



Full wwPDB EM Validation Report ⓘ

Mar 31, 2025 – 01:24 PM EDT

PDB ID : 8UIZ / pdb_00008uiz
EMDB ID : EMD-42306
Title : In situ human P-E state 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2023-10-10
Resolution : 3.43 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

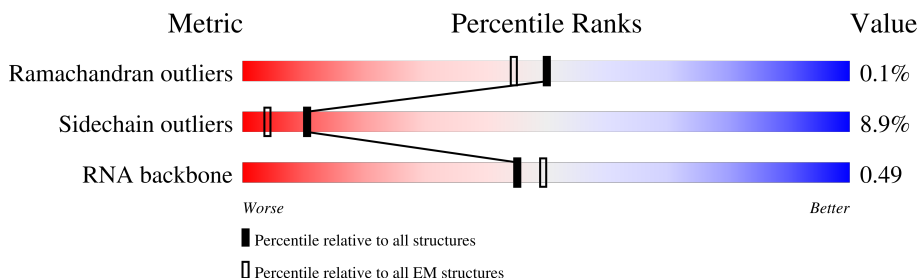
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.43 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	LR	187	
2	SE	262	
3	SI	206	
4	SL	153	
5	SX	141	
6	SG	237	
7	SJ	185	
8	SY	131	

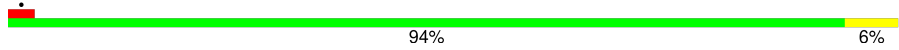
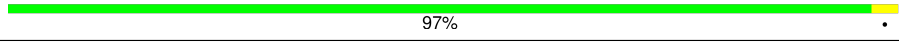
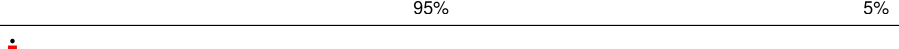
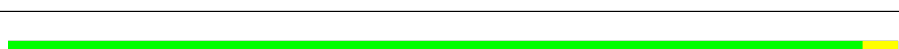
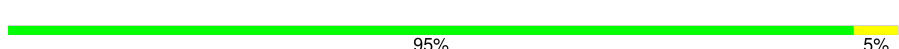
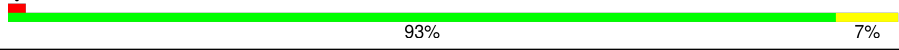

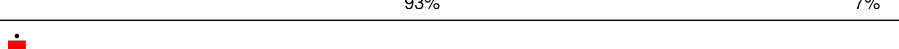
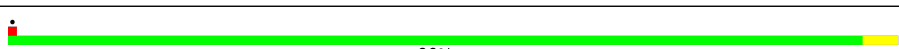

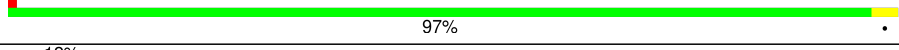
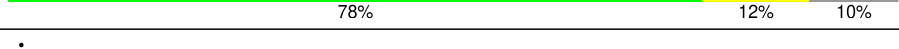
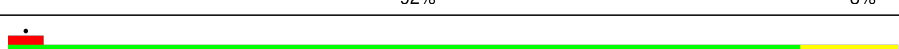
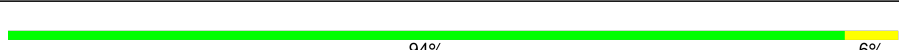
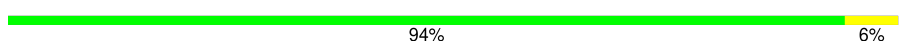
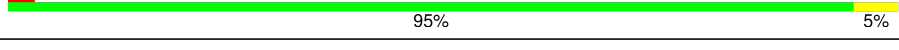
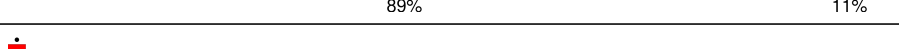

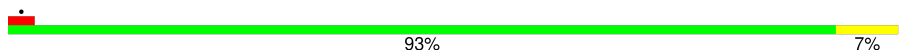
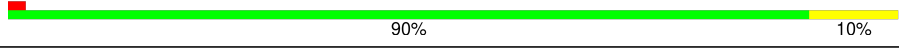
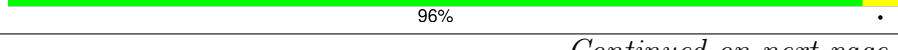



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Mol	Chain	Length	Quality of chain
9	Se	58	
10	SA	221	
11	SB	214	
12	SH	189	
13	SV	83	
14	Sa	102	
15	SC	222	
16	SN	150	
17	SO	140	
18	SW	129	
19	Sb	83	
20	L5	5070	
21	L7	120	
22	L8	156	
23	LA	248	
24	LB	402	
25	LC	368	
26	LD	293	
27	LE	247	
28	LF	225	
29	LG	241	
30	LH	190	
31	LI	213	
32	LJ	176	
33	LL	210	

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

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Mol	Chain	Length	Quality of chain
59	Ln	24	
60	Lo	105	
61	Lp	91	
62	Lr	125	
63	SR	135	
64	SD	227	
65	SF	189	
66	SK	98	
67	SP	121	
68	SQ	144	
69	SS	145	
70	ST	143	
71	SU	104	
72	Sc	64	
73	Sd	55	
74	Sg	313	
75	SM	122	
76	SZ	75	
77	Sf	67	
78	S2	1740	
79	Et	76	
80	Pt	76	
81	Lt	157	
82	Lz	217	
83	Ls	196	

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Mol	Chain	Length	Quality of chain
84	LW	124	<div><div></div><div>32%</div><div></div><div>89%</div><div></div><div>6%</div><div>5%</div></div>

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 222714 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 60S ribosomal protein L19.

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

- Molecule 2 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 3 is a protein called 40S ribosomal protein S8.

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

- Molecule 4 is a protein called 40S ribosomal protein S11.

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

- Molecule 5 is a protein called 40S ribosomal protein S23.

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

- Molecule 6 is a protein called 40S ribosomal protein S6.

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

- Molecule 7 is a protein called 40S ribosomal protein S9.

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

- Molecule 8 is a protein called 40S ribosomal protein S24.

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

- Molecule 9 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 10 is a protein called 40S ribosomal protein SA.

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

- Molecule 11 is a protein called 40S ribosomal protein S3a.

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

- Molecule 12 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 13 is a protein called 40S ribosomal protein S21.

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

- Molecule 14 is a protein called 40S ribosomal protein S26.

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

- Molecule 15 is a protein called 40S ribosomal protein S2.

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

- Molecule 16 is a protein called 40S ribosomal protein S13.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 18 is a protein called 40S ribosomal protein S15a.

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

- Molecule 19 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 20 is a RNA chain called 28S rRNA.

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

- Molecule 21 is a RNA chain called 5S rRNA [Homo sapiens].

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

- Molecule 22 is a RNA chain called 5.8S rRNA [Homo sapiens].

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

- Molecule 23 is a protein called 60S ribosomal protein L8.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 25 is a protein called 60S ribosomal protein L4.

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

- Molecule 26 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 27 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 28 is a protein called 60S ribosomal protein L7.

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

- Molecule 29 is a protein called 60S ribosomal protein L7a.

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

- Molecule 30 is a protein called 60S ribosomal protein L9.

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

- Molecule 31 is a protein called Ribosomal protein uL16-like.

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

- Molecule 32 is a protein called 60S ribosomal protein L11.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 34 is a protein called 60S ribosomal protein L14.

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

- Molecule 35 is a protein called 60S ribosomal protein L15.

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

- Molecule 36 is a protein called 60S ribosomal protein L13a.

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

- Molecule 37 is a protein called 60S ribosomal protein L17.

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

- Molecule 38 is a protein called 60S ribosomal protein L18.

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

- Molecule 39 is a protein called 60S ribosomal protein L18a.

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

- Molecule 40 is a protein called 60S ribosomal protein L21.

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

- Molecule 41 is a protein called Heparin-binding protein HBp15.

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

- Molecule 42 is a protein called 60S ribosomal protein L23.

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

- Molecule 43 is a protein called 60S ribosomal protein L23a.

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

- Molecule 44 is a protein called 60S ribosomal protein L26.

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

- Molecule 45 is a protein called 60S ribosomal protein L27.

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

- Molecule 46 is a protein called 60S ribosomal protein L27a.

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

- Molecule 47 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 48 is a protein called 60S ribosomal protein L30.

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

- Molecule 49 is a protein called 60S ribosomal protein L31.

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

- Molecule 50 is a protein called 60S ribosomal protein L32.

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

- Molecule 51 is a protein called 60S ribosomal protein L35a.

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

- Molecule 52 is a protein called 60S ribosomal protein L34.

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

- Molecule 53 is a protein called 60S ribosomal protein L35.

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

- Molecule 54 is a protein called 60S ribosomal protein L36.

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

- Molecule 55 is a protein called 60S ribosomal protein L37.

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

- Molecule 56 is a protein called 60S ribosomal protein L38.

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

- Molecule 57 is a protein called 60S ribosomal protein L39.

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

- Molecule 58 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 59 is a protein called 60S ribosomal protein L41.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L37a.

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

- Molecule 62 is a protein called 60S ribosomal protein L28.

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

- Molecule 63 is a protein called 40S ribosomal protein S17.

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

- Molecule 64 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 65 is a protein called 40S ribosomal protein S5.

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

- Molecule 66 is a protein called 40S ribosomal protein S10.

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

- Molecule 67 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 68 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 69 is a protein called 40S ribosomal protein S18.

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

- Molecule 70 is a protein called 40S ribosomal protein S19.

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

- Molecule 71 is a protein called 40S ribosomal protein S20.

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

- Molecule 72 is a protein called 40S ribosomal protein S28.

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

- Molecule 73 is a protein called 40S ribosomal protein S29.

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

- Molecule 74 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 75 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 76 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 77 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 78 is a RNA chain called 18S rRNA [Homo sapiens].

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

- Molecule 79 is a RNA chain called E site tRNA.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Pt	74	Total	C	N	O	P	0	0
			1576	705	286	512	73		

- Molecule 81 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 82 is a protein called 60S ribosomal protein L10a.

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

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

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

- Molecule 84 is a protein called Ribosomal protein L24.

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

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

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	

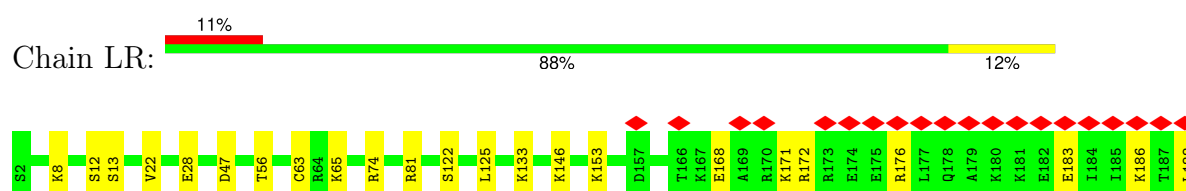
- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	L5	212	Total	Mg	0
			212	212	
86	L7	3	Total	Mg	0
			3	3	
86	L8	5	Total	Mg	0
			5	5	
86	LA	1	Total	Mg	0
			1	1	
86	LB	1	Total	Mg	0
			1	1	
86	LP	1	Total	Mg	0
			1	1	
86	LV	1	Total	Mg	0
			1	1	
86	Le	1	Total	Mg	0
			1	1	
86	Lg	1	Total	Mg	0
			1	1	
86	S2	29	Total	Mg	0
			29	29	

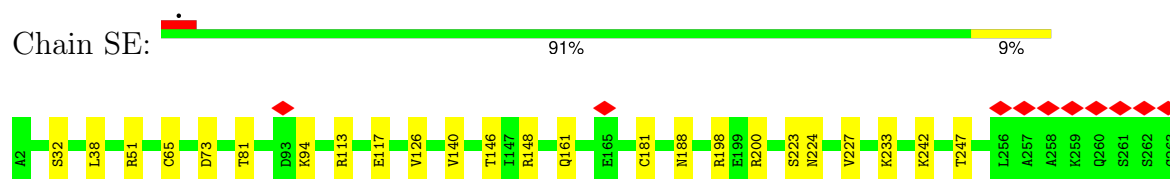
3 Residue-property plots [i](#)

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.

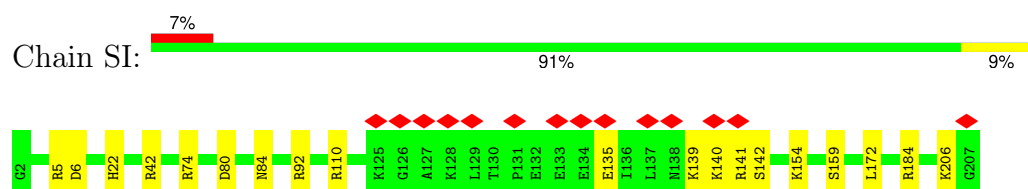
- Molecule 1: 60S ribosomal protein L19



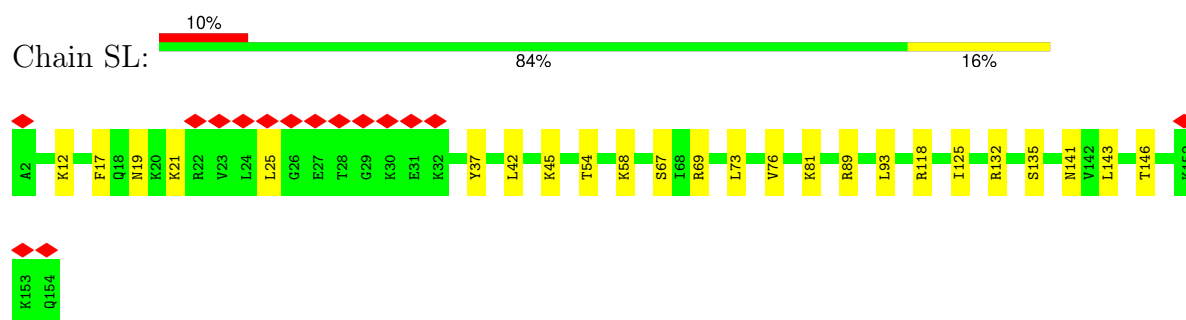
- Molecule 2: Small ribosomal subunit protein eS4, X isoform



- Molecule 3: 40S ribosomal protein S8



- Molecule 4: 40S ribosomal protein S11

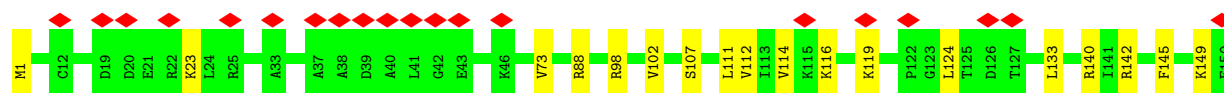
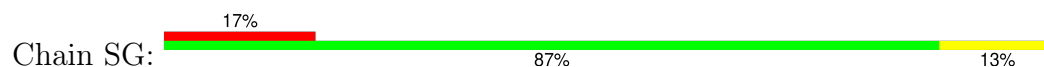


- Molecule 5: 40S ribosomal protein S23

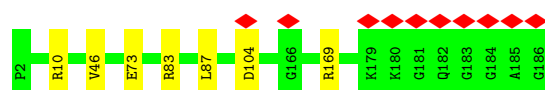




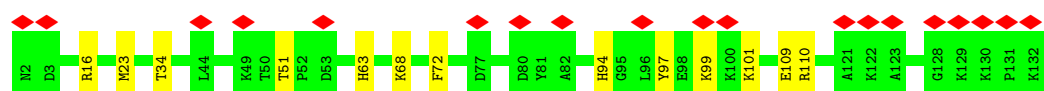
- Molecule 6: 40S ribosomal protein S6



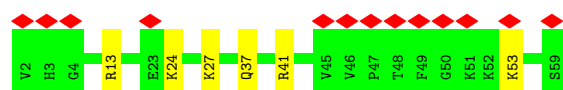
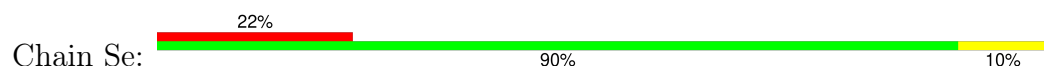
- Molecule 7: 40S ribosomal protein S9



- Molecule 8: 40S ribosomal protein S24



- Molecule 9: Small ribosomal subunit protein eS30



- Molecule 10: 40S ribosomal protein SA

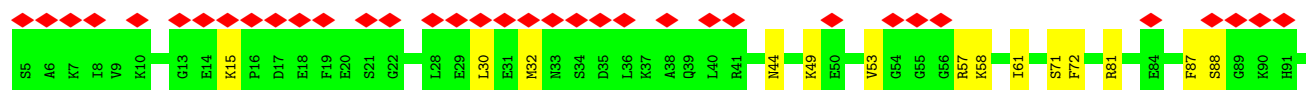
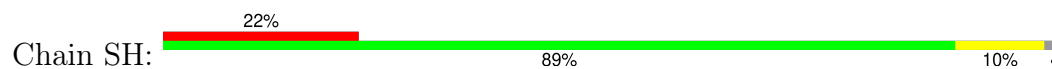


- Molecule 11: 40S ribosomal protein S3a

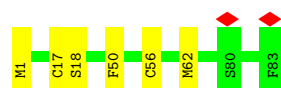




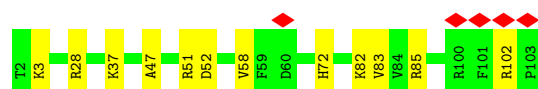
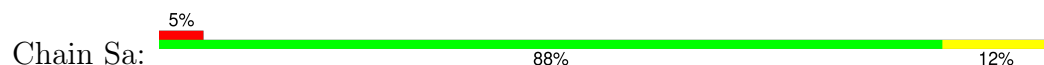
- Molecule 12: Small ribosomal subunit protein eS7



- Molecule 13: 40S ribosomal protein S21



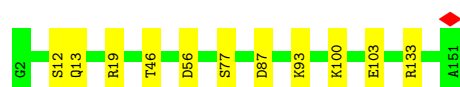
- Molecule 14: 40S ribosomal protein S26



- Molecule 15: 40S ribosomal protein S2



- Molecule 16: 40S ribosomal protein S13



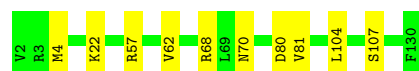
- Molecule 17: Small ribosomal subunit protein uS11





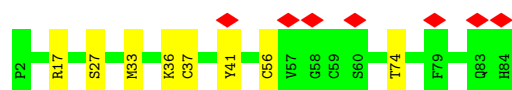
- Molecule 18: 40S ribosomal protein S15a

Chain SW: 92% 8%



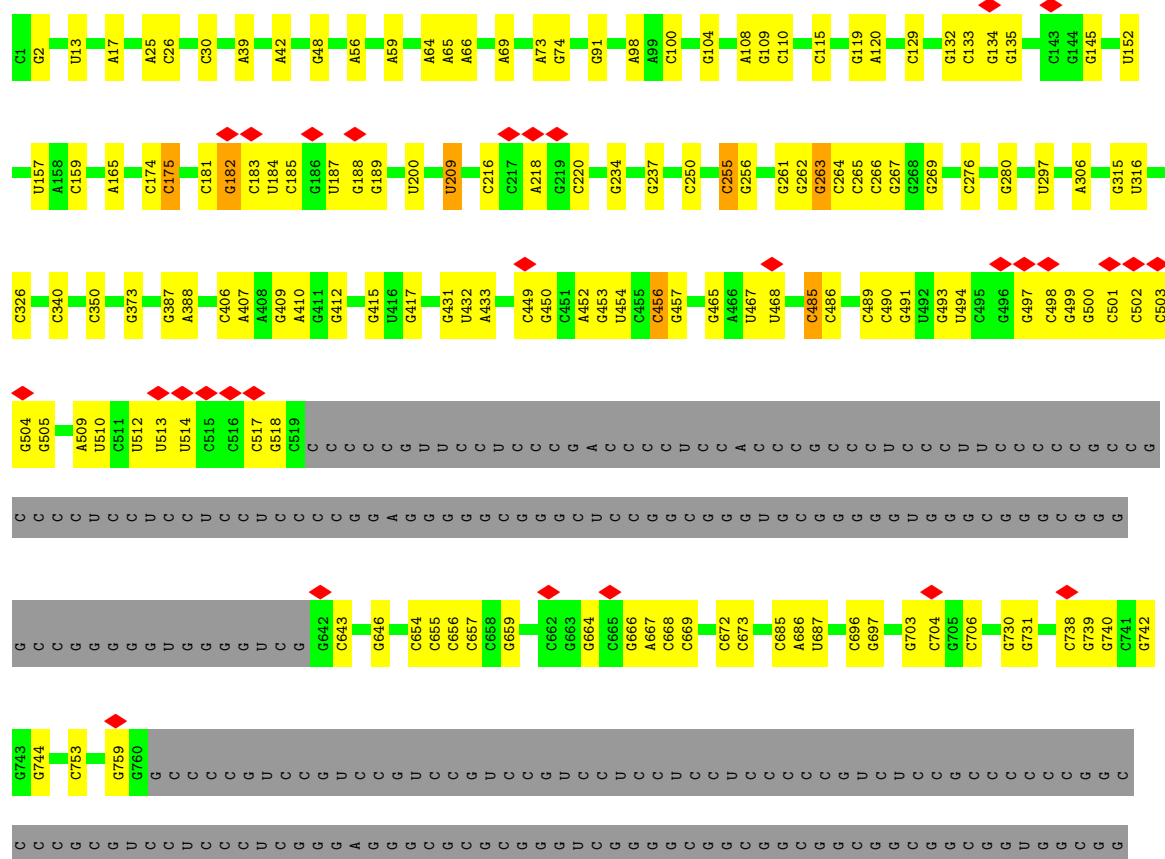
- Molecule 19: Small ribosomal subunit protein eS27

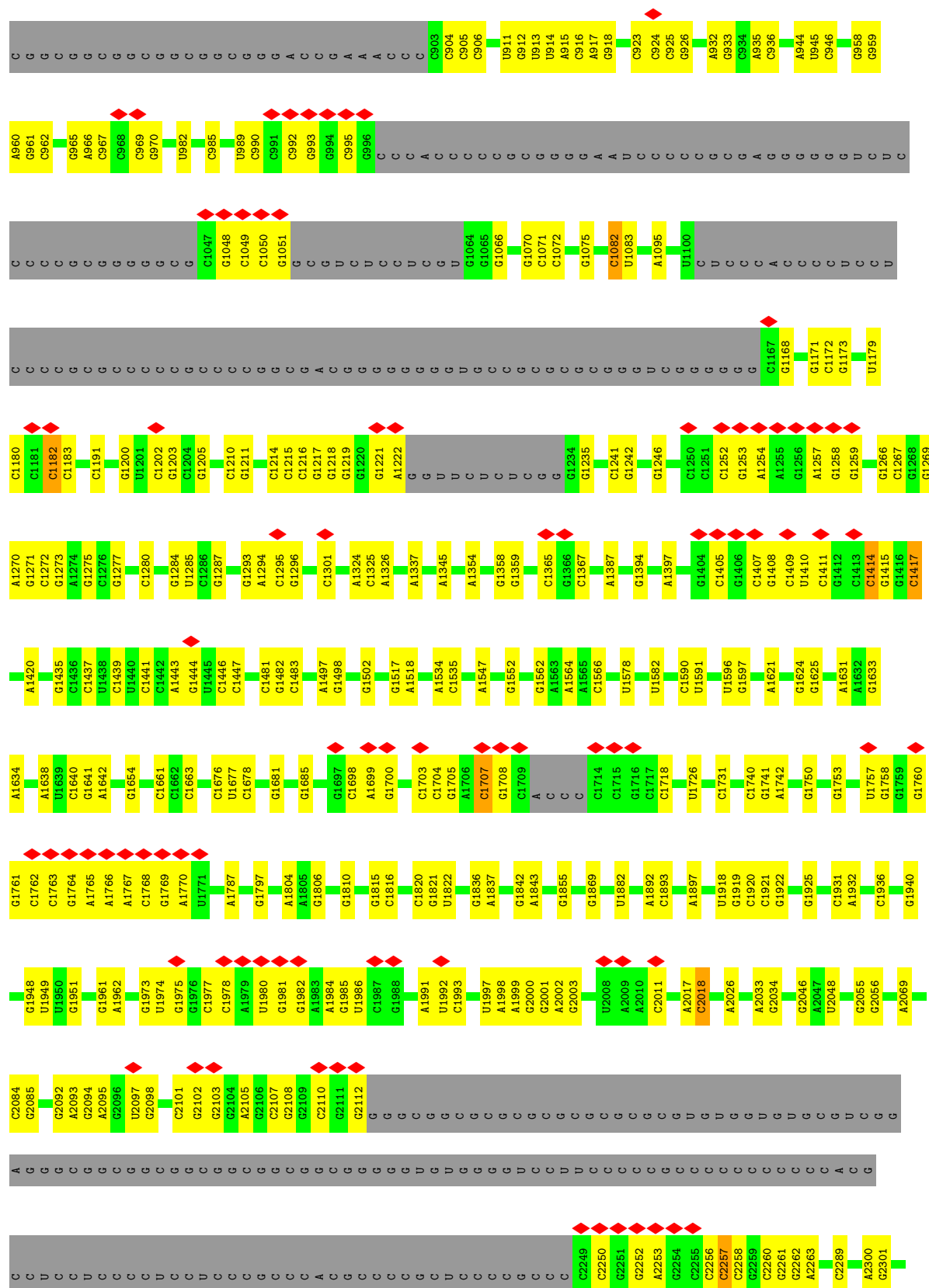
Chain Sb: 8% 90% 10%



- Molecule 20: 28S rRNA

Chain L5: 5% 56% 18% 26%





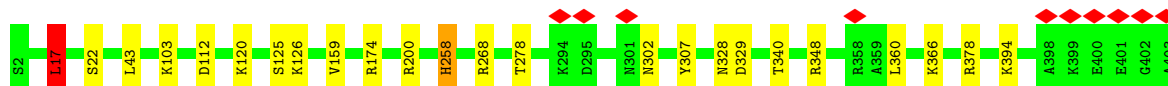


Chain LA:  92% 8%



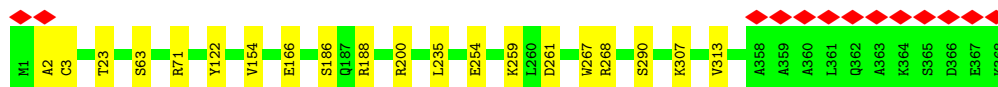
- Molecule 24: Large ribosomal subunit protein uL3

Chain LB:  94% 5%



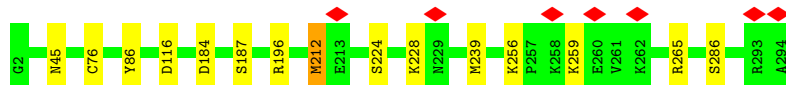
- Molecule 25: 60S ribosomal protein L4

Chain LC:  95% 5%




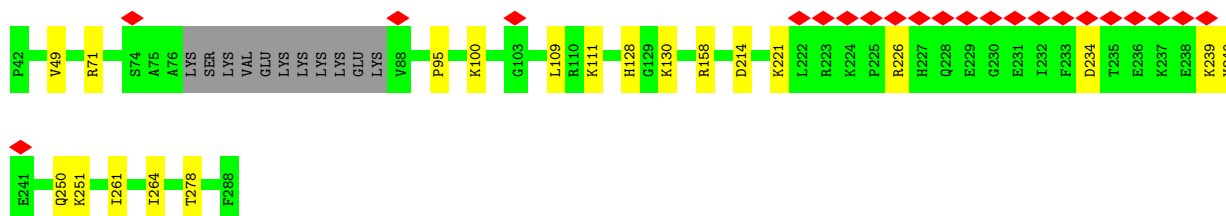
- Molecule 26: Large ribosomal subunit protein uL18

Chain LD:  95% 5%



- Molecule 27: Large ribosomal subunit protein eL6

Chain LE:  9% 87% 8%



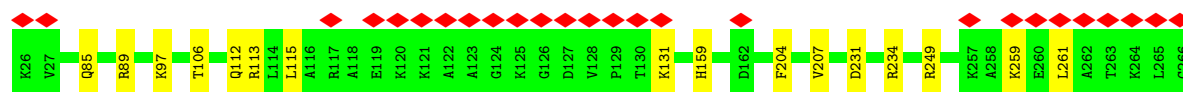
- Molecule 28: 60S ribosomal protein L7

Chain LF:  96%



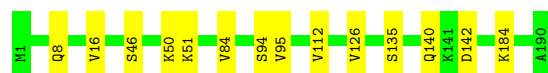
- Molecule 29: 60S ribosomal protein L7a

Chain LG:  11% 93% 7%



- Molecule 30: 60S ribosomal protein L9

Chain LH: 93% 7%



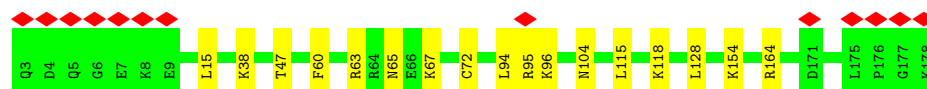
- Molecule 31: Ribosomal protein uL16-like

Chain LI: 89% 6% 5%



- Molecule 32: 60S ribosomal protein L11

Chain LJ: 7% 90% 10%



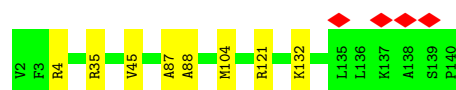
- Molecule 33: Large ribosomal subunit protein eL13

Chain LL: 93% 7%



- Molecule 34: 60S ribosomal protein L14

Chain LM: 94% 6%



- Molecule 35: 60S ribosomal protein L15

Chain LN: 97%



- Molecule 36: 60S ribosomal protein L13a

Chain LO:  95% 5%



- Molecule 37: 60S ribosomal protein L17

Chain LP:  91% 9%



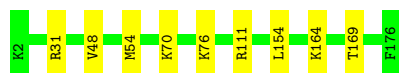
- Molecule 38: 60S ribosomal protein L18

Chain LQ:  96% .



- Molecule 39: 60S ribosomal protein L18a

Chain LS:  95% 5%




- Molecule 40: 60S ribosomal protein L21

Chain LT:  93% 7%



- Molecule 41: Heparin-binding protein HBp15

Chain LU:  86% 14%

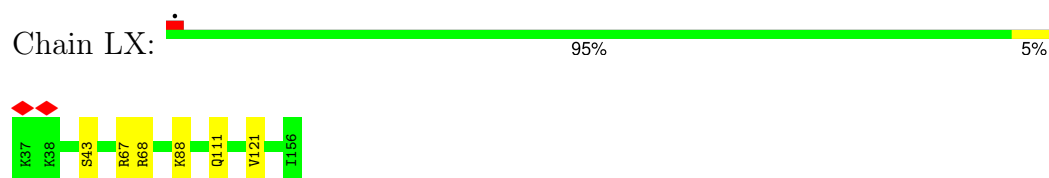


- Molecule 42: 60S ribosomal protein L23

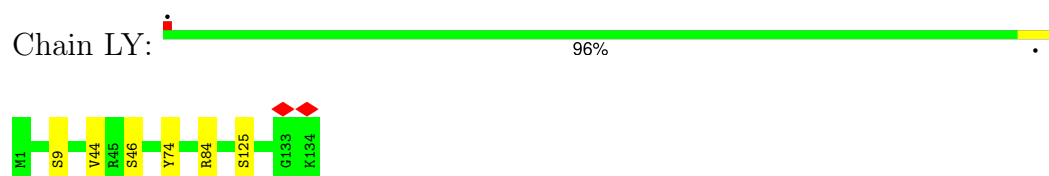
Chain LV:  93% 7%



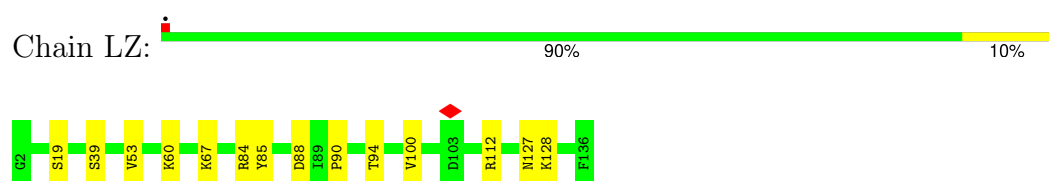
- Molecule 43: 60S ribosomal protein L23a



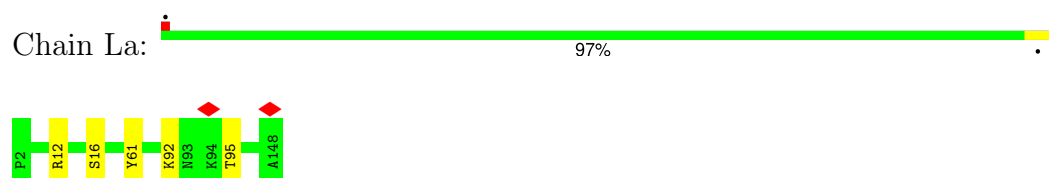
- Molecule 44: 60S ribosomal protein L26



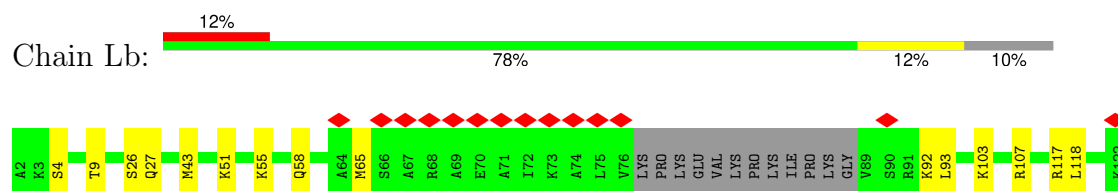
- Molecule 45: 60S ribosomal protein L27



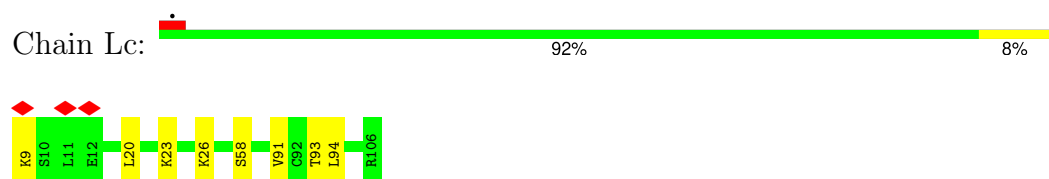
- Molecule 46: 60S ribosomal protein L27a



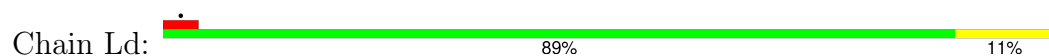
- Molecule 47: Large ribosomal subunit protein eL29

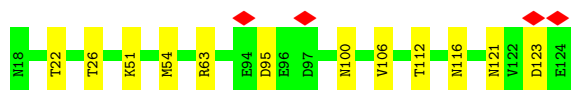


- Molecule 48: 60S ribosomal protein L30

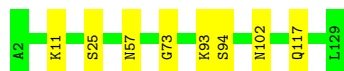


- Molecule 49: 60S ribosomal protein L31

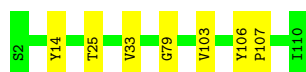




- Molecule 50: 60S ribosomal protein L32



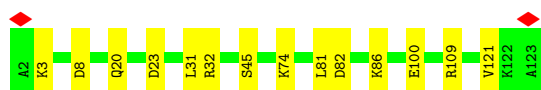
- Molecule 51: 60S ribosomal protein L35a



- Molecule 52: 60S ribosomal protein L34



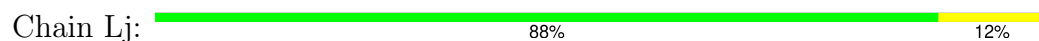
- Molecule 53: 60S ribosomal protein L35



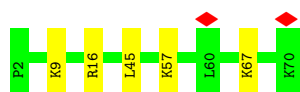
- Molecule 54: 60S ribosomal protein L36



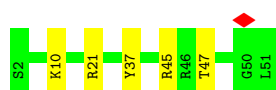
- Molecule 55: 60S ribosomal protein L37



- Molecule 56: 60S ribosomal protein L38



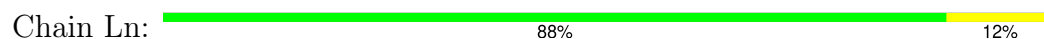
- Molecule 57: 60S ribosomal protein L39



- Molecule 58: Large ribosomal subunit protein eL40



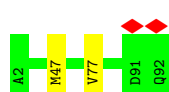
- Molecule 59: 60S ribosomal protein L41



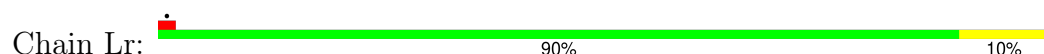
- Molecule 60: 60S ribosomal protein L36a



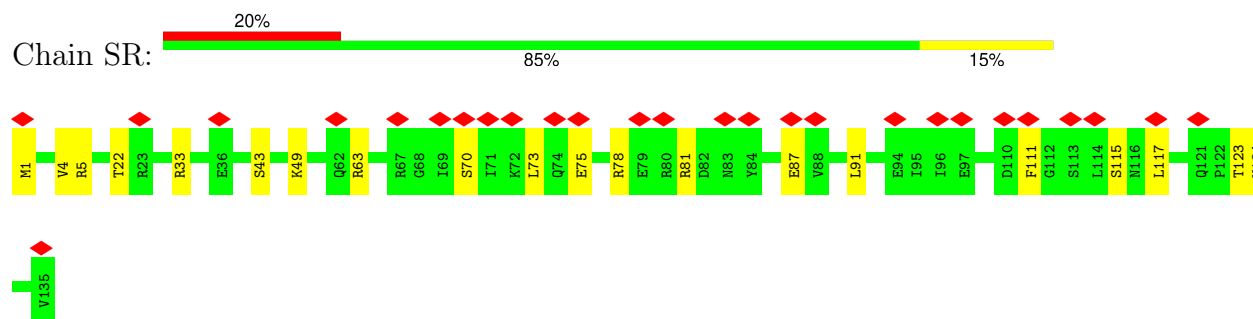
- Molecule 61: 60S ribosomal protein L37a



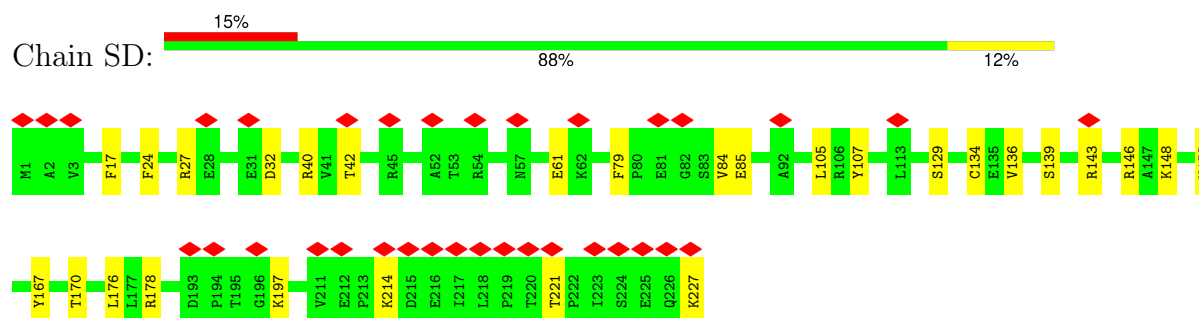
- Molecule 62: 60S ribosomal protein L28



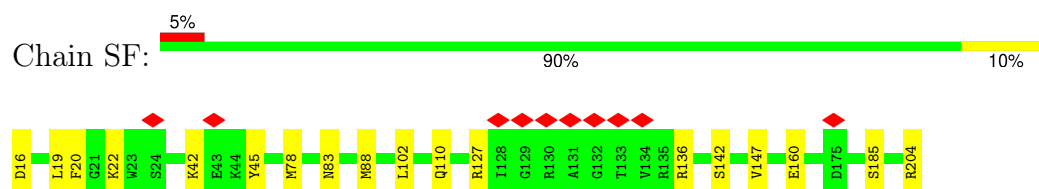
- Molecule 63: 40S ribosomal protein S17



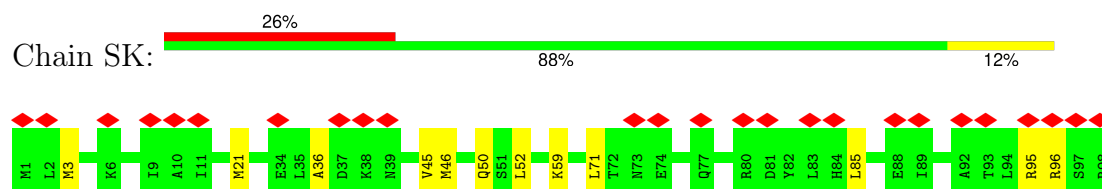
- Molecule 64: Small ribosomal subunit protein uS3



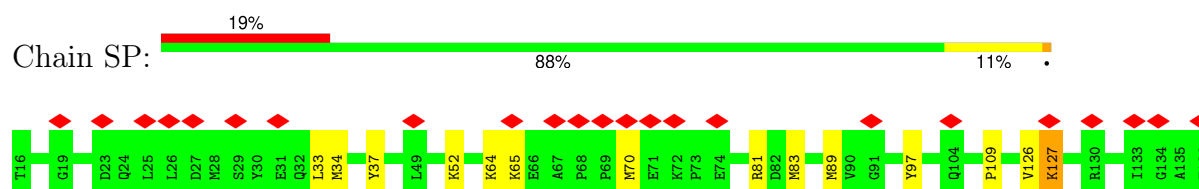
- Molecule 65: 40S ribosomal protein S5



- Molecule 66: 40S ribosomal protein S10

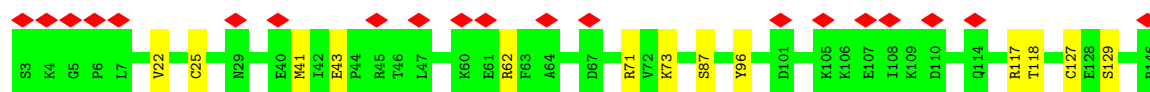


- Molecule 67: Small ribosomal subunit protein uS19

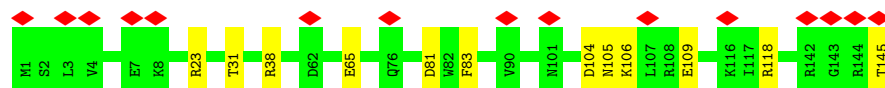


- Molecule 68: Small ribosomal subunit protein uS9

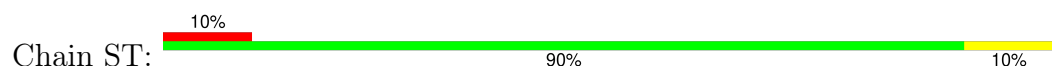




- Molecule 69: 40S ribosomal protein S18



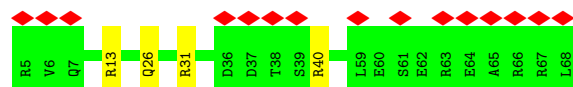
- Molecule 70: 40S ribosomal protein S19



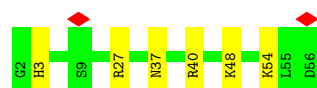
- Molecule 71: 40S ribosomal protein S20



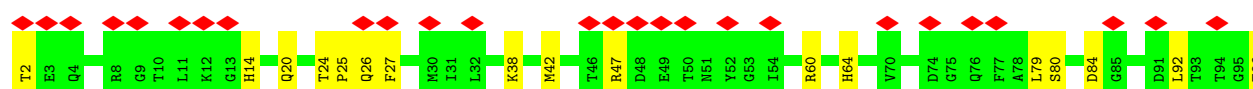
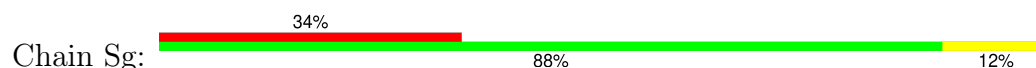
- Molecule 72: 40S ribosomal protein S28

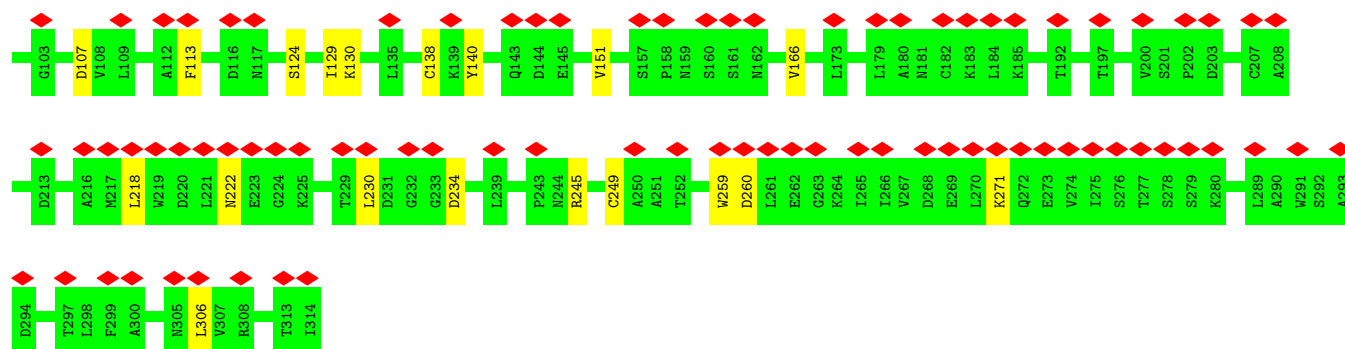


- Molecule 73: 40S ribosomal protein S29

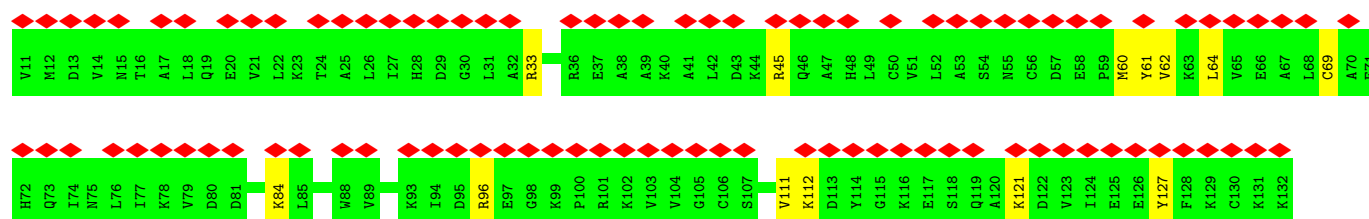
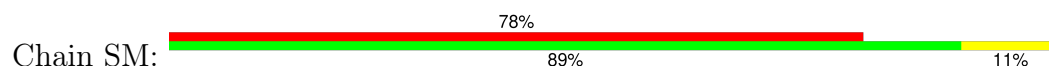


- Molecule 74: Receptor of activated protein C kinase 1

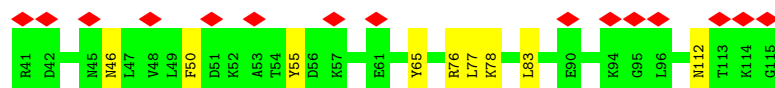
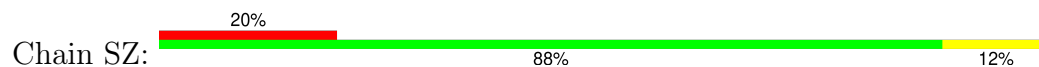




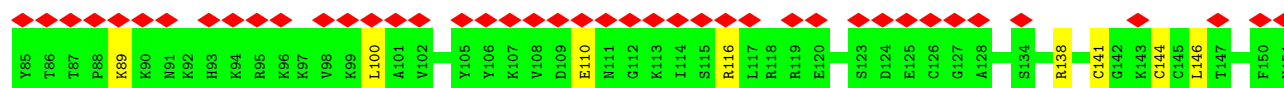
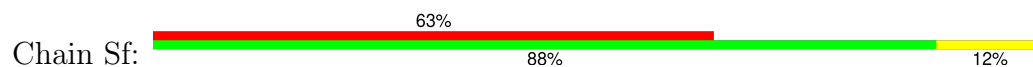
- Molecule 75: Small ribosomal subunit protein eS12



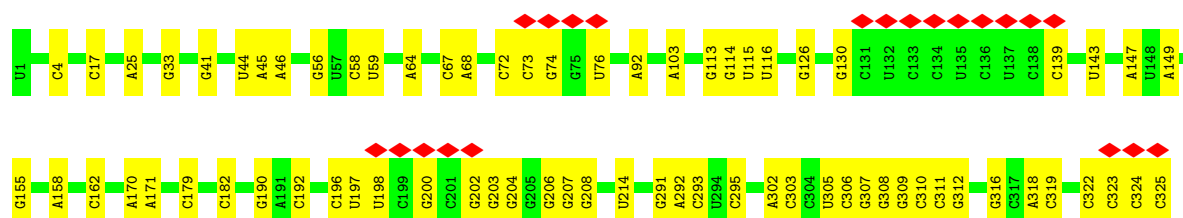
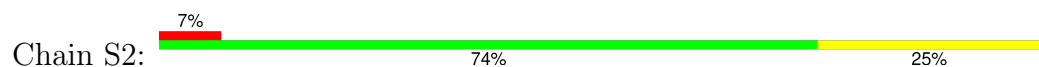
- Molecule 76: Small ribosomal subunit protein eS25

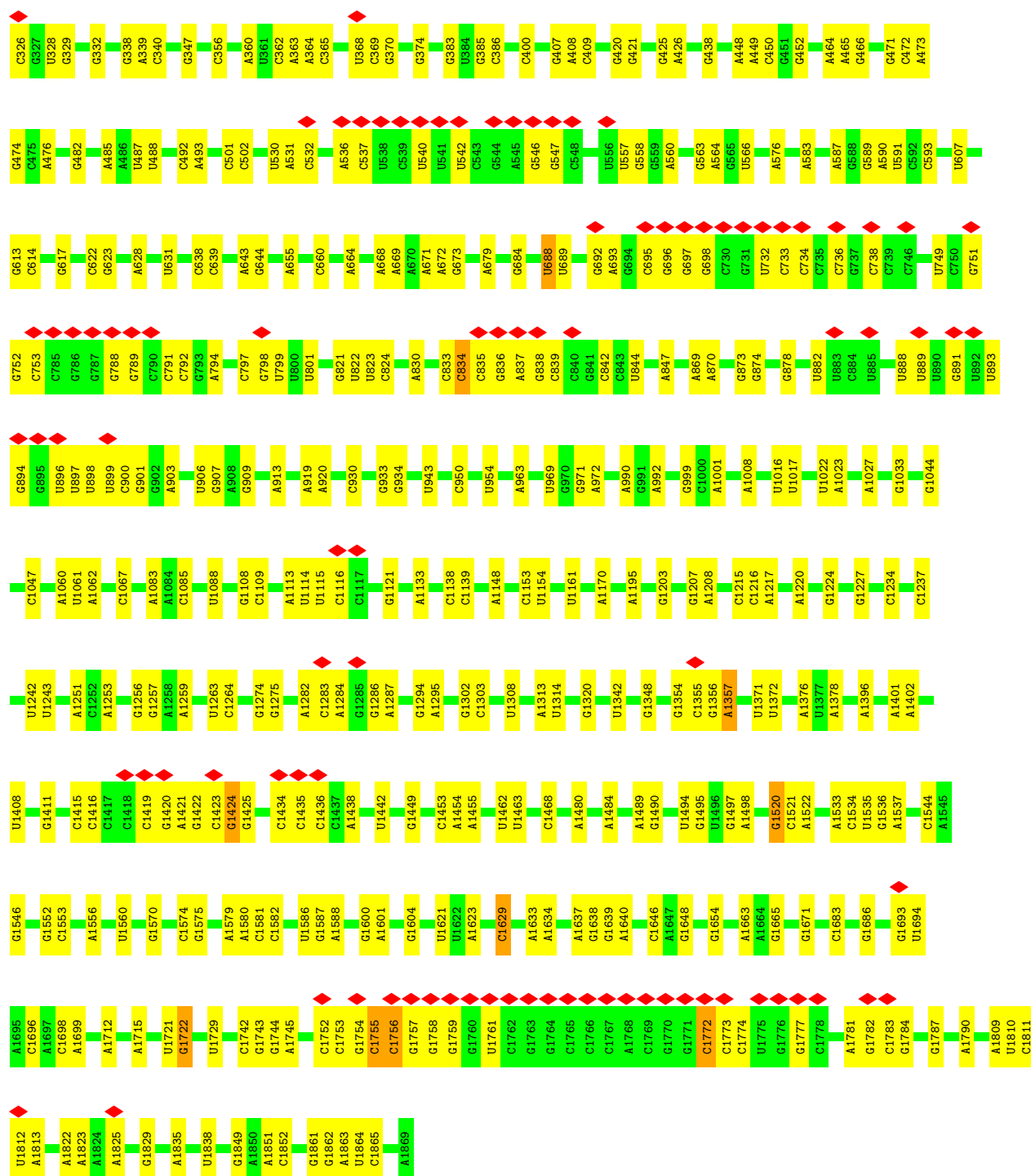


- Molecule 77: Ubiquitin-40S ribosomal protein S27a

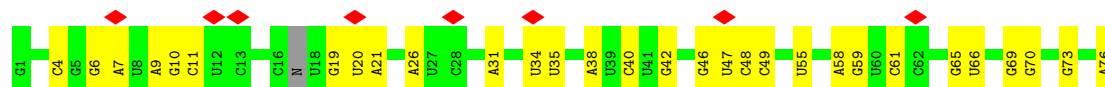


- Molecule 78: 18S rRNA [Homo sapiens]

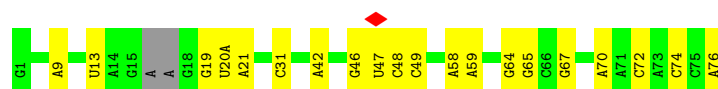




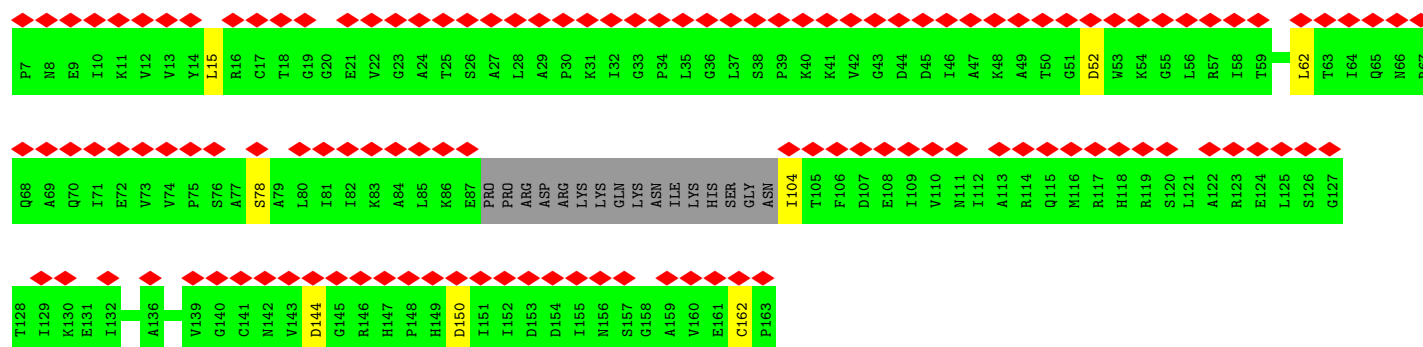
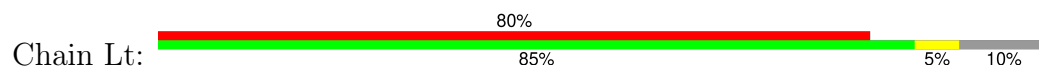
• Molecule 79: E site tRNA



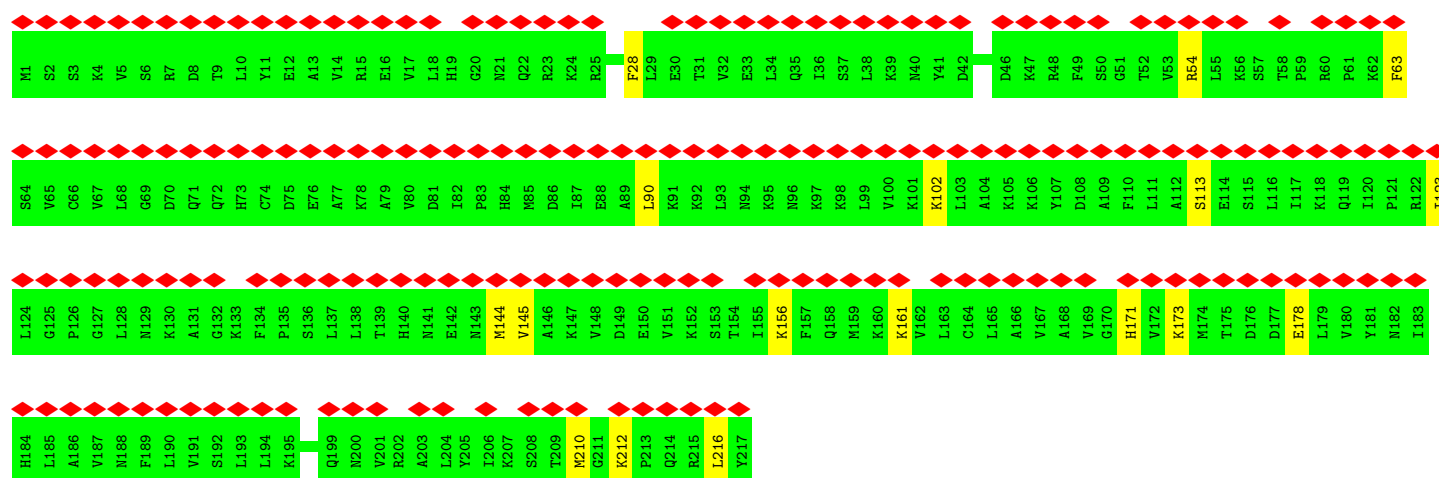
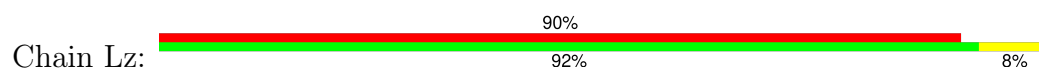
• Molecule 80: P site tRNA



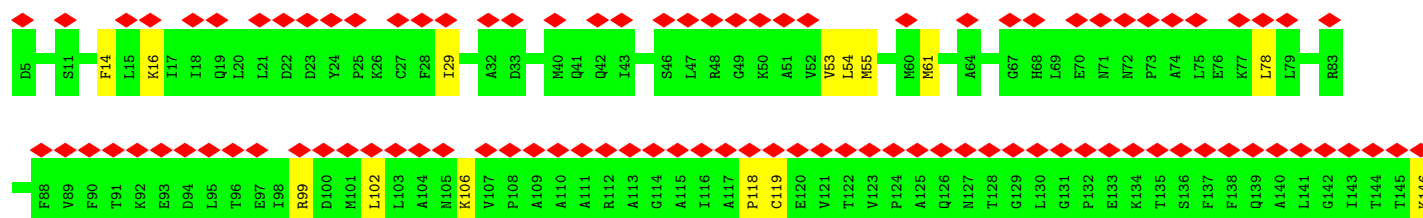
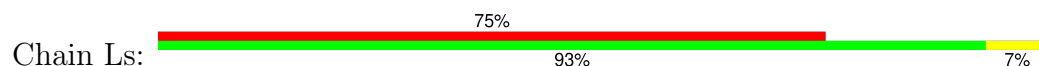
• Molecule 81: Large ribosomal subunit protein uL11

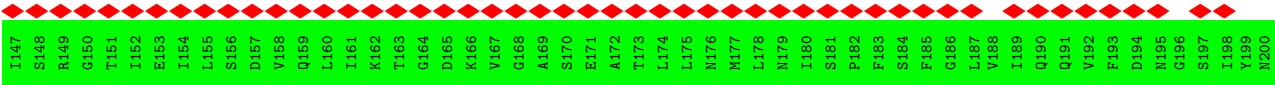


• Molecule 82: 60S ribosomal protein L10a

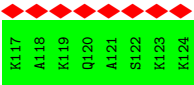
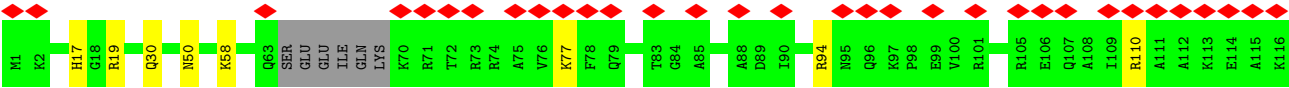


• Molecule 83: 60S acidic ribosomal protein P0





● Molecule 84: Ribosomal protein L24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12376	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	0.286	Depositor
Minimum map value	-0.129	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0264	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: ZN, MG

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	LR	0.40	0/1582	0.63	0/2091
2	SE	0.34	0/2118	0.58	0/2849
3	SI	0.36	0/1715	0.62	1/2287 (0.0%)
4	SL	0.40	0/1268	0.62	0/1696
5	SX	0.36	0/1116	0.56	0/1490
6	SG	0.33	0/1946	0.66	1/2590 (0.0%)
7	SJ	0.33	0/1550	0.60	0/2069
8	SY	0.31	0/1083	0.60	0/1438
9	Se	0.29	0/465	0.60	0/612
10	SA	0.35	0/1778	0.60	0/2416
11	SB	0.35	0/1765	0.57	0/2362
12	SH	0.33	0/1519	0.61	1/2033 (0.0%)
13	SV	0.32	0/643	0.63	0/860
14	Sa	0.39	0/836	0.64	0/1121
15	SC	0.36	0/1762	0.59	0/2381
16	SN	0.38	0/1232	0.56	0/1656
17	SO	0.35	0/1062	0.64	1/1425 (0.1%)
18	SW	0.37	0/1051	0.59	0/1406
19	Sb	0.34	0/665	0.56	0/891
20	L5	0.90	0/89312	0.91	93/139287 (0.1%)
21	L7	0.88	0/2861	0.84	0/4459
22	L8	0.92	0/3701	0.83	1/5766 (0.0%)
23	LA	0.50	0/1936	0.65	0/2596
24	LB	0.46	0/3306	0.61	1/4424 (0.0%)
25	LC	0.45	0/2981	0.62	1/4002 (0.0%)
26	LD	0.45	0/2428	0.61	2/3252 (0.1%)
27	LE	0.51	2/1942 (0.1%)	0.73	4/2606 (0.2%)
28	LF	0.48	0/1905	0.59	0/2539
29	LG	0.42	0/1960	0.60	1/2637 (0.0%)
30	LH	0.42	0/1537	0.65	1/2066 (0.0%)
31	LI	0.45	0/1673	0.59	0/2233
32	LJ	0.38	0/1433	0.61	0/1915

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LL	0.42	0/1732	0.63	1/2315 (0.0%)
34	LM	0.43	0/1161	0.59	0/1554
35	LN	0.49	0/1746	0.62	0/2338
36	LO	0.46	0/1682	0.60	0/2250
37	LP	0.47	0/1268	0.60	0/1701
38	LQ	0.47	0/1537	0.65	0/2052
39	LS	0.49	0/1493	0.63	0/2003
40	LT	0.46	0/1326	0.61	0/1770
41	LU	0.45	0/839	0.65	0/1126
42	LV	0.47	0/993	0.61	0/1332
43	LX	0.42	0/1002	0.61	0/1345
44	LY	0.44	0/1132	0.60	0/1504
45	LZ	0.46	0/1130	0.57	0/1507
46	La	0.48	0/1191	0.58	0/1591
47	Lb	0.38	0/889	0.71	1/1175 (0.1%)
48	Lc	0.44	0/774	0.59	1/1038 (0.1%)
49	Ld	0.44	0/903	0.61	0/1216
50	Le	0.48	0/1071	0.63	0/1429
51	Lf	0.50	0/895	0.66	0/1198
52	Lg	0.46	0/916	0.66	1/1220 (0.1%)
53	Lh	0.41	0/1023	0.58	0/1351
54	Li	0.38	0/843	0.60	0/1115
55	Lj	0.51	0/720	0.66	0/952
56	Lk	0.39	0/575	0.59	0/761
57	Ll	0.43	0/454	0.62	0/599
58	Lm	0.42	0/435	0.57	0/575
59	Ln	0.40	0/231	0.81	1/294 (0.3%)
60	Lo	0.46	0/876	0.62	0/1156
61	Lp	0.47	0/718	0.55	0/953
62	Lr	0.45	0/1017	0.62	0/1364
63	SR	0.33	0/1105	0.68	0/1484
64	SD	0.36	0/1793	0.59	0/2414
65	SF	0.33	0/1516	0.62	1/2037 (0.0%)
66	SK	0.31	0/851	0.63	0/1147
67	SP	0.35	0/1003	0.68	0/1342
68	SQ	0.32	0/1160	0.60	0/1553
69	SS	0.32	0/1216	0.66	0/1628
70	ST	0.31	0/1131	0.58	0/1515
71	SU	0.29	0/831	0.59	0/1115
72	Sc	0.32	0/508	0.67	0/680
73	Sd	0.34	0/470	0.62	0/623
74	Sg	0.28	0/2493	0.58	0/3394
75	SM	0.33	0/950	0.64	1/1275 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SZ	0.30	0/604	0.72	1/810 (0.1%)
77	Sf	0.28	0/560	0.57	0/745
78	S2	0.63	0/41242	0.85	52/64255 (0.1%)
79	Et	0.38	0/1778	0.90	0/2767
80	Pt	0.48	0/1761	0.82	1/2741 (0.0%)
81	Lt	0.27	0/1058	0.57	0/1430
82	Lz	0.27	0/1769	0.59	0/2371
83	Ls	0.29	0/1519	0.61	0/2052
84	LW	0.43	0/979	0.62	0/1295
All	All	0.68	2/239000 (0.0%)	0.80	169/350912 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	SX	0	1
12	SH	0	1
23	LA	0	1
24	LB	0	3
32	LJ	0	1
34	LM	0	1
36	LO	0	1
40	LT	0	1
51	Lf	0	3
53	Lh	0	1
55	Lj	0	2
65	SF	0	1
67	SP	0	1
68	SQ	0	1
76	SZ	0	1
All	All	0	20

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	LE	95	PRO	CG-CD	-10.47	1.16	1.50
27	LE	95	PRO	N-CD	5.43	1.55	1.47

All (169) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	LE	95	PRO	CA-N-CD	-12.04	94.64	111.50
27	LE	95	PRO	N-CD-CG	-10.71	87.14	103.20
20	L5	3773	U	N3-C2-O2	-9.81	115.33	122.20
20	L5	174	C	N3-C2-O2	-9.73	115.09	121.90
20	L5	485	C	C2-N1-C1'	9.16	128.88	118.80
20	L5	456	C	O4'-C1'-N1	8.99	115.40	108.20
20	L5	1481	C	C4-C5-C6	8.74	121.77	117.40
20	L5	1481	C	C5-C6-N1	-8.68	116.66	121.00
78	S2	1772	C	N1-C2-O2	8.51	124.01	118.90
78	S2	1772	C	N3-C2-O2	-8.51	115.94	121.90
78	S2	1416	C	N3-C2-O2	-8.43	116.00	121.90
20	L5	417	G	O4'-C1'-N9	8.38	114.90	108.20
78	S2	1629	C	N3-C2-O2	-8.36	116.05	121.90
78	S2	1694	U	C5-C6-N1	8.22	126.81	122.70
78	S2	1722	G	N3-C4-N9	8.03	130.82	126.00
20	L5	2710	C	N1-C2-O2	8.02	123.71	118.90
20	L5	2710	C	C2-N1-C1'	7.95	127.55	118.80
20	L5	181	C	N1-C2-O2	7.93	123.66	118.90
20	L5	1707	C	C6-N1-C2	-7.77	117.19	120.30
20	L5	181	C	C2-N1-C1'	7.72	127.29	118.80
20	L5	181	C	N3-C2-O2	-7.65	116.55	121.90
20	L5	181	C	C6-N1-C2	-7.62	117.25	120.30
78	S2	1453	C	C2-N1-C1'	7.59	127.15	118.80
20	L5	1082	C	O4'-C1'-N1	7.43	114.14	108.20
20	L5	3773	U	N1-C2-O2	7.31	127.92	122.80
78	S2	356	C	C2-N1-C1'	7.23	126.75	118.80
78	S2	1424	G	N3-C4-N9	7.15	130.29	126.00
20	L5	485	C	C6-N1-C1'	-7.11	112.27	120.80
78	S2	1722	G	C6-C5-N7	-7.08	126.15	130.40
20	L5	456	C	N3-C2-O2	-7.05	116.96	121.90
78	S2	1811	C	N1-C2-O2	6.95	123.07	118.90
17	SO	14	VAL	C-N-CA	6.94	139.04	121.70
20	L5	4709	U	C2-N1-C1'	6.87	125.94	117.70
20	L5	490	C	N3-C2-O2	-6.85	117.11	121.90
20	L5	1414	C	N3-C2-O2	-6.83	117.12	121.90
20	L5	2710	C	N3-C2-O2	-6.81	117.13	121.90
78	S2	356	C	N1-C2-O2	6.78	122.97	118.90
20	L5	129	C	N3-C2-O2	-6.77	117.16	121.90
20	L5	175	C	N3-C2-O2	-6.70	117.21	121.90
78	S2	1022	U	C2-N1-C1'	6.70	125.74	117.70
78	S2	1722	G	C4-N9-C1'	6.70	135.20	126.50
75	SM	64	LEU	CA-CB-CG	6.65	130.60	115.30
20	L5	255	C	N3-C2-O2	-6.60	117.28	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	L5	1414	C	N1-C2-O2	6.59	122.86	118.90
78	S2	1453	C	N1-C2-O2	6.48	122.79	118.90
26	LD	212	MET	CA-CB-CG	6.44	124.25	113.30
20	L5	3761	C	C2-N1-C1'	6.43	125.88	118.80
78	S2	293	C	C2-N1-C1'	6.43	125.87	118.80
78	S2	1722	G	C8-N9-C1'	-6.42	118.66	127.00
78	S2	1694	U	C2-N1-C1'	6.38	125.35	117.70
78	S2	834	C	C6-N1-C2	-6.34	117.76	120.30
20	L5	2410	C	C2-N1-C1'	6.29	125.71	118.80
20	L5	1082	C	N3-C2-O2	-6.28	117.50	121.90
20	L5	925	C	N1-C2-O2	6.18	122.61	118.90
29	LG	115	LEU	CA-CB-CG	6.17	129.49	115.30
47	Lb	118	LEU	CA-CB-CG	6.17	129.49	115.30
20	L5	1481	C	C2-N3-C4	-6.15	116.82	119.90
27	LE	95	PRO	N-CA-CB	-6.11	95.88	102.60
78	S2	834	C	N3-C2-O2	-6.10	117.63	121.90
20	L5	1707	C	C5-C6-N1	6.09	124.05	121.00
20	L5	3773	U	O4'-C1'-N1	6.08	113.07	108.20
20	L5	4924	C	N3-C2-O2	-6.05	117.66	121.90
33	LL	17	ASP	CB-CG-OD2	6.03	123.72	118.30
20	L5	4447	C	C6-N1-C1'	6.02	128.03	120.80
20	L5	4928	C	C2-N1-C1'	6.00	125.40	118.80
20	L5	925	C	N3-C2-O2	-5.98	117.72	121.90
20	L5	1417	C	C2-N1-C1'	5.98	125.37	118.80
20	L5	4709	U	C5-C4-O4	-5.96	122.33	125.90
78	S2	293	C	N1-C2-O2	5.94	122.47	118.90
20	L5	4447	C	C2-N1-C1'	-5.93	112.27	118.80
20	L5	2018	C	C6-N1-C2	-5.87	117.95	120.30
78	S2	1424	G	N3-C4-C5	-5.87	125.67	128.60
78	S2	688	U	P-O3'-C3'	5.86	126.73	119.70
78	S2	1629	C	C6-N1-C2	-5.86	117.96	120.30
20	L5	174	C	N1-C2-O2	5.82	122.39	118.90
6	SG	161	PRO	CA-N-CD	-5.80	103.38	111.50
20	L5	1252	C	N3-C2-O2	-5.79	117.84	121.90
78	S2	1424	G	C4-N9-C1'	5.79	134.03	126.50
78	S2	501	C	C2-N1-C1'	5.78	125.16	118.80
12	SH	30	LEU	CA-CB-CG	5.78	128.59	115.30
20	L5	2257	C	N1-C2-O2	5.77	122.36	118.90
20	L5	1597	G	O4'-C1'-N9	5.75	112.80	108.20
78	S2	1811	C	N3-C2-O2	-5.74	117.88	121.90
20	L5	1182	C	N1-C2-O2	5.74	122.34	118.90
20	L5	1216	C	C2-N1-C1'	5.74	125.11	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	L5	4928	C	N1-C2-O2	5.73	122.34	118.90
20	L5	1816	C	C6-N1-C2	-5.71	118.01	120.30
78	S2	356	C	N3-C2-O2	-5.69	117.92	121.90
78	S2	1722	G	N9-C4-C5	-5.68	103.13	105.40
20	L5	1191	C	N3-C2-O2	-5.66	117.94	121.90
20	L5	4926	C	C2-N1-C1'	5.65	125.02	118.80
25	LC	2	ALA	C-N-CA	5.65	135.82	121.70
78	S2	1520	G	C4-N9-C1'	5.63	133.82	126.50
27	LE	95	PRO	CA-CB-CG	-5.62	93.33	104.00
20	L5	1182	C	C2-N1-C1'	5.61	124.97	118.80
78	S2	1453	C	C6-N1-C2	-5.57	118.07	120.30
22	L8	51	U	N3-C2-O2	-5.57	118.30	122.20
26	LD	212	MET	CB-CG-SD	5.55	129.04	112.40
20	L5	2257	C	C2-N1-C1'	5.53	124.88	118.80
30	LH	142	ASP	CB-CG-OD2	5.51	123.26	118.30
20	L5	100	C	C2-N1-C1'	5.50	124.85	118.80
20	L5	2710	C	C6-N1-C1'	-5.50	114.20	120.80
20	L5	4898	G	N1-C6-O6	-5.48	116.61	119.90
20	L5	4926	C	N1-C2-O2	5.48	122.19	118.90
78	S2	1016	U	N3-C2-O2	-5.44	118.39	122.20
20	L5	262	G	N1-C6-O6	-5.44	116.63	119.90
3	SI	172	LEU	CA-CB-CG	5.43	127.79	115.30
20	L5	664	G	N1-C6-O6	-5.42	116.65	119.90
78	S2	1453	C	N3-C2-O2	-5.41	118.11	121.90
78	S2	1755	C	N1-C2-O2	5.37	122.12	118.90
20	L5	2710	C	C6-N1-C2	-5.37	118.15	120.30
65	SF	102	LEU	CA-CB-CG	5.36	127.63	115.30
76	SZ	83	LEU	CA-CB-CG	5.35	127.60	115.30
20	L5	4922	C	N1-C2-O2	5.34	122.11	118.90
20	L5	3765	G	C8-N9-C4	-5.34	104.26	106.40
52	Lg	96	LEU	CA-CB-CG	5.32	127.53	115.30
78	S2	1357	A	N1-C6-N6	-5.31	115.41	118.60
20	L5	740	G	N3-C4-N9	-5.30	122.82	126.00
20	L5	3773	U	C2-N1-C1'	5.30	124.06	117.70
78	S2	1772	C	C2-N1-C1'	5.30	124.63	118.80
78	S2	1694	U	N1-C2-O2	5.30	126.51	122.80
20	L5	4709	U	C6-N1-C1'	-5.29	113.79	121.20
78	S2	1629	C	N1-C2-N3	5.29	122.90	119.20
78	S2	1424	G	C6-C5-N7	-5.26	127.24	130.40
59	Ln	13	LEU	CA-CB-CG	5.26	127.41	115.30
20	L5	209	U	C2-N1-C1'	5.26	124.01	117.70
20	L5	4281	A	O4'-C1'-N9	5.26	112.41	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	Pt	31	C	C2-N1-C1'	5.25	124.58	118.80
78	S2	1756	C	N3-C2-O2	-5.25	118.23	121.90
20	L5	1259	G	C5-C6-O6	5.25	131.75	128.60
20	L5	2018	C	C5-C6-N1	5.23	123.62	121.00
20	L5	2000	G	N3-C4-N9	5.23	129.14	126.00
20	L5	3775	A	O4'-C1'-N9	5.21	112.37	108.20
20	L5	664	G	C5-C6-O6	5.21	131.72	128.60
20	L5	4898	G	C5-C6-O6	5.21	131.72	128.60
20	L5	4897	G	C5-C6-O6	5.19	131.71	128.60
20	L5	3761	C	N1-C2-O2	5.18	122.01	118.90
20	L5	4694	G	O4'-C1'-N9	5.18	112.34	108.20
78	S2	1425	G	C5-C6-O6	5.17	131.70	128.60
78	S2	293	C	N3-C2-O2	-5.17	118.28	121.90
48	Lc	20	LEU	CA-CB-CG	5.17	127.18	115.30
20	L5	740	G	N3-C4-C5	5.16	131.18	128.60
20	L5	4694	G	C4-N9-C1'	5.16	133.20	126.50
78	S2	1520	G	C8-N9-C1'	-5.15	120.30	127.00
20	L5	1259	G	N1-C6-O6	-5.15	116.81	119.90
20	L5	4447	C	O4'-C1'-N1	5.15	112.32	108.20
78	S2	322	C	N1-C2-O2	5.14	121.98	118.90
78	S2	1694	U	C6-N1-C2	-5.13	117.92	121.00
20	L5	182	G	N3-C4-N9	-5.13	122.92	126.00
20	L5	263	G	N1-C2-N2	-5.13	111.59	116.20
20	L5	1552	G	O4'-C1'-N9	5.13	112.30	108.20
78	S2	1424	G	C8-N9-C1'	-5.10	120.37	127.00
20	L5	2000	G	N3-C4-C5	-5.10	126.05	128.60
20	L5	115	C	C6-N1-C2	-5.10	118.26	120.30
78	S2	1314	U	C2-N1-C1'	5.10	123.82	117.70
78	S2	1722	G	N3-C4-C5	-5.09	126.06	128.60
78	S2	501	C	N1-C2-O2	5.08	121.95	118.90
20	L5	2760	G	P-O3'-C3'	5.07	125.79	119.70
24	LB	17	LEU	CA-CB-CG	5.07	126.96	115.30
20	L5	4068	U	C2-N1-C1'	5.06	123.77	117.70
78	S2	1520	G	N3-C4-N9	5.06	129.03	126.00
78	S2	356	C	C6-N1-C1'	-5.04	114.76	120.80
20	L5	4303	C	N3-C2-O2	-5.03	118.38	121.90
20	L5	2528	G	C4-N9-C1'	5.03	133.04	126.50
78	S2	1453	C	C6-N1-C1'	-5.02	114.78	120.80
20	L5	129	C	C6-N1-C2	-5.02	118.29	120.30
20	L5	3775	A	C6-C5-N7	-5.02	128.79	132.30
20	L5	3775	A	N7-C8-N9	5.00	116.30	113.80
20	L5	3641	U	C4-C5-C6	5.00	122.70	119.70

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	LA	13	GLY	Peptide
24	LB	17	LEU	Peptide
24	LB	258	HIS	Peptide
24	LB	302	ASN	Peptide
32	LJ	94	LEU	Peptide
34	LM	87	ALA	Peptide
36	LO	110	PRO	Peptide
40	LT	136	ARG	Peptide
51	Lf	103	VAL	Peptide
51	Lf	106	TYR	Peptide
51	Lf	79	GLY	Peptide
53	Lh	86	LYS	Peptide
55	Lj	39	TYR	Peptide
55	Lj	40	PRO	Peptide
65	SF	78	MET	Peptide
12	SH	15	LYS	Peptide
67	SP	127	LYS	Peptide
68	SQ	43	GLU	Peptide
5	SX	126	ALA	Peptide
76	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	LR	185/187 (99%)	177 (96%)	8 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	SE	260/262 (99%)	243 (94%)	17 (6%)	0	100	100
3	SI	204/206 (99%)	193 (95%)	11 (5%)	0	100	100
4	SL	151/153 (99%)	137 (91%)	14 (9%)	0	100	100
5	SX	139/141 (99%)	128 (92%)	10 (7%)	1 (1%)	19	52
6	SG	235/237 (99%)	221 (94%)	14 (6%)	0	100	100
7	SJ	183/185 (99%)	167 (91%)	16 (9%)	0	100	100
8	SY	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
9	Se	56/58 (97%)	48 (86%)	8 (14%)	0	100	100
10	SA	219/221 (99%)	194 (89%)	25 (11%)	0	100	100
11	SB	212/214 (99%)	203 (96%)	9 (4%)	0	100	100
12	SH	182/189 (96%)	160 (88%)	22 (12%)	0	100	100
13	SV	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
14	Sa	100/102 (98%)	90 (90%)	9 (9%)	1 (1%)	13	44
15	SC	220/222 (99%)	205 (93%)	15 (7%)	0	100	100
16	SN	148/150 (99%)	144 (97%)	4 (3%)	0	100	100
17	SO	138/140 (99%)	125 (91%)	13 (9%)	0	100	100
18	SW	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
19	Sb	81/83 (98%)	72 (89%)	9 (11%)	0	100	100
23	LA	246/248 (99%)	223 (91%)	22 (9%)	1 (0%)	30	63
24	LB	400/402 (100%)	375 (94%)	25 (6%)	0	100	100
25	LC	366/368 (100%)	341 (93%)	25 (7%)	0	100	100
26	LD	291/293 (99%)	272 (94%)	19 (6%)	0	100	100
27	LE	232/247 (94%)	211 (91%)	21 (9%)	0	100	100
28	LF	223/225 (99%)	212 (95%)	11 (5%)	0	100	100
29	LG	239/241 (99%)	220 (92%)	19 (8%)	0	100	100
30	LH	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
31	LI	198/213 (93%)	188 (95%)	10 (5%)	0	100	100
32	LJ	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
33	LL	208/210 (99%)	190 (91%)	18 (9%)	0	100	100
34	LM	137/139 (99%)	128 (93%)	8 (6%)	1 (1%)	19	52
35	LN	201/203 (99%)	189 (94%)	10 (5%)	2 (1%)	13	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	LO	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
37	LP	151/153 (99%)	142 (94%)	9 (6%)	0	100	100
38	LQ	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
39	LS	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
40	LT	157/159 (99%)	146 (93%)	11 (7%)	0	100	100
41	LU	99/101 (98%)	82 (83%)	17 (17%)	0	100	100
42	LV	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
43	LX	118/120 (98%)	115 (98%)	3 (2%)	0	100	100
44	LY	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
45	LZ	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
46	La	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
47	Lb	105/121 (87%)	96 (91%)	9 (9%)	0	100	100
48	Lc	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
49	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
50	Le	126/128 (98%)	115 (91%)	10 (8%)	1 (1%)	16	49
51	Lf	107/109 (98%)	98 (92%)	8 (8%)	1 (1%)	14	46
52	Lg	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
53	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
54	Li	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
55	Lj	84/86 (98%)	79 (94%)	5 (6%)	0	100	100
56	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
57	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
58	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
59	Ln	22/24 (92%)	22 (100%)	0	0	100	100
60	Lo	103/105 (98%)	95 (92%)	8 (8%)	0	100	100
61	Lp	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
62	Lr	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
63	SR	133/135 (98%)	120 (90%)	12 (9%)	1 (1%)	16	49
64	SD	225/227 (99%)	209 (93%)	16 (7%)	0	100	100
65	SF	187/189 (99%)	168 (90%)	19 (10%)	0	100	100
66	SK	96/98 (98%)	81 (84%)	13 (14%)	2 (2%)	5	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	SP	119/121 (98%)	109 (92%)	10 (8%)	0	100	100
68	SQ	142/144 (99%)	123 (87%)	19 (13%)	0	100	100
69	SS	143/145 (99%)	135 (94%)	8 (6%)	0	100	100
70	ST	141/143 (99%)	128 (91%)	12 (8%)	1 (1%)	19	52
71	SU	102/104 (98%)	94 (92%)	8 (8%)	0	100	100
72	Sc	62/64 (97%)	54 (87%)	8 (13%)	0	100	100
73	Sd	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
74	Sg	311/313 (99%)	275 (88%)	36 (12%)	0	100	100
75	SM	120/122 (98%)	108 (90%)	11 (9%)	1 (1%)	16	49
76	SZ	73/75 (97%)	58 (80%)	15 (20%)	0	100	100
77	Sf	65/67 (97%)	54 (83%)	11 (17%)	0	100	100
81	Lt	137/157 (87%)	103 (75%)	33 (24%)	1 (1%)	19	52
82	Lz	215/217 (99%)	169 (79%)	46 (21%)	0	100	100
83	Ls	194/196 (99%)	183 (94%)	11 (6%)	0	100	100
84	LW	114/124 (92%)	108 (95%)	6 (5%)	0	100	100
All	All	11863/12090 (98%)	10927 (92%)	922 (8%)	14 (0%)	50	79

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	SX	127	ASN
34	LM	88	ALA
35	LN	124	ASP
63	SR	124	VAL
66	SK	36	ALA
70	ST	41	LYS
81	Lt	144	ASP
14	Sa	47	ALA
75	SM	96	ARG
66	SK	96	ARG
23	LA	55	GLY
50	Le	73	GLY
51	Lf	107	PRO
35	LN	84	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	LR	166/166 (100%)	143 (86%)	23 (14%)	3	15
2	SE	224/224 (100%)	200 (89%)	24 (11%)	5	23
3	SI	178/178 (100%)	160 (90%)	18 (10%)	6	25
4	SL	137/137 (100%)	113 (82%)	24 (18%)	1	8
5	SX	113/113 (100%)	105 (93%)	8 (7%)	12	38
6	SG	207/207 (100%)	177 (86%)	30 (14%)	2	13
7	SJ	161/161 (100%)	154 (96%)	7 (4%)	25	53
8	SY	113/113 (100%)	100 (88%)	13 (12%)	4	20
9	Se	47/47 (100%)	41 (87%)	6 (13%)	3	17
10	SA	183/183 (100%)	166 (91%)	17 (9%)	7	28
11	SB	195/195 (100%)	176 (90%)	19 (10%)	6	26
12	SH	166/169 (98%)	150 (90%)	16 (10%)	7	27
13	SV	67/67 (100%)	61 (91%)	6 (9%)	8	29
14	Sa	89/89 (100%)	78 (88%)	11 (12%)	4	18
15	SC	188/188 (100%)	169 (90%)	19 (10%)	6	25
16	SN	130/130 (100%)	119 (92%)	11 (8%)	8	31
17	SO	110/110 (100%)	99 (90%)	11 (10%)	6	26
18	SW	112/112 (100%)	102 (91%)	10 (9%)	8	30
19	Sb	75/75 (100%)	67 (89%)	8 (11%)	5	23
23	LA	190/190 (100%)	173 (91%)	17 (9%)	8	30
24	LB	348/348 (100%)	325 (93%)	23 (7%)	14	41
25	LC	306/306 (100%)	287 (94%)	19 (6%)	15	42
26	LD	246/247 (100%)	231 (94%)	15 (6%)	15	43
27	LE	209/220 (95%)	190 (91%)	19 (9%)	7	29
28	LF	194/194 (100%)	186 (96%)	8 (4%)	26	54
29	LG	203/205 (99%)	188 (93%)	15 (7%)	11	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	LH	169/169 (100%)	156 (92%)	13 (8%)	10	35
31	LI	172/180 (96%)	160 (93%)	12 (7%)	12	39
32	LJ	148/148 (100%)	132 (89%)	16 (11%)	5	23
33	LL	176/176 (100%)	163 (93%)	13 (7%)	11	36
34	LM	118/118 (100%)	112 (95%)	6 (5%)	20	48
35	LN	171/171 (100%)	166 (97%)	5 (3%)	37	64
36	LO	173/173 (100%)	163 (94%)	10 (6%)	17	44
37	LP	134/134 (100%)	120 (90%)	14 (10%)	5	24
38	LQ	164/164 (100%)	156 (95%)	8 (5%)	21	49
39	LS	156/156 (100%)	147 (94%)	9 (6%)	17	44
40	LT	139/139 (100%)	129 (93%)	10 (7%)	12	38
41	LU	91/91 (100%)	77 (85%)	14 (15%)	2	11
42	LV	101/101 (100%)	92 (91%)	9 (9%)	8	30
43	LX	108/108 (100%)	102 (94%)	6 (6%)	17	45
44	LY	124/124 (100%)	118 (95%)	6 (5%)	21	50
45	LZ	117/117 (100%)	103 (88%)	14 (12%)	4	19
46	La	120/120 (100%)	115 (96%)	5 (4%)	25	53
47	Lb	88/101 (87%)	74 (84%)	14 (16%)	2	11
48	Lc	83/83 (100%)	76 (92%)	7 (8%)	9	31
49	Ld	98/98 (100%)	86 (88%)	12 (12%)	4	18
50	Le	114/114 (100%)	107 (94%)	7 (6%)	15	43
51	Lf	88/88 (100%)	85 (97%)	3 (3%)	32	60
52	Lg	98/98 (100%)	93 (95%)	5 (5%)	20	48
53	Lh	109/109 (100%)	96 (88%)	13 (12%)	4	19
54	Li	86/86 (100%)	83 (96%)	3 (4%)	31	59
55	Lj	73/73 (100%)	65 (89%)	8 (11%)	5	22
56	Lk	64/64 (100%)	59 (92%)	5 (8%)	10	34
57	Ll	47/47 (100%)	42 (89%)	5 (11%)	5	23
58	Lm	48/48 (100%)	46 (96%)	2 (4%)	25	53
59	Ln	23/23 (100%)	21 (91%)	2 (9%)	8	30
60	Lo	93/93 (100%)	88 (95%)	5 (5%)	18	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	Lp	74/74 (100%)	72 (97%)	2 (3%)	40	66
62	Lr	109/109 (100%)	96 (88%)	13 (12%)	4	19
63	SR	122/122 (100%)	103 (84%)	19 (16%)	2	11
64	SD	190/190 (100%)	162 (85%)	28 (15%)	2	13
65	SF	159/159 (100%)	143 (90%)	16 (10%)	6	25
66	SK	89/89 (100%)	79 (89%)	10 (11%)	5	21
67	SP	107/107 (100%)	93 (87%)	14 (13%)	3	16
68	SQ	119/119 (100%)	107 (90%)	12 (10%)	6	25
69	SS	126/126 (100%)	114 (90%)	12 (10%)	7	27
70	ST	113/113 (100%)	98 (87%)	15 (13%)	3	16
71	SU	94/94 (100%)	88 (94%)	6 (6%)	14	41
72	Sc	57/57 (100%)	53 (93%)	4 (7%)	12	39
73	Sd	48/48 (100%)	42 (88%)	6 (12%)	3	18
74	Sg	272/272 (100%)	236 (87%)	36 (13%)	3	16
75	SM	102/104 (98%)	91 (89%)	11 (11%)	5	23
76	SZ	66/66 (100%)	59 (89%)	7 (11%)	5	23
77	Sf	60/60 (100%)	52 (87%)	8 (13%)	3	16
81	Lt	112/130 (86%)	105 (94%)	7 (6%)	15	42
82	Lz	195/196 (100%)	178 (91%)	17 (9%)	8	30
83	Ls	162/164 (99%)	148 (91%)	14 (9%)	8	31
84	LW	97/103 (94%)	89 (92%)	8 (8%)	9	33
All	All	10323/10390 (99%)	9400 (91%)	923 (9%)	10	30

All (923) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	LR	8	LYS
1	LR	12	SER
1	LR	13	SER
1	LR	22	VAL
1	LR	28	GLU
1	LR	47	ASP
1	LR	56	THR
1	LR	63	CYS
1	LR	65	LYS

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Mol	Chain	Res	Type
1	LR	74	ARG
1	LR	81	ARG
1	LR	122	SER
1	LR	125	LEU
1	LR	133	LYS
1	LR	146	LYS
1	LR	153	LYS
1	LR	168	GLU
1	LR	171	LYS
1	LR	172	ARG
1	LR	176	ARG
1	LR	183	GLU
1	LR	186	LYS
1	LR	188	LEU
2	SE	32	SER
2	SE	38	LEU
2	SE	51	ARG
2	SE	65	CYS
2	SE	73	ASP
2	SE	81	THR
2	SE	94	LYS
2	SE	113	ARG
2	SE	117	GLU
2	SE	126	VAL
2	SE	140	VAL
2	SE	146	THR
2	SE	148	ARG
2	SE	161	GLN
2	SE	181	CYS
2	SE	188	ASN
2	SE	198	ARG
2	SE	200	ARG
2	SE	223	SER
2	SE	224	ASN
2	SE	227	VAL
2	SE	233	LYS
2	SE	242	LYS
2	SE	247	THR
3	SI	5	ARG
3	SI	6	ASP
3	SI	22	HIS
3	SI	42	ARG

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Mol	Chain	Res	Type
3	SI	74	ARG
3	SI	80	ASP
3	SI	84	ASN
3	SI	92	ARG
3	SI	110	ARG
3	SI	135	GLU
3	SI	139	LYS
3	SI	140	LYS
3	SI	141	ARG
3	SI	142	SER
3	SI	154	LYS
3	SI	159	SER
3	SI	184	ARG
3	SI	206	LYS
4	SL	12	LYS
4	SL	17	PHE
4	SL	19	ASN
4	SL	21	LYS
4	SL	25	LEU
4	SL	37	TYR
4	SL	42	LEU
4	SL	45	LYS
4	SL	54	THR
4	SL	58	LYS
4	SL	67	SER
4	SL	69	ARG
4	SL	73	LEU
4	SL	76	VAL
4	SL	81	LYS
4	SL	89	ARG
4	SL	93	LEU
4	SL	118	ARG
4	SL	125	ILE
4	SL	132	ARG
4	SL	135	SER
4	SL	141	ASN
4	SL	143	LEU
4	SL	146	THR
5	SX	7	LEU
5	SX	45	SER
5	SX	57	VAL
5	SX	69	CYS

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Mol	Chain	Res	Type
5	SX	98	ASP
5	SX	105	PHE
5	SX	114	ASP
5	SX	129	SER
6	SG	1	MET
6	SG	23	LYS
6	SG	73	VAL
6	SG	88	ARG
6	SG	98	ARG
6	SG	102	VAL
6	SG	107	SER
6	SG	111	LEU
6	SG	112	VAL
6	SG	114	VAL
6	SG	116	LYS
6	SG	119	LYS
6	SG	124	LEU
6	SG	133	LEU
6	SG	140	ARG
6	SG	142	ARG
6	SG	145	PHE
6	SG	149	LYS
6	SG	151	ASP
6	SG	153	VAL
6	SG	154	ARG
6	SG	168	LYS
6	SG	181	THR
6	SG	186	GLN
6	SG	188	LYS
6	SG	201	LYS
6	SG	203	LYS
6	SG	215	LYS
6	SG	217	MET
6	SG	221	LYS
7	SJ	10	ARG
7	SJ	46	VAL
7	SJ	73	GLU
7	SJ	83	ARG
7	SJ	87	LEU
7	SJ	104	ASP
7	SJ	169	ARG
8	SY	16	ARG

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Mol	Chain	Res	Type
8	SY	23	MET
8	SY	34	THR
8	SY	51	THR
8	SY	63	HIS
8	SY	68	LYS
8	SY	72	PHE
8	SY	94	HIS
8	SY	97	TYR
8	SY	99	LYS
8	SY	101	LYS
8	SY	109	GLU
8	SY	110	ARG
9	Se	13	ARG
9	Se	24	LYS
9	Se	27	LYS
9	Se	37	GLN
9	Se	41	ARG
9	Se	53	LYS
10	SA	18	PHE
10	SA	25	LEU
10	SA	31	ASP
10	SA	38	ILE
10	SA	39	TYR
10	SA	40	LYS
10	SA	55	TRP
10	SA	79	SER
10	SA	130	ASP
10	SA	138	SER
10	SA	144	THR
10	SA	178	LEU
10	SA	180	ARG
10	SA	185	MET
10	SA	193	HIS
10	SA	200	ASP
10	SA	208	GLU
11	SB	38	MET
11	SB	46	LYS
11	SB	50	THR
11	SB	53	GLN
11	SB	73	ASP
11	SB	83	LYS
11	SB	85	LYS

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Mol	Chain	Res	Type
11	SB	92	GLN
11	SB	107	ARG
11	SB	131	ASP
11	SB	137	LEU
11	SB	162	ARG
11	SB	167	LYS
11	SB	174	ARG
11	SB	181	LEU
11	SB	204	ILE
11	SB	210	VAL
11	SB	211	PHE
11	SB	218	LEU
12	SH	32	MET
12	SH	44	ASN
12	SH	49	LYS
12	SH	53	VAL
12	SH	57	ARG
12	SH	58	LYS
12	SH	61	ILE
12	SH	71	SER
12	SH	72	PHE
12	SH	81	ARG
12	SH	87	PHE
12	SH	88	SER
12	SH	98	ARG
12	SH	116	ARG
12	SH	145	ARG
12	SH	163	GLN
13	SV	1	MET
13	SV	17	CYS
13	SV	18	SER
13	SV	50	PHE
13	SV	56	CYS
13	SV	62	MET
14	Sa	3	LYS
14	Sa	28	ARG
14	Sa	37	LYS
14	Sa	51	ARG
14	Sa	52	ASP
14	Sa	58	VAL
14	Sa	72	HIS
14	Sa	82	LYS

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Mol	Chain	Res	Type
14	Sa	83	VAL
14	Sa	85	ARG
14	Sa	102	ARG
15	SC	71	LYS
15	SC	75	ILE
15	SC	76	LYS
15	SC	78	LEU
15	SC	80	GLU
15	SC	86	LEU
15	SC	101	SER
15	SC	108	LYS
15	SC	117	ARG
15	SC	132	ASP
15	SC	167	ARG
15	SC	205	VAL
15	SC	229	CYS
15	SC	248	TYR
15	SC	254	ASP
15	SC	256	TRP
15	SC	267	GLN
15	SC	271	ASP
15	SC	280	VAL
16	SN	12	SER
16	SN	13	GLN
16	SN	19	ARG
16	SN	46	THR
16	SN	56	ASP
16	SN	77	SER
16	SN	87	ASP
16	SN	93	LYS
16	SN	100	LYS
16	SN	103	GLU
16	SN	133	ARG
17	SO	27	VAL
17	SO	40	THR
17	SO	60	MET
17	SO	88	LEU
17	SO	97	LEU
17	SO	98	ARG
17	SO	100	THR
17	SO	104	ARG
17	SO	122	SER

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Mol	Chain	Res	Type
17	SO	143	LYS
17	SO	151	LEU
18	SW	4	MET
18	SW	22	LYS
18	SW	57	ARG
18	SW	62	VAL
18	SW	68	ARG
18	SW	70	ASN
18	SW	80	ASP
18	SW	81	VAL
18	SW	104	LEU
18	SW	107	SER
19	Sb	17	ARG
19	Sb	27	SER
19	Sb	33	MET
19	Sb	36	LYS
19	Sb	37	CYS
19	Sb	41	TYR
19	Sb	56	CYS
19	Sb	74	THR
23	LA	15	VAL
23	LA	32	VAL
23	LA	45	VAL
23	LA	54	ARG
23	LA	68	ARG
23	LA	80	GLU
23	LA	101	VAL
23	LA	102	LEU
23	LA	114	CYS
23	LA	135	THR
23	LA	155	LYS
23	LA	159	SER
23	LA	198	ARG
23	LA	207	VAL
23	LA	223	SER
23	LA	228	ASP
23	LA	245	ARG
24	LB	17	LEU
24	LB	22	SER
24	LB	43	LEU
24	LB	103	LYS
24	LB	112	ASP

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Mol	Chain	Res	Type
24	LB	120	LYS
24	LB	125	SER
24	LB	126	LYS
24	LB	159	VAL
24	LB	174	ARG
24	LB	200	ARG
24	LB	258	HIS
24	LB	268	ARG
24	LB	278	THR
24	LB	307	TYR
24	LB	328	ASN
24	LB	329	ASP
24	LB	340	THR
24	LB	348	ARG
24	LB	360	LEU
24	LB	366	LYS
24	LB	378	ARG
24	LB	394	LYS
25	LC	3	CYS
25	LC	23	THR
25	LC	63	SER
25	LC	71	ARG
25	LC	122	TYR
25	LC	154	VAL
25	LC	166	GLU
25	LC	186	SER
25	LC	188	ARG
25	LC	200	ARG
25	LC	235	LEU
25	LC	254	GLU
25	LC	259	LYS
25	LC	261	ASP
25	LC	267	TRP
25	LC	268	ARG
25	LC	290	SER
25	LC	307	LYS
25	LC	313	VAL
26	LD	45	ASN
26	LD	76	CYS
26	LD	86	TYR
26	LD	116	ASP
26	LD	184	ASP

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Mol	Chain	Res	Type
26	LD	187	SER
26	LD	196	ARG
26	LD	212	MET
26	LD	224	SER
26	LD	228	LYS
26	LD	239	MET
26	LD	256	LYS
26	LD	259	LYS
26	LD	265	ARG
26	LD	286	SER
27	LE	49	VAL
27	LE	71	ARG
27	LE	100	LYS
27	LE	109	LEU
27	LE	111	LYS
27	LE	128	HIS
27	LE	130	LYS
27	LE	158	ARG
27	LE	214	ASP
27	LE	221	LYS
27	LE	226	ARG
27	LE	234	ASP
27	LE	239	LYS
27	LE	240	TYR
27	LE	250	GLN
27	LE	251	LYS
27	LE	261	ILE
27	LE	264	ILE
27	LE	278	THR
28	LF	34	ARG
28	LF	48	LYS
28	LF	99	ASN
28	LF	119	ASN
28	LF	152	GLU
28	LF	200	ARG
28	LF	232	ASP
28	LF	237	GLU
29	LG	85	GLN
29	LG	89	ARG
29	LG	97	LYS
29	LG	106	THR
29	LG	112	GLN

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Mol	Chain	Res	Type
29	LG	113	ARG
29	LG	131	LYS
29	LG	159	HIS
29	LG	204	PHE
29	LG	207	VAL
29	LG	231	ASP
29	LG	234	ARG
29	LG	249	ARG
29	LG	259	LYS
29	LG	261	LEU
30	LH	8	GLN
30	LH	16	VAL
30	LH	46	SER
30	LH	50	LYS
30	LH	51	LYS
30	LH	84	VAL
30	LH	94	SER
30	LH	95	VAL
30	LH	112	VAL
30	LH	126	VAL
30	LH	135	SER
30	LH	140	GLN
30	LH	184	LYS
31	LI	44	ASP
31	LI	71	CYS
31	LI	82	ARG
31	LI	133	GLN
31	LI	136	MET
31	LI	162	ARG
31	LI	168	SER
31	LI	179	ASP
31	LI	188	LYS
31	LI	207	ASP
31	LI	210	ARG
31	LI	214	SER
32	LJ	15	LEU
32	LJ	38	LYS
32	LJ	47	THR
32	LJ	60	PHE
32	LJ	63	ARG
32	LJ	65	ASN
32	LJ	67	LYS

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Mol	Chain	Res	Type
32	LJ	72	CYS
32	LJ	95	ARG
32	LJ	96	LYS
32	LJ	104	ASN
32	LJ	115	LEU
32	LJ	118	LYS
32	LJ	128	LEU
32	LJ	154	LYS
32	LJ	164	ARG
33	LL	59	VAL
33	LL	64	VAL
33	LL	67	HIS
33	LL	70	VAL
33	LL	79	GLU
33	LL	90	VAL
33	LL	103	ARG
33	LL	106	SER
33	LL	135	LYS
33	LL	142	GLU
33	LL	158	ARG
33	LL	184	MET
33	LL	190	ARG
34	LM	4	ARG
34	LM	35	ARG
34	LM	45	VAL
34	LM	104	MET
34	LM	121	ARG
34	LM	132	LYS
35	LN	18	VAL
35	LN	20	ARG
35	LN	118	SER
35	LN	126	THR
35	LN	147	ASP
36	LO	27	VAL
36	LO	29	LEU
36	LO	32	LYS
36	LO	37	ARG
36	LO	67	SER
36	LO	127	VAL
36	LO	140	ARG
36	LO	180	GLN
36	LO	188	LYS

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Mol	Chain	Res	Type
36	LO	189	ILE
37	LP	18	ARG
37	LP	20	SER
37	LP	23	ARG
37	LP	24	VAL
37	LP	30	ARG
37	LP	57	CYS
37	LP	58	VAL
37	LP	69	ARG
37	LP	80	GLN
37	LP	100	SER
37	LP	108	ASP
37	LP	113	VAL
37	LP	139	TYR
37	LP	141	SER
38	LQ	28	LEU
38	LQ	62	SER
38	LQ	79	THR
38	LQ	82	VAL
38	LQ	124	ASP
38	LQ	137	VAL
38	LQ	150	ARG
38	LQ	164	LYS
39	LS	31	ARG
39	LS	48	VAL
39	LS	54	MET
39	LS	70	LYS
39	LS	76	LYS
39	LS	111	ARG
39	LS	154	LEU
39	LS	164	LYS
39	LS	169	THR
40	LT	5	LYS
40	LT	45	MET
40	LT	68	THR
40	LT	69	GLN
40	LT	83	LYS
40	LT	102	ARG
40	LT	111	GLU
40	LT	127	GLN
40	LT	137	GLU
40	LT	158	PHE

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Mol	Chain	Res	Type
41	LU	19	LEU
41	LU	20	LYS
41	LU	21	PHE
41	LU	34	MET
41	LU	62	THR
41	LU	66	SER
41	LU	69	LYS
41	LU	76	VAL
41	LU	94	ASN
41	LU	97	ARG
41	LU	99	TRP
41	LU	109	SER
41	LU	110	TYR
41	LU	116	GLN
42	LV	25	VAL
42	LV	48	ARG
42	LV	67	LYS
42	LV	72	LEU
42	LV	91	LYS
42	LV	94	VAL
42	LV	101	ASN
42	LV	115	SER
42	LV	135	ASN
43	LX	43	SER
43	LX	67	ARG
43	LX	68	ARG
43	LX	88	LYS
43	LX	111	GLN
43	LX	121	VAL
44	LY	9	SER
44	LY	44	VAL
44	LY	46	SER
44	LY	74	TYR
44	LY	84	ARG
44	LY	125	SER
45	LZ	19	SER
45	LZ	39	SER
45	LZ	53	VAL
45	LZ	60	LYS
45	LZ	67	LYS
45	LZ	84	ARG
45	LZ	85	TYR

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Mol	Chain	Res	Type
45	LZ	88	ASP
45	LZ	90	PRO
45	LZ	94	THR
45	LZ	100	VAL
45	LZ	112	ARG
45	LZ	127	ASN
45	LZ	128	LYS
46	La	12	ARG
46	La	16	SER
46	La	61	TYR
46	La	92	LYS
46	La	95	THR
47	Lb	4	SER
47	Lb	9	THR
47	Lb	26	SER
47	Lb	27	GLN
47	Lb	43	MET
47	Lb	51	LYS
47	Lb	55	LYS
47	Lb	58	GLN
47	Lb	65	MET
47	Lb	92	LYS
47	Lb	93	LEU
47	Lb	103	LYS
47	Lb	107	ARG
47	Lb	117	ARG
48	Lc	9	LYS
48	Lc	23	LYS
48	Lc	26	LYS
48	Lc	58	SER
48	Lc	91	VAL
48	Lc	93	THR
48	Lc	94	LEU
49	Ld	22	THR
49	Ld	26	THR
49	Ld	51	LYS
49	Ld	54	MET
49	Ld	63	ARG
49	Ld	95	ASP
49	Ld	100	ASN
49	Ld	106	VAL
49	Ld	112	THR

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Mol	Chain	Res	Type
49	Ld	116	ASN
49	Ld	121	ASN
49	Ld	123	ASP
50	Le	11	LYS
50	Le	25	SER
50	Le	57	ASN
50	Le	93	LYS
50	Le	94	SER
50	Le	102	ASN
50	Le	117	GLN
51	Lf	14	TYR
51	Lf	25	THR
51	Lf	33	VAL
52	Lg	20	THR
52	Lg	32	TYR
52	Lg	63	VAL
52	Lg	75	SER
52	Lg	110	GLN
53	Lh	3	LYS
53	Lh	8	ASP
53	Lh	20	GLN
53	Lh	23	ASP
53	Lh	31	LEU
53	Lh	32	ARG
53	Lh	45	SER
53	Lh	74	LYS
53	Lh	81	LEU
53	Lh	82	ASP
53	Lh	100	GLU
53	Lh	109	ARG
53	Lh	121	VAL
54	Li	23	LYS
54	Li	48	CYS
54	Li	99	LYS
55	Lj	2	THR
55	Lj	20	ARG
55	Lj	22	CYS
55	Lj	32	SER
55	Lj	42	LYS
55	Lj	55	ARG
55	Lj	63	ARG
55	Lj	83	THR

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Mol	Chain	Res	Type
56	Lk	9	LYS
56	Lk	16	ARG
56	Lk	45	LEU
56	Lk	57	LYS
56	Lk	67	LYS
57	Ll	10	LYS
57	Ll	21	ARG
57	Ll	37	TYR
57	Ll	45	ARG
57	Ll	47	THR
58	Lm	85	LEU
58	Lm	94	MET
59	Ln	15	ARG
59	Ln	21	ARG
60	Lo	15	CYS
60	Lo	31	ASP
60	Lo	57	ARG
60	Lo	77	CYS
60	Lo	99	ARG
61	Lp	47	MET
61	Lp	77	VAL
62	Lr	8	MET
62	Lr	14	SER
62	Lr	21	ASN
62	Lr	35	ARG
62	Lr	37	SER
62	Lr	46	ARG
62	Lr	49	VAL
62	Lr	58	LYS
62	Lr	60	VAL
62	Lr	80	THR
62	Lr	81	THR
62	Lr	83	ASN
62	Lr	122	LYS
63	SR	1	MET
63	SR	4	VAL
63	SR	5	ARG
63	SR	22	THR
63	SR	33	ARG
63	SR	43	SER
63	SR	49	LYS
63	SR	63	ARG

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Mol	Chain	Res	Type
63	SR	70	SER
63	SR	73	LEU
63	SR	75	GLU
63	SR	78	ARG
63	SR	81	ARG
63	SR	87	GLU
63	SR	91	LEU
63	SR	111	PHE
63	SR	115	SER
63	SR	117	LEU
63	SR	123	THR
64	SD	17	PHE
64	SD	24	PHE
64	SD	27	ARG
64	SD	32	ASP
64	SD	40	ARG
64	SD	42	THR
64	SD	61	GLU
64	SD	79	PHE
64	SD	84	VAL
64	SD	85	GLU
64	SD	105	LEU
64	SD	107	TYR
64	SD	129	SER
64	SD	134	CYS
64	SD	136	VAL
64	SD	139	SER
64	SD	143	ARG
64	SD	146	ARG
64	SD	148	LYS
64	SD	153	VAL
64	SD	167	TYR
64	SD	170	THR
64	SD	176	LEU
64	SD	178	ARG
64	SD	197	LYS
64	SD	214	LYS
64	SD	221	THR
64	SD	227	LYS
65	SF	16	ASP
65	SF	19	LEU
65	SF	20	PHE

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Mol	Chain	Res	Type
65	SF	22	LYS
65	SF	42	LYS
65	SF	45	TYR
65	SF	83	ASN
65	SF	88	MET
65	SF	110	GLN
65	SF	127	ARG
65	SF	136	ARG
65	SF	142	SER
65	SF	147	VAL
65	SF	160	GLU
65	SF	185	SER
65	SF	204	ARG
66	SK	3	MET
66	SK	21	MET
66	SK	45	VAL
66	SK	46	MET
66	SK	50	GLN
66	SK	52	LEU
66	SK	59	LYS
66	SK	71	LEU
66	SK	85	LEU
66	SK	95	ARG
67	SP	33	LEU
67	SP	34	MET
67	SP	37	TYR
67	SP	52	LYS
67	SP	64	LYS
67	SP	65	LYS
67	SP	70	MET
67	SP	81	ARG
67	SP	83	MET
67	SP	89	MET
67	SP	97	TYR
67	SP	109	PRO
67	SP	126	VAL
67	SP	127	LYS
68	SQ	22	VAL
68	SQ	25	CYS
68	SQ	41	MET
68	SQ	62	ARG
68	SQ	71	ARG

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Mol	Chain	Res	Type
68	SQ	73	LYS
68	SQ	87	SER
68	SQ	96	TYR
68	SQ	117	ARG
68	SQ	118	THR
68	SQ	127	CYS
68	SQ	129	SER
69	SS	23	ARG
69	SS	31	THR
69	SS	38	ARG
69	SS	65	GLU
69	SS	81	ASP
69	SS	83	PHE
69	SS	104	ASP
69	SS	105	ASN
69	SS	106	LYS
69	SS	109	GLU
69	SS	118	ARG
69	SS	145	THR
70	ST	6	VAL
70	ST	41	LYS
70	ST	44	GLU
70	ST	51	ASN
70	ST	67	ARG
70	ST	87	VAL
70	ST	93	SER
70	ST	102	ARG
70	ST	111	LYS
70	ST	112	MET
70	ST	116	ASP
70	ST	122	LYS
70	ST	128	GLN
70	ST	129	ARG
70	ST	133	ARG
71	SU	19	ARG
71	SU	23	THR
71	SU	36	CYS
71	SU	62	ARG
71	SU	78	ASP
71	SU	86	LYS
72	Sc	13	ARG
72	Sc	26	GLN

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Mol	Chain	Res	Type
72	Sc	31	ARG
72	Sc	40	ARG
73	Sd	3	HIS
73	Sd	27	ARG
73	Sd	37	ASN
73	Sd	40	ARG
73	Sd	48	LYS
73	Sd	54	LYS
74	Sg	2	THR
74	Sg	14	HIS
74	Sg	20	GLN
74	Sg	24	THR
74	Sg	25	PRO
74	Sg	26	GLN
74	Sg	27	PHE
74	Sg	38	LYS
74	Sg	42	MET
74	Sg	47	ARG
74	Sg	60	ARG
74	Sg	64	HIS
74	Sg	79	LEU
74	Sg	80	SER
74	Sg	84	ASP
74	Sg	92	LEU
74	Sg	96	THR
74	Sg	107	ASP
74	Sg	113	PHE
74	Sg	124	SER
74	Sg	129	ILE
74	Sg	130	LYS
74	Sg	138	CYS
74	Sg	140	TYR
74	Sg	151	VAL
74	Sg	166	VAL
74	Sg	218	LEU
74	Sg	222	ASN
74	Sg	230	LEU
74	Sg	234	ASP
74	Sg	245	ARG
74	Sg	249	CYS
74	Sg	259	TRP
74	Sg	260	ASP

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Mol	Chain	Res	Type
74	Sg	271	LYS
74	Sg	306	LEU
75	SM	33	ARG
75	SM	45	ARG
75	SM	60	MET
75	SM	61	TYR
75	SM	62	VAL
75	SM	69	CYS
75	SM	84	LYS
75	SM	111	VAL
75	SM	112	LYS
75	SM	121	LYS
75	SM	127	TYR
76	SZ	50	PHE
76	SZ	55	TYR
76	SZ	65	TYR
76	SZ	76	ARG
76	SZ	77	LEU
76	SZ	78	LYS
76	SZ	112	ASN
77	Sf	89	LYS
77	Sf	100	LEU
77	Sf	110	GLU
77	Sf	116	ARG
77	Sf	138	ARG
77	Sf	141	CYS
77	Sf	144	CYS
77	Sf	146	LEU
81	Lt	15	LEU
81	Lt	52	ASP
81	Lt	62	LEU
81	Lt	78	SER
81	Lt	104	ILE
81	Lt	150	ASP
81	Lt	162	CYS
82	Lz	28	PHE
82	Lz	54	ARG
82	Lz	63	PHE
82	Lz	90	LEU
82	Lz	102	LYS
82	Lz	113	SER
82	Lz	123	ILE

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Mol	Chain	Res	Type
82	Lz	144	MET
82	Lz	145	VAL
82	Lz	156	LYS
82	Lz	161	LYS
82	Lz	171	HIS
82	Lz	173	LYS
82	Lz	178	GLU
82	Lz	210	MET
82	Lz	212	LYS
82	Lz	216	LEU
83	Ls	14	PHE
83	Ls	16	LYS
83	Ls	29	ILE
83	Ls	53	VAL
83	Ls	54	LEU
83	Ls	55	MET
83	Ls	61	MET
83	Ls	78	LEU
83	Ls	99	ARG
83	Ls	102	LEU
83	Ls	106	LYS
83	Ls	118	PRO
83	Ls	119	CYS
83	Ls	146	LYS
84	LW	17	HIS
84	LW	19	ARG
84	LW	30	GLN
84	LW	50	ASN
84	LW	58	LYS
84	LW	77	LYS
84	LW	94	ARG
84	LW	110	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
6	SG	56	ASN
6	SG	186	GLN
7	SJ	154	GLN
13	SV	21	ASN
17	SO	32	HIS
17	SO	79	GLN

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Mol	Chain	Res	Type
18	SW	98	GLN
26	LD	275	GLN
27	LE	250	GLN
37	LP	80	GLN
37	LP	118	GLN
37	LP	120	ASN
42	LV	84	GLN
43	LX	93	ASN
47	Lb	58	GLN
62	Lr	23	GLN
63	SR	31	ASN
66	SK	44	HIS
68	SQ	80	GLN
74	Sg	188	HIS
83	Ls	39	GLN
83	Ls	81	HIS
83	Ls	127	ASN
83	Ls	159	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	L5	3704/5070 (73%)	883 (23%)	20 (0%)
21	L7	119/120 (99%)	13 (10%)	0
22	L8	155/156 (99%)	29 (18%)	0
78	S2	1715/1740 (98%)	437 (25%)	7 (0%)
79	Et	73/76 (96%)	30 (41%)	0
80	Pt	72/76 (94%)	19 (26%)	0
All	All	5838/7238 (80%)	1411 (24%)	27 (0%)

All (1411) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	L5	2	G
20	L5	13	U
20	L5	17	A
20	L5	25	A
20	L5	26	C
20	L5	30	C
20	L5	39	A
20	L5	42	A

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Mol	Chain	Res	Type
20	L5	48	G
20	L5	56	A
20	L5	59	A
20	L5	64	A
20	L5	65	A
20	L5	66	A
20	L5	69	A
20	L5	73	A
20	L5	74	G
20	L5	91	G
20	L5	98	A
20	L5	104	G
20	L5	108	A
20	L5	109	G
20	L5	110	C
20	L5	119	G
20	L5	120	A
20	L5	132	G
20	L5	133	C
20	L5	134	G
20	L5	135	G
20	L5	145	G
20	L5	152	U
20	L5	157	U
20	L5	159	C
20	L5	165	A
20	L5	175	C
20	L5	182	G
20	L5	183	C
20	L5	184	U
20	L5	185	C
20	L5	187	U
20	L5	188	G
20	L5	189	G
20	L5	200	U
20	L5	209	U
20	L5	216	C
20	L5	218	A
20	L5	220	C
20	L5	234	G
20	L5	237	G
20	L5	250	C

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Mol	Chain	Res	Type
20	L5	255	C
20	L5	256	G
20	L5	261	G
20	L5	263	G
20	L5	264	C
20	L5	265	C
20	L5	266	C
20	L5	267	G
20	L5	269	G
20	L5	276	C
20	L5	280	G
20	L5	297	U
20	L5	306	A
20	L5	315	G
20	L5	316	U
20	L5	326	C
20	L5	340	C
20	L5	350	C
20	L5	373	G
20	L5	387	G
20	L5	388	A
20	L5	407	A
20	L5	409	G
20	L5	410	A
20	L5	412	G
20	L5	415	G
20	L5	431	G
20	L5	432	U
20	L5	433	A
20	L5	449	C
20	L5	450	G
20	L5	452	A
20	L5	453	G
20	L5	454	U
20	L5	456	C
20	L5	457	G
20	L5	465	G
20	L5	467	U
20	L5	468	U
20	L5	485	C
20	L5	486	C
20	L5	489	C

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Mol	Chain	Res	Type
20	L5	491	G
20	L5	493	G
20	L5	494	U
20	L5	497	G
20	L5	498	C
20	L5	499	G
20	L5	500	G
20	L5	501	C
20	L5	502	C
20	L5	503	C
20	L5	504	G
20	L5	505	G
20	L5	509	A
20	L5	510	U
20	L5	512	U
20	L5	513	U
20	L5	514	U
20	L5	517	C
20	L5	518	G
20	L5	643	C
20	L5	646	G
20	L5	654	C
20	L5	655	C
20	L5	656	C
20	L5	657	C
20	L5	659	G
20	L5	666	G
20	L5	667	A
20	L5	668	C
20	L5	669	C
20	L5	672	C
20	L5	673	C
20	L5	685	C
20	L5	686	A
20	L5	687	U
20	L5	696	C
20	L5	697	G
20	L5	703	G
20	L5	704	C
20	L5	706	C
20	L5	730	G
20	L5	731	G

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Mol	Chain	Res	Type
20	L5	738	C
20	L5	739	G
20	L5	742	G
20	L5	744	G
20	L5	753	C
20	L5	759	G
20	L5	904	C
20	L5	905	C
20	L5	906	C
20	L5	911	U
20	L5	912	G
20	L5	913	U
20	L5	914	U
20	L5	915	A
20	L5	916	C
20	L5	917	A
20	L5	918	G
20	L5	923	C
20	L5	924	C
20	L5	926	G
20	L5	932	A
20	L5	933	G
20	L5	935	A
20	L5	936	C
20	L5	944	A
20	L5	945	U
20	L5	946	C
20	L5	958	G
20	L5	959	G
20	L5	960	A
20	L5	961	G
20	L5	962	C
20	L5	965	G
20	L5	966	A
20	L5	967	C
20	L5	969	C
20	L5	970	G
20	L5	982	U
20	L5	985	C
20	L5	989	U
20	L5	990	C
20	L5	992	C

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Mol	Chain	Res	Type
20	L5	993	G
20	L5	995	C
20	L5	1048	G
20	L5	1049	C
20	L5	1050	C
20	L5	1051	G
20	L5	1066	G
20	L5	1070	G
20	L5	1071	C
20	L5	1072	C
20	L5	1075	G
20	L5	1082	C
20	L5	1083	U
20	L5	1095	A
20	L5	1168	G
20	L5	1171	G
20	L5	1172	C
20	L5	1173	G
20	L5	1179	U
20	L5	1180	C
20	L5	1182	C
20	L5	1183	C
20	L5	1200	G
20	L5	1202	C
20	L5	1203	G
20	L5	1205	G
20	L5	1210	C
20	L5	1211	G
20	L5	1214	C
20	L5	1215	C
20	L5	1217	G
20	L5	1218	G
20	L5	1219	G
20	L5	1221	G
20	L5	1222	A
20	L5	1235	G
20	L5	1241	C
20	L5	1242	G
20	L5	1246	G
20	L5	1253	G
20	L5	1254	A
20	L5	1257	A

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Mol	Chain	Res	Type
20	L5	1258	G
20	L5	1266	G
20	L5	1267	C
20	L5	1269	G
20	L5	1270	A
20	L5	1271	G
20	L5	1272	C
20	L5	1273	G
20	L5	1275	G
20	L5	1277	G
20	L5	1280	C
20	L5	1284	G
20	L5	1285	U
20	L5	1287	G
20	L5	1293	G
20	L5	1294	A
20	L5	1295	C
20	L5	1296	G
20	L5	1301	C
20	L5	1325	C
20	L5	1326	A
20	L5	1337	A
20	L5	1345	A
20	L5	1354	A
20	L5	1358	G
20	L5	1359	G
20	L5	1365	C
20	L5	1367	C
20	L5	1387	A
20	L5	1394	G
20	L5	1397	A
20	L5	1405	C
20	L5	1407	C
20	L5	1408	G
20	L5	1409	C
20	L5	1410	U
20	L5	1411	C
20	L5	1414	C
20	L5	1415	G
20	L5	1417	C
20	L5	1420	A
20	L5	1435	G

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Mol	Chain	Res	Type
20	L5	1437	C
20	L5	1439	C
20	L5	1441	C
20	L5	1443	A
20	L5	1444	G
20	L5	1446	C
20	L5	1447	C
20	L5	1482	G
20	L5	1483	C
20	L5	1497	A
20	L5	1498	G
20	L5	1502	G
20	L5	1517	G
20	L5	1518	A
20	L5	1534	A
20	L5	1535	C
20	L5	1547	A
20	L5	1562	G
20	L5	1564	A
20	L5	1566	C
20	L5	1578	U
20	L5	1582	U
20	L5	1591	U
20	L5	1596	U
20	L5	1621	A
20	L5	1624	G
20	L5	1625	G
20	L5	1631	A
20	L5	1633	G
20	L5	1634	A
20	L5	1638	A
20	L5	1640	C
20	L5	1641	G
20	L5	1642	A
20	L5	1654	G
20	L5	1661	C
20	L5	1663	C
20	L5	1676	C
20	L5	1677	U
20	L5	1678	C
20	L5	1681	G
20	L5	1685	G

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Mol	Chain	Res	Type
20	L5	1698	C
20	L5	1699	A
20	L5	1700	G
20	L5	1703	C
20	L5	1704	C
20	L5	1705	G
20	L5	1707	C
20	L5	1708	G
20	L5	1718	C
20	L5	1726	U
20	L5	1731	C
20	L5	1740	C
20	L5	1741	G
20	L5	1742	A
20	L5	1750	G
20	L5	1753	G
20	L5	1757	U
20	L5	1758	G
20	L5	1760	G
20	L5	1761	G
20	L5	1762	C
20	L5	1763	C
20	L5	1764	G
20	L5	1765	A
20	L5	1766	A
20	L5	1767	A
20	L5	1768	C
20	L5	1769	G
20	L5	1770	A
20	L5	1787	A
20	L5	1797	G
20	L5	1804	A
20	L5	1806	G
20	L5	1810	G
20	L5	1815	G
20	L5	1820	C
20	L5	1821	G
20	L5	1822	U
20	L5	1836	G
20	L5	1837	A
20	L5	1842	G
20	L5	1843	A

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Mol	Chain	Res	Type
20	L5	1855	G
20	L5	1869	G
20	L5	1882	U
20	L5	1892	A
20	L5	1893	C
20	L5	1897	A
20	L5	1918	U
20	L5	1919	G
20	L5	1920	C
20	L5	1921	C
20	L5	1922	G
20	L5	1925	G
20	L5	1931	C
20	L5	1932	A
20	L5	1936	C
20	L5	1940	G
20	L5	1948	G
20	L5	1949	U
20	L5	1951	G
20	L5	1961	G
20	L5	1962	A
20	L5	1973	G
20	L5	1974	U
20	L5	1975	G
20	L5	1978	C
20	L5	1980	U
20	L5	1981	G
20	L5	1982	G
20	L5	1984	A
20	L5	1985	G
20	L5	1986	U
20	L5	1991	A
20	L5	1992	U
20	L5	1993	C
20	L5	1997	U
20	L5	1998	A
20	L5	1999	A
20	L5	2001	G
20	L5	2002	A
20	L5	2003	G
20	L5	2011	C
20	L5	2017	A

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Mol	Chain	Res	Type
20	L5	2018	C
20	L5	2026	A
20	L5	2033	A
20	L5	2034	G
20	L5	2046	G
20	L5	2048	U
20	L5	2055	G
20	L5	2056	G
20	L5	2069	A
20	L5	2084	C
20	L5	2085	G
20	L5	2092	G
20	L5	2093	A
20	L5	2094	G
20	L5	2095	A
20	L5	2097	U
20	L5	2098	G
20	L5	2101	C
20	L5	2102	G
20	L5	2103	G
20	L5	2105	A
20	L5	2107	C
20	L5	2108	G
20	L5	2110	C
20	L5	2112	G
20	L5	2250	C
20	L5	2252	G
20	L5	2253	A
20	L5	2256	C
20	L5	2257	C
20	L5	2258	C
20	L5	2260	C
20	L5	2261	G
20	L5	2262	G
20	L5	2263	A
20	L5	2289	C
20	L5	2300	A
20	L5	2301	G
20	L5	2313	A
20	L5	2333	G
20	L5	2345	G
20	L5	2348	G

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Mol	Chain	Res	Type
20	L5	2351	C
20	L5	2360	A
20	L5	2364	G
20	L5	2389	A
20	L5	2395	A
20	L5	2397	G
20	L5	2402	G
20	L5	2408	U
20	L5	2411	C
20	L5	2412	A
20	L5	2417	A
20	L5	2421	G
20	L5	2425	U
20	L5	2441	C
20	L5	2450	G
20	L5	2453	A
20	L5	2464	C
20	L5	2465	C
20	L5	2469	C
20	L5	2474	G
20	L5	2475	G
20	L5	2478	C
20	L5	2479	G
20	L5	2483	G
20	L5	2484	A
20	L5	2485	U
20	L5	2486	G
20	L5	2487	G
20	L5	2488	C
20	L5	2489	C
20	L5	2494	U
20	L5	2503	G
20	L5	2504	C
20	L5	2505	C
20	L5	2506	G
20	L5	2513	A
20	L5	2519	U
20	L5	2520	C
20	L5	2529	A
20	L5	2536	A
20	L5	2537	A
20	L5	2544	G

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Mol	Chain	Res	Type
20	L5	2546	G
20	L5	2547	G
20	L5	2554	U
20	L5	2556	G
20	L5	2560	C
20	L5	2565	A
20	L5	2573	A
20	L5	2583	C
20	L5	2587	A
20	L5	2589	C
20	L5	2601	A
20	L5	2618	G
20	L5	2627	C
20	L5	2652	G
20	L5	2653	C
20	L5	2662	G
20	L5	2669	C
20	L5	2670	C
20	L5	2675	G
20	L5	2676	A
20	L5	2686	G
20	L5	2687	U
20	L5	2694	G
20	L5	2695	A
20	L5	2696	A
20	L5	2703	G
20	L5	2707	U
20	L5	2708	U
20	L5	2709	C
20	L5	2710	C
20	L5	2711	G
20	L5	2712	G
20	L5	2721	G
20	L5	2724	G
20	L5	2726	G
20	L5	2738	C
20	L5	2739	C
20	L5	2742	G
20	L5	2743	A
20	L5	2746	A
20	L5	2761	U
20	L5	2762	G

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Mol	Chain	Res	Type
20	L5	2763	U
20	L5	2764	A
20	L5	2769	U
20	L5	2770	C
20	L5	2782	U
20	L5	2787	A
20	L5	2788	U
20	L5	2790	U
20	L5	2806	A
20	L5	2814	C
20	L5	2815	A
20	L5	2826	U
20	L5	2827	G
20	L5	2833	A
20	L5	2847	G
20	L5	2848	G
20	L5	2855	G
20	L5	2867	C
20	L5	2877	G
20	L5	2892	C
20	L5	2894	A
20	L5	2895	A
20	L5	2899	C
20	L5	2900	U
20	L5	2902	G
20	L5	2903	G
20	L5	2904	U
20	L5	2905	C
20	L5	2906	G
20	L5	2908	U
20	L5	3585	G
20	L5	3586	G
20	L5	3590	G
20	L5	3591	C
20	L5	3594	C
20	L5	3595	U
20	L5	3596	A
20	L5	3597	G
20	L5	3605	C
20	L5	3615	G
20	L5	3616	U
20	L5	3618	C

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Mol	Chain	Res	Type
20	L5	3626	G
20	L5	3630	A
20	L5	3635	A
20	L5	3644	U
20	L5	3646	A
20	L5	3648	A
20	L5	3650	C
20	L5	3662	A
20	L5	3664	G
20	L5	3670	C
20	L5	3672	G
20	L5	3673	C
20	L5	3674	G
20	L5	3675	G
20	L5	3711	A
20	L5	3713	U
20	L5	3714	G
20	L5	3727	A
20	L5	3740	G
20	L5	3748	A
20	L5	3750	G
20	L5	3753	G
20	L5	3756	A
20	L5	3757	G
20	L5	3758	U
20	L5	3759	A
20	L5	3760	A
20	L5	3761	C
20	L5	3766	A
20	L5	3767	C
20	L5	3772	U
20	L5	3773	U
20	L5	3776	G
20	L5	3777	G
20	L5	3784	A
20	L5	3786	U
20	L5	3788	C
20	L5	3802	U
20	L5	3811	G
20	L5	3812	C
20	L5	3813	A
20	L5	3814	U

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Mol	Chain	Res	Type
20	L5	3817	A
20	L5	3818	U
20	L5	3819	G
20	L5	3823	G
20	L5	3838	U
20	L5	3839	G
20	L5	3840	U
20	L5	3841	C
20	L5	3867	A
20	L5	3877	A
20	L5	3878	C
20	L5	3879	G
20	L5	3880	G
20	L5	3885	G
20	L5	3887	C
20	L5	3890	A
20	L5	3892	U
20	L5	3897	G
20	L5	3898	G
20	L5	3901	A
20	L5	3906	A
20	L5	3907	G
20	L5	3908	A
20	L5	3915	U
20	L5	3938	G
20	L5	3939	G
20	L5	3943	A
20	L5	3944	G
20	L5	3947	A
20	L5	3948	C
20	L5	3949	A
20	L5	3951	G
20	L5	3953	G
20	L5	3955	G
20	L5	3956	G
20	L5	3957	U
20	L5	3959	U
20	L5	3960	A
20	L5	3962	A
20	L5	3963	A
20	L5	3964	U
20	L5	3965	A

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Mol	Chain	Res	Type
20	L5	3966	A
20	L5	3968	U
20	L5	3969	G
20	L5	3971	G
20	L5	3973	G
20	L5	3974	G
20	L5	3975	C
20	L5	3976	C
20	L5	3977	C
20	L5	4034	G
20	L5	4037	C
20	L5	4038	C
20	L5	4039	G
20	L5	4041	C
20	L5	4042	G
20	L5	4043	G
20	L5	4044	U
20	L5	4046	A
20	L5	4047	A
20	L5	4048	A
20	L5	4049	U
20	L5	4050	A
20	L5	4051	C
20	L5	4052	C
20	L5	4053	A
20	L5	4054	C
20	L5	4055	U
20	L5	4057	C
20	L5	4058	U
20	L5	4059	C
20	L5	4060	U
20	L5	4061	G
20	L5	4062	A
20	L5	4063	U
20	L5	4065	G
20	L5	4067	U
20	L5	4068	U
20	L5	4069	U
20	L5	4076	G
20	L5	4084	G
20	L5	4092	G
20	L5	4093	G

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Mol	Chain	Res	Type
20	L5	4096	C
20	L5	4097	G
20	L5	4099	G
20	L5	4102	C
20	L5	4104	G
20	L5	4107	G
20	L5	4108	G
20	L5	4111	U
20	L5	4114	C
20	L5	4115	G
20	L5	4116	C
20	L5	4117	U
20	L5	4119	C
20	L5	4121	G
20	L5	4122	G
20	L5	4127	A
20	L5	4133	C
20	L5	4134	C
20	L5	4138	C
20	L5	4140	C
20	L5	4141	G
20	L5	4142	C
20	L5	4143	G
20	L5	4144	C
20	L5	4146	G
20	L5	4149	C
20	L5	4150	G
20	L5	4157	A
20	L5	4160	C
20	L5	4162	C
20	L5	4163	U
20	L5	4166	G
20	L5	4168	G
20	L5	4170	A
20	L5	4177	C
20	L5	4183	G
20	L5	4184	G
20	L5	4191	G
20	L5	4196	G
20	L5	4197	G
20	L5	4201	G
20	L5	4203	A

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Mol	Chain	Res	Type
20	L5	4212	A
20	L5	4214	A
20	L5	4222	G
20	L5	4229	U
20	L5	4232	U
20	L5	4233	A
20	L5	4242	U
20	L5	4249	G
20	L5	4251	A
20	L5	4254	G
20	L5	4255	A
20	L5	4257	A
20	L5	4258	C
20	L5	4265	U
20	L5	4268	A
20	L5	4273	A
20	L5	4281	A
20	L5	4282	A
20	L5	4296	U
20	L5	4304	A
20	L5	4305	G
20	L5	4314	C
20	L5	4319	C
20	L5	4330	G
20	L5	4332	C
20	L5	4338	G
20	L5	4349	C
20	L5	4350	C
20	L5	4354	U
20	L5	4373	G
20	L5	4376	A
20	L5	4377	G
20	L5	4378	A
20	L5	4380	A
20	L5	4387	C
20	L5	4391	G
20	L5	4394	A
20	L5	4420	U
20	L5	4422	A
20	L5	4438	U
20	L5	4448	G
20	L5	4449	A

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Mol	Chain	Res	Type
20	L5	4453	C
20	L5	4464	A
20	L5	4466	C
20	L5	4475	G
20	L5	4484	A
20	L5	4488	A
20	L5	4500	U
20	L5	4512	U
20	L5	4513	A
20	L5	4515	G
20	L5	4519	C
20	L5	4524	G
20	L5	4525	C
20	L5	4527	G
20	L5	4545	G
20	L5	4548	A
20	L5	4549	G
20	L5	4557	U
20	L5	4560	C
20	L5	4567	G
20	L5	4573	G
20	L5	4575	G
20	L5	4584	A
20	L5	4589	A
20	L5	4590	A
20	L5	4600	G
20	L5	4601	U
20	L5	4617	G
20	L5	4626	A
20	L5	4627	U
20	L5	4635	A
20	L5	4636	U
20	L5	4637	G
20	L5	4656	A
20	L5	4657	U
20	L5	4659	G
20	L5	4670	C
20	L5	4672	A
20	L5	4679	G
20	L5	4687	A
20	L5	4694	G
20	L5	4695	C

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Mol	Chain	Res	Type
20	L5	4700	A
20	L5	4708	A
20	L5	4709	U
20	L5	4719	G
20	L5	4734	A
20	L5	4740	G
20	L5	4741	C
20	L5	4742	G
20	L5	4745	G
20	L5	4750	G
20	L5	4754	G
20	L5	4757	C
20	L5	4759	C
20	L5	4761	G
20	L5	4765	G
20	L5	4771	C
20	L5	4772	C
20	L5	4773	C
20	L5	4775	C
20	L5	4867	G
20	L5	4870	G
20	L5	4871	C
20	L5	4874	A
20	L5	4875	G
20	L5	4880	C
20	L5	4881	U
20	L5	4882	U
20	L5	4883	C
20	L5	4889	G
20	L5	4895	C
20	L5	4896	G
20	L5	4897	G
20	L5	4900	C
20	L5	4901	G
20	L5	4902	C
20	L5	4909	A
20	L5	4910	G
20	L5	4912	G
20	L5	4914	C
20	L5	4918	C
20	L5	4922	C
20	L5	4923	C

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Mol	Chain	Res	Type
20	L5	4924	C
20	L5	4925	U
20	L5	4926	C
20	L5	4927	G
20	L5	4928	C
20	L5	4934	A
20	L5	4941	G
20	L5	4943	A
20	L5	4951	G
20	L5	4955	A
20	L5	4960	G
20	L5	4973	U
20	L5	4976	U
20	L5	4985	U
20	L5	4988	U
20	L5	4989	U
20	L5	4990	C
20	L5	4991	U
20	L5	5009	G
20	L5	5013	C
20	L5	5014	A
20	L5	5017	G
20	L5	5022	U
20	L5	5024	C
20	L5	5027	C
20	L5	5028	G
20	L5	5029	C
20	L5	5030	U
20	L5	5034	A
20	L5	5041	G
20	L5	5050	C
20	L5	5054	C
20	L5	5055	G
20	L5	5061	A
20	L5	5069	U
21	L7	4	U
21	L7	22	A
21	L7	33	U
21	L7	37	G
21	L7	38	U
21	L7	42	A
21	L7	53	U

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Mol	Chain	Res	Type
21	L7	54	A
21	L7	63	C
21	L7	64	G
21	L7	66	G
21	L7	100	A
21	L7	110	G
22	L8	25	G
22	L8	34	U
22	L8	35	C
22	L8	48	A
22	L8	52	A
22	L8	59	A
22	L8	62	A
22	L8	63	U
22	L8	68	G
22	L8	80	A
22	L8	82	A
22	L8	83	C
22	L8	84	A
22	L8	85	U
22	L8	86	U
22	L8	87	G
22	L8	94	G
22	L8	103	A
22	L8	105	C
22	L8	110	U
22	L8	111	U
22	L8	112	G
22	L8	114	G
22	L8	123	U
22	L8	124	U
22	L8	125	C
22	L8	126	C
22	L8	127	U
22	L8	151	G
78	S2	4	C
78	S2	17	C
78	S2	25	A
78	S2	33	G
78	S2	41	G
78	S2	44	U
78	S2	45	A

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Mol	Chain	Res	Type
78	S2	46	A
78	S2	56	G
78	S2	58	C
78	S2	59	U
78	S2	64	A
78	S2	67	C
78	S2	68	A
78	S2	72	C
78	S2	73	C
78	S2	74	G
78	S2	76	U
78	S2	92	A
78	S2	103	A
78	S2	113	G
78	S2	114	G
78	S2	115	U
78	S2	116	U
78	S2	126	G
78	S2	130	G
78	S2	139	C
78	S2	143	U
78	S2	147	A
78	S2	149	A
78	S2	155	G
78	S2	158	A
78	S2	162	C
78	S2	170	A
78	S2	171	A
78	S2	179	C
78	S2	182	C
78	S2	190	G
78	S2	192	C
78	S2	196	C
78	S2	197	U
78	S2	198	U
78	S2	200	G
78	S2	202	G
78	S2	203	G
78	S2	204	G
78	S2	206	G
78	S2	207	G
78	S2	208	G

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Mol	Chain	Res	Type
78	S2	214	U
78	S2	291	G
78	S2	292	A
78	S2	295	C
78	S2	302	A
78	S2	303	C
78	S2	305	U
78	S2	306	C
78	S2	307	G
78	S2	308	G
78	S2	309	G
78	S2	310	C
78	S2	311	C
78	S2	312	G
78	S2	316	G
78	S2	318	A
78	S2	319	C
78	S2	323	C
78	S2	324	C
78	S2	325	C
78	S2	326	C
78	S2	328	U
78	S2	329	G
78	S2	332	G
78	S2	338	G
78	S2	339	A
78	S2	340	C
78	S2	347	G
78	S2	360	A
78	S2	362	C
78	S2	363	A
78	S2	364	A
78	S2	365	C
78	S2	368	U
78	S2	369	C
78	S2	370	G
78	S2	374	G
78	S2	383	G
78	S2	385	G
78	S2	386	C
78	S2	400	C
78	S2	407	G

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Mol	Chain	Res	Type
78	S2	408	A
78	S2	409	C
78	S2	421	G
78	S2	425	G
78	S2	426	A
78	S2	438	G
78	S2	448	A
78	S2	449	A
78	S2	450	C
78	S2	452	G
78	S2	464	A
78	S2	465	A
78	S2	466	G
78	S2	471	G
78	S2	472	C
78	S2	473	A
78	S2	474	G
78	S2	476	A
78	S2	482	G
78	S2	485	A
78	S2	487	U
78	S2	488	U
78	S2	492	C
78	S2	493	A
78	S2	502	C
78	S2	530	U
78	S2	531	A
78	S2	532	C
78	S2	536	A
78	S2	537	C
78	S2	540	U
78	S2	542	U
78	S2	546	G
78	S2	547	G
78	S2	557	U
78	S2	558	G
78	S2	560	A
78	S2	563	G
78	S2	564	A
78	S2	566	U
78	S2	576	A
78	S2	583	A

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Mol	Chain	Res	Type
78	S2	587	A
78	S2	589	G
78	S2	590	A
78	S2	591	U
78	S2	593	C
78	S2	607	U
78	S2	613	G
78	S2	614	C
78	S2	617	G
78	S2	622	C
78	S2	623	G
78	S2	628	A
78	S2	631	U
78	S2	638	C
78	S2	639	C
78	S2	643	A
78	S2	644	G
78	S2	655	A
78	S2	660	C
78	S2	664	A
78	S2	668	A
78	S2	669	A
78	S2	671	A
78	S2	672	A
78	S2	673	G
78	S2	679	A
78	S2	684	G
78	S2	688	U
78	S2	689	U
78	S2	692	G
78	S2	693	A
78	S2	695	C
78	S2	696	G
78	S2	697	G
78	S2	698	G
78	S2	732	U
78	S2	733	C
78	S2	734	C
78	S2	736	C
78	S2	738	C
78	S2	749	U
78	S2	751	G

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Mol	Chain	Res	Type
78	S2	752	G
78	S2	753	C
78	S2	788	G
78	S2	789	G
78	S2	791	C
78	S2	792	C
78	S2	794	A
78	S2	797	C
78	S2	798	G
78	S2	799	U
78	S2	801	U
78	S2	821	G
78	S2	822	U
78	S2	823	U
78	S2	824	C
78	S2	830	A
78	S2	833	C
78	S2	834	C
78	S2	835	C
78	S2	836	G
78	S2	837	A
78	S2	838	G
78	S2	839	C
78	S2	842	C
78	S2	844	U
78	S2	847	A
78	S2	869	A
78	S2	870	A
78	S2	873	G
78	S2	874	G
78	S2	878	G
78	S2	882	U
78	S2	888	U
78	S2	889	U
78	S2	891	G
78	S2	893	U
78	S2	894	G
78	S2	896	U
78	S2	897	U
78	S2	898	U
78	S2	899	U
78	S2	900	C

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Mol	Chain	Res	Type
78	S2	901	G
78	S2	903	A
78	S2	906	U
78	S2	907	G
78	S2	909	G
78	S2	913	A
78	S2	919	A
78	S2	920	A
78	S2	930	C
78	S2	933	G
78	S2	934	G
78	S2	943	U
78	S2	950	C
78	S2	954	U
78	S2	963	A
78	S2	969	U
78	S2	971	G
78	S2	972	A
78	S2	990	A
78	S2	992	A
78	S2	999	G
78	S2	1001	A
78	S2	1008	A
78	S2	1017	U
78	S2	1023	A
78	S2	1027	A
78	S2	1033	G
78	S2	1044	G
78	S2	1047	C
78	S2	1060	A
78	S2	1061	U
78	S2	1062	A
78	S2	1067	C
78	S2	1083	A
78	S2	1085	C
78	S2	1088	U
78	S2	1108	G
78	S2	1109	C
78	S2	1113	A
78	S2	1114	U
78	S2	1115	U
78	S2	1116	C

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Mol	Chain	Res	Type
78	S2	1121	G
78	S2	1133	A
78	S2	1138	C
78	S2	1139	C
78	S2	1148	A
78	S2	1153	C
78	S2	1154	U
78	S2	1161	U
78	S2	1170	A
78	S2	1195	A
78	S2	1203	G
78	S2	1207	G
78	S2	1208	A
78	S2	1215	C
78	S2	1216	C
78	S2	1217	A
78	S2	1220	A
78	S2	1224	G
78	S2	1227	G
78	S2	1234	C
78	S2	1237	C
78	S2	1242	U
78	S2	1243	U
78	S2	1251	A
78	S2	1253	A
78	S2	1256	G
78	S2	1257	G
78	S2	1259	A
78	S2	1263	U
78	S2	1264	C
78	S2	1274	G
78	S2	1275	G
78	S2	1282	A
78	S2	1283	C
78	S2	1284	A
78	S2	1286	G
78	S2	1287	A
78	S2	1294	G
78	S2	1295	A
78	S2	1302	G
78	S2	1303	C
78	S2	1308	U

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Mol	Chain	Res	Type
78	S2	1313	A
78	S2	1320	G
78	S2	1342	U
78	S2	1348	G
78	S2	1354	G
78	S2	1355	C
78	S2	1356	G
78	S2	1357	A
78	S2	1371	U
78	S2	1372	U
78	S2	1376	A
78	S2	1378	A
78	S2	1396	A
78	S2	1401	A
78	S2	1402	A
78	S2	1408	U
78	S2	1411	G
78	S2	1415	C
78	S2	1419	C
78	S2	1420	G
78	S2	1421	A
78	S2	1422	G
78	S2	1423	C
78	S2	1424	G
78	S2	1434	C
78	S2	1435	C
78	S2	1436	C
78	S2	1438	A
78	S2	1442	U
78	S2	1449	G
78	S2	1454	A
78	S2	1455	A
78	S2	1462	U
78	S2	1463	U
78	S2	1468	C
78	S2	1480	A
78	S2	1484	A
78	S2	1489	A
78	S2	1490	G
78	S2	1494	U
78	S2	1495	G
78	S2	1497	G

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Mol	Chain	Res	Type
78	S2	1498	A
78	S2	1520	G
78	S2	1521	C
78	S2	1522	A
78	S2	1533	A
78	S2	1534	C
78	S2	1535	U
78	S2	1536	G
78	S2	1537	A
78	S2	1544	C
78	S2	1546	G
78	S2	1552	G
78	S2	1553	C
78	S2	1556	A
78	S2	1560	U
78	S2	1570	G
78	S2	1574	C
78	S2	1575	G
78	S2	1579	A
78	S2	1580	A
78	S2	1581	C
78	S2	1582	C
78	S2	1586	U
78	S2	1587	G
78	S2	1588	A
78	S2	1600	G
78	S2	1601	A
78	S2	1604	G
78	S2	1621	U
78	S2	1623	A
78	S2	1629	C
78	S2	1633	A
78	S2	1634	A
78	S2	1637	A
78	S2	1638	G
78	S2	1639	G
78	S2	1640	A
78	S2	1646	C
78	S2	1648	G
78	S2	1654	G
78	S2	1663	A
78	S2	1665	G

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Mol	Chain	Res	Type
78	S2	1671	G
78	S2	1683	C
78	S2	1686	G
78	S2	1693	G
78	S2	1696	C
78	S2	1698	C
78	S2	1699	A
78	S2	1712	A
78	S2	1715	A
78	S2	1721	U
78	S2	1722	G
78	S2	1729	U
78	S2	1742	C
78	S2	1743	G
78	S2	1744	G
78	S2	1745	A
78	S2	1752	C
78	S2	1753	C
78	S2	1754	G
78	S2	1755	C
78	S2	1756	C
78	S2	1757	G
78	S2	1758	G
78	S2	1759	G
78	S2	1761	U
78	S2	1772	C
78	S2	1773	C
78	S2	1774	C
78	S2	1777	G
78	S2	1782	G
78	S2	1783	C
78	S2	1784	G
78	S2	1787	G
78	S2	1790	A
78	S2	1809	A
78	S2	1810	U
78	S2	1812	U
78	S2	1813	A
78	S2	1822	A
78	S2	1823	A
78	S2	1825	A
78	S2	1829	G

Continued on next page...

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Mol	Chain	Res	Type
78	S2	1835	A
78	S2	1838	U
78	S2	1849	G
78	S2	1851	A
78	S2	1852	C
78	S2	1861	G
78	S2	1862	G
78	S2	1863	A
78	S2	1864	U
78	S2	1865	C
79	Et	4	C
79	Et	6	G
79	Et	7	A
79	Et	9	A
79	Et	10	G
79	Et	11	C
79	Et	19	G
79	Et	20	U
79	Et	21	A
79	Et	26	A
79	Et	31	A
79	Et	34	U
79	Et	35	U
79	Et	38	A
79	Et	40	C
79	Et	42	G
79	Et	46	G
79	Et	47	U
79	Et	48	C
79	Et	49	C
79	Et	55	U
79	Et	58	A
79	Et	59	G
79	Et	61	C
79	Et	65	G
79	Et	66	U
79	Et	69	G
79	Et	70	G
79	Et	73	G
79	Et	76	A
80	Pt	9	A
80	Pt	13	U

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Mol	Chain	Res	Type
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	59	A
80	Pt	64	G
80	Pt	65	G
80	Pt	67	G
80	Pt	70	A
80	Pt	72	C
80	Pt	74	C
80	Pt	76	A

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	L5	265	C
20	L5	406	C
20	L5	493	G
20	L5	914	U
20	L5	1082	C
20	L5	1324	A
20	L5	1590	C
20	L5	1633	G
20	L5	1977	C
20	L5	2033	A
20	L5	2416	G
20	L5	2485	U
20	L5	2675	G
20	L5	2760	G
20	L5	2786	C
20	L5	3614	G
20	L5	3673	C
20	L5	4600	G
20	L5	4699	U
20	L5	4913	G
78	S2	291	G

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Mol	Chain	Res	Type
78	S2	420	G
78	S2	563	G
78	S2	688	U
78	S2	1355	C
78	S2	1434	C
78	S2	1781	A

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
78	S2	6
20	L5	1

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	26.73
1	S2	698:G	O3'	730:C	P	16.85
1	S2	739:C	O3'	746:C	P	12.91
1	S2	225:G	O3'	287:U	P	7.44
1	S2	1693:G	O3'	1694:U	P	5.77
1	L5	3949:A	O3'	3950:U	P	4.48
1	S2	1210:G	O3'	1211:G	P	3.18

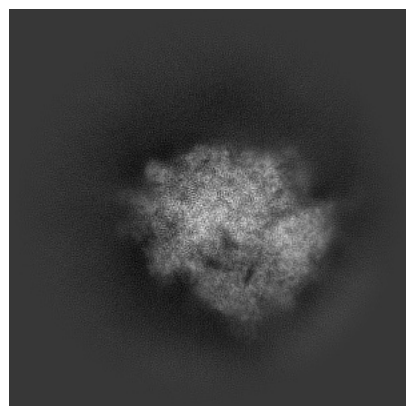
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42306. These allow visual inspection of the internal detail of the map and identification of artifacts.

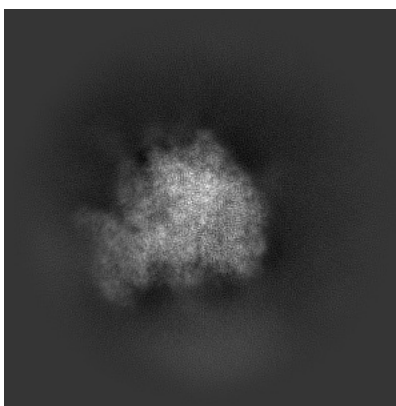
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

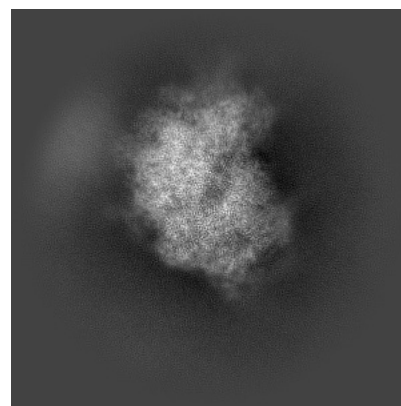
6.1.1 Primary map



X

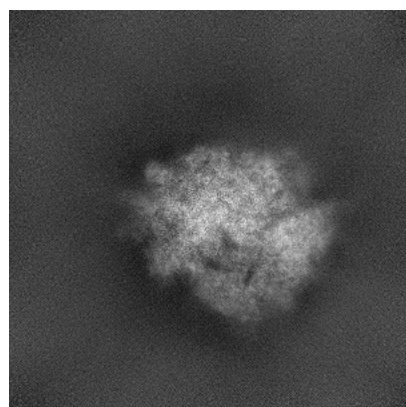


Y

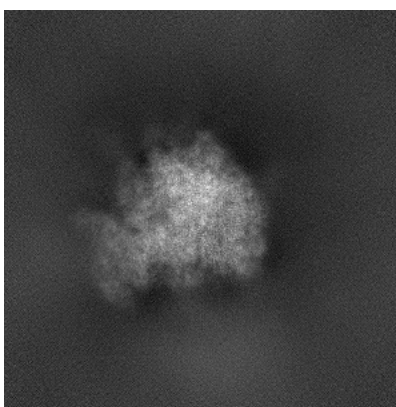


Z

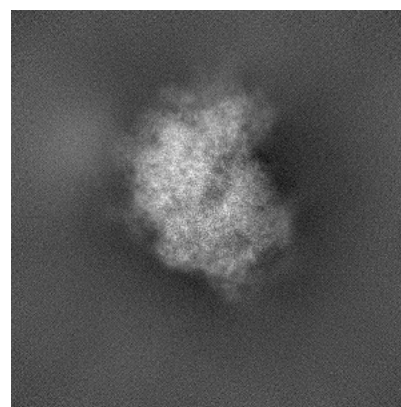
6.1.2 Raw map



X



Y

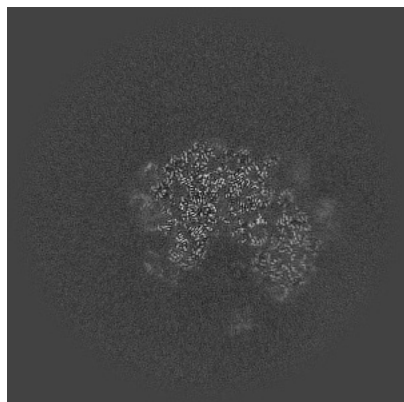


Z

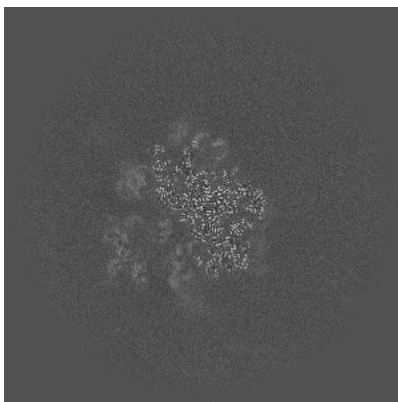
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

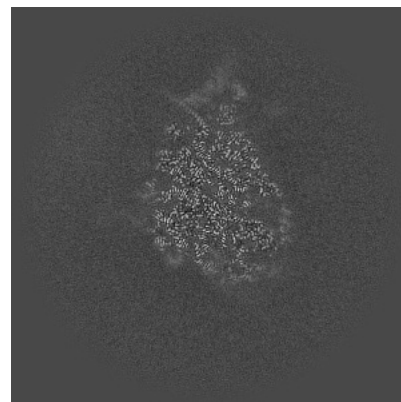
6.2.1 Primary map



X Index: 256

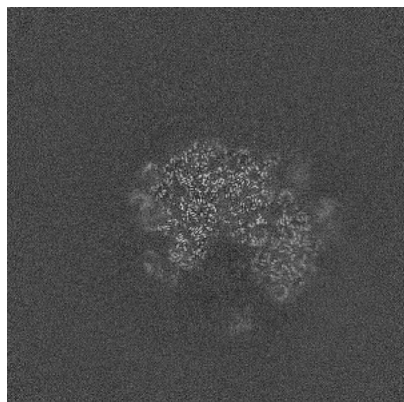


Y Index: 256

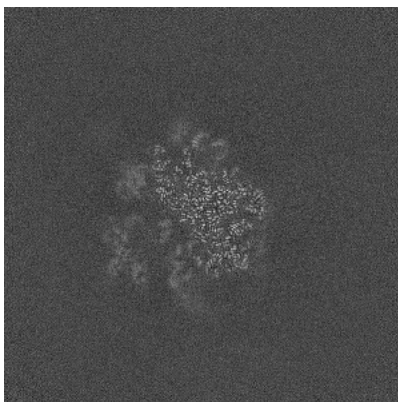


Z Index: 256

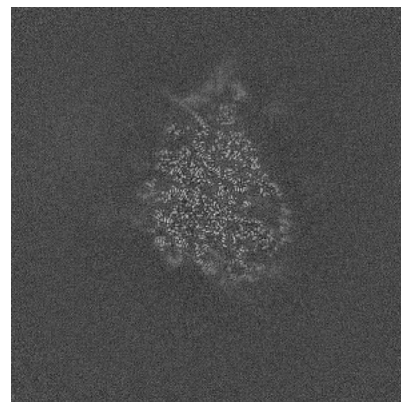
6.2.2 Raw map



X Index: 256



Y Index: 256

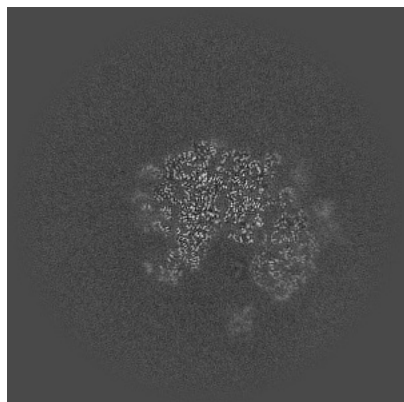


Z Index: 256

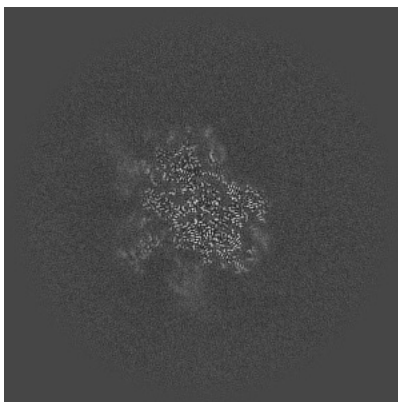
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

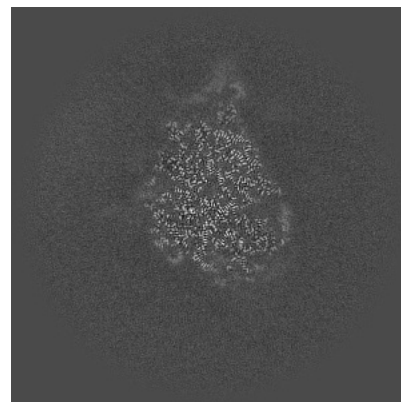
6.3.1 Primary map



X Index: 253

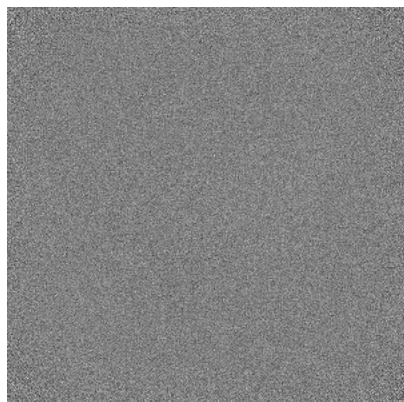


Y Index: 243

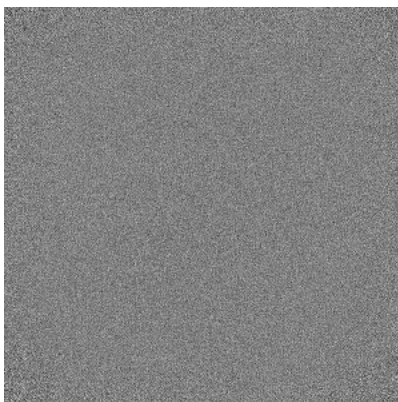


Z Index: 258

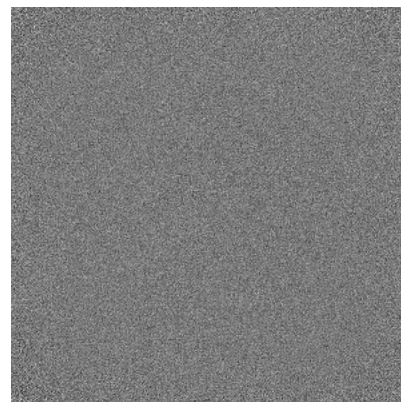
6.3.2 Raw map



X Index: 0



Y Index: 0

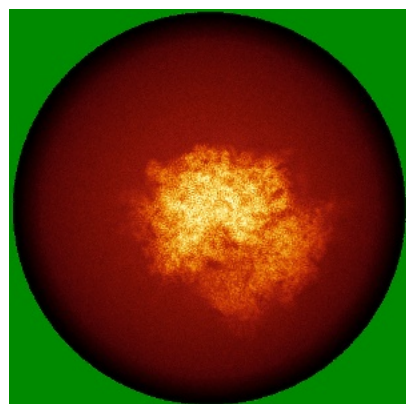


Z Index: 0

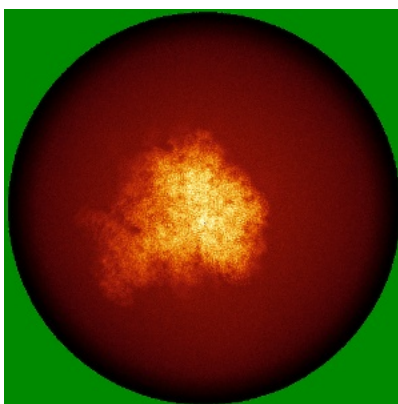
The images above show the largest variance slices of the map in three orthogonal directions.

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

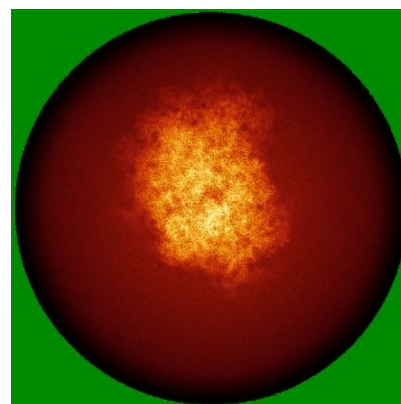
6.4.1 Primary map



X

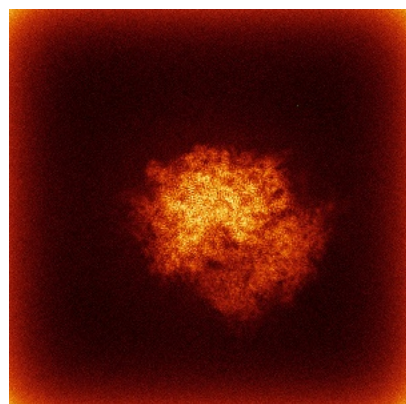


Y

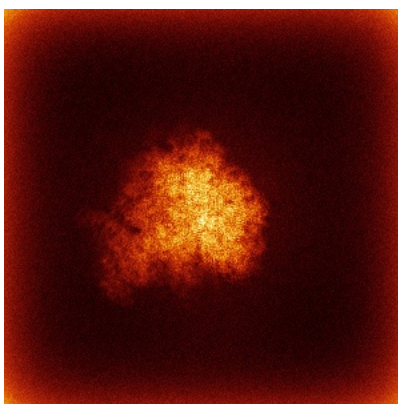


Z

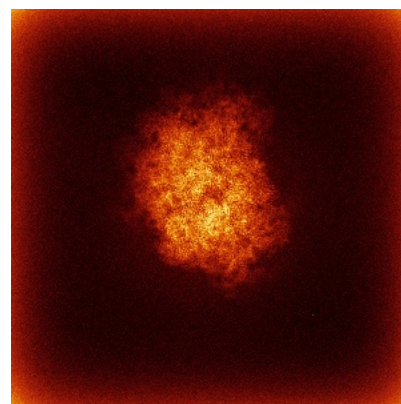
6.4.2 Raw map



X



Y

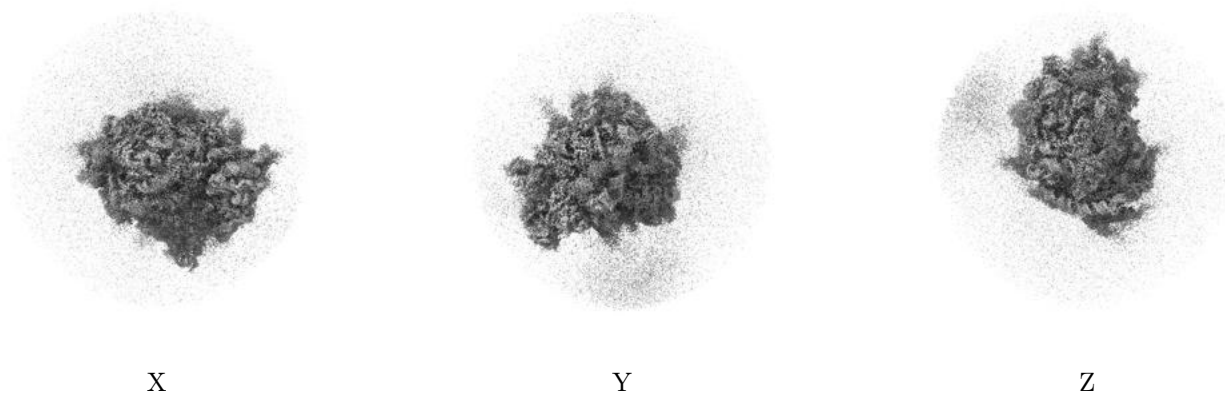


Z

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.

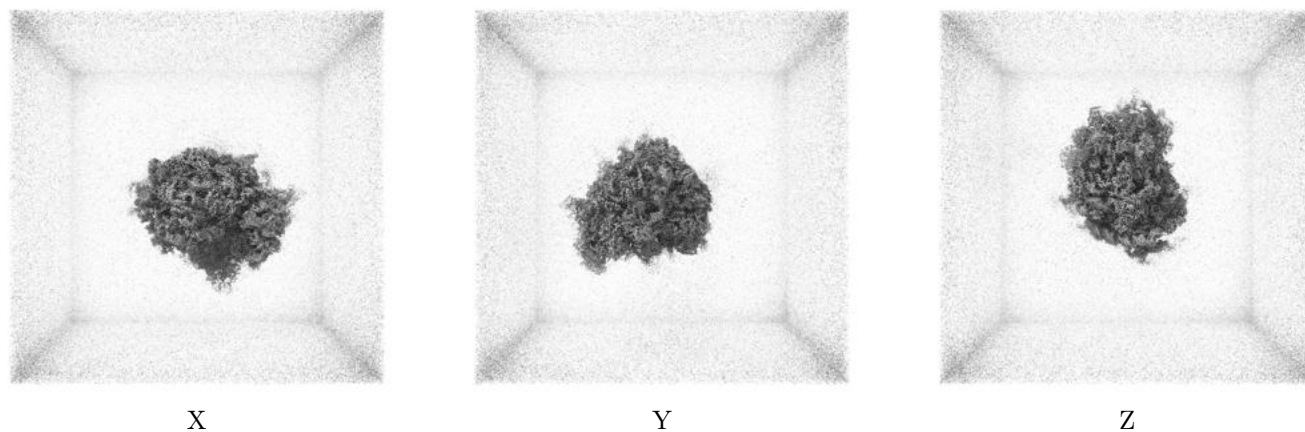
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0264. 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.

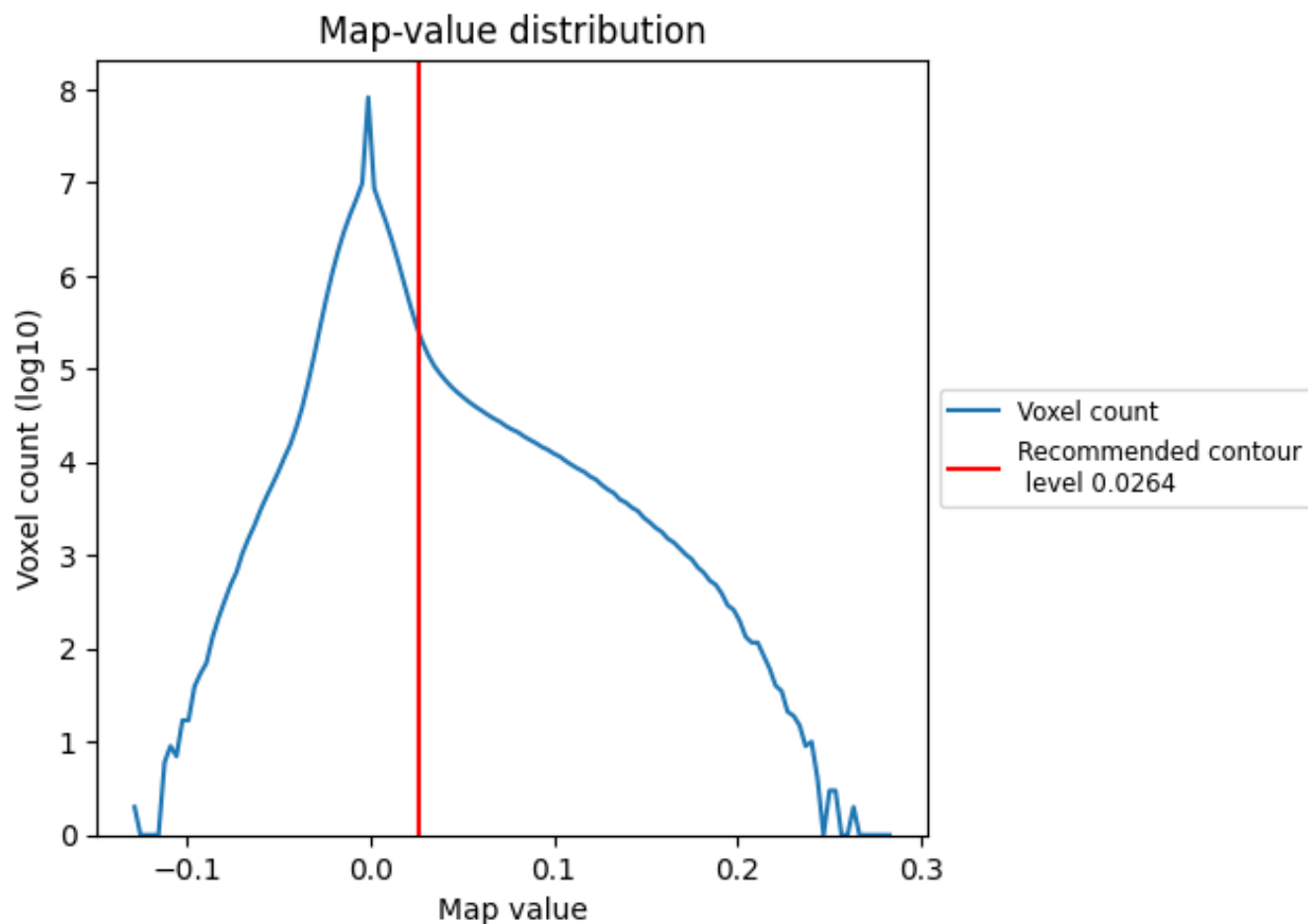
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

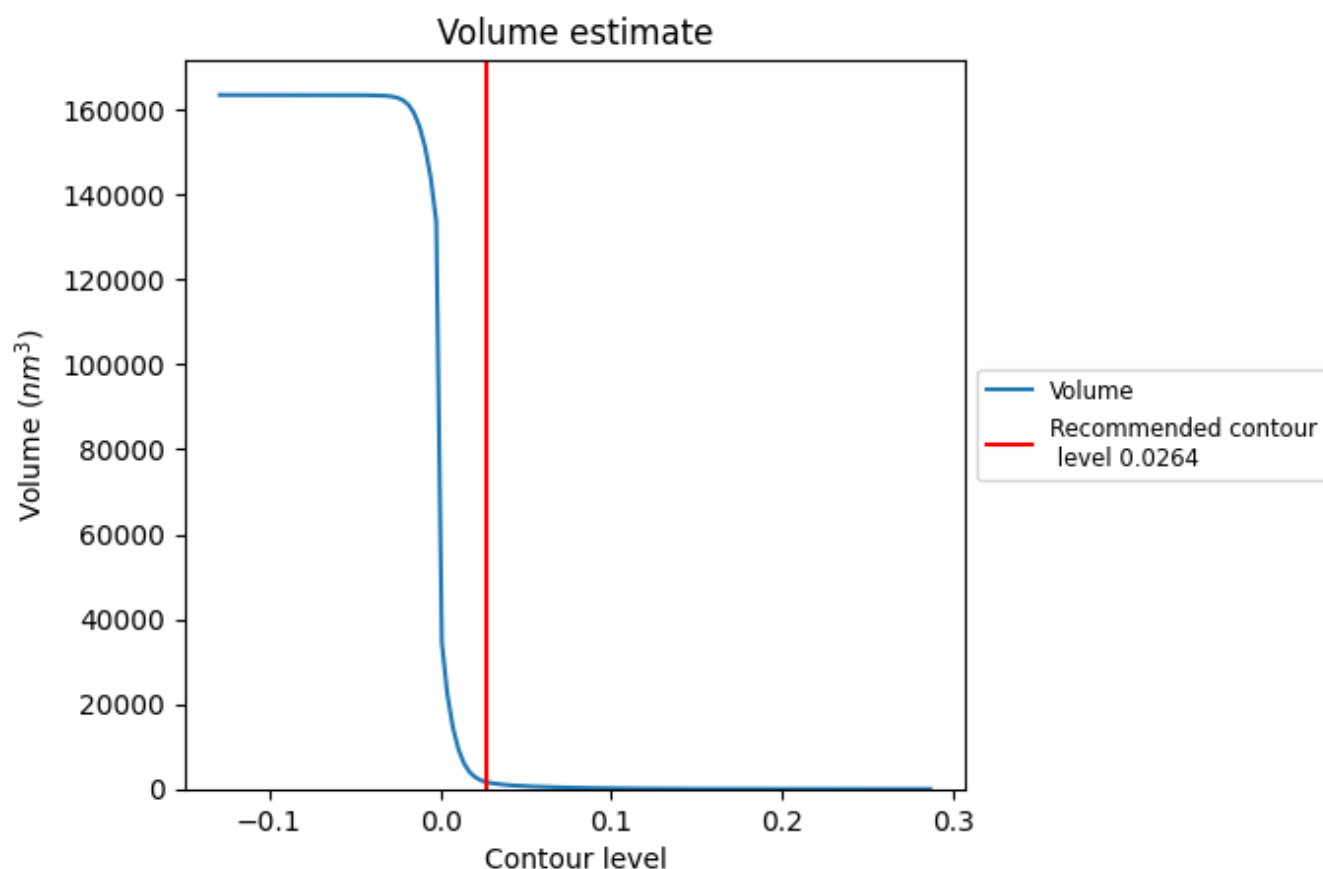
This section contains the results of statistical analysis of the map.

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.

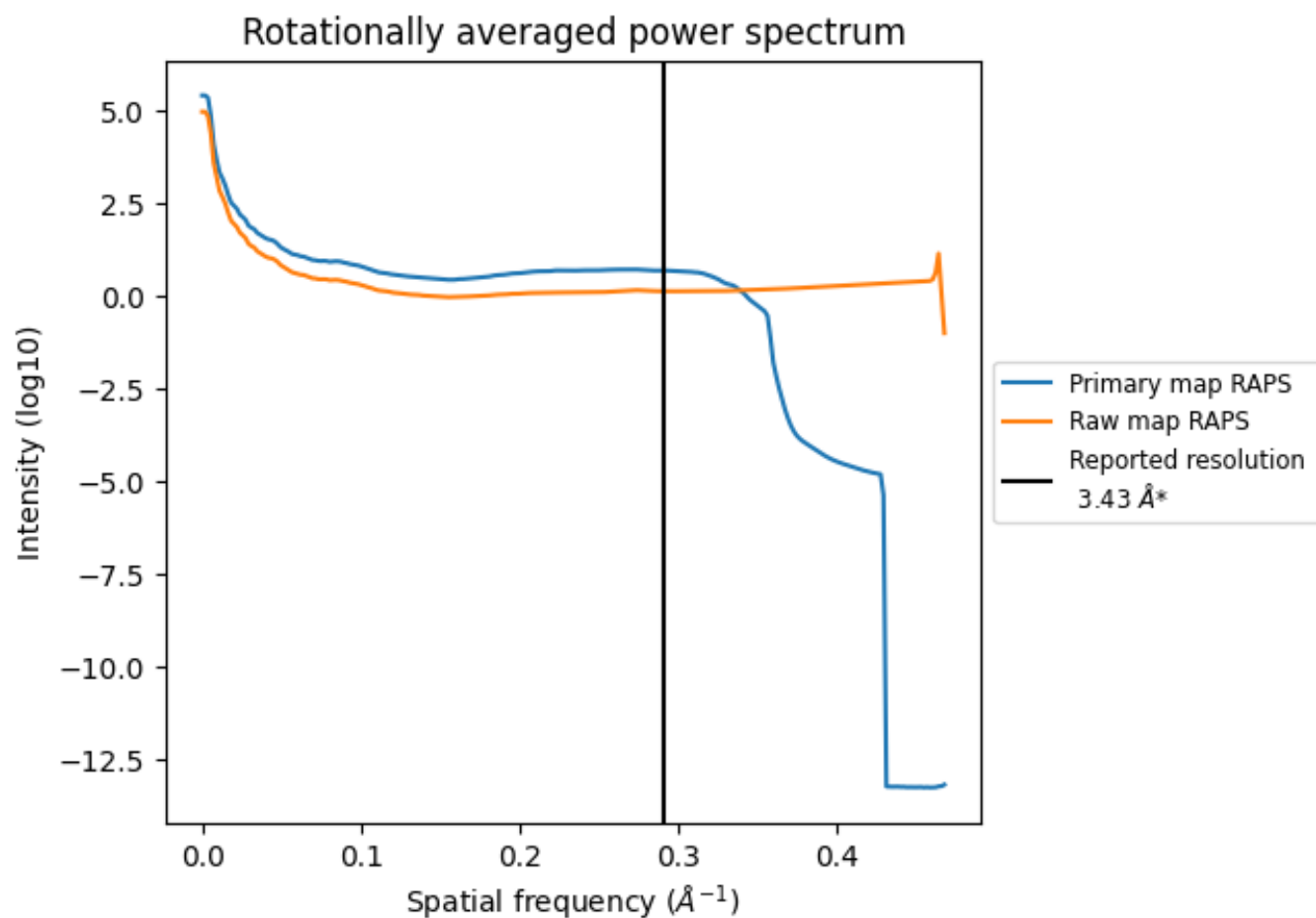
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1700 nm^3 ; this corresponds to an approximate mass of 1535 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 ⓘ

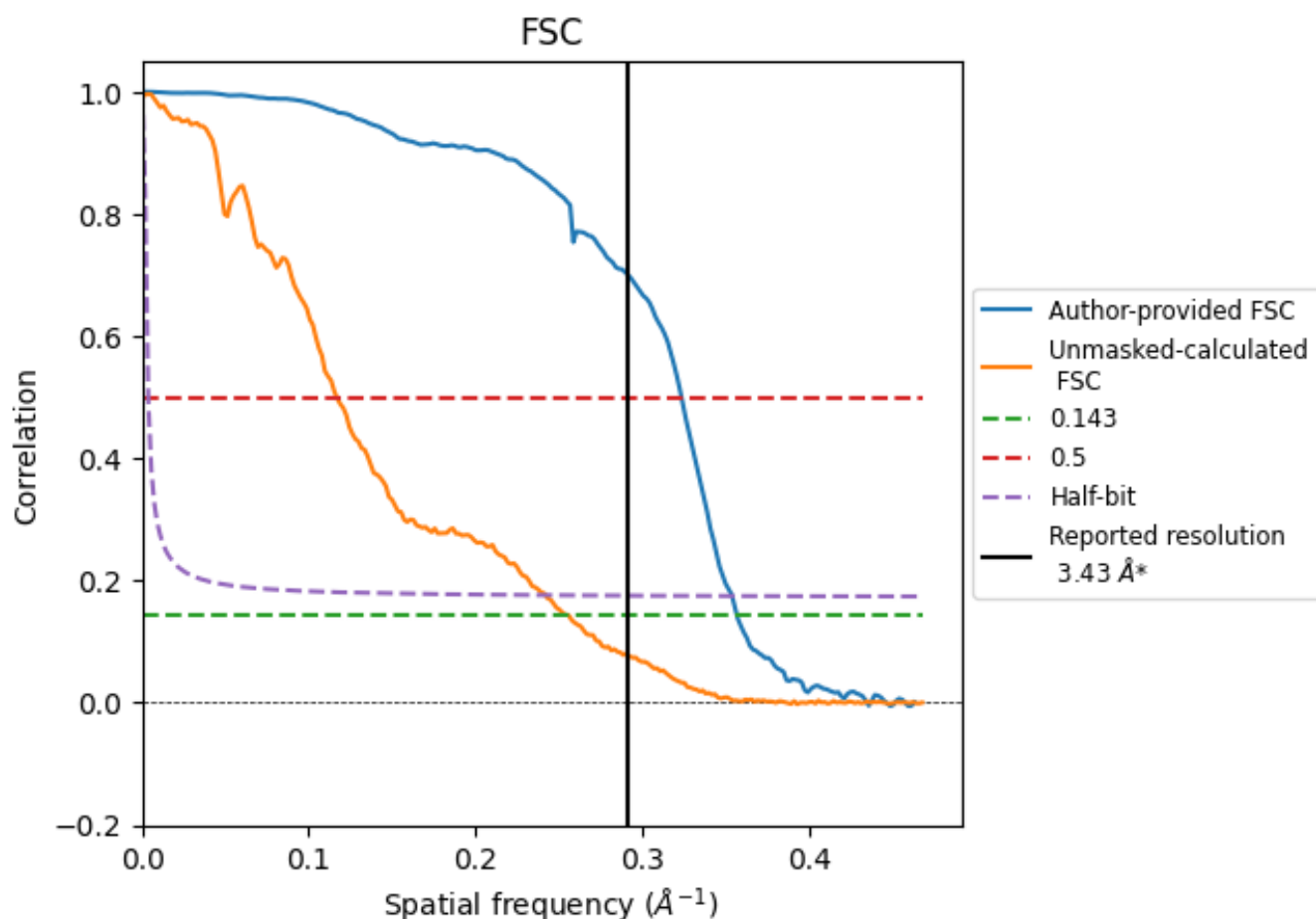


*Reported resolution corresponds to spatial frequency of 0.292 Å⁻¹

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 0.292 \AA^{-1}

8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.43	-	-
Author-provided FSC curve	2.80	3.09	2.82
Unmasked-calculated*	3.91	8.56	4.13

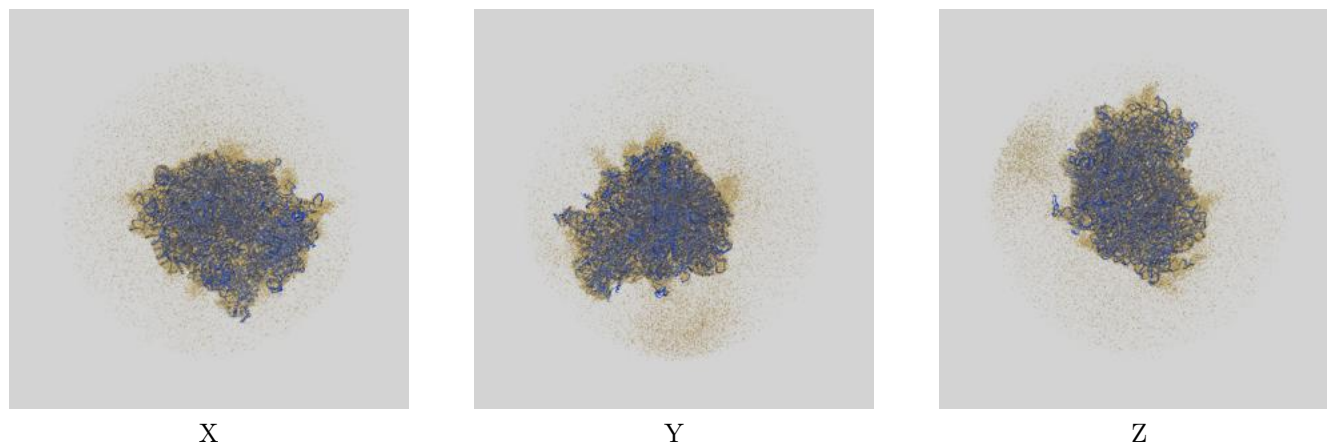
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.80 differs from the reported value 3.43 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.91 differs from the reported value 3.43 by more than 10 %

9 Map-model fit [i](#)

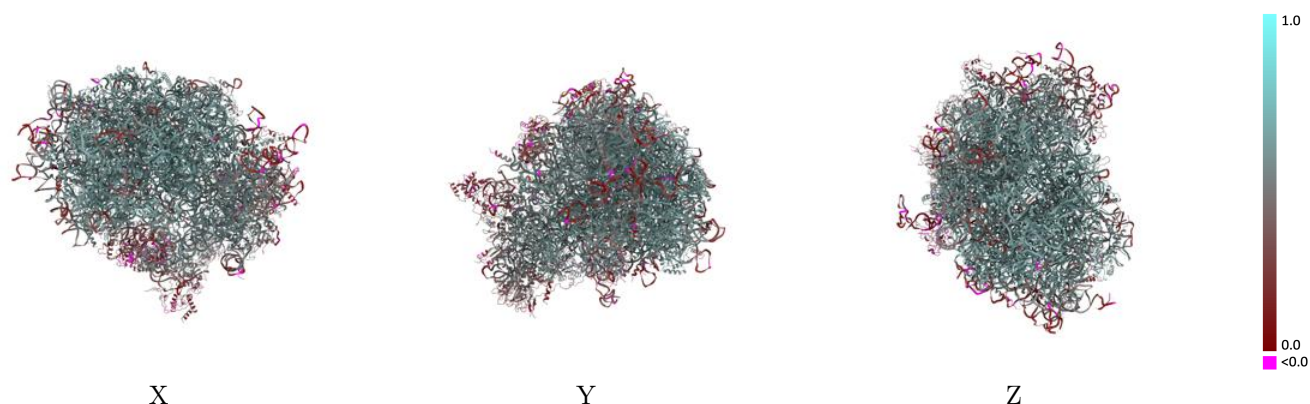
This section contains information regarding the fit between EMDB map EMD-42306 and PDB model 8UIZ. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



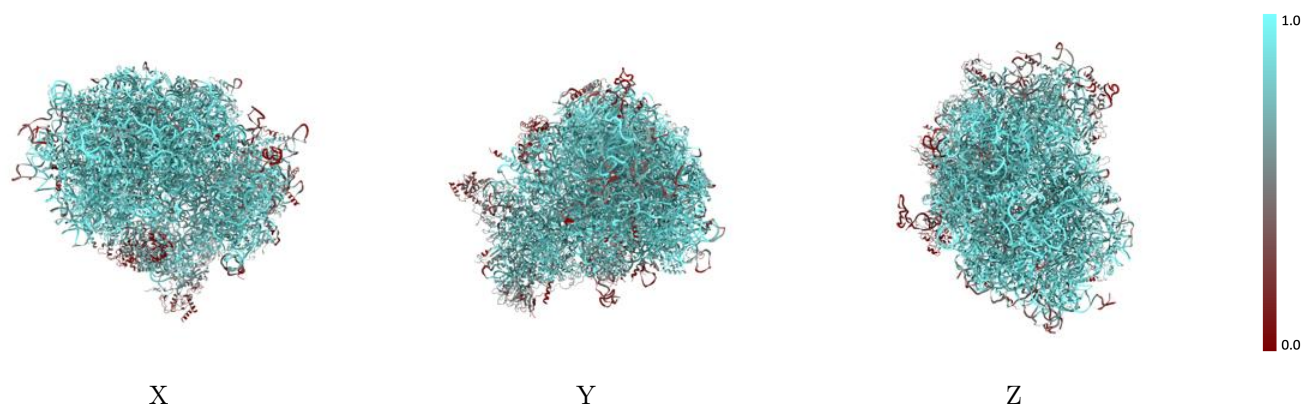
The images above show the 3D surface view of the map at the recommended contour level 0.0264 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



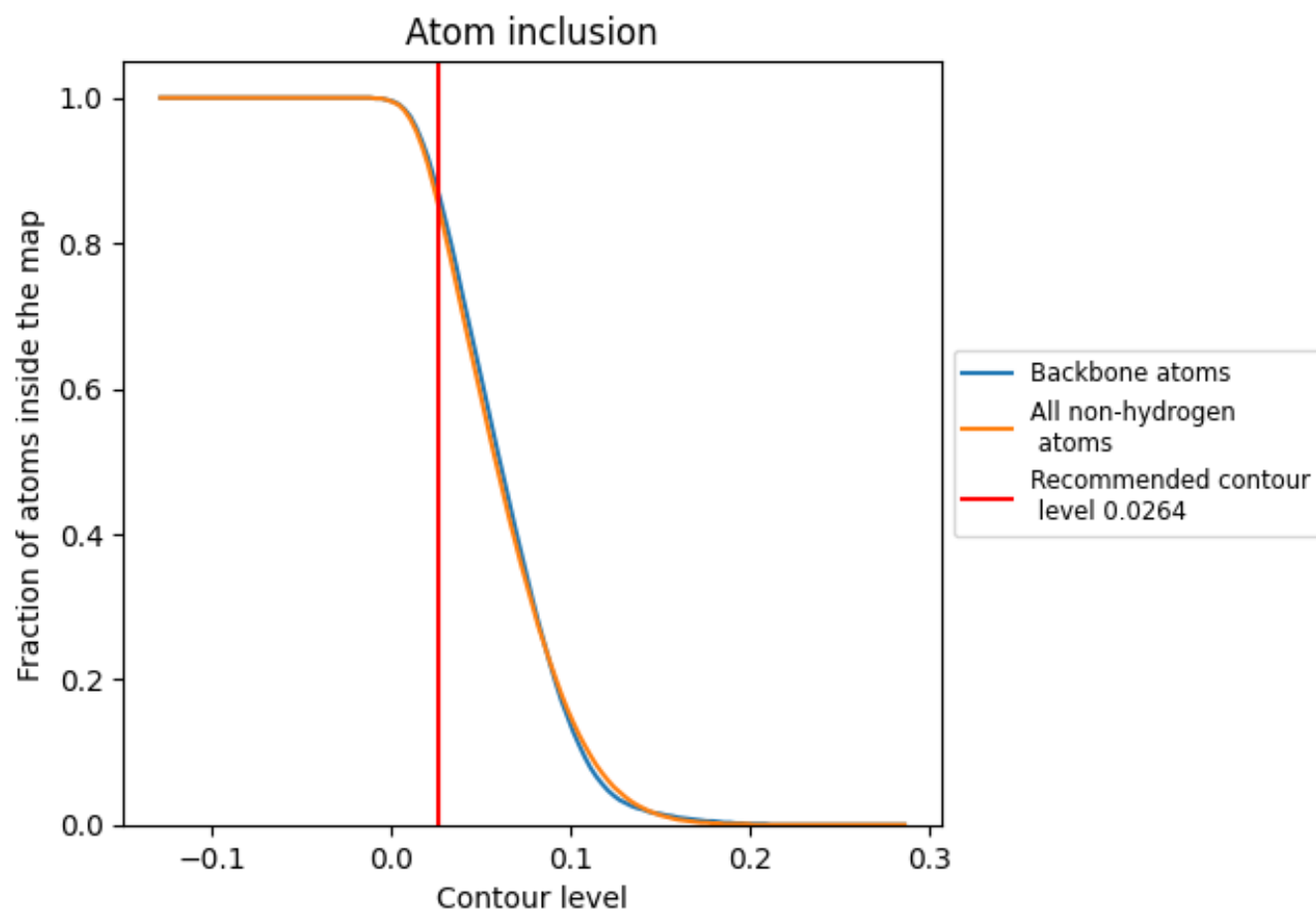
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0264).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 85% 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 (0.0264) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8510	 0.5270
Et	 0.6410	 0.2420
L5	 0.8970	 0.5440
L7	 0.9810	 0.6070
L8	 0.9390	 0.5810
LA	 0.9650	 0.6240
LB	 0.9180	 0.6030
LC	 0.9200	 0.6020
LD	 0.8710	 0.5690
LE	 0.8260	 0.5360
LF	 0.9310	 0.6090
LG	 0.8140	 0.5460
LH	 0.9090	 0.5940
LI	 0.9200	 0.6050
LJ	 0.7910	 0.5230
LL	 0.8860	 0.5780
LM	 0.9140	 0.5810
LN	 0.9830	 0.6330
LO	 0.9410	 0.6110
LP	 0.9420	 0.6160
LQ	 0.9570	 0.6260
LR	 0.8390	 0.5460
LS	 0.9550	 0.6240
LT	 0.9040	 0.5930
LU	 0.7990	 0.5020
LV	 0.9310	 0.6150
LW	 0.6340	 0.4200
LX	 0.8970	 0.5890
LY	 0.9120	 0.6000
LZ	 0.9050	 0.5850
La	 0.9560	 0.6290
Lb	 0.8190	 0.5290
Lc	 0.9160	 0.5790
Ld	 0.9000	 0.5880
Le	 0.9660	 0.6300



















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Chain	Atom inclusion	Q-score
Lf	 0.9640	 0.6200
Lg	 0.9230	 0.5960
Lh	 0.9180	 0.6010
Li	 0.8900	 0.5890
Lj	 0.9730	 0.6190
Lk	 0.8100	 0.5460
Ll	 0.9480	 0.6090
Lm	 0.9210	 0.6090
Ln	 0.9620	 0.6140
Lo	 0.9290	 0.6060
Lp	 0.9260	 0.6100
Lr	 0.9350	 0.6060
Ls	 0.2720	 0.2200
Lt	 0.1610	 0.1590
Lz	 0.1200	 0.1390
Pt	 0.8500	 0.4960
S2	 0.8850	 0.5060
SA	 0.7710	 0.5100
SB	 0.8230	 0.5500
SC	 0.8600	 0.5490
SD	 0.6710	 0.4490
SE	 0.8110	 0.5170
SF	 0.7500	 0.4750
SG	 0.6590	 0.4250
SH	 0.6310	 0.4300
SI	 0.8000	 0.5300
SJ	 0.7950	 0.5070
SK	 0.5880	 0.3660
SL	 0.8200	 0.5370
SM	 0.2360	 0.2110
SN	 0.8870	 0.5750
SO	 0.8170	 0.5440
SP	 0.6430	 0.4180
SQ	 0.7090	 0.4700
SR	 0.6380	 0.4200
SS	 0.7030	 0.4550
ST	 0.7130	 0.4590
SU	 0.6110	 0.3910
SV	 0.8090	 0.5310
SW	 0.9180	 0.5780
SX	 0.8510	 0.5590
SY	 0.7050	 0.4400

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Chain	Atom inclusion	Q-score
SZ	 0.6000	 0.3990
Sa	 0.8620	 0.5560
Sb	 0.7610	 0.4980
Sc	 0.6540	 0.4240
Sd	 0.8120	 0.4970
Se	 0.6350	 0.4210
Sf	 0.3420	 0.2230
Sg	 0.5040	 0.3610