



Full wwPDB EM Validation Report ⓘ

Mar 31, 2025 – 01:12 PM EDT

PDB ID : 8UIY / pdb_00008uiy
EMDB ID : EMD-42305
Title : In situ human P-Z state 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2023-10-10
Resolution : 3.44 Å(reported)

This is a Full wwPDB EM Validation 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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

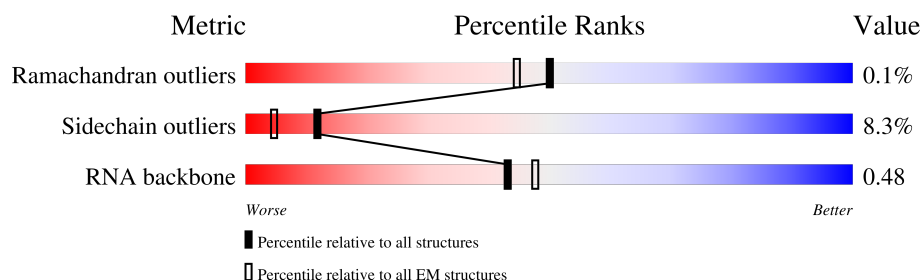
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.44 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	LW	124	
2	LR	187	
3	SE	262	
4	SI	206	
5	SL	153	
6	SX	141	
7	SG	237	
8	SJ	185	

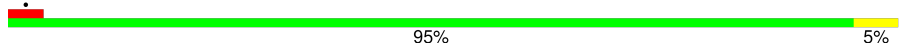
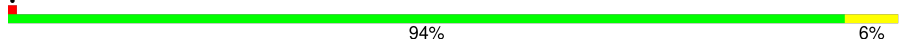
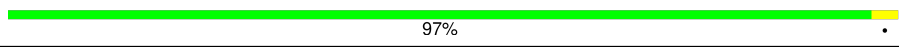
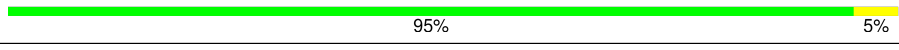
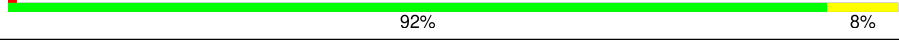
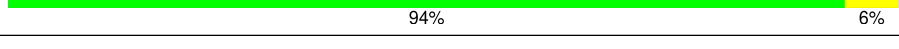
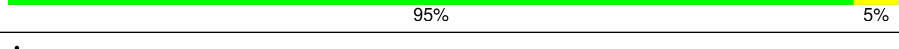
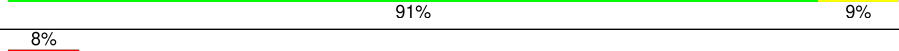
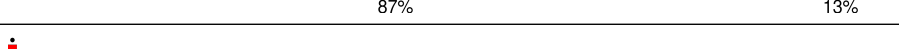
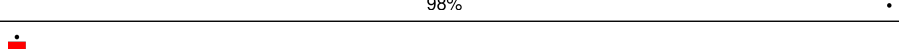
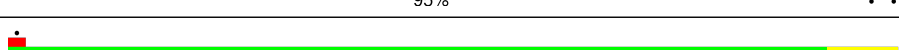
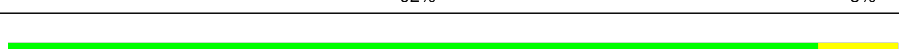
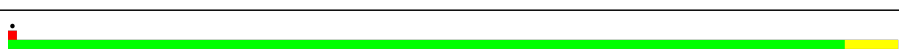

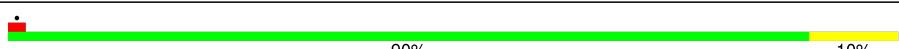

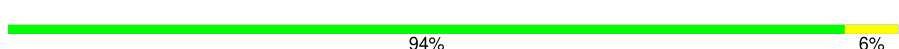
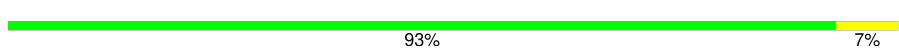
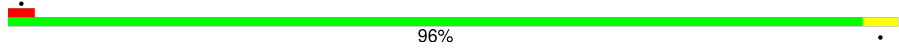
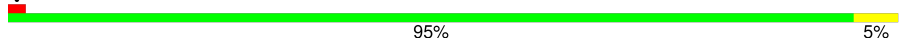
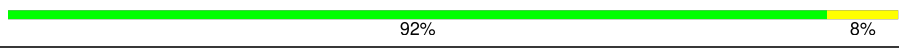
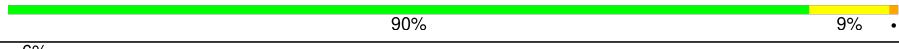
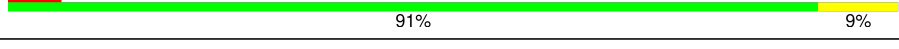
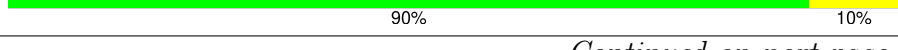

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Mol	Chain	Length	Quality of chain
9	SY	131	
10	Se	58	
11	SA	221	
12	SB	214	
13	SH	189	
14	SV	83	
15	Sa	102	
16	SC	222	
17	SN	150	
18	SO	140	
19	SW	129	
20	Sb	83	
21	L5	5070	
22	L7	120	
23	L8	156	
24	LA	248	
25	LB	402	
26	LC	368	
27	LD	293	
28	LE	247	
29	LF	225	
30	LG	241	
31	LH	190	
32	LI	213	
33	LJ	176	


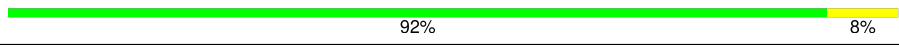
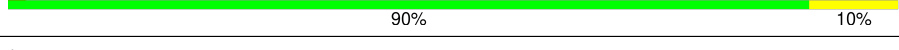
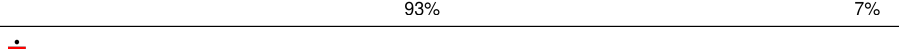
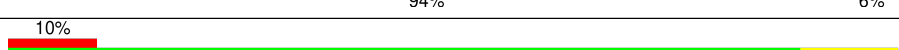
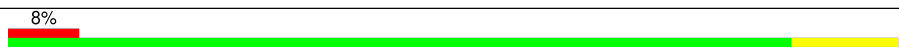


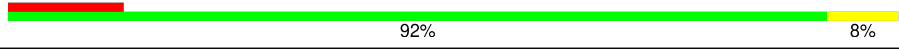
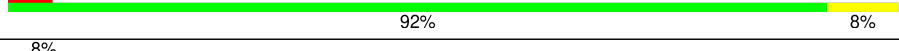
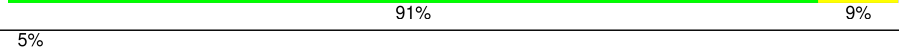
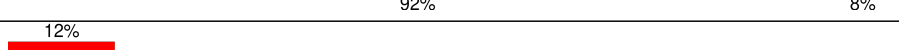

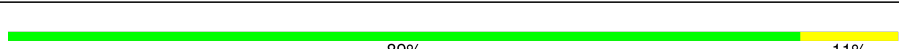



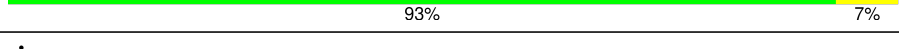
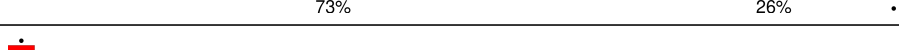






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Mol	Chain	Length	Quality of chain
34	LL	210	
35	LM	139	
36	LN	203	
37	LO	201	
38	LP	153	
39	LQ	187	
40	LS	175	
41	LT	159	
42	LU	101	
43	LV	131	
44	LX	120	
45	LY	134	
46	LZ	135	
47	La	147	
48	Lb	121	
49	Lc	98	
50	Ld	107	
51	Le	128	
52	Lf	109	
53	Lg	114	
54	Lh	122	
55	Li	102	
56	Lj	86	
57	Lk	69	
58	Ll	50	

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Mol	Chain	Length	Quality of chain
59	Lm	52	
60	Ln	24	
61	Lo	105	
62	Lp	91	
63	Lr	125	
64	SR	135	
65	SD	227	
66	SF	189	
67	SK	98	
68	SP	121	
69	SQ	144	
70	SS	145	
71	ST	143	
72	SU	104	
73	Sc	64	
74	Sd	55	
75	Sg	313	
76	SM	122	
77	SZ	75	
78	Sf	67	
79	S2	1740	
80	Pt	76	
81	Zt	75	
82	Ls	196	
83	Lt	157	

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Mol	Chain	Length	Quality of chain
84	Lz	217	<div><div></div><div>90%</div><div></div><div>93%</div><div></div><div>6%</div></div>

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 222758 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 protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		

- Molecule 2 is a protein called 60S ribosomal protein L19.

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

- Molecule 3 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 4 is a protein called 40S ribosomal protein S8.

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

- Molecule 5 is a protein called 40S ribosomal protein S11.

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

- Molecule 6 is a protein called 40S ribosomal protein S23.

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

- Molecule 7 is a protein called 40S ribosomal protein S6.

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

- Molecule 8 is a protein called 40S ribosomal protein S9.

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

- Molecule 9 is a protein called 40S ribosomal protein S24.

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

- Molecule 10 is a protein called Small ribosomal subunit protein eS30.

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

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

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

- Molecule 12 is a protein called 40S ribosomal protein S3a.

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

- Molecule 13 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 14 is a protein called 40S ribosomal protein S21.

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

- Molecule 15 is a protein called 40S ribosomal protein S26.

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

- Molecule 16 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 17 is a protein called 40S ribosomal protein S13.

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

- Molecule 18 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 19 is a protein called 40S ribosomal protein S15a.

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

- Molecule 20 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 21 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L5	3740	Total	C	N	O	P	0	0
			79860	35549	14585	25987	3739		

- Molecule 22 is a RNA chain called 5S rRNA [Homo sapiens].

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

- Molecule 23 is a RNA chain called 5.8S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 24 is a protein called 60S ribosomal protein L8.

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

- Molecule 25 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 26 is a protein called 60S ribosomal protein L4.

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

- Molecule 27 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 29 is a protein called 60S ribosomal protein L7.

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

- Molecule 30 is a protein called 60S ribosomal protein L7a.

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

- Molecule 31 is a protein called 60S ribosomal protein L9.

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

- Molecule 32 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 33 is a protein called 60S ribosomal protein L11.

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

- Molecule 34 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 35 is a protein called 60S ribosomal protein L14.

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

- Molecule 36 is a protein called 60S ribosomal protein L15.

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

- Molecule 37 is a protein called 60S ribosomal protein L13a.

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

- Molecule 38 is a protein called 60S ribosomal protein L17.

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

- Molecule 39 is a protein called 60S ribosomal protein L18.

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

- Molecule 40 is a protein called 60S ribosomal protein L18a.

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

- Molecule 41 is a protein called 60S ribosomal protein L21.

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

- Molecule 42 is a protein called Heparin-binding protein HBp15.

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

- Molecule 43 is a protein called 60S ribosomal protein L23.

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

- Molecule 44 is a protein called 60S ribosomal protein L23a.

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

- Molecule 45 is a protein called 60S ribosomal protein L26.

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

- Molecule 46 is a protein called 60S ribosomal protein L27.

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

- Molecule 47 is a protein called 60S ribosomal protein L27a.

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

- Molecule 48 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 49 is a protein called 60S ribosomal protein L30.

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

- Molecule 50 is a protein called 60S ribosomal protein L31.

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

- Molecule 51 is a protein called 60S ribosomal protein L32.

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

- Molecule 52 is a protein called 60S ribosomal protein L35a.

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

- Molecule 53 is a protein called 60S ribosomal protein L34.

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

- Molecule 54 is a protein called 60S ribosomal protein L35.

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

- Molecule 55 is a protein called 60S ribosomal protein L36.

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

- Molecule 56 is a protein called 60S ribosomal protein L37.

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

- Molecule 57 is a protein called 60S ribosomal protein L38.

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

- Molecule 58 is a protein called 60S ribosomal protein L39.

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

- Molecule 59 is a protein called Large ribosomal subunit protein eL40.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L36a.

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

- Molecule 62 is a protein called 60S ribosomal protein L37a.

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

- Molecule 63 is a protein called 60S ribosomal protein L28.

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

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

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

- Molecule 65 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 66 is a protein called 40S ribosomal protein S5.

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

- Molecule 67 is a protein called 40S ribosomal protein S10.

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

- Molecule 68 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 69 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 70 is a protein called 40S ribosomal protein S18.

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

- Molecule 71 is a protein called 40S ribosomal protein S19.

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

- Molecule 72 is a protein called 40S ribosomal protein S20.

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

- Molecule 73 is a protein called 40S ribosomal protein S28.

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

- Molecule 74 is a protein called 40S ribosomal protein S29.

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

- Molecule 75 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 76 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 77 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 79 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

- Molecule 80 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Pt	76	Total	C	N	O	P	0	0
			1620	725	296	524	75		

- Molecule 81 is a RNA chain called Z site tRNA.

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

- Molecule 82 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 83 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 84 is a protein called 60S ribosomal protein L10a.

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

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

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

Mol	Chain	Residues	Atoms		AltConf
86	L5	212	Total	Mg	0
			212	212	
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	LP	1	Total	Mg	0
			1	1	
86	LV	1	Total	Mg	0
			1	1	
86	La	1	Total	Mg	0
			1	1	
86	Le	1	Total	Mg	0
			1	1	
86	Lg	1	Total	Mg	0
			1	1	
86	Lj	1	Total	Mg	0
			1	1	

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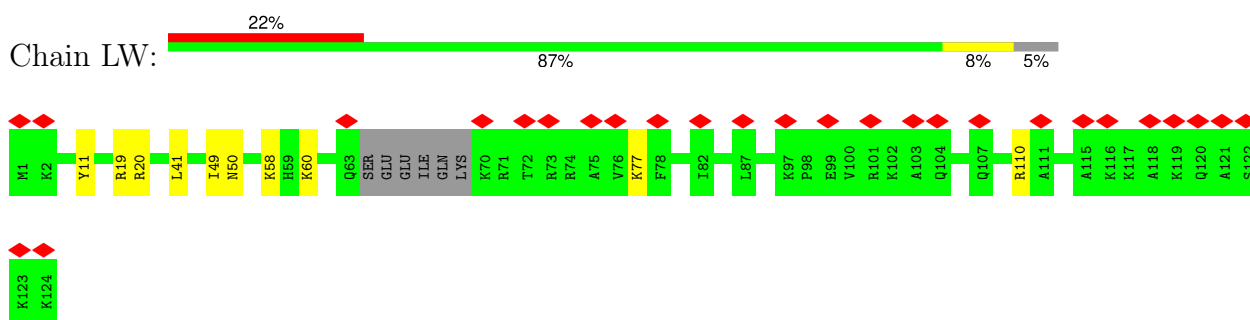
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Mol	Chain	Residues	Atoms		AltConf
86	S2	29	Total	Mg	0
			29	29	

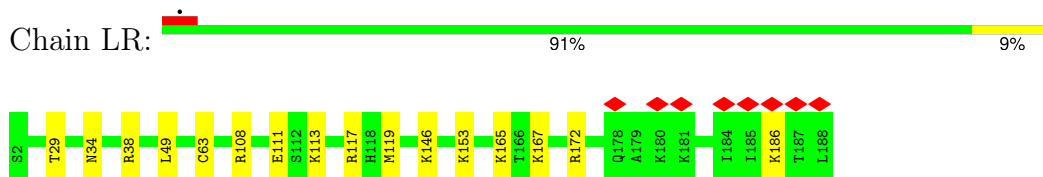
3 Residue-property plots [i](#)

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

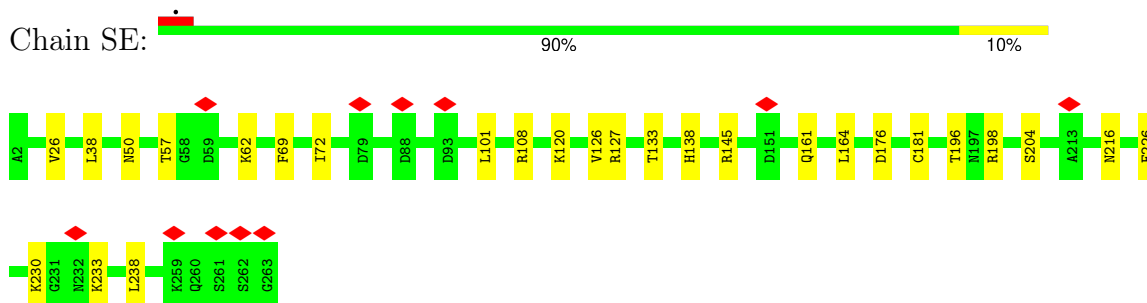
- Molecule 1: Ribosomal protein L24



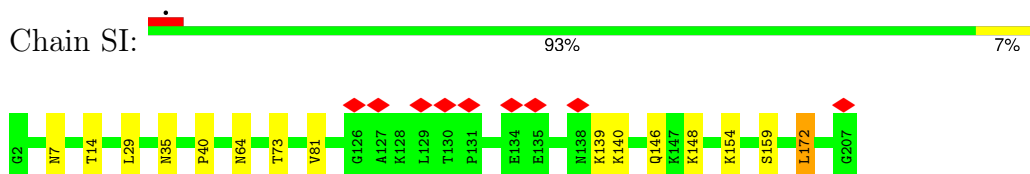
- Molecule 2: 60S ribosomal protein L19



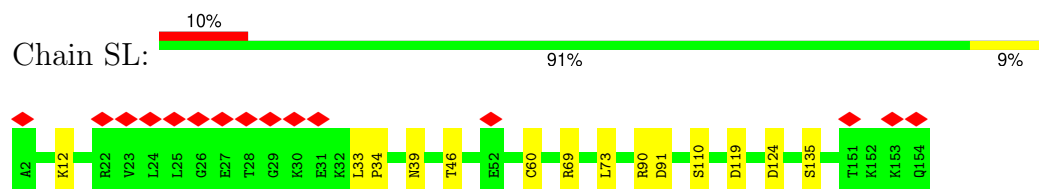
- Molecule 3: Small ribosomal subunit protein eS4, X isoform



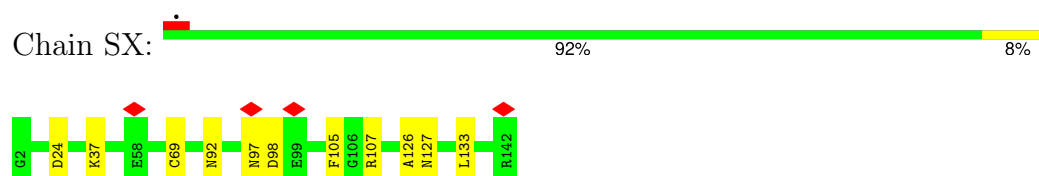
- Molecule 4: 40S ribosomal protein S8



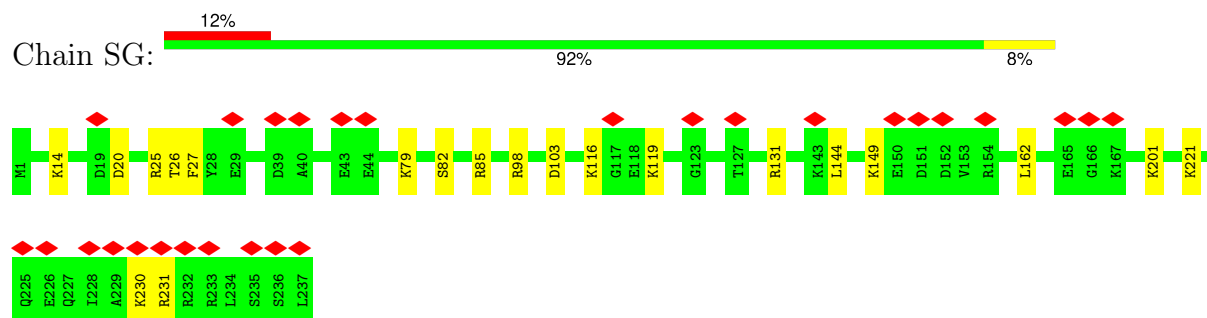
- Molecule 5: 40S ribosomal protein S11



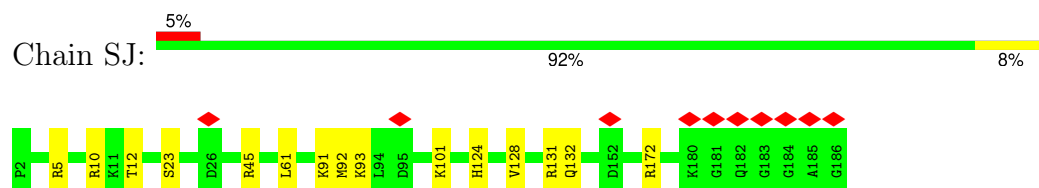
- Molecule 6: 40S ribosomal protein S23



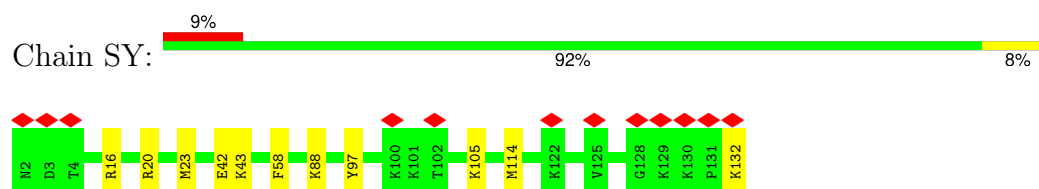
- Molecule 7: 40S ribosomal protein S6



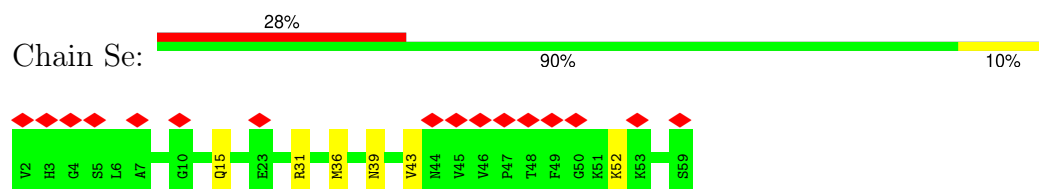
- Molecule 8: 40S ribosomal protein S9



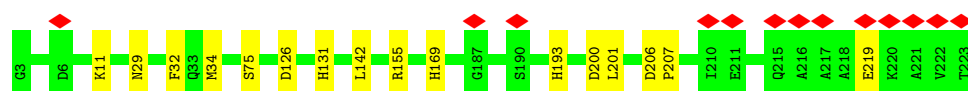
- Molecule 9: 40S ribosomal protein S24



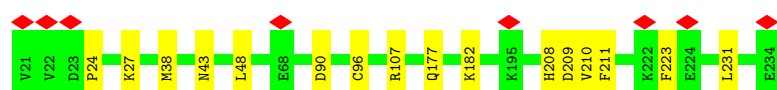
- Molecule 10: Small ribosomal subunit protein eS30



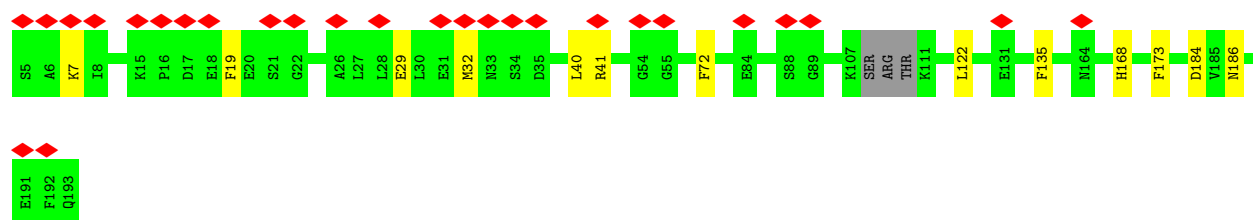
- Molecule 11: 40S ribosomal protein SA



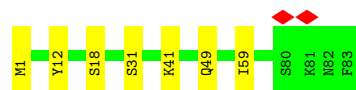
- Molecule 12: 40S ribosomal protein S3a



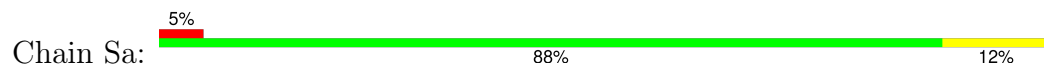
- Molecule 13: Small ribosomal subunit protein eS7



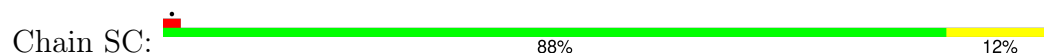
- Molecule 14: 40S ribosomal protein S21



- Molecule 15: 40S ribosomal protein S26

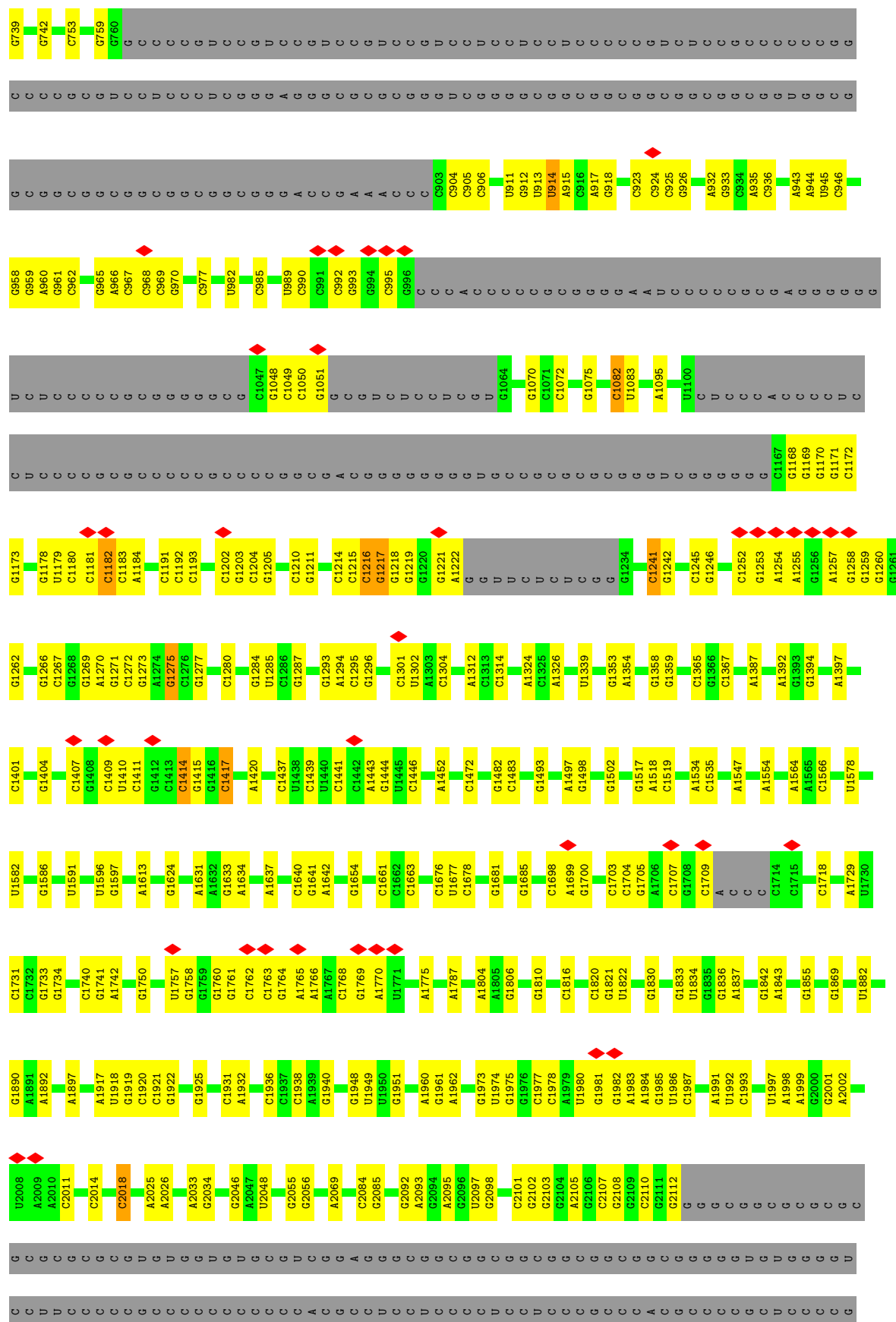


- Molecule 16: 40S ribosomal protein S2




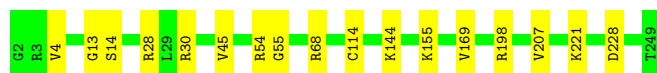
- Molecule 17: 40S ribosomal protein S13





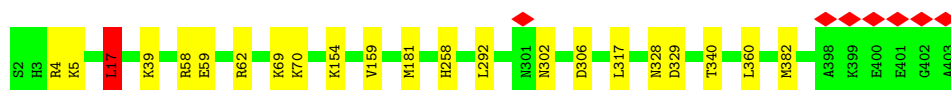


Chain LA:  93% 7%



- Molecule 25: Large ribosomal subunit protein uL3

Chain LB:  95% 5%



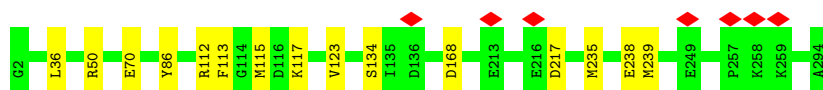
- Molecule 26: 60S ribosomal protein L4

Chain LC:  96% 4%



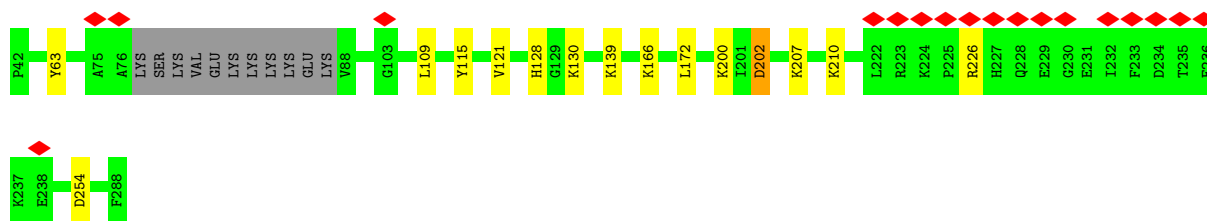
- Molecule 27: Large ribosomal subunit protein uL18

Chain LD:  95% 5%



- Molecule 28: Large ribosomal subunit protein eL6

Chain LE:  89% 7% 6%



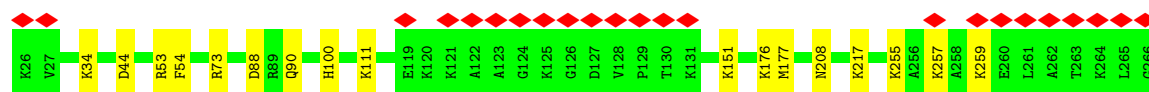
- Molecule 29: 60S ribosomal protein L7

Chain LF:  96% 4%

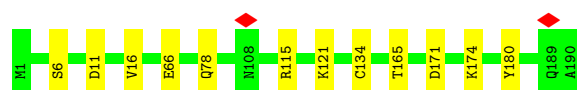


- Molecule 30: 60S ribosomal protein L7a

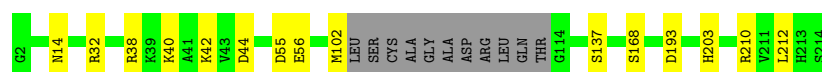
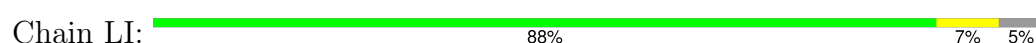
Chain LG:  93% 7% 10%



- Molecule 31: 60S ribosomal protein L9



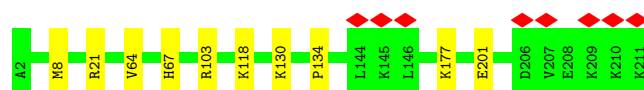
- Molecule 32: Ribosomal protein uL16-like



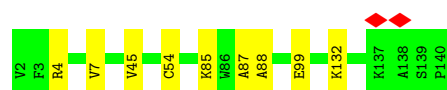
- Molecule 33: 60S ribosomal protein L11



- Molecule 34: Large ribosomal subunit protein eL13



- Molecule 35: 60S ribosomal protein L14



- Molecule 36: 60S ribosomal protein L15



- Molecule 37: 60S ribosomal protein L13a

Chain LO:  95% 5%



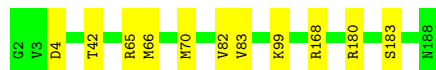
- Molecule 38: 60S ribosomal protein L17

Chain LP:  92% 8%



- Molecule 39: 60S ribosomal protein L18

Chain LQ:  94% 6%




- Molecule 40: 60S ribosomal protein L18a

Chain LS:  95% 5%




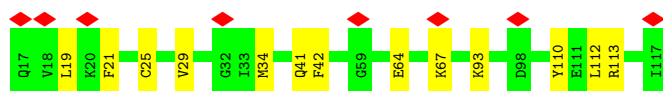
- Molecule 41: 60S ribosomal protein L21

Chain LT:  91% 9%



- Molecule 42: Heparin-binding protein HBp15

Chain LU:  87% 13% 8%

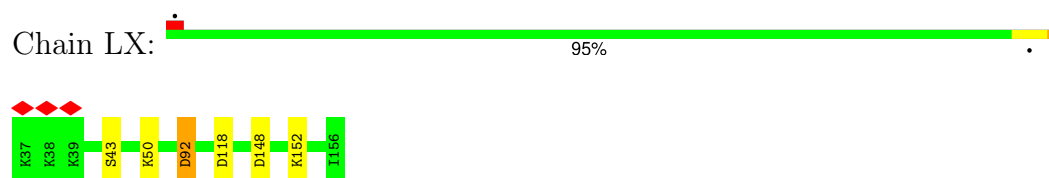


- Molecule 43: 60S ribosomal protein L23

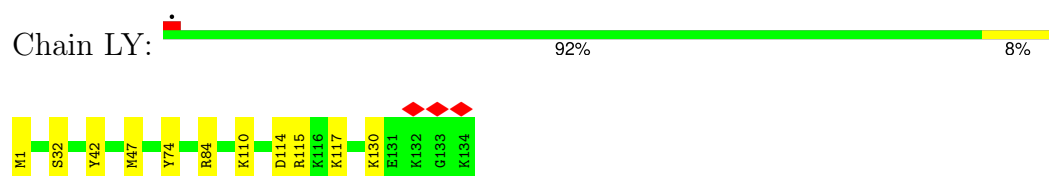
Chain LV:  98%



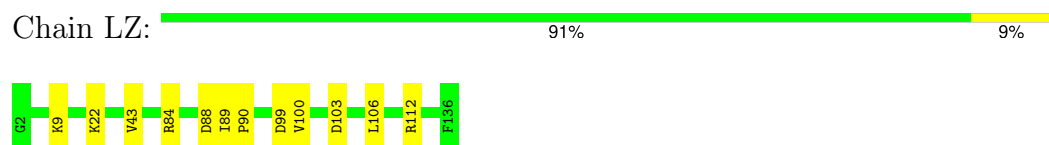
- Molecule 44: 60S ribosomal protein L23a



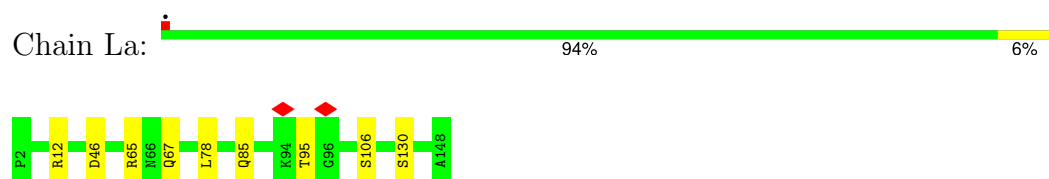
- Molecule 45: 60S ribosomal protein L26



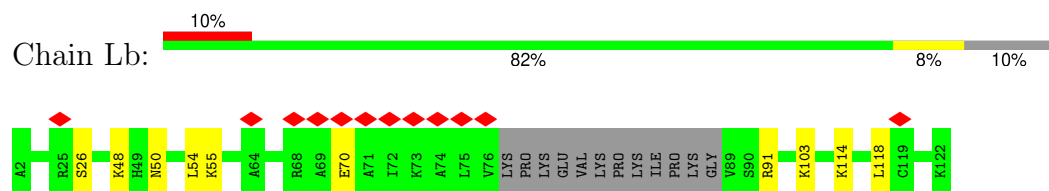
- Molecule 46: 60S ribosomal protein L27



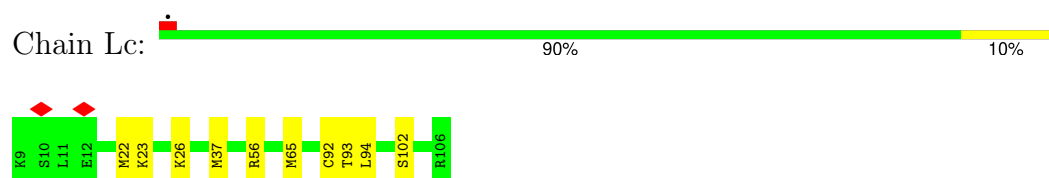
- Molecule 47: 60S ribosomal protein L27a



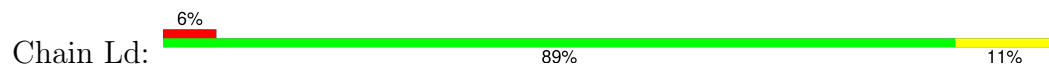
- Molecule 48: Large ribosomal subunit protein eL29



- Molecule 49: 60S ribosomal protein L30



- Molecule 50: 60S ribosomal protein L31





- Molecule 51: 60S ribosomal protein L32



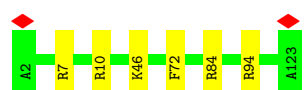
- Molecule 52: 60S ribosomal protein L35a



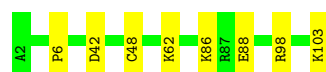
- Molecule 53: 60S ribosomal protein L34



- Molecule 54: 60S ribosomal protein L35



- Molecule 55: 60S ribosomal protein L36

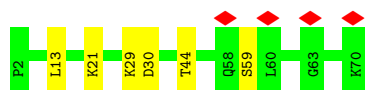


- Molecule 56: 60S ribosomal protein L37



- Molecule 57: 60S ribosomal protein L38





- Molecule 58: 60S ribosomal protein L39

Chain Ll: 90% 10%



- Molecule 59: Large ribosomal subunit protein eL40

Chain Lm: 90% 10%



- Molecule 60: 60S ribosomal protein L41

Chain Ln: 92% 8%



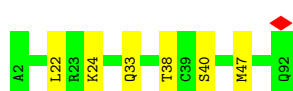
- Molecule 61: 60S ribosomal protein L36a

Chain Lo: 90% 10%



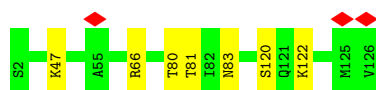
- Molecule 62: 60S ribosomal protein L37a

Chain Lp: 93% 7%

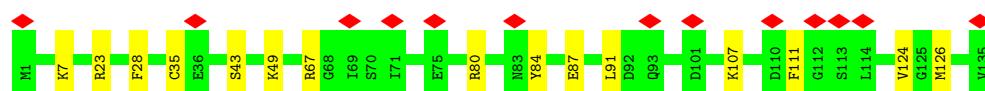
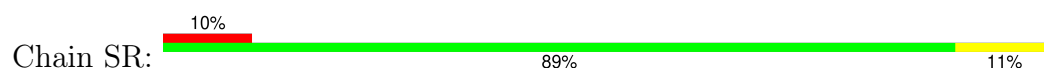


- Molecule 63: 60S ribosomal protein L28

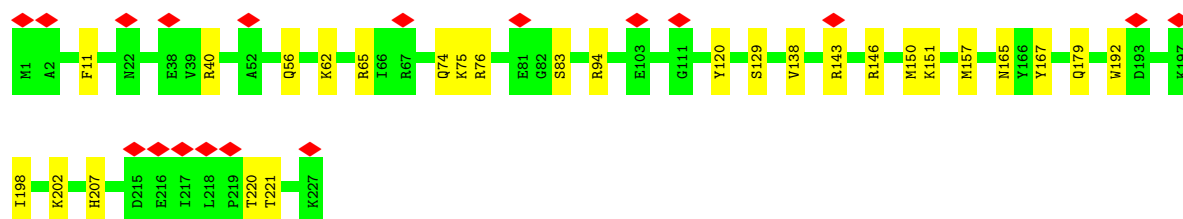
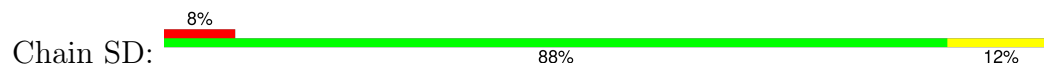
Chain Lr: 94% 6%



- Molecule 64: 40S ribosomal protein S17



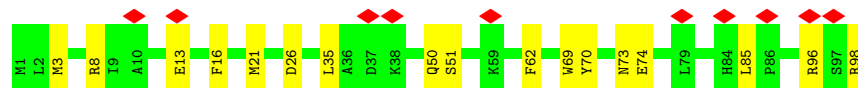
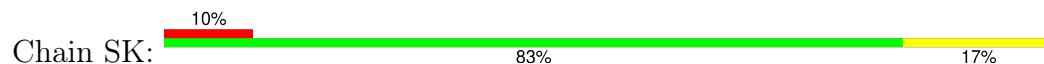
- Molecule 65: Small ribosomal subunit protein uS3



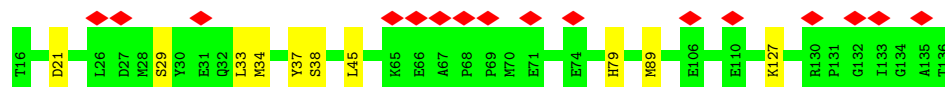
- Molecule 66: 40S ribosomal protein S5



- Molecule 67: 40S ribosomal protein S10



- Molecule 68: Small ribosomal subunit protein uS19

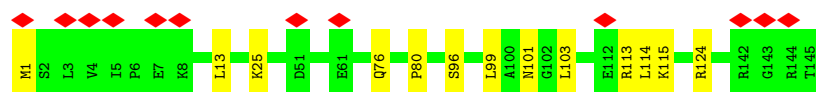


- Molecule 69: Small ribosomal subunit protein uS9

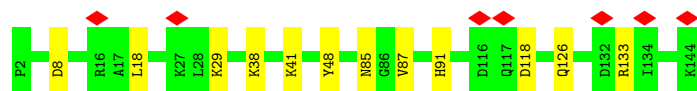


- Molecule 70: 40S ribosomal protein S18

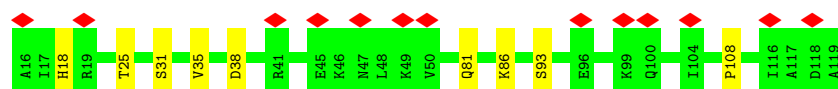




- Molecule 71: 40S ribosomal protein S19



- Molecule 72: 40S ribosomal protein S20



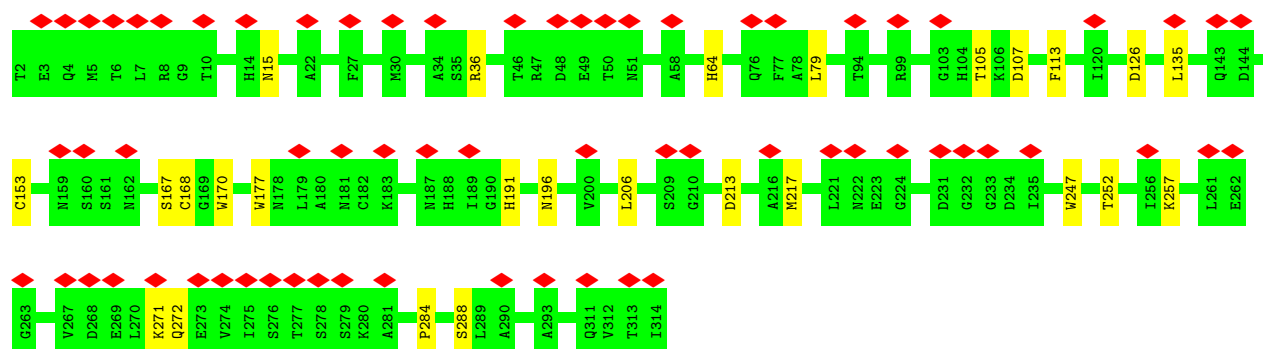
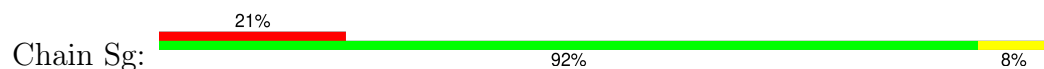
- Molecule 73: 40S ribosomal protein S28



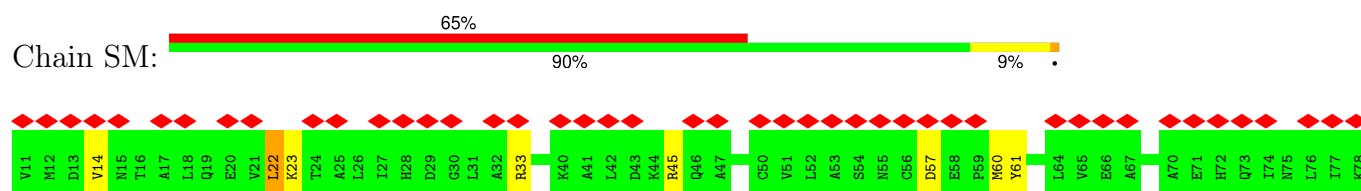
- Molecule 74: 40S ribosomal protein S29



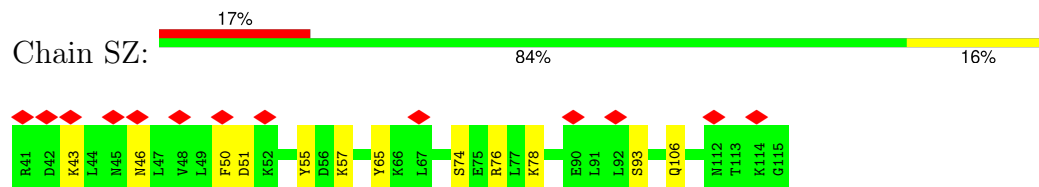
- Molecule 75: Receptor of activated protein C kinase 1



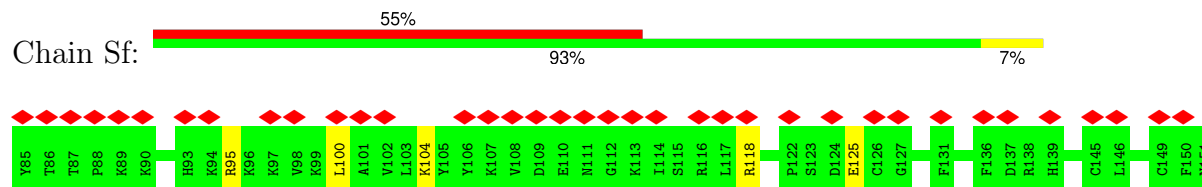
- Molecule 76: Small ribosomal subunit protein eS12



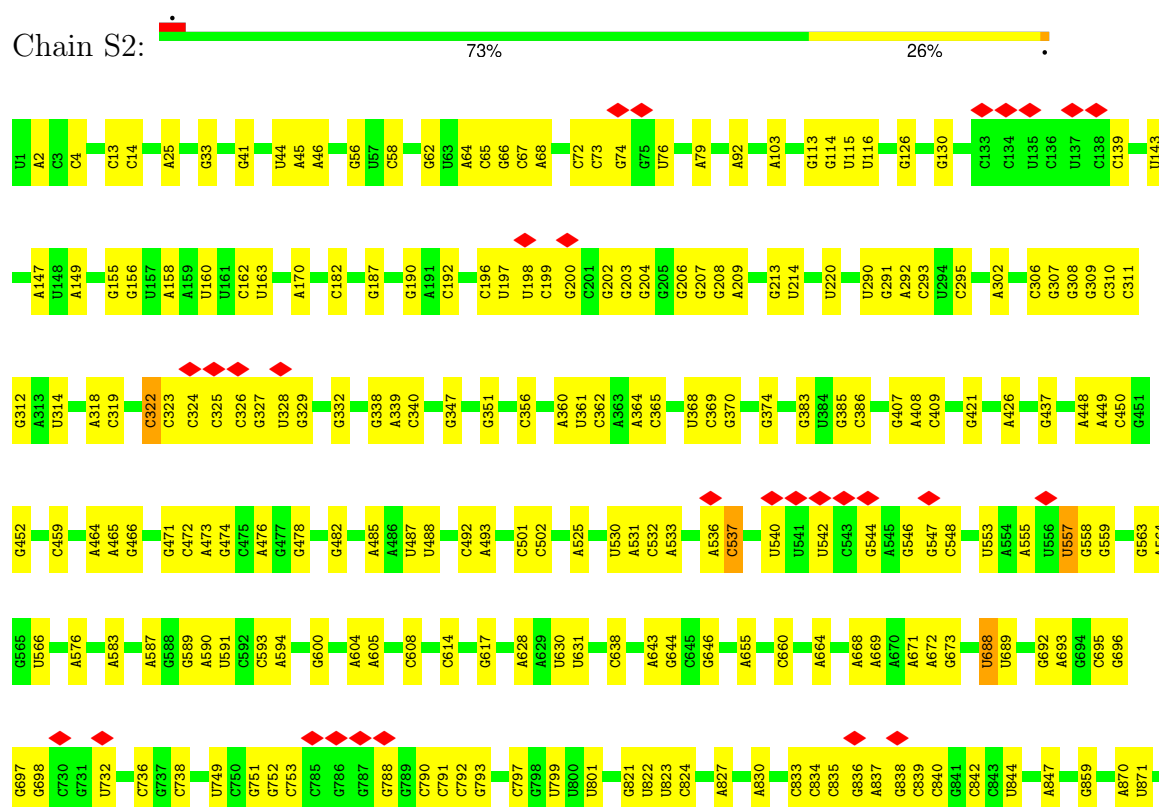
- Molecule 77: Small ribosomal subunit protein eS25

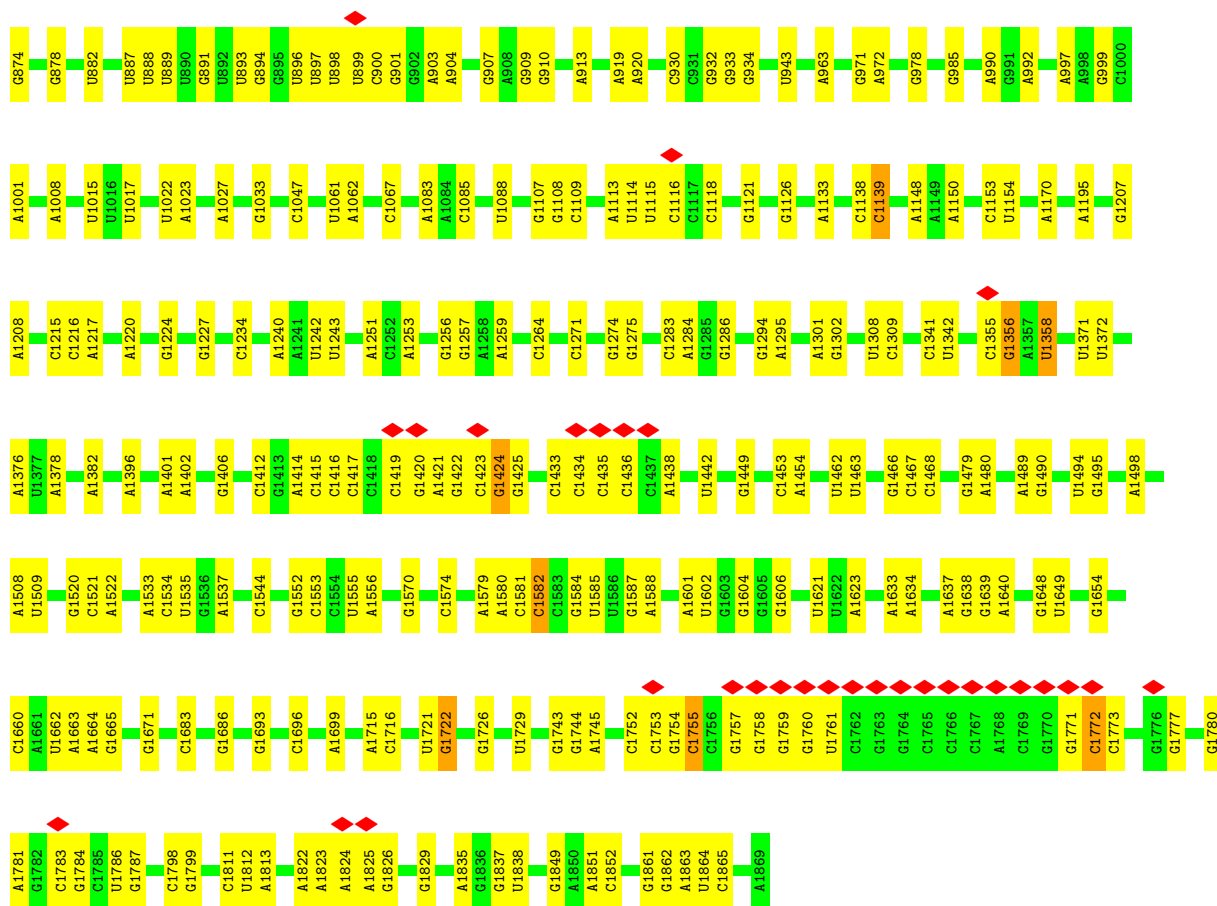


- Molecule 78: Ubiquitin-40S ribosomal protein S27a

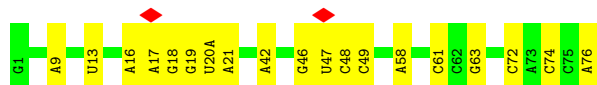
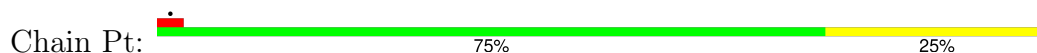


- Molecule 79: 18S rRNA

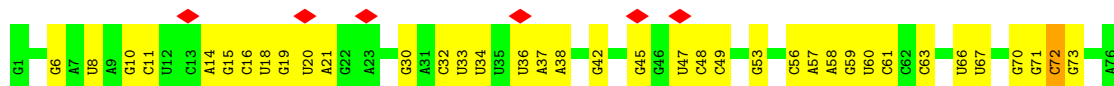




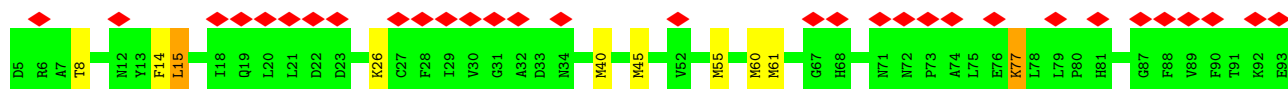
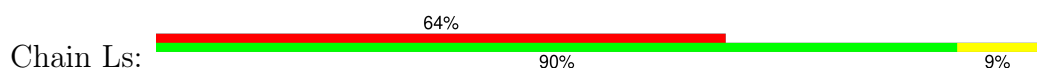
• Molecule 80: P site tRNA

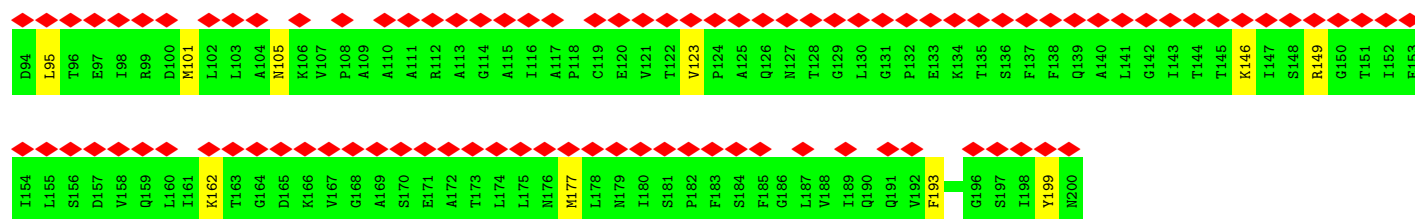


• Molecule 81: Z site tRNA

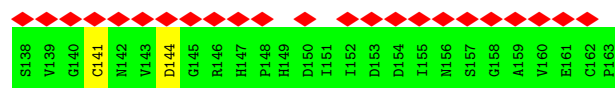
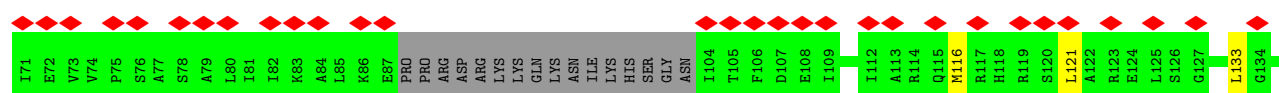
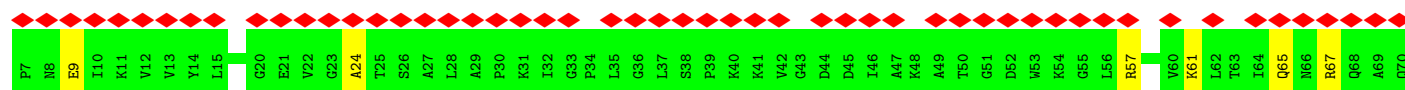
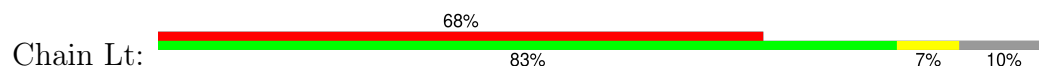


• Molecule 82: 60S acidic ribosomal protein P0

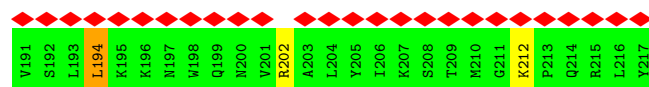
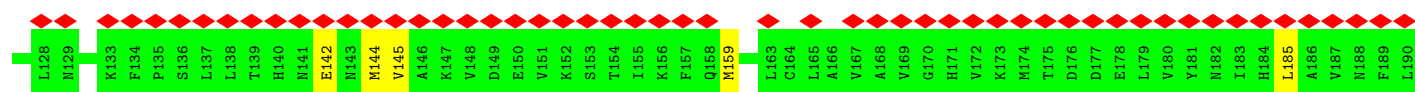
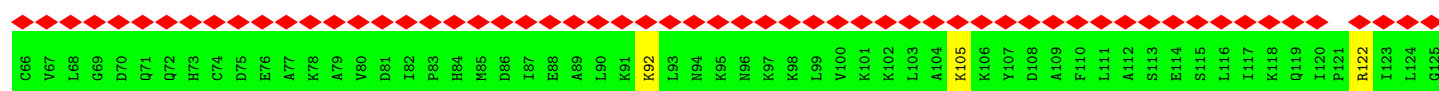
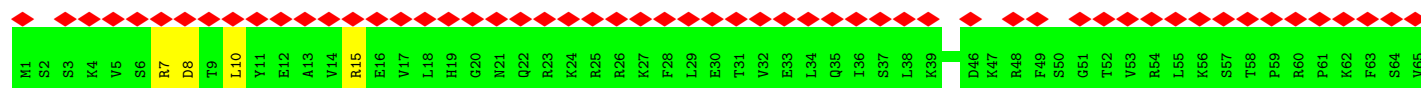




• Molecule 83: Large ribosomal subunit protein uL11



• Molecule 84: 60S ribosomal protein L10a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10889	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.188	Depositor
Minimum map value	-0.078	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0237	Depositor
Map size (\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 (\AA)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	LW	0.44	0/979	0.67	0/1295
2	LR	0.42	0/1582	0.67	0/2091
3	SE	0.36	0/2118	0.60	0/2849
4	SI	0.42	0/1715	0.66	2/2287 (0.1%)
5	SL	0.63	2/1268 (0.2%)	0.79	3/1696 (0.2%)
6	SX	0.43	0/1116	0.64	1/1490 (0.1%)
7	SG	0.34	0/1946	0.65	0/2590
8	SJ	0.37	0/1550	0.64	0/2069
9	SY	0.35	0/1083	0.68	0/1438
10	Se	0.33	0/465	0.65	0/612
11	SA	0.43	0/1778	0.70	2/2416 (0.1%)
12	SB	0.43	0/1765	0.65	1/2362 (0.0%)
13	SH	0.34	0/1519	0.65	0/2033
14	SV	0.36	0/643	0.65	0/860
15	Sa	0.45	0/836	0.68	0/1121
16	SC	0.40	0/1762	0.65	1/2381 (0.0%)
17	SN	0.41	0/1232	0.59	0/1656
18	SO	0.40	0/1062	0.66	1/1425 (0.1%)
19	SW	0.44	1/1051 (0.1%)	0.68	1/1406 (0.1%)
20	Sb	0.41	0/665	0.67	0/891
21	L5	0.98	0/89311	0.98	127/139283 (0.1%)
22	L7	0.98	0/2861	0.90	0/4459
23	L8	0.99	0/3701	0.90	2/5766 (0.0%)
24	LA	0.55	0/1936	0.68	0/2596
25	LB	0.51	0/3306	0.63	3/4424 (0.1%)
26	LC	0.50	0/2981	0.66	2/4002 (0.0%)
27	LD	0.49	0/2428	0.61	0/3252
28	LE	0.45	0/1942	0.67	1/2606 (0.0%)
29	LF	0.51	0/1905	0.63	0/2539
30	LG	0.46	0/1960	0.60	0/2637
31	LH	0.48	0/1537	0.67	0/2066
32	LI	0.49	0/1673	0.69	2/2233 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LJ	0.46	0/1433	0.68	1/1915 (0.1%)
34	LL	0.53	2/1732 (0.1%)	0.73	3/2315 (0.1%)
35	LM	0.49	0/1161	0.61	0/1554
36	LN	0.56	0/1746	0.66	0/2338
37	LO	0.53	0/1682	0.63	0/2250
38	LP	0.52	0/1268	0.61	0/1701
39	LQ	0.53	0/1537	0.70	1/2052 (0.0%)
40	LS	0.55	0/1493	0.62	0/2003
41	LT	0.54	0/1326	0.65	0/1770
42	LU	0.49	0/839	0.74	0/1126
43	LV	0.51	0/993	0.64	0/1332
44	LX	0.47	0/1002	0.67	1/1345 (0.1%)
45	LY	0.50	0/1132	0.64	0/1504
46	LZ	0.64	1/1130 (0.1%)	0.85	4/1507 (0.3%)
47	La	0.52	0/1191	0.60	0/1591
48	Lb	0.39	0/889	0.69	1/1175 (0.1%)
49	Lc	0.49	0/774	0.60	0/1038
50	Ld	0.51	0/903	0.63	0/1216
51	Le	0.54	0/1071	0.64	0/1429
52	Lf	0.56	0/895	0.65	0/1198
53	Lg	0.50	0/916	0.65	0/1220
54	Lh	0.42	0/1023	0.61	0/1351
55	Li	0.61	2/843 (0.2%)	0.82	3/1115 (0.3%)
56	Lj	0.57	0/720	0.68	0/952
57	Lk	0.40	0/575	0.63	0/761
58	Ll	0.48	0/454	0.67	0/599
59	Lm	0.47	0/435	0.65	0/575
60	Ln	0.43	0/231	0.76	0/294
61	Lo	0.48	0/876	0.62	0/1156
62	Lp	0.50	0/718	0.66	1/953 (0.1%)
63	Lr	0.49	0/1017	0.64	0/1364
64	SR	0.34	0/1105	0.67	0/1484
65	SD	0.37	0/1793	0.62	0/2414
66	SF	0.38	0/1516	0.66	1/2037 (0.0%)
67	SK	0.37	0/851	0.72	1/1147 (0.1%)
68	SP	0.39	0/1003	0.68	0/1342
69	SQ	0.37	0/1160	0.73	0/1553
70	SS	0.36	0/1216	0.68	0/1628
71	ST	0.34	0/1131	0.61	0/1515
72	SU	0.33	0/831	0.67	0/1115
73	Sc	0.36	0/508	0.70	0/680
74	Sd	0.42	0/470	0.69	1/623 (0.2%)
75	Sg	0.37	1/2493 (0.0%)	0.70	2/3394 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SM	0.30	0/950	0.62	1/1275 (0.1%)
77	SZ	0.35	0/604	0.71	0/810
78	Sf	0.35	0/560	0.62	0/745
79	S2	0.72	0/41242	0.92	47/64255 (0.1%)
80	Pt	0.58	0/1812	0.87	0/2823
81	Zt	0.44	0/1779	0.95	2/2771 (0.1%)
82	Ls	0.33	0/1519	0.65	2/2052 (0.1%)
83	Lt	0.28	0/1058	0.64	2/1430 (0.1%)
84	Lz	0.30	0/1769	0.60	1/2371 (0.0%)
All	All	0.75	9/239051 (0.0%)	0.86	224/350994 (0.1%)

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
1	LW	0	1
6	SX	0	1
24	LA	0	2
25	LB	0	3
32	LI	0	1
33	LJ	0	1
35	LM	0	1
37	LO	0	1
41	LT	0	1
42	LU	0	1
52	Lf	0	2
56	Lj	0	1
64	SR	0	1
68	SP	0	1
69	SQ	0	1
77	SZ	0	1
All	All	0	20

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	SL	34	PRO	CG-CD	-13.49	1.06	1.50
46	LZ	90	PRO	CG-CD	-11.44	1.12	1.50
55	Li	6	PRO	CG-CD	-9.21	1.20	1.50
34	LL	134	PRO	CG-CD	-7.35	1.26	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	SL	34	PRO	N-CD	6.45	1.56	1.47
75	Sg	284	PRO	N-CD	5.70	1.55	1.47
34	LL	134	PRO	N-CD	5.33	1.55	1.47
55	Li	6	PRO	CB-CG	5.18	1.75	1.50
19	SW	93	LEU	C-N	-5.09	1.22	1.34

All (224) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	LZ	90	PRO	CA-N-CD	-13.39	92.75	111.50
34	LL	134	PRO	CA-N-CD	-13.05	93.23	111.50
55	Li	6	PRO	CA-N-CD	-12.60	93.86	111.50
11	SA	207	PRO	CA-N-CD	-12.56	93.91	111.50
5	SL	34	PRO	CA-N-CD	-12.09	94.57	111.50
46	LZ	90	PRO	N-CD-CG	-11.91	85.34	103.20
75	Sg	284	PRO	CA-N-CD	-11.87	94.89	111.50
79	S2	1722	G	N3-C4-N9	11.34	132.80	126.00
5	SL	34	PRO	N-CD-CG	-11.22	86.37	103.20
21	L5	655	C	N3-C2-O2	-10.88	114.28	121.90
21	L5	129	C	N3-C2-O2	-10.73	114.39	121.90
21	L5	260	C	N3-C2-O2	-9.80	115.04	121.90
21	L5	485	C	C2-N1-C1'	9.14	128.86	118.80
21	L5	3773	U	N3-C2-O2	-9.06	115.86	122.20
21	L5	174	C	N3-C2-O2	-8.84	115.72	121.90
79	S2	1722	G	N3-C4-C5	-8.80	124.20	128.60
21	L5	456	C	N3-C2-O2	-8.32	116.08	121.90
34	LL	134	PRO	N-CD-CG	-8.26	90.81	103.20
21	L5	655	C	N1-C2-O2	8.21	123.83	118.90
21	L5	1082	C	O4'-C1'-N1	8.15	114.72	108.20
46	LZ	90	PRO	CA-CB-CG	-8.13	88.56	104.00
4	SI	40	PRO	CA-N-CD	-8.11	100.15	111.50
79	S2	1772	C	N1-C2-O2	8.05	123.73	118.90
75	Sg	284	PRO	N-CD-CG	-8.04	91.14	103.20
79	S2	1811	C	N3-C2-O2	-8.02	116.28	121.90
21	L5	4101	C	N3-C4-C5	8.02	125.11	121.90
79	S2	1811	C	N1-C2-O2	7.93	123.66	118.90
55	Li	6	PRO	N-CD-CG	-7.81	91.48	103.20
79	S2	293	C	N1-C2-O2	7.81	123.58	118.90
12	SB	24	PRO	CA-N-CD	-7.73	100.67	111.50
79	S2	1722	G	C6-C5-N7	-7.71	125.78	130.40
21	L5	130	C	N3-C2-O2	-7.67	116.53	121.90
79	S2	1722	G	C4-N9-C1'	7.63	136.42	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	SL	34	PRO	CA-CB-CG	-7.59	89.57	104.00
79	S2	293	C	C2-N1-C1'	7.59	127.15	118.80
21	L5	3773	U	O4'-C1'-N1	7.58	114.27	108.20
21	L5	3773	U	N1-C2-O2	7.49	128.04	122.80
21	L5	260	C	N1-C2-O2	7.49	123.39	118.90
21	L5	1252	C	N3-C2-O2	-7.49	116.66	121.90
79	S2	1358	U	C5-C6-N1	7.46	126.43	122.70
21	L5	417	G	O4'-C1'-N9	7.43	114.14	108.20
79	S2	1722	G	C8-N9-C1'	-7.34	117.45	127.00
21	L5	1414	C	N1-C2-O2	7.33	123.30	118.90
79	S2	1416	C	N3-C2-O2	-7.32	116.78	121.90
21	L5	456	C	O4'-C1'-N1	7.31	114.05	108.20
28	LE	202	ASP	CB-CG-OD2	7.29	124.86	118.30
21	L5	209	U	C2-N1-C1'	7.27	126.42	117.70
21	L5	4303	C	C6-N1-C2	-7.24	117.41	120.30
18	SO	14	VAL	C-N-CA	7.22	139.75	121.70
21	L5	490	C	N3-C2-O2	-7.22	116.84	121.90
79	S2	356	C	C2-N1-C1'	7.13	126.65	118.80
32	LI	212	LEU	CA-CB-CG	7.09	131.61	115.30
76	SM	22	LEU	CA-CB-CG	6.98	131.36	115.30
21	L5	925	C	N3-C2-O2	-6.94	117.04	121.90
21	L5	2018	C	C5-C6-N1	6.94	124.47	121.00
79	S2	293	C	N3-C2-O2	-6.94	117.04	121.90
21	L5	499	G	O4'-C1'-N9	6.94	113.75	108.20
66	SF	121	PRO	CA-N-CD	-6.93	101.80	111.50
48	Lb	118	LEU	CA-CB-CG	6.87	131.09	115.30
79	S2	1772	C	N3-C2-O2	-6.78	117.16	121.90
21	L5	175	C	N3-C2-O2	-6.77	117.16	121.90
21	L5	485	C	C6-N1-C1'	-6.70	112.76	120.80
79	S2	356	C	N1-C2-O2	6.61	122.86	118.90
21	L5	925	C	N1-C2-O2	6.54	122.83	118.90
84	Lz	194	LEU	CA-CB-CG	6.54	130.33	115.30
79	S2	1015	U	C2-N3-C4	-6.52	123.09	127.00
21	L5	4709	U	C2-N1-C1'	6.51	125.51	117.70
21	L5	4147	G	C5-C6-O6	6.46	132.48	128.60
21	L5	2410	C	C2-N1-C1'	6.45	125.89	118.80
21	L5	2018	C	C6-N1-C2	-6.42	117.73	120.30
21	L5	1417	C	C2-N1-C1'	6.40	125.84	118.80
21	L5	485	C	N1-C2-O2	6.36	122.71	118.90
79	S2	833	C	N1-C2-O2	6.32	122.69	118.90
21	L5	654	C	N1-C2-O2	6.28	122.67	118.90
79	S2	1582	C	N1-C2-O2	6.27	122.66	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	L5	4922	C	N3-C2-O2	-6.26	117.51	121.90
21	L5	129	C	N1-C2-O2	6.25	122.65	118.90
23	L8	51	U	N3-C2-O2	-6.21	117.86	122.20
79	S2	1722	G	N1-C2-N2	-6.18	110.64	116.20
79	S2	557	U	N3-C2-O2	-6.16	117.89	122.20
11	SA	207	PRO	N-CD-CG	-6.15	93.97	103.20
55	Li	6	PRO	CA-CB-CG	-6.15	92.31	104.00
21	L5	914	U	C5-C4-O4	-6.14	122.22	125.90
79	S2	1139	C	C6-N1-C2	-6.06	117.88	120.30
21	L5	261	G	C4-C5-N7	6.05	113.22	110.80
21	L5	4924	C	C6-N1-C1'	6.04	128.05	120.80
21	L5	2257	C	N1-C2-O2	6.02	122.51	118.90
79	S2	1722	G	N9-C4-C5	-6.01	103.00	105.40
21	L5	100	C	C2-N1-C1'	6.00	125.41	118.80
25	LB	17	LEU	CA-CB-CG	6.00	129.09	115.30
79	S2	1722	G	N3-C2-N2	5.98	124.08	119.90
21	L5	3955	G	N3-C4-N9	-5.94	122.43	126.00
79	S2	1520	G	C4-N9-C1'	5.94	134.22	126.50
21	L5	175	C	N1-C2-O2	5.92	122.45	118.90
79	S2	1772	C	C2-N1-C1'	5.89	125.28	118.80
21	L5	129	C	C6-N1-C2	-5.87	117.95	120.30
33	LJ	91	GLU	CA-CB-CG	5.86	126.29	113.40
79	S2	501	C	C2-N1-C1'	5.86	125.25	118.80
21	L5	209	U	C6-N1-C1'	-5.85	113.02	121.20
21	L5	499	G	N9-C4-C5	-5.83	103.07	105.40
32	LI	193	ASP	CB-CG-OD2	5.80	123.52	118.30
21	L5	262	G	C8-N9-C4	-5.79	104.08	106.40
39	LQ	4	ASP	CB-CG-OD2	5.78	123.50	118.30
21	L5	1414	C	N3-C2-O2	-5.77	117.86	121.90
79	S2	1453	C	C2-N1-C1'	5.77	125.14	118.80
81	Zt	72	C	N1-C2-O2	5.75	122.35	118.90
21	L5	181	C	C2-N1-C1'	5.75	125.12	118.80
21	L5	2627	C	C2-N1-C1'	5.75	125.12	118.80
21	L5	130	C	C6-N1-C2	-5.73	118.01	120.30
21	L5	664	G	C5-C6-O6	5.72	132.03	128.60
21	L5	456	C	N1-C2-O2	5.72	122.33	118.90
79	S2	688	U	P-O3'-C3'	5.71	126.55	119.70
21	L5	4138	C	N3-C2-O2	-5.70	117.91	121.90
4	SI	172	LEU	CA-CB-CG	5.70	128.41	115.30
21	L5	1082	C	N3-C2-O2	-5.70	117.91	121.90
21	L5	4922	C	N1-C2-O2	5.70	122.32	118.90
21	L5	3761	C	C2-N1-C1'	5.70	125.06	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	L5	500	G	N1-C2-N2	-5.69	111.08	116.20
21	L5	2257	C	C2-N1-C1'	5.66	125.03	118.80
19	SW	29	PRO	CA-N-CD	-5.66	103.58	111.50
21	L5	263	G	C5-C6-O6	5.63	131.98	128.60
26	LC	2	ALA	C-N-CA	5.62	135.76	121.70
21	L5	174	C	N1-C2-N3	5.62	123.14	119.20
21	L5	456	C	C6-N1-C2	-5.62	118.05	120.30
21	L5	4898	G	N3-C4-N9	-5.62	122.63	126.00
21	L5	181	C	N1-C2-O2	5.61	122.27	118.90
21	L5	3761	C	N1-C2-O2	5.61	122.26	118.90
21	L5	4147	G	N1-C6-O6	-5.61	116.53	119.90
21	L5	4147	G	N3-C4-N9	-5.60	122.64	126.00
21	L5	255	C	N3-C2-O2	-5.56	118.01	121.90
82	Ls	77	LYS	CA-CB-CG	5.56	125.62	113.40
21	L5	1082	C	C2-N1-C1'	-5.55	112.69	118.80
21	L5	1217	G	N3-C4-N9	5.53	129.32	126.00
81	Zt	66	U	C2-N1-C1'	5.53	124.34	117.70
79	S2	293	C	C6-N1-C1'	-5.53	114.16	120.80
21	L5	1082	C	P-O3'-C3'	5.53	126.33	119.70
79	S2	1139	C	N3-C2-O2	-5.52	118.04	121.90
21	L5	177	G	N1-C2-N2	-5.52	111.23	116.20
21	L5	1191	C	N3-C2-O2	-5.50	118.05	121.90
79	S2	1520	G	C8-N9-C1'	-5.49	119.86	127.00
21	L5	1082	C	C6-N1-C1'	5.49	127.38	120.80
21	L5	174	C	C6-N1-C2	-5.48	118.11	120.30
25	LB	17	LEU	CB-CG-CD2	-5.48	101.69	111.00
83	Lt	133	LEU	CA-CB-CG	5.46	127.86	115.30
21	L5	4107	G	N3-C4-C5	-5.46	125.87	128.60
21	L5	2519	U	O4'-C1'-N1	5.46	112.56	108.20
21	L5	489	C	N1-C2-O2	5.45	122.17	118.90
79	S2	1424	G	N3-C4-N9	5.44	129.26	126.00
74	Sd	30	LEU	CA-CB-CG	5.44	127.81	115.30
44	LX	92	ASP	CB-CG-OD1	5.43	123.19	118.30
21	L5	1241	C	C2-N1-C1'	5.42	124.76	118.80
21	L5	4887	C	C2-N1-C1'	5.42	124.76	118.80
25	LB	360	LEU	CA-CB-CG	5.41	127.74	115.30
21	L5	1816	C	C6-N1-C2	-5.40	118.14	120.30
21	L5	1493	G	N3-C4-N9	5.40	129.24	126.00
21	L5	914	U	N3-C4-O4	5.40	123.18	119.40
21	L5	4895	C	N1-C2-O2	5.37	122.12	118.90
21	L5	1217	G	C4-N9-C1'	5.36	133.47	126.50
21	L5	1182	C	N1-C2-O2	5.36	122.11	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	L5	499	G	N3-C4-N9	5.35	129.21	126.00
21	L5	3955	G	N3-C4-C5	5.35	131.27	128.60
46	LZ	89	ILE	C-N-CD	5.35	139.63	128.40
82	Ls	15	LEU	CA-CB-CG	5.35	127.60	115.30
21	L5	499	G	C8-N9-C1'	-5.34	120.05	127.00
21	L5	2786	C	C6-N1-C2	-5.34	118.16	120.30
21	L5	664	G	N1-C6-O6	-5.33	116.70	119.90
21	L5	4924	C	C2-N1-C1'	-5.32	112.95	118.80
21	L5	1973	G	N1-C6-O6	-5.30	116.72	119.90
21	L5	259	C	N1-C2-O2	5.29	122.08	118.90
79	S2	356	C	C6-N1-C1'	-5.29	114.45	120.80
21	L5	3775	A	C6-C5-N7	-5.28	128.60	132.30
21	L5	261	G	N9-C4-C5	-5.28	103.29	105.40
21	L5	4303	C	N3-C2-O2	-5.28	118.21	121.90
21	L5	177	G	N3-C2-N2	5.27	123.59	119.90
21	L5	1241	C	N1-C2-O2	5.27	122.06	118.90
79	S2	1780	G	O4'-C1'-N9	5.27	112.41	108.20
21	L5	1275	G	C4-N9-C1'	-5.26	119.66	126.50
21	L5	4926	C	C6-N1-C2	-5.25	118.20	120.30
21	L5	3765	G	N3-C2-N2	-5.25	116.22	119.90
21	L5	1192	C	N3-C2-O2	-5.25	118.23	121.90
21	L5	255	C	C2-N3-C4	-5.24	117.28	119.90
21	L5	4709	U	C5-C4-O4	-5.24	122.76	125.90
21	L5	3773	U	C2-N1-C1'	5.23	123.97	117.70
21	L5	4101	C	C2-N3-C4	-5.22	117.29	119.90
21	L5	1216	C	C2-N1-C1'	5.22	124.54	118.80
21	L5	4281	A	C2-N3-C4	-5.22	107.99	110.60
62	Lp	47	MET	CA-CB-CG	5.21	122.16	113.30
21	L5	4897	G	C5-C6-O6	5.18	131.71	128.60
21	L5	499	G	C4-C5-N7	5.18	112.87	110.80
21	L5	1493	G	N3-C4-C5	-5.17	126.02	128.60
79	S2	537	C	C2-N1-C1'	5.17	124.49	118.80
79	S2	557	U	N1-C2-O2	5.16	126.41	122.80
21	L5	3955	G	C4-N9-C1'	-5.16	119.80	126.50
79	S2	1755	C	N1-C2-O2	5.15	121.99	118.90
21	L5	4107	G	C2-N3-C4	5.14	114.47	111.90
21	L5	1414	C	C2-N1-C1'	5.13	124.44	118.80
79	S2	1660	C	N3-C2-O2	-5.13	118.31	121.90
21	L5	262	G	N1-C2-N2	-5.13	111.58	116.20
21	L5	2018	C	O4'-C1'-N1	5.12	112.30	108.20
21	L5	4626	A	O4'-C1'-N9	5.12	112.30	108.20
79	S2	1425	G	C5-C6-O6	5.12	131.67	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	L5	4926	C	C2-N1-C1'	5.11	124.42	118.80
6	SX	133	LEU	CA-CB-CG	5.10	127.04	115.30
21	L5	100	C	C6-N1-C2	-5.09	118.26	120.30
16	SC	233	LEU	CA-CB-CG	5.08	126.99	115.30
79	S2	1722	G	C4-C5-C6	5.08	121.85	118.80
21	L5	4107	G	N1-C6-O6	-5.07	116.86	119.90
21	L5	701	G	N3-C4-N9	-5.06	122.96	126.00
79	S2	1520	G	N3-C4-N9	5.05	129.03	126.00
79	S2	1772	C	C6-N1-C2	-5.05	118.28	120.30
34	LL	134	PRO	CA-CB-CG	-5.05	94.41	104.00
21	L5	3598	C	N1-C2-O2	5.04	121.92	118.90
21	L5	4592	C	N1-C2-O2	-5.04	115.88	118.90
79	S2	322	C	N1-C2-O2	5.04	121.92	118.90
83	Lt	121	LEU	CA-CB-CG	5.04	126.88	115.30
21	L5	1216	C	N3-C2-O2	-5.03	118.38	121.90
23	L8	128	C	C2-N1-C1'	5.03	124.33	118.80
79	S2	1022	U	C2-N1-C1'	5.03	123.73	117.70
67	SK	85	LEU	CA-CB-CG	5.02	126.85	115.30
79	S2	356	C	N3-C2-O2	-5.02	118.39	121.90
26	LC	235	LEU	CA-CB-CG	5.01	126.82	115.30
79	S2	1356	G	C6-C5-N7	5.01	133.41	130.40
21	L5	1259	G	C5-C6-O6	5.01	131.60	128.60
21	L5	500	G	N3-C2-N2	5.00	123.40	119.90

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
24	LA	13	GLY	Peptide
24	LA	54	ARG	Peptide
25	LB	17	LEU	Peptide
25	LB	258	HIS	Peptide
25	LB	302	ASN	Peptide
32	LI	14	ASN	Peptide
33	LJ	94	LEU	Peptide
35	LM	87	ALA	Peptide
37	LO	110	PRO	Peptide
41	LT	136	ARG	Peptide
42	LU	41	GLN	Peptide
1	LW	49	ILE	Peptide
52	Lf	106	TYR	Peptide
52	Lf	79	GLY	Peptide

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Mol	Chain	Res	Type	Group
56	Lj	39	TYR	Peptide
68	SP	127	LYS	Peptide
69	SQ	43	GLU	Peptide
64	SR	84	TYR	Peptide
6	SX	126	ALA	Peptide
77	SZ	46	ASN	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LW	114/124 (92%)	109 (96%)	5 (4%)	0	100	100
2	LR	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
3	SE	260/262 (99%)	245 (94%)	15 (6%)	0	100	100
4	SI	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
5	SL	151/153 (99%)	139 (92%)	12 (8%)	0	100	100
6	SX	139/141 (99%)	121 (87%)	17 (12%)	1 (1%)	19	52
7	SG	235/237 (99%)	216 (92%)	19 (8%)	0	100	100
8	SJ	183/185 (99%)	173 (94%)	10 (6%)	0	100	100
9	SY	129/131 (98%)	112 (87%)	17 (13%)	0	100	100
10	Se	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
11	SA	219/221 (99%)	194 (89%)	25 (11%)	0	100	100
12	SB	212/214 (99%)	197 (93%)	15 (7%)	0	100	100
13	SH	182/189 (96%)	154 (85%)	28 (15%)	0	100	100
14	SV	81/83 (98%)	70 (86%)	11 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	Sa	100/102 (98%)	88 (88%)	11 (11%)	1 (1%)	13	44
16	SC	220/222 (99%)	203 (92%)	17 (8%)	0	100	100
17	SN	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
18	SO	138/140 (99%)	126 (91%)	12 (9%)	0	100	100
19	SW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
20	Sb	81/83 (98%)	69 (85%)	12 (15%)	0	100	100
24	LA	246/248 (99%)	222 (90%)	22 (9%)	2 (1%)	16	49
25	LB	400/402 (100%)	363 (91%)	37 (9%)	0	100	100
26	LC	366/368 (100%)	336 (92%)	30 (8%)	0	100	100
27	LD	291/293 (99%)	268 (92%)	23 (8%)	0	100	100
28	LE	232/247 (94%)	204 (88%)	28 (12%)	0	100	100
29	LF	223/225 (99%)	207 (93%)	16 (7%)	0	100	100
30	LG	239/241 (99%)	221 (92%)	18 (8%)	0	100	100
31	LH	188/190 (99%)	176 (94%)	12 (6%)	0	100	100
32	LI	198/213 (93%)	183 (92%)	15 (8%)	0	100	100
33	LJ	174/176 (99%)	157 (90%)	17 (10%)	0	100	100
34	LL	208/210 (99%)	189 (91%)	19 (9%)	0	100	100
35	LM	137/139 (99%)	127 (93%)	9 (7%)	1 (1%)	19	52
36	LN	201/203 (99%)	187 (93%)	13 (6%)	1 (0%)	25	58
37	LO	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
38	LP	151/153 (99%)	141 (93%)	10 (7%)	0	100	100
39	LQ	185/187 (99%)	176 (95%)	9 (5%)	0	100	100
40	LS	173/175 (99%)	158 (91%)	15 (9%)	0	100	100
41	LT	157/159 (99%)	145 (92%)	12 (8%)	0	100	100
42	LU	99/101 (98%)	80 (81%)	19 (19%)	0	100	100
43	LV	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
44	LX	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
45	LY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
46	LZ	133/135 (98%)	120 (90%)	13 (10%)	0	100	100
47	La	145/147 (99%)	136 (94%)	9 (6%)	0	100	100
48	Lb	105/121 (87%)	99 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	Lc	96/98 (98%)	87 (91%)	9 (9%)	0	100	100
50	Ld	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
51	Le	126/128 (98%)	117 (93%)	9 (7%)	0	100	100
52	Lf	107/109 (98%)	98 (92%)	8 (8%)	1 (1%)	14	46
53	Lg	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
54	Lh	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
55	Li	100/102 (98%)	93 (93%)	7 (7%)	0	100	100
56	Lj	84/86 (98%)	75 (89%)	9 (11%)	0	100	100
57	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
58	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
59	Lm	50/52 (96%)	50 (100%)	0	0	100	100
60	Ln	22/24 (92%)	22 (100%)	0	0	100	100
61	Lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
62	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
63	Lr	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
64	SR	133/135 (98%)	117 (88%)	15 (11%)	1 (1%)	16	49
65	SD	225/227 (99%)	200 (89%)	25 (11%)	0	100	100
66	SF	187/189 (99%)	167 (89%)	20 (11%)	0	100	100
67	SK	96/98 (98%)	84 (88%)	11 (12%)	1 (1%)	13	44
68	SP	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
69	SQ	142/144 (99%)	121 (85%)	20 (14%)	1 (1%)	19	52
70	SS	143/145 (99%)	132 (92%)	11 (8%)	0	100	100
71	ST	141/143 (99%)	129 (92%)	12 (8%)	0	100	100
72	SU	102/104 (98%)	90 (88%)	11 (11%)	1 (1%)	13	44
73	Sc	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
74	Sd	53/55 (96%)	49 (92%)	3 (6%)	1 (2%)	6	31
75	Sg	311/313 (99%)	269 (86%)	42 (14%)	0	100	100
76	SM	120/122 (98%)	107 (89%)	13 (11%)	0	100	100
77	SZ	73/75 (97%)	55 (75%)	18 (25%)	0	100	100
78	Sf	65/67 (97%)	56 (86%)	9 (14%)	0	100	100
82	Ls	194/196 (99%)	178 (92%)	16 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
83	Lt	137/157 (87%)	107 (78%)	27 (20%)	3 (2%)	5	29
84	Lz	215/217 (99%)	166 (77%)	49 (23%)	0	100	100
All	All	11863/12090 (98%)	10808 (91%)	1040 (9%)	15 (0%)	50	79

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	SX	127	ASN
67	SK	96	ARG
15	Sa	47	ALA
35	LM	88	ALA
36	LN	124	ASP
64	SR	124	VAL
74	Sd	14	PHE
83	Lt	24	ALA
83	Lt	67	ARG
83	Lt	144	ASP
24	LA	14	SER
24	LA	55	GLY
52	Lf	107	PRO
69	SQ	44	PRO
72	SU	108	PRO

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	
1	LW	97/103 (94%)	88 (91%)	9 (9%)	7	28
2	LR	166/166 (100%)	150 (90%)	16 (10%)	7	27
3	SE	224/224 (100%)	197 (88%)	27 (12%)	4	18
4	SI	178/178 (100%)	164 (92%)	14 (8%)	10	34
5	SL	137/137 (100%)	124 (90%)	13 (10%)	7	27
6	SX	113/113 (100%)	105 (93%)	8 (7%)	12	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	SG	207/207 (100%)	187 (90%)	20 (10%)	6	26
8	SJ	161/161 (100%)	146 (91%)	15 (9%)	7	28
9	SY	113/113 (100%)	102 (90%)	11 (10%)	6	26
10	Se	47/47 (100%)	41 (87%)	6 (13%)	3	17
11	SA	183/183 (100%)	168 (92%)	15 (8%)	9	33
12	SB	195/195 (100%)	180 (92%)	15 (8%)	10	35
13	SH	166/169 (98%)	153 (92%)	13 (8%)	10	34
14	SV	67/67 (100%)	60 (90%)	7 (10%)	5	24
15	Sa	89/89 (100%)	78 (88%)	11 (12%)	4	18
16	SC	188/188 (100%)	163 (87%)	25 (13%)	3	16
17	SN	130/130 (100%)	119 (92%)	11 (8%)	8	31
18	SO	110/110 (100%)	103 (94%)	7 (6%)	14	41
19	SW	112/112 (100%)	101 (90%)	11 (10%)	6	26
20	Sb	75/75 (100%)	66 (88%)	9 (12%)	4	19
24	LA	190/190 (100%)	177 (93%)	13 (7%)	13	40
25	LB	348/348 (100%)	329 (94%)	19 (6%)	18	46
26	LC	306/306 (100%)	293 (96%)	13 (4%)	25	53
27	LD	246/247 (100%)	231 (94%)	15 (6%)	15	43
28	LE	209/220 (95%)	194 (93%)	15 (7%)	12	38
29	LF	194/194 (100%)	186 (96%)	8 (4%)	26	54
30	LG	203/205 (99%)	186 (92%)	17 (8%)	9	31
31	LH	169/169 (100%)	157 (93%)	12 (7%)	12	38
32	LI	172/180 (96%)	160 (93%)	12 (7%)	12	39
33	LJ	148/148 (100%)	141 (95%)	7 (5%)	22	51
34	LL	176/176 (100%)	167 (95%)	9 (5%)	20	48
35	LM	118/118 (100%)	111 (94%)	7 (6%)	16	44
36	LN	171/171 (100%)	166 (97%)	5 (3%)	37	64
37	LO	173/173 (100%)	164 (95%)	9 (5%)	19	47
38	LP	134/134 (100%)	122 (91%)	12 (9%)	8	29
39	LQ	164/164 (100%)	154 (94%)	10 (6%)	15	43
40	LS	156/156 (100%)	147 (94%)	9 (6%)	17	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	LT	139/139 (100%)	126 (91%)	13 (9%)	7	27
42	LU	91/91 (100%)	79 (87%)	12 (13%)	3	16
43	LV	101/101 (100%)	98 (97%)	3 (3%)	36	63
44	LX	108/108 (100%)	102 (94%)	6 (6%)	17	45
45	LY	124/124 (100%)	113 (91%)	11 (9%)	8	30
46	LZ	117/117 (100%)	107 (92%)	10 (8%)	8	31
47	La	120/120 (100%)	111 (92%)	9 (8%)	11	36
48	Lb	88/101 (87%)	79 (90%)	9 (10%)	6	25
49	Lc	83/83 (100%)	73 (88%)	10 (12%)	4	19
50	Ld	98/98 (100%)	86 (88%)	12 (12%)	4	18
51	Le	114/114 (100%)	106 (93%)	8 (7%)	12	39
52	Lf	88/88 (100%)	83 (94%)	5 (6%)	17	45
53	Lg	98/98 (100%)	93 (95%)	5 (5%)	20	48
54	Lh	109/109 (100%)	103 (94%)	6 (6%)	18	46
55	Li	86/86 (100%)	79 (92%)	7 (8%)	9	33
56	Lj	73/73 (100%)	64 (88%)	9 (12%)	4	18
57	Lk	64/64 (100%)	58 (91%)	6 (9%)	7	27
58	Ll	47/47 (100%)	42 (89%)	5 (11%)	5	23
59	Lm	48/48 (100%)	43 (90%)	5 (10%)	5	24
60	Ln	23/23 (100%)	21 (91%)	2 (9%)	8	30
61	Lo	93/93 (100%)	83 (89%)	10 (11%)	5	23
62	Lp	74/74 (100%)	69 (93%)	5 (7%)	13	40
63	Lr	109/109 (100%)	102 (94%)	7 (6%)	14	41
64	SR	122/122 (100%)	109 (89%)	13 (11%)	5	23
65	SD	190/190 (100%)	163 (86%)	27 (14%)	2	14
66	SF	159/159 (100%)	147 (92%)	12 (8%)	11	36
67	SK	89/89 (100%)	74 (83%)	15 (17%)	1	9
68	SP	107/107 (100%)	98 (92%)	9 (8%)	9	31
69	SQ	119/119 (100%)	109 (92%)	10 (8%)	9	31
70	SS	126/126 (100%)	113 (90%)	13 (10%)	6	25
71	ST	113/113 (100%)	101 (89%)	12 (11%)	5	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	SU	94/94 (100%)	86 (92%)	8 (8%)	8	31
73	Sc	57/57 (100%)	52 (91%)	5 (9%)	8	30
74	Sd	48/48 (100%)	44 (92%)	4 (8%)	9	32
75	Sg	272/272 (100%)	247 (91%)	25 (9%)	7	28
76	SM	102/104 (98%)	90 (88%)	12 (12%)	4	19
77	SZ	66/66 (100%)	55 (83%)	11 (17%)	2	9
78	Sf	60/60 (100%)	55 (92%)	5 (8%)	9	32
82	Ls	162/164 (99%)	142 (88%)	20 (12%)	4	18
83	Lt	112/130 (86%)	106 (95%)	6 (5%)	18	46
84	Lz	195/196 (100%)	180 (92%)	15 (8%)	10	35
All	All	10323/10390 (99%)	9471 (92%)	852 (8%)	12	32

All (852) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	LW	11	TYR
1	LW	19	ARG
1	LW	20	ARG
1	LW	41	LEU
1	LW	50	ASN
1	LW	58	LYS
1	LW	60	LYS
1	LW	77	LYS
1	LW	110	ARG
2	LR	29	THR
2	LR	34	ASN
2	LR	38	ARG
2	LR	49	LEU
2	LR	63	CYS
2	LR	108	ARG
2	LR	111	GLU
2	LR	113	LYS
2	LR	117	ARG
2	LR	119	MET
2	LR	146	LYS
2	LR	153	LYS
2	LR	165	LYS
2	LR	167	LYS

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Mol	Chain	Res	Type
2	LR	172	ARG
2	LR	186	LYS
3	SE	26	VAL
3	SE	38	LEU
3	SE	50	ASN
3	SE	57	THR
3	SE	62	LYS
3	SE	69	PHE
3	SE	72	ILE
3	SE	101	LEU
3	SE	108	ARG
3	SE	120	LYS
3	SE	126	VAL
3	SE	127	ARG
3	SE	133	THR
3	SE	138	HIS
3	SE	145	ARG
3	SE	161	GLN
3	SE	164	LEU
3	SE	176	ASP
3	SE	181	CYS
3	SE	196	THR
3	SE	198	ARG
3	SE	204	SER
3	SE	216	ASN
3	SE	226	PHE
3	SE	230	LYS
3	SE	233	LYS
3	SE	238	LEU
4	SI	7	ASN
4	SI	14	THR
4	SI	29	LEU
4	SI	35	ASN
4	SI	64	ASN
4	SI	73	THR
4	SI	81	VAL
4	SI	139	LYS
4	SI	140	LYS
4	SI	146	GLN
4	SI	148	LYS
4	SI	154	LYS
4	SI	159	SER

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Mol	Chain	Res	Type
4	SI	172	LEU
5	SL	12	LYS
5	SL	33	LEU
5	SL	39	ASN
5	SL	46	THR
5	SL	60	CYS
5	SL	69	ARG
5	SL	73	LEU
5	SL	90	ARG
5	SL	91	ASP
5	SL	110	SER
5	SL	119	ASP
5	SL	124	ASP
5	SL	135	SER
6	SX	24	ASP
6	SX	37	LYS
6	SX	69	CYS
6	SX	92	ASN
6	SX	97	ASN
6	SX	98	ASP
6	SX	105	PHE
6	SX	107	ARG
7	SG	14	LYS
7	SG	20	ASP
7	SG	25	ARG
7	SG	26	THR
7	SG	27	PHE
7	SG	79	LYS
7	SG	82	SER
7	SG	85	ARG
7	SG	98	ARG
7	SG	103	ASP
7	SG	116	LYS
7	SG	119	LYS
7	SG	131	ARG
7	SG	144	LEU
7	SG	149	LYS
7	SG	162	LEU
7	SG	201	LYS
7	SG	221	LYS
7	SG	230	LYS
7	SG	231	ARG

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Mol	Chain	Res	Type
8	SJ	5	ARG
8	SJ	10	ARG
8	SJ	12	THR
8	SJ	23	SER
8	SJ	45	ARG
8	SJ	61	LEU
8	SJ	91	LYS
8	SJ	92	MET
8	SJ	93	LYS
8	SJ	101	LYS
8	SJ	124	HIS
8	SJ	128	VAL
8	SJ	131	ARG
8	SJ	132	GLN
8	SJ	172	ARG
9	SY	16	ARG
9	SY	20	ARG
9	SY	23	MET
9	SY	42	GLU
9	SY	43	LYS
9	SY	58	PHE
9	SY	88	LYS
9	SY	97	TYR
9	SY	105	LYS
9	SY	114	MET
9	SY	132	LYS
10	Se	15	GLN
10	Se	31	ARG
10	Se	36	MET
10	Se	39	ASN
10	Se	43	VAL
10	Se	52	LYS
11	SA	11	LYS
11	SA	29	ASN
11	SA	32	PHE
11	SA	34	MET
11	SA	75	SER
11	SA	126	ASP
11	SA	131	HIS
11	SA	142	LEU
11	SA	155	ARG
11	SA	169	HIS

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Mol	Chain	Res	Type
11	SA	193	HIS
11	SA	200	ASP
11	SA	201	LEU
11	SA	206	ASP
11	SA	219	GLU
12	SB	27	LYS
12	SB	38	MET
12	SB	43	ASN
12	SB	48	LEU
12	SB	90	ASP
12	SB	96	CYS
12	SB	107	ARG
12	SB	177	GLN
12	SB	182	LYS
12	SB	208	HIS
12	SB	209	ASP
12	SB	210	VAL
12	SB	211	PHE
12	SB	223	PHE
12	SB	231	LEU
13	SH	7	LYS
13	SH	19	PHE
13	SH	29	GLU
13	SH	32	MET
13	SH	40	LEU
13	SH	41	ARG
13	SH	72	PHE
13	SH	122	LEU
13	SH	135	PHE
13	SH	168	HIS
13	SH	173	PHE
13	SH	184	ASP
13	SH	186	ASN
14	SV	1	MET
14	SV	12	TYR
14	SV	18	SER
14	SV	31	SER
14	SV	41	LYS
14	SV	49	GLN
14	SV	59	ILE
15	Sa	3	LYS
15	Sa	23	CYS

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Mol	Chain	Res	Type
15	Sa	33	ASP
15	Sa	39	PHE
15	Sa	42	ARG
15	Sa	52	ASP
15	Sa	57	SER
15	Sa	71	LEU
15	Sa	75	VAL
15	Sa	81	SER
15	Sa	92	ARG
16	SC	68	ARG
16	SC	73	MET
16	SC	77	SER
16	SC	81	ILE
16	SC	92	GLU
16	SC	97	PHE
16	SC	102	LEU
16	SC	116	THR
16	SC	117	ARG
16	SC	121	ARG
16	SC	123	ARG
16	SC	134	ASN
16	SC	152	ARG
16	SC	161	SER
16	SC	163	VAL
16	SC	184	VAL
16	SC	187	ARG
16	SC	188	CYS
16	SC	206	SER
16	SC	220	ASP
16	SC	227	ARG
16	SC	236	PHE
16	SC	248	TYR
16	SC	256	TRP
16	SC	263	LYS
17	SN	26	LEU
17	SN	29	THR
17	SN	35	GLU
17	SN	36	GLN
17	SN	48	SER
17	SN	65	PHE
17	SN	87	ASP
17	SN	103	GLU

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Mol	Chain	Res	Type
17	SN	106	ARG
17	SN	110	ASP
17	SN	143	SER
18	SO	26	ASN
18	SO	93	LEU
18	SO	103	ASN
18	SO	114	SER
18	SO	121	ARG
18	SO	138	ASP
18	SO	147	ARG
19	SW	5	ASN
19	SW	22	LYS
19	SW	29	PRO
19	SW	36	ARG
19	SW	49	GLU
19	SW	52	ILE
19	SW	54	ASP
19	SW	64	ASN
19	SW	80	ASP
19	SW	82	GLN
19	SW	103	VAL
20	Sb	6	ASP
20	Sb	9	HIS
20	Sb	29	ASN
20	Sb	33	MET
20	Sb	36	LYS
20	Sb	41	TYR
20	Sb	60	SER
20	Sb	79	PHE
20	Sb	80	ARG
24	LA	4	VAL
24	LA	28	ARG
24	LA	30	ARG
24	LA	45	VAL
24	LA	68	ARG
24	LA	114	CYS
24	LA	144	LYS
24	LA	155	LYS
24	LA	169	VAL
24	LA	198	ARG
24	LA	207	VAL
24	LA	221	LYS

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Mol	Chain	Res	Type
24	LA	228	ASP
25	LB	4	ARG
25	LB	5	LYS
25	LB	17	LEU
25	LB	39	LYS
25	LB	58	ARG
25	LB	59	GLU
25	LB	62	ARG
25	LB	69	LYS
25	LB	70	LYS
25	LB	154	LYS
25	LB	159	VAL
25	LB	181	MET
25	LB	292	LEU
25	LB	306	ASP
25	LB	317	LEU
25	LB	328	ASN
25	LB	329	ASP
25	LB	340	THR
25	LB	382	MET
26	LC	3	CYS
26	LC	14	LYS
26	LC	71	ARG
26	LC	95	MET
26	LC	106	LYS
26	LC	122	TYR
26	LC	186	SER
26	LC	188	ARG
26	LC	189	MET
26	LC	201	ARG
26	LC	261	ASP
26	LC	266	THR
26	LC	341	LEU
27	LD	36	LEU
27	LD	50	ARG
27	LD	70	GLU
27	LD	86	TYR
27	LD	112	ARG
27	LD	113	PHE
27	LD	115	MET
27	LD	117	LYS
27	LD	123	VAL

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Mol	Chain	Res	Type
27	LD	134	SER
27	LD	168	ASP
27	LD	217	ASP
27	LD	235	MET
27	LD	238	GLU
27	LD	239	MET
28	LE	63	TYR
28	LE	109	LEU
28	LE	115	TYR
28	LE	121	VAL
28	LE	128	HIS
28	LE	130	LYS
28	LE	139	LYS
28	LE	166	LYS
28	LE	172	LEU
28	LE	200	LYS
28	LE	202	ASP
28	LE	207	LYS
28	LE	210	LYS
28	LE	226	ARG
28	LE	254	ASP
29	LF	74	MET
29	LF	80	ASN
29	LF	119	ASN
29	LF	127	LYS
29	LF	177	ARG
29	LF	181	LYS
29	LF	221	LYS
29	LF	236	ARG
30	LG	34	LYS
30	LG	44	ASP
30	LG	53	ARG
30	LG	54	PHE
30	LG	73	ARG
30	LG	88	ASP
30	LG	90	GLN
30	LG	100	HIS
30	LG	111	LYS
30	LG	151	LYS
30	LG	176	LYS
30	LG	177	MET
30	LG	208	ASN

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Mol	Chain	Res	Type
30	LG	217	LYS
30	LG	255	LYS
30	LG	257	LYS
30	LG	259	LYS
31	LH	6	SER
31	LH	11	ASP
31	LH	16	VAL
31	LH	66	GLU
31	LH	78	GLN
31	LH	115	ARG
31	LH	121	LYS
31	LH	134	CYS
31	LH	165	THR
31	LH	171	ASP
31	LH	174	LYS
31	LH	180	TYR
32	LI	32	ARG
32	LI	38	ARG
32	LI	40	LYS
32	LI	42	LYS
32	LI	44	ASP
32	LI	55	ASP
32	LI	56	GLU
32	LI	102	MET
32	LI	137	SER
32	LI	168	SER
32	LI	203	HIS
32	LI	210	ARG
33	LJ	51	SER
33	LJ	65	ASN
33	LJ	92	TYR
33	LJ	95	ARG
33	LJ	100	SER
33	LJ	101	ASP
33	LJ	128	LEU
34	LL	8	MET
34	LL	21	ARG
34	LL	64	VAL
34	LL	67	HIS
34	LL	103	ARG
34	LL	118	LYS
34	LL	130	LYS

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Mol	Chain	Res	Type
34	LL	177	LYS
34	LL	201	GLU
35	LM	4	ARG
35	LM	7	VAL
35	LM	45	VAL
35	LM	54	CYS
35	LM	85	LYS
35	LM	99	GLU
35	LM	132	LYS
36	LN	100	SER
36	LN	108	ARG
36	LN	110	CYS
36	LN	147	ASP
36	LN	193	ARG
37	LO	29	LEU
37	LO	31	ARG
37	LO	85	ARG
37	LO	88	LEU
37	LO	140	ARG
37	LO	145	VAL
37	LO	169	ARG
37	LO	170	LYS
37	LO	199	HIS
38	LP	9	GLU
38	LP	18	ARG
38	LP	20	SER
38	LP	30	ARG
38	LP	39	MET
38	LP	46	LYS
38	LP	69	ARG
38	LP	93	HIS
38	LP	100	SER
38	LP	107	LEU
38	LP	118	GLN
38	LP	125	MET
39	LQ	42	THR
39	LQ	65	ARG
39	LQ	66	MET
39	LQ	70	MET
39	LQ	82	VAL
39	LQ	83	VAL
39	LQ	99	LYS

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Mol	Chain	Res	Type
39	LQ	168	ARG
39	LQ	180	ARG
39	LQ	183	SER
40	LS	8	ARG
40	LS	31	ARG
40	LS	54	MET
40	LS	77	ASN
40	LS	88	SER
40	LS	92	ASN
40	LS	111	ARG
40	LS	127	MET
40	LS	161	ARG
41	LT	3	ASN
41	LT	32	ARG
41	LT	38	ASP
41	LT	56	CYS
41	LT	63	ARG
41	LT	79	GLN
41	LT	81	LYS
41	LT	83	LYS
41	LT	85	LEU
41	LT	102	ARG
41	LT	147	GLU
41	LT	157	GLU
41	LT	158	PHE
42	LU	19	LEU
42	LU	21	PHE
42	LU	25	CYS
42	LU	29	VAL
42	LU	34	MET
42	LU	42	PHE
42	LU	64	GLU
42	LU	67	LYS
42	LU	93	LYS
42	LU	110	TYR
42	LU	112	LEU
42	LU	113	ARG
43	LV	99	GLU
43	LV	131	ARG
43	LV	135	ASN
44	LX	43	SER
44	LX	50	LYS

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Mol	Chain	Res	Type
44	LX	92	ASP
44	LX	118	ASP
44	LX	148	ASP
44	LX	152	LYS
45	LY	1	MET
45	LY	32	SER
45	LY	42	TYR
45	LY	47	MET
45	LY	74	TYR
45	LY	84	ARG
45	LY	110	LYS
45	LY	114	ASP
45	LY	115	ARG
45	LY	117	LYS
45	LY	130	LYS
46	LZ	9	LYS
46	LZ	22	LYS
46	LZ	43	VAL
46	LZ	84	ARG
46	LZ	88	ASP
46	LZ	99	ASP
46	LZ	100	VAL
46	LZ	103	ASP
46	LZ	106	LEU
46	LZ	112	ARG
47	La	12	ARG
47	La	46	ASP
47	La	65	ARG
47	La	67	GLN
47	La	78	LEU
47	La	85	GLN
47	La	95	THR
47	La	106	SER
47	La	130	SER
48	Lb	26	SER
48	Lb	48	LYS
48	Lb	50	ASN
48	Lb	54	LEU
48	Lb	55	LYS
48	Lb	70	GLU
48	Lb	91	ARG
48	Lb	103	LYS

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Mol	Chain	Res	Type
48	Lb	114	LYS
49	Lc	22	MET
49	Lc	23	LYS
49	Lc	26	LYS
49	Lc	37	MET
49	Lc	56	ARG
49	Lc	65	MET
49	Lc	92	CYS
49	Lc	93	THR
49	Lc	94	LEU
49	Lc	102	SER
50	Ld	19	GLU
50	Ld	26	THR
50	Ld	44	ARG
50	Ld	55	LYS
50	Ld	57	MET
50	Ld	61	ASP
50	Ld	67	ARG
50	Ld	87	ARG
50	Ld	91	LYS
50	Ld	95	ASP
50	Ld	100	ASN
50	Ld	118	GLN
51	Le	4	LEU
51	Le	13	VAL
51	Le	25	SER
51	Le	26	ASP
51	Le	34	ASN
51	Le	86	GLU
51	Le	102	ASN
51	Le	129	LEU
52	Lf	7	SER
52	Lf	46	ARG
52	Lf	47	CYS
52	Lf	90	SER
52	Lf	109	ARG
53	Lg	32	TYR
53	Lg	65	MET
53	Lg	69	LYS
53	Lg	73	HIS
53	Lg	83	CYS
54	Lh	7	ARG

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Mol	Chain	Res	Type
54	Lh	10	ARG
54	Lh	46	LYS
54	Lh	72	PHE
54	Lh	84	ARG
54	Lh	94	ARG
55	Li	42	ASP
55	Li	48	CYS
55	Li	62	LYS
55	Li	86	LYS
55	Li	88	GLU
55	Li	98	ARG
55	Li	103	LYS
56	Lj	11	ARG
56	Lj	12	ARG
56	Lj	22	CYS
56	Lj	25	LYS
56	Lj	30	GLN
56	Lj	36	LYS
56	Lj	39	TYR
56	Lj	63	ARG
56	Lj	79	ARG
57	Lk	13	LEU
57	Lk	21	LYS
57	Lk	29	LYS
57	Lk	30	ASP
57	Lk	44	THR
57	Lk	59	SER
58	Ll	25	GLN
58	Ll	28	ARG
58	Ll	36	ARG
58	Ll	37	TYR
58	Ll	45	ARG
59	Lm	88	LYS
59	Lm	94	MET
59	Lm	97	ARG
59	Lm	106	ARG
59	Lm	122	ARG
60	Ln	2	ARG
60	Ln	6	ARG
61	Lo	15	CYS
61	Lo	19	GLN
61	Lo	33	LEU

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Mol	Chain	Res	Type
61	Lo	63	THR
61	Lo	72	CYS
61	Lo	77	CYS
61	Lo	78	ARG
61	Lo	79	SER
61	Lo	82	MET
61	Lo	96	ASP
62	Lp	22	LEU
62	Lp	24	LYS
62	Lp	33	GLN
62	Lp	38	THR
62	Lp	40	SER
63	Lr	47	LYS
63	Lr	66	ARG
63	Lr	80	THR
63	Lr	81	THR
63	Lr	83	ASN
63	Lr	120	SER
63	Lr	122	LYS
64	SR	7	LYS
64	SR	23	ARG
64	SR	28	PHE
64	SR	35	CYS
64	SR	43	SER
64	SR	49	LYS
64	SR	67	ARG
64	SR	80	ARG
64	SR	87	GLU
64	SR	91	LEU
64	SR	107	LYS
64	SR	111	PHE
64	SR	126	MET
65	SD	11	PHE
65	SD	40	ARG
65	SD	56	GLN
65	SD	62	LYS
65	SD	65	ARG
65	SD	74	GLN
65	SD	75	LYS
65	SD	76	ARG
65	SD	83	SER
65	SD	94	ARG

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Mol	Chain	Res	Type
65	SD	120	TYR
65	SD	129	SER
65	SD	138	VAL
65	SD	143	ARG
65	SD	146	ARG
65	SD	150	MET
65	SD	151	LYS
65	SD	157	MET
65	SD	165	ASN
65	SD	167	TYR
65	SD	179	GLN
65	SD	192	TRP
65	SD	198	ILE
65	SD	202	LYS
65	SD	207	HIS
65	SD	220	THR
65	SD	221	THR
66	SF	19	LEU
66	SF	27	ASP
66	SF	37	ASP
66	SF	45	TYR
66	SF	60	ARG
66	SF	66	CYS
66	SF	74	ASN
66	SF	75	SER
66	SF	78	MET
66	SF	86	LYS
66	SF	140	ASP
66	SF	149	GLN
67	SK	3	MET
67	SK	8	ARG
67	SK	13	GLU
67	SK	16	PHE
67	SK	21	MET
67	SK	26	ASP
67	SK	35	LEU
67	SK	50	GLN
67	SK	51	SER
67	SK	62	PHE
67	SK	69	TRP
67	SK	70	TYR
67	SK	73	ASN

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Mol	Chain	Res	Type
67	SK	74	GLU
67	SK	98	ARG
68	SP	21	ASP
68	SP	29	SER
68	SP	33	LEU
68	SP	34	MET
68	SP	37	TYR
68	SP	38	SER
68	SP	45	LEU
68	SP	79	HIS
68	SP	89	MET
69	SQ	7	LEU
69	SQ	51	LEU
69	SQ	60	LYS
69	SQ	71	ARG
69	SQ	95	TYR
69	SQ	98	LYS
69	SQ	109	LYS
69	SQ	117	ARG
69	SQ	140	ARG
69	SQ	145	TYR
70	SS	1	MET
70	SS	13	LEU
70	SS	25	LYS
70	SS	76	GLN
70	SS	80	PRO
70	SS	96	SER
70	SS	99	LEU
70	SS	101	ASN
70	SS	103	LEU
70	SS	113	ARG
70	SS	114	LEU
70	SS	115	LYS
70	SS	124	ARG
71	ST	8	ASP
71	ST	18	LEU
71	ST	29	LYS
71	ST	38	LYS
71	ST	41	LYS
71	ST	48	TYR
71	ST	85	ASN
71	ST	87	VAL

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Mol	Chain	Res	Type
71	ST	91	HIS
71	ST	118	ASP
71	ST	126	GLN
71	ST	133	ARG
72	SU	18	HIS
72	SU	25	THR
72	SU	31	SER
72	SU	35	VAL
72	SU	38	ASP
72	SU	81	GLN
72	SU	86	LYS
72	SU	93	SER
73	Sc	7	GLN
73	Sc	16	LYS
73	Sc	27	CYS
73	Sc	35	MET
73	Sc	55	VAL
74	Sd	7	TYR
74	Sd	8	TRP
74	Sd	13	LYS
74	Sd	22	ARG
75	Sg	15	ASN
75	Sg	36	ARG
75	Sg	64	HIS
75	Sg	79	LEU
75	Sg	105	THR
75	Sg	107	ASP
75	Sg	113	PHE
75	Sg	126	ASP
75	Sg	135	LEU
75	Sg	153	CYS
75	Sg	167	SER
75	Sg	168	CYS
75	Sg	170	TRP
75	Sg	177	TRP
75	Sg	191	HIS
75	Sg	196	ASN
75	Sg	206	LEU
75	Sg	213	ASP
75	Sg	217	MET
75	Sg	247	TRP
75	Sg	252	THR

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Mol	Chain	Res	Type
75	Sg	257	LYS
75	Sg	271	LYS
75	Sg	272	GLN
75	Sg	288	SER
76	SM	14	VAL
76	SM	22	LEU
76	SM	23	LYS
76	SM	33	ARG
76	SM	45	ARG
76	SM	57	ASP
76	SM	60	MET
76	SM	61	TYR
76	SM	83	LYS
76	SM	93	LYS
76	SM	127	TYR
76	SM	128	PHE
77	SZ	43	LYS
77	SZ	50	PHE
77	SZ	51	ASP
77	SZ	55	TYR
77	SZ	57	LYS
77	SZ	65	TYR
77	SZ	74	SER
77	SZ	76	ARG
77	SZ	78	LYS
77	SZ	93	SER
77	SZ	106	GLN
78	Sf	95	ARG
78	Sf	100	LEU
78	Sf	104	LYS
78	Sf	118	ARG
78	Sf	125	GLU
82	Ls	8	THR
82	Ls	14	PHE
82	Ls	15	LEU
82	Ls	26	LYS
82	Ls	40	MET
82	Ls	45	MET
82	Ls	55	MET
82	Ls	60	MET
82	Ls	61	MET
82	Ls	77	LYS

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Mol	Chain	Res	Type
82	Ls	95	LEU
82	Ls	101	MET
82	Ls	105	ASN
82	Ls	123	VAL
82	Ls	146	LYS
82	Ls	149	ARG
82	Ls	162	LYS
82	Ls	177	MET
82	Ls	193	PHE
82	Ls	199	TYR
83	Lt	9	GLU
83	Lt	57	ARG
83	Lt	61	LYS
83	Lt	65	GLN
83	Lt	116	MET
83	Lt	141	CYS
84	Lz	7	ARG
84	Lz	8	ASP
84	Lz	10	LEU
84	Lz	15	ARG
84	Lz	92	LYS
84	Lz	105	LYS
84	Lz	122	ARG
84	Lz	142	GLU
84	Lz	144	MET
84	Lz	145	VAL
84	Lz	159	MET
84	Lz	185	LEU
84	Lz	194	LEU
84	Lz	202	ARG
84	Lz	212	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
3	SE	157	ASN
4	SI	64	ASN
7	SG	186	GLN
8	SJ	113	GLN
10	Se	44	ASN
11	SA	141	ASN
12	SB	75	GLN

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Mol	Chain	Res	Type
13	SH	25	GLN
13	SH	168	HIS
14	SV	49	GLN
18	SO	32	HIS
20	Sb	51	GLN
24	LA	139	HIS
25	LB	186	ASN
27	LD	111	ASN
27	LD	229	ASN
28	LE	128	HIS
29	LF	151	ASN
30	LG	43	GLN
33	LJ	42	GLN
33	LJ	98	ASN
34	LL	40	GLN
38	LP	137	ASN
39	LQ	125	GLN
40	LS	77	ASN
40	LS	146	HIS
45	LY	14	ASN
46	LZ	40	HIS
46	LZ	127	ASN
51	Le	107	ASN
59	Lm	109	ASN
61	Lo	25	GLN
62	Lp	33	GLN
63	Lr	31	ASN
65	SD	101	GLN
66	SF	110	GLN
66	SF	114	ASN
68	SP	35	GLN
68	SP	41	GLN
69	SQ	24	HIS
70	SS	11	HIS
71	ST	126	GLN
73	Sc	24	GLN
75	Sg	62	HIS
75	Sg	162	ASN
75	Sg	178	ASN
75	Sg	191	HIS
75	Sg	272	GLN
78	Sf	139	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	L5	3703/5070 (73%)	920 (24%)	26 (0%)
22	L7	119/120 (99%)	14 (11%)	0
23	L8	155/156 (99%)	35 (22%)	0
79	S2	1715/1740 (98%)	458 (26%)	5 (0%)
80	Pt	75/76 (98%)	19 (25%)	0
81	Zt	74/75 (98%)	36 (48%)	0
All	All	5841/7237 (80%)	1482 (25%)	31 (0%)

All (1482) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	L5	25	A
21	L5	26	C
21	L5	30	C
21	L5	39	A
21	L5	42	A
21	L5	48	G
21	L5	56	A
21	L5	59	A
21	L5	64	A
21	L5	65	A
21	L5	69	A
21	L5	72	C
21	L5	73	A
21	L5	74	G
21	L5	91	G
21	L5	108	A
21	L5	109	G
21	L5	110	C
21	L5	119	G
21	L5	120	A
21	L5	132	G
21	L5	133	C
21	L5	134	G
21	L5	135	G
21	L5	137	G
21	L5	139	G
21	L5	152	U
21	L5	159	C
21	L5	165	A
21	L5	166	C

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Mol	Chain	Res	Type
21	L5	171	U
21	L5	172	C
21	L5	175	C
21	L5	181	C
21	L5	182	G
21	L5	183	C
21	L5	184	U
21	L5	185	C
21	L5	186	G
21	L5	188	G
21	L5	189	G
21	L5	200	U
21	L5	209	U
21	L5	216	C
21	L5	218	A
21	L5	220	C
21	L5	234	G
21	L5	237	G
21	L5	250	C
21	L5	255	C
21	L5	256	G
21	L5	261	G
21	L5	262	G
21	L5	263	G
21	L5	264	C
21	L5	265	C
21	L5	266	C
21	L5	267	G
21	L5	269	G
21	L5	275	C
21	L5	276	C
21	L5	280	G
21	L5	297	U
21	L5	306	A
21	L5	310	G
21	L5	315	G
21	L5	316	U
21	L5	340	C
21	L5	350	C
21	L5	373	G
21	L5	385	A
21	L5	387	G

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Mol	Chain	Res	Type
21	L5	388	A
21	L5	396	A
21	L5	407	A
21	L5	409	G
21	L5	410	A
21	L5	411	G
21	L5	412	G
21	L5	413	G
21	L5	415	G
21	L5	431	G
21	L5	432	U
21	L5	433	A
21	L5	438	G
21	L5	449	C
21	L5	450	G
21	L5	452	A
21	L5	453	G
21	L5	454	U
21	L5	456	C
21	L5	457	G
21	L5	465	G
21	L5	467	U
21	L5	468	U
21	L5	484	U
21	L5	485	C
21	L5	486	C
21	L5	489	C
21	L5	493	G
21	L5	494	U
21	L5	497	G
21	L5	498	C
21	L5	499	G
21	L5	500	G
21	L5	501	C
21	L5	502	C
21	L5	503	C
21	L5	504	G
21	L5	505	G
21	L5	509	A
21	L5	510	U
21	L5	512	U
21	L5	513	U

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Mol	Chain	Res	Type
21	L5	514	U
21	L5	515	C
21	L5	517	C
21	L5	518	G
21	L5	643	C
21	L5	644	G
21	L5	645	G
21	L5	646	G
21	L5	654	C
21	L5	655	C
21	L5	656	C
21	L5	657	C
21	L5	658	C
21	L5	659	G
21	L5	666	G
21	L5	667	A
21	L5	668	C
21	L5	669	C
21	L5	672	C
21	L5	673	C
21	L5	685	C
21	L5	686	A
21	L5	687	U
21	L5	696	C
21	L5	703	G
21	L5	704	C
21	L5	706	C
21	L5	731	G
21	L5	738	C
21	L5	739	G
21	L5	742	G
21	L5	753	C
21	L5	759	G
21	L5	904	C
21	L5	905	C
21	L5	906	C
21	L5	911	U
21	L5	912	G
21	L5	913	U
21	L5	914	U
21	L5	915	A
21	L5	917	A

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Mol	Chain	Res	Type
21	L5	918	G
21	L5	923	C
21	L5	924	C
21	L5	926	G
21	L5	932	A
21	L5	933	G
21	L5	936	C
21	L5	943	A
21	L5	944	A
21	L5	945	U
21	L5	946	C
21	L5	958	G
21	L5	959	G
21	L5	960	A
21	L5	961	G
21	L5	962	C
21	L5	965	G
21	L5	966	A
21	L5	967	C
21	L5	968	C
21	L5	969	C
21	L5	970	G
21	L5	977	C
21	L5	982	U
21	L5	985	C
21	L5	989	U
21	L5	990	C
21	L5	992	C
21	L5	993	G
21	L5	995	C
21	L5	1048	G
21	L5	1049	C
21	L5	1050	C
21	L5	1051	G
21	L5	1070	G
21	L5	1072	C
21	L5	1075	G
21	L5	1082	C
21	L5	1083	U
21	L5	1095	A
21	L5	1168	G
21	L5	1169	G

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Mol	Chain	Res	Type
21	L5	1170	G
21	L5	1171	G
21	L5	1172	C
21	L5	1173	G
21	L5	1178	G
21	L5	1179	U
21	L5	1180	C
21	L5	1181	C
21	L5	1182	C
21	L5	1183	C
21	L5	1184	A
21	L5	1193	C
21	L5	1202	C
21	L5	1203	G
21	L5	1204	C
21	L5	1205	G
21	L5	1210	C
21	L5	1211	G
21	L5	1214	C
21	L5	1215	C
21	L5	1216	C
21	L5	1217	G
21	L5	1218	G
21	L5	1219	G
21	L5	1221	G
21	L5	1222	A
21	L5	1241	C
21	L5	1242	G
21	L5	1245	C
21	L5	1246	G
21	L5	1253	G
21	L5	1254	A
21	L5	1255	A
21	L5	1257	A
21	L5	1258	G
21	L5	1260	G
21	L5	1262	G
21	L5	1266	G
21	L5	1267	C
21	L5	1269	G
21	L5	1270	A
21	L5	1271	G

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Mol	Chain	Res	Type
21	L5	1272	C
21	L5	1273	G
21	L5	1275	G
21	L5	1277	G
21	L5	1280	C
21	L5	1284	G
21	L5	1285	U
21	L5	1287	G
21	L5	1293	G
21	L5	1294	A
21	L5	1295	C
21	L5	1296	G
21	L5	1301	C
21	L5	1302	U
21	L5	1304	C
21	L5	1312	A
21	L5	1314	C
21	L5	1324	A
21	L5	1326	A
21	L5	1339	U
21	L5	1353	G
21	L5	1354	A
21	L5	1358	G
21	L5	1359	G
21	L5	1365	C
21	L5	1367	C
21	L5	1387	A
21	L5	1392	A
21	L5	1394	G
21	L5	1397	A
21	L5	1401	C
21	L5	1404	G
21	L5	1407	C
21	L5	1409	C
21	L5	1410	U
21	L5	1411	C
21	L5	1414	C
21	L5	1415	G
21	L5	1417	C
21	L5	1420	A
21	L5	1437	C
21	L5	1439	C

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Mol	Chain	Res	Type
21	L5	1441	C
21	L5	1443	A
21	L5	1444	G
21	L5	1446	C
21	L5	1452	A
21	L5	1472	C
21	L5	1482	G
21	L5	1483	C
21	L5	1497	A
21	L5	1498	G
21	L5	1502	G
21	L5	1517	G
21	L5	1518	A
21	L5	1519	C
21	L5	1534	A
21	L5	1535	C
21	L5	1547	A
21	L5	1554	A
21	L5	1564	A
21	L5	1566	C
21	L5	1578	U
21	L5	1582	U
21	L5	1586	G
21	L5	1591	U
21	L5	1596	U
21	L5	1597	G
21	L5	1613	A
21	L5	1624	G
21	L5	1631	A
21	L5	1633	G
21	L5	1634	A
21	L5	1637	A
21	L5	1640	C
21	L5	1641	G
21	L5	1642	A
21	L5	1654	G
21	L5	1661	C
21	L5	1663	C
21	L5	1676	C
21	L5	1677	U
21	L5	1678	C
21	L5	1681	G

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Mol	Chain	Res	Type
21	L5	1685	G
21	L5	1698	C
21	L5	1699	A
21	L5	1700	G
21	L5	1703	C
21	L5	1704	C
21	L5	1705	G
21	L5	1707	C
21	L5	1709	C
21	L5	1718	C
21	L5	1729	A
21	L5	1731	C
21	L5	1733	G
21	L5	1734	G
21	L5	1740	C
21	L5	1741	G
21	L5	1742	A
21	L5	1750	G
21	L5	1757	U
21	L5	1758	G
21	L5	1760	G
21	L5	1761	G
21	L5	1762	C
21	L5	1763	C
21	L5	1764	G
21	L5	1765	A
21	L5	1766	A
21	L5	1768	C
21	L5	1769	G
21	L5	1770	A
21	L5	1775	A
21	L5	1787	A
21	L5	1804	A
21	L5	1806	G
21	L5	1810	G
21	L5	1820	C
21	L5	1821	G
21	L5	1822	U
21	L5	1830	G
21	L5	1833	G
21	L5	1834	U
21	L5	1836	G

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Mol	Chain	Res	Type
21	L5	1837	A
21	L5	1842	G
21	L5	1843	A
21	L5	1855	G
21	L5	1869	G
21	L5	1882	U
21	L5	1890	G
21	L5	1892	A
21	L5	1897	A
21	L5	1917	A
21	L5	1918	U
21	L5	1919	G
21	L5	1920	C
21	L5	1921	C
21	L5	1922	G
21	L5	1925	G
21	L5	1931	C
21	L5	1932	A
21	L5	1936	C
21	L5	1938	C
21	L5	1940	G
21	L5	1948	G
21	L5	1949	U
21	L5	1951	G
21	L5	1960	A
21	L5	1961	G
21	L5	1962	A
21	L5	1974	U
21	L5	1975	G
21	L5	1978	C
21	L5	1980	U
21	L5	1981	G
21	L5	1982	G
21	L5	1983	A
21	L5	1984	A
21	L5	1985	G
21	L5	1986	U
21	L5	1987	C
21	L5	1991	A
21	L5	1992	U
21	L5	1993	C
21	L5	1997	U

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Mol	Chain	Res	Type
21	L5	1998	A
21	L5	1999	A
21	L5	2001	G
21	L5	2002	A
21	L5	2011	C
21	L5	2014	C
21	L5	2018	C
21	L5	2025	A
21	L5	2026	A
21	L5	2033	A
21	L5	2034	G
21	L5	2046	G
21	L5	2048	U
21	L5	2055	G
21	L5	2056	G
21	L5	2069	A
21	L5	2084	C
21	L5	2085	G
21	L5	2092	G
21	L5	2093	A
21	L5	2095	A
21	L5	2097	U
21	L5	2098	G
21	L5	2101	C
21	L5	2102	G
21	L5	2103	G
21	L5	2105	A
21	L5	2107	C
21	L5	2108	G
21	L5	2110	C
21	L5	2112	G
21	L5	2250	C
21	L5	2252	G
21	L5	2253	A
21	L5	2255	C
21	L5	2256	C
21	L5	2257	C
21	L5	2258	C
21	L5	2260	C
21	L5	2261	G
21	L5	2289	C
21	L5	2300	A

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Mol	Chain	Res	Type
21	L5	2301	G
21	L5	2306	G
21	L5	2313	A
21	L5	2333	G
21	L5	2344	U
21	L5	2345	G
21	L5	2348	G
21	L5	2351	C
21	L5	2360	A
21	L5	2364	G
21	L5	2382	A
21	L5	2395	A
21	L5	2397	G
21	L5	2402	G
21	L5	2404	A
21	L5	2409	U
21	L5	2411	C
21	L5	2417	A
21	L5	2421	G
21	L5	2422	C
21	L5	2425	U
21	L5	2441	C
21	L5	2464	C
21	L5	2465	C
21	L5	2469	C
21	L5	2471	G
21	L5	2474	G
21	L5	2475	G
21	L5	2478	C
21	L5	2483	G
21	L5	2484	A
21	L5	2485	U
21	L5	2486	G
21	L5	2487	G
21	L5	2488	C
21	L5	2489	C
21	L5	2490	U
21	L5	2491	C
21	L5	2493	G
21	L5	2503	G
21	L5	2504	C
21	L5	2505	C

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Mol	Chain	Res	Type
21	L5	2506	G
21	L5	2511	A
21	L5	2513	A
21	L5	2514	G
21	L5	2519	U
21	L5	2520	C
21	L5	2529	A
21	L5	2536	A
21	L5	2537	A
21	L5	2544	G
21	L5	2546	G
21	L5	2547	G
21	L5	2554	U
21	L5	2557	G
21	L5	2559	G
21	L5	2560	C
21	L5	2573	A
21	L5	2583	C
21	L5	2587	A
21	L5	2589	C
21	L5	2600	A
21	L5	2601	A
21	L5	2611	A
21	L5	2623	A
21	L5	2627	C
21	L5	2639	U
21	L5	2652	G
21	L5	2653	C
21	L5	2658	G
21	L5	2662	G
21	L5	2664	G
21	L5	2669	C
21	L5	2675	G
21	L5	2676	A
21	L5	2687	U
21	L5	2694	G
21	L5	2695	A
21	L5	2696	A
21	L5	2703	G
21	L5	2707	U
21	L5	2708	U
21	L5	2711	G

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Mol	Chain	Res	Type
21	L5	2712	G
21	L5	2721	G
21	L5	2724	G
21	L5	2726	G
21	L5	2738	C
21	L5	2739	C
21	L5	2742	G
21	L5	2743	A
21	L5	2746	A
21	L5	2754	G
21	L5	2761	U
21	L5	2763	U
21	L5	2764	A
21	L5	2769	U
21	L5	2770	C
21	L5	2787	A
21	L5	2788	U
21	L5	2790	U
21	L5	2806	A
21	L5	2826	U
21	L5	2827	G
21	L5	2834	C
21	L5	2847	G
21	L5	2848	G
21	L5	2855	G
21	L5	2875	C
21	L5	2877	G
21	L5	2892	C
21	L5	2895	A
21	L5	2900	U
21	L5	2902	G
21	L5	2903	G
21	L5	2904	U
21	L5	2905	C
21	L5	2906	G
21	L5	2907	G
21	L5	2908	U
21	L5	3588	C
21	L5	3590	G
21	L5	3591	C
21	L5	3594	C
21	L5	3595	U

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Mol	Chain	Res	Type
21	L5	3596	A
21	L5	3597	G
21	L5	3599	A
21	L5	3604	A
21	L5	3605	C
21	L5	3615	G
21	L5	3616	U
21	L5	3626	G
21	L5	3630	A
21	L5	3635	A
21	L5	3644	U
21	L5	3646	A
21	L5	3648	A
21	L5	3662	A
21	L5	3670	C
21	L5	3673	C
21	L5	3674	G
21	L5	3685	C
21	L5	3691	G
21	L5	3692	A
21	L5	3711	A
21	L5	3713	U
21	L5	3714	G
21	L5	3726	A
21	L5	3727	A
21	L5	3736	A
21	L5	3740	G
21	L5	3748	A
21	L5	3750	G
21	L5	3753	G
21	L5	3758	U
21	L5	3759	A
21	L5	3760	A
21	L5	3761	C
21	L5	3766	A
21	L5	3769	C
21	L5	3771	C
21	L5	3772	U
21	L5	3773	U
21	L5	3774	A
21	L5	3776	G
21	L5	3777	G

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Mol	Chain	Res	Type
21	L5	3784	A
21	L5	3786	U
21	L5	3802	U
21	L5	3811	G
21	L5	3814	U
21	L5	3817	A
21	L5	3818	U
21	L5	3819	G
21	L5	3823	G
21	L5	3838	U
21	L5	3839	G
21	L5	3840	U
21	L5	3841	C
21	L5	3843	C
21	L5	3867	A
21	L5	3877	A
21	L5	3878	C
21	L5	3879	G
21	L5	3885	G
21	L5	3887	C
21	L5	3890	A
21	L5	3892	U
21	L5	3897	G
21	L5	3901	A
21	L5	3905	A
21	L5	3906	A
21	L5	3907	G
21	L5	3908	A
21	L5	3915	U
21	L5	3920	U
21	L5	3923	A
21	L5	3930	U
21	L5	3938	G
21	L5	3939	G
21	L5	3940	U
21	L5	3943	A
21	L5	3944	G
21	L5	3946	G
21	L5	3947	A
21	L5	3948	C
21	L5	3949	A
21	L5	3950	U

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Mol	Chain	Res	Type
21	L5	3953	G
21	L5	3955	G
21	L5	3956	G
21	L5	3957	U
21	L5	3959	U
21	L5	3960	A
21	L5	3962	A
21	L5	3963	A
21	L5	3965	A
21	L5	3966	A
21	L5	3968	U
21	L5	3970	G
21	L5	3971	G
21	L5	3972	A
21	L5	3973	G
21	L5	3975	C
21	L5	3976	C
21	L5	3977	C
21	L5	4034	G
21	L5	4035	G
21	L5	4038	C
21	L5	4039	G
21	L5	4041	C
21	L5	4042	G
21	L5	4043	G
21	L5	4044	U
21	L5	4046	A
21	L5	4047	A
21	L5	4048	A
21	L5	4049	U
21	L5	4050	A
21	L5	4051	C
21	L5	4052	C
21	L5	4053	A
21	L5	4055	U
21	L5	4056	A
21	L5	4057	C
21	L5	4058	U
21	L5	4059	C
21	L5	4060	U
21	L5	4061	G
21	L5	4062	A

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Mol	Chain	Res	Type
21	L5	4063	U
21	L5	4065	G
21	L5	4068	U
21	L5	4076	G
21	L5	4084	G
21	L5	4088	C
21	L5	4092	G
21	L5	4097	G
21	L5	4098	A
21	L5	4099	G
21	L5	4100	C
21	L5	4101	C
21	L5	4102	C
21	L5	4103	C
21	L5	4104	G
21	L5	4108	G
21	L5	4111	U
21	L5	4112	C
21	L5	4114	C
21	L5	4115	G
21	L5	4116	C
21	L5	4119	C
21	L5	4121	G
21	L5	4122	G
21	L5	4127	A
21	L5	4133	C
21	L5	4134	C
21	L5	4138	C
21	L5	4140	C
21	L5	4141	G
21	L5	4142	C
21	L5	4143	G
21	L5	4144	C
21	L5	4146	G
21	L5	4160	C
21	L5	4162	C
21	L5	4163	U
21	L5	4170	A
21	L5	4177	C
21	L5	4183	G
21	L5	4184	G
21	L5	4191	G

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Mol	Chain	Res	Type
21	L5	4196	G
21	L5	4197	G
21	L5	4201	G
21	L5	4203	A
21	L5	4212	A
21	L5	4222	G
21	L5	4229	U
21	L5	4232	U
21	L5	4233	A
21	L5	4237	C
21	L5	4249	G
21	L5	4251	A
21	L5	4254	G
21	L5	4255	A
21	L5	4257	A
21	L5	4258	C
21	L5	4265	U
21	L5	4267	G
21	L5	4268	A
21	L5	4273	A
21	L5	4281	A
21	L5	4282	A
21	L5	4291	G
21	L5	4295	U
21	L5	4304	A
21	L5	4305	G
21	L5	4306	U
21	L5	4313	A
21	L5	4314	C
21	L5	4319	C
21	L5	4329	G
21	L5	4330	G
21	L5	4332	C
21	L5	4339	A
21	L5	4349	C
21	L5	4354	U
21	L5	4364	G
21	L5	4373	G
21	L5	4376	A
21	L5	4377	G
21	L5	4378	A
21	L5	4380	A

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Mol	Chain	Res	Type
21	L5	4387	C
21	L5	4391	G
21	L5	4394	A
21	L5	4398	C
21	L5	4421	C
21	L5	4422	A
21	L5	4448	G
21	L5	4449	A
21	L5	4452	U
21	L5	4453	C
21	L5	4464	A
21	L5	4466	C
21	L5	4475	G
21	L5	4488	A
21	L5	4500	U
21	L5	4512	U
21	L5	4513	A
21	L5	4519	C
21	L5	4524	G
21	L5	4525	C
21	L5	4528	G
21	L5	4545	G
21	L5	4548	A
21	L5	4549	G
21	L5	4560	C
21	L5	4567	G
21	L5	4569	U
21	L5	4572	U
21	L5	4575	G
21	L5	4581	G
21	L5	4584	A
21	L5	4589	A
21	L5	4590	A
21	L5	4594	U
21	L5	4600	G
21	L5	4601	U
21	L5	4606	G
21	L5	4617	G
21	L5	4627	U
21	L5	4635	A
21	L5	4636	U
21	L5	4637	G

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Mol	Chain	Res	Type
21	L5	4647	G
21	L5	4648	A
21	L5	4652	G
21	L5	4656	A
21	L5	4659	G
21	L5	4670	C
21	L5	4672	A
21	L5	4694	G
21	L5	4695	C
21	L5	4700	A
21	L5	4707	A
21	L5	4708	A
21	L5	4709	U
21	L5	4719	G
21	L5	4733	C
21	L5	4734	A
21	L5	4740	G
21	L5	4741	C
21	L5	4742	G
21	L5	4745	G
21	L5	4754	G
21	L5	4757	C
21	L5	4759	C
21	L5	4761	G
21	L5	4765	G
21	L5	4771	C
21	L5	4772	C
21	L5	4775	C
21	L5	4859	C
21	L5	4860	G
21	L5	4862	G
21	L5	4863	G
21	L5	4870	G
21	L5	4871	C
21	L5	4875	G
21	L5	4877	G
21	L5	4880	C
21	L5	4881	U
21	L5	4882	U
21	L5	4883	C
21	L5	4889	G
21	L5	4895	C

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Mol	Chain	Res	Type
21	L5	4896	G
21	L5	4899	G
21	L5	4900	C
21	L5	4901	G
21	L5	4909	A
21	L5	4910	G
21	L5	4912	G
21	L5	4914	C
21	L5	4922	C
21	L5	4923	C
21	L5	4924	C
21	L5	4925	U
21	L5	4926	C
21	L5	4927	G
21	L5	4928	C
21	L5	4934	A
21	L5	4937	C
21	L5	4940	C
21	L5	4941	G
21	L5	4943	A
21	L5	4944	C
21	L5	4951	G
21	L5	4960	G
21	L5	4976	U
21	L5	4979	A
21	L5	4988	U
21	L5	4989	U
21	L5	4991	U
21	L5	4995	U
21	L5	5008	C
21	L5	5009	G
21	L5	5013	C
21	L5	5014	A
21	L5	5017	G
21	L5	5023	C
21	L5	5024	C
21	L5	5025	C
21	L5	5026	U
21	L5	5027	C
21	L5	5028	G
21	L5	5030	U
21	L5	5034	A

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Mol	Chain	Res	Type
21	L5	5037	U
21	L5	5040	U
21	L5	5041	G
21	L5	5050	C
21	L5	5055	G
21	L5	5060	A
21	L5	5061	A
21	L5	5069	U
22	L7	7	G
22	L7	22	A
22	L7	24	C
22	L7	33	U
22	L7	37	G
22	L7	38	U
22	L7	42	A
22	L7	53	U
22	L7	54	A
22	L7	63	C
22	L7	64	G
22	L7	66	G
22	L7	100	A
22	L7	111	C
23	L8	2	G
23	L8	23	C
23	L8	25	G
23	L8	34	U
23	L8	35	C
23	L8	38	U
23	L8	48	A
23	L8	52	A
23	L8	59	A
23	L8	62	A
23	L8	63	U
23	L8	68	G
23	L8	80	A
23	L8	82	A
23	L8	84	A
23	L8	85	U
23	L8	86	U
23	L8	87	G
23	L8	94	G
23	L8	101	C

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Mol	Chain	Res	Type
23	L8	103	A
23	L8	104	A
23	L8	105	C
23	L8	110	U
23	L8	111	U
23	L8	112	G
23	L8	114	G
23	L8	123	U
23	L8	124	U
23	L8	125	C
23	L8	126	C
23	L8	127	U
23	L8	147	G
23	L8	151	G
23	L8	153	C
79	S2	2	A
79	S2	4	C
79	S2	13	C
79	S2	14	C
79	S2	25	A
79	S2	33	G
79	S2	41	G
79	S2	44	U
79	S2	45	A
79	S2	46	A
79	S2	56	G
79	S2	58	C
79	S2	62	G
79	S2	64	A
79	S2	65	C
79	S2	66	G
79	S2	67	C
79	S2	68	A
79	S2	72	C
79	S2	73	C
79	S2	74	G
79	S2	76	U
79	S2	79	A
79	S2	92	A
79	S2	103	A
79	S2	113	G
79	S2	114	G

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Mol	Chain	Res	Type
79	S2	115	U
79	S2	116	U
79	S2	126	G
79	S2	130	G
79	S2	139	C
79	S2	143	U
79	S2	147	A
79	S2	149	A
79	S2	155	G
79	S2	156	G
79	S2	158	A
79	S2	160	U
79	S2	162	C
79	S2	163	U
79	S2	170	A
79	S2	182	C
79	S2	187	G
79	S2	190	G
79	S2	192	C
79	S2	196	C
79	S2	197	U
79	S2	198	U
79	S2	199	C
79	S2	200	G
79	S2	202	G
79	S2	203	G
79	S2	204	G
79	S2	206	G
79	S2	207	G
79	S2	208	G
79	S2	209	A
79	S2	213	G
79	S2	214	U
79	S2	220	U
79	S2	290	U
79	S2	291	G
79	S2	292	A
79	S2	295	C
79	S2	302	A
79	S2	306	C
79	S2	307	G
79	S2	308	G

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Mol	Chain	Res	Type
79	S2	309	G
79	S2	310	C
79	S2	311	C
79	S2	312	G
79	S2	314	U
79	S2	318	A
79	S2	319	C
79	S2	322	C
79	S2	323	C
79	S2	324	C
79	S2	325	C
79	S2	326	C
79	S2	327	G
79	S2	328	U
79	S2	329	G
79	S2	332	G
79	S2	338	G
79	S2	339	A
79	S2	340	C
79	S2	347	G
79	S2	351	G
79	S2	360	A
79	S2	361	U
79	S2	362	C
79	S2	364	A
79	S2	365	C
79	S2	368	U
79	S2	369	C
79	S2	370	G
79	S2	374	G
79	S2	383	G
79	S2	385	G
79	S2	386	C
79	S2	407	G
79	S2	408	A
79	S2	409	C
79	S2	421	G
79	S2	426	A
79	S2	437	G
79	S2	448	A
79	S2	449	A
79	S2	450	C

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Mol	Chain	Res	Type
79	S2	452	G
79	S2	459	C
79	S2	464	A
79	S2	465	A
79	S2	466	G
79	S2	471	G
79	S2	472	C
79	S2	473	A
79	S2	474	G
79	S2	476	A
79	S2	478	G
79	S2	482	G
79	S2	485	A
79	S2	487	U
79	S2	488	U
79	S2	492	C
79	S2	493	A
79	S2	502	C
79	S2	525	A
79	S2	530	U
79	S2	531	A
79	S2	532	C
79	S2	533	A
79	S2	536	A
79	S2	537	C
79	S2	540	U
79	S2	542	U
79	S2	544	G
79	S2	546	G
79	S2	547	G
79	S2	548	C
79	S2	553	U
79	S2	555	A
79	S2	557	U
79	S2	558	G
79	S2	559	G
79	S2	563	G
79	S2	564	A
79	S2	566	U
79	S2	576	A
79	S2	583	A
79	S2	587	A

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Mol	Chain	Res	Type
79	S2	589	G
79	S2	590	A
79	S2	591	U
79	S2	593	C
79	S2	594	A
79	S2	600	G
79	S2	604	A
79	S2	605	A
79	S2	608	C
79	S2	614	C
79	S2	617	G
79	S2	628	A
79	S2	630	U
79	S2	631	U
79	S2	638	C
79	S2	643	A
79	S2	644	G
79	S2	646	G
79	S2	655	A
79	S2	660	C
79	S2	664	A
79	S2	668	A
79	S2	669	A
79	S2	671	A
79	S2	672	A
79	S2	673	G
79	S2	688	U
79	S2	689	U
79	S2	692	G
79	S2	693	A
79	S2	695	C
79	S2	696	G
79	S2	697	G
79	S2	698	G
79	S2	732	U
79	S2	736	C
79	S2	738	C
79	S2	749	U
79	S2	751	G
79	S2	752	G
79	S2	753	C
79	S2	788	G

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Mol	Chain	Res	Type
79	S2	790	C
79	S2	791	C
79	S2	792	C
79	S2	793	G
79	S2	797	C
79	S2	799	U
79	S2	801	U
79	S2	821	G
79	S2	822	U
79	S2	823	U
79	S2	824	C
79	S2	827	A
79	S2	830	A
79	S2	834	C
79	S2	835	C
79	S2	836	G
79	S2	837	A
79	S2	838	G
79	S2	839	C
79	S2	840	C
79	S2	842	C
79	S2	844	U
79	S2	847	A
79	S2	859	G
79	S2	870	A
79	S2	871	U
79	S2	874	G
79	S2	878	G
79	S2	882	U
79	S2	887	U
79	S2	888	U
79	S2	889	U
79	S2	891	G
79	S2	893	U
79	S2	894	G
79	S2	896	U
79	S2	897	U
79	S2	898	U
79	S2	899	U
79	S2	900	C
79	S2	901	G
79	S2	903	A

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Mol	Chain	Res	Type
79	S2	904	A
79	S2	907	G
79	S2	909	G
79	S2	910	G
79	S2	913	A
79	S2	919	A
79	S2	920	A
79	S2	930	C
79	S2	932	G
79	S2	933	G
79	S2	934	G
79	S2	943	U
79	S2	963	A
79	S2	971	G
79	S2	972	A
79	S2	978	G
79	S2	985	G
79	S2	990	A
79	S2	992	A
79	S2	997	A
79	S2	999	G
79	S2	1001	A
79	S2	1008	A
79	S2	1017	U
79	S2	1023	A
79	S2	1027	A
79	S2	1033	G
79	S2	1047	C
79	S2	1061	U
79	S2	1062	A
79	S2	1067	C
79	S2	1083	A
79	S2	1085	C
79	S2	1088	U
79	S2	1107	G
79	S2	1108	G
79	S2	1109	C
79	S2	1113	A
79	S2	1114	U
79	S2	1115	U
79	S2	1116	C
79	S2	1118	C

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Mol	Chain	Res	Type
79	S2	1121	G
79	S2	1126	G
79	S2	1133	A
79	S2	1138	C
79	S2	1139	C
79	S2	1148	A
79	S2	1150	A
79	S2	1153	C
79	S2	1154	U
79	S2	1170	A
79	S2	1195	A
79	S2	1207	G
79	S2	1208	A
79	S2	1215	C
79	S2	1216	C
79	S2	1217	A
79	S2	1220	A
79	S2	1224	G
79	S2	1227	G
79	S2	1234	C
79	S2	1240	A
79	S2	1242	U
79	S2	1243	U
79	S2	1251	A
79	S2	1253	A
79	S2	1256	G
79	S2	1257	G
79	S2	1259	A
79	S2	1264	C
79	S2	1271	C
79	S2	1274	G
79	S2	1275	G
79	S2	1283	C
79	S2	1284	A
79	S2	1286	G
79	S2	1294	G
79	S2	1295	A
79	S2	1301	A
79	S2	1302	G
79	S2	1308	U
79	S2	1309	C
79	S2	1341	C

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Mol	Chain	Res	Type
79	S2	1342	U
79	S2	1355	C
79	S2	1356	G
79	S2	1358	U
79	S2	1371	U
79	S2	1372	U
79	S2	1376	A
79	S2	1378	A
79	S2	1382	A
79	S2	1396	A
79	S2	1401	A
79	S2	1402	A
79	S2	1406	G
79	S2	1412	C
79	S2	1414	A
79	S2	1415	C
79	S2	1417	C
79	S2	1419	C
79	S2	1420	G
79	S2	1421	A
79	S2	1422	G
79	S2	1423	C
79	S2	1424	G
79	S2	1433	C
79	S2	1435	C
79	S2	1436	C
79	S2	1438	A
79	S2	1442	U
79	S2	1449	G
79	S2	1454	A
79	S2	1462	U
79	S2	1463	U
79	S2	1466	G
79	S2	1468	C
79	S2	1479	G
79	S2	1480	A
79	S2	1489	A
79	S2	1490	G
79	S2	1494	U
79	S2	1495	G
79	S2	1498	A
79	S2	1508	A

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Mol	Chain	Res	Type
79	S2	1509	U
79	S2	1521	C
79	S2	1522	A
79	S2	1533	A
79	S2	1534	C
79	S2	1535	U
79	S2	1537	A
79	S2	1544	C
79	S2	1552	G
79	S2	1553	C
79	S2	1555	U
79	S2	1556	A
79	S2	1570	G
79	S2	1574	C
79	S2	1579	A
79	S2	1580	A
79	S2	1581	C
79	S2	1582	C
79	S2	1584	G
79	S2	1585	U
79	S2	1587	G
79	S2	1588	A
79	S2	1601	A
79	S2	1602	U
79	S2	1604	G
79	S2	1606	G
79	S2	1621	U
79	S2	1623	A
79	S2	1633	A
79	S2	1634	A
79	S2	1637	A
79	S2	1638	G
79	S2	1639	G
79	S2	1640	A
79	S2	1648	G
79	S2	1649	U
79	S2	1654	G
79	S2	1662	U
79	S2	1663	A
79	S2	1664	A
79	S2	1665	G
79	S2	1671	G

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Mol	Chain	Res	Type
79	S2	1683	C
79	S2	1686	G
79	S2	1693	G
79	S2	1696	C
79	S2	1699	A
79	S2	1715	A
79	S2	1716	C
79	S2	1721	U
79	S2	1722	G
79	S2	1726	G
79	S2	1729	U
79	S2	1743	G
79	S2	1744	G
79	S2	1745	A
79	S2	1752	C
79	S2	1753	C
79	S2	1754	G
79	S2	1755	C
79	S2	1757	G
79	S2	1758	G
79	S2	1759	G
79	S2	1760	G
79	S2	1761	U
79	S2	1771	G
79	S2	1772	C
79	S2	1773	C
79	S2	1777	G
79	S2	1781	A
79	S2	1783	C
79	S2	1784	G
79	S2	1786	U
79	S2	1787	G
79	S2	1798	C
79	S2	1799	G
79	S2	1812	U
79	S2	1813	A
79	S2	1822	A
79	S2	1823	A
79	S2	1824	A
79	S2	1825	A
79	S2	1826	G
79	S2	1829	G

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Mol	Chain	Res	Type
79	S2	1835	A
79	S2	1837	G
79	S2	1838	U
79	S2	1849	G
79	S2	1851	A
79	S2	1852	C
79	S2	1861	G
79	S2	1862	G
79	S2	1863	A
79	S2	1864	U
79	S2	1865	C
80	Pt	9	A
80	Pt	13	U
80	Pt	16	A
80	Pt	17	A
80	Pt	18	G
80	Pt	19	G
80	Pt	20(A)	U
80	Pt	21	A
80	Pt	42	A
80	Pt	46	G
80	Pt	47	U
80	Pt	48	C
80	Pt	49	C
80	Pt	58	A
80	Pt	61	C
80	Pt	63	G
80	Pt	72	C
80	Pt	74	C
80	Pt	76	A
81	Zt	6	G
81	Zt	8	U
81	Zt	10	G
81	Zt	11	C
81	Zt	14	A
81	Zt	15	G
81	Zt	16	C
81	Zt	18	U
81	Zt	19	G
81	Zt	20	U
81	Zt	21	A
81	Zt	30	G

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Mol	Chain	Res	Type
81	Zt	32	C
81	Zt	33	U
81	Zt	34	U
81	Zt	36	U
81	Zt	37	A
81	Zt	38	A
81	Zt	42	G
81	Zt	45	G
81	Zt	47	U
81	Zt	48	C
81	Zt	49	C
81	Zt	53	G
81	Zt	56	C
81	Zt	57	A
81	Zt	58	A
81	Zt	59	G
81	Zt	60	U
81	Zt	61	C
81	Zt	63	C
81	Zt	67	U
81	Zt	70	G
81	Zt	71	G
81	Zt	72	C
81	Zt	73	G

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	L5	181	C
21	L5	183	C
21	L5	185	C
21	L5	265	C
21	L5	406	C
21	L5	493	G
21	L5	914	U
21	L5	935	A
21	L5	1082	C
21	L5	1633	G
21	L5	1733	G
21	L5	1977	C
21	L5	2033	A
21	L5	2055	G

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Mol	Chain	Res	Type
21	L5	2416	G
21	L5	2485	U
21	L5	2675	G
21	L5	2760	G
21	L5	2786	C
21	L5	3614	G
21	L5	3673	C
21	L5	4055	U
21	L5	4061	G
21	L5	4600	G
21	L5	4699	U
21	L5	4913	G
79	S2	291	G
79	S2	563	G
79	S2	688	U
79	S2	1434	C
79	S2	1467	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 261 ligands modelled in this entry, 261 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
79	S2	6
21	L5	2

All 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	27.67
1	S2	698:G	O3'	730:C	P	17.12
1	S2	739:C	O3'	746:C	P	13.36
1	S2	225:G	O3'	287:U	P	7.94
1	S2	1693:G	O3'	1694:U	P	5.36
1	L5	4068:U	O3'	4069:U	P	3.32
1	L5	3944:G	O3'	3945:A	P	3.13
1	S2	1210:G	O3'	1211:G	P	3.02

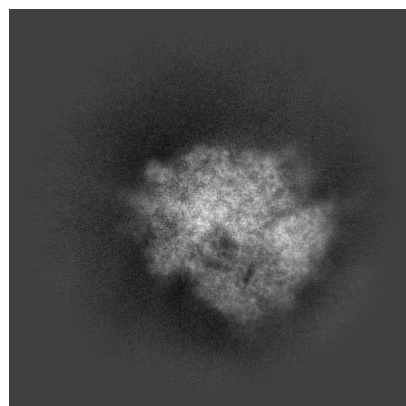
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42305. These allow visual inspection of the internal detail of the map and identification of artifacts.

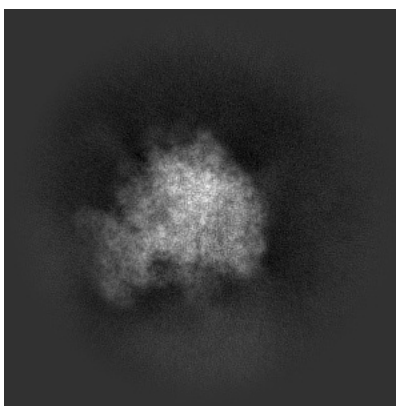
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

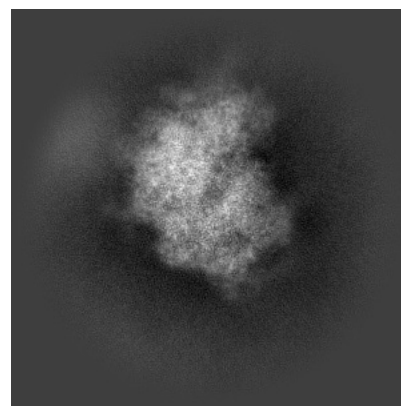
6.1.1 Primary map



X

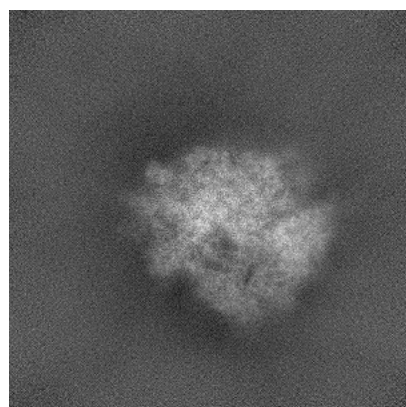


Y

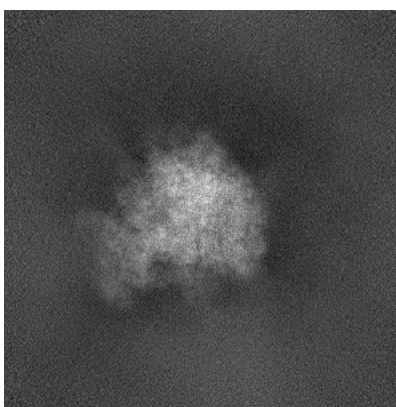


Z

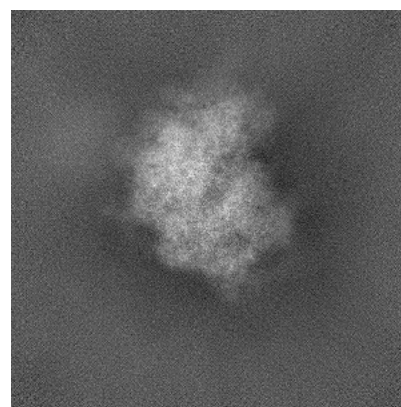
6.1.2 Raw map



X



Y

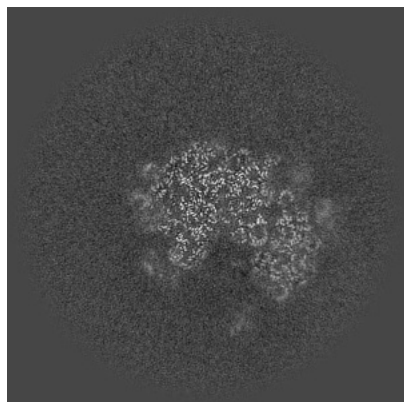


Z

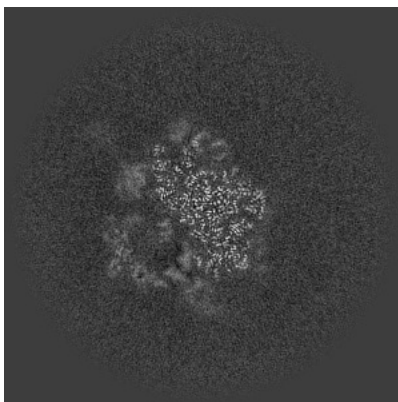
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

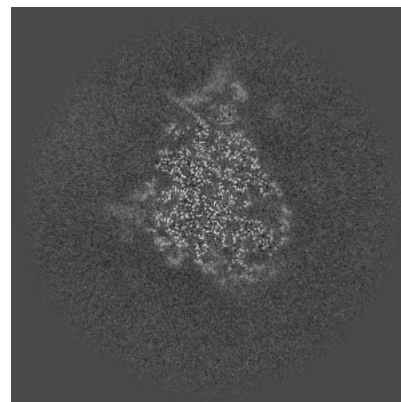
6.2.1 Primary map



X Index: 256

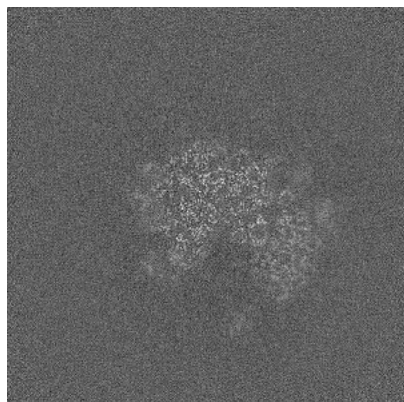


Y Index: 256

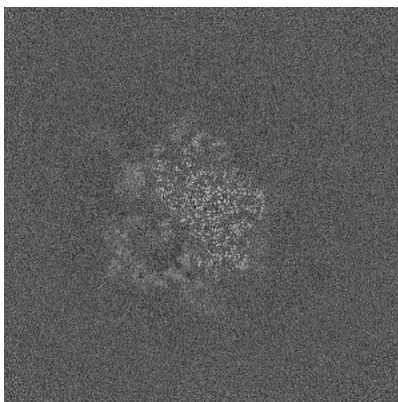


Z Index: 256

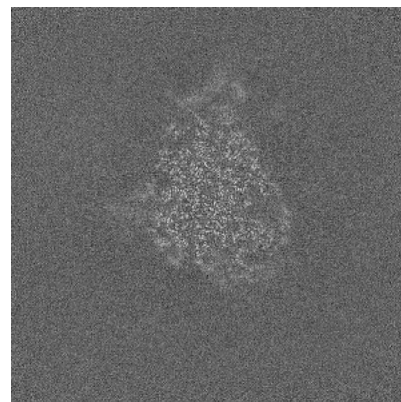
6.2.2 Raw map



X Index: 256



Y Index: 256

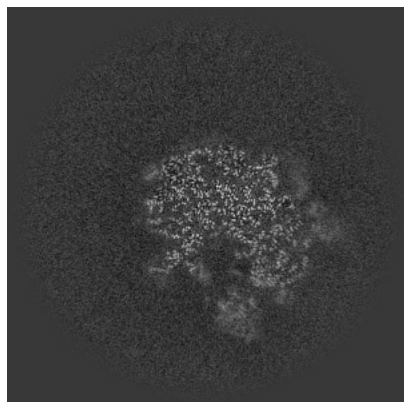


Z Index: 256

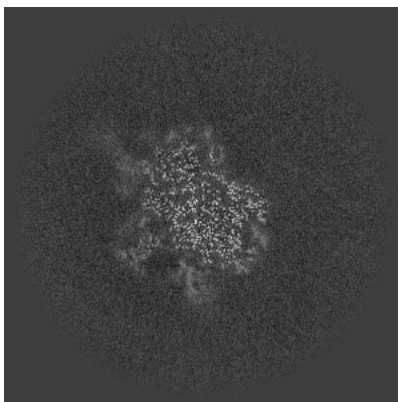
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

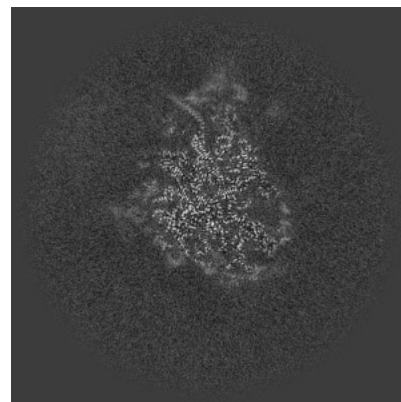
6.3.1 Primary map



X Index: 243

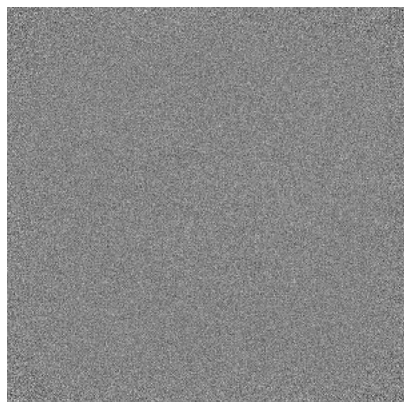


Y Index: 243

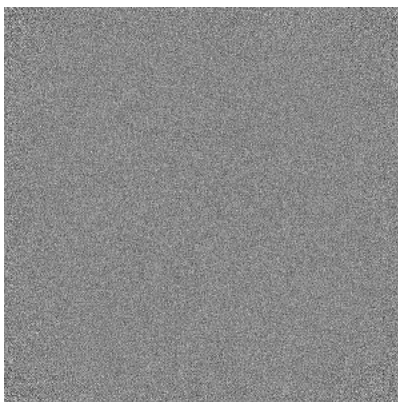


Z Index: 254

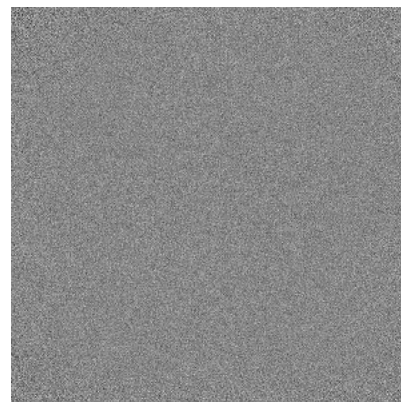
6.3.2 Raw map



X Index: 0



Y Index: 0

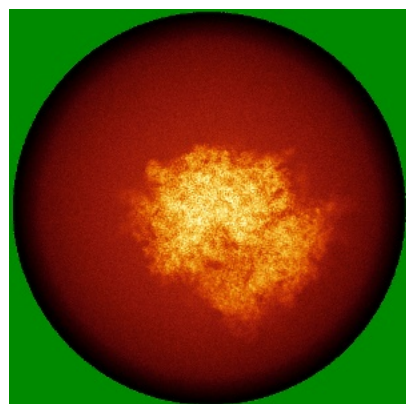


Z Index: 0

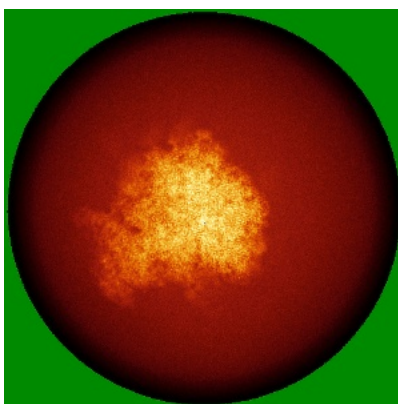
The images above show the largest variance slices of the map in three orthogonal directions.

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

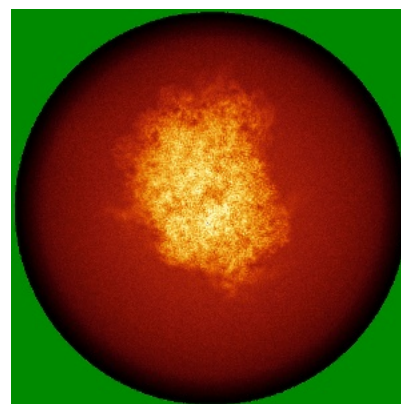
6.4.1 Primary map



X

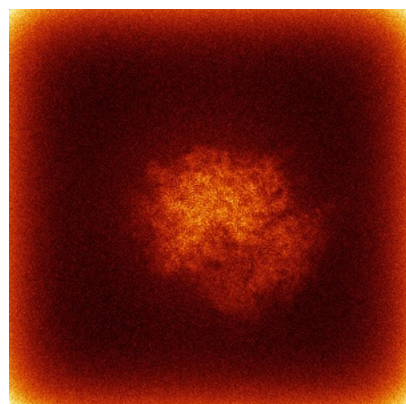


Y

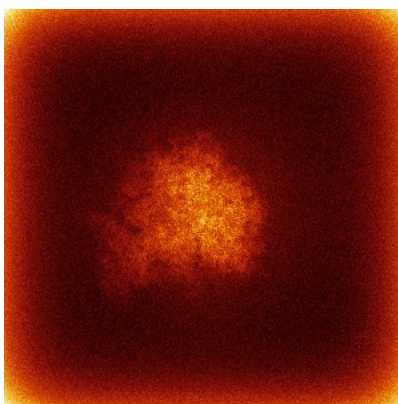


Z

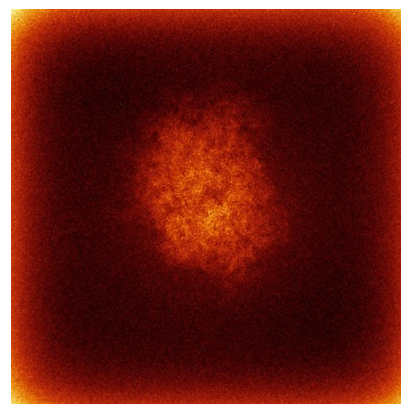
6.4.2 Raw map



X



Y

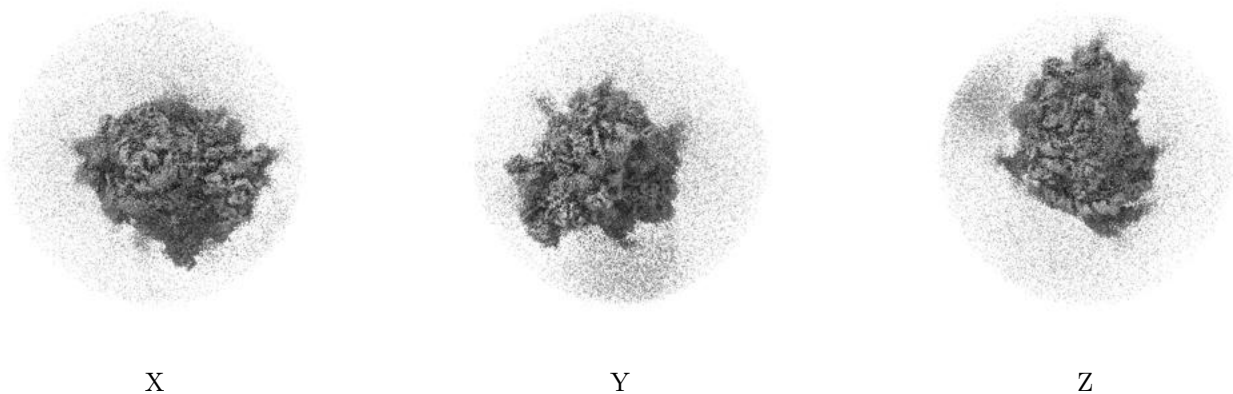


Z

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.

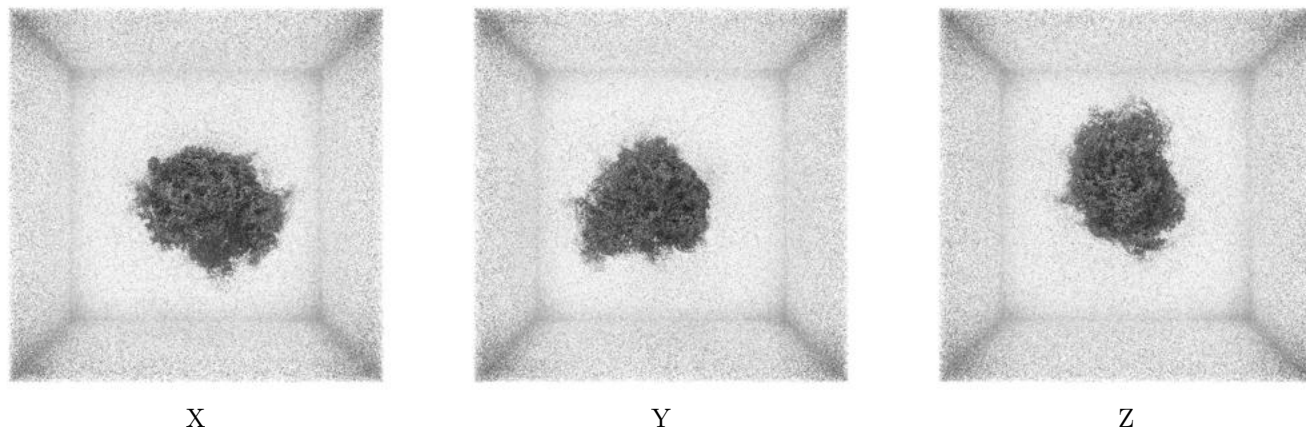
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0237. 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.

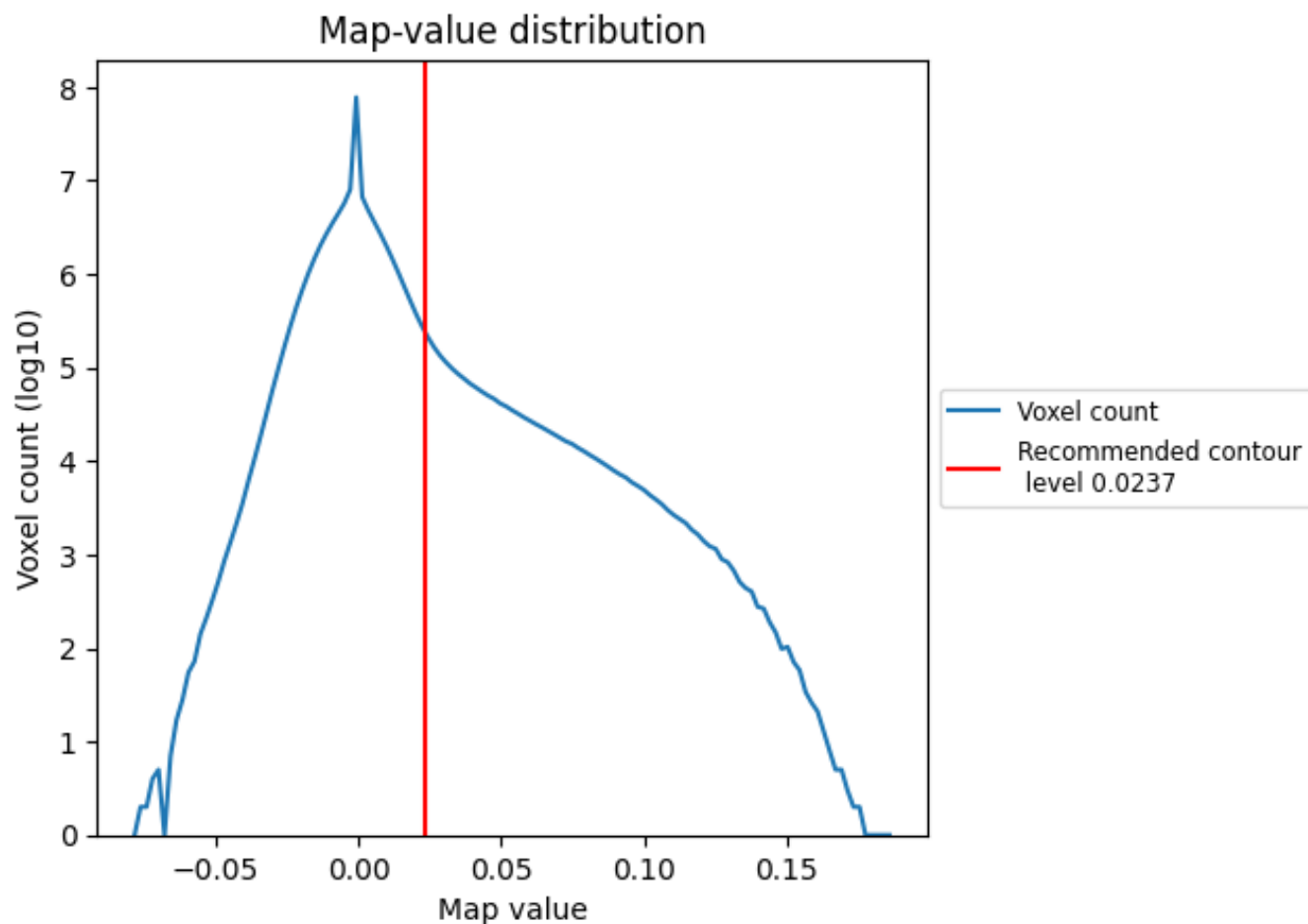
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

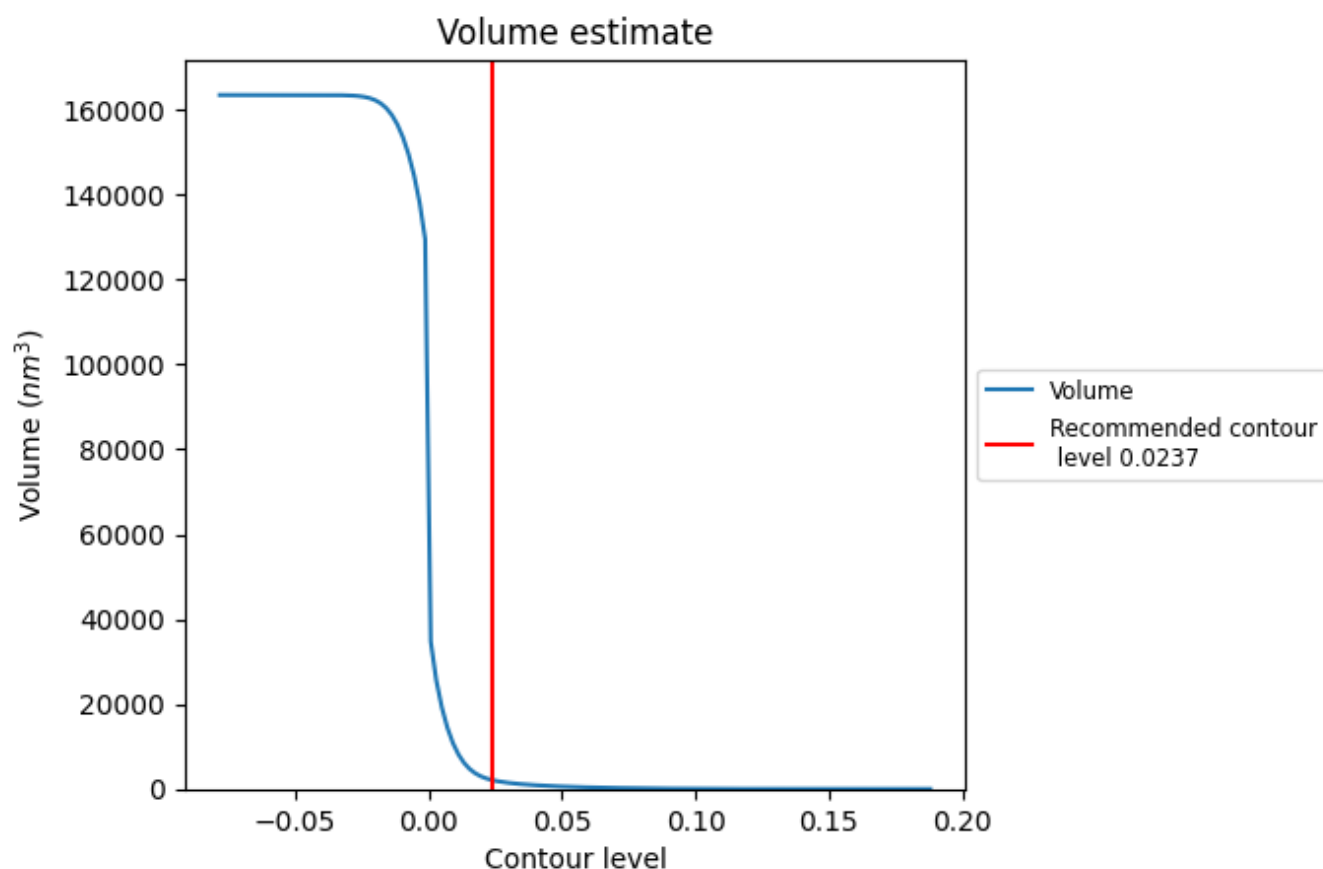
This section contains the results of statistical analysis of the map.

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.

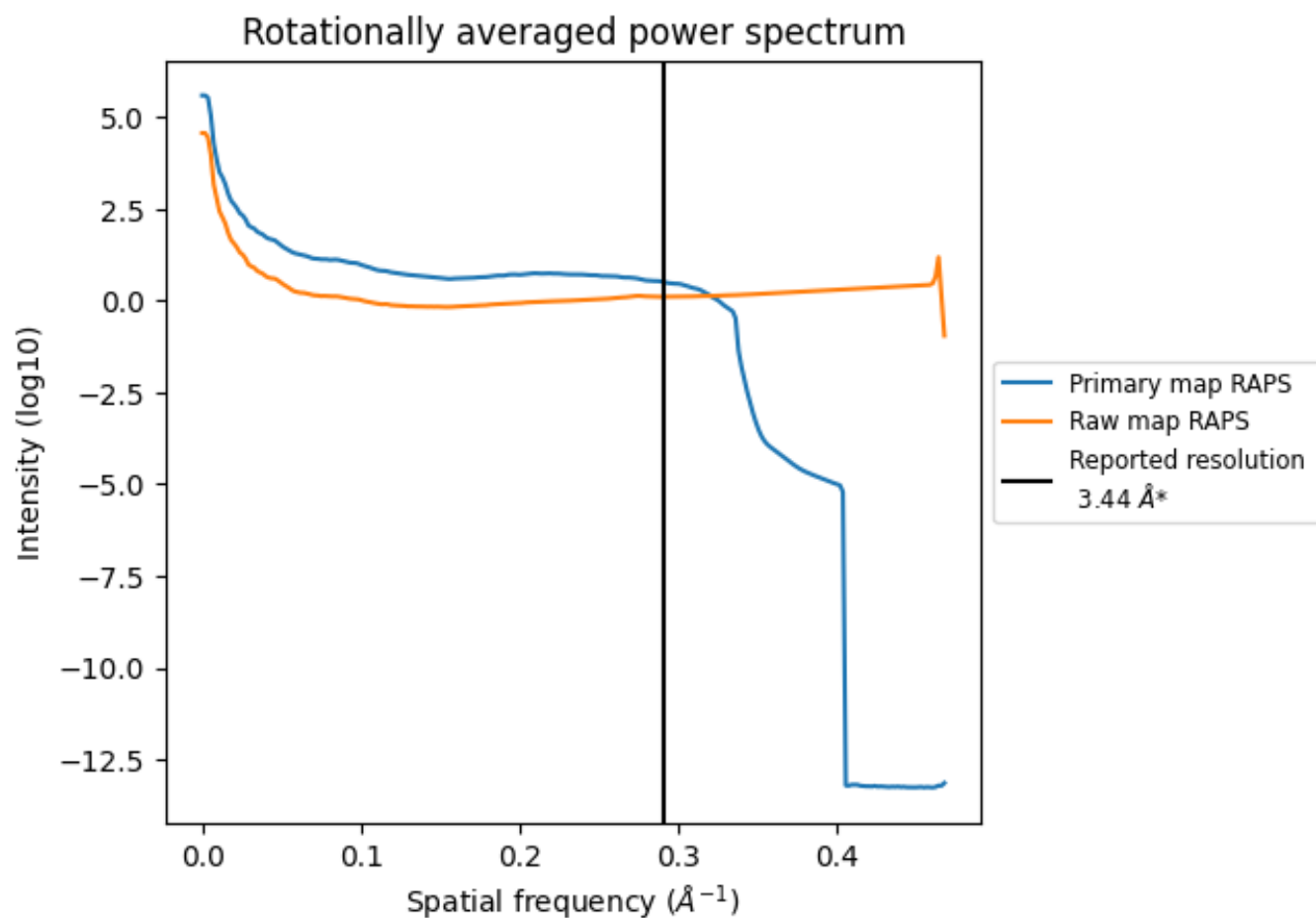
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2116 nm^3 ; this corresponds to an approximate mass of 1911 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 ⓘ

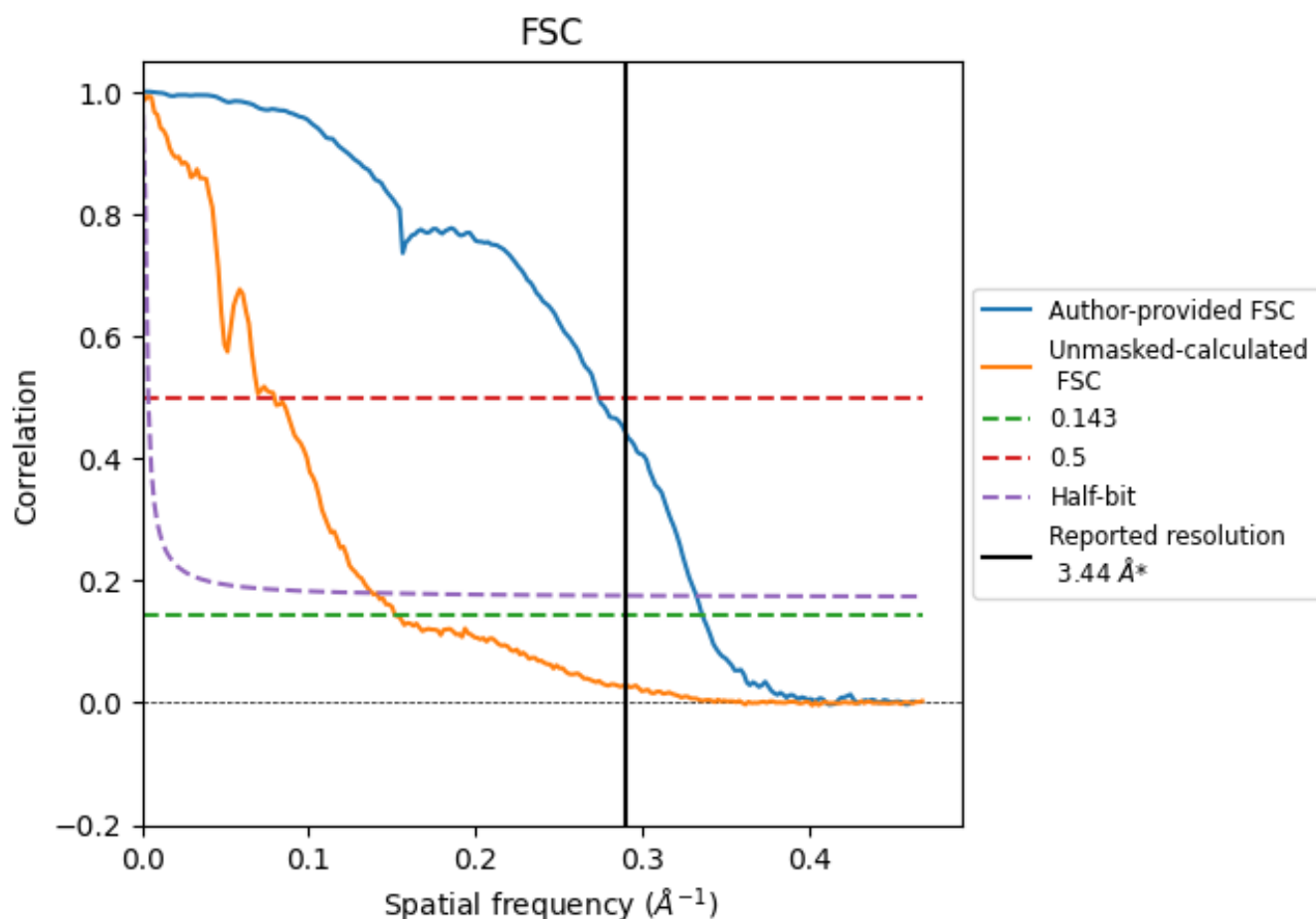


*Reported resolution corresponds to spatial frequency of 0.291 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.291 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.44	-	-
Author-provided FSC curve	2.97	3.65	3.01
Unmasked-calculated*	6.59	12.61	7.24

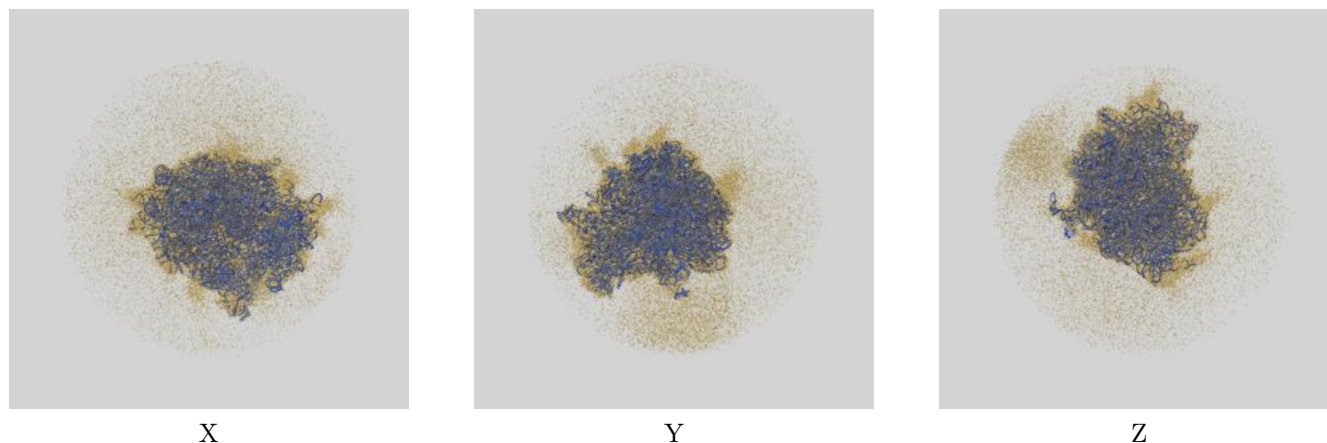
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.97 differs from the reported value 3.44 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.59 differs from the reported value 3.44 by more than 10 %

9 Map-model fit [i](#)

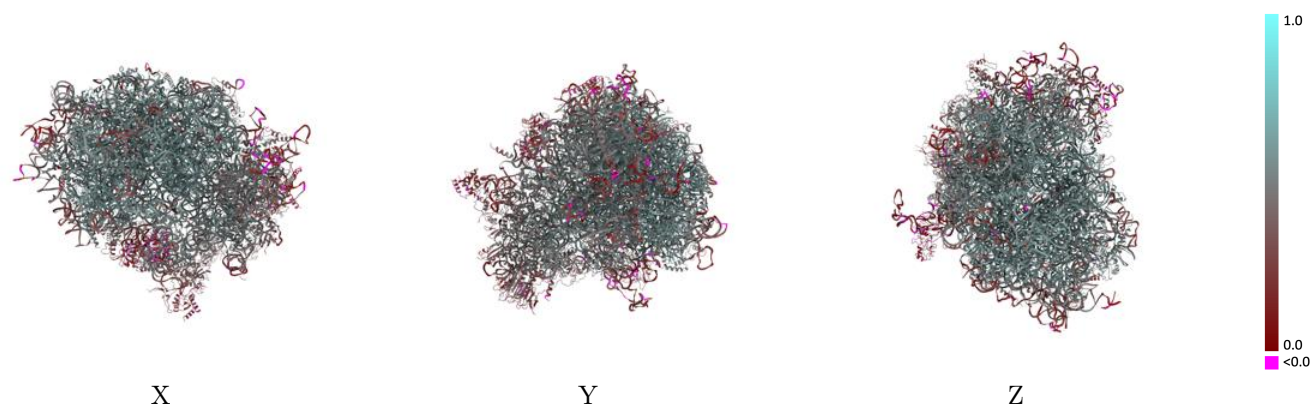
This section contains information regarding the fit between EMDB map EMD-42305 and PDB model 8UIY. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



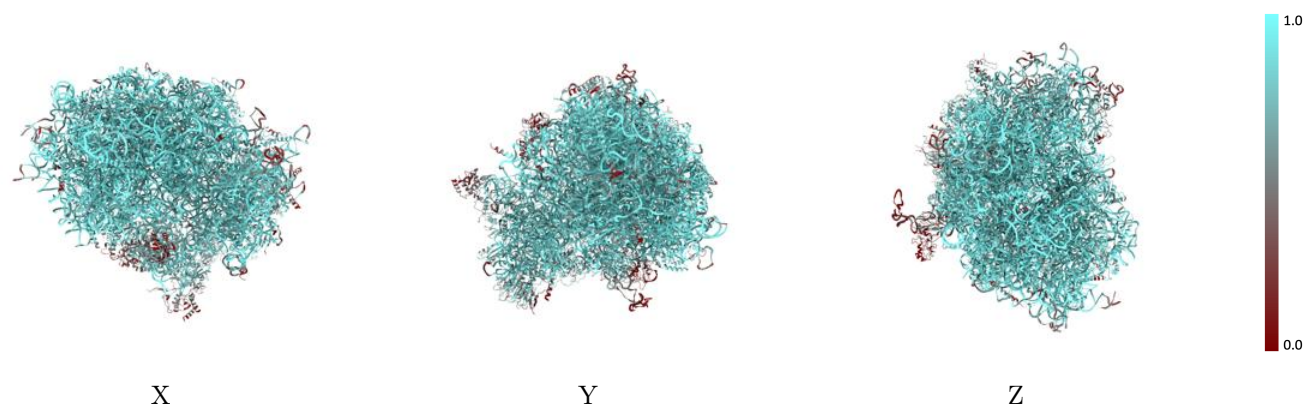
The images above show the 3D surface view of the map at the recommended contour level 0.0237 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



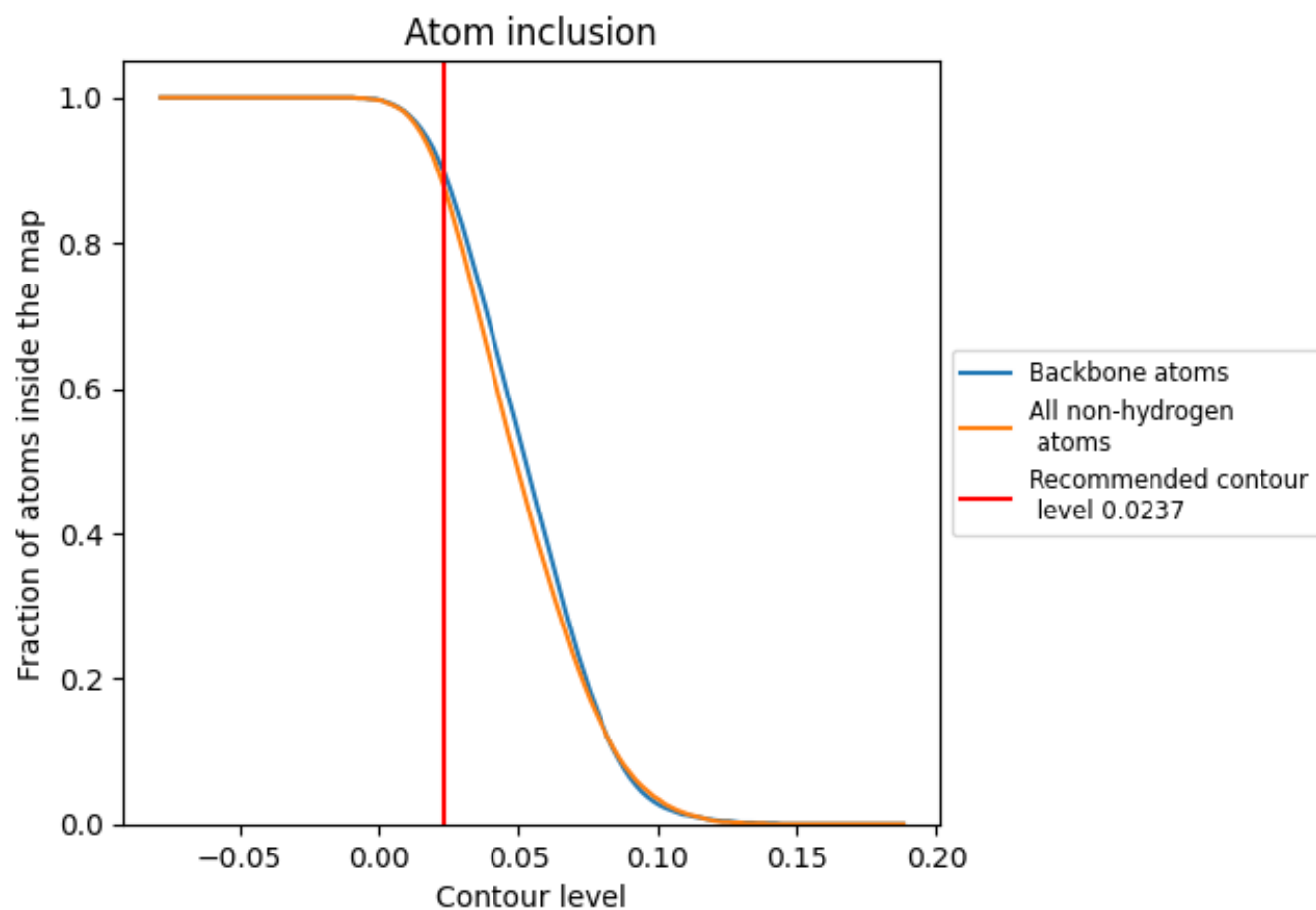
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0237).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 87% 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 (0.0237) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.4870
L5	 0.9230	 0.5060
L7	 0.9840	 0.5640
L8	 0.9520	 0.5330
LA	 0.9530	 0.5880
LB	 0.9140	 0.5660
LC	 0.9170	 0.5660
LD	 0.8800	 0.5230
LE	 0.8370	 0.5040
LF	 0.9290	 0.5680
LG	 0.8220	 0.5050
LH	 0.8900	 0.5470
LI	 0.9130	 0.5600
LJ	 0.7710	 0.4810
LL	 0.8740	 0.5330
LM	 0.9280	 0.5490
LN	 0.9720	 0.5910
LO	 0.9360	 0.5700
LP	 0.9450	 0.5750
LQ	 0.9400	 0.5830
LR	 0.8620	 0.5250
LS	 0.9340	 0.5840
LT	 0.9070	 0.5510
LU	 0.8040	 0.4650
LV	 0.9170	 0.5710
LW	 0.6810	 0.3930
LX	 0.8960	 0.5540
LY	 0.9010	 0.5560
LZ	 0.9070	 0.5430
La	 0.9460	 0.5800
Lb	 0.7980	 0.4950
Lc	 0.9250	 0.5440
Ld	 0.8720	 0.5410
Le	 0.9400	 0.5830
Lf	 0.9540	 0.5890



















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Chain	Atom inclusion	Q-score
Lg	 0.9130	 0.5530
Lh	 0.8810	 0.5410
Li	 0.9170	 0.5420
Lj	 0.9660	 0.5830
Lk	 0.8060	 0.5010
Ll	 0.9460	 0.5660
Lm	 0.9090	 0.5660
Ln	 0.9470	 0.5780
Lo	 0.9380	 0.5590
Lp	 0.9140	 0.5620
Lr	 0.9270	 0.5690
Ls	 0.3350	 0.2160
Lt	 0.2570	 0.1720
Lz	 0.1280	 0.1500
Pt	 0.8550	 0.4300
S2	 0.9190	 0.4580
SA	 0.7970	 0.4630
SB	 0.8200	 0.4970
SC	 0.8650	 0.5000
SD	 0.7280	 0.4030
SE	 0.8260	 0.4610
SF	 0.7950	 0.4410
SG	 0.7150	 0.3750
SH	 0.6960	 0.3930
SI	 0.8370	 0.4850
SJ	 0.8330	 0.4680
SK	 0.7010	 0.3790
SL	 0.8280	 0.4980
SM	 0.3240	 0.2000
SN	 0.8730	 0.5150
SO	 0.8010	 0.4950
SP	 0.7120	 0.4040
SQ	 0.7690	 0.4290
SR	 0.7290	 0.3940
SS	 0.7420	 0.4260
ST	 0.7540	 0.4000
SU	 0.7290	 0.3790
SV	 0.8120	 0.4750
SW	 0.9200	 0.5280
SX	 0.8640	 0.5120
SY	 0.7560	 0.3840
SZ	 0.6740	 0.3850

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Chain	Atom inclusion	Q-score
Sa	 0.8660	 0.5110
Sb	 0.7980	 0.4850
Sc	 0.7100	 0.3950
Sd	 0.8780	 0.4490
Se	 0.6890	 0.3960
Sf	 0.4390	 0.2240
Sg	 0.6090	 0.3240
Zt	 0.6550	 0.1770