



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 10:32 AM UTC

PDB ID : 8HKZ / pdb_00008hkz
EMDB ID : EMD-34864
Title : Cryo-EM Structures and Translocation Mechanism of Crenarchaeota Ribosome
Authors : Wang, Y.H.; Zhou, J.
Deposited on : 2022-11-28
Resolution : 4.78 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

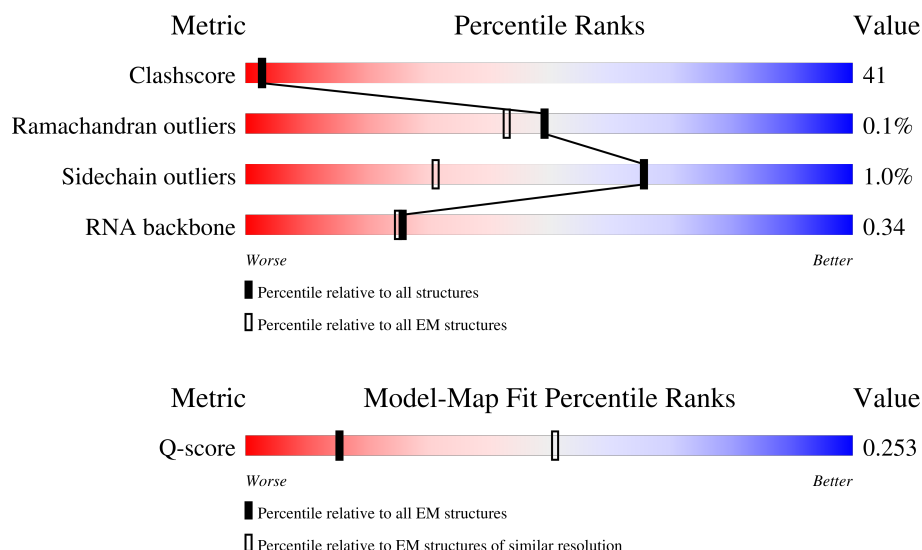
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.78 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1565 (4.28 - 5.27)

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	A23S	3022	
2	A16S	1503	
3	A5S	122	

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Mol	Chain	Length	Quality of chain
4	AL1P	216	95% 100%
5	AL2P	234	46% 98%
6	AL3P	339	38% 99%
7	AL4P	251	26% 99%
8	AL5P	168	40% 99%
9	AL6P	181	36% 99%
10	ALX0	76	30% 96%
11	L10E	164	32% 99%
12	L13P	140	29% 100%
13	L141	86	31% 99%
13	L142	86	53% 100%
14	L14P	134	61% 99%
15	L15E	169	37% 99%
16	L18E	112	7% 100%
17	L18P	193	34% 100%
18	L19E	144	17% 99%
19	L22P	150	37% 99%
20	L23P	81	33% 100%
21	L24E	54	31% 100%
22	L24P	122	18% 99%
23	L29P	63	21% 98%
24	L30E	94	16% 100%
25	L30P	155	26% 99%
26	L31E	75	35% 99%
27	L32E	123	50% 100%

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Mol	Chain	Length	Quality of chain
28	L34E	77	39% 95%
29	L37A	65	25% 100%
30	L37E	54	20% 100%
31	L39E	49	31% 100%
32	L40E	55	87% 100%
33	L44E	92	35% 99%
34	L7A1	123	42% 99%
34	L7A2	123	36% 100%
34	SL7A	123	89% 100%
35	L15P	144	15% 65% 35%
36	L21E	97	25% 99%
37	L45A	101	42% 95% 5%
38	L46A	70	70% 100%
39	L47A	80	94% 99%
40	AS2P	196	51% 100%
41	AS4E	240	37% 99%
42	AS4P	166	29% 99%
43	AS5P	204	30% 100%
44	AS6E	105	64% 98%
45	AS8E	126	55% 100%
46	AS8P	130	15% 98%
47	S11P	128	48% 100%
48	S12P	143	66% 99%
49	S15P	149	23% 97%
50	S17P	111	48% 99%

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Mol	Chain	Length	Quality of chain
51	S24E	96	
52	S27E	59	
53	S3AE	189	
54	AS3P	201	
55	AS7P	193	
56	S10P	100	
57	S13P	147	
58	S14P	52	
59	S17E	62	
60	S19E	150	
61	S19P	115	
62	AS9P	136	
63	S28E	63	
64	S27A	54	
65	APTP	6	
66	AETN	76	
66	APTN	76	
67	AMRN	9	

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 167743 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 23S rRNA (2996-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A23S	2996	Total	C	N	O	P	0	0
			64360	28674	11914	20776	2996		

- Molecule 2 is a RNA chain called 16S rRNA (1493-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A16S	1493	Total	C	N	O	P	0	0
			32063	14279	5930	10361	1493		

- Molecule 3 is a RNA chain called 5S rRNA (122-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A5S	122	Total	C	N	O	P	0	0
			2609	1163	476	849	121		

- Molecule 4 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AL1P	216	Total	C	N	O	S	0	0
			1715	1096	303	312	4		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AL2P	234	Total	C	N	O	S	0	0
			1754	1101	344	307	2		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AL3P	339	Total	C	N	O	S	0	0
			2695	1730	484	477	4		

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AL4P	251	Total	C	N	O	S	0	0
			1926	1223	356	345	2		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AL5P	168	Total	C	N	O	S	0	0
			1343	854	253	232	4		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AL6P	181	Total	C	N	O	S	0	0
			1431	920	246	264	1		

- Molecule 10 is a protein called 50S ribosomal protein L18Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	ALX0	76	Total	C	N	O	S	0	0
			629	403	110	115	1		

- Molecule 11 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L10E	164	Total	C	N	O	S	0	0
			1310	837	239	227	7		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L13P	140	Total	C	N	O	S	0	0
			1109	707	208	190	4		

- Molecule 13 is a protein called 50S ribosomal protein L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L141	86	Total	C	N	O	S	0	0
			669	417	123	127	2		
13	L142	86	Total	C	N	O	S	0	0
			669	417	123	127	2		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L14P	134	Total	C	N	O	S	0	0
			1034	655	194	181	4		

- Molecule 15 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L15E	169	Total	C	N	O	S	0	0
			1423	899	283	236	5		

- Molecule 16 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L18E	112	Total	C	N	O	S	0	0
			895	576	163	153	3		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L18P	193	Total	C	N	O	S	0	0
			1539	990	274	274	1		

- Molecule 18 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	L19E	144	Total	C	N	O	0	0
			1206	753	247	206		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L22P	150	Total	C	N	O	S	0	0
			1223	782	225	213	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L23P	81	Total	C	N	O	S	0	0
			650	419	109	121	1		

- Molecule 21 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L24E	54	Total	C	N	O	S	0	0
			441	282	80	73	6		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L24P	122	Total	C	N	O	S	0	0
			989	620	189	176	4		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L29P	63	Total	C	N	O	S	0	0
			513	319	95	96	3		

- Molecule 24 is a protein called 50S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L30E	94	Total	C	N	O	S	0	0
			729	474	116	136	3		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	L30P	155	Total	C	N	O	S	0	0
			1254	804	222	223	5		

- Molecule 26 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	L31E	75	Total	C	N	O	S	0	0
			625	398	126	97	4		

- Molecule 27 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L32E	123	Total	C	N	O	S	0	0
			1010	650	193	166	1		

- Molecule 28 is a protein called 50S ribosomal protein L34e.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L34E	77	Total	C	N	O	S	0	0
			629	395	119	110	5		

- Molecule 29 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L37A	65	Total	C	N	O	S	0	0
			527	335	99	87	6		

- Molecule 30 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L37E	54	Total	C	N	O	S	0	0
			436	267	94	69	6		

- Molecule 31 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L39E	49	Total	C	N	O		0	0
			414	265	88	61			

- Molecule 32 is a protein called 50S ribosomal protein L40E.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	L40E	55	Total	C	N	O	S	0	0
			439	273	89	72	5		

- Molecule 33 is a protein called 50S ribosomal protein L44e.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L44E	92	Total	C	N	O	S	0	0
			753	474	144	129	6		

- Molecule 34 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L7A1	123	Total	C	N	O	S	0	0
			935	593	155	184	3		
34	L7A2	123	Total	C	N	O	S	0	0
			935	593	155	184	3		
34	SL7A	123	Total	C	N	O	S	0	0
			935	593	155	184	3		

- Molecule 35 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L15P	94	Total	C	N	O	S	0	0
			752	487	131	133	1		

- Molecule 36 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L21E	97	Total	C	N	O	S	0	0
			785	502	152	129	2		

- Molecule 37 is a protein called DUF2280 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L45A	101	Total	C	N	O	S	0	0
			816	515	141	156	4		

- Molecule 38 is a protein called Conserved protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	L46A	70	Total	C	N	O	S	0	0
			586	382	101	102	1		

- Molecule 39 is a protein called 50S ribosomal protein L47A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	L47A	80	Total	C	N	O	S	0	0
			648	405	113	128	2		

- Molecule 40 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AS2P	196	Total	C	N	O	S	0	0
			1587	1022	277	286	2		

- Molecule 41 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AS4E	240	Total	C	N	O	S	0	0
			1925	1238	335	348	4		

- Molecule 42 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AS4P	166	Total	C	N	O	S	0	0
			1370	874	252	241	3		

- Molecule 43 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AS5P	204	Total	C	N	O	S	0	0
			1600	1028	277	287	8		

- Molecule 44 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AS6E	105	Total	C	N	O	S	0	0
			805	506	149	147	3		

- Molecule 45 is a protein called 30S ribosomal protein S8e.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AS8E	126	Total	C	N	O	S	0	0
			993	619	187	187			

- Molecule 46 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AS8P	130	Total	C	N	O	S	0	0
			1028	661	181	182	4		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S11P	128	Total	C	N	O	S	0	0
			960	595	190	173	2		

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S12P	143	Total	C	N	O	S	0	0
			1103	701	209	189	4		

- Molecule 49 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S15P	149	Total	C	N	O	S	0	0
			1225	778	228	214	5		

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S17P	111	Total	C	N	O	S	0	0
			885	557	165	160	3		

- Molecule 51 is a protein called 30S ribosomal protein S24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S24E	96	Total	C	N	O	S	0	0
			759	479	133	147			

- Molecule 52 is a protein called 30S ribosomal protein S27e.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S27E	59	Total	C	N	O	S	0	0
			458	294	83	76	5		

- Molecule 53 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S3AE	189	Total	C	N	O	S	0	0
			1545	1004	264	276	1		

- Molecule 54 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AS3P	201	Total	C	N	O	S	0	0
			1576	1020	274	278	4		

- Molecule 55 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AS7P	193	Total	C	N	O	S	0	0
			1537	969	285	279	4		

- Molecule 56 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S10P	100	Total	C	N	O	S	0	0
			824	522	154	142	6		

- Molecule 57 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S13P	147	Total	C	N	O	S	0	0
			1204	753	230	217	4		

- Molecule 58 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	S14P	52	Total	C	N	O	S	0	0
			432	273	85	69	5		

- Molecule 59 is a protein called 30S ribosomal protein S17e.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	S17E	62	Total	C	N	O	S	0	0
			517	326	92	99			

- Molecule 60 is a protein called 30S ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	S19E	150	Total	C	N	O	S	0	0
			1239	801	223	213	2		

- Molecule 61 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	S19P	115	Total	C	N	O	S	0	0
			968	620	181	162	5		

- Molecule 62 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AS9P	136	Total	C	N	O	S	0	0
			1096	692	200	197	7		

- Molecule 63 is a protein called 30S ribosomal protein S28e.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	S28E	63	Total	C	N	O	0	0
			498	308	99	91		

- Molecule 64 is a protein called 30S ribosomal protein S27ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	S27A	54	Total	C	N	O	S	0	0
			435	274	79	76	6		

- Molecule 65 is a protein called PHE-PHE-PHE-PHE-PHE-PHE.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	APTP	6	Total	C	N	O	0	0
			67	54	6	7		

- Molecule 66 is a RNA chain called tRNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
66	APTN	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		
66	AETN	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 67 is a RNA chain called mRNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AMRN	9	Total	C	N	O	P	0	0
			180	81	18	72	9		

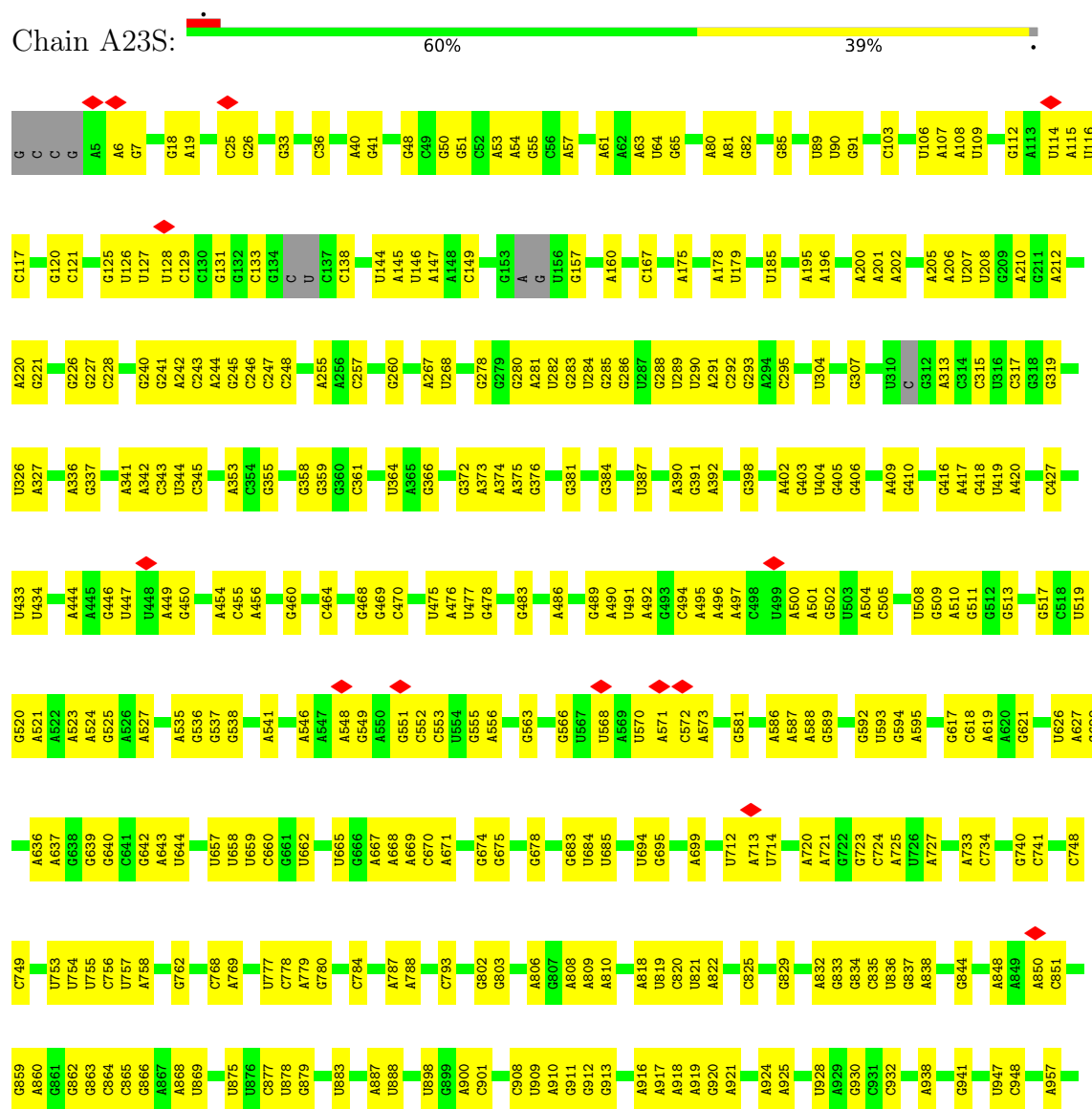
- Molecule 68 is UNKNOWN LIGAND (CCD ID: UNL) (formula:) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms				AltConf
68	AS2P	34	Total	C	N	O	0
			171	102	34	35	
68	AS5P	18	Total	C	N	O	0
			90	54	18	18	
68	AS8P	5	Total	C	N	O	0
			25	15	5	5	

3 Residue-property plots

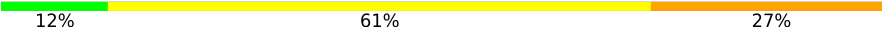
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

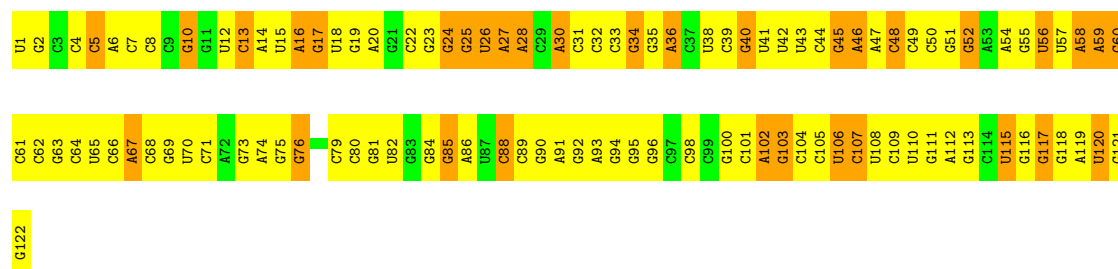
• Molecule 1: 23S rRNA (2996-MER)



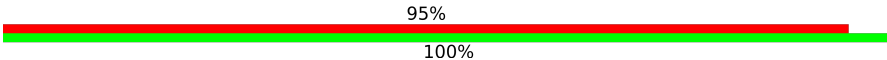


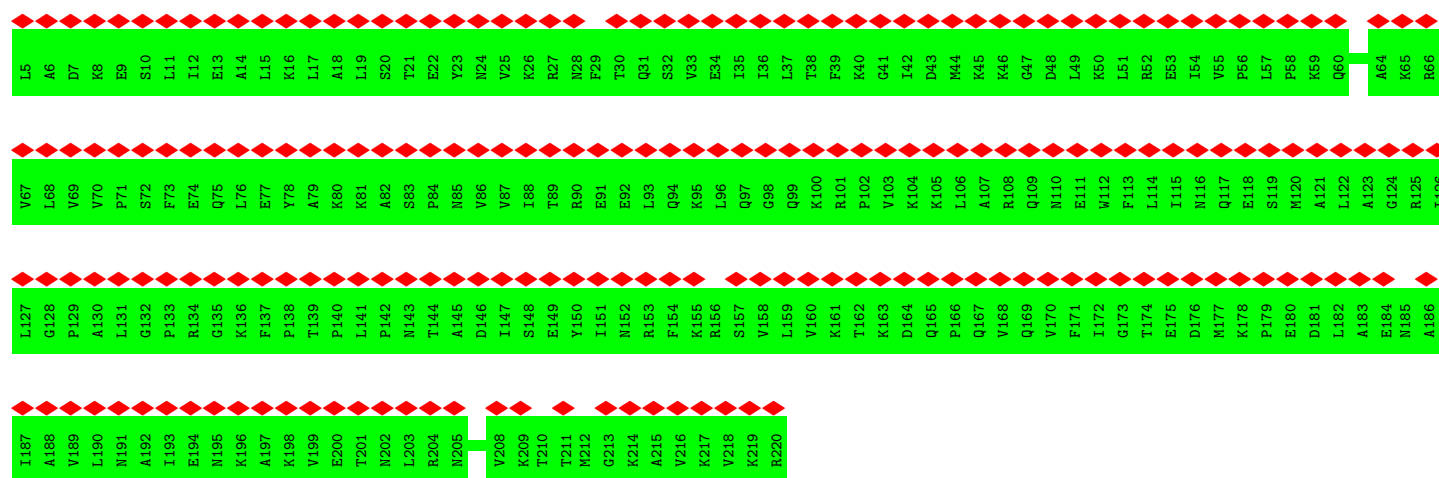


Chain A5S: 

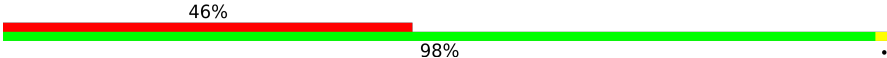


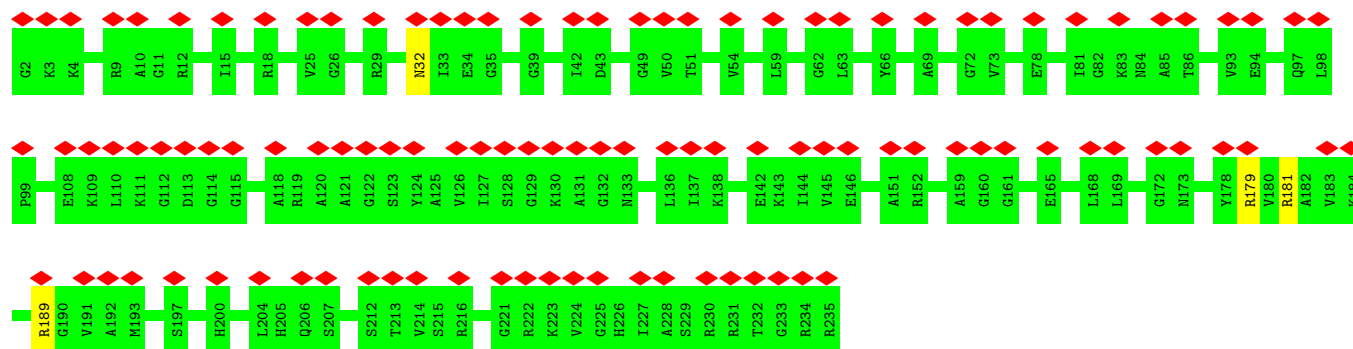
- Molecule 4: 50S ribosomal protein L1

Chain AL1P: 

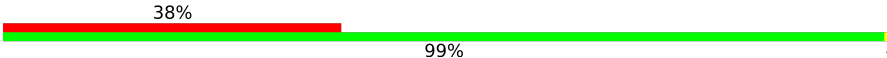


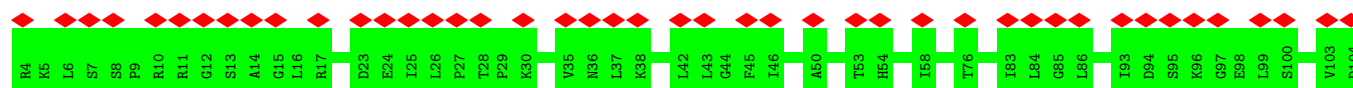
- Molecule 5: 50S ribosomal protein L2

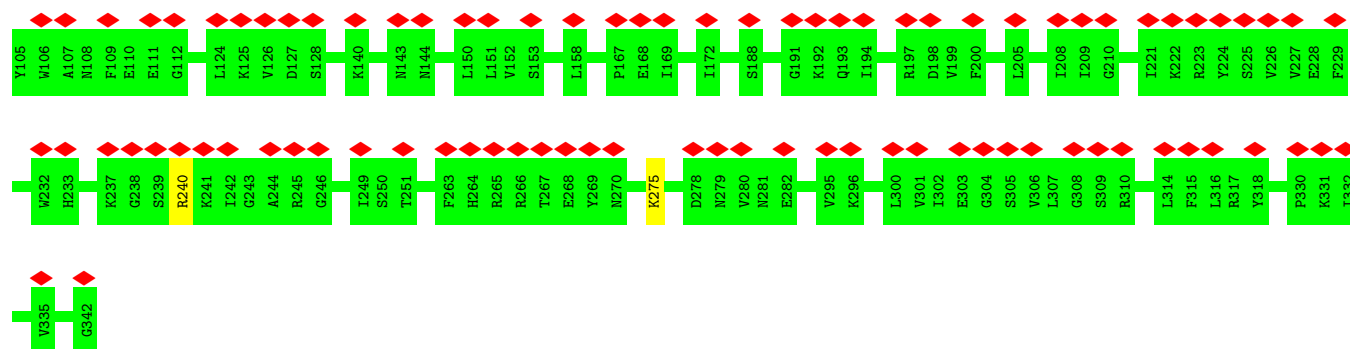
Chain AL2P: 



- Molecule 6: 50S ribosomal protein L3

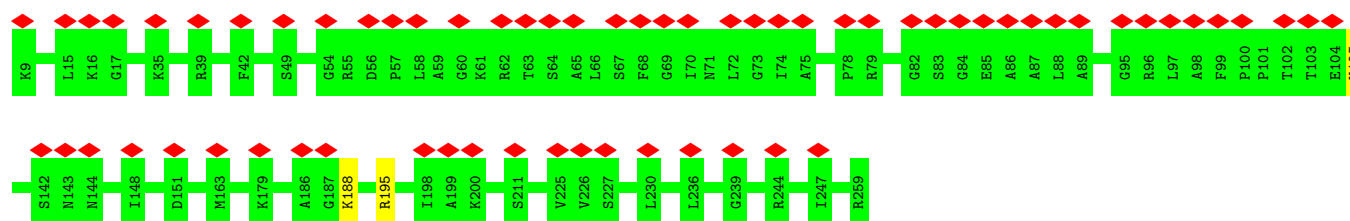
Chain AL3P: 





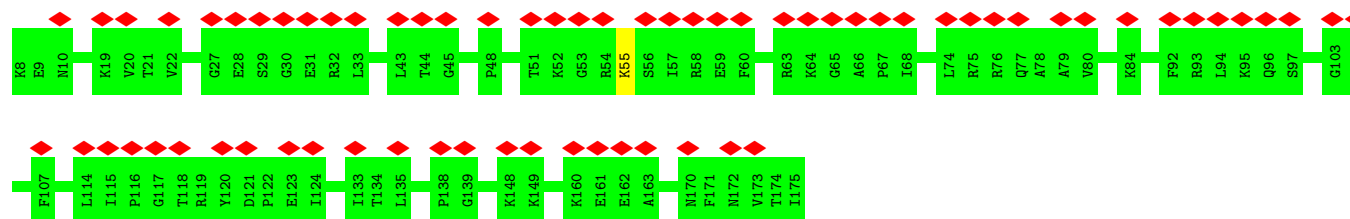
• Molecule 7: 50S ribosomal protein L4

Chain AL4P: 26% 99%



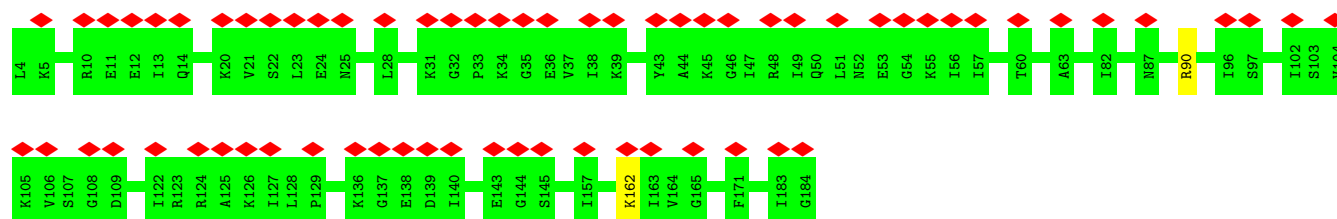
• Molecule 8: 50S ribosomal protein L5

Chain AL5P: 40% 99%



• Molecule 9: 50S ribosomal protein L6

Chain AL6P: 36% 99%

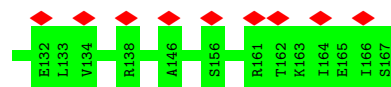
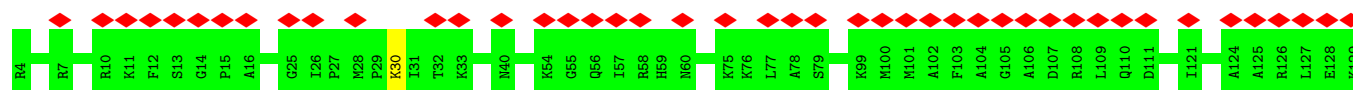


• Molecule 10: 50S ribosomal protein L18Ae

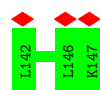
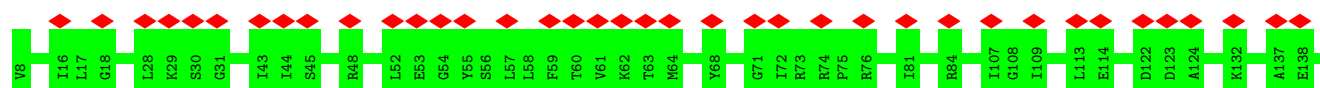
Chain ALX0: 30% 96%



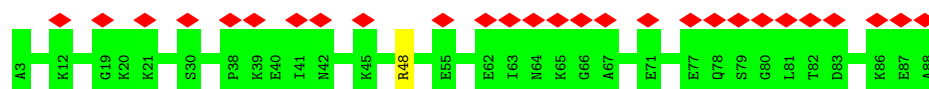
- Molecule 11: 50S ribosomal protein L10e



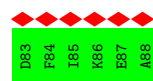
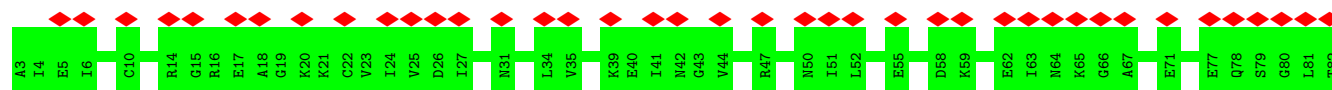
- Molecule 12: 50S ribosomal protein L13



- Molecule 13: 50S ribosomal protein L14e

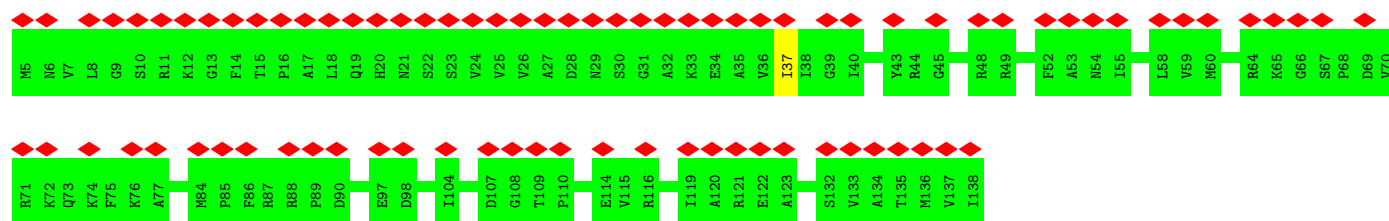


- Molecule 13: 50S ribosomal protein L14e

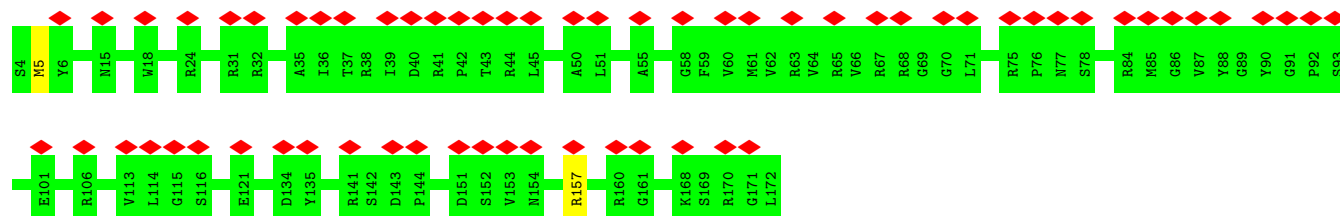


- Molecule 14: 50S ribosomal protein L14

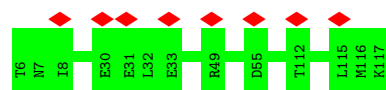




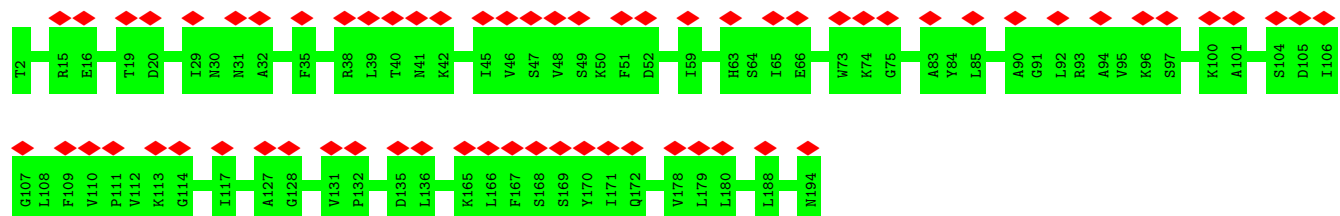
• Molecule 15: 50S ribosomal protein L15e



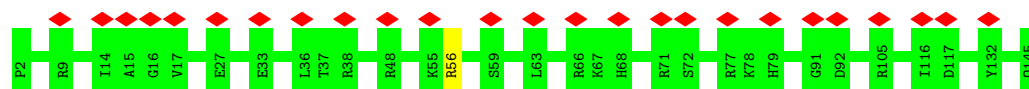
• Molecule 16: 50S ribosomal protein L18e



• Molecule 17: 50S ribosomal protein L18

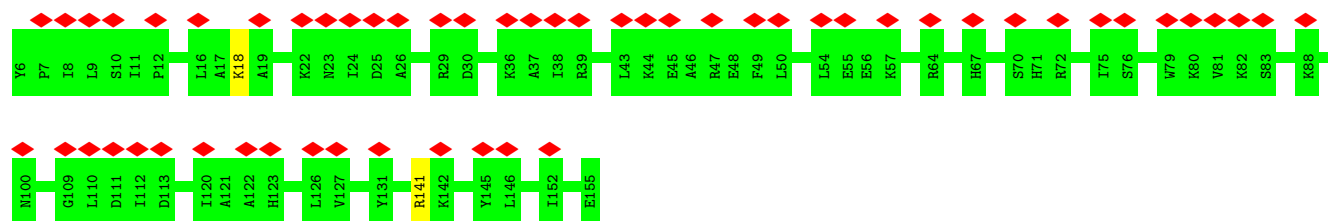


• Molecule 18: 50S ribosomal protein L19e

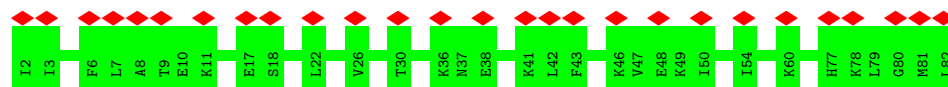


• Molecule 19: 50S ribosomal protein L22

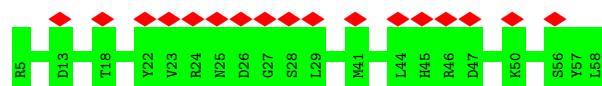




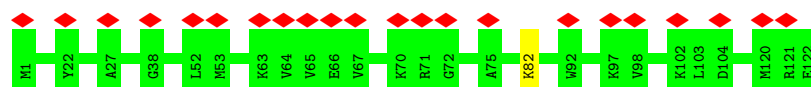
- Molecule 20: 50S ribosomal protein L23



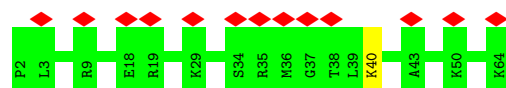
- Molecule 21: 50S ribosomal protein L24e



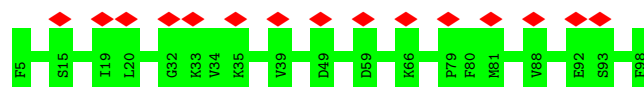
- Molecule 22: 50S ribosomal protein L24



- Molecule 23: 50S ribosomal protein L29

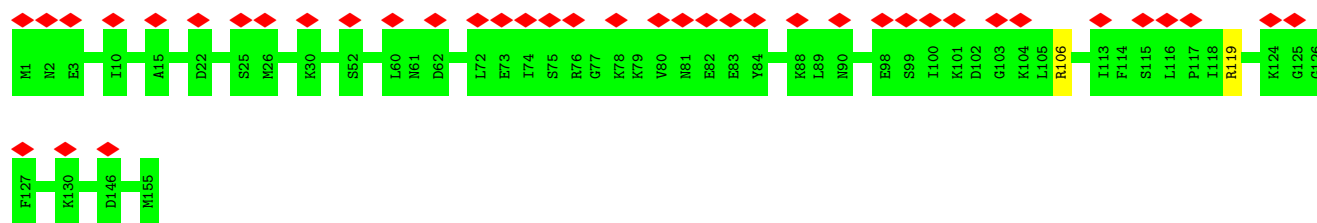


- Molecule 24: 50S ribosomal protein L30e

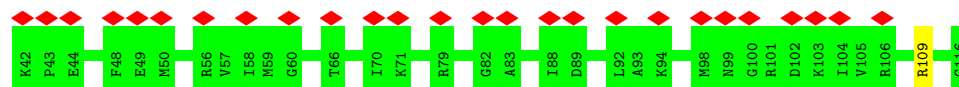
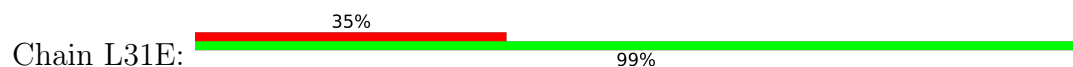


- Molecule 25: 50S ribosomal protein L30

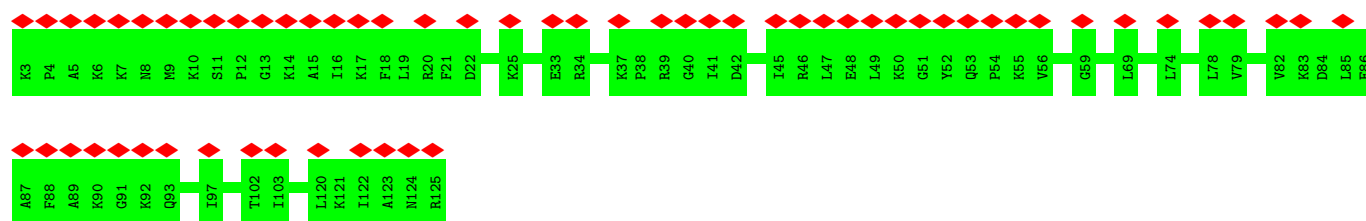




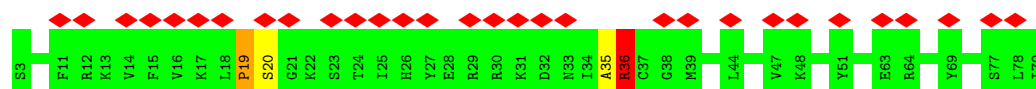
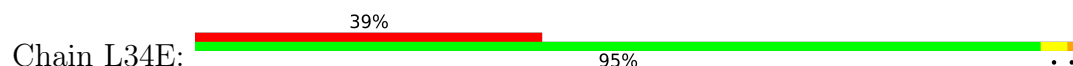
- Molecule 26: 50S ribosomal protein L31e



- Molecule 27: 50S ribosomal protein L32e



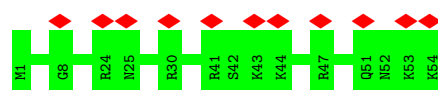
- Molecule 28: 50S ribosomal protein L34e



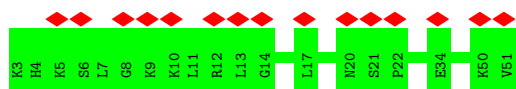
- Molecule 29: 50S ribosomal protein L37Ae



- Molecule 30: 50S ribosomal protein L37e



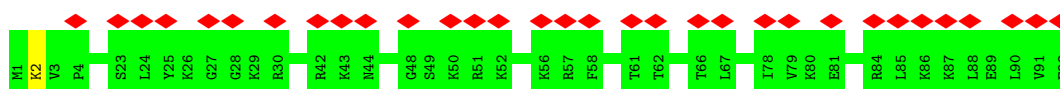
- Molecule 31: 50S ribosomal protein L39e



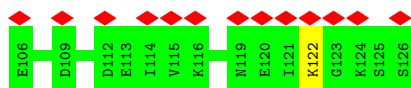
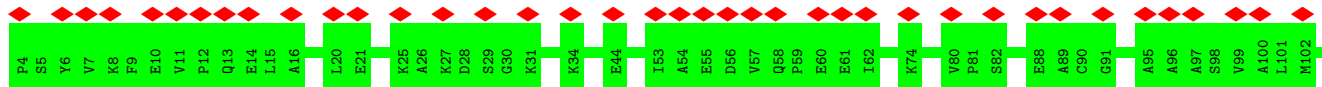
- Molecule 32: 50S ribosomal protein L40E



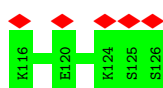
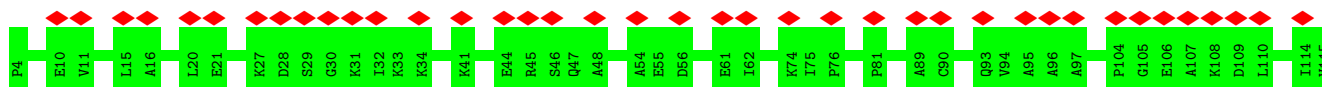
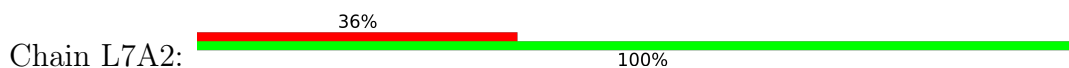
- Molecule 33: 50S ribosomal protein L44e



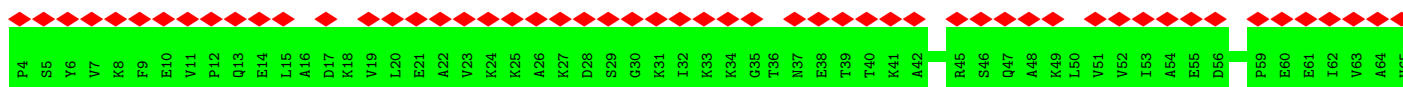
- Molecule 34: 50S ribosomal protein L7Ae

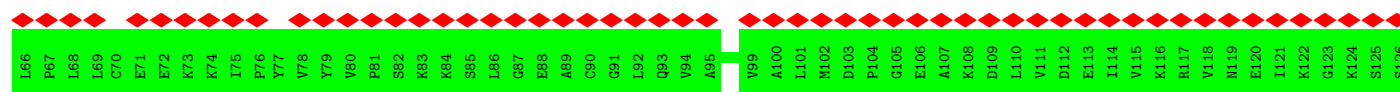


- Molecule 34: 50S ribosomal protein L7Ae

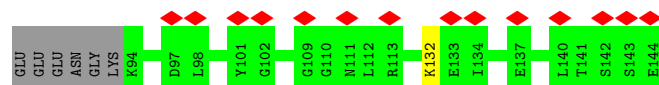
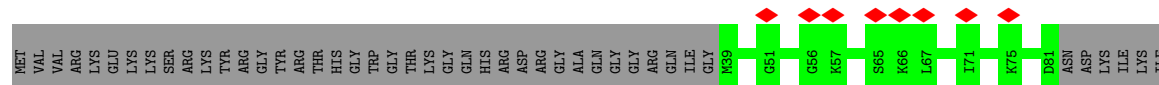


- Molecule 34: 50S ribosomal protein L7Ae

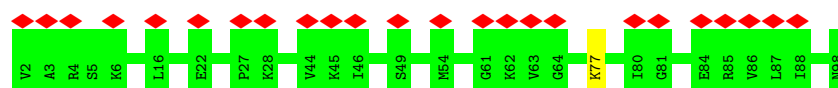




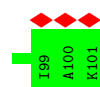
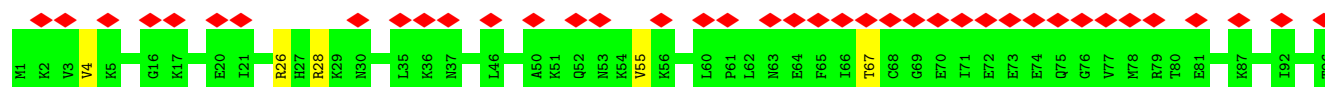
- Molecule 35: Large ribosomal subunit protein uL15



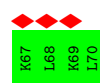
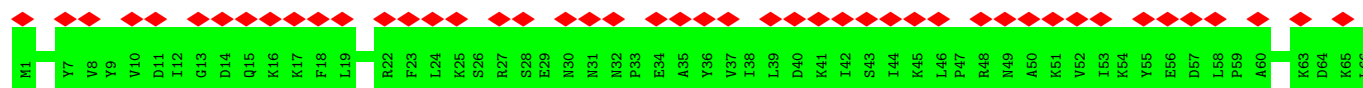
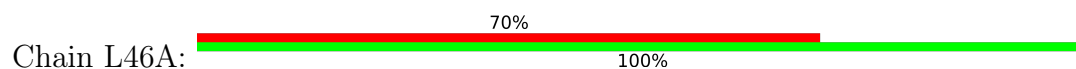
- Molecule 36: 50S ribosomal protein L21e



- Molecule 37: DUF2280 domain-containing protein

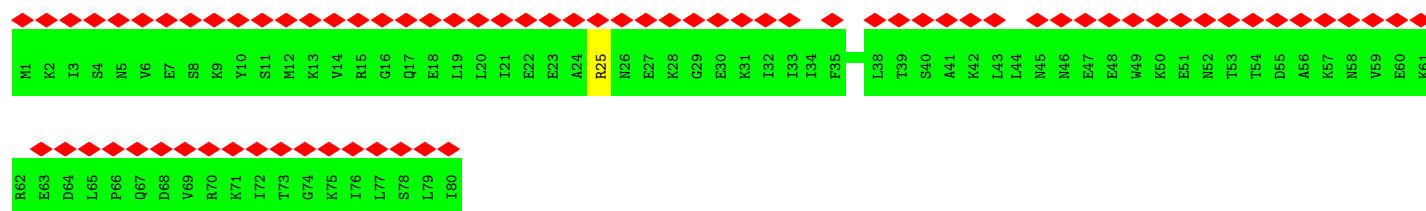


- Molecule 38: Conserved protein

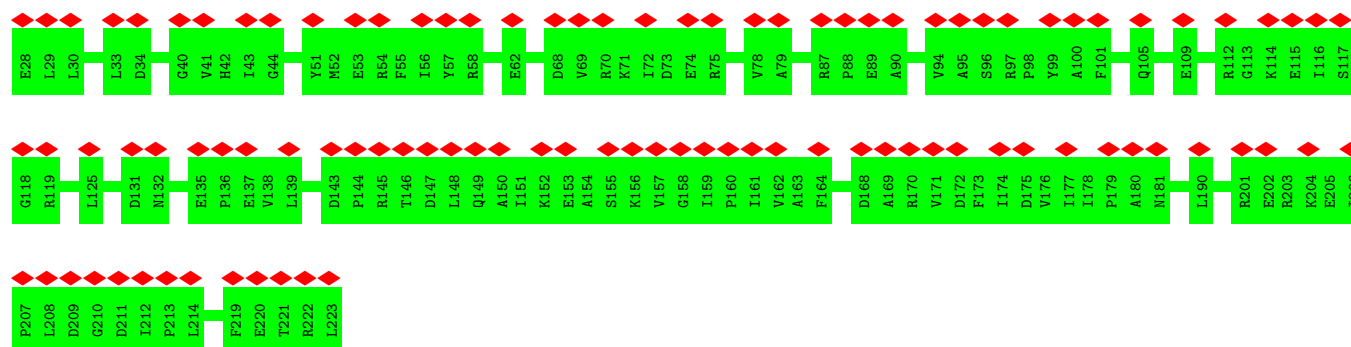


- Molecule 39: 50S ribosomal protein L47A

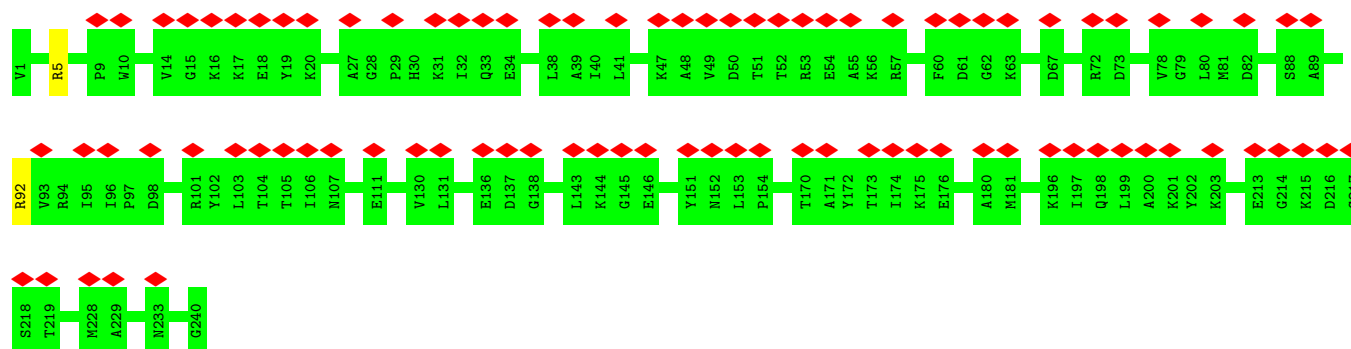
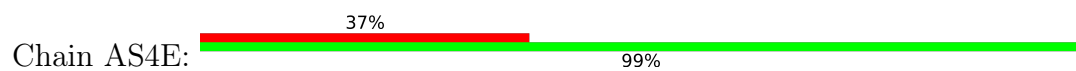




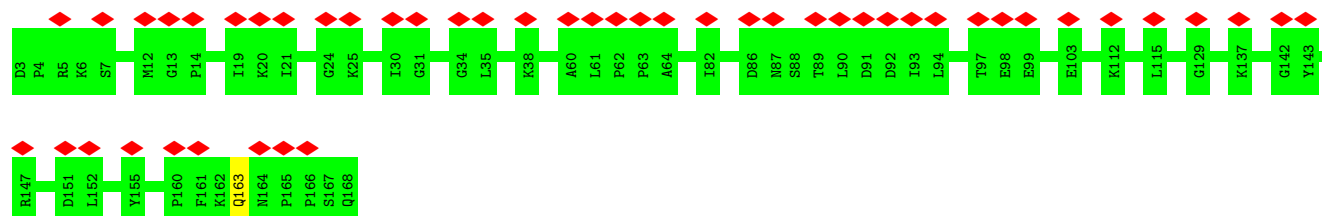
• Molecule 40: 30S ribosomal protein S2



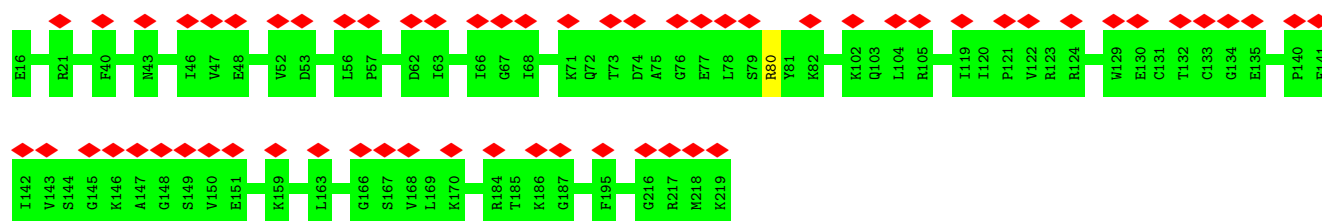
• Molecule 41: 30S ribosomal protein S4e



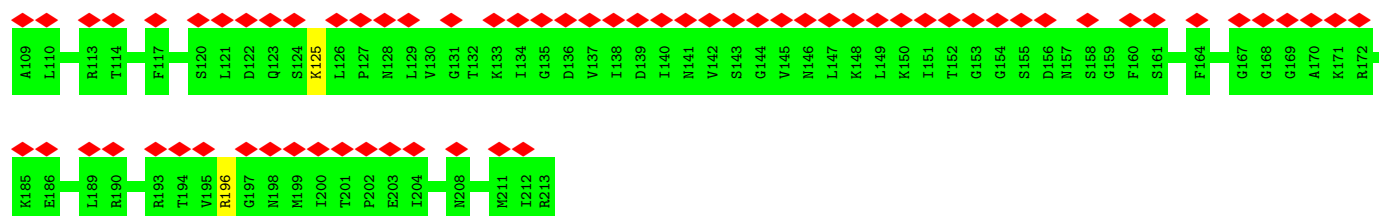
• Molecule 42: 30S ribosomal protein S4



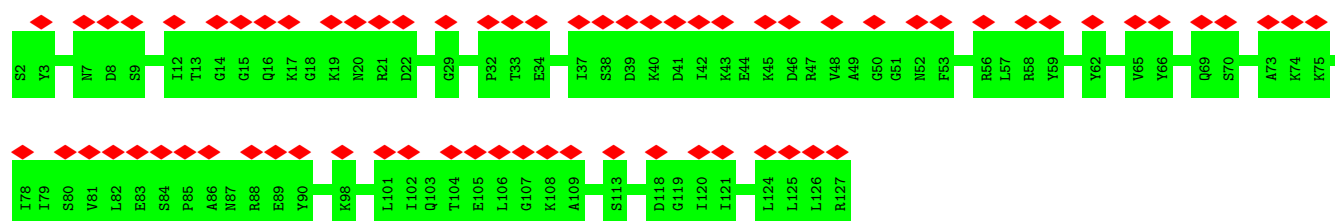
• Molecule 43: 30S ribosomal protein S5



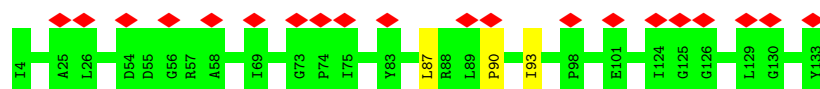
- Molecule 44: 30S ribosomal protein S6e



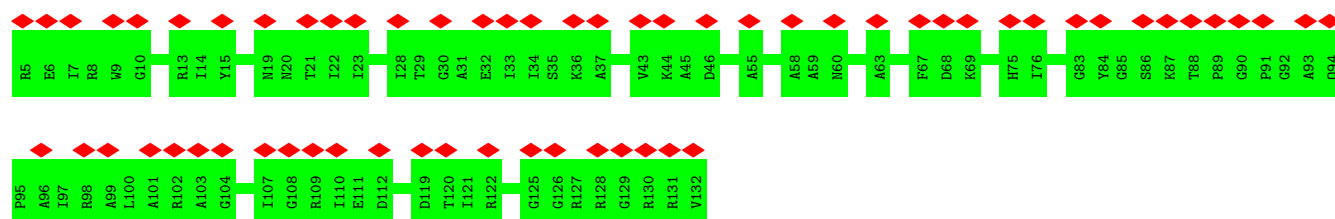
- Molecule 45: 30S ribosomal protein S8e



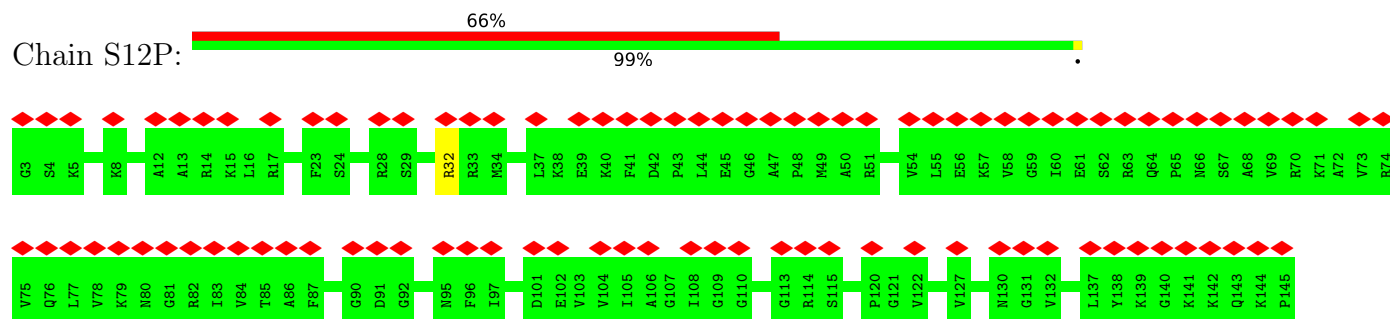
- Molecule 46: 30S ribosomal protein S8



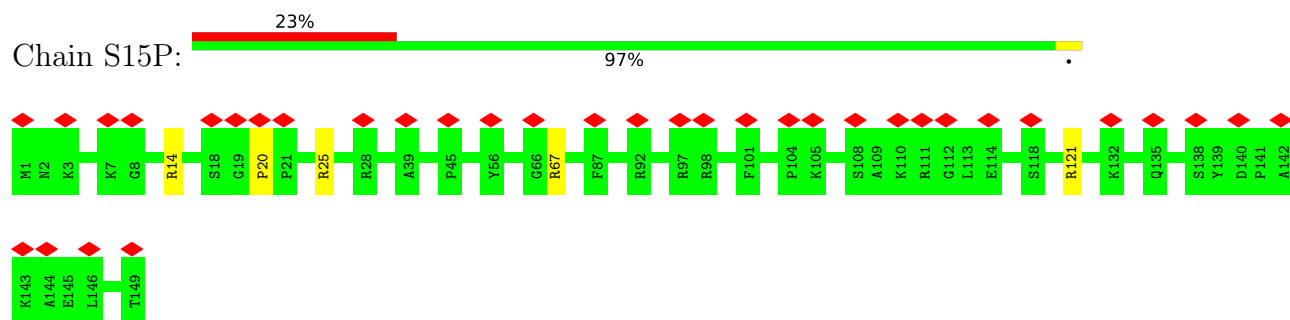
- Molecule 47: 30S ribosomal protein S11



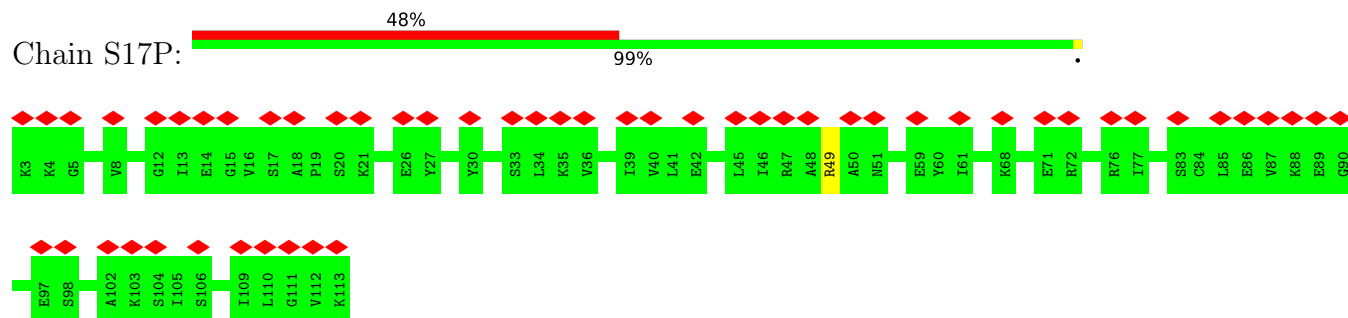
- Molecule 48: 30S ribosomal protein S12



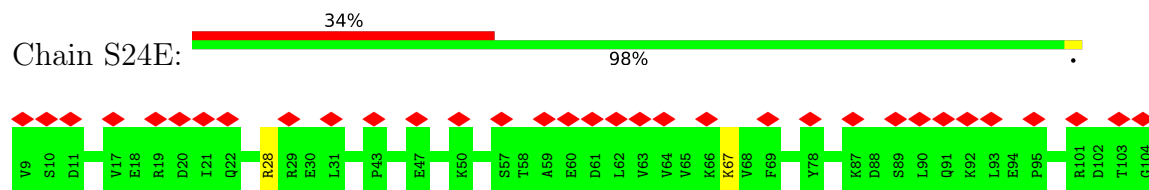
- Molecule 49: 30S ribosomal protein S15



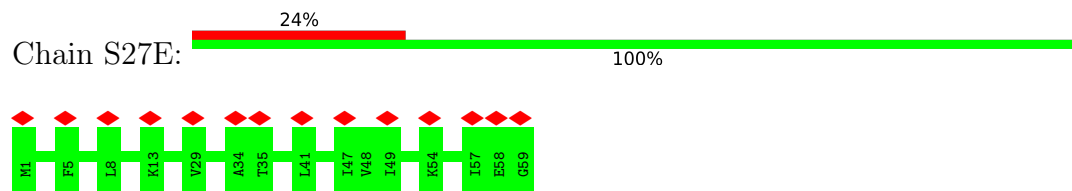
- Molecule 50: 30S ribosomal protein S17



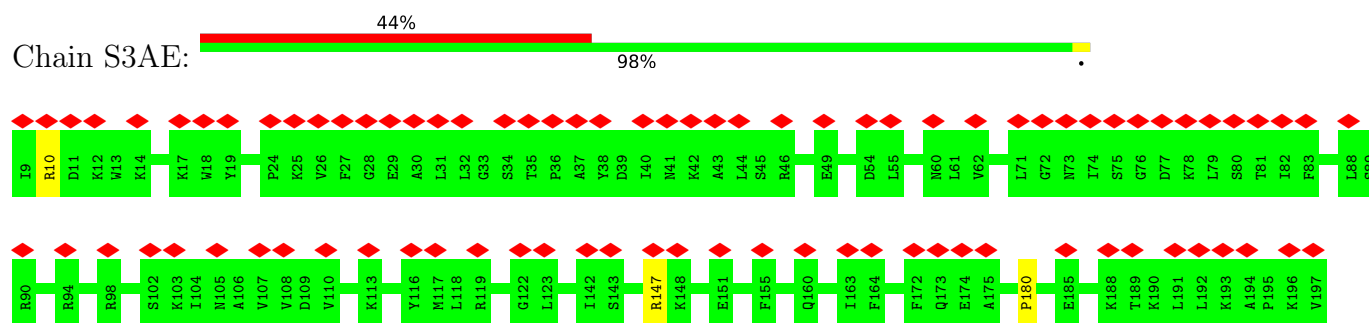
- Molecule 51: 30S ribosomal protein S24e



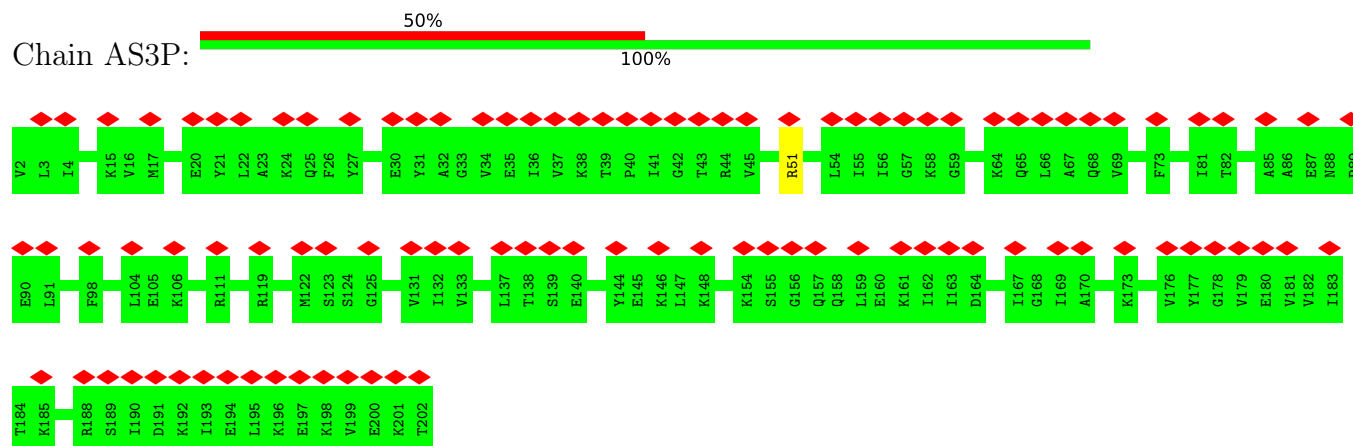
- Molecule 52: 30S ribosomal protein S27e



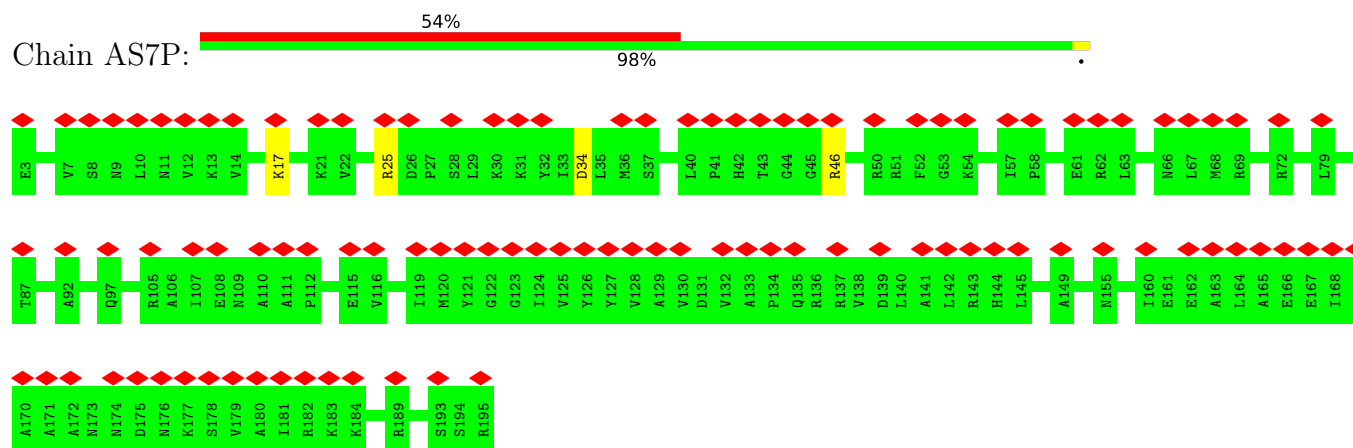
- Molecule 53: 30S ribosomal protein S3Ae



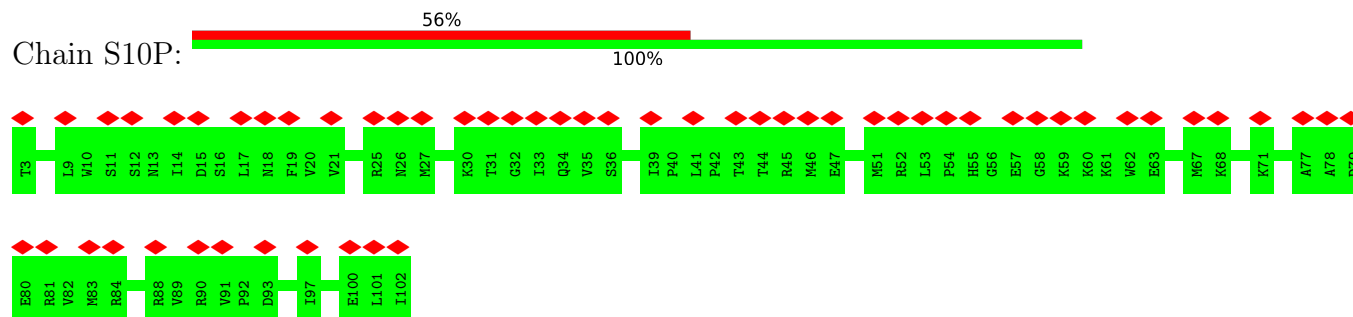
• Molecule 54: 30S ribosomal protein S3



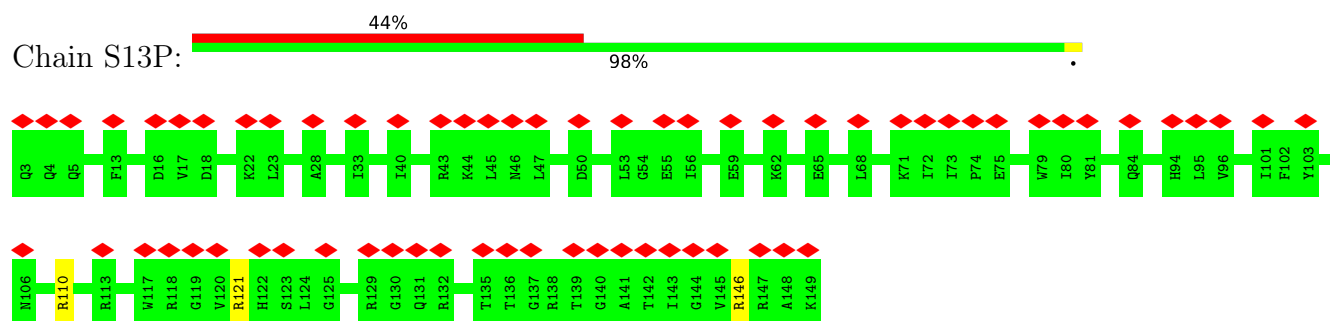
• Molecule 55: 30S ribosomal protein S7



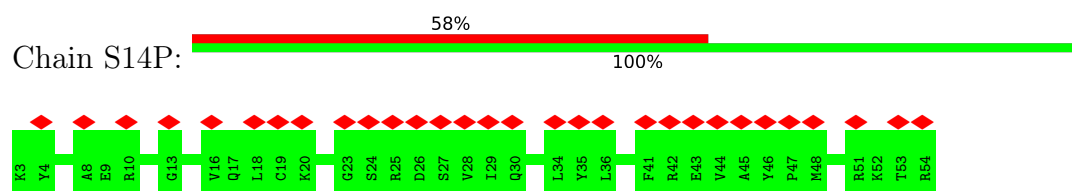
• Molecule 56: 30S ribosomal protein S10



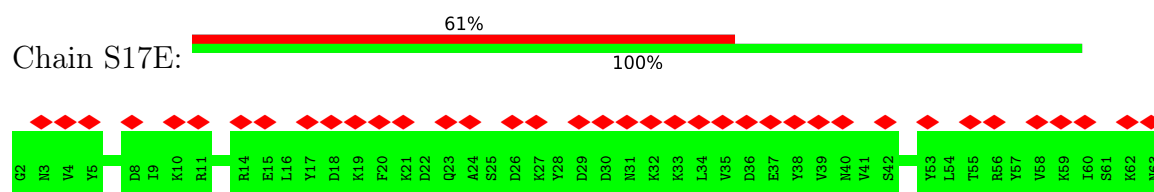
- Molecule 57: 30S ribosomal protein S13



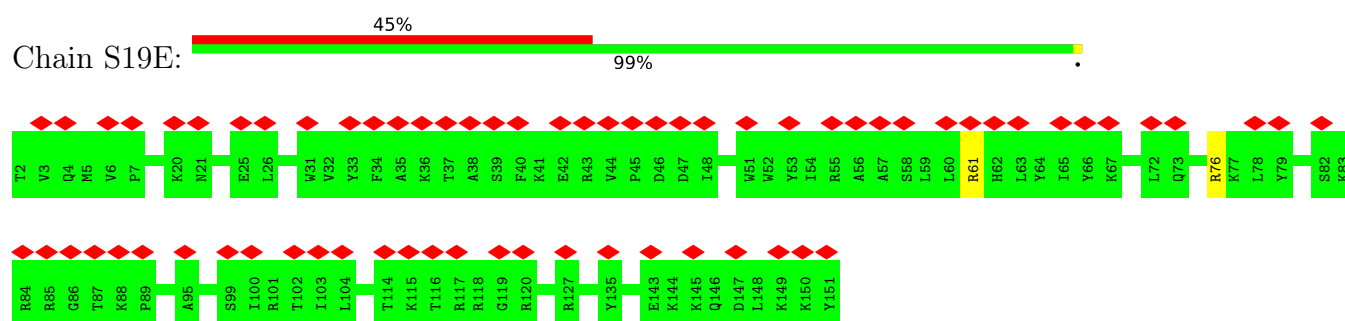
- Molecule 58: 30S ribosomal protein S14 type Z



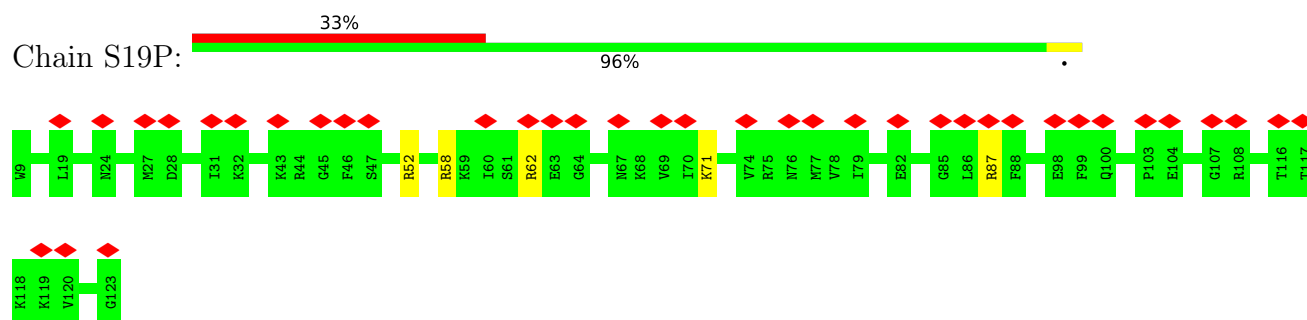
- Molecule 59: 30S ribosomal protein S17e



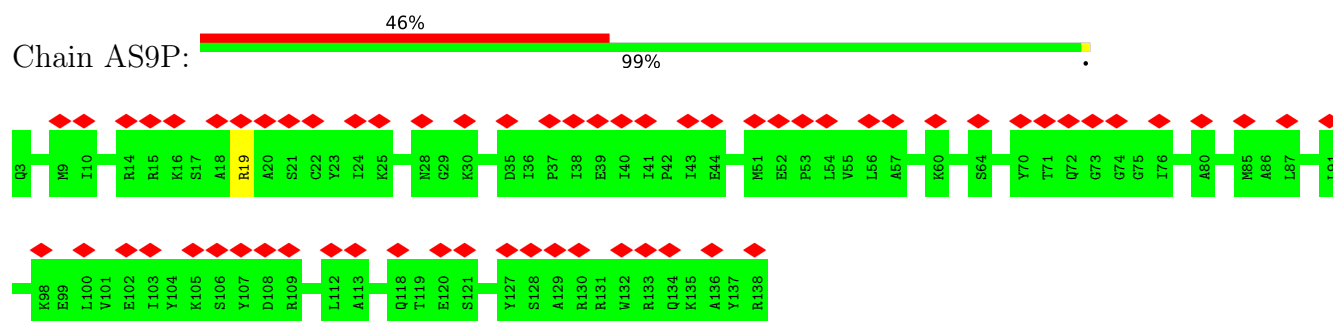
- Molecule 60: 30S ribosomal protein S19e



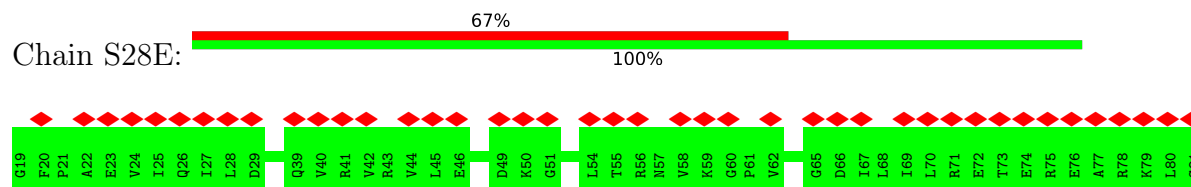
- Molecule 61: 30S ribosomal protein S19



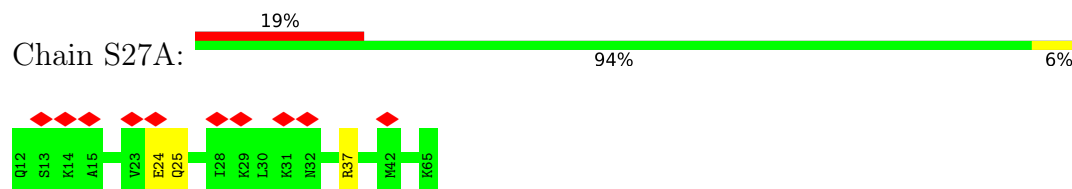
- Molecule 62: 30S ribosomal protein S9



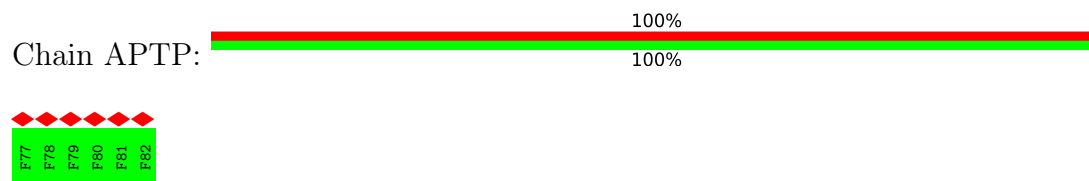
- Molecule 63: 30S ribosomal protein S28e



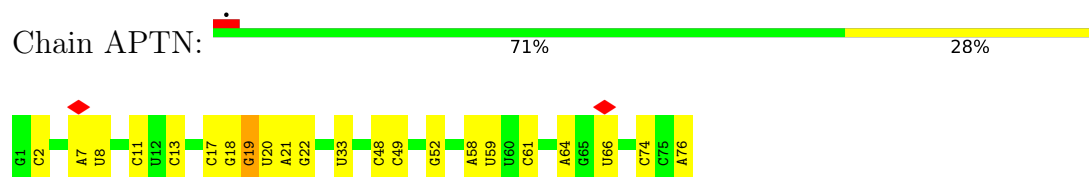
- Molecule 64: 30S ribosomal protein S27ae



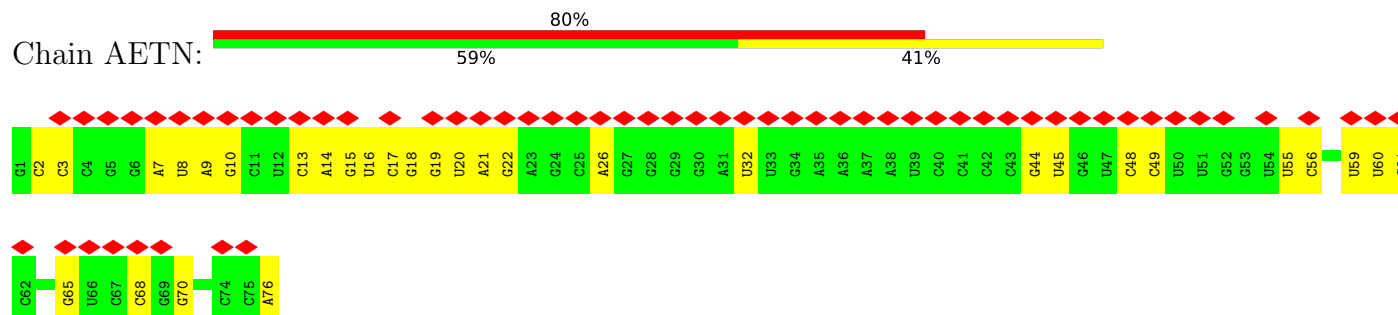
- Molecule 65: PHE-PHE-PHE-PHE-PHE-PHE



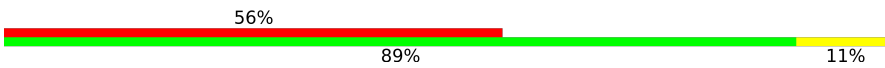
- Molecule 66: tRNA (76-MER)

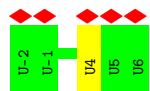


- Molecule 66: tRNA (76-MER)



- Molecule 67: mRNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*U)-3')

Chain AMRN: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3842	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	26.7	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.115	Depositor
Minimum map value	-0.446	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.089	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	413.06, 413.06, 413.06	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.087, 1.087, 1.087	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	A23S	0.25	4/72052 (0.0%)	0.36	11/112414 (0.0%)
2	A16S	0.27	1/35889 (0.0%)	0.42	4/56002 (0.0%)
3	A5S	0.18	0/2917	0.23	0/4549
4	AL1P	0.13	0/1739	0.35	0/2338
5	AL2P	0.18	0/1787	0.37	0/2409
6	AL3P	0.19	0/2758	0.41	0/3727
7	AL4P	0.16	0/1956	0.38	0/2635
8	AL5P	0.16	0/1364	0.38	0/1827
9	AL6P	0.17	0/1450	0.39	0/1949
10	ALX0	0.26	0/638	0.57	0/851
11	L10E	0.17	0/1334	0.35	0/1787
12	L13P	0.17	0/1123	0.41	0/1502
13	L141	0.16	0/673	0.35	0/900
13	L142	0.17	0/673	0.41	0/900
14	L14P	0.17	0/1054	0.38	0/1425
15	L15E	0.19	0/1458	0.41	0/1956
16	L18E	0.16	0/907	0.34	0/1214
17	L18P	0.15	0/1570	0.34	0/2115
18	L19E	0.18	0/1223	0.34	0/1622
19	L22P	0.17	0/1246	0.38	0/1671
20	L23P	0.18	0/655	0.41	0/874
21	L24E	0.17	0/451	0.38	0/599
22	L24P	0.18	0/1000	0.43	0/1329
23	L29P	0.17	0/513	0.43	0/678
24	L30E	0.18	0/738	0.37	0/985
25	L30P	0.20	0/1278	0.50	0/1713
26	L31E	0.18	0/632	0.47	0/837
27	L32E	0.18	0/1027	0.42	0/1366
28	L34E	0.53	2/642 (0.3%)	0.93	10/854 (1.2%)
29	L37A	0.24	0/542	0.49	0/726
30	L37E	0.18	0/445	0.38	0/585
31	L39E	0.20	0/422	0.46	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	L40E	0.17	0/443	0.57	0/587
33	L44E	0.16	0/763	0.33	0/1008
34	L7A1	0.15	0/946	0.32	0/1272
34	L7A2	0.15	0/946	0.34	0/1272
34	SL7A	0.14	0/946	0.38	0/1272
35	L15P	0.16	0/766	0.35	0/1023
36	L21E	0.18	0/800	0.37	0/1067
37	L45A	0.18	0/824	0.44	0/1094
38	L46A	0.14	0/595	0.37	0/793
39	L47A	0.15	0/652	0.43	0/870
40	AS2P	0.15	0/1621	0.35	0/2202
41	AS4E	0.16	0/1956	0.45	0/2635
42	AS4P	0.16	0/1399	0.45	0/1883
43	AS5P	0.18	0/1631	0.37	0/2200
44	AS6E	0.18	0/815	0.43	0/1093
45	AS8E	0.16	0/1005	0.37	0/1342
46	AS8P	0.20	0/1046	0.44	0/1410
47	S11P	0.16	0/976	0.44	0/1315
48	S12P	0.18	0/1120	0.45	0/1495
49	S15P	0.18	0/1250	0.43	0/1677
50	S17P	0.15	0/899	0.36	0/1203
51	S24E	0.15	0/769	0.33	0/1034
52	S27E	0.16	0/465	0.37	0/618
53	S3AE	0.16	0/1573	0.41	0/2115
54	AS3P	0.16	0/1599	0.35	0/2147
55	AS7P	0.18	0/1561	0.45	0/2105
56	S10P	0.16	0/840	0.37	0/1132
57	S13P	0.18	0/1221	0.42	0/1634
58	S14P	0.20	0/441	0.51	0/583
59	S17E	0.14	0/523	0.35	0/696
60	S19E	0.18	0/1267	0.45	0/1705
61	S19P	0.17	0/985	0.39	0/1310
62	AS9P	0.18	0/1115	0.43	0/1496
63	S28E	0.16	0/500	0.40	0/669
64	S27A	0.24	0/444	0.63	0/590
65	APTP	0.23	0/72	0.48	0/93
66	AETN	0.23	0/1809	0.47	0/2819
66	APTN	0.22	0/1809	0.44	1/2819 (0.0%)
67	AMRN	0.14	0/197	0.26	0/302
All	All	0.23	7/180745 (0.0%)	0.39	26/267481 (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
2	A16S	0	1
28	L34E	0	1
42	AS4P	0	1
46	AS8P	0	3
49	S15P	0	1
55	AS7P	0	1
64	S27A	0	1
All	All	0	9

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	L34E	19	PRO	C-N	9.63	1.57	1.32
2	A16S	381	C	C2-O2	-7.39	1.09	1.24
1	A23S	2547	G	C1'-N9	-6.89	1.37	1.48
1	A23S	1315	U	C1'-N1	6.16	1.57	1.48
1	A23S	1316	A	C1'-N9	-5.45	1.38	1.47
1	A23S	1318	U	C1'-N1	5.16	1.56	1.48
28	L34E	20	SER	N-CA	5.11	1.53	1.46

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A16S	381	C	N1-C2-O2	-11.78	83.57	118.90
66	APTN	19	G	N1-C2-N2	-7.86	92.61	116.20
2	A16S	381	C	N3-C2-O2	7.84	145.44	121.90
28	L34E	19	PRO	CA-C-O	-7.35	107.22	120.60
1	A23S	2433	C	N3-C4-N4	-7.25	96.24	118.00
1	A23S	1625	C	P-O3'-C3'	7.00	130.70	120.20
28	L34E	19	PRO	N-CA-C	6.98	126.85	112.47
28	L34E	35	ALA	CA-C-O	-6.59	114.53	121.98
2	A16S	366	C	O4'-C1'-N1	6.57	118.36	108.50
28	L34E	19	PRO	CA-C-N	6.50	140.55	122.15
28	L34E	19	PRO	C-N-CA	6.50	140.55	122.15
28	L34E	36	ARG	N-CA-CB	6.41	121.98	110.83
1	A23S	1626	C	C6-N1-C2	-6.34	101.19	120.20
1	A23S	2433	C	C5-C4-N4	6.21	138.84	120.20
28	L34E	36	ARG	CB-CA-C	-6.07	97.77	109.37
1	A23S	2430	G	N1-C6-O6	-5.93	102.11	119.90
1	A23S	1626	C	C5-C6-N1	5.74	138.21	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A23S	1625	C	N1-C1'-C2'	5.67	122.51	114.00
1	A23S	1626	C	P-O5'-C5'	5.46	129.10	120.90
28	L34E	36	ARG	CB-CG-CD	5.37	123.66	111.30
1	A23S	2640	C	N1-C1'-C2'	5.31	119.96	112.00
28	L34E	35	ALA	CA-C-N	-5.31	114.98	122.94
28	L34E	35	ALA	C-N-CA	-5.31	114.98	122.94
1	A23S	2430	G	C5-C6-O6	5.29	144.47	128.60
2	A16S	1023	C	N1-C1'-C2'	5.16	119.75	112.00
1	A23S	2291	G	O4'-C1'-N9	5.11	115.87	108.20

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A16S	381	C	Sidechain
42	AS4P	163	GLN	Peptide
55	AS7P	34	ASP	Peptide
46	AS8P	87	LEU	Peptide
46	AS8P	90	PRO	Peptide
46	AS8P	93	ILE	Peptide
28	L34E	36	ARG	Peptide
49	S15P	20	PRO	Peptide
64	S27A	24	GLU	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A23S	64360	0	0	0	0
2	A16S	32063	0	0	0	0
3	A5S	2609	0	1324	102	0
4	AL1P	1715	0	0	0	0
5	AL2P	1754	0	0	0	0
6	AL3P	2695	0	0	0	0
7	AL4P	1926	0	0	0	0
8	AL5P	1343	0	0	0	0
9	AL6P	1431	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	ALX0	629	0	0	0	0
11	L10E	1310	0	0	0	0
12	L13P	1109	0	0	0	0
13	L141	669	0	0	0	0
13	L142	669	0	0	0	0
14	L14P	1034	0	0	0	0
15	L15E	1423	0	0	0	0
16	L18E	895	0	0	0	0
17	L18P	1539	0	0	0	0
18	L19E	1206	0	0	0	0
19	L22P	1223	0	0	0	0
20	L23P	650	0	0	0	0
21	L24E	441	0	0	0	0
22	L24P	989	0	0	0	0
23	L29P	513	0	0	0	0
24	L30E	729	0	0	0	0
25	L30P	1254	0	0	0	0
26	L31E	625	0	0	0	0
27	L32E	1010	0	0	0	0
28	L34E	629	0	0	0	0
29	L37A	527	0	0	0	0
30	L37E	436	0	0	0	0
31	L39E	414	0	0	0	0
32	L40E	439	0	0	0	0
33	L44E	753	0	0	0	0
34	L7A1	935	0	0	0	0
34	L7A2	935	0	0	0	0
34	SL7A	935	0	0	0	0
35	L15P	752	0	0	0	0
36	L21E	785	0	0	0	0
37	L45A	816	0	0	0	0
38	L46A	586	0	0	0	0
39	L47A	648	0	0	0	0
40	AS2P	1587	0	0	0	0
41	AS4E	1925	0	0	0	0
42	AS4P	1370	0	0	0	0
43	AS5P	1600	0	0	0	0
44	AS6E	805	0	0	0	0
45	AS8E	993	0	0	0	0
46	AS8P	1028	0	0	0	0
47	S11P	960	0	0	0	0
48	S12P	1103	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	S15P	1225	0	0	0	0
50	S17P	885	0	0	0	0
51	S24E	759	0	0	0	0
52	S27E	458	0	0	0	0
53	S3AE	1545	0	0	0	0
54	AS3P	1576	0	0	0	0
55	AS7P	1537	0	0	0	0
56	S10P	824	0	0	0	0
57	S13P	1204	0	0	0	0
58	S14P	432	0	0	0	0
59	S17E	517	0	0	0	0
60	S19E	1239	0	0	0	0
61	S19P	968	0	0	0	0
62	AS9P	1096	0	0	0	0
63	S28E	498	0	0	0	0
64	S27A	435	0	0	0	0
65	APTP	67	0	0	0	0
66	AETN	1619	0	0	0	0
66	APTN	1619	0	0	0	0
67	AMRN	180	0	0	0	0
68	AS2P	171	0	0	0	0
68	AS5P	90	0	0	0	0
68	AS8P	25	0	0	0	0
All	All	167743	0	1324	102	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 41.

All (102) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A5S:75:G:N1	3:A5S:107:C:O2	2.13	0.81
3:A5S:10:G:N1	3:A5S:115:U:O2	2.15	0.75
3:A5S:35:G:C6	3:A5S:45:G:H1'	2.23	0.73
3:A5S:2:G:H1	3:A5S:122:G:H2'	1.53	0.73
3:A5S:121:G:H2'	3:A5S:122:G:C8	2.28	0.69
3:A5S:15:U:O2'	3:A5S:113:G:OP2	2.12	0.67
3:A5S:85:G:H2'	3:A5S:86:A:C8	2.31	0.64
3:A5S:90:G:N2	3:A5S:93:A:OP2	2.31	0.63
3:A5S:12:U:O2	3:A5S:113:G:N1	2.32	0.63
3:A5S:31:C:O2'	3:A5S:58:A:N6	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A5S:30:A:N6	3:A5S:55:G:O6	2.32	0.62
3:A5S:41:U:O2'	3:A5S:46:A:N6	2.31	0.62
3:A5S:121:G:H2'	3:A5S:122:G:H8	1.66	0.60
3:A5S:34:G:O6	3:A5S:49:C:N4	2.34	0.59
3:A5S:82:U:O2	3:A5S:100:G:N2	2.33	0.59
3:A5S:94:G:H2'	3:A5S:95:G:H8	1.68	0.58
3:A5S:95:G:H2'	3:A5S:96:G:C8	2.39	0.57
3:A5S:1:U:H3'	3:A5S:2:G:C8	2.39	0.57
3:A5S:38:U:N3	3:A5S:49:C:O2'	2.37	0.56
3:A5S:40:G:N2	3:A5S:45:G:OP2	2.39	0.55
3:A5S:76:G:H1	3:A5S:106:U:H3	1.55	0.55
3:A5S:40:G:H21	3:A5S:47:A:H62	1.55	0.54
3:A5S:62:C:H2'	3:A5S:63:G:C8	2.43	0.54
3:A5S:109:C:H2'	3:A5S:110:U:H6	1.72	0.54
3:A5S:16:A:OP2	3:A5S:69:G:N2	2.33	0.54
3:A5S:2:G:N1	3:A5S:122:G:H2'	2.24	0.53
3:A5S:105:C:H2'	3:A5S:106:U:C6	2.44	0.53
3:A5S:1:U:H2'	3:A5S:2:G:O4'	2.09	0.52
3:A5S:65:U:H2'	3:A5S:66:C:C6	2.45	0.52
3:A5S:94:G:H2'	3:A5S:95:G:C8	2.45	0.51
3:A5S:73:G:H2'	3:A5S:74:A:H8	1.75	0.51
3:A5S:104:C:H2'	3:A5S:105:C:C6	2.46	0.51
3:A5S:59:A:H5''	3:A5S:60:G:O5'	2.11	0.51
3:A5S:15:U:H4'	3:A5S:70:U:O2	2.10	0.51
3:A5S:50:C:H2'	3:A5S:51:G:H8	1.75	0.51
3:A5S:95:G:H2'	3:A5S:96:G:H8	1.75	0.51
3:A5S:108:U:H2'	3:A5S:109:C:C6	2.47	0.50
3:A5S:15:U:H5'	3:A5S:71:C:O4'	2.10	0.50
3:A5S:22:C:H2'	3:A5S:23:G:C8	2.47	0.50
3:A5S:45:G:O4'	3:A5S:48:C:N4	2.45	0.50
3:A5S:44:C:H2'	3:A5S:46:A:C8	2.47	0.50
3:A5S:102:A:C2	3:A5S:103:G:H1'	2.47	0.49
3:A5S:106:U:H2'	3:A5S:107:C:C6	2.47	0.49
3:A5S:109:C:H2'	3:A5S:110:U:C6	2.47	0.49
3:A5S:4:C:O2'	3:A5S:5:C:O5'	2.28	0.49
3:A5S:13:C:H1'	3:A5S:16:A:N1	2.28	0.49
3:A5S:32:C:H2'	3:A5S:33:C:C6	2.48	0.49
3:A5S:18:U:H2'	3:A5S:19:G:C8	2.47	0.49
3:A5S:23:G:H2'	3:A5S:24:G:C8	2.49	0.48
3:A5S:33:C:H2'	3:A5S:34:G:O4'	2.14	0.48
3:A5S:45:G:N2	3:A5S:48:C:N3	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A5S:4:C:O2'	3:A5S:5:C:H6	1.98	0.46
3:A5S:116:G:C6	3:A5S:117:G:C6	3.03	0.46
3:A5S:50:C:H2'	3:A5S:51:G:C8	2.50	0.46
3:A5S:7:C:H2'	3:A5S:8:C:C6	2.50	0.46
3:A5S:63:G:H2'	3:A5S:64:C:C6	2.51	0.46
3:A5S:91:A:H2'	3:A5S:92:G:O4'	2.15	0.46
3:A5S:51:G:H2'	3:A5S:52:G:O4'	2.16	0.46
3:A5S:66:C:H2'	3:A5S:67:A:C8	2.51	0.46
3:A5S:4:C:HO2'	3:A5S:5:C:C5'	2.29	0.46
3:A5S:32:C:H4'	3:A5S:54:A:N1	2.31	0.45
3:A5S:93:A:H2'	3:A5S:94:G:O4'	2.17	0.45
3:A5S:93:A:C2	3:A5S:94:G:H1'	2.52	0.45
3:A5S:17:G:C6	3:A5S:69:G:C5	3.04	0.44
3:A5S:76:G:N2	3:A5S:106:U:O2	2.41	0.44
3:A5S:120:U:H2'	3:A5S:121:G:C8	2.52	0.44
3:A5S:84:G:H2'	3:A5S:85:G:H8	1.83	0.44
3:A5S:121:G:C2	3:A5S:122:G:C5	3.05	0.44
3:A5S:85:G:C6	3:A5S:98:C:N3	2.87	0.43
3:A5S:27:A:H2'	3:A5S:120:U:O2'	2.18	0.43
3:A5S:88:C:H2'	3:A5S:89:C:C6	2.52	0.43
3:A5S:56:U:H2'	3:A5S:57:U:O4'	2.19	0.43
3:A5S:60:G:H2'	3:A5S:61:C:O4'	2.19	0.43
3:A5S:92:G:H2'	3:A5S:93:A:C8	2.54	0.43
3:A5S:79:C:H2'	3:A5S:80:C:O4'	2.19	0.43
3:A5S:15:U:H1'	3:A5S:112:A:H2'	2.01	0.43
3:A5S:5:C:H2'	3:A5S:6:A:O4'	2.18	0.42
3:A5S:22:C:N4	3:A5S:23:G:O6	2.52	0.42
3:A5S:19:G:H2'	3:A5S:20:A:H8	1.84	0.42
3:A5S:54:A:H2'	3:A5S:55:G:O4'	2.19	0.42
3:A5S:18:U:H2'	3:A5S:19:G:H8	1.83	0.42
3:A5S:35:G:O2'	3:A5S:36:A:N7	2.52	0.42
3:A5S:81:G:N2	3:A5S:102:A:H1'	2.35	0.42
3:A5S:34:G:C2	3:A5S:51:G:C4	3.08	0.42
3:A5S:40:G:H21	3:A5S:47:A:N6	2.16	0.42
3:A5S:103:G:H2'	3:A5S:104:C:C6	2.55	0.42
3:A5S:27:A:C2	3:A5S:28:A:H1'	2.55	0.42
3:A5S:92:G:H2'	3:A5S:93:A:O4'	2.20	0.42
3:A5S:19:G:H2'	3:A5S:20:A:C8	2.55	0.41
3:A5S:25:G:H1'	3:A5S:28:A:N6	2.35	0.41
3:A5S:88:C:H2'	3:A5S:89:C:H6	1.83	0.41
3:A5S:31:C:H2'	3:A5S:32:C:H5'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A5S:4:C:O2	3:A5S:122:G:N1	2.53	0.41
3:A5S:30:A:C6	3:A5S:31:C:C2	3.08	0.41
3:A5S:46:A:C5	3:A5S:47:A:C5	3.08	0.41
3:A5S:61:C:H2'	3:A5S:62:C:O4'	2.21	0.41
3:A5S:39:C:H2'	3:A5S:40:G:O4'	2.21	0.41
3:A5S:67:A:H2'	3:A5S:68:C:C6	2.57	0.40
3:A5S:90:G:H1'	3:A5S:93:A:N6	2.36	0.40
3:A5S:26:U:H5''	3:A5S:28:A:N7	2.36	0.40
3:A5S:40:G:H1	3:A5S:45:G:P	2.44	0.40
3:A5S:40:G:C5	3:A5S:45:G:C6	3.09	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AL1P	214/216 (99%)	194 (91%)	20 (9%)	0	100	100
5	AL2P	232/234 (99%)	219 (94%)	13 (6%)	0	100	100
6	AL3P	337/339 (99%)	295 (88%)	42 (12%)	0	100	100
7	AL4P	249/251 (99%)	229 (92%)	20 (8%)	0	100	100
8	AL5P	166/168 (99%)	145 (87%)	21 (13%)	0	100	100
9	AL6P	179/181 (99%)	156 (87%)	23 (13%)	0	100	100
10	ALX0	74/76 (97%)	63 (85%)	11 (15%)	0	100	100
11	L10E	162/164 (99%)	148 (91%)	14 (9%)	0	100	100
12	L13P	138/140 (99%)	122 (88%)	16 (12%)	0	100	100
13	L141	84/86 (98%)	74 (88%)	10 (12%)	0	100	100
13	L142	84/86 (98%)	69 (82%)	15 (18%)	0	100	100
14	L14P	132/134 (98%)	118 (89%)	14 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	L15E	167/169 (99%)	156 (93%)	11 (7%)	0	100	100
16	L18E	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
17	L18P	191/193 (99%)	178 (93%)	13 (7%)	0	100	100
18	L19E	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
19	L22P	148/150 (99%)	136 (92%)	12 (8%)	0	100	100
20	L23P	79/81 (98%)	70 (89%)	9 (11%)	0	100	100
21	L24E	52/54 (96%)	49 (94%)	3 (6%)	0	100	100
22	L24P	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
23	L29P	61/63 (97%)	52 (85%)	9 (15%)	0	100	100
24	L30E	92/94 (98%)	83 (90%)	9 (10%)	0	100	100
25	L30P	153/155 (99%)	128 (84%)	25 (16%)	0	100	100
26	L31E	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
27	L32E	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
28	L34E	75/77 (97%)	57 (76%)	17 (23%)	1 (1%)	9	41
29	L37A	63/65 (97%)	50 (79%)	13 (21%)	0	100	100
30	L37E	52/54 (96%)	47 (90%)	5 (10%)	0	100	100
31	L39E	47/49 (96%)	37 (79%)	10 (21%)	0	100	100
32	L40E	53/55 (96%)	43 (81%)	10 (19%)	0	100	100
33	L44E	90/92 (98%)	85 (94%)	5 (6%)	0	100	100
34	L7A1	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
34	L7A2	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
34	SL7A	121/123 (98%)	107 (88%)	14 (12%)	0	100	100
35	L15P	90/144 (62%)	81 (90%)	9 (10%)	0	100	100
36	L21E	95/97 (98%)	89 (94%)	6 (6%)	0	100	100
37	L45A	99/101 (98%)	77 (78%)	19 (19%)	3 (3%)	3	22
38	L46A	68/70 (97%)	62 (91%)	6 (9%)	0	100	100
39	L47A	78/80 (98%)	67 (86%)	11 (14%)	0	100	100
40	AS2P	194/196 (99%)	178 (92%)	16 (8%)	0	100	100
41	AS4E	238/240 (99%)	199 (84%)	39 (16%)	0	100	100
42	AS4P	164/166 (99%)	138 (84%)	26 (16%)	0	100	100
43	AS5P	202/204 (99%)	177 (88%)	25 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	AS6E	103/105 (98%)	79 (77%)	24 (23%)	0	100	100
45	AS8E	124/126 (98%)	114 (92%)	10 (8%)	0	100	100
46	AS8P	128/130 (98%)	107 (84%)	21 (16%)	0	100	100
47	S11P	126/128 (98%)	108 (86%)	18 (14%)	0	100	100
48	S12P	141/143 (99%)	116 (82%)	25 (18%)	0	100	100
49	S15P	147/149 (99%)	129 (88%)	18 (12%)	0	100	100
50	S17P	109/111 (98%)	96 (88%)	13 (12%)	0	100	100
51	S24E	94/96 (98%)	84 (89%)	10 (11%)	0	100	100
52	S27E	57/59 (97%)	47 (82%)	10 (18%)	0	100	100
53	S3AE	187/189 (99%)	164 (88%)	22 (12%)	1 (0%)	24	63
54	AS3P	199/201 (99%)	183 (92%)	16 (8%)	0	100	100
55	AS7P	191/193 (99%)	165 (86%)	26 (14%)	0	100	100
56	S10P	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
57	S13P	145/147 (99%)	124 (86%)	21 (14%)	0	100	100
58	S14P	50/52 (96%)	40 (80%)	10 (20%)	0	100	100
59	S17E	60/62 (97%)	55 (92%)	5 (8%)	0	100	100
60	S19E	148/150 (99%)	125 (84%)	23 (16%)	0	100	100
61	S19P	113/115 (98%)	98 (87%)	15 (13%)	0	100	100
62	AS9P	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
63	S28E	61/63 (97%)	52 (85%)	9 (15%)	0	100	100
64	S27A	52/54 (96%)	39 (75%)	12 (23%)	1 (2%)	6	32
65	AFTP	4/6 (67%)	2 (50%)	2 (50%)	0	100	100
All	All	8002/8184 (98%)	7073 (88%)	923 (12%)	6 (0%)	49	83

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	L34E	19	PRO
37	L45A	55	VAL
37	L45A	4	VAL
37	L45A	67	THR
64	S27A	25	GLN
53	S3AE	180	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AL1P	189/190 (100%)	189 (100%)	0	100	100
5	AL2P	181/181 (100%)	177 (98%)	4 (2%)	45	64
6	AL3P	297/297 (100%)	295 (99%)	2 (1%)	76	79
7	AL4P	212/212 (100%)	209 (99%)	3 (1%)	59	71
8	AL5P	144/144 (100%)	143 (99%)	1 (1%)	76	79
9	AL6P	157/157 (100%)	155 (99%)	2 (1%)	61	72
10	ALX0	68/68 (100%)	65 (96%)	3 (4%)	25	47
11	L10E	137/137 (100%)	136 (99%)	1 (1%)	76	79
12	L13P	121/121 (100%)	121 (100%)	0	100	100
13	L141	74/74 (100%)	73 (99%)	1 (1%)	59	71
13	L142	74/74 (100%)	74 (100%)	0	100	100
14	L14P	110/110 (100%)	109 (99%)	1 (1%)	70	77
15	L15E	146/146 (100%)	144 (99%)	2 (1%)	59	71
16	L18E	98/98 (100%)	98 (100%)	0	100	100
17	L18P	162/162 (100%)	162 (100%)	0	100	100
18	L19E	126/126 (100%)	125 (99%)	1 (1%)	73	78
19	L22P	131/131 (100%)	129 (98%)	2 (2%)	57	71
20	L23P	74/74 (100%)	74 (100%)	0	100	100
21	L24E	50/50 (100%)	50 (100%)	0	100	100
22	L24P	108/108 (100%)	107 (99%)	1 (1%)	70	77
23	L29P	59/59 (100%)	58 (98%)	1 (2%)	53	68
24	L30E	83/83 (100%)	83 (100%)	0	100	100
25	L30P	136/136 (100%)	134 (98%)	2 (2%)	57	71
26	L31E	66/66 (100%)	65 (98%)	1 (2%)	57	71
27	L32E	106/106 (100%)	106 (100%)	0	100	100
28	L34E	70/70 (100%)	69 (99%)	1 (1%)	59	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	L37A	53/53 (100%)	53 (100%)	0	100	100
30	L37E	45/45 (100%)	45 (100%)	0	100	100
31	L39E	44/44 (100%)	44 (100%)	0	100	100
32	L40E	50/50 (100%)	50 (100%)	0	100	100
33	L44E	84/84 (100%)	83 (99%)	1 (1%)	63	73
34	L7A1	104/104 (100%)	103 (99%)	1 (1%)	68	76
34	L7A2	104/104 (100%)	104 (100%)	0	100	100
34	SL7A	104/104 (100%)	104 (100%)	0	100	100
35	L15P	78/118 (66%)	77 (99%)	1 (1%)	61	72
36	L21E	85/85 (100%)	84 (99%)	1 (1%)	63	73
37	L45A	91/91 (100%)	89 (98%)	2 (2%)	45	64
38	L46A	66/66 (100%)	66 (100%)	0	100	100
39	L47A	74/74 (100%)	73 (99%)	1 (1%)	59	71
40	AS2P	174/174 (100%)	174 (100%)	0	100	100
41	AS4E	210/210 (100%)	208 (99%)	2 (1%)	68	76
42	AS4P	149/149 (100%)	149 (100%)	0	100	100
43	AS5P	174/174 (100%)	173 (99%)	1 (1%)	78	81
44	AS6E	88/88 (100%)	86 (98%)	2 (2%)	44	64
45	AS8E	106/106 (100%)	106 (100%)	0	100	100
46	AS8P	111/111 (100%)	111 (100%)	0	100	100
47	S11P	94/94 (100%)	94 (100%)	0	100	100
48	S12P	116/116 (100%)	115 (99%)	1 (1%)	70	77
49	S15P	133/133 (100%)	129 (97%)	4 (3%)	36	57
50	S17P	97/97 (100%)	96 (99%)	1 (1%)	68	76
51	S24E	84/84 (100%)	82 (98%)	2 (2%)	43	63
52	S27E	51/51 (100%)	51 (100%)	0	100	100
53	S3AE	170/170 (100%)	168 (99%)	2 (1%)	63	73
54	AS3P	165/165 (100%)	164 (99%)	1 (1%)	78	81
55	AS7P	166/166 (100%)	163 (98%)	3 (2%)	51	67
56	S10P	92/92 (100%)	92 (100%)	0	100	100
57	S13P	129/129 (100%)	126 (98%)	3 (2%)	44	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	S14P	45/45 (100%)	45 (100%)	0	100	100
59	S17E	57/57 (100%)	57 (100%)	0	100	100
60	S19E	134/134 (100%)	132 (98%)	2 (2%)	57	71
61	S19P	106/106 (100%)	101 (95%)	5 (5%)	23	45
62	AS9P	113/113 (100%)	112 (99%)	1 (1%)	70	77
63	S28E	54/54 (100%)	54 (100%)	0	100	100
64	S27A	47/47 (100%)	46 (98%)	1 (2%)	47	65
65	APTP	6/6 (100%)	6 (100%)	0	100	100
All	All	7032/7073 (99%)	6965 (99%)	67 (1%)	65	76

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	AL2P	32	ASN
5	AL2P	179	ARG
5	AL2P	181	ARG
5	AL2P	189	ARG
6	AL3P	240	ARG
6	AL3P	275	LYS
7	AL4P	105	LYS
7	AL4P	188	LYS
7	AL4P	195	ARG
8	AL5P	55	LYS
9	AL6P	90	ARG
9	AL6P	162	LYS
10	ALX0	6	ILE
10	ALX0	14	ILE
10	ALX0	36	LYS
11	L10E	30	LYS
13	L14I	48	ARG
14	L14P	37	ILE
15	L15E	5	MET
15	L15E	157	ARG
18	L19E	56	ARG
19	L22P	18	LYS
19	L22P	141	ARG
22	L24P	82	LYS
23	L29P	40	LYS
25	L30P	106	ARG

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Mol	Chain	Res	Type
25	L30P	119	ARG
26	L31E	109	ARG
28	L34E	36	ARG
33	L44E	2	LYS
34	L7A1	122	LYS
35	L15P	132	LYS
36	L21E	77	LYS
37	L45A	26	ARG
37	L45A	28	ARG
39	L47A	25	ARG
41	AS4E	5	ARG
41	AS4E	92	ARG
43	AS5P	80	ARG
44	AS6E	125	LYS
44	AS6E	196	ARG
48	S12P	32	ARG
49	S15P	14	ARG
49	S15P	25	ARG
49	S15P	67	ARG
49	S15P	121	ARG
50	S17P	49	ARG
51	S24E	28	ARG
51	S24E	67	LYS
53	S3AE	10	ARG
53	S3AE	147	ARG
54	AS3P	51	ARG
55	AS7P	17	LYS
55	AS7P	25	ARG
55	AS7P	46	ARG
57	S13P	110	ARG
57	S13P	121	ARG
57	S13P	146	ARG
60	S19E	61	ARG
60	S19E	76	ARG
61	S19P	52	ARG
61	S19P	58	ARG
61	S19P	62	ARG
61	S19P	71	LYS
61	S19P	87	ARG
62	AS9P	19	ARG
64	S27A	37	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are

no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A23S	2986/3022 (98%)	1168 (39%)	55 (1%)
2	A16S	1491/1503 (99%)	618 (41%)	58 (3%)
3	A5S	121/122 (99%)	39 (32%)	1 (0%)
66	AETN	75/76 (98%)	31 (41%)	2 (2%)
66	APTN	75/76 (98%)	21 (28%)	1 (1%)
67	AMRN	8/9 (88%)	1 (12%)	0
All	All	4756/4808 (98%)	1878 (39%)	117 (2%)

All (1878) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A23S	6	A
1	A23S	7	G
1	A23S	18	G
1	A23S	19	A
1	A23S	25	C
1	A23S	26	G
1	A23S	33	G
1	A23S	36	C
1	A23S	40	A
1	A23S	41	G
1	A23S	48	G
1	A23S	50	G
1	A23S	51	G
1	A23S	53	A
1	A23S	54	A
1	A23S	55	G
1	A23S	57	A
1	A23S	61	A
1	A23S	63	A
1	A23S	64	U
1	A23S	65	G
1	A23S	80	A
1	A23S	81	A
1	A23S	82	G
1	A23S	85	G
1	A23S	89	U
1	A23S	90	U

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Mol	Chain	Res	Type
1	A23S	91	G
1	A23S	103	C
1	A23S	106	U
1	A23S	107	A
1	A23S	108	A
1	A23S	109	U
1	A23S	112	G
1	A23S	114	U
1	A23S	115	A
1	A23S	116	U
1	A23S	117	C
1	A23S	120	G
1	A23S	121	C
1	A23S	125	G
1	A23S	126	U
1	A23S	127	U
1	A23S	128	U
1	A23S	129	C
1	A23S	131	G
1	A23S	133	C
1	A23S	138	C
1	A23S	144	U
1	A23S	145	A
1	A23S	146	U
1	A23S	147	A
1	A23S	149	C
1	A23S	157	G
1	A23S	160	A
1	A23S	167	C
1	A23S	175	A
1	A23S	178	A
1	A23S	179	U
1	A23S	185	U
1	A23S	195	A
1	A23S	196	A
1	A23S	200	A
1	A23S	201	A
1	A23S	202	A
1	A23S	205	A
1	A23S	206	A
1	A23S	207	U
1	A23S	208	U

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Mol	Chain	Res	Type
1	A23S	210	A
1	A23S	212	A
1	A23S	220	A
1	A23S	221	G
1	A23S	226	G
1	A23S	227	G
1	A23S	228	C
1	A23S	240	G
1	A23S	241	G
1	A23S	242	A
1	A23S	243	C
1	A23S	244	A
1	A23S	245	G
1	A23S	246	C
1	A23S	247	C
1	A23S	248	C
1	A23S	255	A
1	A23S	257	C
1	A23S	260	G
1	A23S	267	A
1	A23S	268	U
1	A23S	278	G
1	A23S	280	G
1	A23S	281	A
1	A23S	282	U
1	A23S	283	G
1	A23S	284	U
1	A23S	285	G
1	A23S	286	G
1	A23S	288	G
1	A23S	289	U
1	A23S	291	A
1	A23S	292	C
1	A23S	293	G
1	A23S	295	C
1	A23S	304	U
1	A23S	307	G
1	A23S	313	A
1	A23S	315	C
1	A23S	317	C
1	A23S	319	G
1	A23S	327	A

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Mol	Chain	Res	Type
1	A23S	336	A
1	A23S	337	G
1	A23S	341	A
1	A23S	342	A
1	A23S	343	C
1	A23S	344	U
1	A23S	345	C
1	A23S	353	A
1	A23S	355	G
1	A23S	358	G
1	A23S	359	G
1	A23S	361	C
1	A23S	364	U
1	A23S	366	G
1	A23S	372	G
1	A23S	373	A
1	A23S	374	A
1	A23S	375	A
1	A23S	376	G
1	A23S	381	G
1	A23S	384	G
1	A23S	387	U
1	A23S	390	A
1	A23S	391	G
1	A23S	392	A
1	A23S	398	G
1	A23S	403	G
1	A23S	404	U
1	A23S	405	G
1	A23S	406	G
1	A23S	409	A
1	A23S	410	G
1	A23S	416	G
1	A23S	417	A
1	A23S	418	G
1	A23S	419	U
1	A23S	420	A
1	A23S	427	C
1	A23S	433	U
1	A23S	434	U
1	A23S	444	A
1	A23S	446	G

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Mol	Chain	Res	Type
1	A23S	447	U
1	A23S	449	A
1	A23S	450	G
1	A23S	454	A
1	A23S	455	C
1	A23S	456	A
1	A23S	460	G
1	A23S	464	C
1	A23S	468	G
1	A23S	469	G
1	A23S	470	C
1	A23S	475	U
1	A23S	476	A
1	A23S	477	U
1	A23S	478	G
1	A23S	483	G
1	A23S	486	A
1	A23S	489	G
1	A23S	490	A
1	A23S	491	U
1	A23S	492	A
1	A23S	494	C
1	A23S	495	A
1	A23S	496	A
1	A23S	497	A
1	A23S	500	A
1	A23S	501	A
1	A23S	502	G
1	A23S	505	C
1	A23S	508	U
1	A23S	509	G
1	A23S	510	A
1	A23S	511	G
1	A23S	513	G
1	A23S	517	G
1	A23S	519	U
1	A23S	520	G
1	A23S	521	A
1	A23S	523	A
1	A23S	524	A
1	A23S	525	G
1	A23S	527	A

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Mol	Chain	Res	Type
1	A23S	535	A
1	A23S	536	G
1	A23S	537	G
1	A23S	538	G
1	A23S	541	A
1	A23S	546	A
1	A23S	548	A
1	A23S	549	G
1	A23S	551	G
1	A23S	552	C
1	A23S	553	C
1	A23S	555	G
1	A23S	556	A
1	A23S	563	G
1	A23S	566	G
1	A23S	568	U
1	A23S	570	U
1	A23S	571	A
1	A23S	572	C
1	A23S	573	A
1	A23S	581	G
1	A23S	586	A
1	A23S	587	A
1	A23S	588	A
1	A23S	589	G
1	A23S	592	G
1	A23S	593	U
1	A23S	594	G
1	A23S	595	A
1	A23S	617	G
1	A23S	618	C
1	A23S	619	A
1	A23S	621	G
1	A23S	626	U
1	A23S	627	A
1	A23S	628	G
1	A23S	636	A
1	A23S	637	A
1	A23S	639	G
1	A23S	640	G
1	A23S	643	A
1	A23S	644	U

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Mol	Chain	Res	Type
1	A23S	657	U
1	A23S	658	U
1	A23S	659	U
1	A23S	660	C
1	A23S	662	U
1	A23S	665	U
1	A23S	668	A
1	A23S	669	A
1	A23S	670	C
1	A23S	671	A
1	A23S	674	G
1	A23S	675	G
1	A23S	678	G
1	A23S	683	G
1	A23S	684	U
1	A23S	685	U
1	A23S	694	U
1	A23S	695	G
1	A23S	699	A
1	A23S	712	U
1	A23S	713	A
1	A23S	714	U
1	A23S	720	A
1	A23S	721	A
1	A23S	723	G
1	A23S	724	C
1	A23S	725	A
1	A23S	727	A
1	A23S	733	A
1	A23S	734	C
1	A23S	740	G
1	A23S	741	C
1	A23S	748	C
1	A23S	749	C
1	A23S	753	U
1	A23S	754	U
1	A23S	755	U
1	A23S	756	C
1	A23S	757	U
1	A23S	758	A
1	A23S	762	G
1	A23S	768	C

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Mol	Chain	Res	Type
1	A23S	769	A
1	A23S	777	U
1	A23S	778	C
1	A23S	779	A
1	A23S	780	G
1	A23S	784	C
1	A23S	787	A
1	A23S	788	A
1	A23S	793	C
1	A23S	802	G
1	A23S	803	G
1	A23S	806	A
1	A23S	808	A
1	A23S	809	A
1	A23S	810	A
1	A23S	818	A
1	A23S	819	U
1	A23S	820	C
1	A23S	821	U
1	A23S	822	A
1	A23S	825	C
1	A23S	829	G
1	A23S	832	A
1	A23S	833	G
1	A23S	834	G
1	A23S	835	C
1	A23S	837	G
1	A23S	838	A
1	A23S	844	G
1	A23S	848	A
1	A23S	850	A
1	A23S	851	C
1	A23S	859	G
1	A23S	860	A
1	A23S	862	G
1	A23S	863	G
1	A23S	864	C
1	A23S	865	C
1	A23S	866	G
1	A23S	868	A
1	A23S	869	U
1	A23S	875	U

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Mol	Chain	Res	Type
1	A23S	878	U
1	A23S	879	G
1	A23S	883	U
1	A23S	887	A
1	A23S	888	U
1	A23S	898	U
1	A23S	900	A
1	A23S	901	C
1	A23S	908	C
1	A23S	909	U
1	A23S	910	A
1	A23S	911	G
1	A23S	912	G
1	A23S	913	G
1	A23S	916	A
1	A23S	917	A
1	A23S	918	A
1	A23S	919	A
1	A23S	920	G
1	A23S	921	A
1	A23S	924	A
1	A23S	925	A
1	A23S	928	U
1	A23S	930	G
1	A23S	932	C
1	A23S	938	A
1	A23S	941	G
1	A23S	947	U
1	A23S	948	C
1	A23S	957	A
1	A23S	963	C
1	A23S	964	C
1	A23S	966	A
1	A23S	967	G
1	A23S	968	C
1	A23S	970	C
1	A23S	981	A
1	A23S	982	A
1	A23S	983	G
1	A23S	985	C
1	A23S	986	A
1	A23S	993	G

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Mol	Chain	Res	Type
1	A23S	995	G
1	A23S	996	G
1	A23S	1000	A
1	A23S	1001	G
1	A23S	1002	U
1	A23S	1003	G
1	A23S	1004	A
1	A23S	1006	A
1	A23S	1007	G
1	A23S	1008	A
1	A23S	1011	G
1	A23S	1012	G
1	A23S	1013	G
1	A23S	1030	C
1	A23S	1044	C
1	A23S	1046	A
1	A23S	1047	A
1	A23S	1048	C
1	A23S	1050	C
1	A23S	1051	C
1	A23S	1055	C
1	A23S	1060	G
1	A23S	1066	C
1	A23S	1069	A
1	A23S	1070	G
1	A23S	1071	A
1	A23S	1072	A
1	A23S	1082	G
1	A23S	1083	G
1	A23S	1084	G
1	A23S	1085	U
1	A23S	1089	U
1	A23S	1090	C
1	A23S	1094	G
1	A23S	1095	U
1	A23S	1098	G
1	A23S	1099	G
1	A23S	1102	G
1	A23S	1103	G
1	A23S	1105	U
1	A23S	1108	C
1	A23S	1110	A

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Mol	Chain	Res	Type
1	A23S	1112	A
1	A23S	1113	G
1	A23S	1114	G
1	A23S	1117	A
1	A23S	1118	A
1	A23S	1119	C
1	A23S	1120	A
1	A23S	1122	C
1	A23S	1125	A
1	A23S	1127	A
1	A23S	1128	C
1	A23S	1136	A
1	A23S	1137	A
1	A23S	1139	G
1	A23S	1141	C
1	A23S	1144	A
1	A23S	1148	U
1	A23S	1149	C
1	A23S	1153	G
1	A23S	1154	C
1	A23S	1155	U
1	A23S	1156	A
1	A23S	1158	G
1	A23S	1162	C
1	A23S	1163	A
1	A23S	1165	C
1	A23S	1166	G
1	A23S	1167	A
1	A23S	1168	A
1	A23S	1173	C
1	A23S	1174	G
1	A23S	1176	C
1	A23S	1177	U
1	A23S	1178	C
1	A23S	1179	C
1	A23S	1181	G
1	A23S	1185	U
1	A23S	1186	A
1	A23S	1187	G
1	A23S	1188	A
1	A23S	1190	A
1	A23S	1192	C

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Mol	Chain	Res	Type
1	A23S	1193	G
1	A23S	1196	A
1	A23S	1198	G
1	A23S	1199	G
1	A23S	1200	U
1	A23S	1202	G
1	A23S	1204	C
1	A23S	1206	C
1	A23S	1207	A
1	A23S	1208	G
1	A23S	1209	C
1	A23S	1210	A
1	A23S	1211	G
1	A23S	1212	C
1	A23S	1213	A
1	A23S	1214	G
1	A23S	1216	C
1	A23S	1219	C
1	A23S	1220	C
1	A23S	1221	U
1	A23S	1222	C
1	A23S	1227	G
1	A23S	1229	G
1	A23S	1231	G
1	A23S	1233	G
1	A23S	1235	A
1	A23S	1236	A
1	A23S	1237	C
1	A23S	1241	U
1	A23S	1248	C
1	A23S	1249	C
1	A23S	1250	G
1	A23S	1252	G
1	A23S	1257	G
1	A23S	1259	G
1	A23S	1266	A
1	A23S	1270	U
1	A23S	1272	G
1	A23S	1273	G
1	A23S	1274	U
1	A23S	1276	G
1	A23S	1281	U

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Mol	Chain	Res	Type
1	A23S	1282	C
1	A23S	1283	A
1	A23S	1284	A
1	A23S	1289	G
1	A23S	1292	G
1	A23S	1296	A
1	A23S	1299	C
1	A23S	1300	C
1	A23S	1301	C
1	A23S	1306	G
1	A23S	1312	C
1	A23S	1316	A
1	A23S	1317	C
1	A23S	1318	U
1	A23S	1322	G
1	A23S	1330	G
1	A23S	1334	G
1	A23S	1338	G
1	A23S	1346	G
1	A23S	1347	A
1	A23S	1348	U
1	A23S	1350	G
1	A23S	1351	G
1	A23S	1352	G
1	A23S	1353	U
1	A23S	1354	A
1	A23S	1355	G
1	A23S	1356	A
1	A23S	1364	U
1	A23S	1366	G
1	A23S	1367	U
1	A23S	1368	G
1	A23S	1369	A
1	A23S	1370	G
1	A23S	1379	G
1	A23S	1380	A
1	A23S	1381	C
1	A23S	1392	U
1	A23S	1394	C
1	A23S	1395	A
1	A23S	1396	G
1	A23S	1397	A

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Mol	Chain	Res	Type
1	A23S	1398	U
1	A23S	1399	C
1	A23S	1406	G
1	A23S	1410	U
1	A23S	1414	A
1	A23S	1416	C
1	A23S	1417	G
1	A23S	1418	A
1	A23S	1419	A
1	A23S	1422	G
1	A23S	1425	G
1	A23S	1426	U
1	A23S	1427	G
1	A23S	1433	C
1	A23S	1444	G
1	A23S	1445	A
1	A23S	1446	A
1	A23S	1447	G
1	A23S	1450	C
1	A23S	1453	G
1	A23S	1458	U
1	A23S	1460	C
1	A23S	1462	G
1	A23S	1465	A
1	A23S	1467	C
1	A23S	1468	G
1	A23S	1469	U
1	A23S	1474	C
1	A23S	1475	A
1	A23S	1476	G
1	A23S	1479	G
1	A23S	1484	U
1	A23S	1485	U
1	A23S	1486	A
1	A23S	1487	G
1	A23S	1489	C
1	A23S	1490	G
1	A23S	1494	C
1	A23S	1501	A
1	A23S	1502	G
1	A23S	1508	A
1	A23S	1509	A

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Mol	Chain	Res	Type
1	A23S	1511	A
1	A23S	1513	G
1	A23S	1514	U
1	A23S	1515	A
1	A23S	1520	C
1	A23S	1523	A
1	A23S	1524	A
1	A23S	1525	A
1	A23S	1526	G
1	A23S	1527	G
1	A23S	1529	A
1	A23S	1530	A
1	A23S	1531	A
1	A23S	1532	G
1	A23S	1536	U
1	A23S	1537	U
1	A23S	1538	A
1	A23S	1539	A
1	A23S	1541	A
1	A23S	1542	U
1	A23S	1544	C
1	A23S	1545	C
1	A23S	1549	G
1	A23S	1555	C
1	A23S	1558	G
1	A23S	1561	G
1	A23S	1563	U
1	A23S	1564	G
1	A23S	1565	C
1	A23S	1566	G
1	A23S	1568	U
1	A23S	1569	A
1	A23S	1570	A
1	A23S	1574	A
1	A23S	1575	A
1	A23S	1576	G
1	A23S	1578	C
1	A23S	1579	A
1	A23S	1581	A
1	A23S	1584	C
1	A23S	1585	C
1	A23S	1587	G

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Mol	Chain	Res	Type
1	A23S	1588	A
1	A23S	1589	C
1	A23S	1594	U
1	A23S	1598	G
1	A23S	1601	G
1	A23S	1602	G
1	A23S	1611	G
1	A23S	1613	C
1	A23S	1614	C
1	A23S	1615	A
1	A23S	1616	C
1	A23S	1617	C
1	A23S	1618	G
1	A23S	1619	U
1	A23S	1625	C
1	A23S	1626	C
1	A23S	1627	A
1	A23S	1630	C
1	A23S	1633	U
1	A23S	1634	C
1	A23S	1635	A
1	A23S	1636	A
1	A23S	1641	U
1	A23S	1644	G
1	A23S	1645	A
1	A23S	1646	G
1	A23S	1647	A
1	A23S	1648	G
1	A23S	1649	C
1	A23S	1654	A
1	A23S	1656	G
1	A23S	1660	A
1	A23S	1661	G
1	A23S	1663	A
1	A23S	1664	G
1	A23S	1666	G
1	A23S	1667	G
1	A23S	1671	A
1	A23S	1674	G
1	A23S	1676	G
1	A23S	1679	A
1	A23S	1680	U

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Mol	Chain	Res	Type
1	A23S	1682	G
1	A23S	1684	C
1	A23S	1686	U
1	A23S	1690	G
1	A23S	1691	U
1	A23S	1693	A
1	A23S	1694	G
1	A23S	1696	A
1	A23S	1700	U
1	A23S	1701	U
1	A23S	1704	C
1	A23S	1708	A
1	A23S	1710	C
1	A23S	1713	U
1	A23S	1715	G
1	A23S	1720	C
1	A23S	1721	A
1	A23S	1722	U
1	A23S	1724	A
1	A23S	1726	A
1	A23S	1729	G
1	A23S	1730	G
1	A23S	1734	C
1	A23S	1740	C
1	A23S	1741	G
1	A23S	1742	A
1	A23S	1743	U
1	A23S	1744	C
1	A23S	1748	G
1	A23S	1751	G
1	A23S	1752	A
1	A23S	1757	A
1	A23S	1762	G
1	A23S	1764	A
1	A23S	1770	A
1	A23S	1771	C
1	A23S	1772	U
1	A23S	1773	G
1	A23S	1776	G
1	A23S	1785	U
1	A23S	1786	G
1	A23S	1789	A

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Mol	Chain	Res	Type
1	A23S	1790	A
1	A23S	1796	A
1	A23S	1800	G
1	A23S	1801	U
1	A23S	1802	C
1	A23S	1803	U
1	A23S	1804	G
1	A23S	1809	G
1	A23S	1810	U
1	A23S	1811	A
1	A23S	1817	G
1	A23S	1818	G
1	A23S	1822	G
1	A23S	1825	A
1	A23S	1826	A
1	A23S	1827	C
1	A23S	1828	U
1	A23S	1829	C
1	A23S	1830	G
1	A23S	1832	C
1	A23S	1836	U
1	A23S	1846	A
1	A23S	1847	A
1	A23S	1851	C
1	A23S	1855	A
1	A23S	1857	A
1	A23S	1861	G
1	A23S	1864	G
1	A23S	1865	C
1	A23S	1866	C
1	A23S	1868	A
1	A23S	1873	G
1	A23S	1878	A
1	A23S	1879	A
1	A23S	1880	C
1	A23S	1890	A
1	A23S	1893	G
1	A23S	1903	A
1	A23S	1905	C
1	A23S	1907	G
1	A23S	1908	A
1	A23S	1909	G

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Mol	Chain	Res	Type
1	A23S	1912	A
1	A23S	1917	A
1	A23S	1918	C
1	A23S	1923	U
1	A23S	1924	A
1	A23S	1925	A
1	A23S	1928	A
1	A23S	1929	A
1	A23S	1931	A
1	A23S	1933	A
1	A23S	1935	A
1	A23S	1943	G
1	A23S	1944	C
1	A23S	1945	U
1	A23S	1951	G
1	A23S	1952	A
1	A23S	1953	A
1	A23S	1955	G
1	A23S	1959	G
1	A23S	1961	G
1	A23S	1973	A
1	A23S	1976	C
1	A23S	1977	C
1	A23S	1979	G
1	A23S	1980	G
1	A23S	1982	C
1	A23S	1985	U
1	A23S	1991	U
1	A23S	1992	U
1	A23S	2004	G
1	A23S	2005	G
1	A23S	2007	U
1	A23S	2008	C
1	A23S	2013	G
1	A23S	2015	G
1	A23S	2017	G
1	A23S	2020	G
1	A23S	2026	C
1	A23S	2028	G
1	A23S	2030	A
1	A23S	2032	G
1	A23S	2035	G

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Mol	Chain	Res	Type
1	A23S	2036	G
1	A23S	2038	G
1	A23S	2040	U
1	A23S	2041	A
1	A23S	2042	A
1	A23S	2043	C
1	A23S	2044	U
1	A23S	2045	C
1	A23S	2047	G
1	A23S	2049	C
1	A23S	2051	C
1	A23S	2053	C
1	A23S	2054	U
1	A23S	2055	U
1	A23S	2056	A
1	A23S	2057	A
1	A23S	2058	G
1	A23S	2059	G
1	A23S	2061	A
1	A23S	2062	G
1	A23S	2065	A
1	A23S	2066	A
1	A23S	2067	A
1	A23S	2074	G
1	A23S	2080	U
1	A23S	2082	A
1	A23S	2084	U
1	A23S	2085	U
1	A23S	2092	C
1	A23S	2093	G
1	A23S	2094	C
1	A23S	2095	A
1	A23S	2098	A
1	A23S	2099	A
1	A23S	2100	U
1	A23S	2101	G
1	A23S	2105	C
1	A23S	2106	A
1	A23S	2108	C
1	A23S	2110	C
1	A23S	2111	G
1	A23S	2120	U

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Mol	Chain	Res	Type
1	A23S	2121	G
1	A23S	2125	C
1	A23S	2132	G
1	A23S	2135	C
1	A23S	2140	U
1	A23S	2142	A
1	A23S	2145	G
1	A23S	2147	C
1	A23S	2148	C
1	A23S	2149	U
1	A23S	2150	G
1	A23S	2151	A
1	A23S	2152	G
1	A23S	2155	G
1	A23S	2156	G
1	A23S	2159	C
1	A23S	2160	A
1	A23S	2161	C
1	A23S	2162	A
1	A23S	2163	G
1	A23S	2165	C
1	A23S	2170	A
1	A23S	2171	U
1	A23S	2181	C
1	A23S	2182	C
1	A23S	2183	G
1	A23S	2184	A
1	A23S	2185	G
1	A23S	2186	A
1	A23S	2187	G
1	A23S	2188	A
1	A23S	2189	A
1	A23S	2190	G
1	A23S	2191	A
1	A23S	2192	C
1	A23S	2197	U
1	A23S	2198	G
1	A23S	2199	G
1	A23S	2204	U
1	A23S	2205	C
1	A23S	2207	C
1	A23S	2216	G

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Mol	Chain	Res	Type
1	A23S	2221	U
1	A23S	2223	U
1	A23S	2225	C
1	A23S	2231	G
1	A23S	2234	U
1	A23S	2235	U
1	A23S	2240	C
1	A23S	2241	G
1	A23S	2242	U
1	A23S	2244	G
1	A23S	2245	A
1	A23S	2246	G
1	A23S	2247	U
1	A23S	2248	A
1	A23S	2249	G
1	A23S	2251	U
1	A23S	2255	A
1	A23S	2256	G
1	A23S	2258	G
1	A23S	2259	G
1	A23S	2260	U
1	A23S	2262	G
1	A23S	2263	A
1	A23S	2264	A
1	A23S	2268	G
1	A23S	2269	U
1	A23S	2270	C
1	A23S	2271	C
1	A23S	2272	U
1	A23S	2275	C
1	A23S	2276	G
1	A23S	2278	G
1	A23S	2280	G
1	A23S	2281	C
1	A23S	2285	G
1	A23S	2287	A
1	A23S	2288	C
1	A23S	2290	C
1	A23S	2291	G
1	A23S	2292	A
1	A23S	2293	A
1	A23S	2294	A

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Mol	Chain	Res	Type
1	A23S	2295	G
1	A23S	2297	G
1	A23S	2298	A
1	A23S	2299	A
1	A23S	2300	A
1	A23S	2301	C
1	A23S	2302	A
1	A23S	2305	A
1	A23S	2308	C
1	A23S	2310	U
1	A23S	2313	A
1	A23S	2317	U
1	A23S	2326	U
1	A23S	2327	A
1	A23S	2328	A
1	A23S	2336	A
1	A23S	2337	A
1	A23S	2339	G
1	A23S	2342	A
1	A23S	2346	A
1	A23S	2357	U
1	A23S	2359	G
1	A23S	2363	G
1	A23S	2366	C
1	A23S	2367	G
1	A23S	2370	U
1	A23S	2371	G
1	A23S	2372	G
1	A23S	2374	G
1	A23S	2379	A
1	A23S	2380	C
1	A23S	2388	A
1	A23S	2390	A
1	A23S	2401	G
1	A23S	2403	A
1	A23S	2405	C
1	A23S	2408	A
1	A23S	2409	A
1	A23S	2410	A
1	A23S	2414	C
1	A23S	2419	C
1	A23S	2422	G

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Mol	Chain	Res	Type
1	A23S	2427	A
1	A23S	2428	C
1	A23S	2429	A
1	A23S	2433	C
1	A23S	2435	C
1	A23S	2440	G
1	A23S	2442	A
1	A23S	2443	G
1	A23S	2444	A
1	A23S	2449	A
1	A23S	2456	A
1	A23S	2457	A
1	A23S	2463	G
1	A23S	2467	G
1	A23S	2468	A
1	A23S	2469	C
1	A23S	2473	A
1	A23S	2480	C
1	A23S	2484	U
1	A23S	2486	C
1	A23S	2488	G
1	A23S	2492	C
1	A23S	2493	A
1	A23S	2498	G
1	A23S	2499	C
1	A23S	2502	A
1	A23S	2503	A
1	A23S	2504	G
1	A23S	2505	C
1	A23S	2507	G
1	A23S	2508	G
1	A23S	2510	C
1	A23S	2515	C
1	A23S	2517	A
1	A23S	2518	A
1	A23S	2523	C
1	A23S	2526	G
1	A23S	2527	C
1	A23S	2531	C
1	A23S	2532	A
1	A23S	2533	C
1	A23S	2547	G

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Mol	Chain	Res	Type
1	A23S	2548	C
1	A23S	2549	A
1	A23S	2551	G
1	A23S	2552	A
1	A23S	2553	C
1	A23S	2554	A
1	A23S	2555	G
1	A23S	2556	A
1	A23S	2558	A
1	A23S	2559	A
1	A23S	2564	C
1	A23S	2565	C
1	A23S	2568	G
1	A23S	2571	G
1	A23S	2572	A
1	A23S	2573	U
1	A23S	2574	A
1	A23S	2577	A
1	A23S	2578	G
1	A23S	2581	U
1	A23S	2582	C
1	A23S	2583	G
1	A23S	2589	G
1	A23S	2593	A
1	A23S	2594	G
1	A23S	2596	G
1	A23S	2601	C
1	A23S	2602	A
1	A23S	2604	C
1	A23S	2605	G
1	A23S	2607	C
1	A23S	2610	C
1	A23S	2613	G
1	A23S	2616	U
1	A23S	2617	U
1	A23S	2618	G
1	A23S	2619	C
1	A23S	2620	U
1	A23S	2621	A
1	A23S	2623	A
1	A23S	2624	U
1	A23S	2626	G

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Mol	Chain	Res	Type
1	A23S	2627	A
1	A23S	2629	G
1	A23S	2632	G
1	A23S	2635	U
1	A23S	2638	U
1	A23S	2641	C
1	A23S	2642	A
1	A23S	2643	C
1	A23S	2644	C
1	A23S	2645	C
1	A23S	2650	G
1	A23S	2653	G
1	A23S	2654	C
1	A23S	2655	A
1	A23S	2656	G
1	A23S	2657	C
1	A23S	2659	G
1	A23S	2669	G
1	A23S	2678	C
1	A23S	2688	A
1	A23S	2689	A
1	A23S	2690	A
1	A23S	2691	G
1	A23S	2694	G
1	A23S	2696	G
1	A23S	2697	C
1	A23S	2698	G
1	A23S	2700	G
1	A23S	2701	A
1	A23S	2706	G
1	A23S	2709	U
1	A23S	2718	C
1	A23S	2720	C
1	A23S	2721	G
1	A23S	2722	A
1	A23S	2723	G
1	A23S	2726	A
1	A23S	2727	G
1	A23S	2728	G
1	A23S	2729	U
1	A23S	2730	C
1	A23S	2731	G

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Mol	Chain	Res	Type
1	A23S	2732	G
1	A23S	2733	A
1	A23S	2735	U
1	A23S	2738	A
1	A23S	2741	G
1	A23S	2747	G
1	A23S	2753	G
1	A23S	2755	A
1	A23S	2756	C
1	A23S	2761	U
1	A23S	2762	G
1	A23S	2763	A
1	A23S	2764	G
1	A23S	2767	G
1	A23S	2768	A
1	A23S	2769	A
1	A23S	2770	G
1	A23S	2773	A
1	A23S	2776	C
1	A23S	2779	A
1	A23S	2780	G
1	A23S	2781	U
1	A23S	2801	G
1	A23S	2804	G
1	A23S	2807	U
1	A23S	2808	C
1	A23S	2813	U
1	A23S	2814	U
1	A23S	2815	A
1	A23S	2824	C
1	A23S	2826	G
1	A23S	2828	U
1	A23S	2831	G
1	A23S	2832	G
1	A23S	2835	A
1	A23S	2836	U
1	A23S	2837	G
1	A23S	2841	G
1	A23S	2848	G
1	A23S	2849	C
1	A23S	2850	G
1	A23S	2855	G

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Mol	Chain	Res	Type
1	A23S	2866	G
1	A23S	2870	A
1	A23S	2871	A
1	A23S	2878	U
1	A23S	2879	A
1	A23S	2880	A
1	A23S	2884	G
1	A23S	2886	A
1	A23S	2887	A
1	A23S	2888	C
1	A23S	2891	C
1	A23S	2893	C
1	A23S	2896	C
1	A23S	2897	U
1	A23S	2898	A
1	A23S	2899	A
1	A23S	2901	A
1	A23S	2902	G
1	A23S	2903	A
1	A23S	2904	G
1	A23S	2911	A
1	A23S	2924	G
1	A23S	2935	A
1	A23S	2937	A
1	A23S	2939	G
1	A23S	2943	G
1	A23S	2947	U
1	A23S	2948	G
1	A23S	2949	A
1	A23S	2952	G
1	A23S	2961	U
1	A23S	2963	U
1	A23S	2971	A
1	A23S	2972	A
1	A23S	2973	G
1	A23S	2976	U
1	A23S	2983	C
1	A23S	2993	U
1	A23S	2995	G
1	A23S	2999	G
1	A23S	3000	C
1	A23S	3005	C

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Mol	Chain	Res	Type
1	A23S	3006	C
1	A23S	3007	C
1	A23S	3010	U
1	A23S	3012	A
1	A23S	3019	C
1	A23S	3020	C
1	A23S	3021	C
2	A16S	10	U
2	A16S	11	C
2	A16S	16	U
2	A16S	17	G
2	A16S	19	U
2	A16S	29	C
2	A16S	39	A
2	A16S	41	C
2	A16S	48	G
2	A16S	49	G
2	A16S	50	G
2	A16S	51	A
2	A16S	52	U
2	A16S	53	A
2	A16S	54	A
2	A16S	55	G
2	A16S	56	C
2	A16S	57	C
2	A16S	60	G
2	A16S	61	G
2	A16S	62	G
2	A16S	63	A
2	A16S	64	G
2	A16S	66	C
2	A16S	69	A
2	A16S	70	C
2	A16S	72	C
2	A16S	73	U
2	A16S	74	C
2	A16S	76	C
2	A16S	77	G
2	A16S	78	G
2	A16S	79	G
2	A16S	80	U
2	A16S	81	A

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Mol	Chain	Res	Type
2	A16S	83	G
2	A16S	86	A
2	A16S	87	G
2	A16S	88	U
2	A16S	89	G
2	A16S	91	G
2	A16S	96	A
2	A16S	97	C
2	A16S	101	U
2	A16S	103	A
2	A16S	107	A
2	A16S	108	C
2	A16S	109	A
2	A16S	113	G
2	A16S	115	C
2	A16S	117	A
2	A16S	118	A
2	A16S	119	C
2	A16S	120	C
2	A16S	123	C
2	A16S	131	A
2	A16S	132	C
2	A16S	137	A
2	A16S	138	U
2	A16S	141	C
2	A16S	148	A
2	A16S	149	A
2	A16S	150	A
2	A16S	151	C
2	A16S	152	U
2	A16S	153	G
2	A16S	156	G
2	A16S	157	A
2	A16S	159	A
2	A16S	162	C
2	A16S	169	A
2	A16S	174	A
2	A16S	176	G
2	A16S	177	A
2	A16S	178	G
2	A16S	180	C
2	A16S	185	A

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Mol	Chain	Res	Type
2	A16S	187	U
2	A16S	191	U
2	A16S	192	C
2	A16S	196	C
2	A16S	197	C
2	A16S	200	A
2	A16S	202	A
2	A16S	203	G
2	A16S	204	G
2	A16S	210	A
2	A16S	213	C
2	A16S	214	U
2	A16S	215	A
2	A16S	216	U
2	A16S	217	U
2	A16S	218	U
2	A16S	220	C
2	A16S	221	C
2	A16S	224	U
2	A16S	228	A
2	A16S	229	G
2	A16S	230	C
2	A16S	231	C
2	A16S	240	A
2	A16S	241	U
2	A16S	242	G
2	A16S	243	G
2	A16S	247	U
2	A16S	248	A
2	A16S	249	C
2	A16S	252	C
2	A16S	255	A
2	A16S	256	U
2	A16S	257	C
2	A16S	259	G
2	A16S	263	G
2	A16S	266	G
2	A16S	270	G
2	A16S	272	G
2	A16S	274	A
2	A16S	275	A
2	A16S	276	A

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Mol	Chain	Res	Type
2	A16S	277	G
2	A16S	278	G
2	A16S	279	C
2	A16S	280	C
2	A16S	287	A
2	A16S	292	U
2	A16S	293	A
2	A16S	294	A
2	A16S	301	G
2	A16S	303	G
2	A16S	308	U
2	A16S	313	G
2	A16S	319	G
2	A16S	320	C
2	A16S	321	C
2	A16S	323	C
2	A16S	326	G
2	A16S	327	U
2	A16S	328	U
2	A16S	333	A
2	A16S	340	C
2	A16S	341	A
2	A16S	342	A
2	A16S	344	G
2	A16S	345	G
2	A16S	346	C
2	A16S	350	G
2	A16S	351	G
2	A16S	355	U
2	A16S	356	A
2	A16S	358	G
2	A16S	363	G
2	A16S	364	C
2	A16S	365	A
2	A16S	366	C
2	A16S	367	C
2	A16S	369	G
2	A16S	372	G
2	A16S	373	C
2	A16S	375	A
2	A16S	377	A
2	A16S	378	C

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Mol	Chain	Res	Type
2	A16S	379	G
2	A16S	380	U
2	A16S	381	C
2	A16S	385	A
2	A16S	388	G
2	A16S	400	G
2	A16S	405	C
2	A16S	409	A
2	A16S	410	C
2	A16S	412	C
2	A16S	416	G
2	A16S	418	G
2	A16S	419	C
2	A16S	420	C
2	A16S	424	G
2	A16S	428	G
2	A16S	433	C
2	A16S	435	U
2	A16S	439	C
2	A16S	444	U
2	A16S	445	C
2	A16S	446	U
2	A16S	447	A
2	A16S	449	A
2	A16S	451	A
2	A16S	452	G
2	A16S	456	G
2	A16S	457	G
2	A16S	460	A
2	A16S	461	A
2	A16S	462	U
2	A16S	463	A
2	A16S	465	G
2	A16S	471	G
2	A16S	472	G
2	A16S	473	C
2	A16S	474	A
2	A16S	475	A
2	A16S	476	G
2	A16S	478	C
2	A16S	482	U
2	A16S	484	U

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Mol	Chain	Res	Type
2	A16S	485	C
2	A16S	487	G
2	A16S	490	G
2	A16S	491	C
2	A16S	494	C
2	A16S	495	G
2	A16S	496	G
2	A16S	497	U
2	A16S	498	A
2	A16S	499	A
2	A16S	500	U
2	A16S	502	C
2	A16S	504	A
2	A16S	512	G
2	A16S	513	A
2	A16S	525	G
2	A16S	526	A
2	A16S	527	U
2	A16S	529	A
2	A16S	530	C
2	A16S	532	G
2	A16S	537	U
2	A16S	538	A
2	A16S	539	A
2	A16S	542	C
2	A16S	543	G
2	A16S	552	C
2	A16S	554	G
2	A16S	562	A
2	A16S	563	G
2	A16S	570	C
2	A16S	573	A
2	A16S	585	U
2	A16S	586	C
2	A16S	596	A
2	A16S	597	C
2	A16S	598	U
2	A16S	600	G
2	A16S	601	G
2	A16S	608	A
2	A16S	609	C
2	A16S	610	U

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Mol	Chain	Res	Type
2	A16S	619	A
2	A16S	620	G
2	A16S	624	G
2	A16S	627	G
2	A16S	628	G
2	A16S	631	A
2	A16S	632	G
2	A16S	639	G
2	A16S	640	G
2	A16S	644	U
2	A16S	652	U
2	A16S	653	A
2	A16S	654	G
2	A16S	656	G
2	A16S	658	C
2	A16S	659	G
2	A16S	661	A
2	A16S	665	C
2	A16S	668	A
2	A16S	669	G
2	A16S	675	G
2	A16S	684	A
2	A16S	685	C
2	A16S	687	A
2	A16S	695	A
2	A16S	696	A
2	A16S	697	G
2	A16S	698	C
2	A16S	700	C
2	A16S	714	G
2	A16S	715	C
2	A16S	716	C
2	A16S	718	G
2	A16S	719	A
2	A16S	721	G
2	A16S	725	A
2	A16S	726	G
2	A16S	727	A
2	A16S	731	G
2	A16S	733	A
2	A16S	741	G
2	A16S	742	C

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Mol	Chain	Res	Type
2	A16S	743	A
2	A16S	747	A
2	A16S	748	A
2	A16S	753	A
2	A16S	754	U
2	A16S	755	U
2	A16S	756	A
2	A16S	757	G
2	A16S	758	A
2	A16S	759	U
2	A16S	760	A
2	A16S	761	C
2	A16S	762	C
2	A16S	765	G
2	A16S	771	C
2	A16S	774	G
2	A16S	779	U
2	A16S	781	A
2	A16S	782	A
2	A16S	783	C
2	A16S	784	G
2	A16S	785	A
2	A16S	787	G
2	A16S	789	G
2	A16S	794	A
2	A16S	795	G
2	A16S	796	G
2	A16S	797	U
2	A16S	810	U
2	A16S	811	A
2	A16S	812	G
2	A16S	813	A
2	A16S	814	G
2	A16S	820	U
2	A16S	829	C
2	A16S	834	A
2	A16S	835	A
2	A16S	837	C
2	A16S	841	U
2	A16S	842	A
2	A16S	850	C
2	A16S	855	G

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Mol	Chain	Res	Type
2	A16S	861	U
2	A16S	865	G
2	A16S	870	A
2	A16S	872	G
2	A16S	877	A
2	A16S	884	A
2	A16S	891	U
2	A16S	892	G
2	A16S	896	G
2	A16S	897	G
2	A16S	898	G
2	A16S	900	A
2	A16S	901	G
2	A16S	902	C
2	A16S	904	C
2	A16S	905	C
2	A16S	906	A
2	A16S	909	A
2	A16S	916	G
2	A16S	921	U
2	A16S	927	U
2	A16S	928	C
2	A16S	929	A
2	A16S	930	A
2	A16S	931	U
2	A16S	936	G
2	A16S	937	U
2	A16S	938	C
2	A16S	939	A
2	A16S	940	A
2	A16S	945	U
2	A16S	946	G
2	A16S	947	G
2	A16S	948	A
2	A16S	949	A
2	A16S	950	U
2	A16S	953	U
2	A16S	954	A
2	A16S	955	C
2	A16S	957	G
2	A16S	959	G
2	A16S	960	G

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Mol	Chain	Res	Type
2	A16S	962	A
2	A16S	963	G
2	A16S	965	C
2	A16S	971	U
2	A16S	972	A
2	A16S	973	U
2	A16S	974	G
2	A16S	975	A
2	A16S	976	C
2	A16S	977	G
2	A16S	981	A
2	A16S	983	G
2	A16S	985	U
2	A16S	986	A
2	A16S	987	A
2	A16S	988	C
2	A16S	989	G
2	A16S	990	A
2	A16S	995	G
2	A16S	998	U
2	A16S	999	G
2	A16S	1001	C
2	A16S	1003	C
2	A16S	1004	G
2	A16S	1005	C
2	A16S	1006	G
2	A16S	1014	G
2	A16S	1017	G
2	A16S	1018	C
2	A16S	1025	G
2	A16S	1029	C
2	A16S	1030	C
2	A16S	1031	A
2	A16S	1032	G
2	A16S	1038	G
2	A16S	1041	G
2	A16S	1042	U
2	A16S	1044	A
2	A16S	1045	A
2	A16S	1046	A
2	A16S	1047	U
2	A16S	1048	G

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Mol	Chain	Res	Type
2	A16S	1049	U
2	A16S	1050	C
2	A16S	1052	G
2	A16S	1053	G
2	A16S	1055	U
2	A16S	1056	A
2	A16S	1057	A
2	A16S	1058	G
2	A16S	1060	C
2	A16S	1063	G
2	A16S	1065	A
2	A16S	1066	A
2	A16S	1068	G
2	A16S	1075	A
2	A16S	1076	C
2	A16S	1082	C
2	A16S	1083	C
2	A16S	1088	G
2	A16S	1089	U
2	A16S	1091	G
2	A16S	1092	G
2	A16S	1093	U
2	A16S	1094	A
2	A16S	1095	U
2	A16S	1097	C
2	A16S	1098	U
2	A16S	1099	G
2	A16S	1102	C
2	A16S	1104	C
2	A16S	1105	C
2	A16S	1106	G
2	A16S	1107	G
2	A16S	1109	C
2	A16S	1110	C
2	A16S	1111	A
2	A16S	1112	G
2	A16S	1113	A
2	A16S	1114	A
2	A16S	1115	C
2	A16S	1116	C
2	A16S	1117	A
2	A16S	1118	C

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Mol	Chain	Res	Type
2	A16S	1123	G
2	A16S	1127	G
2	A16S	1128	A
2	A16S	1129	C
2	A16S	1130	U
2	A16S	1136	C
2	A16S	1138	U
2	A16S	1139	A
2	A16S	1145	G
2	A16S	1146	A
2	A16S	1150	A
2	A16S	1151	G
2	A16S	1152	G
2	A16S	1153	A
2	A16S	1154	G
2	A16S	1158	G
2	A16S	1160	C
2	A16S	1161	A
2	A16S	1162	C
2	A16S	1166	A
2	A16S	1167	G
2	A16S	1168	G
2	A16S	1170	C
2	A16S	1171	A
2	A16S	1172	G
2	A16S	1181	G
2	A16S	1182	A
2	A16S	1187	C
2	A16S	1188	C
2	A16S	1192	G
2	A16S	1193	C
2	A16S	1195	G
2	A16S	1196	C
2	A16S	1197	A
2	A16S	1200	C
2	A16S	1202	G
2	A16S	1208	A
2	A16S	1210	U
2	A16S	1211	G
2	A16S	1214	A
2	A16S	1220	A
2	A16S	1222	C

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Mol	Chain	Res	Type
2	A16S	1226	A
2	A16S	1227	U
2	A16S	1228	G
2	A16S	1232	C
2	A16S	1234	U
2	A16S	1236	G
2	A16S	1237	A
2	A16S	1238	A
2	A16S	1240	G
2	A16S	1244	G
2	A16S	1245	A
2	A16S	1247	C
2	A16S	1248	C
2	A16S	1249	A
2	A16S	1250	A
2	A16S	1251	U
2	A16S	1252	C
2	A16S	1253	C
2	A16S	1254	U
2	A16S	1255	U
2	A16S	1256	A
2	A16S	1262	U
2	A16S	1263	G
2	A16S	1264	C
2	A16S	1267	C
2	A16S	1268	A
2	A16S	1269	G
2	A16S	1270	U
2	A16S	1271	U
2	A16S	1272	G
2	A16S	1273	G
2	A16S	1274	G
2	A16S	1275	A
2	A16S	1277	C
2	A16S	1278	G
2	A16S	1280	G
2	A16S	1283	C
2	A16S	1287	A
2	A16S	1288	A
2	A16S	1289	C
2	A16S	1290	C
2	A16S	1291	C

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Mol	Chain	Res	Type
2	A16S	1292	G
2	A16S	1295	C
2	A16S	1300	G
2	A16S	1307	G
2	A16S	1309	A
2	A16S	1312	C
2	A16S	1314	U
2	A16S	1315	A
2	A16S	1316	G
2	A16S	1317	U
2	A16S	1324	G
2	A16S	1327	U
2	A16S	1328	C
2	A16S	1329	A
2	A16S	1330	A
2	A16S	1331	C
2	A16S	1332	A
2	A16S	1337	G
2	A16S	1338	C
2	A16S	1344	A
2	A16S	1346	A
2	A16S	1348	G
2	A16S	1350	C
2	A16S	1351	C
2	A16S	1362	C
2	A16S	1363	A
2	A16S	1366	C
2	A16S	1367	A
2	A16S	1369	C
2	A16S	1370	G
2	A16S	1371	C
2	A16S	1372	C
2	A16S	1379	U
2	A16S	1380	C
2	A16S	1382	A
2	A16S	1388	G
2	A16S	1390	G
2	A16S	1391	A
2	A16S	1401	G
2	A16S	1404	G
2	A16S	1412	C
2	A16S	1414	A

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Mol	Chain	Res	Type
2	A16S	1415	U
2	A16S	1416	A
2	A16S	1417	A
2	A16S	1418	G
2	A16S	1443	G
2	A16S	1452	G
2	A16S	1453	A
2	A16S	1454	A
2	A16S	1455	G
2	A16S	1456	U
2	A16S	1458	G
2	A16S	1459	U
2	A16S	1460	A
2	A16S	1461	A
2	A16S	1462	C
2	A16S	1463	A
2	A16S	1464	A
2	A16S	1465	G
2	A16S	1466	G
2	A16S	1476	G
2	A16S	1478	G
2	A16S	1479	A
2	A16S	1480	A
2	A16S	1481	C
2	A16S	1484	G
2	A16S	1487	G
2	A16S	1488	C
2	A16S	1489	U
2	A16S	1490	G
2	A16S	1491	G
2	A16S	1493	U
2	A16S	1494	C
2	A16S	1495	A
2	A16S	1496	C
2	A16S	1497	C
2	A16S	1498	U
2	A16S	1499	C
3	A5S	5	C
3	A5S	10	G
3	A5S	13	C
3	A5S	14	A
3	A5S	16	A

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Mol	Chain	Res	Type
3	A5S	17	G
3	A5S	25	G
3	A5S	26	U
3	A5S	27	A
3	A5S	28	A
3	A5S	30	A
3	A5S	34	G
3	A5S	36	A
3	A5S	40	G
3	A5S	42	U
3	A5S	43	U
3	A5S	45	G
3	A5S	46	A
3	A5S	48	C
3	A5S	52	G
3	A5S	56	U
3	A5S	58	A
3	A5S	59	A
3	A5S	60	G
3	A5S	67	A
3	A5S	76	G
3	A5S	85	G
3	A5S	88	C
3	A5S	101	C
3	A5S	102	A
3	A5S	103	G
3	A5S	106	U
3	A5S	107	C
3	A5S	111	G
3	A5S	115	U
3	A5S	117	G
3	A5S	118	G
3	A5S	119	A
3	A5S	120	U
66	APTN	2	C
66	APTN	7	A
66	APTN	8	U
66	APTN	11	C
66	APTN	13	C
66	APTN	17	C
66	APTN	18	G
66	APTN	20	U

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Mol	Chain	Res	Type
66	APTN	21	A
66	APTN	22	G
66	APTN	33	U
66	APTN	48	C
66	APTN	49	C
66	APTN	52	G
66	APTN	58	A
66	APTN	59	U
66	APTN	61	C
66	APTN	64	A
66	APTN	66	U
66	APTN	74	C
66	APTN	76	A
66	AETN	2	C
66	AETN	3	C
66	AETN	7	A
66	AETN	8	U
66	AETN	9	A
66	AETN	10	G
66	AETN	13	C
66	AETN	14	A
66	AETN	15	G
66	AETN	16	U
66	AETN	17	C
66	AETN	18	G
66	AETN	19	G
66	AETN	20	U
66	AETN	21	A
66	AETN	22	G
66	AETN	26	A
66	AETN	32	U
66	AETN	44	G
66	AETN	45	U
66	AETN	48	C
66	AETN	49	C
66	AETN	55	U
66	AETN	56	C
66	AETN	59	U
66	AETN	60	U
66	AETN	61	C
66	AETN	65	G
66	AETN	68	C

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Mol	Chain	Res	Type
66	AETN	70	G
66	AETN	76	A
67	AMRN	4	U

All (117) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A23S	116	U
1	A23S	125	G
1	A23S	280	G
1	A23S	290	U
1	A23S	326	U
1	A23S	336	A
1	A23S	341	A
1	A23S	402	A
1	A23S	404	U
1	A23S	504	A
1	A23S	571	A
1	A23S	618	C
1	A23S	642	G
1	A23S	658	U
1	A23S	667	A
1	A23S	668	A
1	A23S	836	U
1	A23S	877	C
1	A23S	920	G
1	A23S	1003	G
1	A23S	1068	A
1	A23S	1198	G
1	A23S	1211	G
1	A23S	1333	A
1	A23S	1452	A
1	A23S	1500	U
1	A23S	1508	A
1	A23S	1529	A
1	A23S	1560	A
1	A23S	1613	C
1	A23S	1646	G
1	A23S	1689	C
1	A23S	1700	U
1	A23S	1750	A
1	A23S	1801	U

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Mol	Chain	Res	Type
1	A23S	1864	G
1	A23S	1904	C
1	A23S	1932	C
1	A23S	1934	U
1	A23S	2081	A
1	A23S	2105	C
1	A23S	2147	C
1	A23S	2148	C
1	A23S	2183	G
1	A23S	2191	A
1	A23S	2291	G
1	A23S	2292	A
1	A23S	2293	A
1	A23S	2466	U
1	A23S	2483	G
1	A23S	2695	A
1	A23S	2700	G
1	A23S	2761	U
1	A23S	2807	U
1	A23S	2878	U
2	A16S	47	A
2	A16S	49	G
2	A16S	63	A
2	A16S	76	C
2	A16S	85	G
2	A16S	102	G
2	A16S	108	C
2	A16S	117	A
2	A16S	147	G
2	A16S	149	A
2	A16S	186	A
2	A16S	214	U
2	A16S	216	U
2	A16S	220	C
2	A16S	255	A
2	A16S	274	A
2	A16S	293	A
2	A16S	319	G
2	A16S	384	C
2	A16S	444	U
2	A16S	450	A
2	A16S	475	A

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Mol	Chain	Res	Type
2	A16S	541	G
2	A16S	653	A
2	A16S	655	G
2	A16S	694	G
2	A16S	732	A
2	A16S	741	G
2	A16S	746	A
2	A16S	883	A
2	A16S	927	U
2	A16S	929	A
2	A16S	938	C
2	A16S	954	A
2	A16S	972	A
2	A16S	975	A
2	A16S	1052	G
2	A16S	1057	A
2	A16S	1065	A
2	A16S	1088	G
2	A16S	1111	A
2	A16S	1116	C
2	A16S	1127	G
2	A16S	1151	G
2	A16S	1165	C
2	A16S	1166	A
2	A16S	1171	A
2	A16S	1227	U
2	A16S	1254	U
2	A16S	1270	U
2	A16S	1274	G
2	A16S	1316	G
2	A16S	1349	U
2	A16S	1417	A
2	A16S	1451	A
2	A16S	1453	A
2	A16S	1483	U
2	A16S	1489	U
3	A5S	24	G
66	APTN	19	G
66	AETN	2	C
66	AETN	8	U

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 57 ligands modelled in this entry, 57 are unknown - 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](#)

There are no chain breaks in this entry.

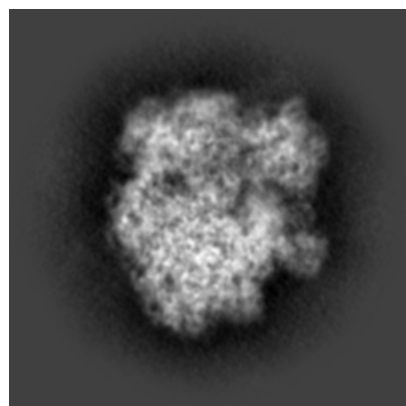
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34864. These allow visual inspection of the internal detail of the map and identification of artifacts.

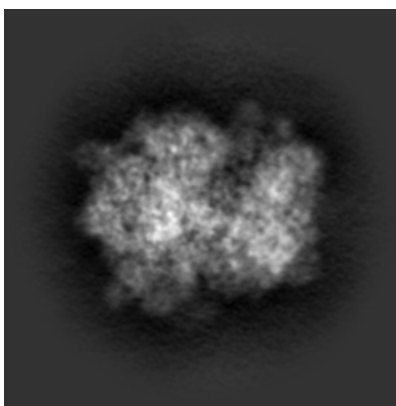
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

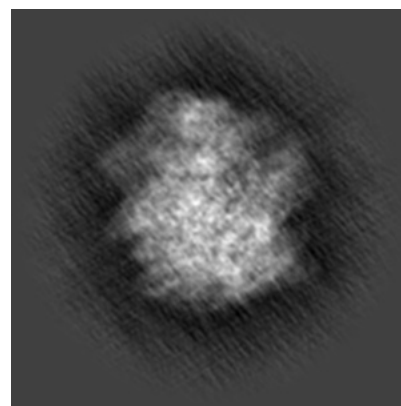
6.1.1 Primary map



X

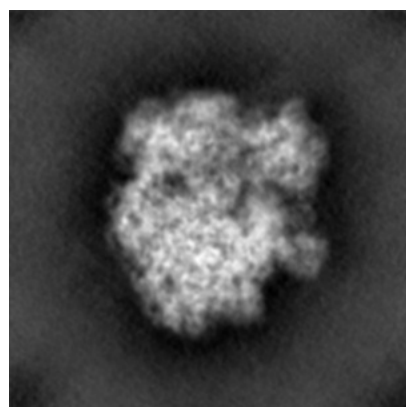


Y

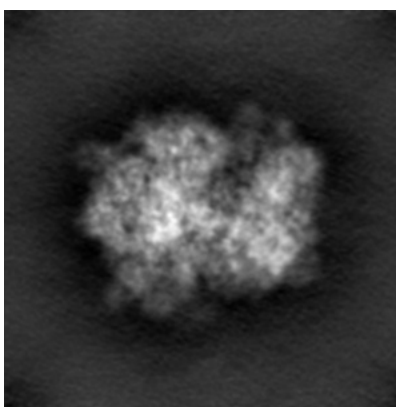


Z

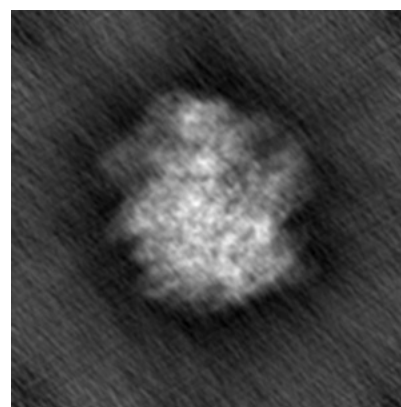
6.1.2 Raw map



X



Y

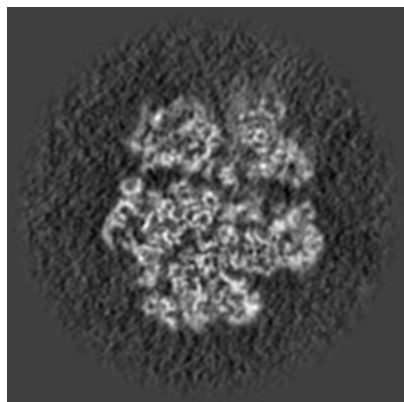


Z

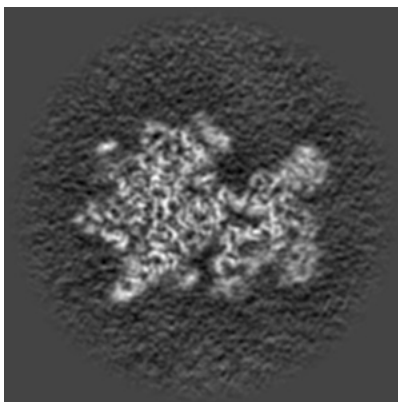
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

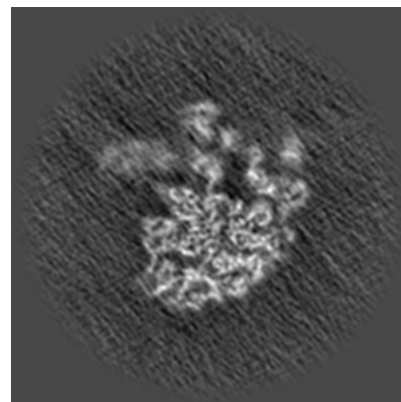
6.2.1 Primary map



X Index: 190

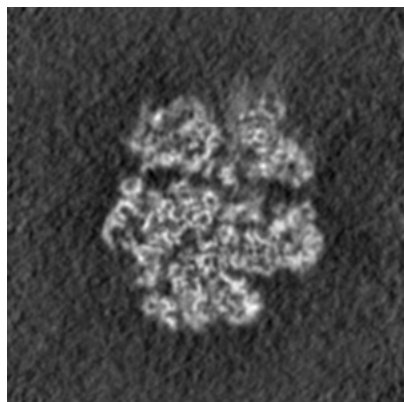


Y Index: 190

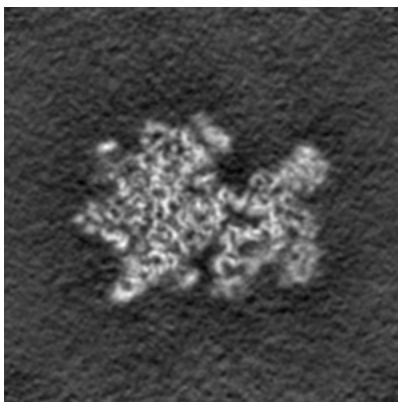


Z Index: 190

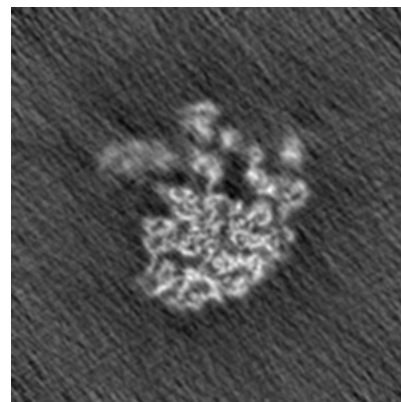
6.2.2 Raw map



X Index: 190



Y Index: 190

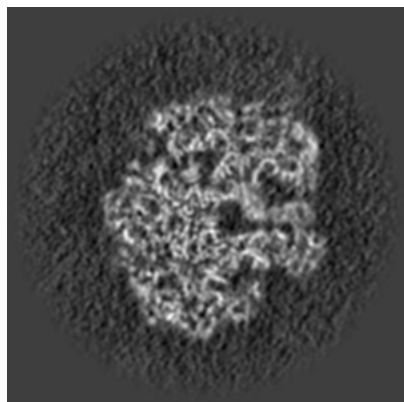


Z Index: 190

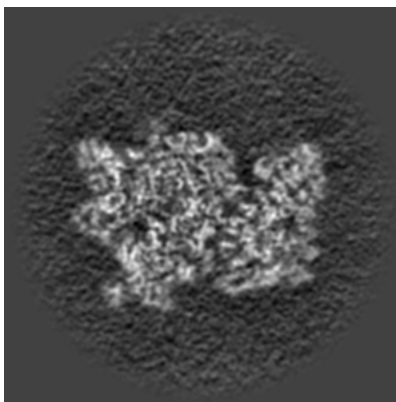
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

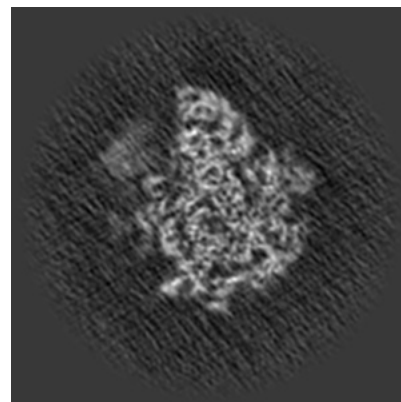
6.3.1 Primary map



X Index: 177

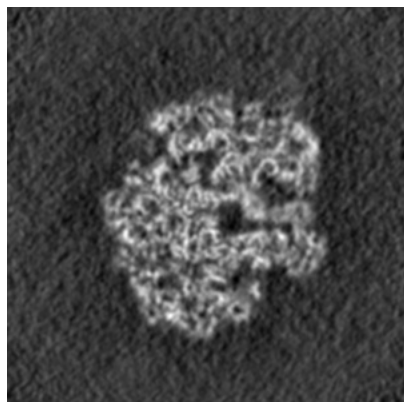


Y Index: 178

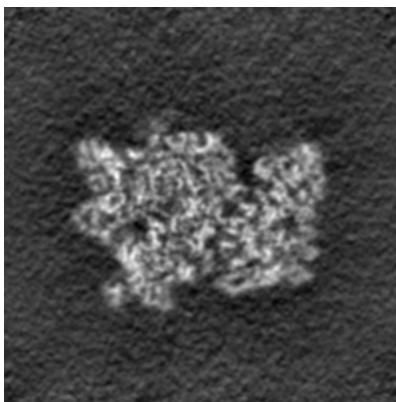


Z Index: 159

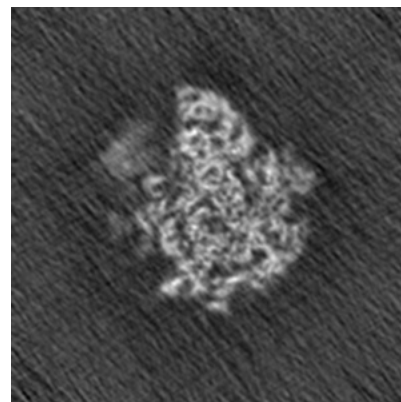
6.3.2 Raw map



X Index: 176



Y Index: 178

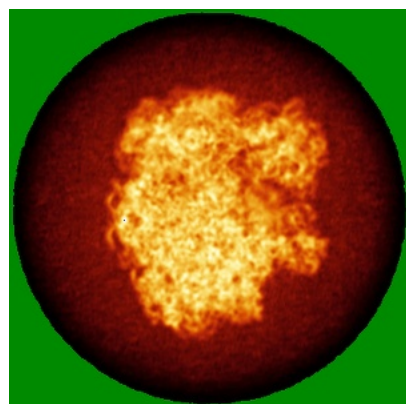


Z Index: 159

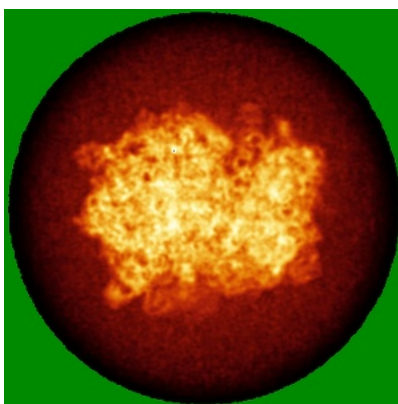
The images above show the largest variance slices of the map in three orthogonal directions.

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

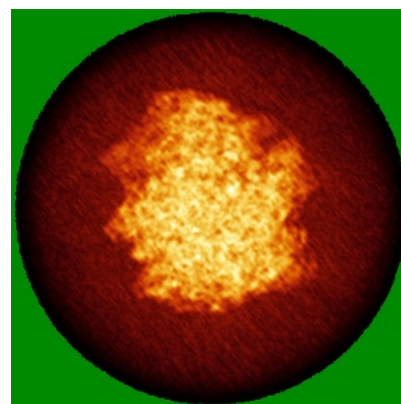
6.4.1 Primary map



X

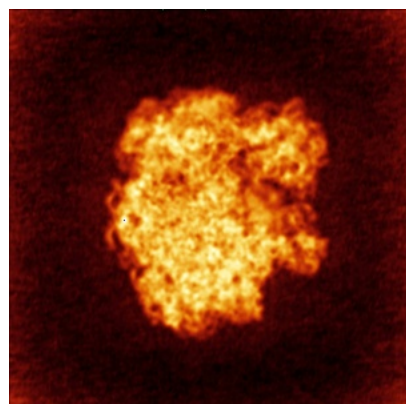


Y

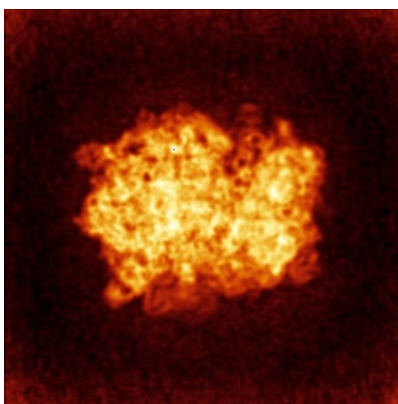


Z

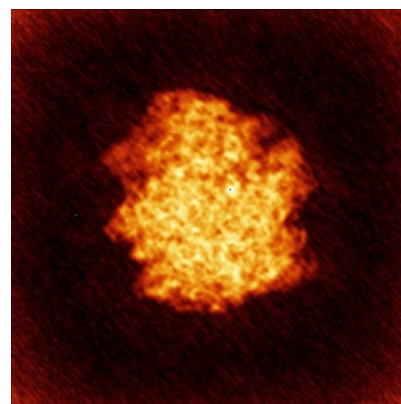
6.4.2 Raw map



X



Y

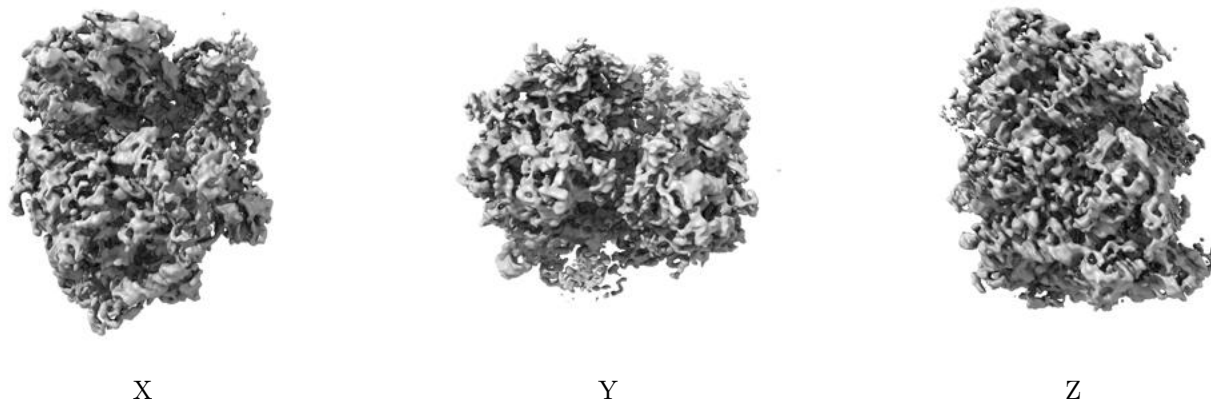


Z

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.

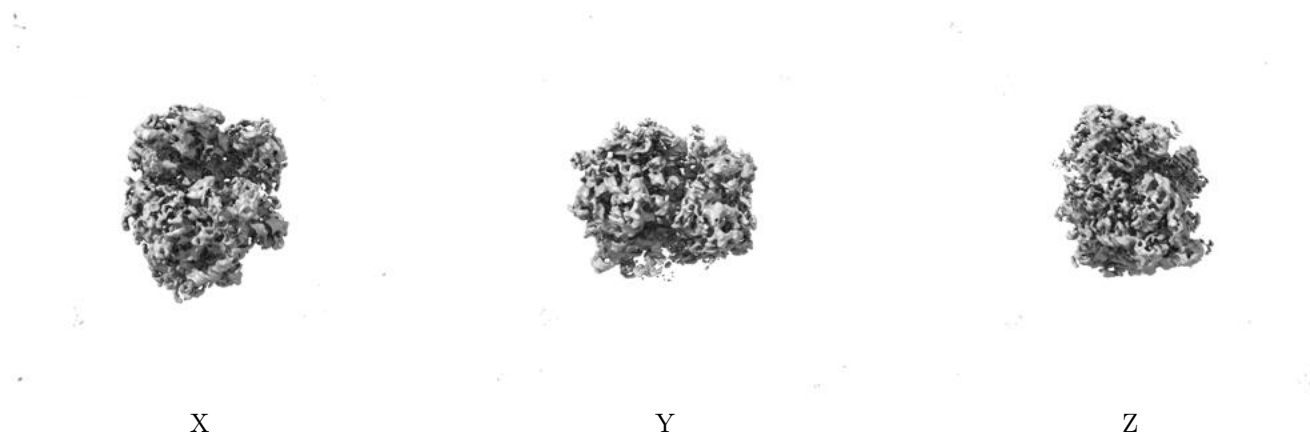
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.33. 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.

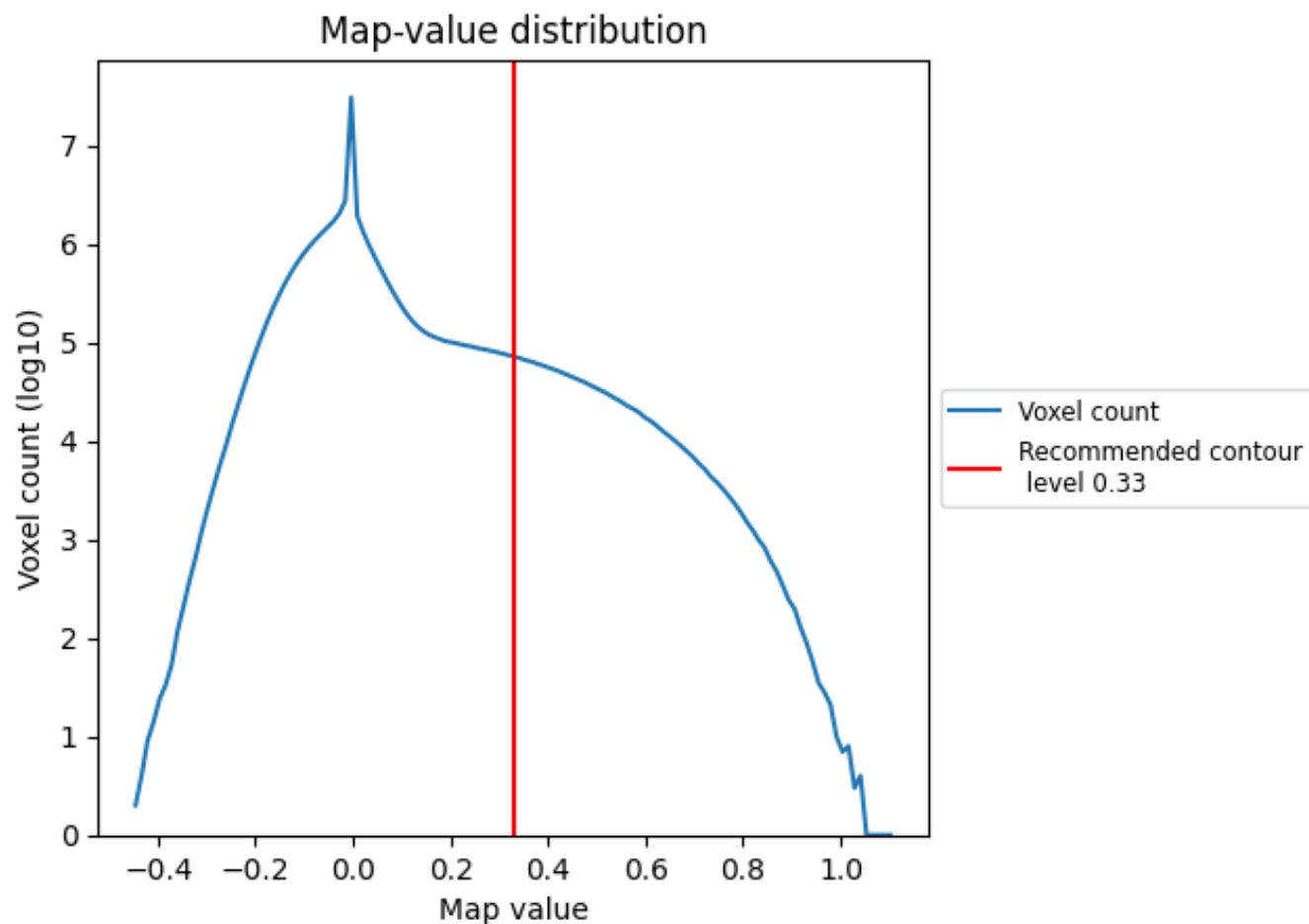
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

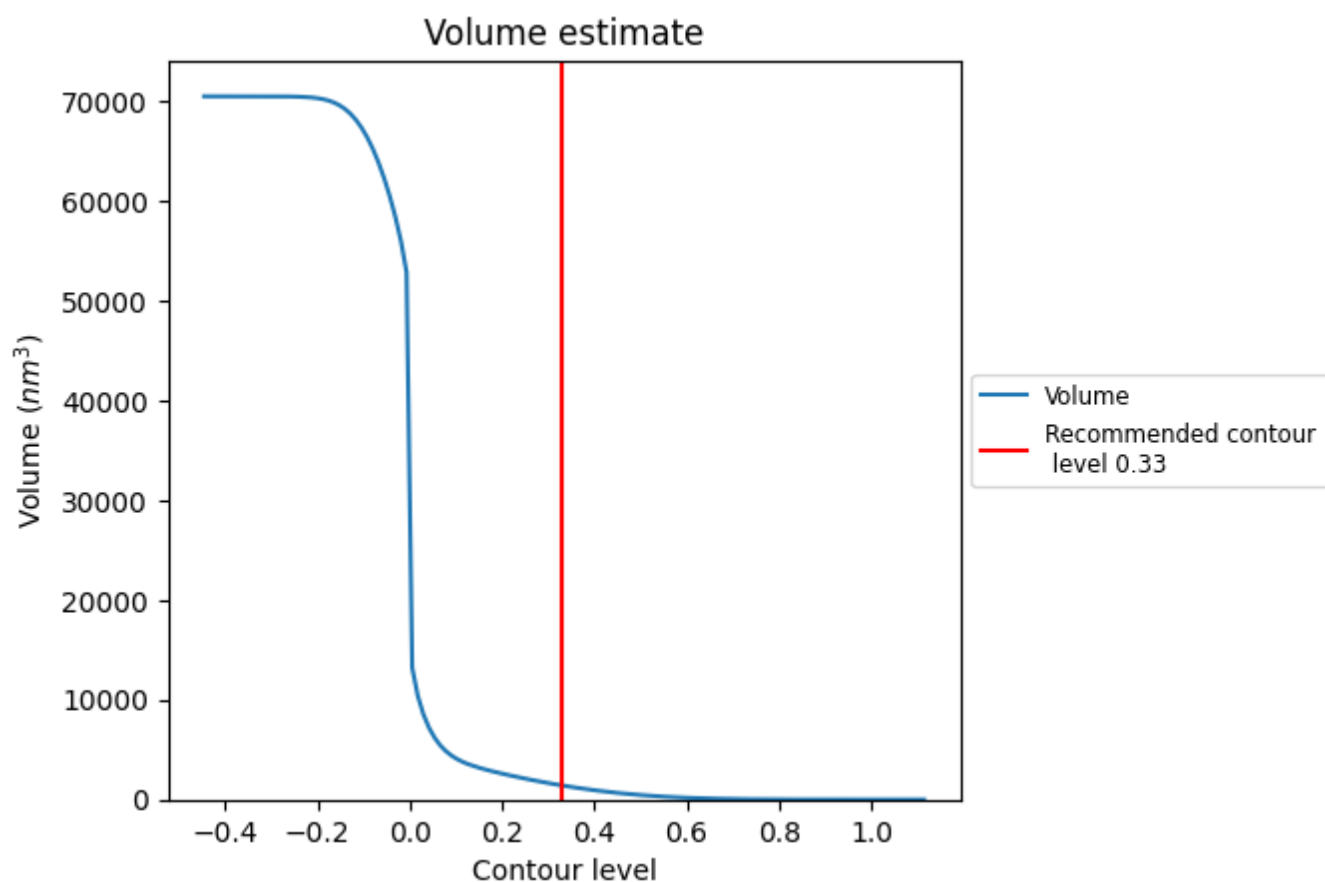
This section contains the results of statistical analysis of the map.

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.

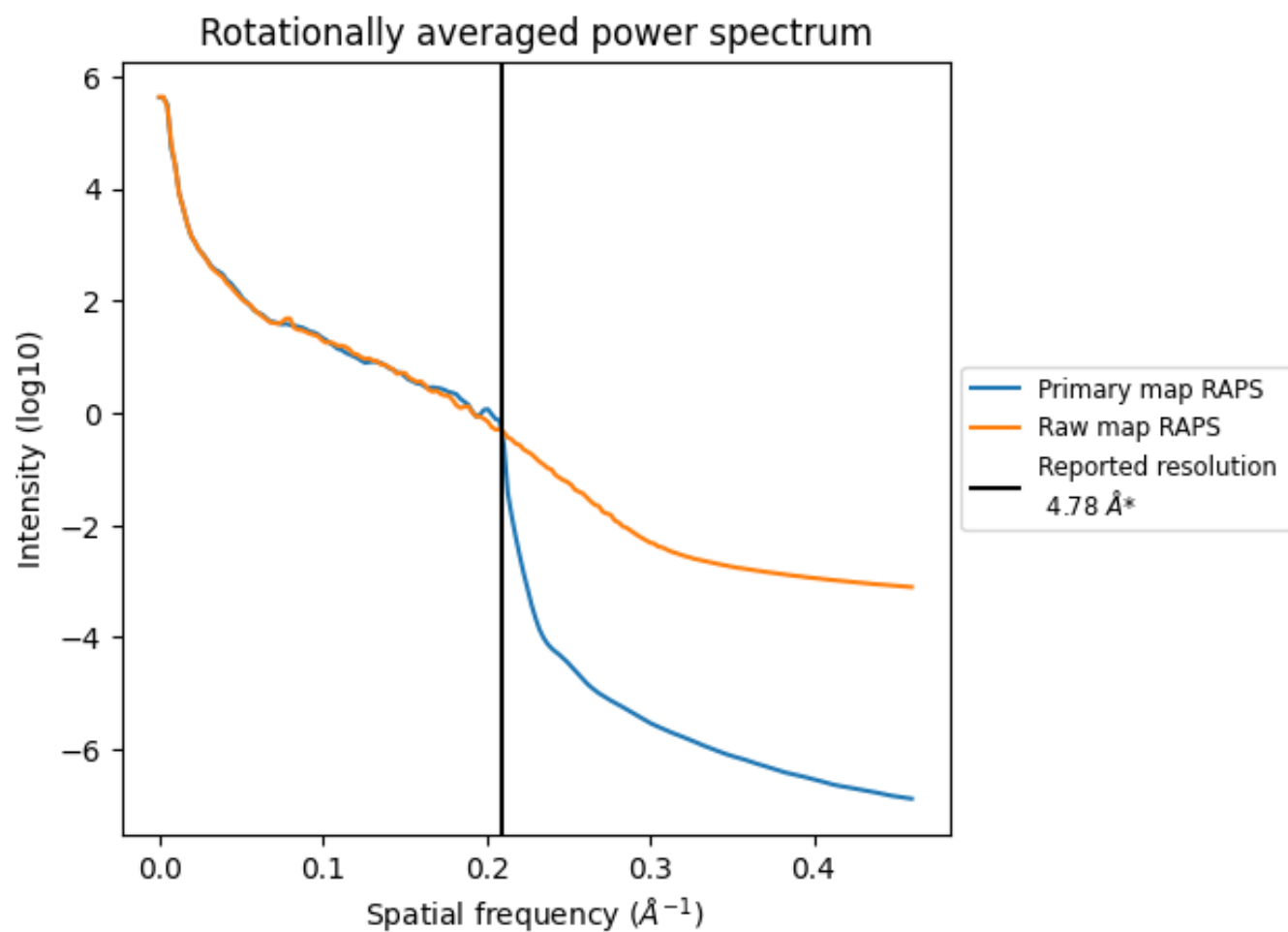
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1414 nm³; this corresponds to an approximate mass of 1277 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 ⓘ

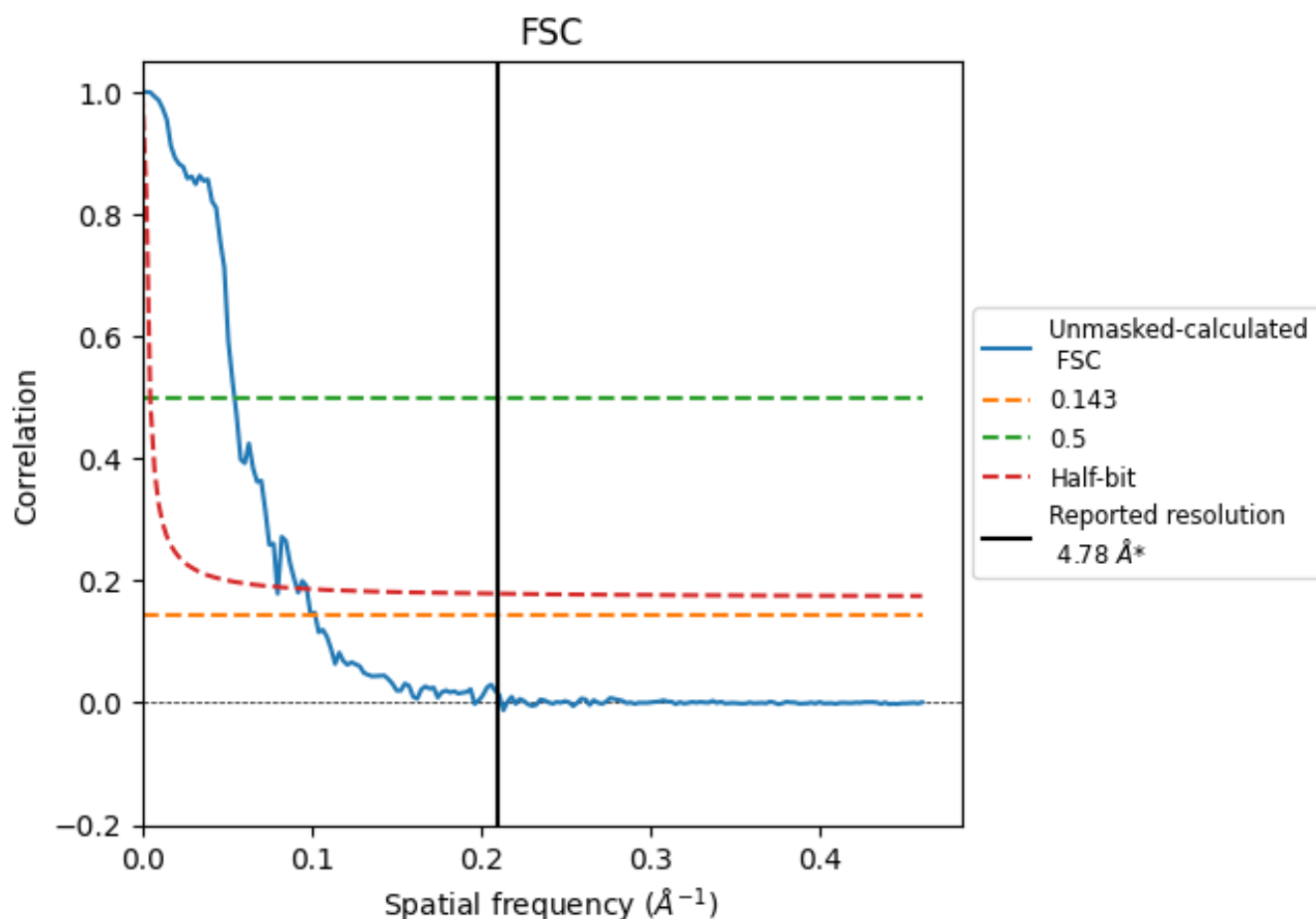


*Reported resolution corresponds to spatial frequency of $0.209 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.209 Å⁻¹

8.2 Resolution estimates [i](#)

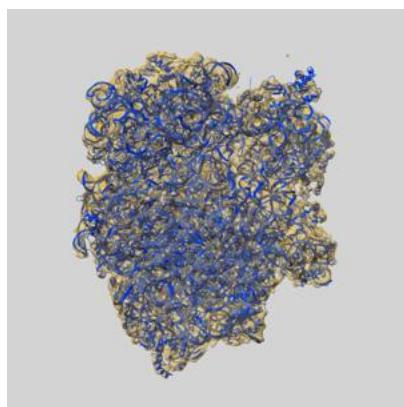
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.78	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.80	18.38	12.56

*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 9.80 differs from the reported value 4.78 by more than 10 %

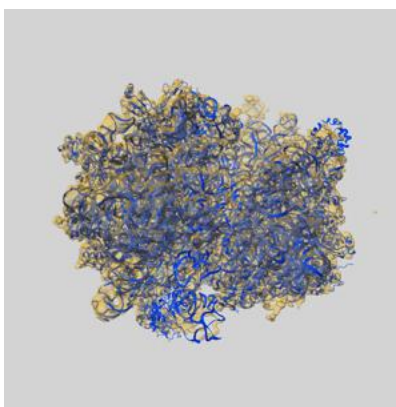
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34864 and PDB model 8HKZ. Per-residue inclusion information can be found in section 3 on page 16.

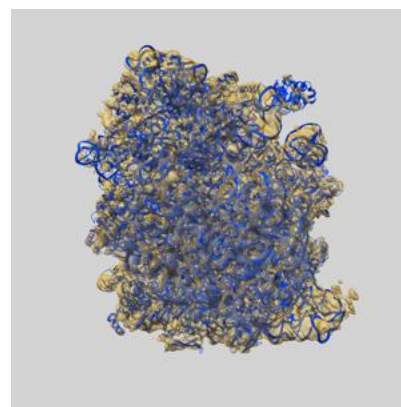
9.1 Map-model overlay [i](#)



X



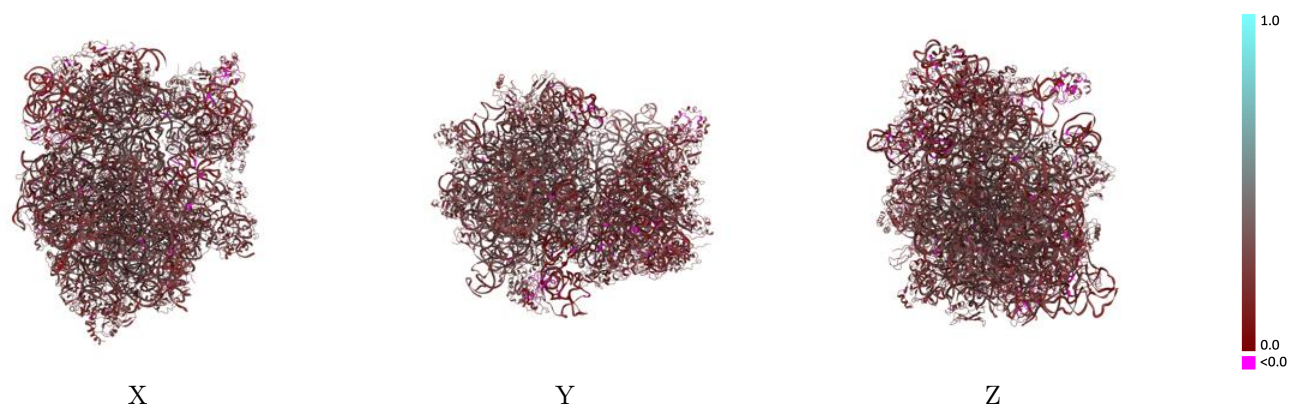
Y



Z

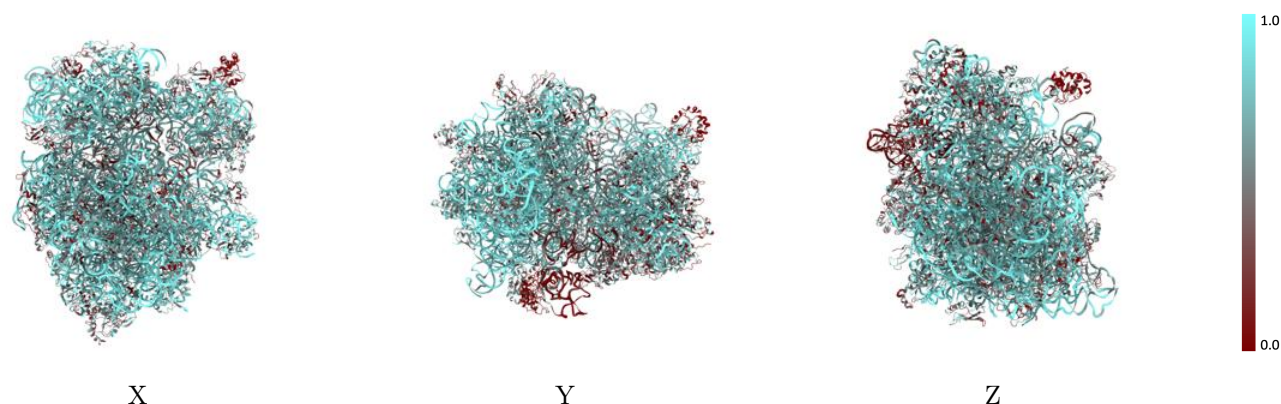
The images above show the 3D surface view of the map at the recommended contour level 0.33 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



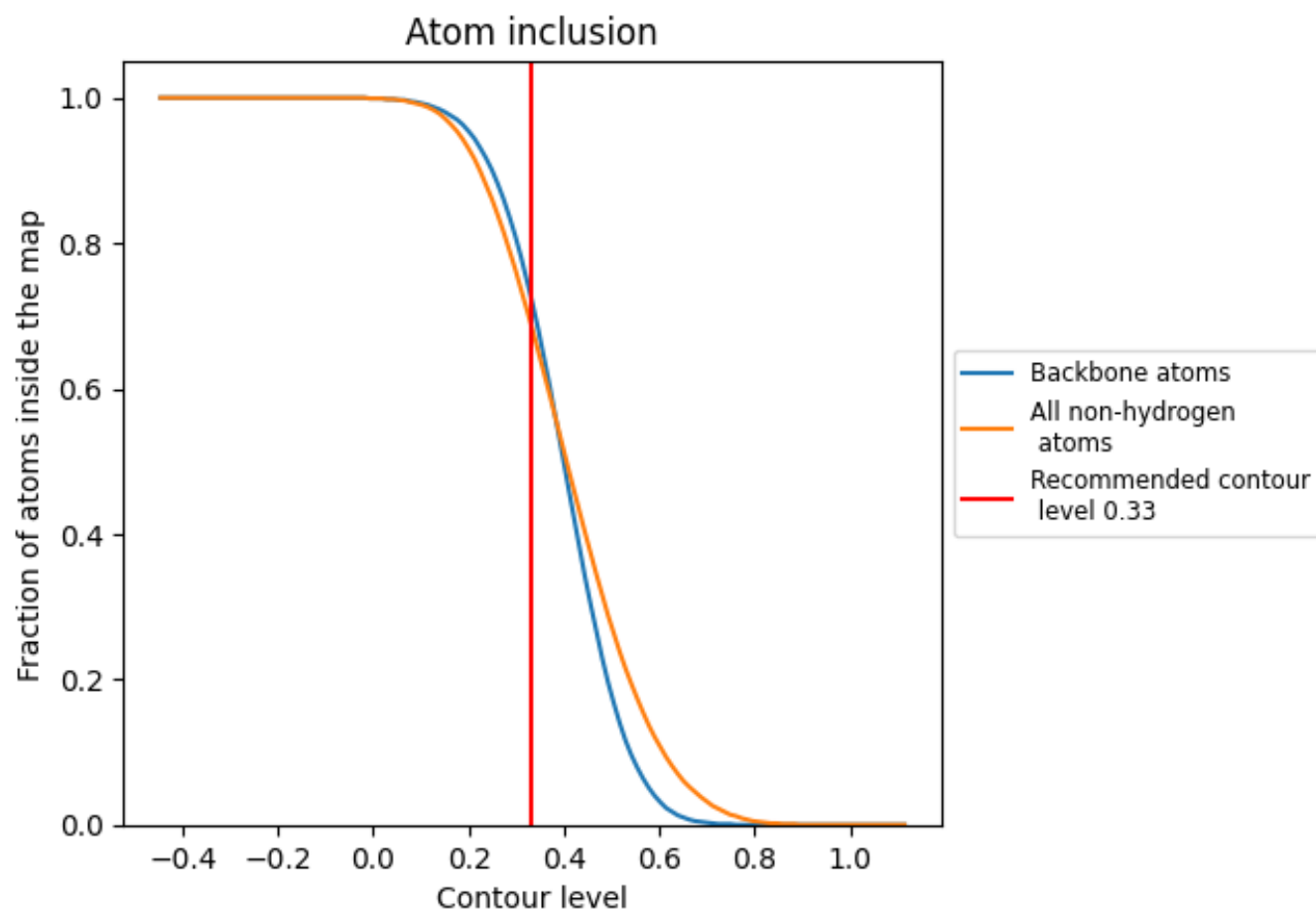
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.33).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 69% 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 (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6920	 0.2530
A16S	 0.8400	 0.2480
A23S	 0.8460	 0.2750
A5S	 0.9210	 0.2650
AETN	 0.1950	 0.1260
AL1P	 0.0500	 0.1750
AL2P	 0.4320	 0.2770
AL3P	 0.4840	 0.2520
AL4P	 0.5370	 0.2670
AL5P	 0.4760	 0.2210
AL6P	 0.4830	 0.2380
ALX0	 0.5380	 0.2160
AMRN	 0.4500	 0.2680
APTN	 0.7740	 0.2250
APTP	 0.0600	 0.1570
AS2P	 0.4410	 0.2550
AS3P	 0.3870	 0.2480
AS4E	 0.5020	 0.2210
AS4P	 0.5550	 0.2290
AS5P	 0.5270	 0.2660
AS6E	 0.3010	 0.2060
AS7P	 0.3840	 0.2200
AS8E	 0.3920	 0.2130
AS8P	 0.6280	 0.2650
AS9P	 0.4410	 0.2020
L10E	 0.5330	 0.2710
L13P	 0.5420	 0.2370
L141	 0.5420	 0.2400
L142	 0.3710	 0.2140
L14P	 0.3420	 0.2620
L15E	 0.4980	 0.2580
L15P	 0.6040	 0.2570
L18E	 0.6840	 0.2760
L18P	 0.5350	 0.2460
L19E	 0.6280	 0.2720



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Chain	Atom inclusion	Q-score
L21E	0.5180	0.2670
L22P	0.4960	0.2550
L23P	0.4910	0.2510
L24E	0.4940	0.2380
L24P	0.6090	0.2350
L29P	0.5570	0.2400
L30E	0.6150	0.2580
L30P	0.5680	0.2300
L31E	0.5170	0.2420
L32E	0.4130	0.2520
L34E	0.5240	0.2360
L37A	0.5520	0.2520
L37E	0.6090	0.2570
L39E	0.5850	0.2320
L40E	0.1550	0.2000
L44E	0.5590	0.2610
L45A	0.4680	0.2480
L46A	0.3110	0.2480
L47A	0.0660	0.2120
L7A1	0.4520	0.2520
L7A2	0.4680	0.2240
S10P	0.3470	0.2120
S11P	0.4090	0.2440
S12P	0.3030	0.2440
S13P	0.4350	0.2120
S14P	0.4010	0.2190
S15P	0.5910	0.2480
S17E	0.3500	0.1850
S17P	0.4620	0.2450
S19E	0.4350	0.1830
S19P	0.5430	0.2130
S24E	0.5360	0.2110
S27A	0.6890	0.1270
S27E	0.6200	0.2340
S28E	0.2590	0.2090
S3AE	0.4680	0.2300
SL7A	0.1180	0.1550