



Full wwPDB EM Validation Report ⓘ

Apr 21, 2025 – 03:09 PM EDT

PDB ID : 9BJ / pdb_00009bj
EMDB ID : EMD-44043
Title : In situ human unrotated hibernating with CCDC124 state 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2024-03-12
Resolution : 2.84 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:

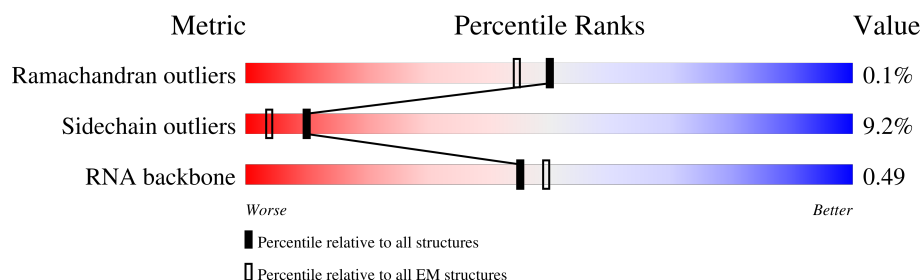
EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 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 2.84 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	SE	262	
2	SI	206	
3	SL	153	
4	SX	282	
5	SG	237	
6	SJ	185	
7	SY	131	
8	Se	58	

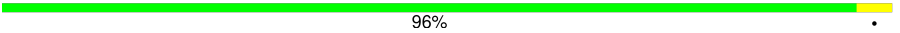
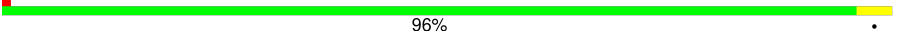

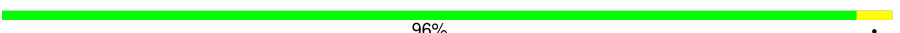












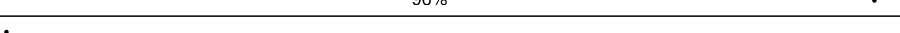
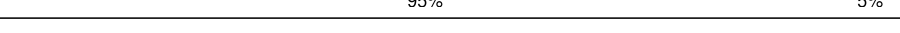

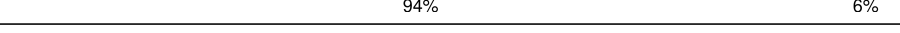

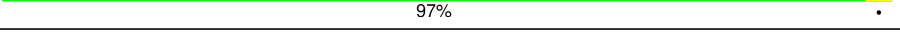

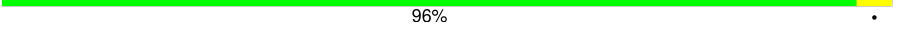

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Mol	Chain	Length	Quality of chain
9	SA	221	
10	SB	214	
11	SH	186	
12	SV	83	
13	Sa	102	
14	SC	222	
15	SN	150	
16	SO	140	
17	SW	129	
18	Sb	83	
19	L5	3740	
20	L7	120	
21	L8	156	
22	LA	248	
23	LB	402	
24	LC	368	
25	LD	293	
26	LE	236	
27	LF	225	
28	LG	241	
29	LH	190	
30	LI	202	
31	LJ	176	
32	LL	210	
33	LM	139	

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Mol	Chain	Length	Quality of chain
34	LN	203	 96% .
35	LO	201	 96% .
36	LP	153	 90% 10%
37	LQ	187	 96% .
38	LR	187	 7% 92% 8%
39	LS	175	 94% 6%
40	LT	159	 91% 9%
41	LU	101	 8% 90% 10%
42	LV	131	 95% 5%
43	LX	120	 93% 7%
44	LY	134	 94% 6%
45	LZ	135	 92% 8%
46	La	147	 97% .
47	Lb	109	 8% 95% 5%
48	Lc	98	 90% 9% .
49	Ld	107	 96% .
50	Le	128	 95% 5%
51	Lf	109	 91% 9%
52	Lg	114	 94% 6%
53	Lh	122	 89% 11%
54	Li	102	 97% .
55	Lj	86	 86% 13% .
56	Lk	69	 6% 96% .
57	Ll	50	 88% 12%
58	Lm	52	 98% .

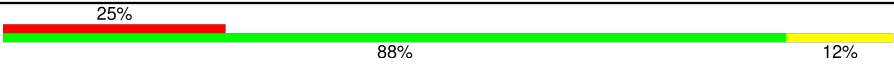

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Mol	Chain	Length	Quality of chain
59	Ln	24	96% .
60	Lo	105	92% 8%
61	Lp	91	96% .
62	Lr	125	87% 13%
63	SR	135	20% 85% 15%
64	SD	227	29% 90% 10%
65	SF	189	27% 88% 12%
66	SK	98	44% 93% 7%
67	SP	121	43% 91% 8% .
68	SQ	144	26% 89% 10% .
69	SS	145	30% 90% 10%
70	ST	143	24% 90% 10% .
71	SU	104	40% 88% 12%
72	Sc	64	27% 92% 8%
73	Sd	55	13% 87% 13%
74	Sg	313	56% 91% 9%
75	SM	122	89% 91% 9%
76	SZ	75	48% 87% 12% .
77	Sf	67	73% 84% 16%
78	S2	1740	5% 75% 25% .
79	Et	75	71% 60% 39% .
80	Lt	141	82% 96% .
81	Lz	217	95% 90% 10%
82	Ls	196	66% 95% 5%
83	CB	846	67% 89% 11%

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Mol	Chain	Length	Quality of chain
84	CE	73	
85	LW	118	

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 228356 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 Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 2 is a protein called 40S ribosomal protein S8.

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

- Molecule 3 is a protein called 40S ribosomal protein S11.

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

- Molecule 4 is a protein called 40S ribosomal protein S23.

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

- Molecule 5 is a protein called 40S ribosomal protein S6.

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

- Molecule 6 is a protein called 40S ribosomal protein S9.

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

- Molecule 7 is a protein called 40S ribosomal protein S24.

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

- Molecule 8 is a protein called Small ribosomal subunit protein eS30.

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

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

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

- Molecule 10 is a protein called 40S ribosomal protein S3a.

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

- Molecule 11 is a protein called 40S ribosomal protein S7 [Homo sapiens].

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

- Molecule 12 is a protein called 40S ribosomal protein S21.

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

- Molecule 13 is a protein called 40S ribosomal protein S26.

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

- Molecule 14 is a protein called 40S ribosomal protein S2.

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

- Molecule 15 is a protein called 40S ribosomal protein S13.

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

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 17 is a protein called 40S ribosomal protein S15a.

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

- Molecule 18 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 19 is a RNA chain called 28S rRNA.

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

- Molecule 20 is a RNA chain called 5S rRNA.

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

- Molecule 21 is a RNA chain called 5.8S rRNA.

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

- Molecule 22 is a protein called 60S ribosomal protein L8.

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

- Molecule 23 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 24 is a protein called 60S ribosomal protein L4.

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

- Molecule 25 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 26 is a protein called 60S ribosomal protein L6.

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

- Molecule 27 is a protein called 60S ribosomal protein L7.

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

- Molecule 28 is a protein called 60S ribosomal protein L7a.

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

- Molecule 29 is a protein called 60S ribosomal protein L9.

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

- Molecule 30 is a protein called 60S ribosomal protein L10-like.

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

- Molecule 31 is a protein called 60S ribosomal protein L11.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 33 is a protein called 60S ribosomal protein L14.

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

- Molecule 34 is a protein called 60S ribosomal protein L15.

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

- Molecule 35 is a protein called 60S ribosomal protein L13a.

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

- Molecule 36 is a protein called 60S ribosomal protein L17.

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

- Molecule 37 is a protein called 60S ribosomal protein L18.

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

- Molecule 38 is a protein called 60S ribosomal protein L19.

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

- 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 60S ribosomal protein L29.

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.

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 protein called 60S ribosomal protein L12.

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

- Molecule 81 is a protein called 60S ribosomal protein L10a.

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

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

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

- Molecule 83 is a protein called eEF2.

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

- Molecule 84 is a protein called Coiled-coil domain-containing protein 124.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CE	73	Total	C	N	O	S	0	0
			613	369	122	121	1		

- Molecule 85 is a protein called 60S ribosomal protein L24.

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

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
87	L5	210	Total	Mg	0
			210	210	
87	L7	3	Total	Mg	0
			3	3	
87	L8	6	Total	Mg	0
			6	6	
87	LA	1	Total	Mg	0
			1	1	
87	LB	1	Total	Mg	0
			1	1	
87	LI	1	Total	Mg	0
			1	1	

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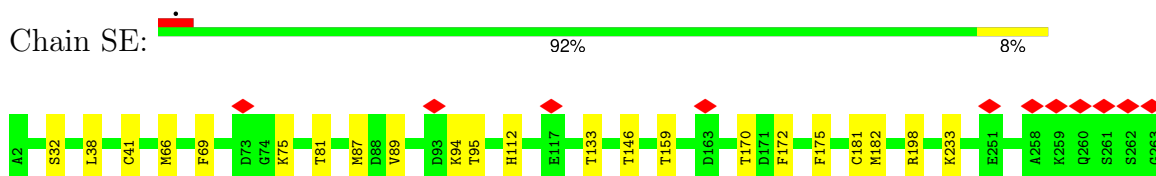
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
87	LP	1	Total 1	Mg 1	0
87	LV	1	Total 1	Mg 1	0
87	Le	1	Total 1	Mg 1	0
87	Lg	1	Total 1	Mg 1	0
87	S2	29	Total 29	Mg 29	0

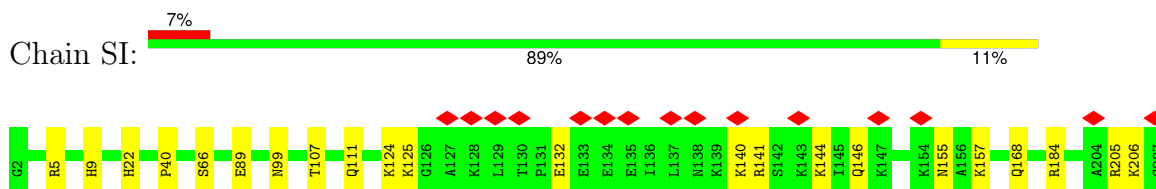
3 Residue-property plots

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

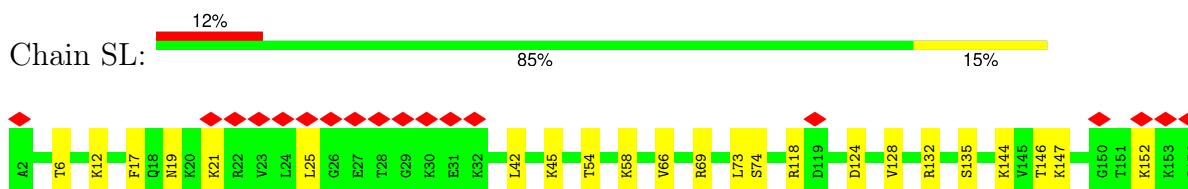
- Molecule 1: Small ribosomal subunit protein eS4, X isoform



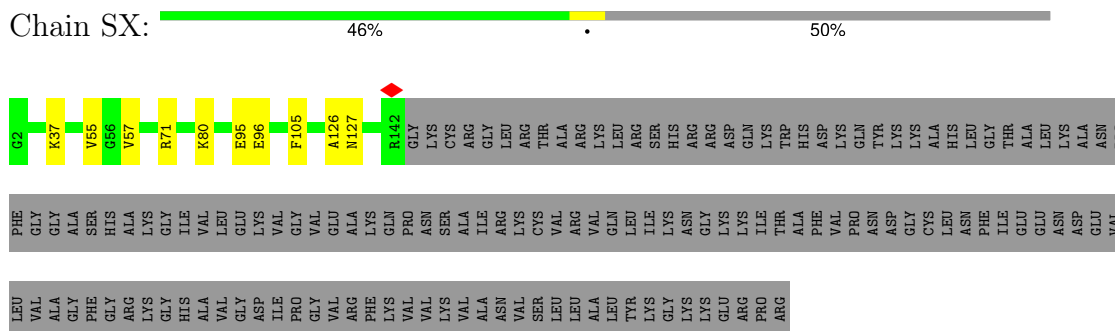
- Molecule 2: 40S ribosomal protein S8



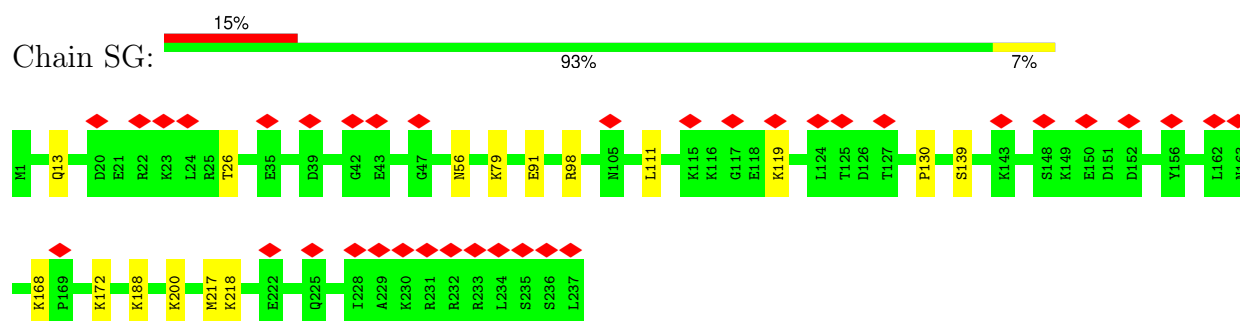
- Molecule 3: 40S ribosomal protein S11



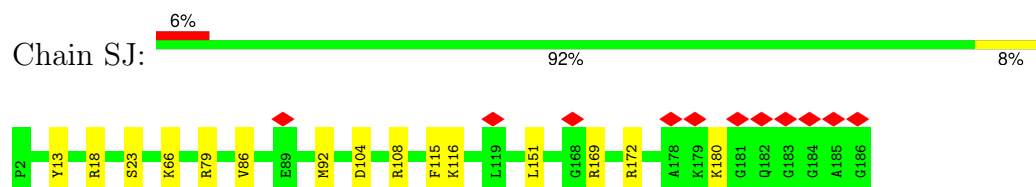
- Molecule 4: 40S ribosomal protein S23



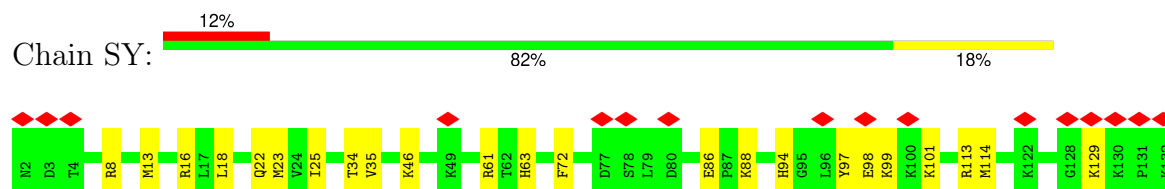
- Molecule 5: 40S ribosomal protein S6



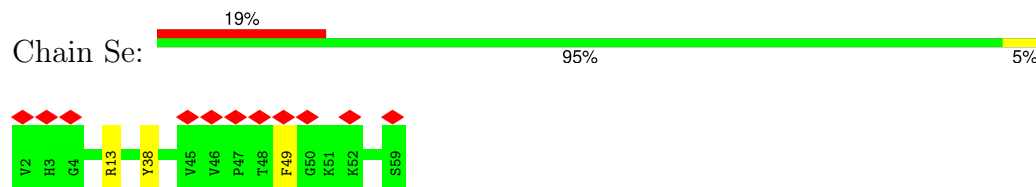
- Molecule 6: 40S ribosomal protein S9



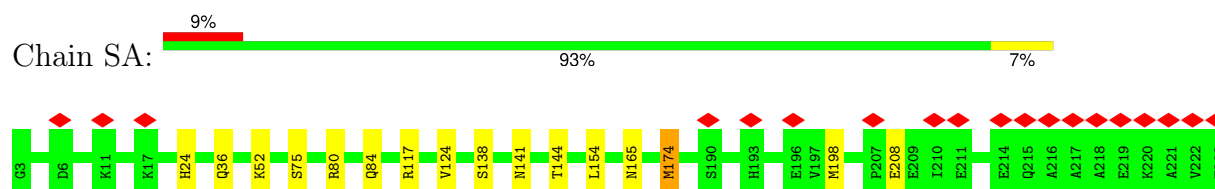
- Molecule 7: 40S ribosomal protein S24



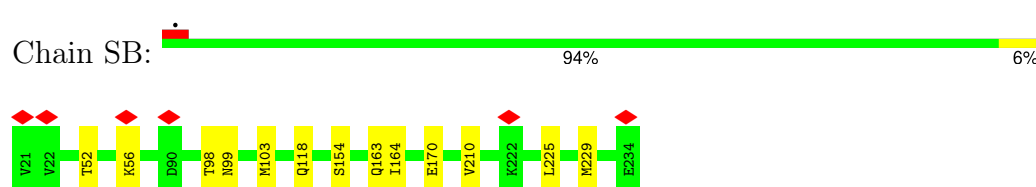
- Molecule 8: Small ribosomal subunit protein eS30



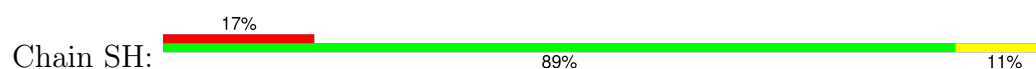
- Molecule 9: 40S ribosomal protein SA

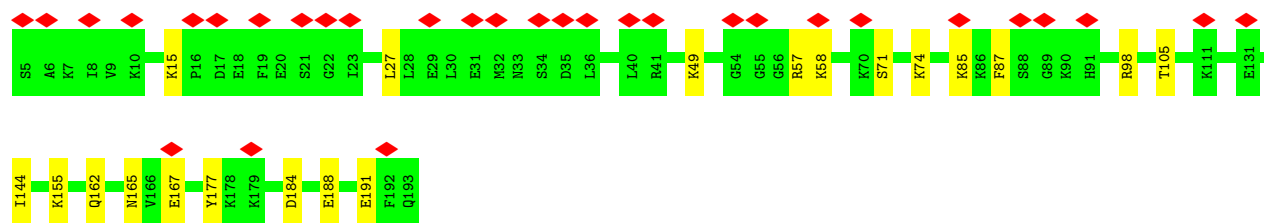


- Molecule 10: 40S ribosomal protein S3a

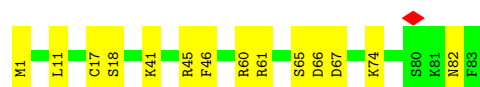
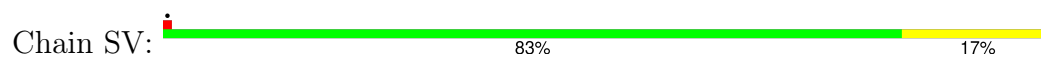


- Molecule 11: 40S ribosomal protein S7 [Homo sapiens]

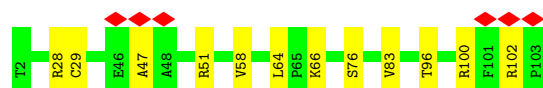
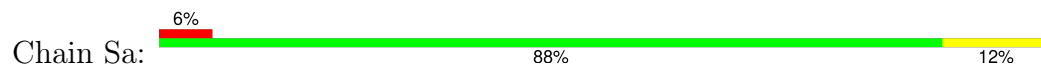




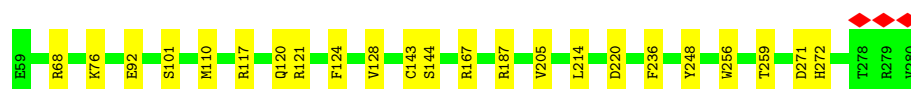
- Molecule 12: 40S ribosomal protein S21



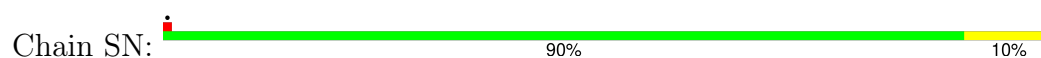
- Molecule 13: 40S ribosomal protein S26



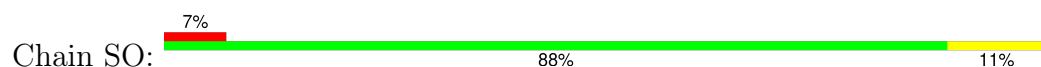
- Molecule 14: 40S ribosomal protein S2



- Molecule 15: 40S ribosomal protein S13

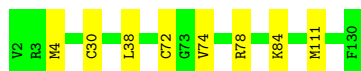


- Molecule 16: Small ribosomal subunit protein uS11

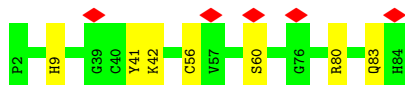


- Molecule 17: 40S ribosomal protein S15a

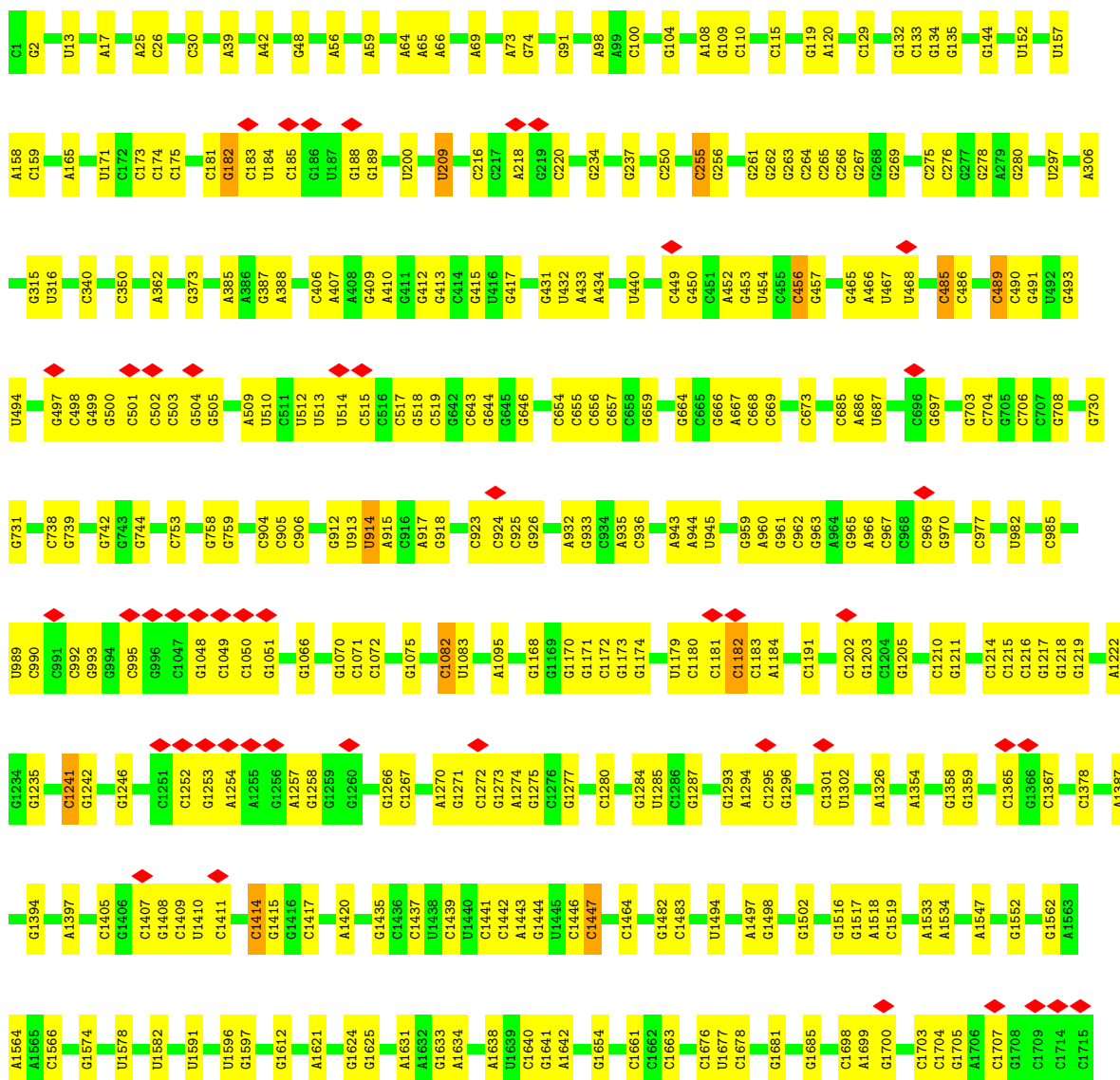
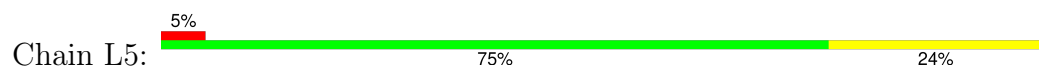




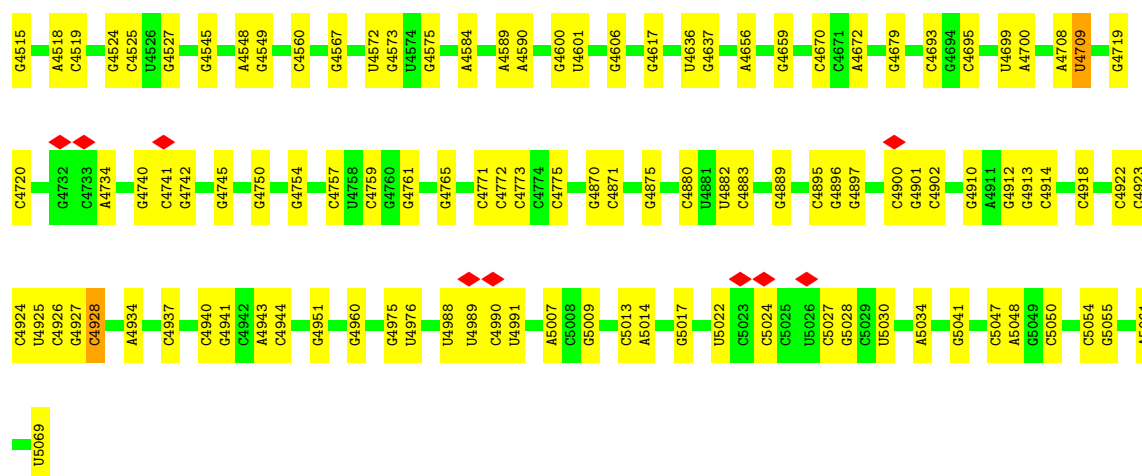
- Molecule 18: Small ribosomal subunit protein eS27



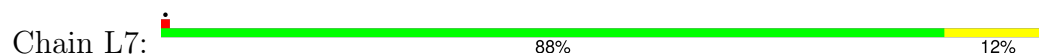
- Molecule 19: 28S rRNA



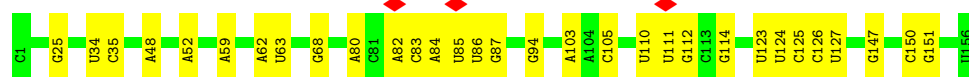
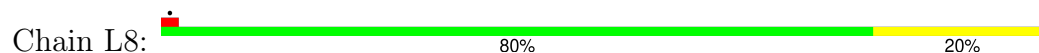




• Molecule 20: 5S rRNA



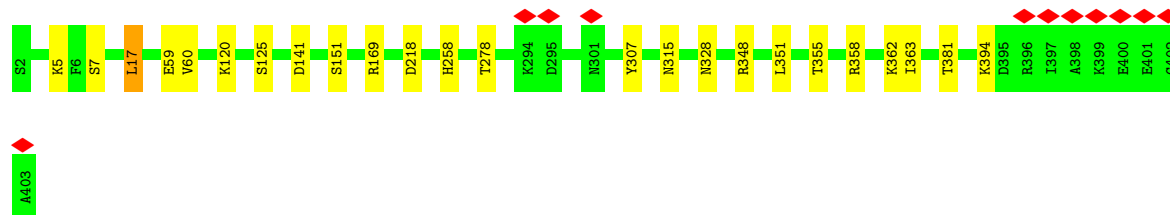
• Molecule 21: 5.8S rRNA



• Molecule 22: 60S ribosomal protein L8



• Molecule 23: Large ribosomal subunit protein uL3



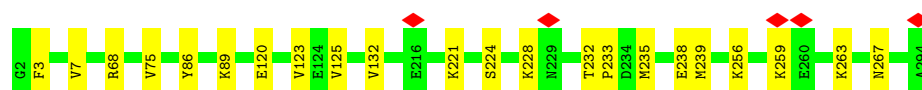
• Molecule 24: 60S ribosomal protein L4

Chain LC:  95% 5%



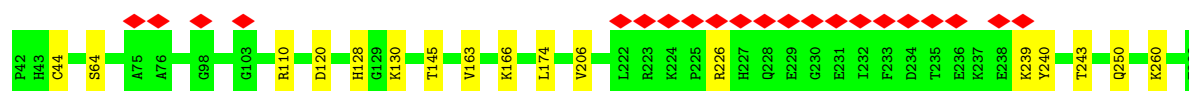
- Molecule 25: Large ribosomal subunit protein uL18

Chain LD:  92% 8%



- Molecule 26: 60S ribosomal protein L6

Chain LE:  9% 93% 7%



- Molecule 27: 60S ribosomal protein L7

Chain LF:  96% 4%



- Molecule 28: 60S ribosomal protein L7a

Chain LG:  12% 94% 6%



- Molecule 29: 60S ribosomal protein L9

Chain LH:  93% 7%

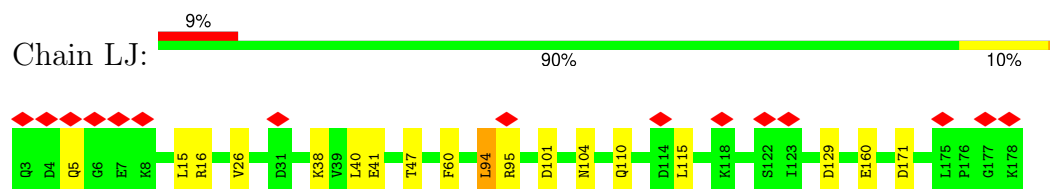


- Molecule 30: 60S ribosomal protein L10-like

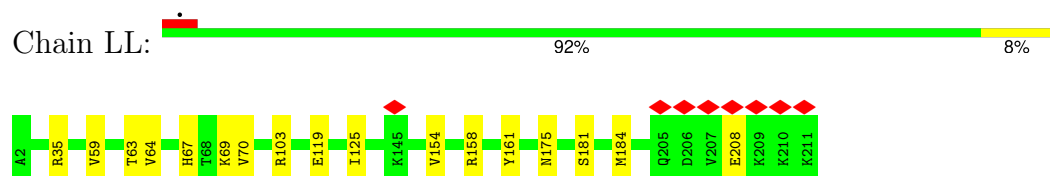
Chain LI:  93% 7%



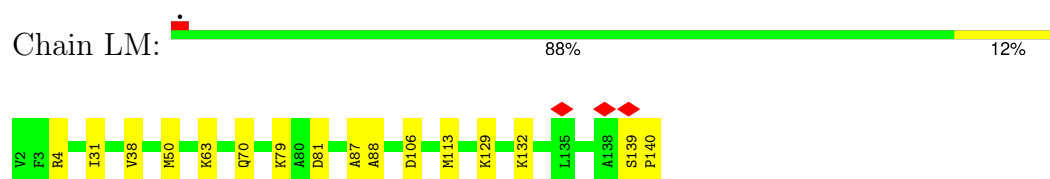
• Molecule 31: 60S ribosomal protein L11



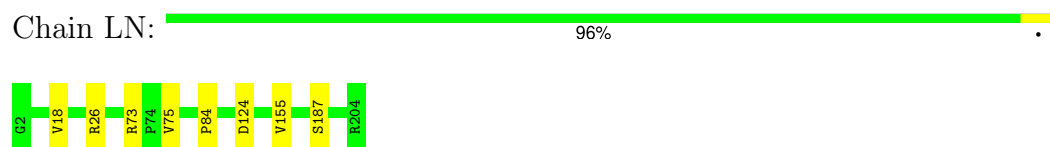
• Molecule 32: Large ribosomal subunit protein eL13



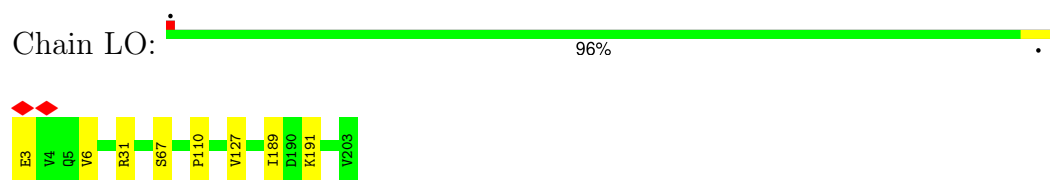
• Molecule 33: 60S ribosomal protein L14



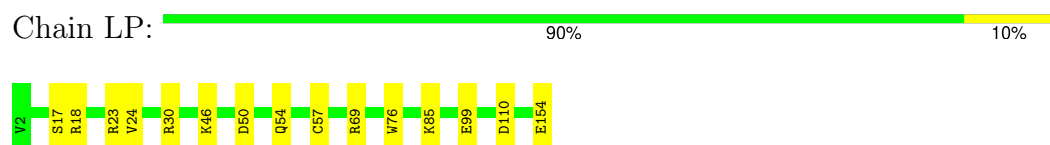
• Molecule 34: 60S ribosomal protein L15



• Molecule 35: 60S ribosomal protein L13a



• Molecule 36: 60S ribosomal protein L17



• Molecule 37: 60S ribosomal protein L18





- Molecule 38: 60S ribosomal protein L19



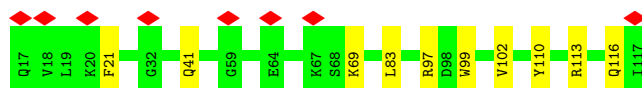
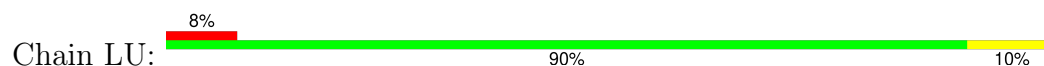
- Molecule 39: 60S ribosomal protein L18a



- Molecule 40: 60S ribosomal protein L21



- Molecule 41: Heparin-binding protein HBp15



- Molecule 42: 60S ribosomal protein L23

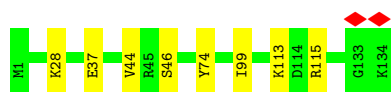


- Molecule 43: 60S ribosomal protein L23a



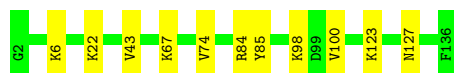
- Molecule 44: 60S ribosomal protein L26

Chain LY:  94% 6%



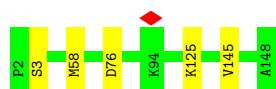
- Molecule 45: 60S ribosomal protein L27

Chain LZ:  92% 8%



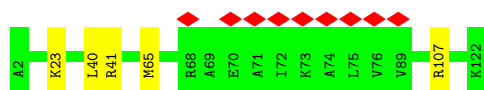
- Molecule 46: 60S ribosomal protein L27a

Chain La:  97% .



- Molecule 47: 60S ribosomal protein L29

Chain Lb:  8% 95% 5%



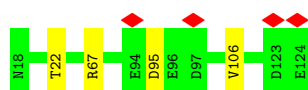
- Molecule 48: 60S ribosomal protein L30

Chain Lc:  90% 9% .



- Molecule 49: 60S ribosomal protein L31

Chain Ld:  96% .



- Molecule 50: 60S ribosomal protein L32

Chain Le:  95% 5%



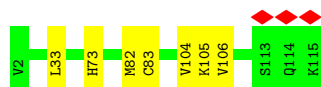
- Molecule 51: 60S ribosomal protein L35a

Chain Lf:  91% 9%



- Molecule 52: 60S ribosomal protein L34

Chain Lg:  94% 6%



- Molecule 53: 60S ribosomal protein L35

Chain Lh:  89% 11%




- Molecule 54: 60S ribosomal protein L36

Chain Li:  97%



- Molecule 55: 60S ribosomal protein L37

Chain Lj:  86% 13%




- Molecule 56: 60S ribosomal protein L38

Chain Lk:  6% 96%



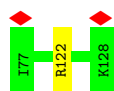
- Molecule 57: 60S ribosomal protein L39

Chain Ll:  88% 12%



- Molecule 58: Large ribosomal subunit protein eL40

Chain Lm: 98%



- Molecule 59: 60S ribosomal protein L41

Chain Ln: 96%



- Molecule 60: 60S ribosomal protein L36a

Chain Lo: 92% 8%



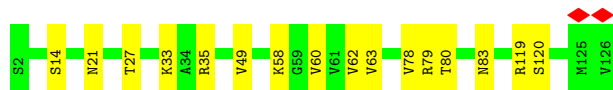
- Molecule 61: 60S ribosomal protein L37a

Chain Lp: 96%



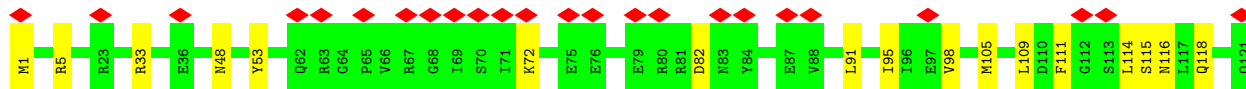
- Molecule 62: 60S ribosomal protein L28

Chain Lr: 87% 13%



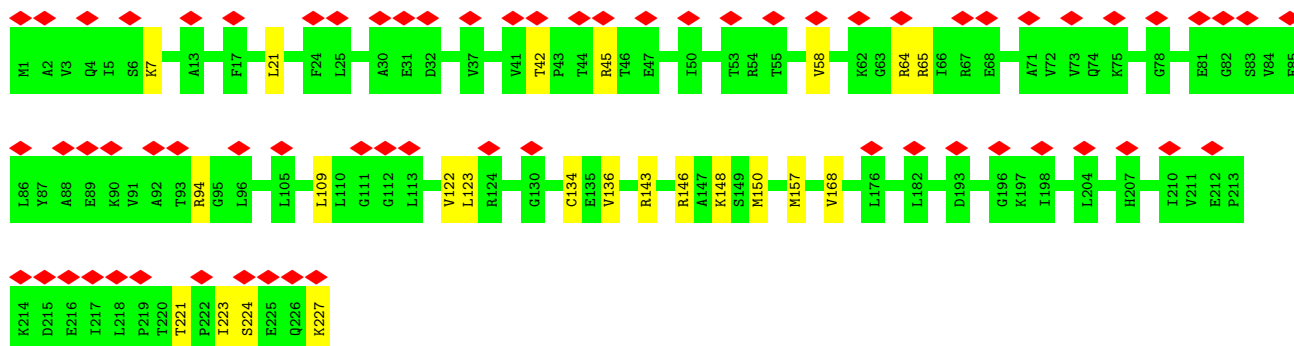
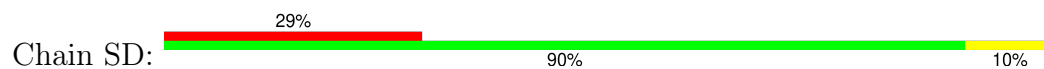
- Molecule 63: 40S ribosomal protein S17

Chain SR: 20% 85% 15%

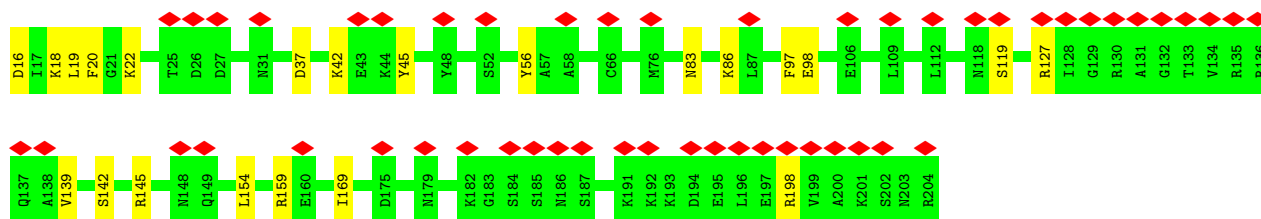
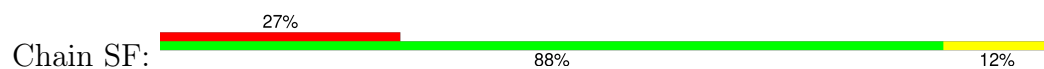




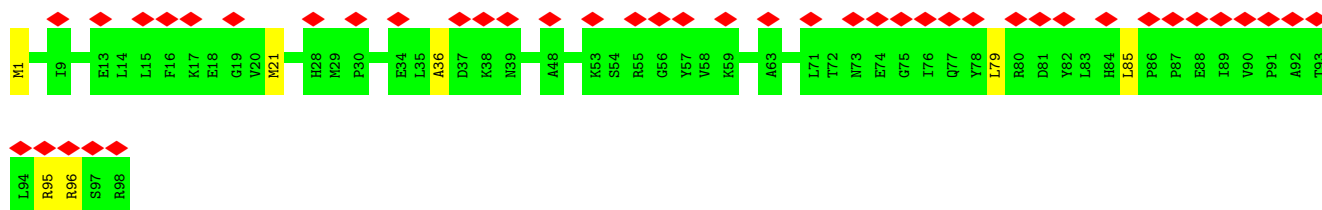
- Molecule 64: Small ribosomal subunit protein uS3



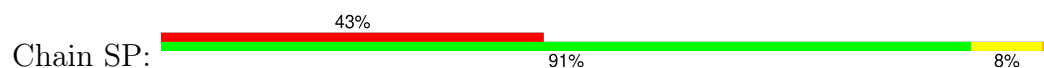
- Molecule 65: 40S ribosomal protein S5

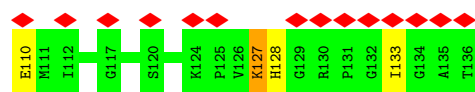


- Molecule 66: 40S ribosomal protein S10

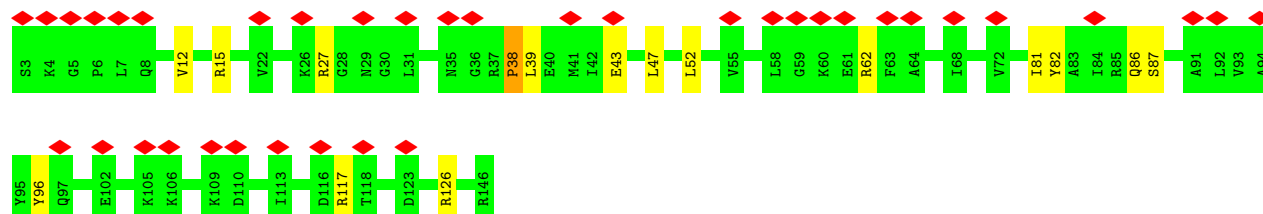
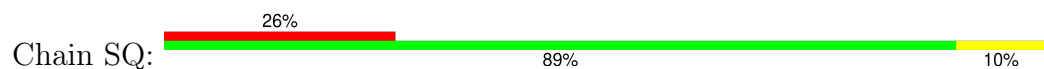


- Molecule 67: Small ribosomal subunit protein uS19

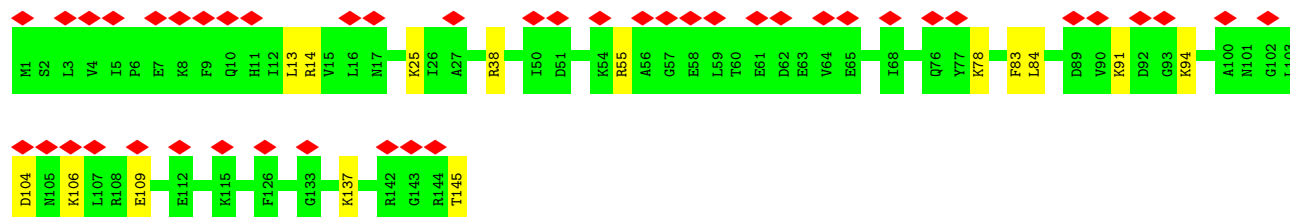
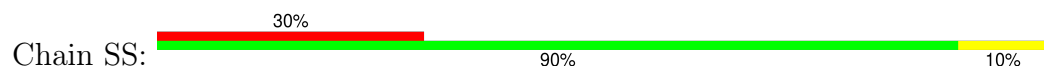




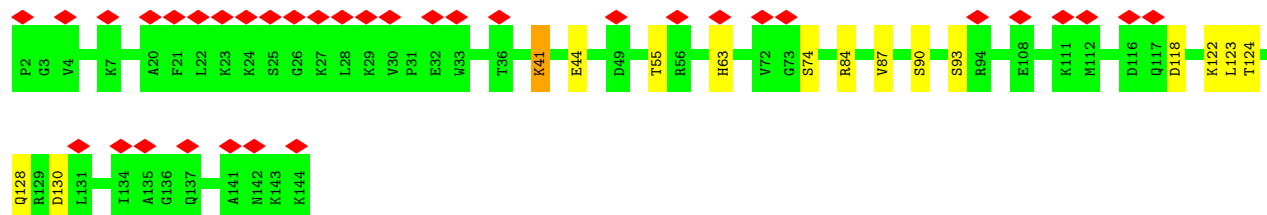
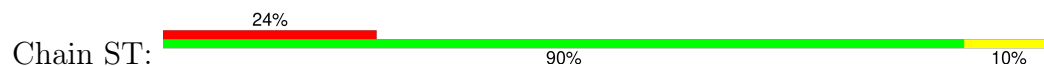
- Molecule 68: Small ribosomal subunit protein uS9



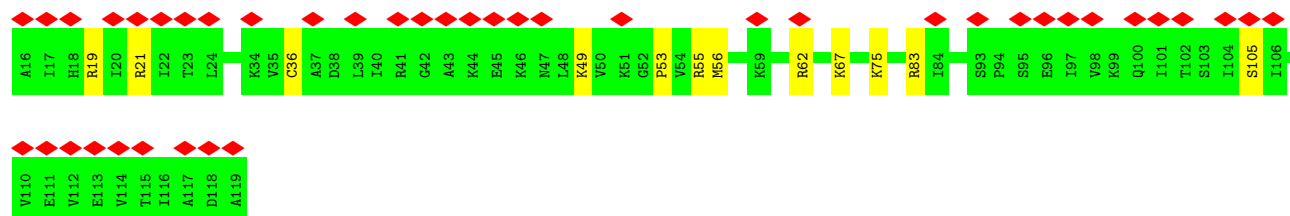
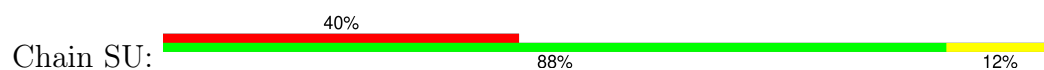
- Molecule 69: 40S ribosomal protein S18



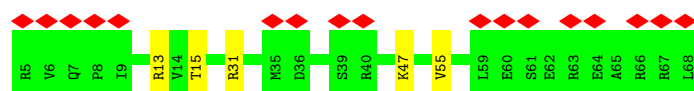
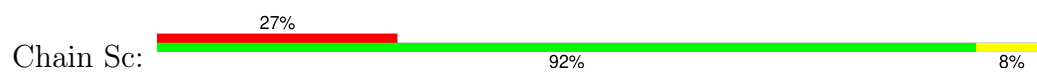
- Molecule 70: 40S ribosomal protein S19



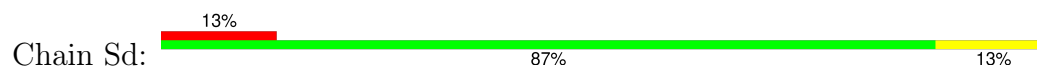
- Molecule 71: 40S ribosomal protein S20



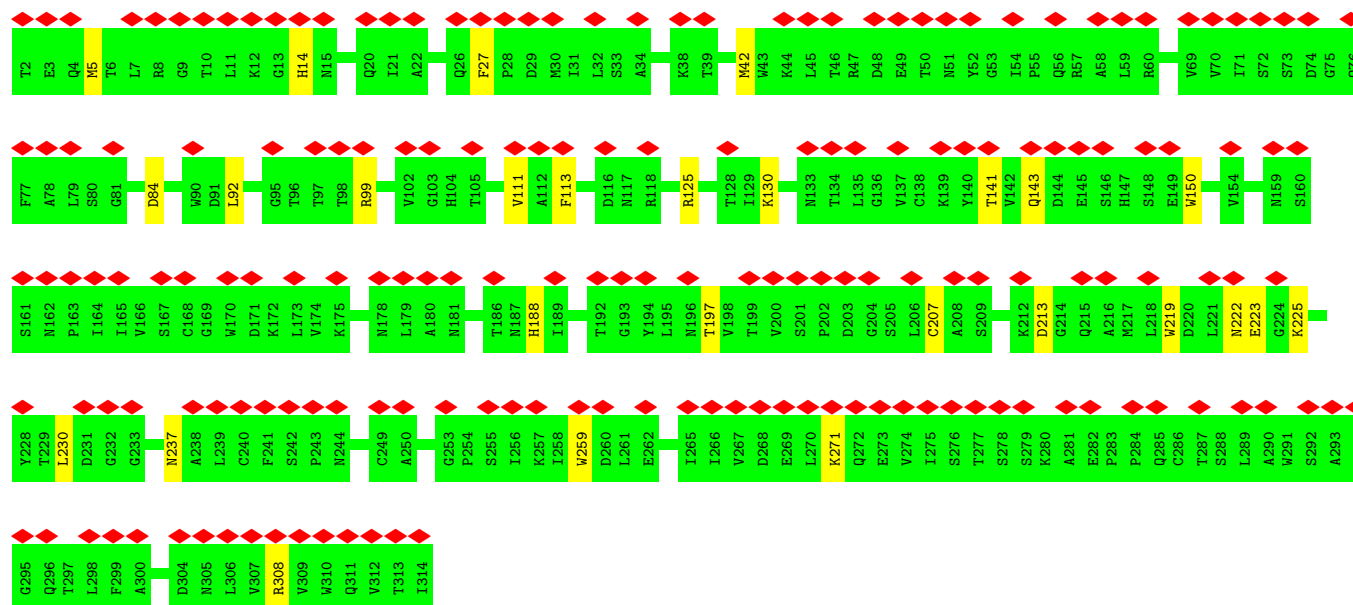
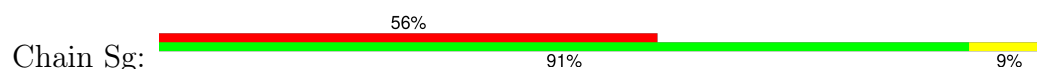
- Molecule 72: 40S ribosomal protein S28



- Molecule 73: 40S ribosomal protein S29



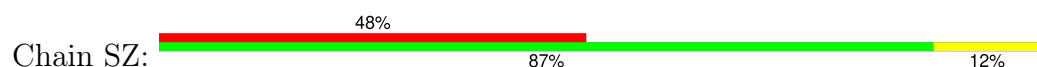
- Molecule 74: Receptor of activated protein C kinase 1

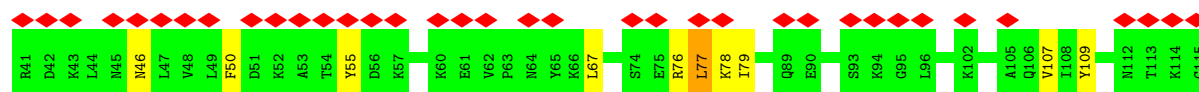


- Molecule 75: Small ribosomal subunit protein eS12

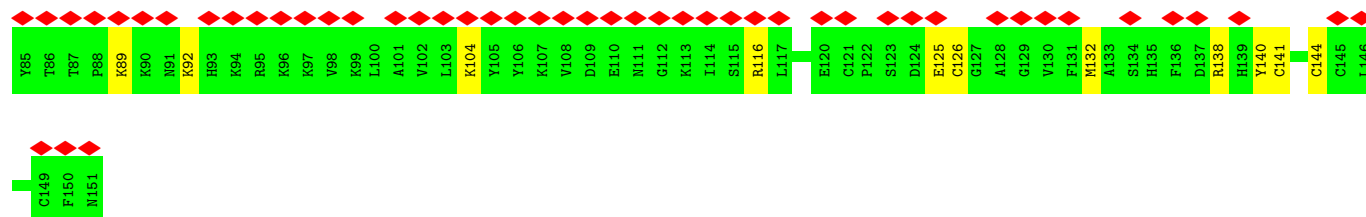
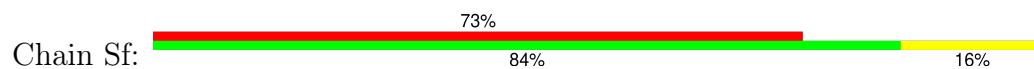


- Molecule 76: Small ribosomal subunit protein eS25

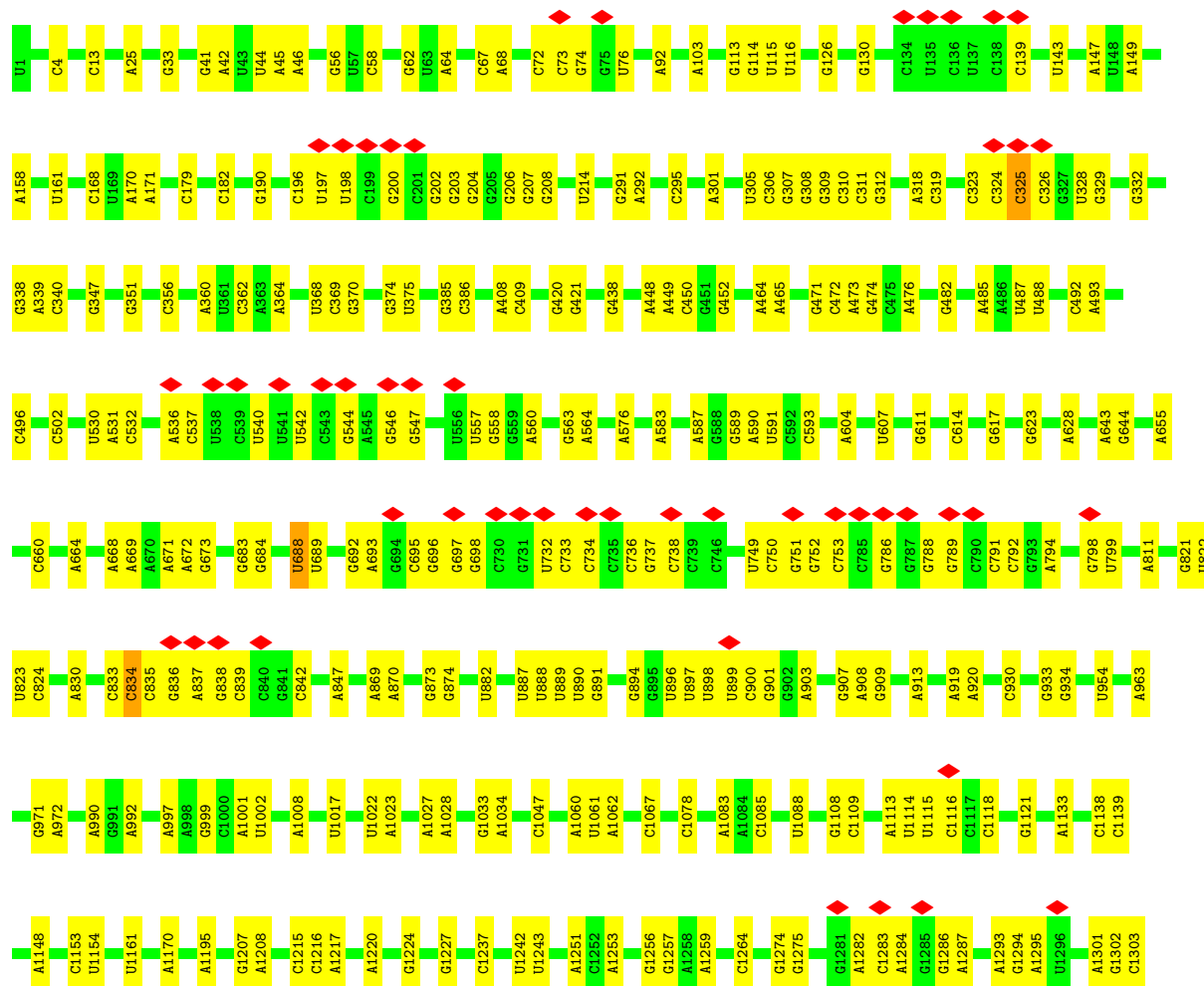
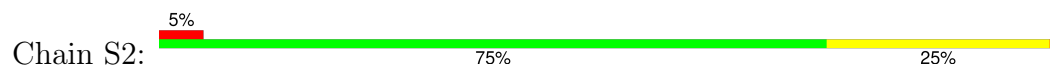


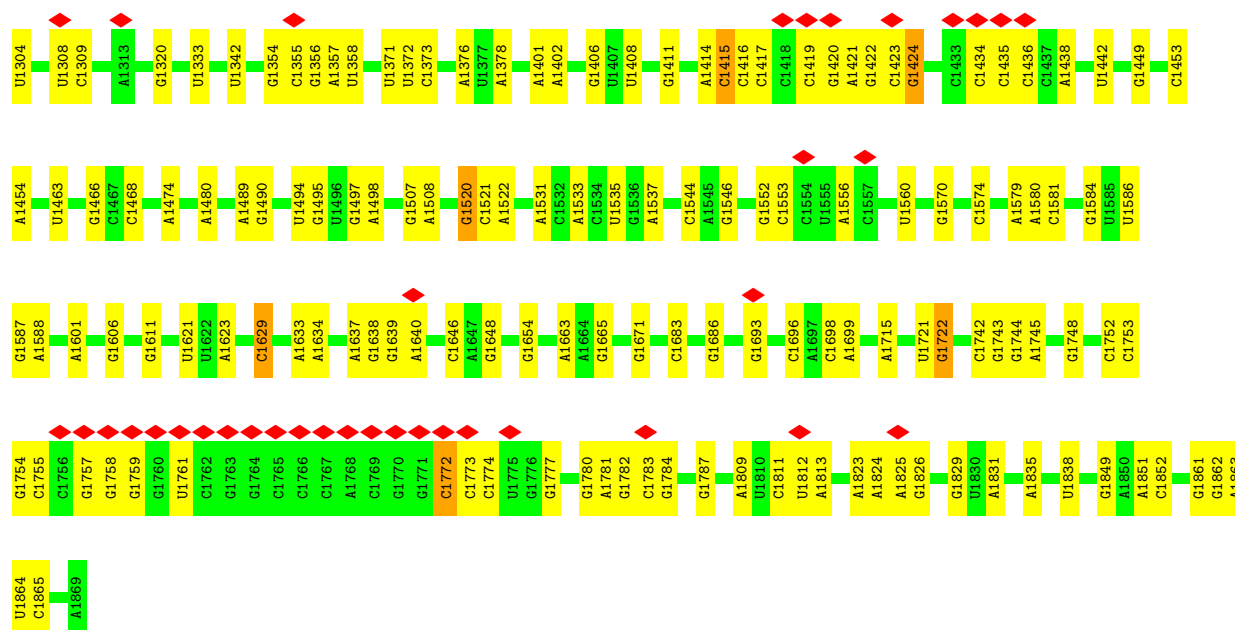


• Molecule 77: Ubiquitin-40S ribosomal protein S27a

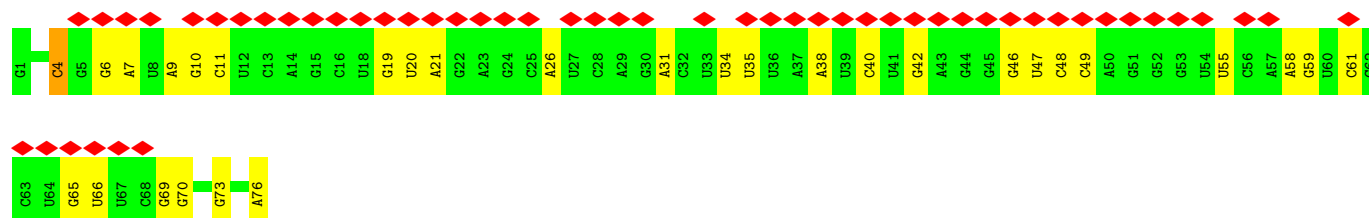
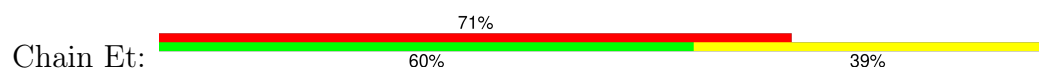


• Molecule 78: 18S rRNA

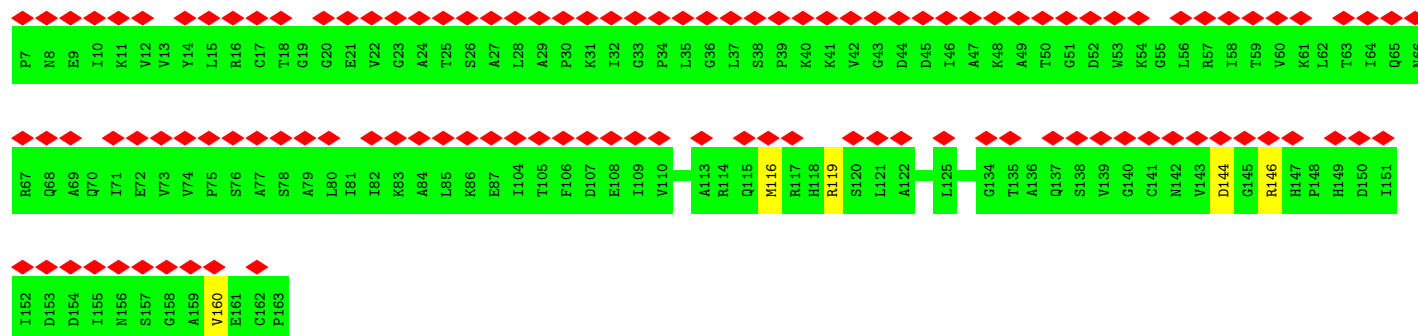
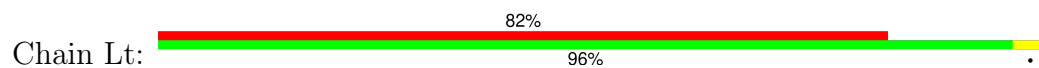




• Molecule 79: E site tRNA

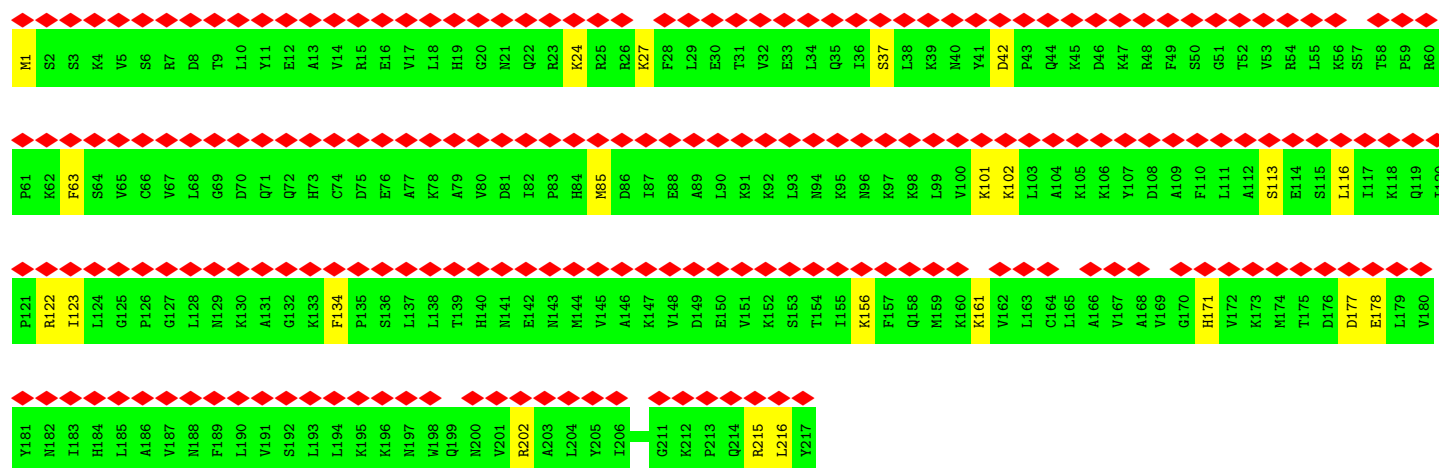


• Molecule 80: 60S ribosomal protein L12

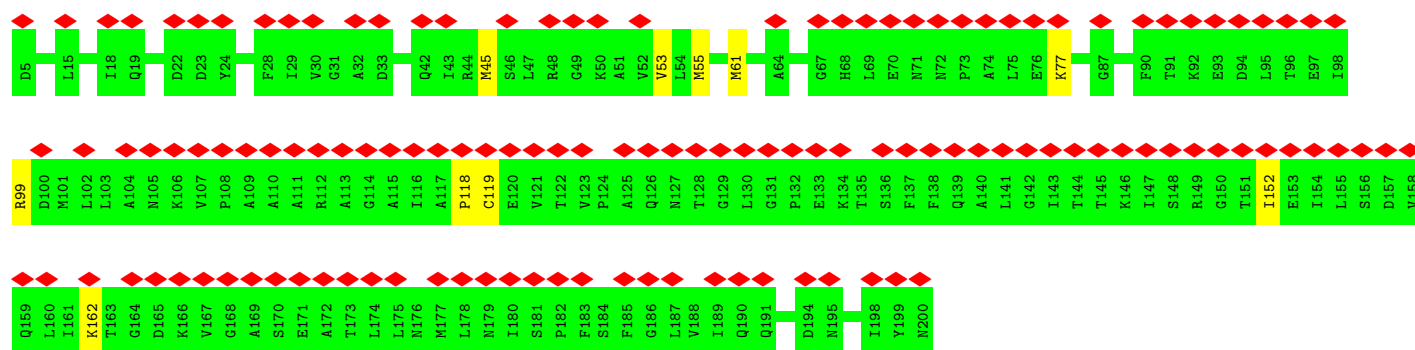


• Molecule 81: 60S ribosomal protein L10a

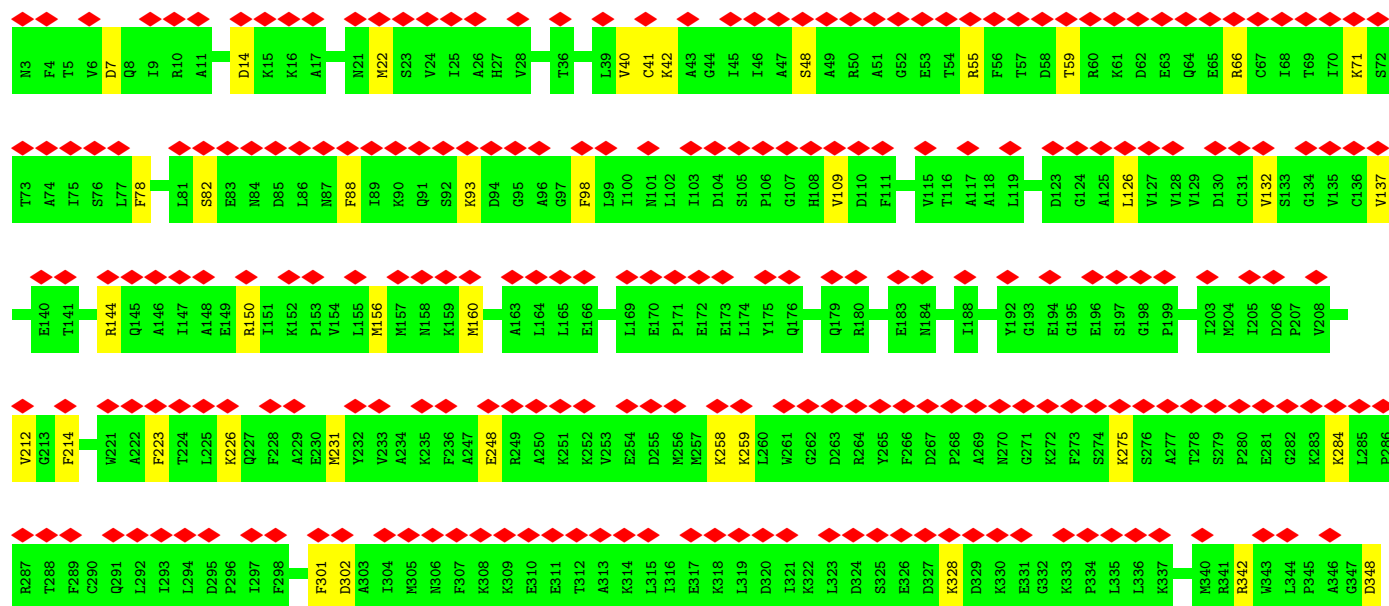
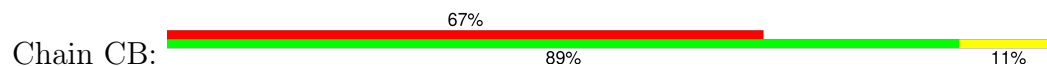


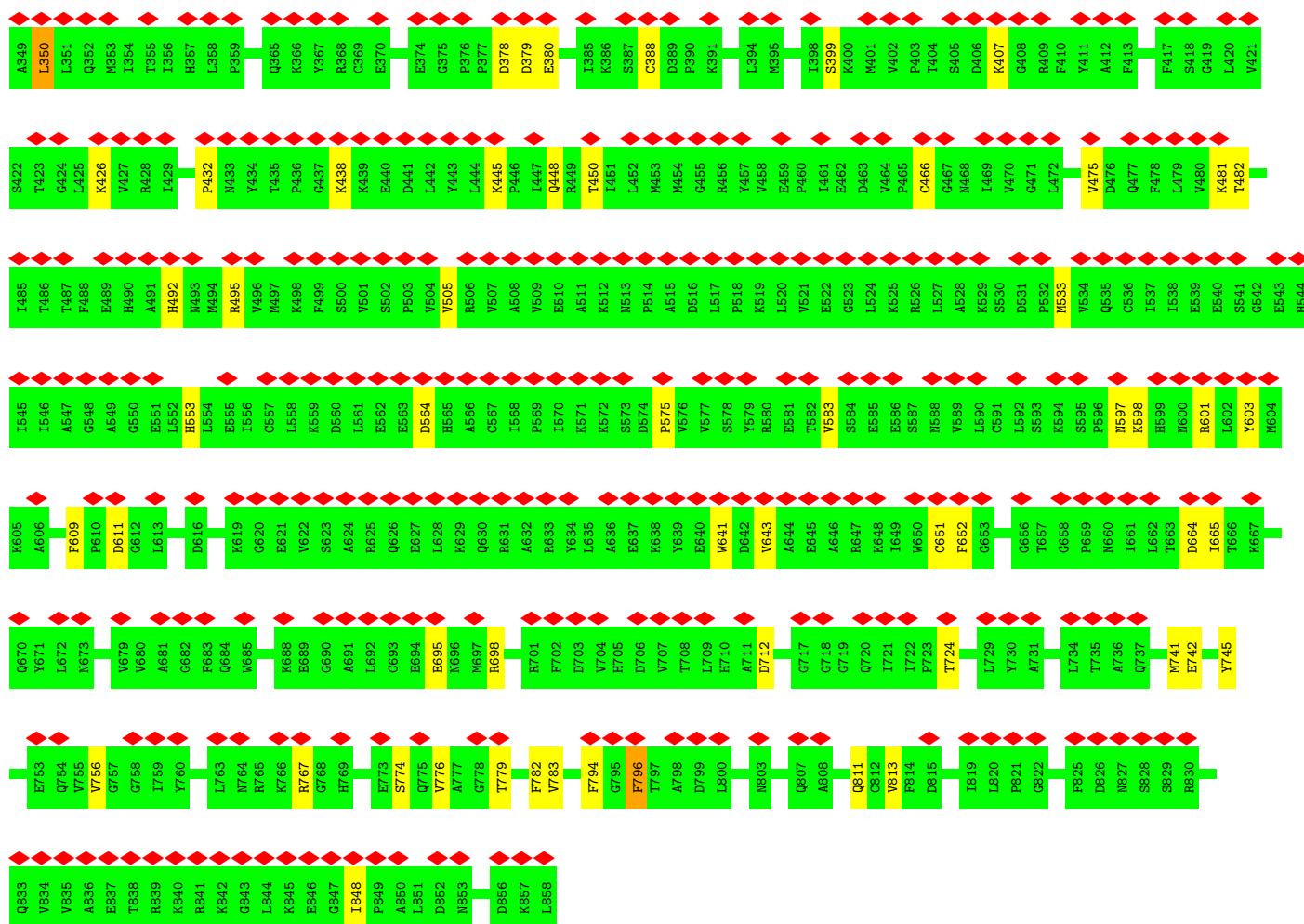


• Molecule 82: 60S acidic ribosomal protein P0

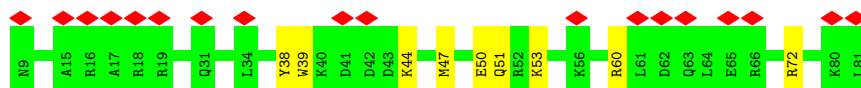
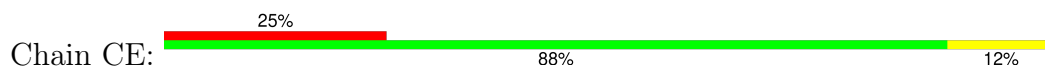


• Molecule 83: eEF2

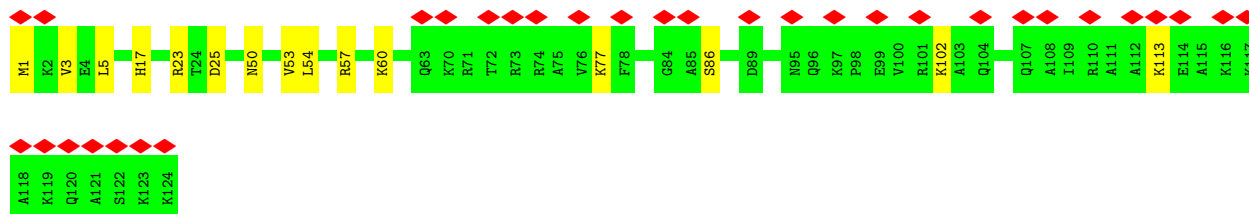




- Molecule 84: Coiled-coil domain-containing protein 124



- Molecule 85: 60S ribosomal protein L24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	86934	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	0.283	Depositor
Minimum map value	-0.113	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0253	Depositor
Map size (\AA)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.068, 1.068, 1.068	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	SE	0.29	0/2118	0.59	1/2849 (0.0%)
2	SI	0.35	1/1715 (0.1%)	0.64	1/2287 (0.0%)
3	SL	0.31	0/1268	0.64	1/1696 (0.1%)
4	SX	0.29	0/1116	0.60	0/1490
5	SG	0.68	4/1946 (0.2%)	0.95	4/2590 (0.2%)
6	SJ	0.29	0/1550	0.61	0/2069
7	SY	0.35	0/1083	0.64	1/1438 (0.1%)
8	Se	0.30	0/465	0.65	0/612
9	SA	0.31	0/1778	0.62	2/2416 (0.1%)
10	SB	0.29	0/1765	0.56	0/2362
11	SH	0.30	0/1519	0.61	0/2033
12	SV	0.28	0/643	0.58	0/860
13	Sa	0.28	0/836	0.61	0/1121
14	SC	0.29	0/1762	0.56	0/2381
15	SN	0.63	2/1232 (0.2%)	1.06	5/1656 (0.3%)
16	SO	0.28	0/1062	0.63	1/1425 (0.1%)
17	SW	0.29	0/1051	0.58	0/1406
18	Sb	0.30	0/665	0.58	0/891
19	L5	0.32	0/89312	0.86	73/139287 (0.1%)
20	L7	0.28	0/2861	0.79	0/4459
21	L8	0.31	0/3701	0.81	0/5766
22	LA	0.31	0/1936	0.63	0/2596
23	LB	0.31	0/3306	0.60	1/4424 (0.0%)
24	LC	0.29	0/2981	0.60	1/4002 (0.0%)
25	LD	0.43	3/2428 (0.1%)	0.81	4/3252 (0.1%)
26	LE	0.30	0/1942	0.60	0/2606
27	LF	0.31	0/1905	0.56	0/2539
28	LG	0.30	0/1960	0.58	1/2637 (0.0%)
29	LH	0.31	0/1537	0.61	0/2066
30	LI	0.30	0/1673	0.58	0/2233
31	LJ	0.31	0/1433	0.63	0/1915
32	LL	0.29	0/1732	0.58	0/2315

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LM	0.69	3/1161 (0.3%)	1.04	5/1554 (0.3%)
34	LN	0.30	0/1746	0.61	0/2338
35	LO	0.30	0/1682	0.56	0/2250
36	LP	0.29	0/1268	0.56	0/1701
37	LQ	0.30	0/1537	0.64	0/2052
38	LR	0.27	0/1581	0.60	0/2088
39	LS	0.32	0/1493	0.60	0/2003
40	LT	0.32	0/1326	0.59	0/1770
41	LU	0.45	0/839	0.66	0/1126
42	LV	0.31	0/993	0.60	0/1332
43	LX	0.28	0/1002	0.56	0/1345
44	LY	0.30	0/1132	0.59	0/1504
45	LZ	0.35	0/1130	0.56	0/1507
46	La	0.30	0/1191	0.57	0/1591
47	Lb	0.28	0/889	0.60	0/1175
48	Lc	0.34	0/774	0.63	1/1038 (0.1%)
49	Ld	0.30	0/903	0.62	0/1216
50	Le	0.31	0/1071	0.58	0/1429
51	Lf	0.32	0/895	0.64	0/1198
52	Lg	0.28	0/916	0.61	0/1220
53	Lh	0.28	0/1023	0.58	0/1351
54	Li	0.29	0/843	0.60	0/1115
55	Lj	0.39	0/720	0.83	3/952 (0.3%)
56	Lk	0.28	0/575	0.52	0/761
57	Ll	0.28	0/454	0.59	0/599
58	Lm	0.26	0/435	0.54	0/575
59	Ln	0.29	0/231	0.76	0/294
60	Lo	0.30	0/876	0.59	0/1156
61	Lp	0.31	0/718	0.56	0/953
62	Lr	0.29	0/1017	0.59	0/1364
63	SR	0.31	0/1105	0.67	1/1484 (0.1%)
64	SD	0.30	0/1793	0.60	0/2414
65	SF	0.36	1/1516 (0.1%)	0.64	1/2037 (0.0%)
66	SK	0.29	0/851	0.59	0/1147
67	SP	0.54	2/1003 (0.2%)	0.73	1/1342 (0.1%)
68	SQ	0.75	4/1160 (0.3%)	0.99	5/1553 (0.3%)
69	SS	0.29	0/1216	0.65	0/1628
70	ST	0.30	0/1131	0.59	0/1515
71	SU	0.25	0/831	0.56	0/1115
72	Sc	0.27	0/508	0.69	0/680
73	Sd	0.30	0/470	0.59	0/623
74	Sg	0.30	0/2493	0.59	1/3394 (0.0%)
75	SM	0.26	0/950	0.52	0/1275

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SZ	0.29	0/604	0.76	2/810 (0.2%)
77	Sf	0.28	0/560	0.62	0/745
78	S2	0.25	0/41242	0.82	39/64255 (0.1%)
79	Et	0.26	0/1778	0.89	1/2767 (0.0%)
80	Lt	0.25	0/1058	0.57	0/1430
81	Lz	0.38	2/1769 (0.1%)	0.63	1/2371 (0.0%)
82	Ls	0.28	0/1519	0.57	0/2052
83	CB	0.42	6/6734 (0.1%)	0.64	7/9094 (0.1%)
84	CE	0.63	2/616 (0.3%)	0.70	1/812 (0.1%)
85	LW	0.31	0/979	0.61	0/1295
All	All	0.32	30/244588 (0.0%)	0.77	165/358074 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	SX	0	1
11	SH	0	1
22	LA	0	1
23	LB	0	2
31	LJ	0	1
32	LL	0	1
33	LM	0	1
35	LO	0	1
51	Lf	0	3
55	Lj	0	2
62	Lr	0	1
67	SP	0	1
68	SQ	0	1
76	SZ	0	1
All	All	0	18

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	SG	130	PRO	CB-CG	21.28	2.56	1.50
68	SQ	38	PRO	CG-CD	-18.38	0.90	1.50
15	SN	23	PRO	CB-CG	17.41	2.37	1.50
33	LM	140	PRO	CB-CG	16.55	2.32	1.50
83	CB	575	PRO	CB-CG	11.72	2.08	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	SG	130	PRO	CG-CD	-11.25	1.13	1.50
83	CB	575	PRO	CG-CD	-10.77	1.15	1.50
84	CE	51	GLN	CG-CD	-10.73	1.26	1.51
68	SQ	47	LEU	CG-CD1	-10.02	1.14	1.51
5	SG	130	PRO	CA-CB	-9.63	1.34	1.53
83	CB	651	CYS	CB-SG	-9.27	1.66	1.82
33	LM	140	PRO	CG-CD	-8.57	1.22	1.50
83	CB	796	PHE	CD2-CE2	-8.25	1.22	1.39
67	SP	108	LYS	CG-CD	-8.06	1.25	1.52
15	SN	23	PRO	CG-CD	-7.75	1.25	1.50
25	LD	233	PRO	CA-CB	7.74	1.69	1.53
25	LD	233	PRO	CG-CD	-7.65	1.25	1.50
25	LD	233	PRO	CB-CG	-7.55	1.12	1.50
33	LM	140	PRO	CA-CB	7.05	1.67	1.53
83	CB	575	PRO	N-CD	6.73	1.57	1.47
67	SP	110	GLU	CB-CG	6.54	1.64	1.52
81	Lz	134	PHE	CD1-CE1	-6.34	1.26	1.39
84	CE	51	GLN	CD-NE2	-6.28	1.17	1.32
5	SG	130	PRO	N-CD	6.27	1.56	1.47
68	SQ	38	PRO	N-CD	6.10	1.56	1.47
83	CB	796	PHE	CE1-CZ	-5.95	1.26	1.37
65	SF	45	TYR	CD2-CE2	-5.89	1.30	1.39
2	SI	89	GLU	CD-OE2	-5.67	1.19	1.25
81	Lz	134	PHE	CE2-CZ	-5.17	1.27	1.37
68	SQ	81	ILE	CG1-CD1	-5.05	1.15	1.50

All (165) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	SN	23	PRO	CA-N-CD	-23.22	78.99	111.50
5	SG	130	PRO	N-CD-CG	-22.13	70.01	103.20
33	LM	140	PRO	CA-N-CD	-20.97	82.14	111.50
68	SQ	38	PRO	N-CD-CG	-19.84	73.44	103.20
33	LM	140	PRO	CB-CG-CD	-19.79	29.34	106.50
15	SN	23	PRO	CB-CG-CD	-19.70	29.67	106.50
25	LD	233	PRO	N-CD-CG	-19.10	74.55	103.20
25	LD	233	PRO	CB-CG-CD	18.84	179.97	106.50
5	SG	130	PRO	N-CA-CB	-18.42	81.19	103.30
5	SG	130	PRO	CB-CG-CD	-17.86	36.85	106.50
25	LD	233	PRO	CA-CB-CG	-17.66	70.45	104.00
15	SN	23	PRO	N-CD-CG	17.15	128.92	103.20
33	LM	140	PRO	N-CD-CG	14.87	125.51	103.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	CB	575	PRO	N-CD-CG	-14.43	81.55	103.20
68	SQ	38	PRO	CA-N-CD	-12.15	94.48	111.50
55	Lj	40	PRO	N-CD-CG	-11.97	85.25	103.20
68	SQ	38	PRO	CA-CB-CG	-11.55	82.06	104.00
15	SN	22	VAL	C-N-CD	11.10	151.71	128.40
5	SG	130	PRO	CA-CB-CG	-10.60	83.86	104.00
67	SP	108	LYS	CD-CE-NZ	9.77	134.16	111.70
19	L5	456	C	O4'-C1'-N1	9.60	115.88	108.20
78	S2	1453	C	C2-N1-C1'	9.29	129.01	118.80
19	L5	174	C	N3-C2-O2	-9.26	115.42	121.90
55	Lj	40	PRO	CA-CB-CG	-8.83	87.22	104.00
83	CB	575	PRO	CA-CB-CG	-8.65	87.57	104.00
19	L5	2710	C	N1-C2-O2	8.59	124.05	118.90
19	L5	485	C	C2-N1-C1'	8.51	128.17	118.80
19	L5	3773	U	N3-C2-O2	-8.44	116.30	122.20
78	S2	1629	C	N3-C2-O2	-8.33	116.07	121.90
19	L5	2710	C	C2-N1-C1'	8.31	127.94	118.80
78	S2	1453	C	N1-C2-O2	7.87	123.62	118.90
19	L5	490	C	N3-C2-O2	-7.87	116.39	121.90
19	L5	1082	C	O4'-C1'-N1	7.65	114.32	108.20
19	L5	181	C	N1-C2-O2	7.60	123.46	118.90
78	S2	356	C	C2-N1-C1'	7.60	127.16	118.80
19	L5	925	C	N1-C2-O2	7.54	123.43	118.90
68	SQ	81	ILE	CA-CB-CG1	-7.53	96.70	111.00
19	L5	417	G	O4'-C1'-N9	7.50	114.20	108.20
2	SI	40	PRO	CA-N-CD	-7.48	101.03	111.50
19	L5	1252	C	N3-C2-O2	-7.40	116.72	121.90
19	L5	2710	C	N3-C2-O2	-7.36	116.75	121.90
19	L5	1414	C	N3-C2-O2	-7.33	116.77	121.90
19	L5	456	C	N3-C2-O2	-7.30	116.79	121.90
78	S2	1722	G	N3-C4-N9	7.25	130.35	126.00
19	L5	1082	C	N3-C2-O2	-7.21	116.86	121.90
83	CB	575	PRO	CB-CG-CD	-7.20	78.41	106.50
78	S2	356	C	N1-C2-O2	7.19	123.21	118.90
78	S2	1416	C	N3-C2-O2	-7.19	116.87	121.90
19	L5	181	C	C2-N1-C1'	7.13	126.64	118.80
19	L5	1414	C	N1-C2-O2	7.12	123.17	118.90
78	S2	1772	C	N1-C2-O2	7.12	123.17	118.90
19	L5	2257	C	C2-N1-C1'	7.08	126.59	118.80
19	L5	2257	C	N1-C2-O2	6.98	123.09	118.90
78	S2	1772	C	N3-C2-O2	-6.89	117.08	121.90
78	S2	1811	C	N1-C2-O2	6.87	123.02	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	L5	925	C	N3-C2-O2	-6.84	117.11	121.90
19	L5	255	C	N3-C2-O2	-6.71	117.21	121.90
9	SA	154	LEU	CA-CB-CG	6.64	130.58	115.30
24	LC	2	ALA	C-N-CA	6.61	138.23	121.70
3	SL	25	LEU	CA-CB-CG	6.60	130.48	115.30
78	S2	1811	C	N3-C2-O2	-6.58	117.30	121.90
78	S2	1453	C	C6-N1-C1'	-6.56	112.93	120.80
19	L5	485	C	C6-N1-C1'	-6.45	113.07	120.80
19	L5	3773	U	N1-C2-O2	6.40	127.28	122.80
19	L5	100	C	C2-N1-C1'	6.35	125.78	118.80
78	S2	786	G	C4-C5-N7	-6.29	108.28	110.80
19	L5	3773	U	O4'-C1'-N1	6.29	113.23	108.20
33	LM	140	PRO	N-CA-CB	-6.28	95.70	102.60
33	LM	139	SER	C-N-CD	6.26	141.55	128.40
76	SZ	77	LEU	CA-CB-CG	6.26	129.69	115.30
78	S2	1629	C	C6-N1-C2	-6.25	117.80	120.30
19	L5	181	C	N3-C2-O2	-6.23	117.54	121.90
78	S2	1722	G	C6-C5-N7	-6.18	126.69	130.40
78	S2	1453	C	C5-C6-N1	6.14	124.07	121.00
19	L5	182	G	N3-C4-N9	-6.14	122.32	126.00
83	CB	350	LEU	CA-CB-CG	6.13	129.39	115.30
19	L5	4709	U	C2-N1-C1'	6.06	124.98	117.70
83	CB	575	PRO	N-CA-CB	-6.06	95.94	102.60
55	Lj	40	PRO	CA-N-CD	-6.05	103.03	111.50
19	L5	4068	U	C2-N1-C1'	6.01	124.91	117.70
78	S2	356	C	N3-C2-O2	-5.99	117.71	121.90
19	L5	175	C	N3-C2-O2	-5.94	117.74	121.90
19	L5	4709	U	C5-C4-O4	-5.92	122.35	125.90
1	SE	87	MET	CG-SD-CE	-5.88	90.80	100.20
78	S2	1309	C	C2-N1-C1'	5.80	125.18	118.80
19	L5	2710	C	C6-N1-C2	-5.79	117.98	120.30
19	L5	2018	C	C5-C6-N1	5.79	123.89	121.00
48	Lc	98	ASP	CB-CG-OD2	5.77	123.49	118.30
19	L5	3761	C	C2-N1-C1'	5.76	125.14	118.80
78	S2	1416	C	C6-N1-C2	-5.75	118.00	120.30
19	L5	1216	C	C2-N1-C1'	5.74	125.11	118.80
19	L5	2257	C	N3-C2-O2	-5.71	117.90	121.90
19	L5	4924	C	N3-C2-O2	-5.70	117.91	121.90
78	S2	1722	G	C4-N9-C1'	5.69	133.89	126.50
78	S2	1453	C	N3-C2-O2	-5.67	117.93	121.90
78	S2	1453	C	C6-N1-C2	-5.66	118.04	120.30
78	S2	688	U	P-O3'-C3'	5.65	126.48	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	LD	267	ASN	C-N-CA	-5.64	107.59	121.70
19	L5	2710	C	C6-N1-C1'	-5.64	114.04	120.80
68	SQ	38	PRO	N-CA-CB	-5.60	96.44	102.60
19	L5	3767	C	C2-N1-C1'	5.58	124.94	118.80
23	LB	17	LEU	CA-CB-CG	5.57	128.10	115.30
78	S2	1424	G	N3-C4-N9	5.49	129.29	126.00
15	SN	23	PRO	N-CA-CB	-5.49	96.57	102.60
78	S2	786	G	N7-C8-N9	-5.47	110.37	113.10
19	L5	1191	C	N3-C2-O2	-5.46	118.08	121.90
19	L5	263	G	N1-C2-N2	-5.46	111.28	116.20
19	L5	914	U	P-O3'-C3'	5.46	126.25	119.70
78	S2	834	C	N3-C2-O2	-5.46	118.08	121.90
78	S2	834	C	N1-C2-O2	5.45	122.17	118.90
19	L5	3773	U	C2-N1-C1'	5.44	124.22	117.70
19	L5	489	C	N1-C2-O2	5.43	122.16	118.90
19	L5	914	U	C5-C4-O4	-5.41	122.66	125.90
19	L5	3761	C	N1-C2-O2	5.41	122.14	118.90
19	L5	4928	C	C2-N1-C1'	5.39	124.73	118.80
16	SO	14	VAL	C-N-CA	5.36	135.10	121.70
78	S2	1722	G	C8-N9-C1'	-5.36	120.04	127.00
65	SF	154	LEU	CB-CG-CD2	5.35	120.10	111.00
78	S2	1415	C	N1-C2-O2	5.33	122.10	118.90
19	L5	1182	C	N1-C2-O2	5.32	122.09	118.90
78	S2	1022	U	C2-N1-C1'	5.32	124.08	117.70
78	S2	356	C	C6-N1-C1'	-5.31	114.43	120.80
76	SZ	67	LEU	CA-CB-CG	5.30	127.50	115.30
19	L5	1552	G	O4'-C1'-N9	5.29	112.43	108.20
78	S2	786	G	C5-N7-C8	5.29	106.94	104.30
78	S2	1520	G	C4-N9-C1'	5.28	133.36	126.50
19	L5	262	G	N1-C6-O6	-5.24	116.75	119.90
19	L5	129	C	C6-N1-C1'	5.24	127.08	120.80
28	LG	136	LEU	CA-CB-CG	5.23	127.32	115.30
19	L5	963	G	C4-N9-C1'	5.22	133.28	126.50
19	L5	174	C	N1-C2-O2	5.21	122.03	118.90
19	L5	1182	C	C2-N1-C1'	5.21	124.53	118.80
84	CE	53	LYS	CA-CB-CG	5.21	124.86	113.40
74	Sg	5	MET	CA-CB-CG	5.19	122.12	113.30
79	Et	4	C	C2-N1-C1'	5.17	124.49	118.80
78	S2	1139	C	N1-C2-O2	5.17	122.00	118.90
19	L5	2018	C	C6-N1-C2	-5.16	118.23	120.30
19	L5	1241	C	N1-C2-O2	5.16	122.00	118.90
7	SY	18	LEU	CA-CB-CG	5.15	127.14	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	SA	174	MET	CB-CG-SD	-5.15	96.96	112.40
63	SR	109	LEU	CA-CB-CG	5.14	127.13	115.30
19	L5	4476	C	C2-N1-C1'	5.13	124.44	118.80
19	L5	4527	G	O4'-C1'-N9	5.12	112.30	108.20
19	L5	664	G	C5-C6-O6	5.11	131.67	128.60
83	CB	126	LEU	CA-CB-CG	5.11	127.04	115.30
19	L5	1597	G	O4'-C1'-N9	5.10	112.28	108.20
81	Lz	216	LEU	CA-CB-CG	5.10	127.03	115.30
19	L5	262	G	C5-C6-O6	5.09	131.65	128.60
19	L5	1447	C	C6-N1-C2	-5.09	118.26	120.30
83	CB	432	PRO	CA-N-CD	-5.09	104.38	111.50
78	S2	1611	G	C5-C6-O6	5.08	131.65	128.60
19	L5	4447	C	C2-N1-C1'	-5.06	113.23	118.80
19	L5	3610	A	C8-N9-C4	5.06	107.82	105.80
19	L5	115	C	N1-C2-O2	5.04	121.93	118.90
19	L5	181	C	C6-N1-C2	-5.04	118.28	120.30
78	S2	325	C	C2-N1-C1'	5.03	124.33	118.80
19	L5	209	U	C2-N1-C1'	5.03	123.73	117.70
19	L5	1241	C	C2-N1-C1'	5.03	124.33	118.80
19	L5	2627	C	C2-N1-C1'	5.02	124.32	118.80
19	L5	129	C	N3-C2-O2	-5.01	118.39	121.90
78	S2	1520	G	N3-C4-N9	5.01	129.01	126.00
19	L5	2410	C	C2-N1-C1'	5.01	124.31	118.80
19	L5	1252	C	N1-C2-O2	5.00	121.90	118.90
78	S2	325	C	N1-C2-O2	5.00	121.90	118.90
78	S2	1139	C	N3-C2-O2	-5.00	118.40	121.90

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	LA	13	GLY	Peptide
23	LB	17	LEU	Peptide
23	LB	258	HIS	Peptide
31	LJ	94	LEU	Peptide
32	LL	154	VAL	Peptide
33	LM	87	ALA	Peptide
35	LO	110	PRO	Peptide
51	Lf	103	VAL	Peptide
51	Lf	106	TYR	Peptide
51	Lf	79	GLY	Peptide
55	Lj	39	TYR	Peptide

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Mol	Chain	Res	Type	Group
55	Lj	40	PRO	Peptide
62	Lr	119	ARG	Sidechain
11	SH	15	LYS	Peptide
67	SP	127	LYS	Peptide
68	SQ	43	GLU	Peptide
4	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	SE	260/262 (99%)	243 (94%)	17 (6%)	0	100	100
2	SI	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
3	SL	151/153 (99%)	138 (91%)	13 (9%)	0	100	100
4	SX	139/282 (49%)	127 (91%)	11 (8%)	1 (1%)	19	36
5	SG	235/237 (99%)	225 (96%)	10 (4%)	0	100	100
6	SJ	183/185 (99%)	170 (93%)	13 (7%)	0	100	100
7	SY	129/131 (98%)	118 (92%)	11 (8%)	0	100	100
8	Se	56/58 (97%)	48 (86%)	8 (14%)	0	100	100
9	SA	219/221 (99%)	193 (88%)	26 (12%)	0	100	100
10	SB	212/214 (99%)	201 (95%)	11 (5%)	0	100	100
11	SH	182/186 (98%)	165 (91%)	17 (9%)	0	100	100
12	SV	81/83 (98%)	71 (88%)	10 (12%)	0	100	100
13	Sa	100/102 (98%)	91 (91%)	8 (8%)	1 (1%)	13	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	SC	220/222 (99%)	205 (93%)	15 (7%)	0	100	100
15	SN	148/150 (99%)	146 (99%)	2 (1%)	0	100	100
16	SO	138/140 (99%)	124 (90%)	14 (10%)	0	100	100
17	SW	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
18	Sb	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
22	LA	246/248 (99%)	224 (91%)	21 (8%)	1 (0%)	30	49
23	LB	400/402 (100%)	371 (93%)	29 (7%)	0	100	100
24	LC	366/368 (100%)	337 (92%)	29 (8%)	0	100	100
25	LD	291/293 (99%)	273 (94%)	18 (6%)	0	100	100
26	LE	232/236 (98%)	203 (88%)	29 (12%)	0	100	100
27	LF	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
28	LG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
29	LH	188/190 (99%)	177 (94%)	11 (6%)	0	100	100
30	LI	198/202 (98%)	186 (94%)	12 (6%)	0	100	100
31	LJ	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
32	LL	208/210 (99%)	197 (95%)	11 (5%)	0	100	100
33	LM	137/139 (99%)	126 (92%)	10 (7%)	1 (1%)	19	36
34	LN	201/203 (99%)	191 (95%)	8 (4%)	2 (1%)	13	25
35	LO	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
36	LP	151/153 (99%)	138 (91%)	13 (9%)	0	100	100
37	LQ	185/187 (99%)	178 (96%)	7 (4%)	0	100	100
38	LR	183/187 (98%)	175 (96%)	8 (4%)	0	100	100
39	LS	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
40	LT	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
41	LU	99/101 (98%)	81 (82%)	18 (18%)	0	100	100
42	LV	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
43	LX	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
44	LY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
45	LZ	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
46	La	145/147 (99%)	136 (94%)	9 (6%)	0	100	100
47	Lb	105/109 (96%)	97 (92%)	8 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	Lc	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
49	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
50	Le	126/128 (98%)	117 (93%)	8 (6%)	1 (1%)	16	32
51	Lf	107/109 (98%)	96 (90%)	10 (9%)	1 (1%)	14	28
52	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
53	Lh	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
54	Li	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
55	Lj	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
56	Lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
57	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
58	Lm	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
59	Ln	22/24 (92%)	22 (100%)	0	0	100	100
60	Lo	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
61	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
62	Lr	123/125 (98%)	116 (94%)	7 (6%)	0	100	100
63	SR	133/135 (98%)	118 (89%)	14 (10%)	1 (1%)	16	32
64	SD	225/227 (99%)	205 (91%)	20 (9%)	0	100	100
65	SF	187/189 (99%)	166 (89%)	21 (11%)	0	100	100
66	SK	96/98 (98%)	86 (90%)	8 (8%)	2 (2%)	5	12
67	SP	119/121 (98%)	109 (92%)	10 (8%)	0	100	100
68	SQ	142/144 (99%)	120 (84%)	21 (15%)	1 (1%)	19	36
69	SS	143/145 (99%)	137 (96%)	6 (4%)	0	100	100
70	ST	141/143 (99%)	127 (90%)	13 (9%)	1 (1%)	19	36
71	SU	102/104 (98%)	96 (94%)	6 (6%)	0	100	100
72	Sc	62/64 (97%)	52 (84%)	10 (16%)	0	100	100
73	Sd	53/55 (96%)	49 (92%)	4 (8%)	0	100	100
74	Sg	311/313 (99%)	277 (89%)	34 (11%)	0	100	100
75	SM	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
76	SZ	73/75 (97%)	59 (81%)	14 (19%)	0	100	100
77	Sf	65/67 (97%)	56 (86%)	9 (14%)	0	100	100
80	Lt	137/141 (97%)	102 (74%)	34 (25%)	1 (1%)	19	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
81	Lz	215/217 (99%)	164 (76%)	51 (24%)	0	100	100
82	Ls	194/196 (99%)	175 (90%)	19 (10%)	0	100	100
83	CB	842/846 (100%)	772 (92%)	66 (8%)	4 (0%)	25	44
84	CE	71/73 (97%)	69 (97%)	2 (3%)	0	100	100
85	LW	114/118 (97%)	108 (95%)	6 (5%)	0	100	100
All	All	12774/13091 (98%)	11759 (92%)	997 (8%)	18 (0%)	50	69

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
83	CB	779	THR
4	SX	127	ASN
33	LM	88	ALA
34	LN	124	ASP
63	SR	124	VAL
66	SK	36	ALA
70	ST	41	LYS
80	Lt	144	ASP
83	CB	407	LYS
66	SK	96	ARG
83	CB	481	LYS
83	CB	611	ASP
13	Sa	47	ALA
68	SQ	38	PRO
22	LA	55	GLY
51	Lf	107	PRO
34	LN	84	PRO
50	Le	73	GLY

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	SE	224/224 (100%)	203 (91%)	21 (9%)	7	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	SI	178/178 (100%)	158 (89%)	20 (11%)	5	10
3	SL	137/137 (100%)	115 (84%)	22 (16%)	2	3
4	SX	113/226 (50%)	105 (93%)	8 (7%)	12	26
5	SG	207/207 (100%)	192 (93%)	15 (7%)	12	25
6	SJ	161/161 (100%)	146 (91%)	15 (9%)	7	15
7	SY	113/113 (100%)	91 (80%)	22 (20%)	1	1
8	Se	47/47 (100%)	44 (94%)	3 (6%)	14	30
9	SA	183/183 (100%)	168 (92%)	15 (8%)	9	20
10	SB	195/195 (100%)	182 (93%)	13 (7%)	13	28
11	SH	166/166 (100%)	147 (89%)	19 (11%)	4	9
12	SV	67/67 (100%)	53 (79%)	14 (21%)	1	1
13	Sa	89/89 (100%)	78 (88%)	11 (12%)	4	7
14	SC	188/188 (100%)	165 (88%)	23 (12%)	4	8
15	SN	130/130 (100%)	117 (90%)	13 (10%)	6	13
16	SO	110/110 (100%)	93 (84%)	17 (16%)	2	3
17	SW	112/112 (100%)	104 (93%)	8 (7%)	12	26
18	Sb	75/75 (100%)	68 (91%)	7 (9%)	7	15
22	LA	190/190 (100%)	172 (90%)	18 (10%)	7	14
23	LB	348/348 (100%)	326 (94%)	22 (6%)	15	30
24	LC	306/306 (100%)	288 (94%)	18 (6%)	16	33
25	LD	246/247 (100%)	226 (92%)	20 (8%)	9	20
26	LE	209/209 (100%)	192 (92%)	17 (8%)	9	20
27	LF	194/194 (100%)	186 (96%)	8 (4%)	26	50
28	LG	203/205 (99%)	189 (93%)	14 (7%)	13	26
29	LH	169/169 (100%)	155 (92%)	14 (8%)	9	20
30	LI	172/172 (100%)	158 (92%)	14 (8%)	9	20
31	LJ	148/148 (100%)	130 (88%)	18 (12%)	4	8
32	LL	176/176 (100%)	160 (91%)	16 (9%)	7	16
33	LM	118/118 (100%)	106 (90%)	12 (10%)	6	12
34	LN	171/171 (100%)	165 (96%)	6 (4%)	31	56
35	LO	173/173 (100%)	166 (96%)	7 (4%)	27	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	LP	134/134 (100%)	119 (89%)	15 (11%)	5	10
37	LQ	164/164 (100%)	157 (96%)	7 (4%)	25	48
38	LR	166/166 (100%)	151 (91%)	15 (9%)	8	16
39	LS	156/156 (100%)	146 (94%)	10 (6%)	14	30
40	LT	139/139 (100%)	125 (90%)	14 (10%)	6	12
41	LU	91/91 (100%)	81 (89%)	10 (11%)	5	10
42	LV	101/101 (100%)	94 (93%)	7 (7%)	13	26
43	LX	108/108 (100%)	100 (93%)	8 (7%)	11	24
44	LY	124/124 (100%)	116 (94%)	8 (6%)	14	29
45	LZ	117/117 (100%)	106 (91%)	11 (9%)	7	15
46	La	120/120 (100%)	115 (96%)	5 (4%)	25	49
47	Lb	88/90 (98%)	83 (94%)	5 (6%)	17	34
48	Lc	83/83 (100%)	73 (88%)	10 (12%)	4	8
49	Ld	98/98 (100%)	94 (96%)	4 (4%)	26	50
50	Le	114/114 (100%)	108 (95%)	6 (5%)	19	38
51	Lf	88/88 (100%)	82 (93%)	6 (7%)	13	27
52	Lg	98/98 (100%)	91 (93%)	7 (7%)	12	26
53	Lh	109/109 (100%)	96 (88%)	13 (12%)	4	8
54	Li	86/86 (100%)	83 (96%)	3 (4%)	31	56
55	Lj	73/73 (100%)	63 (86%)	10 (14%)	3	6
56	Lk	64/64 (100%)	61 (95%)	3 (5%)	22	44
57	Ll	47/47 (100%)	41 (87%)	6 (13%)	3	7
58	Lm	48/48 (100%)	47 (98%)	1 (2%)	48	72
59	Ln	23/23 (100%)	22 (96%)	1 (4%)	25	48
60	Lo	93/93 (100%)	85 (91%)	8 (9%)	8	18
61	Lp	74/74 (100%)	70 (95%)	4 (5%)	18	37
62	Lr	109/109 (100%)	94 (86%)	15 (14%)	3	6
63	SR	122/122 (100%)	104 (85%)	18 (15%)	2	4
64	SD	190/190 (100%)	167 (88%)	23 (12%)	4	8
65	SF	159/159 (100%)	139 (87%)	20 (13%)	3	7
66	SK	89/89 (100%)	84 (94%)	5 (6%)	17	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	SP	107/107 (100%)	98 (92%)	9 (8%)	9	19
68	SQ	119/119 (100%)	107 (90%)	12 (10%)	6	12
69	SS	126/126 (100%)	111 (88%)	15 (12%)	4	8
70	ST	113/113 (100%)	98 (87%)	15 (13%)	3	6
71	SU	94/94 (100%)	82 (87%)	12 (13%)	3	7
72	Sc	57/57 (100%)	52 (91%)	5 (9%)	8	17
73	Sd	48/48 (100%)	41 (85%)	7 (15%)	2	5
74	Sg	272/272 (100%)	246 (90%)	26 (10%)	7	14
75	SM	102/104 (98%)	91 (89%)	11 (11%)	5	11
76	SZ	66/66 (100%)	58 (88%)	8 (12%)	4	8
77	Sf	60/60 (100%)	49 (82%)	11 (18%)	1	1
80	Lt	112/115 (97%)	108 (96%)	4 (4%)	30	55
81	Lz	195/196 (100%)	175 (90%)	20 (10%)	6	12
82	Ls	162/164 (99%)	152 (94%)	10 (6%)	15	30
83	CB	722/723 (100%)	635 (88%)	87 (12%)	4	8
84	CE	62/62 (100%)	55 (89%)	7 (11%)	4	9
85	LW	97/97 (100%)	82 (84%)	15 (16%)	2	3
All	All	11107/11234 (99%)	10085 (91%)	1022 (9%)	10	15

All (1022) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	SE	32	SER
1	SE	38	LEU
1	SE	41	CYS
1	SE	66	MET
1	SE	69	PHE
1	SE	75	LYS
1	SE	81	THR
1	SE	89	VAL
1	SE	94	LYS
1	SE	95	THR
1	SE	112	HIS
1	SE	133	THR
1	SE	146	THR
1	SE	159	THR

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Mol	Chain	Res	Type
1	SE	170	THR
1	SE	172	PHE
1	SE	175	PHE
1	SE	181	CYS
1	SE	182	MET
1	SE	198	ARG
1	SE	233	LYS
2	SI	5	ARG
2	SI	9	HIS
2	SI	22	HIS
2	SI	66	SER
2	SI	99	ASN
2	SI	107	THR
2	SI	111	GLN
2	SI	124	LYS
2	SI	125	LYS
2	SI	132	GLU
2	SI	140	LYS
2	SI	141	ARG
2	SI	144	LYS
2	SI	146	GLN
2	SI	155	ASN
2	SI	157	LYS
2	SI	168	GLN
2	SI	184	ARG
2	SI	205	ARG
2	SI	206	LYS
3	SL	6	THR
3	SL	12	LYS
3	SL	17	PHE
3	SL	19	ASN
3	SL	21	LYS
3	SL	42	LEU
3	SL	45	LYS
3	SL	54	THR
3	SL	58	LYS
3	SL	66	VAL
3	SL	69	ARG
3	SL	73	LEU
3	SL	74	SER
3	SL	118	ARG
3	SL	124	ASP

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Mol	Chain	Res	Type
3	SL	128	VAL
3	SL	132	ARG
3	SL	135	SER
3	SL	144	LYS
3	SL	146	THR
3	SL	147	LYS
3	SL	152	LYS
4	SX	37	LYS
4	SX	55	VAL
4	SX	57	VAL
4	SX	71	ARG
4	SX	80	LYS
4	SX	95	GLU
4	SX	96	GLU
4	SX	105	PHE
5	SG	13	GLN
5	SG	26	THR
5	SG	56	ASN
5	SG	79	LYS
5	SG	91	GLU
5	SG	98	ARG
5	SG	111	LEU
5	SG	119	LYS
5	SG	139	SER
5	SG	168	LYS
5	SG	172	LYS
5	SG	188	LYS
5	SG	200	LYS
5	SG	217	MET
5	SG	218	LYS
6	SJ	13	TYR
6	SJ	18	ARG
6	SJ	23	SER
6	SJ	66	LYS
6	SJ	79	ARG
6	SJ	86	VAL
6	SJ	92	MET
6	SJ	104	ASP
6	SJ	108	ARG
6	SJ	115	PHE
6	SJ	116	LYS
6	SJ	151	LEU

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Mol	Chain	Res	Type
6	SJ	169	ARG
6	SJ	172	ARG
6	SJ	180	LYS
7	SY	8	ARG
7	SY	13	MET
7	SY	16	ARG
7	SY	22	GLN
7	SY	23	MET
7	SY	25	ILE
7	SY	34	THR
7	SY	35	VAL
7	SY	46	LYS
7	SY	61	ARG
7	SY	63	HIS
7	SY	72	PHE
7	SY	86	GLU
7	SY	88	LYS
7	SY	94	HIS
7	SY	97	TYR
7	SY	98	GLU
7	SY	99	LYS
7	SY	101	LYS
7	SY	113	ARG
7	SY	114	MET
7	SY	129	LYS
8	Se	13	ARG
8	Se	38	TYR
8	Se	49	PHE
9	SA	24	HIS
9	SA	36	GLN
9	SA	52	LYS
9	SA	75	SER
9	SA	80	ARG
9	SA	84	GLN
9	SA	117	ARG
9	SA	124	VAL
9	SA	138	SER
9	SA	141	ASN
9	SA	144	THR
9	SA	165	ASN
9	SA	174	MET
9	SA	198	MET

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Mol	Chain	Res	Type
9	SA	208	GLU
10	SB	52	THR
10	SB	56	LYS
10	SB	98	THR
10	SB	99	ASN
10	SB	103	MET
10	SB	118	GLN
10	SB	154	SER
10	SB	163	GLN
10	SB	164	ILE
10	SB	170	GLU
10	SB	210	VAL
10	SB	225	LEU
10	SB	229	MET
11	SH	27	LEU
11	SH	49	LYS
11	SH	57	ARG
11	SH	58	LYS
11	SH	71	SER
11	SH	74	LYS
11	SH	85	LYS
11	SH	87	PHE
11	SH	98	ARG
11	SH	105	THR
11	SH	144	ILE
11	SH	155	LYS
11	SH	162	GLN
11	SH	165	ASN
11	SH	167	GLU
11	SH	177	TYR
11	SH	184	ASP
11	SH	188	GLU
11	SH	191	GLU
12	SV	1	MET
12	SV	11	LEU
12	SV	17	CYS
12	SV	18	SER
12	SV	41	LYS
12	SV	45	ARG
12	SV	46	PHE
12	SV	60	ARG
12	SV	61	ARG

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Mol	Chain	Res	Type
12	SV	65	SER
12	SV	66	ASP
12	SV	67	ASP
12	SV	74	LYS
12	SV	82	ASN
13	Sa	28	ARG
13	Sa	29	CYS
13	Sa	51	ARG
13	Sa	58	VAL
13	Sa	64	LEU
13	Sa	66	LYS
13	Sa	76	SER
13	Sa	83	VAL
13	Sa	96	THR
13	Sa	100	ARG
13	Sa	102	ARG
14	SC	68	ARG
14	SC	76	LYS
14	SC	92	GLU
14	SC	101	SER
14	SC	110	MET
14	SC	117	ARG
14	SC	120	GLN
14	SC	121	ARG
14	SC	124	PHE
14	SC	128	VAL
14	SC	143	CYS
14	SC	144	SER
14	SC	167	ARG
14	SC	187	ARG
14	SC	205	VAL
14	SC	214	LEU
14	SC	220	ASP
14	SC	236	PHE
14	SC	248	TYR
14	SC	256	TRP
14	SC	259	THR
14	SC	271	ASP
14	SC	272	HIS
15	SN	12	SER
15	SN	19	ARG
15	SN	21	SER

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Mol	Chain	Res	Type
15	SN	29	THR
15	SN	31	ASP
15	SN	46	THR
15	SN	56	ASP
15	SN	73	ARG
15	SN	77	SER
15	SN	78	LYS
15	SN	87	ASP
15	SN	104	ARG
15	SN	105	ASN
16	SO	14	VAL
16	SO	25	GLU
16	SO	26	ASN
16	SO	28	PHE
16	SO	40	THR
16	SO	45	THR
16	SO	75	MET
16	SO	88	LEU
16	SO	93	LEU
16	SO	98	ARG
16	SO	105	THR
16	SO	106	LYS
16	SO	121	ARG
16	SO	125	LYS
16	SO	133	THR
16	SO	142	ARG
16	SO	151	LEU
17	SW	4	MET
17	SW	30	CYS
17	SW	38	LEU
17	SW	72	CYS
17	SW	74	VAL
17	SW	78	ARG
17	SW	84	LYS
17	SW	111	MET
18	Sb	9	HIS
18	Sb	41	TYR
18	Sb	42	LYS
18	Sb	56	CYS
18	Sb	60	SER
18	Sb	80	ARG
18	Sb	83	GLN

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Mol	Chain	Res	Type
22	LA	15	VAL
22	LA	32	VAL
22	LA	45	VAL
22	LA	54	ARG
22	LA	92	LYS
22	LA	101	VAL
22	LA	102	LEU
22	LA	114	CYS
22	LA	146	THR
22	LA	154	SER
22	LA	155	LYS
22	LA	198	ARG
22	LA	207	VAL
22	LA	221	LYS
22	LA	226	ARG
22	LA	243	THR
22	LA	245	ARG
22	LA	247	ARG
23	LB	5	LYS
23	LB	7	SER
23	LB	59	GLU
23	LB	60	VAL
23	LB	120	LYS
23	LB	125	SER
23	LB	141	ASP
23	LB	151	SER
23	LB	169	ARG
23	LB	218	ASP
23	LB	278	THR
23	LB	307	TYR
23	LB	315	ASN
23	LB	328	ASN
23	LB	348	ARG
23	LB	351	LEU
23	LB	355	THR
23	LB	358	ARG
23	LB	362	LYS
23	LB	363	ILE
23	LB	381	THR
23	LB	394	LYS
24	LC	3	CYS
24	LC	5	ARG

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Mol	Chain	Res	Type
24	LC	17	SER
24	LC	27	VAL
24	LC	63	SER
24	LC	71	ARG
24	LC	84	THR
24	LC	122	TYR
24	LC	154	VAL
24	LC	172	LYS
24	LC	188	ARG
24	LC	233	SER
24	LC	235	LEU
24	LC	261	ASP
24	LC	267	TRP
24	LC	291	ARG
24	LC	322	LEU
24	LC	335	MET
25	LD	3	PHE
25	LD	7	VAL
25	LD	68	ARG
25	LD	75	VAL
25	LD	86	TYR
25	LD	89	LYS
25	LD	120	GLU
25	LD	123	VAL
25	LD	125	VAL
25	LD	132	VAL
25	LD	221	LYS
25	LD	224	SER
25	LD	228	LYS
25	LD	232	THR
25	LD	235	MET
25	LD	238	GLU
25	LD	239	MET
25	LD	256	LYS
25	LD	259	LYS
25	LD	263	LYS
26	LE	44	CYS
26	LE	64	SER
26	LE	110	ARG
26	LE	120	ASP
26	LE	128	HIS
26	LE	130	LYS

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Mol	Chain	Res	Type
26	LE	145	THR
26	LE	163	VAL
26	LE	166	LYS
26	LE	174	LEU
26	LE	206	VAL
26	LE	226	ARG
26	LE	239	LYS
26	LE	240	TYR
26	LE	243	THR
26	LE	250	GLN
26	LE	260	LYS
27	LF	28	LEU
27	LF	35	LYS
27	LF	86	GLU
27	LF	119	ASN
27	LF	196	THR
27	LF	200	ARG
27	LF	220	MET
27	LF	248	ASN
28	LG	88	ASP
28	LG	94	GLN
28	LG	100	HIS
28	LG	103	ARG
28	LG	151	LYS
28	LG	156	VAL
28	LG	168	VAL
28	LG	175	ARG
28	LG	179	VAL
28	LG	209	SER
28	LG	217	LYS
28	LG	228	ASP
28	LG	249	ARG
28	LG	259	LYS
29	LH	8	GLN
29	LH	10	VAL
29	LH	16	VAL
29	LH	46	SER
29	LH	50	LYS
29	LH	51	LYS
29	LH	71	ARG
29	LH	84	VAL
29	LH	94	SER

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Mol	Chain	Res	Type
29	LH	112	VAL
29	LH	126	VAL
29	LH	135	SER
29	LH	181	VAL
29	LH	183	GLU
30	LI	21	ARG
30	LI	32	ARG
30	LI	44	ASP
30	LI	54	SER
30	LI	55	ASP
30	LI	61	SER
30	LI	71	CYS
30	LI	102	MET
30	LI	129	VAL
30	LI	143	GLN
30	LI	146	GLU
30	LI	162	ARG
30	LI	168	SER
30	LI	195	CYS
31	LJ	5	GLN
31	LJ	15	LEU
31	LJ	16	ARG
31	LJ	26	VAL
31	LJ	38	LYS
31	LJ	40	LEU
31	LJ	41	GLU
31	LJ	47	THR
31	LJ	60	PHE
31	LJ	94	LEU
31	LJ	95	ARG
31	LJ	101	ASP
31	LJ	104	ASN
31	LJ	110	GLN
31	LJ	115	LEU
31	LJ	129	ASP
31	LJ	160	GLU
31	LJ	171	ASP
32	LL	35	ARG
32	LL	59	VAL
32	LL	63	THR
32	LL	64	VAL
32	LL	67	HIS

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Mol	Chain	Res	Type
32	LL	69	LYS
32	LL	70	VAL
32	LL	103	ARG
32	LL	119	GLU
32	LL	125	ILE
32	LL	158	ARG
32	LL	161	TYR
32	LL	175	ASN
32	LL	181	SER
32	LL	184	MET
32	LL	208	GLU
33	LM	4	ARG
33	LM	31	ILE
33	LM	38	VAL
33	LM	50	MET
33	LM	63	LYS
33	LM	70	GLN
33	LM	79	LYS
33	LM	81	ASP
33	LM	106	ASP
33	LM	113	MET
33	LM	129	LYS
33	LM	132	LYS
34	LN	18	VAL
34	LN	26	ARG
34	LN	73	ARG
34	LN	75	VAL
34	LN	155	VAL
34	LN	187	SER
35	LO	3	GLU
35	LO	6	VAL
35	LO	31	ARG
35	LO	67	SER
35	LO	127	VAL
35	LO	189	ILE
35	LO	191	LYS
36	LP	17	SER
36	LP	18	ARG
36	LP	23	ARG
36	LP	24	VAL
36	LP	30	ARG
36	LP	46	LYS

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Mol	Chain	Res	Type
36	LP	50	ASP
36	LP	54	GLN
36	LP	57	CYS
36	LP	69	ARG
36	LP	76	TRP
36	LP	85	LYS
36	LP	99	GLU
36	LP	110	ASP
36	LP	154	GLU
37	LQ	3	VAL
37	LQ	4	ASP
37	LQ	6	ARG
37	LQ	28	LEU
37	LQ	79	THR
37	LQ	108	ARG
37	LQ	130	SER
38	LR	12	SER
38	LR	13	SER
38	LR	29	THR
38	LR	38	ARG
38	LR	74	ARG
38	LR	125	LEU
38	LR	146	LYS
38	LR	148	ASP
38	LR	153	LYS
38	LR	158	GLN
38	LR	162	ARG
38	LR	176	ARG
38	LR	183	GLU
38	LR	186	LYS
38	LR	188	LEU
39	LS	24	THR
39	LS	29	ARG
39	LS	82	LEU
39	LS	85	ASP
39	LS	90	THR
39	LS	111	ARG
39	LS	135	SER
39	LS	151	LYS
39	LS	154	LEU
39	LS	160	ARG
40	LT	4	THR

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Mol	Chain	Res	Type
40	LT	5	LYS
40	LT	45	MET
40	LT	69	GLN
40	LT	79	GLN
40	LT	83	LYS
40	LT	85	LEU
40	LT	99	SER
40	LT	102	ARG
40	LT	114	GLN
40	LT	117	LYS
40	LT	122	LYS
40	LT	149	GLU
40	LT	158	PHE
41	LU	21	PHE
41	LU	41	GLN
41	LU	69	LYS
41	LU	83	LEU
41	LU	97	ARG
41	LU	99	TRP
41	LU	102	VAL
41	LU	110	TYR
41	LU	113	ARG
41	LU	116	GLN
42	LV	48	ARG
42	LV	60	MET
42	LV	72	LEU
42	LV	92	ASP
42	LV	94	VAL
42	LV	101	ASN
42	LV	134	SER
43	LX	53	ARG
43	LX	63	LYS
43	LX	67	ARG
43	LX	68	ARG
43	LX	69	ASN
43	LX	70	LYS
43	LX	97	VAL
43	LX	118	ASP
44	LY	28	LYS
44	LY	37	GLU
44	LY	44	VAL
44	LY	46	SER

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Mol	Chain	Res	Type
44	LY	74	TYR
44	LY	99	ILE
44	LY	113	LYS
44	LY	115	ARG
45	LZ	6	LYS
45	LZ	22	LYS
45	LZ	43	VAL
45	LZ	67	LYS
45	LZ	74	VAL
45	LZ	84	ARG
45	LZ	85	TYR
45	LZ	98	LYS
45	LZ	100	VAL
45	LZ	123	LYS
45	LZ	127	ASN
46	La	3	SER
46	La	58	MET
46	La	76	ASP
46	La	125	LYS
46	La	145	VAL
47	Lb	23	LYS
47	Lb	40	LEU
47	Lb	41	ARG
47	Lb	65	MET
47	Lb	107	ARG
48	Lc	9	LYS
48	Lc	17	ARG
48	Lc	19	GLN
48	Lc	23	LYS
48	Lc	50	ASN
48	Lc	57	LYS
48	Lc	65	MET
48	Lc	93	THR
48	Lc	94	LEU
48	Lc	98	ASP
49	Ld	22	THR
49	Ld	67	ARG
49	Ld	95	ASP
49	Ld	106	VAL
50	Le	37	LYS
50	Le	45	VAL
50	Le	86	GLU

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Mol	Chain	Res	Type
50	Le	117	GLN
50	Le	121	ARG
50	Le	126	ASN
51	Lf	8	LYS
51	Lf	25	THR
51	Lf	33	VAL
51	Lf	37	ASP
51	Lf	67	THR
51	Lf	73	LYS
52	Lg	33	LEU
52	Lg	73	HIS
52	Lg	82	MET
52	Lg	83	CYS
52	Lg	104	VAL
52	Lg	105	LYS
52	Lg	106	VAL
53	Lh	5	LYS
53	Lh	14	LYS
53	Lh	21	LEU
53	Lh	22	ASP
53	Lh	26	VAL
53	Lh	29	SER
53	Lh	66	LYS
53	Lh	81	LEU
53	Lh	84	ARG
53	Lh	87	LYS
53	Lh	94	ARG
53	Lh	116	LEU
53	Lh	121	VAL
54	Li	48	CYS
54	Li	86	LYS
54	Li	99	LYS
55	Lj	2	THR
55	Lj	20	ARG
55	Lj	22	CYS
55	Lj	32	SER
55	Lj	36	LYS
55	Lj	55	ARG
55	Lj	63	ARG
55	Lj	65	ARG
55	Lj	79	ARG
55	Lj	83	THR

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Mol	Chain	Res	Type
56	Lk	7	GLU
56	Lk	24	LYS
56	Lk	52	LYS
57	Ll	8	ARG
57	Ll	21	ARG
57	Ll	37	TYR
57	Ll	45	ARG
57	Ll	47	THR
57	Ll	49	LEU
58	Lm	122	ARG
59	Ln	15	ARG
60	Lo	14	LYS
60	Lo	57	ARG
60	Lo	59	LYS
60	Lo	70	LEU
60	Lo	77	CYS
60	Lo	96	ASP
60	Lo	99	ARG
60	Lo	103	VAL
61	Lp	8	VAL
61	Lp	26	VAL
61	Lp	62	LYS
61	Lp	87	LYS
62	Lr	14	SER
62	Lr	21	ASN
62	Lr	27	THR
62	Lr	33	LYS
62	Lr	35	ARG
62	Lr	49	VAL
62	Lr	58	LYS
62	Lr	60	VAL
62	Lr	62	VAL
62	Lr	63	VAL
62	Lr	78	VAL
62	Lr	79	ARG
62	Lr	80	THR
62	Lr	83	ASN
62	Lr	120	SER
63	SR	1	MET
63	SR	5	ARG
63	SR	33	ARG
63	SR	48	ASN

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Mol	Chain	Res	Type
63	SR	53	TYR
63	SR	72	LYS
63	SR	82	ASP
63	SR	91	LEU
63	SR	95	ILE
63	SR	98	VAL
63	SR	105	MET
63	SR	111	PHE
63	SR	114	LEU
63	SR	115	SER
63	SR	116	ASN
63	SR	118	GLN
63	SR	123	THR
63	SR	130	THR
64	SD	7	LYS
64	SD	21	LEU
64	SD	42	THR
64	SD	45	ARG
64	SD	58	VAL
64	SD	64	ARG
64	SD	65	ARG
64	SD	94	ARG
64	SD	109	LEU
64	SD	122	VAL
64	SD	123	LEU
64	SD	134	CYS
64	SD	136	VAL
64	SD	143	ARG
64	SD	146	ARG
64	SD	148	LYS
64	SD	150	MET
64	SD	157	MET
64	SD	168	VAL
64	SD	221	THR
64	SD	223	ILE
64	SD	224	SER
64	SD	227	LYS
65	SF	16	ASP
65	SF	18	LYS
65	SF	19	LEU
65	SF	20	PHE
65	SF	22	LYS

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Mol	Chain	Res	Type
65	SF	37	ASP
65	SF	42	LYS
65	SF	56	TYR
65	SF	83	ASN
65	SF	86	LYS
65	SF	97	PHE
65	SF	98	GLU
65	SF	119	SER
65	SF	127	ARG
65	SF	139	VAL
65	SF	142	SER
65	SF	145	ARG
65	SF	159	ARG
65	SF	169	ILE
65	SF	198	ARG
66	SK	1	MET
66	SK	21	MET
66	SK	79	LEU
66	SK	85	LEU
66	SK	95	ARG
67	SP	40	ARG
67	SP	50	ARG
67	SP	59	ARG
67	SP	65	LYS
67	SP	70	MET
67	SP	89	MET
67	SP	127	LYS
67	SP	128	HIS
67	SP	133	ILE
68	SQ	12	VAL
68	SQ	15	ARG
68	SQ	27	ARG
68	SQ	39	LEU
68	SQ	52	LEU
68	SQ	62	ARG
68	SQ	82	TYR
68	SQ	86	GLN
68	SQ	87	SER
68	SQ	96	TYR
68	SQ	117	ARG
68	SQ	126	ARG
69	SS	13	LEU

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Mol	Chain	Res	Type
69	SS	14	ARG
69	SS	25	LYS
69	SS	38	ARG
69	SS	55	ARG
69	SS	78	LYS
69	SS	83	PHE
69	SS	84	LEU
69	SS	91	LYS
69	SS	94	LYS
69	SS	104	ASP
69	SS	106	LYS
69	SS	109	GLU
69	SS	137	LYS
69	SS	145	THR
70	ST	41	LYS
70	ST	44	GLU
70	ST	55	THR
70	ST	63	HIS
70	ST	74	SER
70	ST	84	ARG
70	ST	87	VAL
70	ST	90	SER
70	ST	93	SER
70	ST	118	ASP
70	ST	122	LYS
70	ST	123	LEU
70	ST	124	THR
70	ST	128	GLN
70	ST	130	ASP
71	SU	19	ARG
71	SU	21	ARG
71	SU	36	CYS
71	SU	49	LYS
71	SU	53	PRO
71	SU	55	ARG
71	SU	56	MET
71	SU	62	ARG
71	SU	67	LYS
71	SU	75	LYS
71	SU	83	ARG
71	SU	105	SER
72	Sc	13	ARG

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Mol	Chain	Res	Type
72	Sc	15	THR
72	Sc	31	ARG
72	Sc	47	LYS
72	Sc	55	VAL
73	Sd	8	TRP
73	Sd	20	SER
73	Sd	22	ARG
73	Sd	30	LEU
73	Sd	32	ARG
73	Sd	38	MET
73	Sd	40	ARG
74	Sg	14	HIS
74	Sg	27	PHE
74	Sg	42	MET
74	Sg	84	ASP
74	Sg	92	LEU
74	Sg	99	ARG
74	Sg	111	VAL
74	Sg	113	PHE
74	Sg	125	ARG
74	Sg	130	LYS
74	Sg	141	THR
74	Sg	143	GLN
74	Sg	150	TRP
74	Sg	188	HIS
74	Sg	197	THR
74	Sg	207	CYS
74	Sg	213	ASP
74	Sg	219	TRP
74	Sg	222	ASN
74	Sg	223	GLU
74	Sg	225	LYS
74	Sg	230	LEU
74	Sg	237	ASN
74	Sg	259	TRP
74	Sg	271	LYS
74	Sg	308	ARG
75	SM	18	LEU
75	SM	44	LYS
75	SM	45	ARG
75	SM	50	CYS
75	SM	60	MET

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Mol	Chain	Res	Type
75	SM	61	TYR
75	SM	63	LYS
75	SM	68	LEU
75	SM	111	VAL
75	SM	119	GLN
75	SM	127	TYR
76	SZ	50	PHE
76	SZ	55	TYR
76	SZ	76	ARG
76	SZ	77	LEU
76	SZ	78	LYS
76	SZ	79	ILE
76	SZ	107	VAL
76	SZ	109	TYR
77	Sf	89	LYS
77	Sf	92	LYS
77	Sf	104	LYS
77	Sf	116	ARG
77	Sf	125	GLU
77	Sf	126	CYS
77	Sf	132	MET
77	Sf	138	ARG
77	Sf	140	TYR
77	Sf	141	CYS
77	Sf	144	CYS
80	Lt	116	MET
80	Lt	119	ARG
80	Lt	146	ARG
80	Lt	160	VAL
81	Lz	1	MET
81	Lz	24	LYS
81	Lz	27	LYS
81	Lz	37	SER
81	Lz	42	ASP
81	Lz	63	PHE
81	Lz	85	MET
81	Lz	101	LYS
81	Lz	102	LYS
81	Lz	113	SER
81	Lz	116	LEU
81	Lz	122	ARG
81	Lz	123	ILE

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Mol	Chain	Res	Type
81	Lz	156	LYS
81	Lz	161	LYS
81	Lz	171	HIS
81	Lz	177	ASP
81	Lz	178	GLU
81	Lz	202	ARG
81	Lz	215	ARG
82	Ls	45	MET
82	Ls	53	VAL
82	Ls	55	MET
82	Ls	61	MET
82	Ls	77	LYS
82	Ls	99	ARG
82	Ls	118	PRO
82	Ls	119	CYS
82	Ls	152	ILE
82	Ls	162	LYS
83	CB	7	ASP
83	CB	14	ASP
83	CB	22	MET
83	CB	40	VAL
83	CB	41	CYS
83	CB	42	LYS
83	CB	48	SER
83	CB	55	ARG
83	CB	59	THR
83	CB	66	ARG
83	CB	71	LYS
83	CB	78	PHE
83	CB	82	SER
83	CB	88	PHE
83	CB	93	LYS
83	CB	98	PHE
83	CB	109	VAL
83	CB	132	VAL
83	CB	137	VAL
83	CB	144	ARG
83	CB	150	ARG
83	CB	156	MET
83	CB	160	MET
83	CB	212	VAL
83	CB	214	PHE

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Mol	Chain	Res	Type
83	CB	223	PHE
83	CB	226	LYS
83	CB	231	MET
83	CB	248	GLU
83	CB	258	LYS
83	CB	259	LYS
83	CB	275	LYS
83	CB	284	LYS
83	CB	301	PHE
83	CB	302	ASP
83	CB	328	LYS
83	CB	342	ARG
83	CB	348	ASP
83	CB	350	LEU
83	CB	378	ASP
83	CB	379	ASP
83	CB	380	GLU
83	CB	388	CYS
83	CB	399	SER
83	CB	426	LYS
83	CB	438	LYS
83	CB	445	LYS
83	CB	448	GLN
83	CB	450	THR
83	CB	466	CYS
83	CB	475	VAL
83	CB	482	THR
83	CB	492	HIS
83	CB	495	ARG
83	CB	505	VAL
83	CB	533	MET
83	CB	553	HIS
83	CB	564	ASP
83	CB	583	VAL
83	CB	597	ASN
83	CB	598	LYS
83	CB	601	ARG
83	CB	603	TYR
83	CB	609	PHE
83	CB	641	TRP
83	CB	643	VAL
83	CB	652	PHE

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Mol	Chain	Res	Type
83	CB	664	ASP
83	CB	665	ILE
83	CB	695	GLU
83	CB	698	ARG
83	CB	712	ASP
83	CB	724	THR
83	CB	741	MET
83	CB	742	GLU
83	CB	745	TYR
83	CB	756	VAL
83	CB	767	ARG
83	CB	774	SER
83	CB	776	VAL
83	CB	782	PHE
83	CB	783	VAL
83	CB	794	PHE
83	CB	796	PHE
83	CB	811	GLN
83	CB	813	VAL
83	CB	848	ILE
84	CE	38	TYR
84	CE	39	TRP
84	CE	44	LYS
84	CE	47	MET
84	CE	50	GLU
84	CE	60	ARG
84	CE	72	ARG
85	LW	1	MET
85	LW	3	VAL
85	LW	5	LEU
85	LW	17	HIS
85	LW	23	ARG
85	LW	25	ASP
85	LW	50	ASN
85	LW	53	VAL
85	LW	54	LEU
85	LW	57	ARG
85	LW	60	LYS
85	LW	77	LYS
85	LW	86	SER
85	LW	102	LYS
85	LW	113	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	SE	36	HIS
5	SG	197	GLN
7	SY	22	GLN
7	SY	29	HIS
9	SA	24	HIS
10	SB	179	ASN
11	SH	91	HIS
12	SV	35	ASN
18	Sb	26	GLN
28	LG	43	GLN
28	LG	64	GLN
28	LG	94	GLN
31	LJ	104	ASN
36	LP	10	ASN
36	LP	118	GLN
36	LP	120	ASN
42	LV	36	ASN
42	LV	84	GLN
42	LV	135	ASN
48	Lc	50	ASN
50	Le	107	ASN
65	SF	110	GLN
65	SF	114	ASN
66	SK	61	GLN
68	SQ	77	HIS
82	Ls	139	GLN
83	CB	8	GLN
83	CB	27	HIS
83	CB	184	ASN
83	CB	553	HIS
83	CB	599	HIS
83	CB	626	GLN
83	CB	660	ASN
84	CE	51	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
19	L5	3704/3740 (99%)	884 (23%)	20 (0%)
20	L7	119/120 (99%)	14 (11%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	L8	155/156 (99%)	31 (20%)	1 (0%)
78	S2	1715/1740 (98%)	428 (24%)	7 (0%)
79	Et	73/75 (97%)	30 (41%)	0
All	All	5766/5831 (98%)	1387 (24%)	28 (0%)

All (1387) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
19	L5	2	G
19	L5	13	U
19	L5	17	A
19	L5	25	A
19	L5	26	C
19	L5	30	C
19	L5	39	A
19	L5	42	A
19	L5	48	G
19	L5	56	A
19	L5	59	A
19	L5	64	A
19	L5	65	A
19	L5	66	A
19	L5	69	A
19	L5	73	A
19	L5	74	G
19	L5	91	G
19	L5	98	A
19	L5	104	G
19	L5	108	A
19	L5	109	G
19	L5	110	C
19	L5	119	G
19	L5	120	A
19	L5	132	G
19	L5	133	C
19	L5	134	G
19	L5	135	G
19	L5	144	G
19	L5	152	U
19	L5	157	U
19	L5	158	A
19	L5	159	C

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Mol	Chain	Res	Type
19	L5	165	A
19	L5	171	U
19	L5	173	C
19	L5	182	G
19	L5	183	C
19	L5	184	U
19	L5	185	C
19	L5	188	G
19	L5	189	G
19	L5	200	U
19	L5	209	U
19	L5	216	C
19	L5	218	A
19	L5	220	C
19	L5	234	G
19	L5	237	G
19	L5	250	C
19	L5	255	C
19	L5	256	G
19	L5	261	G
19	L5	264	C
19	L5	265	C
19	L5	266	C
19	L5	267	G
19	L5	269	G
19	L5	275	C
19	L5	276	C
19	L5	278	G
19	L5	280	G
19	L5	297	U
19	L5	306	A
19	L5	315	G
19	L5	316	U
19	L5	340	C
19	L5	350	C
19	L5	362	A
19	L5	373	G
19	L5	385	A
19	L5	387	G
19	L5	388	A
19	L5	407	A
19	L5	409	G

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Mol	Chain	Res	Type
19	L5	410	A
19	L5	412	G
19	L5	413	G
19	L5	415	G
19	L5	431	G
19	L5	432	U
19	L5	433	A
19	L5	434	A
19	L5	440	U
19	L5	449	C
19	L5	450	G
19	L5	452	A
19	L5	453	G
19	L5	454	U
19	L5	456	C
19	L5	457	G
19	L5	465	G
19	L5	466	A
19	L5	467	U
19	L5	468	U
19	L5	485	C
19	L5	486	C
19	L5	489	C
19	L5	491	G
19	L5	493	G
19	L5	494	U
19	L5	497	G
19	L5	498	C
19	L5	499	G
19	L5	500	G
19	L5	501	C
19	L5	502	C
19	L5	503	C
19	L5	504	G
19	L5	505	G
19	L5	509	A
19	L5	510	U
19	L5	512	U
19	L5	513	U
19	L5	514	U
19	L5	515	C
19	L5	517	C

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Mol	Chain	Res	Type
19	L5	518	G
19	L5	519	C
19	L5	643	C
19	L5	644	G
19	L5	646	G
19	L5	654	C
19	L5	655	C
19	L5	656	C
19	L5	657	C
19	L5	659	G
19	L5	666	G
19	L5	667	A
19	L5	668	C
19	L5	669	C
19	L5	673	C
19	L5	685	C
19	L5	686	A
19	L5	687	U
19	L5	697	G
19	L5	703	G
19	L5	704	C
19	L5	706	C
19	L5	708	G
19	L5	730	G
19	L5	731	G
19	L5	738	C
19	L5	739	G
19	L5	742	G
19	L5	744	G
19	L5	753	C
19	L5	758	G
19	L5	759	G
19	L5	904	C
19	L5	905	C
19	L5	906	C
19	L5	912	G
19	L5	913	U
19	L5	914	U
19	L5	915	A
19	L5	917	A
19	L5	918	G
19	L5	923	C

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Mol	Chain	Res	Type
19	L5	924	C
19	L5	926	G
19	L5	932	A
19	L5	933	G
19	L5	935	A
19	L5	936	C
19	L5	943	A
19	L5	944	A
19	L5	945	U
19	L5	959	G
19	L5	960	A
19	L5	961	G
19	L5	962	C
19	L5	965	G
19	L5	966	A
19	L5	967	C
19	L5	969	C
19	L5	970	G
19	L5	977	C
19	L5	982	U
19	L5	985	C
19	L5	989	U
19	L5	990	C
19	L5	992	C
19	L5	993	G
19	L5	995	C
19	L5	1048	G
19	L5	1049	C
19	L5	1050	C
19	L5	1051	G
19	L5	1066	G
19	L5	1070	G
19	L5	1072	C
19	L5	1075	G
19	L5	1082	C
19	L5	1083	U
19	L5	1095	A
19	L5	1168	G
19	L5	1170	G
19	L5	1171	G
19	L5	1172	C
19	L5	1173	G

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Mol	Chain	Res	Type
19	L5	1174	G
19	L5	1179	U
19	L5	1180	C
19	L5	1181	C
19	L5	1182	C
19	L5	1183	C
19	L5	1184	A
19	L5	1202	C
19	L5	1203	G
19	L5	1205	G
19	L5	1210	C
19	L5	1211	G
19	L5	1214	C
19	L5	1215	C
19	L5	1217	G
19	L5	1218	G
19	L5	1219	G
19	L5	1222	A
19	L5	1235	G
19	L5	1241	C
19	L5	1242	G
19	L5	1246	G
19	L5	1253	G
19	L5	1254	A
19	L5	1257	A
19	L5	1258	G
19	L5	1266	G
19	L5	1267	C
19	L5	1270	A
19	L5	1271	G
19	L5	1272	C
19	L5	1273	G
19	L5	1274	A
19	L5	1275	G
19	L5	1277	G
19	L5	1280	C
19	L5	1284	G
19	L5	1285	U
19	L5	1287	G
19	L5	1293	G
19	L5	1294	A
19	L5	1295	C

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Mol	Chain	Res	Type
19	L5	1296	G
19	L5	1301	C
19	L5	1302	U
19	L5	1326	A
19	L5	1354	A
19	L5	1358	G
19	L5	1359	G
19	L5	1365	C
19	L5	1367	C
19	L5	1378	C
19	L5	1387	A
19	L5	1394	G
19	L5	1397	A
19	L5	1405	C
19	L5	1407	C
19	L5	1408	G
19	L5	1409	C
19	L5	1410	U
19	L5	1411	C
19	L5	1414	C
19	L5	1415	G
19	L5	1417	C
19	L5	1420	A
19	L5	1435	G
19	L5	1437	C
19	L5	1439	C
19	L5	1441	C
19	L5	1442	C
19	L5	1443	A
19	L5	1444	G
19	L5	1446	C
19	L5	1447	C
19	L5	1464	C
19	L5	1482	G
19	L5	1483	C
19	L5	1494	U
19	L5	1497	A
19	L5	1498	G
19	L5	1502	G
19	L5	1516	G
19	L5	1517	G
19	L5	1518	A

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Mol	Chain	Res	Type
19	L5	1519	C
19	L5	1533	A
19	L5	1534	A
19	L5	1547	A
19	L5	1562	G
19	L5	1564	A
19	L5	1566	C
19	L5	1574	G
19	L5	1578	U
19	L5	1582	U
19	L5	1591	U
19	L5	1596	U
19	L5	1612	G
19	L5	1621	A
19	L5	1624	G
19	L5	1625	G
19	L5	1631	A
19	L5	1633	G
19	L5	1634	A
19	L5	1638	A
19	L5	1640	C
19	L5	1641	G
19	L5	1642	A
19	L5	1654	G
19	L5	1661	C
19	L5	1663	C
19	L5	1676	C
19	L5	1677	U
19	L5	1678	C
19	L5	1681	G
19	L5	1685	G
19	L5	1698	C
19	L5	1699	A
19	L5	1700	G
19	L5	1703	C
19	L5	1704	C
19	L5	1705	G
19	L5	1707	C
19	L5	1718	C
19	L5	1726	U
19	L5	1729	A
19	L5	1731	C

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Mol	Chain	Res	Type
19	L5	1734	G
19	L5	1741	G
19	L5	1742	A
19	L5	1750	G
19	L5	1757	U
19	L5	1758	G
19	L5	1760	G
19	L5	1761	G
19	L5	1762	C
19	L5	1763	C
19	L5	1764	G
19	L5	1765	A
19	L5	1766	A
19	L5	1768	C
19	L5	1769	G
19	L5	1770	A
19	L5	1775	A
19	L5	1787	A
19	L5	1803	G
19	L5	1804	A
19	L5	1806	G
19	L5	1810	G
19	L5	1820	C
19	L5	1821	G
19	L5	1822	U
19	L5	1834	U
19	L5	1836	G
19	L5	1837	A
19	L5	1842	G
19	L5	1843	A
19	L5	1855	G
19	L5	1869	G
19	L5	1882	U
19	L5	1890	G
19	L5	1892	A
19	L5	1893	C
19	L5	1897	A
19	L5	1917	A
19	L5	1918	U
19	L5	1919	G
19	L5	1920	C
19	L5	1921	C

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Mol	Chain	Res	Type
19	L5	1922	G
19	L5	1925	G
19	L5	1931	C
19	L5	1932	A
19	L5	1940	G
19	L5	1948	G
19	L5	1949	U
19	L5	1951	G
19	L5	1961	G
19	L5	1962	A
19	L5	1964	A
19	L5	1974	U
19	L5	1975	G
19	L5	1978	C
19	L5	1980	U
19	L5	1981	G
19	L5	1982	G
19	L5	1983	A
19	L5	1984	A
19	L5	1985	G
19	L5	1986	U
19	L5	1991	A
19	L5	1992	U
19	L5	1993	C
19	L5	1997	U
19	L5	1998	A
19	L5	1999	A
19	L5	2001	G
19	L5	2002	A
19	L5	2003	G
19	L5	2011	C
19	L5	2017	A
19	L5	2018	C
19	L5	2024	G
19	L5	2026	A
19	L5	2033	A
19	L5	2034	G
19	L5	2046	G
19	L5	2048	U
19	L5	2055	G
19	L5	2056	G
19	L5	2069	A

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Mol	Chain	Res	Type
19	L5	2084	C
19	L5	2085	G
19	L5	2092	G
19	L5	2093	A
19	L5	2095	A
19	L5	2097	U
19	L5	2098	G
19	L5	2099	G
19	L5	2101	C
19	L5	2102	G
19	L5	2103	G
19	L5	2107	C
19	L5	2108	G
19	L5	2110	C
19	L5	2112	G
19	L5	2250	C
19	L5	2252	G
19	L5	2253	A
19	L5	2255	C
19	L5	2256	C
19	L5	2257	C
19	L5	2258	C
19	L5	2261	G
19	L5	2289	C
19	L5	2300	A
19	L5	2301	G
19	L5	2313	A
19	L5	2331	G
19	L5	2333	G
19	L5	2345	G
19	L5	2348	G
19	L5	2351	C
19	L5	2360	A
19	L5	2383	C
19	L5	2395	A
19	L5	2397	G
19	L5	2398	U
19	L5	2402	G
19	L5	2404	A
19	L5	2408	U
19	L5	2417	A
19	L5	2421	G

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Mol	Chain	Res	Type
19	L5	2425	U
19	L5	2441	C
19	L5	2450	G
19	L5	2453	A
19	L5	2464	C
19	L5	2465	C
19	L5	2471	G
19	L5	2474	G
19	L5	2475	G
19	L5	2478	C
19	L5	2479	G
19	L5	2483	G
19	L5	2484	A
19	L5	2485	U
19	L5	2486	G
19	L5	2487	G
19	L5	2488	C
19	L5	2489	C
19	L5	2490	U
19	L5	2494	U
19	L5	2503	G
19	L5	2504	C
19	L5	2505	C
19	L5	2506	G
19	L5	2513	A
19	L5	2518	G
19	L5	2519	U
19	L5	2520	C
19	L5	2529	A
19	L5	2536	A
19	L5	2537	A
19	L5	2544	G
19	L5	2546	G
19	L5	2547	G
19	L5	2554	U
19	L5	2555	G
19	L5	2559	G
19	L5	2560	C
19	L5	2565	A
19	L5	2573	A
19	L5	2583	C
19	L5	2587	A

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Mol	Chain	Res	Type
19	L5	2588	C
19	L5	2589	C
19	L5	2607	C
19	L5	2618	G
19	L5	2627	C
19	L5	2652	G
19	L5	2653	C
19	L5	2662	G
19	L5	2669	C
19	L5	2675	G
19	L5	2676	A
19	L5	2687	U
19	L5	2694	G
19	L5	2695	A
19	L5	2696	A
19	L5	2703	G
19	L5	2707	U
19	L5	2708	U
19	L5	2710	C
19	L5	2711	G
19	L5	2721	G
19	L5	2723	U
19	L5	2726	G
19	L5	2729	C
19	L5	2739	C
19	L5	2742	G
19	L5	2743	A
19	L5	2746	A
19	L5	2754	G
19	L5	2761	U
19	L5	2763	U
19	L5	2764	A
19	L5	2769	U
19	L5	2770	C
19	L5	2787	A
19	L5	2788	U
19	L5	2790	U
19	L5	2806	A
19	L5	2812	A
19	L5	2814	C
19	L5	2815	A
19	L5	2826	U

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Mol	Chain	Res	Type
19	L5	2827	G
19	L5	2829	U
19	L5	2848	G
19	L5	2855	G
19	L5	2867	C
19	L5	2877	G
19	L5	2897	G
19	L5	2899	C
19	L5	2900	U
19	L5	2902	G
19	L5	2903	G
19	L5	2904	U
19	L5	2905	C
19	L5	2906	G
19	L5	2908	U
19	L5	3586	G
19	L5	3588	C
19	L5	3590	G
19	L5	3591	C
19	L5	3594	C
19	L5	3595	U
19	L5	3596	A
19	L5	3597	G
19	L5	3605	C
19	L5	3615	G
19	L5	3616	U
19	L5	3626	G
19	L5	3630	A
19	L5	3635	A
19	L5	3644	U
19	L5	3646	A
19	L5	3648	A
19	L5	3662	A
19	L5	3664	G
19	L5	3670	C
19	L5	3673	C
19	L5	3674	G
19	L5	3685	C
19	L5	3691	G
19	L5	3692	A
19	L5	3711	A
19	L5	3713	U

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Mol	Chain	Res	Type
19	L5	3714	G
19	L5	3726	A
19	L5	3727	A
19	L5	3729	U
19	L5	3740	G
19	L5	3748	A
19	L5	3750	G
19	L5	3753	G
19	L5	3756	A
19	L5	3757	G
19	L5	3759	A
19	L5	3760	A
19	L5	3761	C
19	L5	3766	A
19	L5	3772	U
19	L5	3773	U
19	L5	3774	A
19	L5	3776	G
19	L5	3777	G
19	L5	3784	A
19	L5	3786	U
19	L5	3788	C
19	L5	3802	U
19	L5	3809	G
19	L5	3811	G
19	L5	3813	A
19	L5	3814	U
19	L5	3817	A
19	L5	3818	U
19	L5	3819	G
19	L5	3823	G
19	L5	3838	U
19	L5	3839	G
19	L5	3840	U
19	L5	3841	C
19	L5	3867	A
19	L5	3876	A
19	L5	3877	A
19	L5	3878	C
19	L5	3879	G
19	L5	3885	G
19	L5	3887	C

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Mol	Chain	Res	Type
19	L5	3890	A
19	L5	3892	U
19	L5	3897	G
19	L5	3901	A
19	L5	3906	A
19	L5	3907	G
19	L5	3908	A
19	L5	3915	U
19	L5	3916	G
19	L5	3922	G
19	L5	3923	A
19	L5	3926	C
19	L5	3930	U
19	L5	3938	G
19	L5	3939	G
19	L5	3943	A
19	L5	3944	G
19	L5	3946	G
19	L5	3947	A
19	L5	3949	A
19	L5	3951	G
19	L5	3953	G
19	L5	3955	G
19	L5	3956	G
19	L5	3957	U
19	L5	3958	G
19	L5	3959	U
19	L5	3960	A
19	L5	3962	A
19	L5	3963	A
19	L5	3964	U
19	L5	3965	A
19	L5	3966	A
19	L5	3969	G
19	L5	3970	G
19	L5	3971	G
19	L5	3973	G
19	L5	3975	C
19	L5	3976	C
19	L5	3977	C
19	L5	4034	G
19	L5	4037	C

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Mol	Chain	Res	Type
19	L5	4038	C
19	L5	4039	G
19	L5	4041	C
19	L5	4042	G
19	L5	4043	G
19	L5	4044	U
19	L5	4045	G
19	L5	4046	A
19	L5	4047	A
19	L5	4048	A
19	L5	4049	U
19	L5	4051	C
19	L5	4052	C
19	L5	4053	A
19	L5	4054	C
19	L5	4055	U
19	L5	4057	C
19	L5	4058	U
19	L5	4059	C
19	L5	4060	U
19	L5	4061	G
19	L5	4062	A
19	L5	4063	U
19	L5	4065	G
19	L5	4067	U
19	L5	4068	U
19	L5	4069	U
19	L5	4076	G
19	L5	4092	G
19	L5	4093	G
19	L5	4097	G
19	L5	4099	G
19	L5	4102	C
19	L5	4104	G
19	L5	4108	G
19	L5	4111	U
19	L5	4114	C
19	L5	4115	G
19	L5	4116	C
19	L5	4117	U
19	L5	4119	C
19	L5	4122	G

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Mol	Chain	Res	Type
19	L5	4127	A
19	L5	4133	C
19	L5	4134	C
19	L5	4138	C
19	L5	4140	C
19	L5	4141	G
19	L5	4142	C
19	L5	4143	G
19	L5	4144	C
19	L5	4146	G
19	L5	4149	C
19	L5	4160	C
19	L5	4162	C
19	L5	4163	U
19	L5	4170	A
19	L5	4177	C
19	L5	4183	G
19	L5	4184	G
19	L5	4191	G
19	L5	4196	G
19	L5	4197	G
19	L5	4203	A
19	L5	4212	A
19	L5	4220	A
19	L5	4222	G
19	L5	4228	G
19	L5	4229	U
19	L5	4233	A
19	L5	4243	C
19	L5	4249	G
19	L5	4251	A
19	L5	4254	G
19	L5	4255	A
19	L5	4257	A
19	L5	4258	C
19	L5	4265	U
19	L5	4268	A
19	L5	4273	A
19	L5	4281	A
19	L5	4297	G
19	L5	4304	A
19	L5	4305	G

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Mol	Chain	Res	Type
19	L5	4306	U
19	L5	4314	C
19	L5	4319	C
19	L5	4330	G
19	L5	4332	C
19	L5	4338	G
19	L5	4349	C
19	L5	4350	C
19	L5	4354	U
19	L5	4364	G
19	L5	4373	G
19	L5	4376	A
19	L5	4377	G
19	L5	4378	A
19	L5	4380	A
19	L5	4387	C
19	L5	4391	G
19	L5	4394	A
19	L5	4422	A
19	L5	4438	U
19	L5	4448	G
19	L5	4449	A
19	L5	4452	U
19	L5	4453	C
19	L5	4464	A
19	L5	4466	C
19	L5	4488	A
19	L5	4500	U
19	L5	4512	U
19	L5	4513	A
19	L5	4515	G
19	L5	4518	A
19	L5	4519	C
19	L5	4524	G
19	L5	4525	C
19	L5	4545	G
19	L5	4548	A
19	L5	4549	G
19	L5	4560	C
19	L5	4567	G
19	L5	4572	U
19	L5	4573	G

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Mol	Chain	Res	Type
19	L5	4575	G
19	L5	4584	A
19	L5	4589	A
19	L5	4590	A
19	L5	4600	G
19	L5	4601	U
19	L5	4606	G
19	L5	4617	G
19	L5	4636	U
19	L5	4637	G
19	L5	4656	A
19	L5	4659	G
19	L5	4670	C
19	L5	4672	A
19	L5	4679	G
19	L5	4693	C
19	L5	4695	C
19	L5	4700	A
19	L5	4708	A
19	L5	4709	U
19	L5	4719	G
19	L5	4720	C
19	L5	4734	A
19	L5	4740	G
19	L5	4741	C
19	L5	4742	G
19	L5	4745	G
19	L5	4750	G
19	L5	4754	G
19	L5	4757	C
19	L5	4759	C
19	L5	4761	G
19	L5	4765	G
19	L5	4771	C
19	L5	4772	C
19	L5	4773	C
19	L5	4775	C
19	L5	4870	G
19	L5	4871	C
19	L5	4875	G
19	L5	4880	C
19	L5	4882	U

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Mol	Chain	Res	Type
19	L5	4883	C
19	L5	4889	G
19	L5	4895	C
19	L5	4896	G
19	L5	4897	G
19	L5	4900	C
19	L5	4901	G
19	L5	4902	C
19	L5	4910	G
19	L5	4912	G
19	L5	4913	G
19	L5	4914	C
19	L5	4918	C
19	L5	4922	C
19	L5	4923	C
19	L5	4925	U
19	L5	4926	C
19	L5	4927	G
19	L5	4928	C
19	L5	4934	A
19	L5	4937	C
19	L5	4940	C
19	L5	4941	G
19	L5	4943	A
19	L5	4944	C
19	L5	4951	G
19	L5	4960	G
19	L5	4975	G
19	L5	4976	U
19	L5	4988	U
19	L5	4989	U
19	L5	4990	C
19	L5	4991	U
19	L5	5007	A
19	L5	5009	G
19	L5	5013	C
19	L5	5014	A
19	L5	5017	G
19	L5	5022	U
19	L5	5024	C
19	L5	5027	C
19	L5	5028	G

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Mol	Chain	Res	Type
19	L5	5030	U
19	L5	5034	A
19	L5	5041	G
19	L5	5047	C
19	L5	5048	A
19	L5	5050	C
19	L5	5054	C
19	L5	5055	G
19	L5	5061	A
19	L5	5069	U
20	L7	3	C
20	L7	4	U
20	L7	5	A
20	L7	22	A
20	L7	24	C
20	L7	33	U
20	L7	38	U
20	L7	53	U
20	L7	54	A
20	L7	63	C
20	L7	64	G
20	L7	66	G
20	L7	100	A
20	L7	110	G
21	L8	25	G
21	L8	34	U
21	L8	35	C
21	L8	48	A
21	L8	52	A
21	L8	59	A
21	L8	62	A
21	L8	63	U
21	L8	68	G
21	L8	80	A
21	L8	82	A
21	L8	83	C
21	L8	84	A
21	L8	85	U
21	L8	86	U
21	L8	87	G
21	L8	94	G
21	L8	103	A

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Mol	Chain	Res	Type
21	L8	105	C
21	L8	110	U
21	L8	111	U
21	L8	112	G
21	L8	114	G
21	L8	123	U
21	L8	124	U
21	L8	125	C
21	L8	126	C
21	L8	127	U
21	L8	147	G
21	L8	150	C
21	L8	151	G
78	S2	4	C
78	S2	13	C
78	S2	25	A
78	S2	33	G
78	S2	41	G
78	S2	42	A
78	S2	44	U
78	S2	45	A
78	S2	46	A
78	S2	56	G
78	S2	58	C
78	S2	62	G
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

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Mol	Chain	Res	Type
78	S2	147	A
78	S2	149	A
78	S2	158	A
78	S2	161	U
78	S2	168	C
78	S2	170	A
78	S2	171	A
78	S2	179	C
78	S2	182	C
78	S2	190	G
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
78	S2	214	U
78	S2	291	G
78	S2	292	A
78	S2	295	C
78	S2	301	A
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	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

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Mol	Chain	Res	Type
78	S2	338	G
78	S2	339	A
78	S2	340	C
78	S2	347	G
78	S2	351	G
78	S2	360	A
78	S2	362	C
78	S2	364	A
78	S2	368	U
78	S2	369	C
78	S2	370	G
78	S2	374	G
78	S2	375	U
78	S2	385	G
78	S2	386	C
78	S2	408	A
78	S2	409	C
78	S2	421	G
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	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	496	C
78	S2	502	C
78	S2	530	U
78	S2	531	A
78	S2	532	C
78	S2	536	A

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Mol	Chain	Res	Type
78	S2	537	C
78	S2	540	U
78	S2	542	U
78	S2	544	G
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	576	A
78	S2	583	A
78	S2	587	A
78	S2	589	G
78	S2	590	A
78	S2	591	U
78	S2	593	C
78	S2	604	A
78	S2	607	U
78	S2	611	G
78	S2	614	C
78	S2	617	G
78	S2	623	G
78	S2	628	A
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	683	G
78	S2	684	G
78	S2	688	U
78	S2	689	U
78	S2	692	G
78	S2	693	A
78	S2	695	C

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Mol	Chain	Res	Type
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	737	G
78	S2	738	C
78	S2	749	U
78	S2	750	C
78	S2	751	G
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	798	G
78	S2	799	U
78	S2	811	A
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	847	A
78	S2	869	A
78	S2	870	A
78	S2	873	G
78	S2	874	G
78	S2	882	U
78	S2	887	U

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Mol	Chain	Res	Type
78	S2	888	U
78	S2	889	U
78	S2	890	U
78	S2	891	G
78	S2	894	G
78	S2	896	U
78	S2	897	U
78	S2	898	U
78	S2	899	U
78	S2	900	C
78	S2	901	G
78	S2	903	A
78	S2	907	G
78	S2	908	A
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	954	U
78	S2	963	A
78	S2	971	G
78	S2	972	A
78	S2	990	A
78	S2	992	A
78	S2	997	A
78	S2	999	G
78	S2	1001	A
78	S2	1002	U
78	S2	1008	A
78	S2	1017	U
78	S2	1023	A
78	S2	1027	A
78	S2	1028	A
78	S2	1033	G
78	S2	1034	A
78	S2	1047	C
78	S2	1060	A
78	S2	1061	U
78	S2	1062	A

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Mol	Chain	Res	Type
78	S2	1067	C
78	S2	1078	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
78	S2	1118	C
78	S2	1121	G
78	S2	1133	A
78	S2	1138	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	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	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	1264	C
78	S2	1274	G
78	S2	1275	G
78	S2	1282	A
78	S2	1283	C

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Mol	Chain	Res	Type
78	S2	1284	A
78	S2	1286	G
78	S2	1287	A
78	S2	1293	A
78	S2	1294	G
78	S2	1295	A
78	S2	1301	A
78	S2	1302	G
78	S2	1303	C
78	S2	1304	U
78	S2	1308	U
78	S2	1320	G
78	S2	1333	U
78	S2	1342	U
78	S2	1354	G
78	S2	1355	C
78	S2	1356	G
78	S2	1357	A
78	S2	1358	U
78	S2	1371	U
78	S2	1372	U
78	S2	1373	C
78	S2	1376	A
78	S2	1378	A
78	S2	1401	A
78	S2	1402	A
78	S2	1406	G
78	S2	1408	U
78	S2	1411	G
78	S2	1414	A
78	S2	1415	C
78	S2	1417	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

Continued on next page...

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Mol	Chain	Res	Type
78	S2	1442	U
78	S2	1449	G
78	S2	1454	A
78	S2	1463	U
78	S2	1466	G
78	S2	1468	C
78	S2	1474	A
78	S2	1480	A
78	S2	1489	A
78	S2	1490	G
78	S2	1494	U
78	S2	1495	G
78	S2	1497	G
78	S2	1498	A
78	S2	1507	G
78	S2	1508	A
78	S2	1520	G
78	S2	1521	C
78	S2	1522	A
78	S2	1531	A
78	S2	1533	A
78	S2	1535	U
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	1579	A
78	S2	1580	A
78	S2	1581	C
78	S2	1584	G
78	S2	1586	U
78	S2	1587	G
78	S2	1588	A
78	S2	1601	A
78	S2	1606	G
78	S2	1621	U
78	S2	1623	A

Continued on next page...

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Mol	Chain	Res	Type
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
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	1715	A
78	S2	1721	U
78	S2	1722	G
78	S2	1742	C
78	S2	1743	G
78	S2	1744	G
78	S2	1745	A
78	S2	1748	G
78	S2	1752	C
78	S2	1753	C
78	S2	1754	G
78	S2	1755	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	1780	G
78	S2	1782	G
78	S2	1783	C

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Mol	Chain	Res	Type
78	S2	1784	G
78	S2	1787	G
78	S2	1809	A
78	S2	1812	U
78	S2	1813	A
78	S2	1823	A
78	S2	1824	A
78	S2	1825	A
78	S2	1826	G
78	S2	1829	G
78	S2	1831	A
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

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Mol	Chain	Res	Type
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

All (28) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
19	L5	265	C
19	L5	406	C
19	L5	493	G
19	L5	912	G
19	L5	914	U
19	L5	1071	C
19	L5	1082	C
19	L5	1633	G
19	L5	1977	C
19	L5	2033	A
19	L5	2416	G
19	L5	2485	U
19	L5	2675	G
19	L5	2760	G
19	L5	2786	C
19	L5	3614	G
19	L5	3673	C
19	L5	4600	G
19	L5	4699	U
19	L5	4913	G
21	L8	86	U
78	S2	291	G
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
19	L5	12
78	S2	6
47	Lb	1
26	LE	1
83	CB	1
85	LW	1
11	SH	1
80	Lt	1
30	LI	1
79	Et	1
38	LR	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lb	76:VAL	C	89:VAL	N	33.86
1	S2	753:C	O3'	785:C	P	27.17
1	LE	76:ALA	C	88:VAL	N	23.48
1	L5	2910:G	O3'	3584:C	P	20.84
1	S2	698:G	O3'	730:C	P	16.88
1	L5	4776:G	O3'	4858:C	P	16.48
1	L5	760:G	O3'	903:C	P	16.21
1	CB	236:PHE	C	247:ALA	N	16.01
1	L5	519:C	O3'	642:G	P	15.61
1	LW	63:GLN	C	70:LYS	N	15.04
1	L5	996:G	O3'	1047:C	P	14.17
1	L5	2112:G	O3'	2249:C	P	13.60
1	S2	739:C	O3'	746:C	P	12.80
1	SH	107:LYS	C	111:LYS	N	11.41
1	L5	1222:A	O3'	1234:G	P	11.20
1	L5	1051:G	O3'	1064:G	P	9.16
1	S2	225:G	O3'	287:U	P	7.94
1	Lt	87:GLU	C	104:ILE	N	7.90
1	L5	1100:U	O3'	1167:C	P	7.85
1	LI	102:MET	C	114:GLY	N	7.57
1	L5	1709:C	O3'	1714:C	P	6.11
1	S2	1693:G	O3'	1694:U	P	5.81
1	Et	16:C	O3'	18:U	P	5.53
1	LR	153:LYS	C	154:LEU	N	5.05
1	L5	3949:A	O3'	3950:U	P	4.40
1	L5	3985:C	O3'	4018:G	P	4.23
1	S2	1210:G	O3'	1211:G	P	3.18

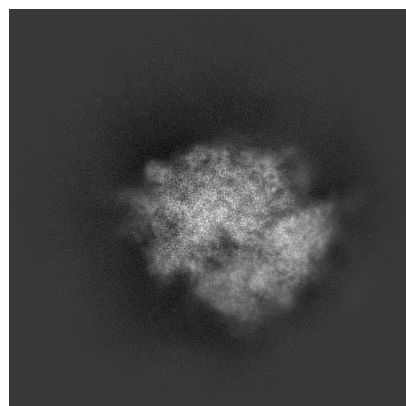
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44043. These allow visual inspection of the internal detail of the map and identification of artifacts.

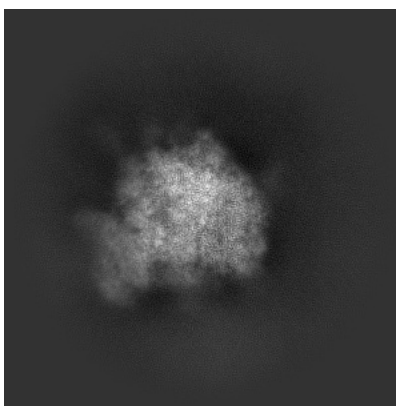
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

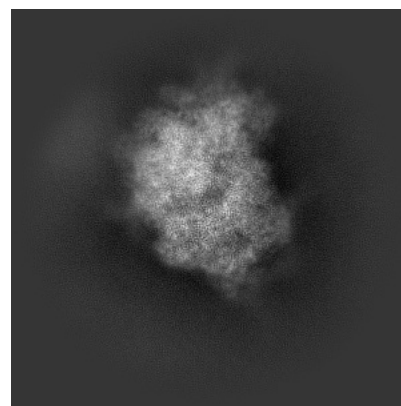
6.1.1 Primary map



X

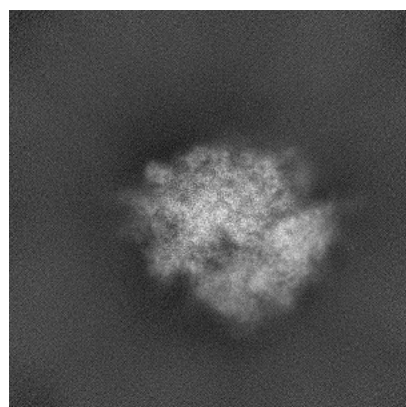


Y

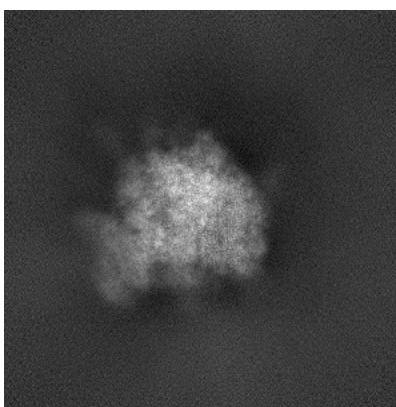


Z

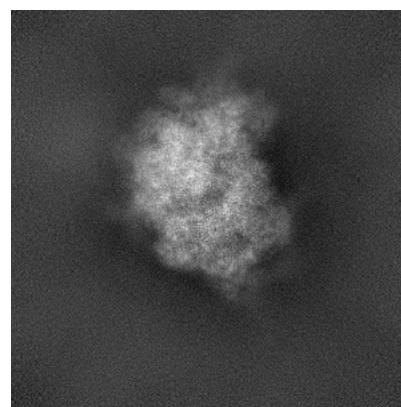
6.1.2 Raw map



X



Y

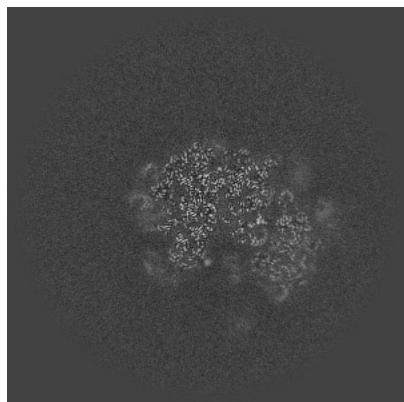


Z

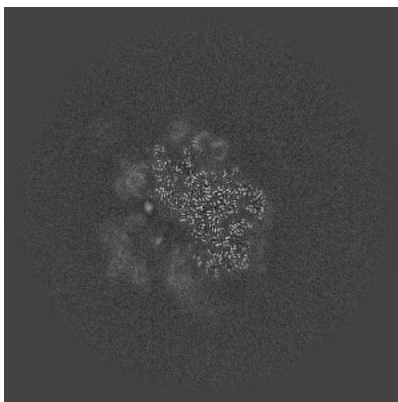
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

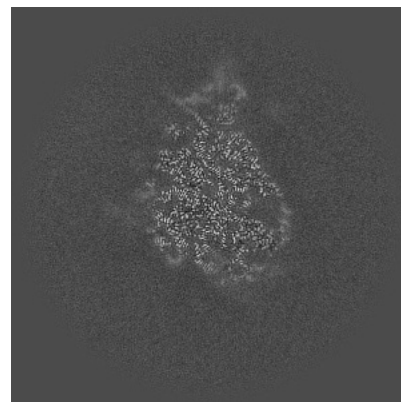
6.2.1 Primary map



X Index: 256

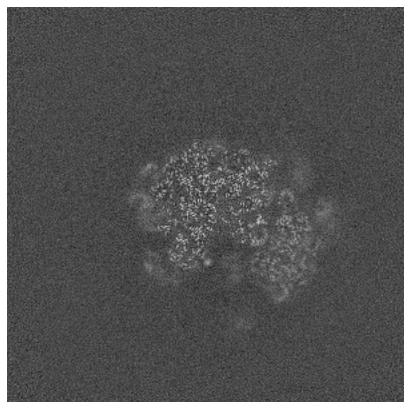


Y Index: 256

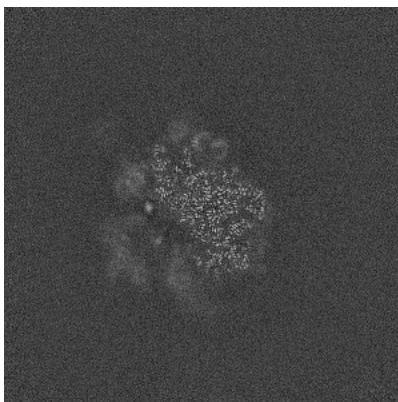


Z Index: 256

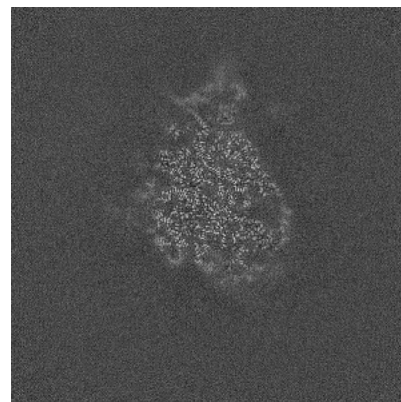
6.2.2 Raw map



X Index: 256



Y Index: 256

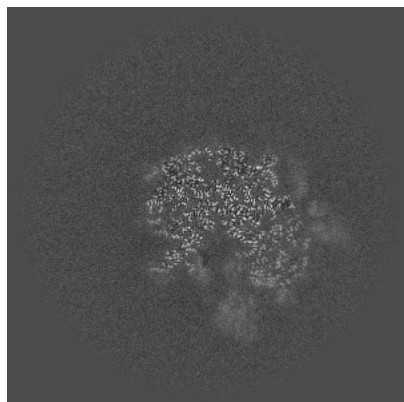


Z Index: 256

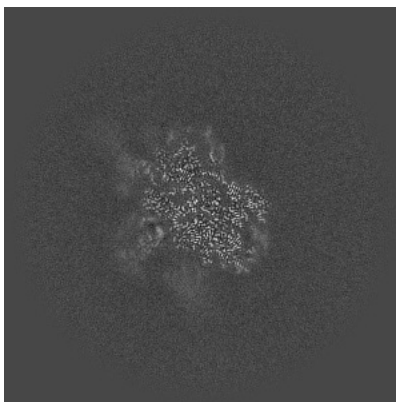
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

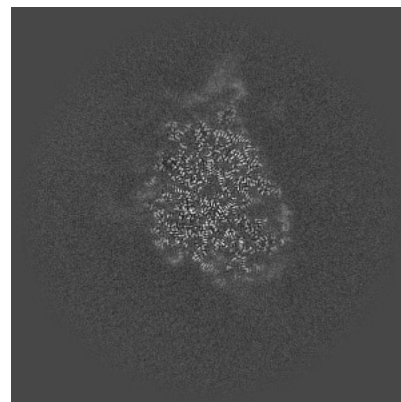
6.3.1 Primary map



X Index: 243

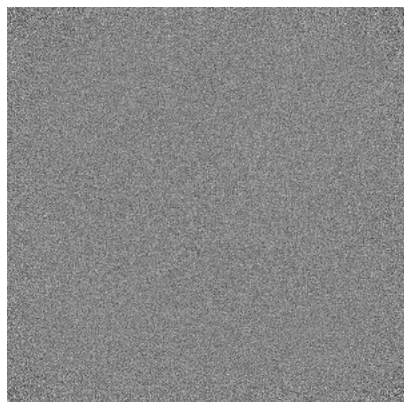


Y Index: 243

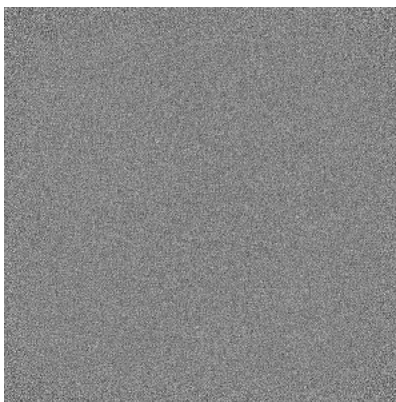


Z Index: 258

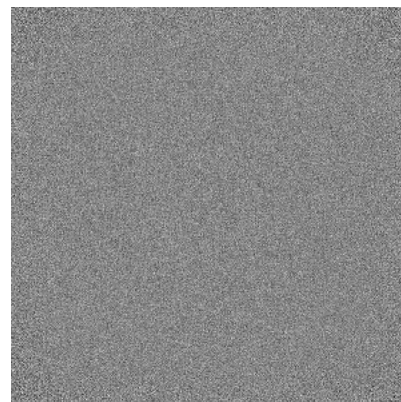
6.3.2 Raw map



X Index: 0



Y Index: 0

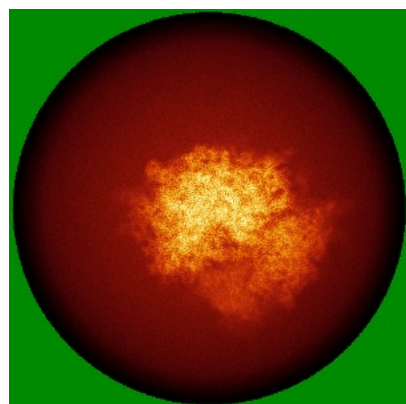


Z Index: 0

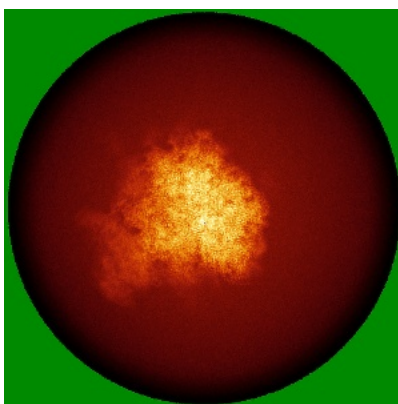
The images above show the largest variance slices of the map in three orthogonal directions.

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

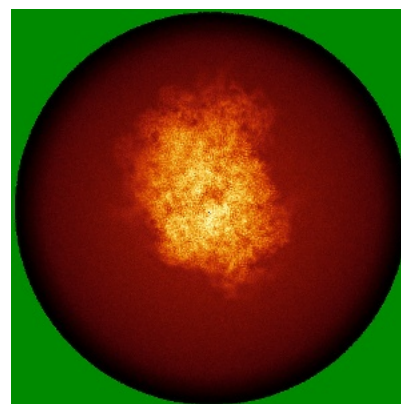
6.4.1 Primary map



X

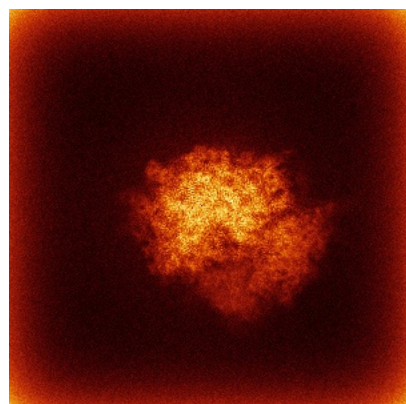


Y

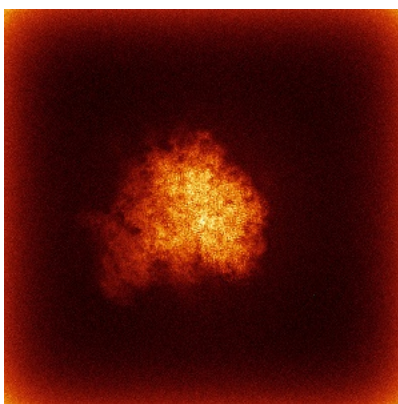


Z

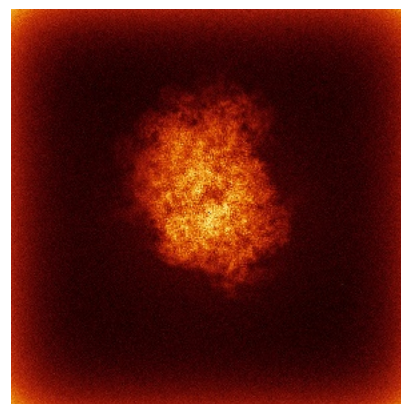
6.4.2 Raw map



X



Y

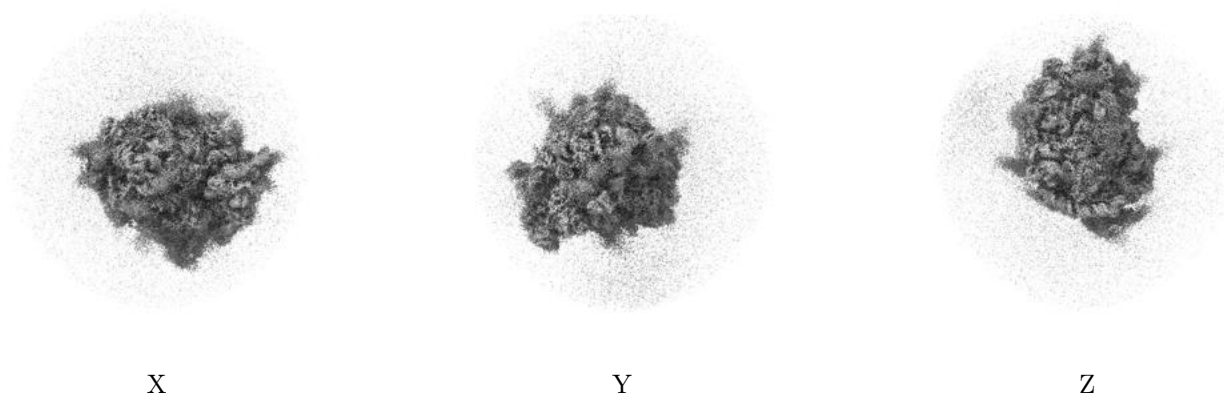


Z

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.

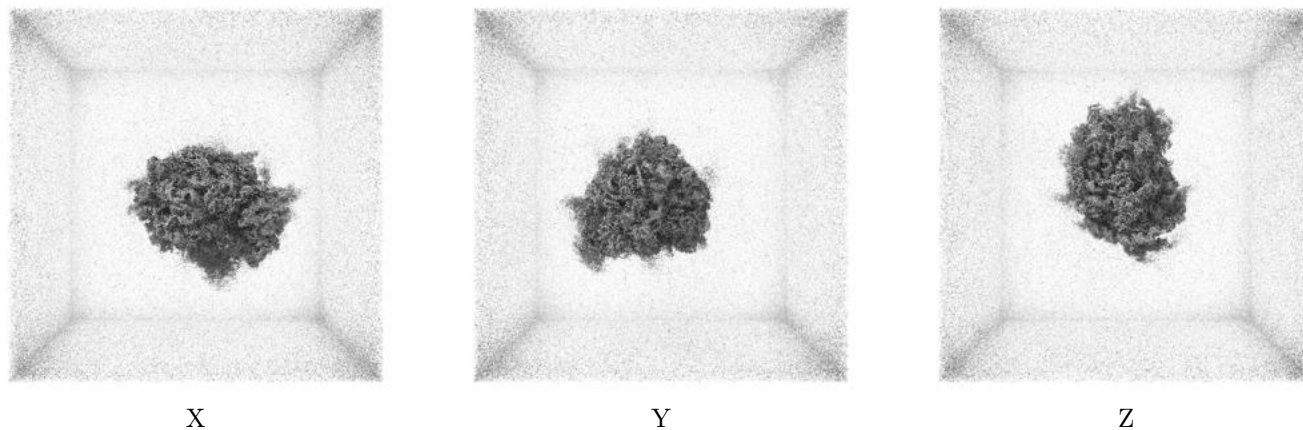
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0253. 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.

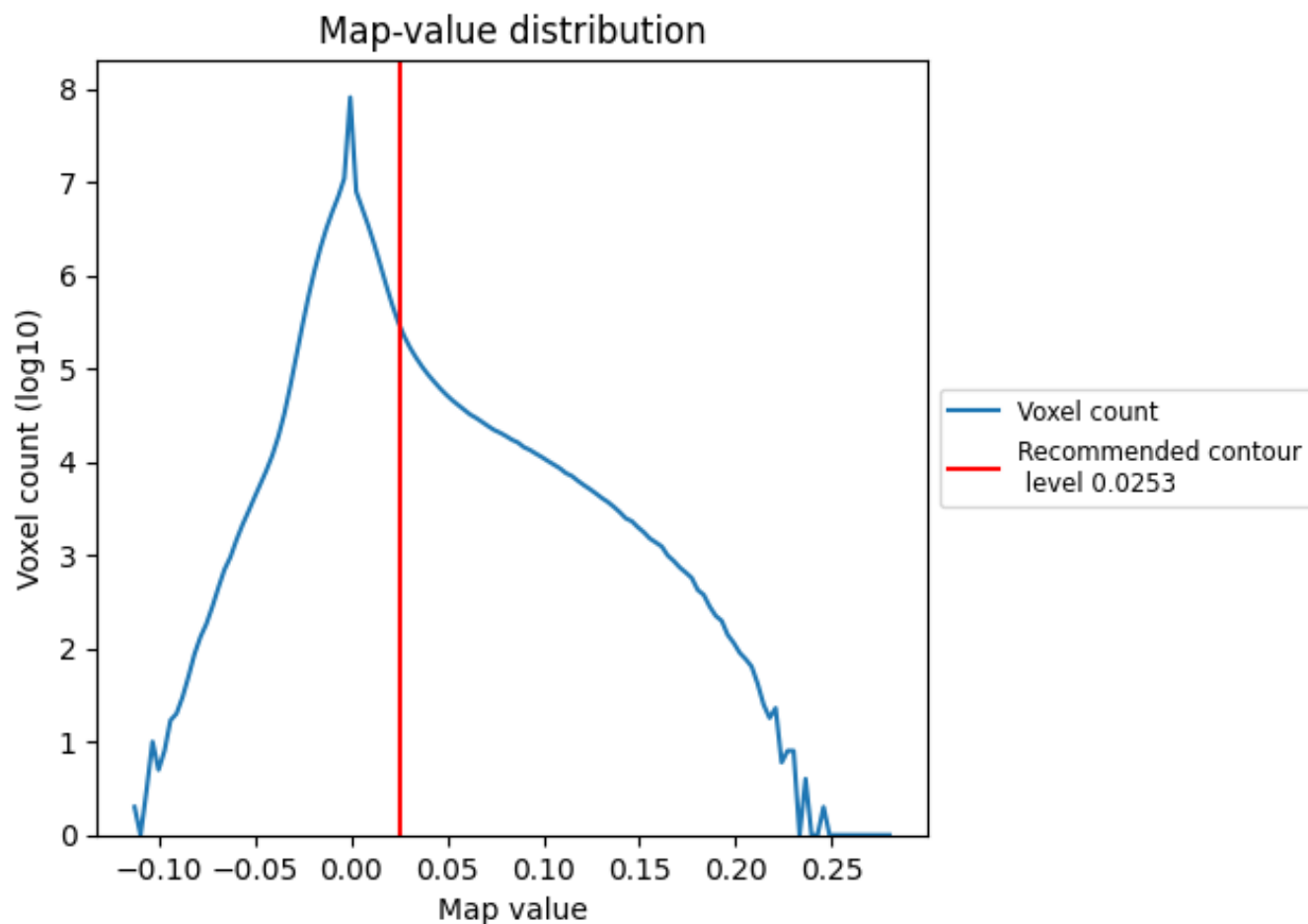
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

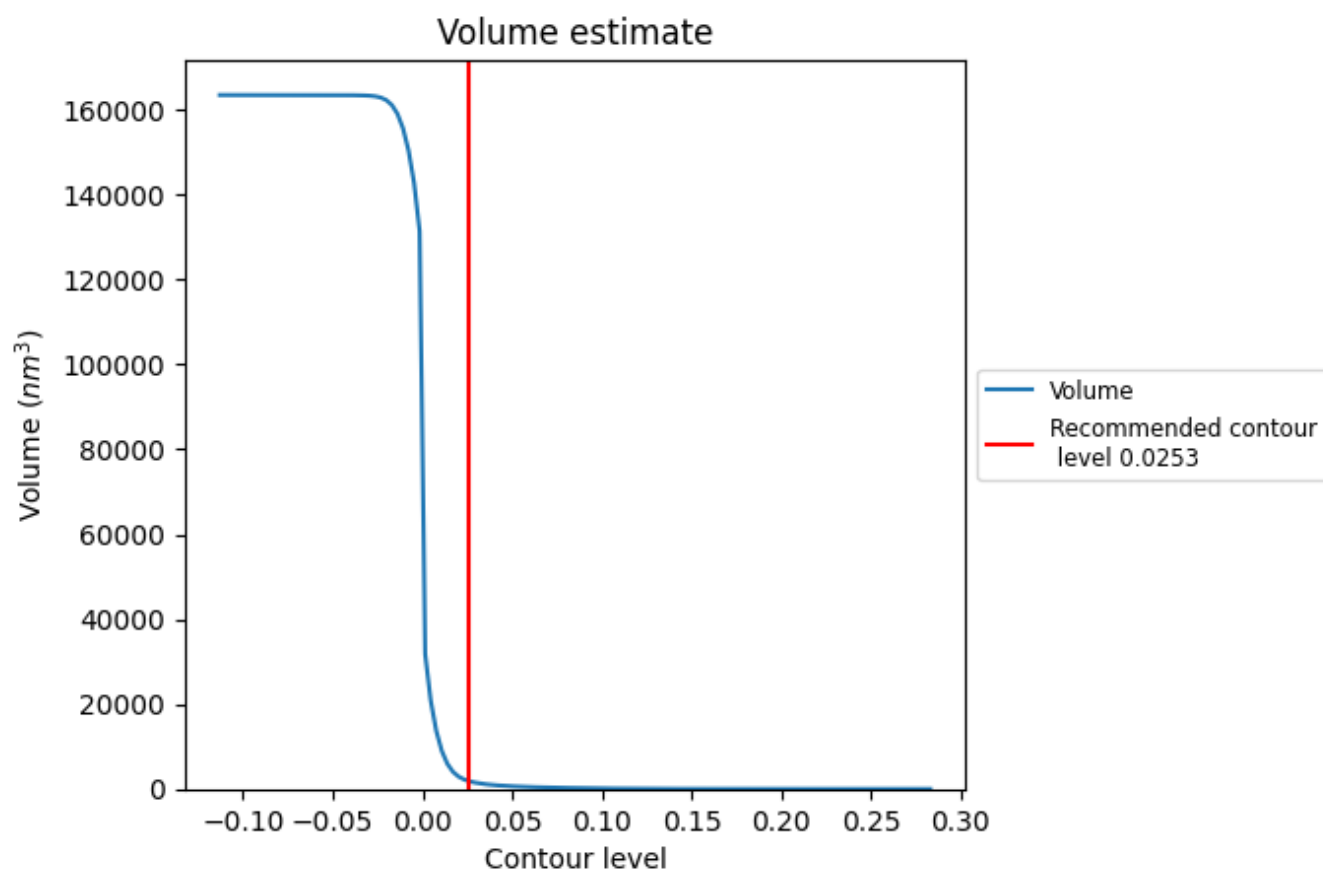
This section contains the results of statistical analysis of the map.

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.

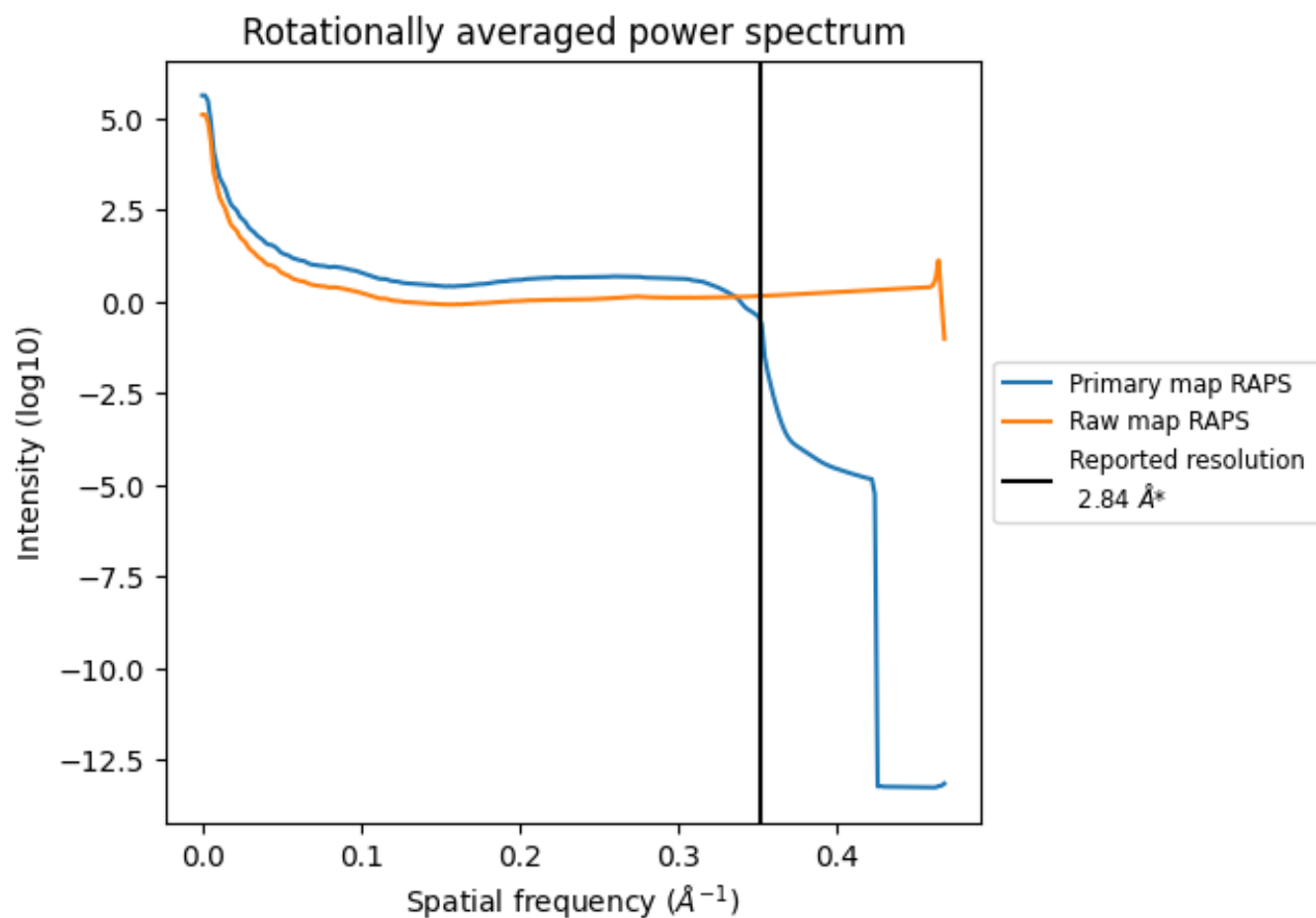
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1946 nm^3 ; this corresponds to an approximate mass of 1758 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 ⓘ

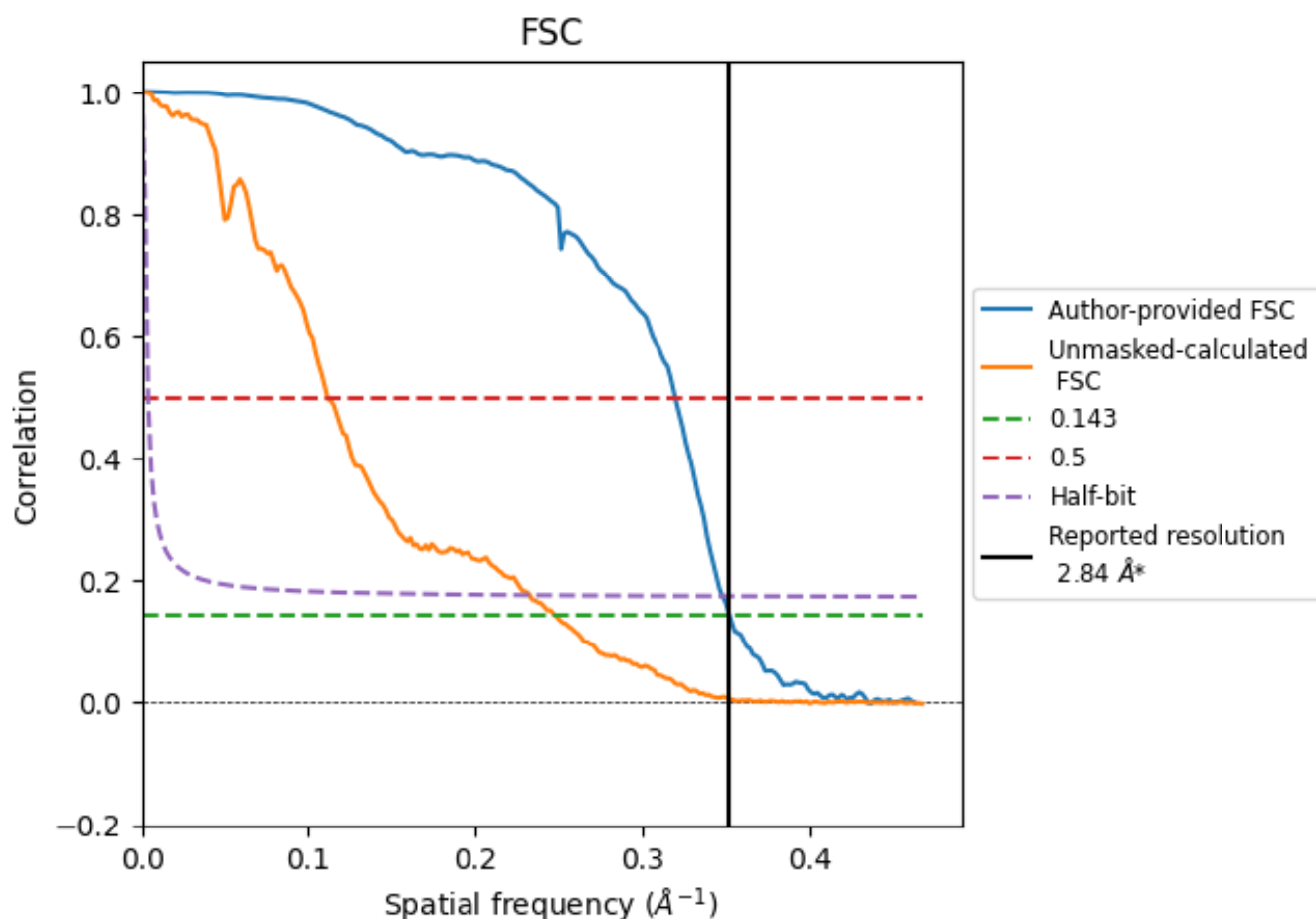


*Reported resolution corresponds to spatial frequency of 0.352 Å⁻¹

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 0.352 \AA^{-1}

8.2 Resolution estimates [i](#)

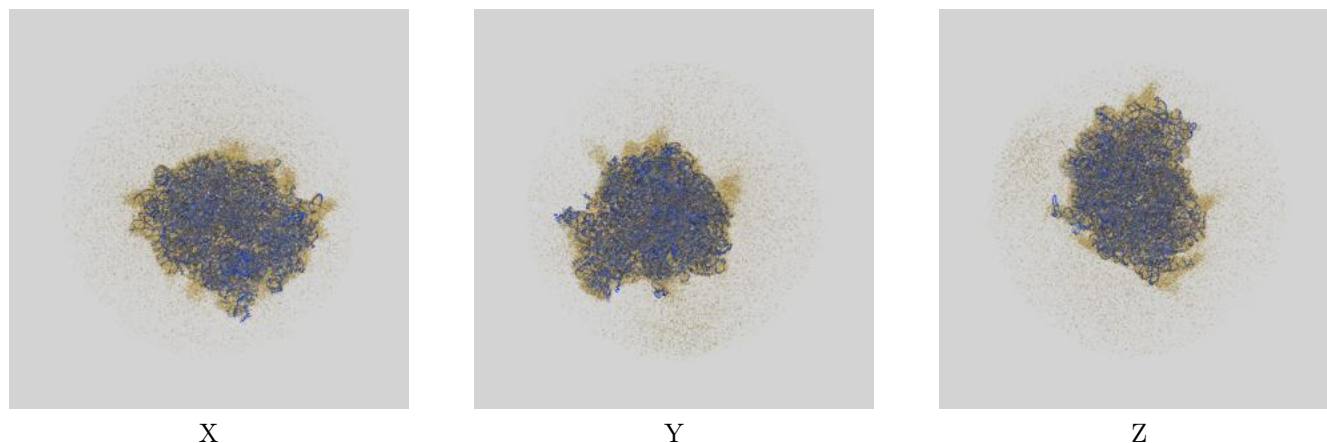
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	2.84	3.12	2.87
Unmasked-calculated*	4.03	8.98	4.30

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.03 differs from the reported value 2.84 by more than 10 %

9 Map-model fit [i](#)

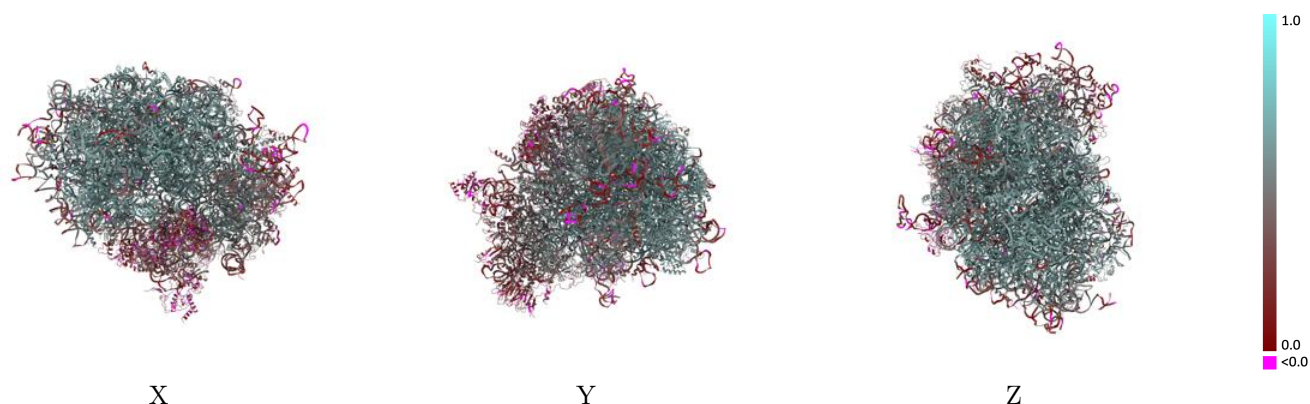
This section contains information regarding the fit between EMDB map EMD-44043 and PDB model 9B0J. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



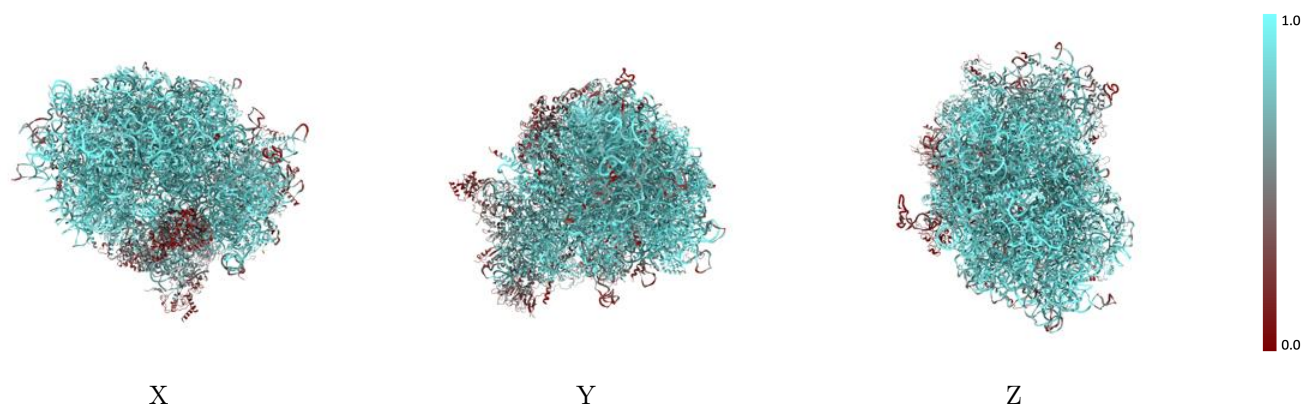
The images above show the 3D surface view of the map at the recommended contour level 0.0253 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



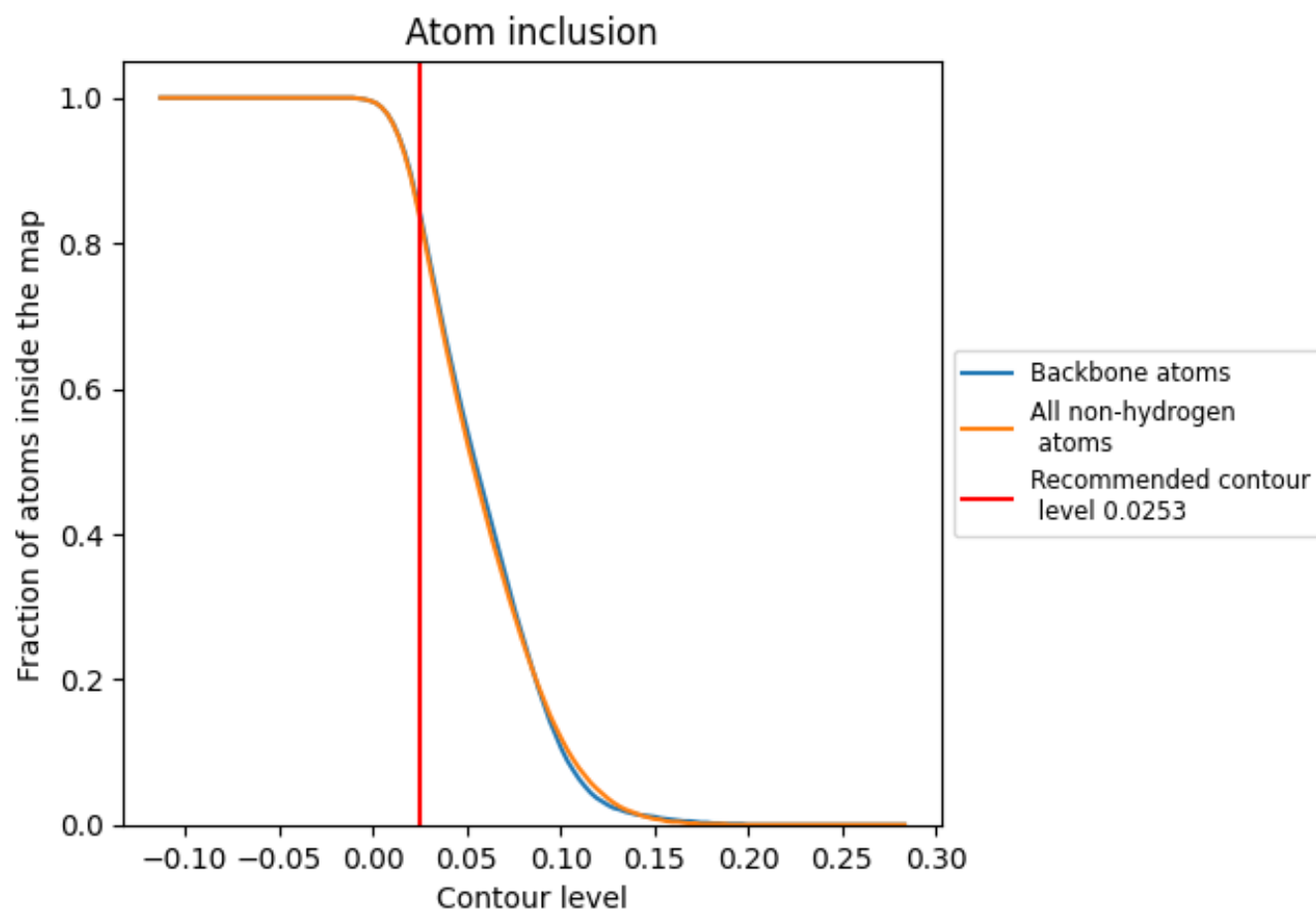
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0253).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 83% 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 (0.0253) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8340	 0.4860
CB	 0.3020	 0.2300
CE	 0.7070	 0.2800
Et	 0.3230	 0.1680
L5	 0.9150	 0.5320
L7	 0.9860	 0.5960
L8	 0.9440	 0.5690
LA	 0.9660	 0.6190
LB	 0.9300	 0.5940
LC	 0.9200	 0.5920
LD	 0.8950	 0.5530
LE	 0.8400	 0.5260
LF	 0.9460	 0.6010
LG	 0.8300	 0.5350
LH	 0.9140	 0.5770
LI	 0.9400	 0.5940
LJ	 0.7870	 0.4790
LL	 0.8960	 0.5660
LM	 0.9320	 0.5810
LN	 0.9810	 0.6270
LO	 0.9490	 0.6040
LP	 0.9440	 0.6120
LQ	 0.9540	 0.6200
LR	 0.8620	 0.5470
LS	 0.9540	 0.6140
LT	 0.9130	 0.5780
LU	 0.8090	 0.4750
LV	 0.9550	 0.6080
LW	 0.6850	 0.4280
LX	 0.9200	 0.5860
LY	 0.9210	 0.5890
LZ	 0.9410	 0.5800
La	 0.9580	 0.6220
Lb	 0.8300	 0.5170
Lc	 0.9210	 0.5570





















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Chain	Atom inclusion	Q-score
Ld	 0.8900	 0.5740
Le	 0.9520	 0.6120
Lf	 0.9640	 0.6180
Lg	 0.9250	 0.5900
Lh	 0.9090	 0.5900
Li	 0.9030	 0.5780
Lj	 0.9630	 0.6160
Lk	 0.8350	 0.5380
Ll	 0.9340	 0.5860
Lm	 0.9300	 0.5980
Ln	 0.9760	 0.6050
Lo	 0.9200	 0.5950
Lp	 0.9160	 0.6010
Lr	 0.9400	 0.6000
Ls	 0.3350	 0.2160
Lt	 0.2110	 0.1330
Lz	 0.0860	 0.1080
S2	 0.8800	 0.4370
SA	 0.7960	 0.4690
SB	 0.8260	 0.5120
SC	 0.8690	 0.5090
SD	 0.5800	 0.3170
SE	 0.8200	 0.4600
SF	 0.5890	 0.3300
SG	 0.6820	 0.3690
SH	 0.6970	 0.4030
SI	 0.8210	 0.4990
SJ	 0.8120	 0.4630
SK	 0.4770	 0.2340
SL	 0.8170	 0.5000
SM	 0.1550	 0.1330
SN	 0.8980	 0.5540
SO	 0.8120	 0.4970
SP	 0.4690	 0.2740
SQ	 0.6090	 0.2910
SR	 0.6340	 0.3400
SS	 0.5450	 0.3160
ST	 0.5880	 0.2760
SU	 0.5170	 0.2710
SV	 0.8550	 0.5060
SW	 0.9230	 0.5560
SX	 0.8530	 0.5250

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Chain	Atom inclusion	Q-score
SY	 0.7290	 0.3700
SZ	 0.4180	 0.2450
Sa	 0.8700	 0.5360
Sb	 0.7900	 0.4740
Sc	 0.6030	 0.3300
Sd	 0.7530	 0.3430
Se	 0.6890	 0.4130
Sf	 0.2760	 0.1630
Sg	 0.3650	 0.2080