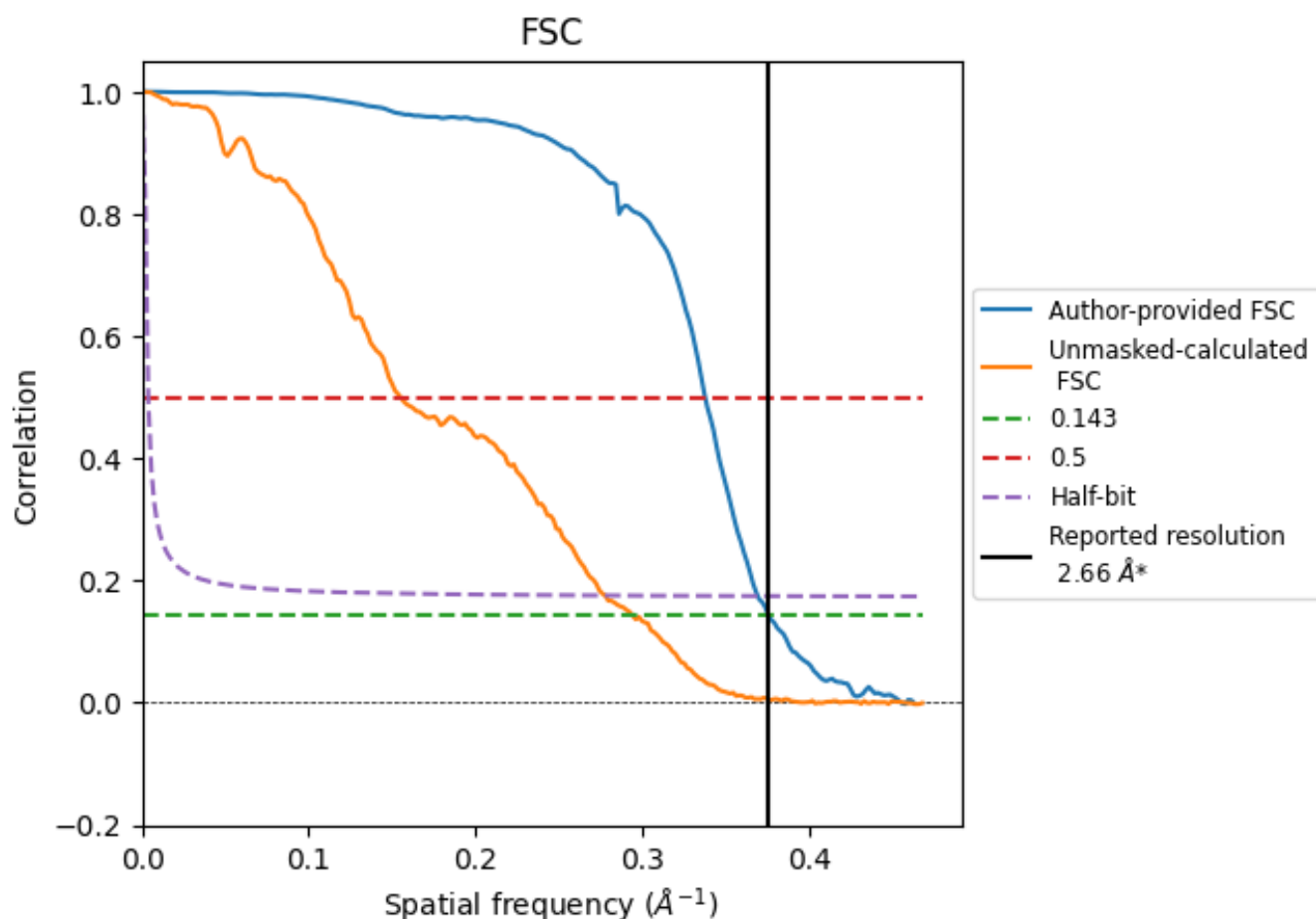


*Reported resolution corresponds to spatial frequency of 0.376 $\text{\AA}^{-1}$

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 0.376 Å⁻¹

8.2 Resolution estimates [i](#)

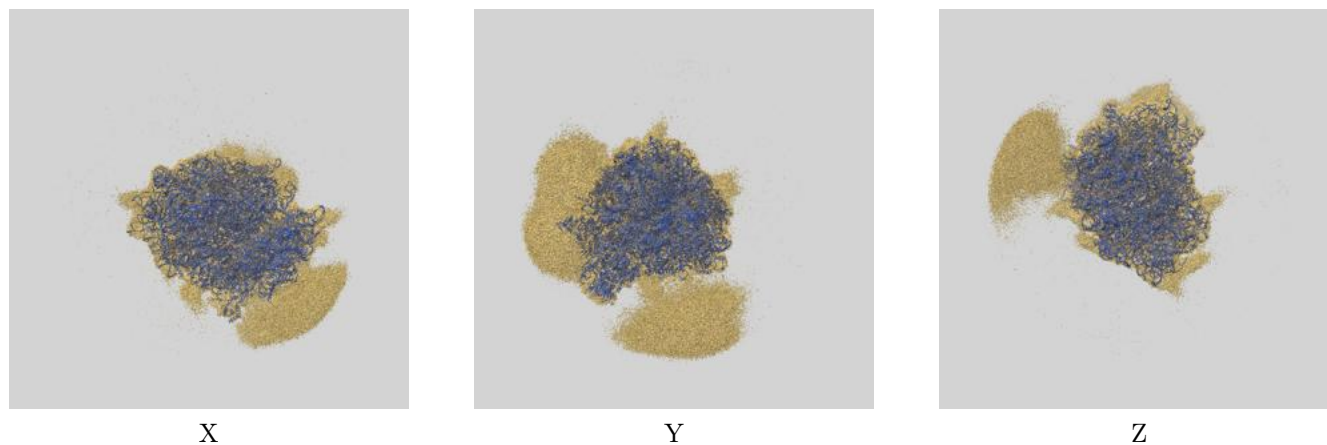
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.66	-	-
Author-provided FSC curve	2.66	2.96	2.71
Unmasked-calculated*	3.40	6.45	3.60

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.40 differs from the reported value 2.66 by more than 10 %

9 Map-model fit [i](#)

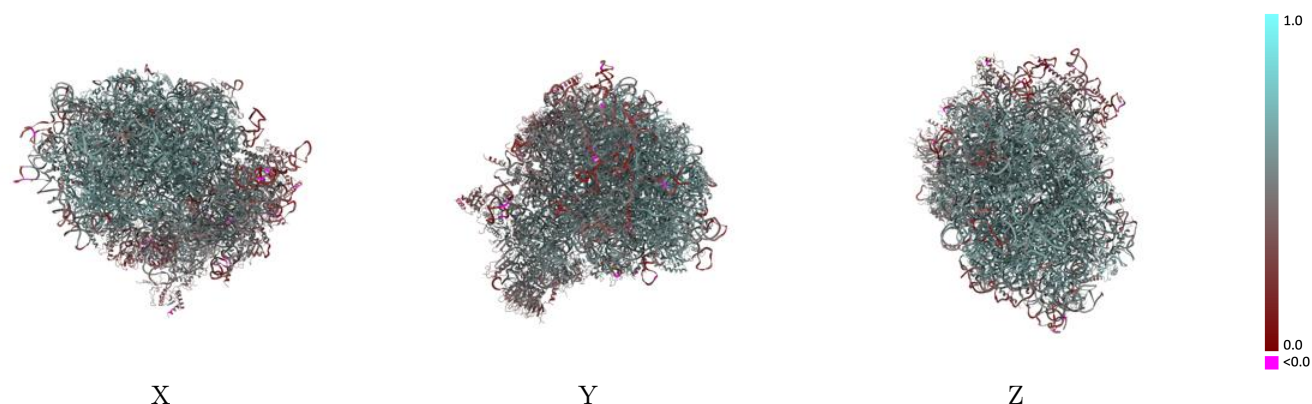
This section contains information regarding the fit between EMDB map EMD-71332 and PDB model 9P73. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



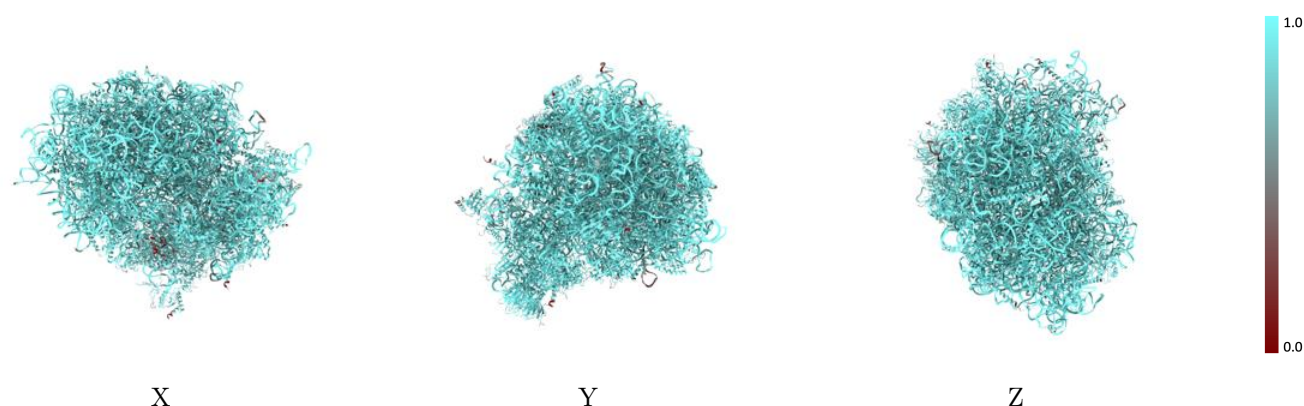
The images above show the 3D surface view of the map at the recommended contour level 0.0159 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



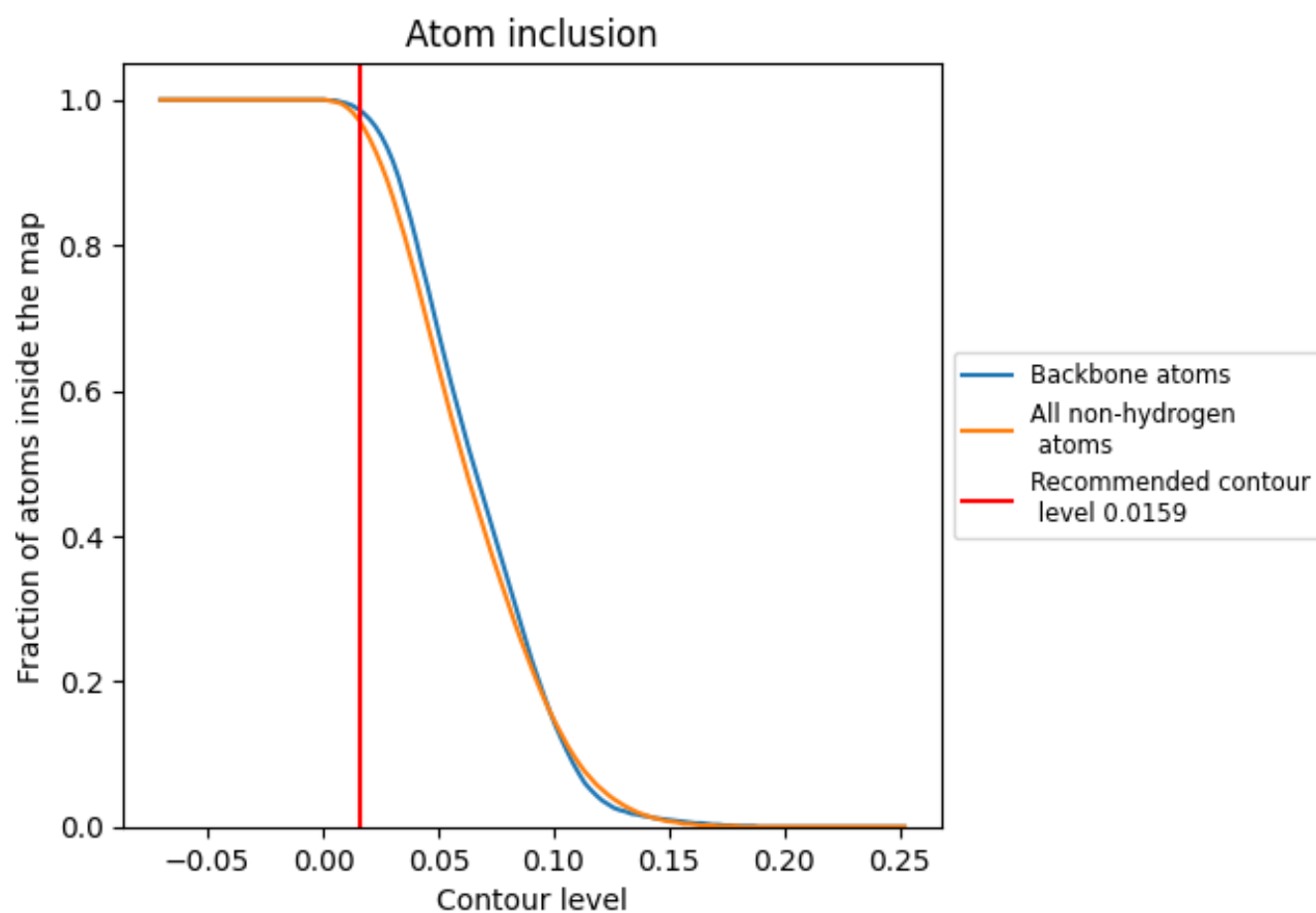
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0159).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 97% 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 (0.0159) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9710	 0.5360
AP	 0.9660	 0.4340
CB	 0.9200	 0.4470
CH	 0.8370	 0.4040
CI	 0.9120	 0.5240
L5	 0.9870	 0.5610
L7	 0.9990	 0.6040
L8	 0.9900	 0.5810
LA	 0.9940	 0.6170
LB	 0.9730	 0.6010
LC	 0.9770	 0.6020
LD	 0.9730	 0.5690
LE	 0.9520	 0.5510
LF	 0.9920	 0.6040
LG	 0.9410	 0.5520
LH	 0.9700	 0.5880
LI	 0.9780	 0.5980
LJ	 0.9580	 0.5480
LL	 0.9490	 0.5820
LM	 0.9800	 0.5860
LN	 0.9980	 0.6290
LO	 0.9870	 0.6040
LP	 0.9840	 0.6120
LQ	 0.9920	 0.6210
LR	 0.9380	 0.5430
LS	 0.9900	 0.6170
LT	 0.9790	 0.5910
LU	 0.9630	 0.5360
LV	 0.9840	 0.6050
LW	 0.8950	 0.4520
LX	 0.9780	 0.5920
LY	 0.9740	 0.5910
LZ	 0.9860	 0.5770
La	 0.9890	 0.6230
Lb	 0.9370	 0.5410



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Chain	Atom inclusion	Q-score
Lc	 0.9520	 0.5480
Ld	 0.9710	 0.5910
Le	 0.9910	 0.6200
Lf	 0.9930	 0.6240
Lg	 0.9830	 0.5980
Lh	 0.9680	 0.5860
Li	 0.9700	 0.5760
Lj	 0.9940	 0.6180
Lk	 0.9520	 0.5400
Ll	 0.9860	 0.6000
Lm	 0.9830	 0.6020
Ln	 0.9900	 0.5720
Lo	 0.9590	 0.5990
Lp	 0.9900	 0.6050
Lr	 0.9810	 0.6040
Ls	 0.6860	 0.3020
Lt	 0.7320	 0.2470
PE	 0.9740	 0.4420
S2	 0.9890	 0.5020
SA	 0.9440	 0.5000
SB	 0.9680	 0.5370
SC	 0.9800	 0.5290
SD	 0.9390	 0.4780
SE	 0.9720	 0.4880
SF	 0.9420	 0.4860
SG	 0.9280	 0.4290
SH	 0.9150	 0.4310
SI	 0.9470	 0.4800
SJ	 0.9450	 0.4680
SK	 0.9380	 0.4610
SL	 0.9360	 0.5200
SM	 0.8010	 0.3030
SN	 0.9700	 0.5360
SO	 0.9550	 0.5340
SP	 0.9490	 0.5080
SQ	 0.9450	 0.4820
SR	 0.9360	 0.4580
SS	 0.9240	 0.4990
ST	 0.9350	 0.4790
SU	 0.9250	 0.4340
SV	 0.9580	 0.5000
SW	 0.9880	 0.5450

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Chain	Atom inclusion	Q-score
SX	 0.9590	 0.5270
SY	 0.8970	 0.4090
SZ	 0.8950	 0.4640
Sa	 0.9680	 0.5410
Sb	 0.9550	 0.5130
Sc	 0.9140	 0.4510
Sd	 0.9820	 0.5480
Sf	 0.8760	 0.3700
Sg	 0.9320	 0.4130