



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 12:40 PM UTC

PDB ID : 9BDN / pdb_00009bdn
EMDB ID : EMD-44463
Title : 80S ribosome with angiogenin and tRNAAla
Authors : Loveland, A.B.; Korostelev, A.A.
Deposited on : 2024-04-12
Resolution : 3.10 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:

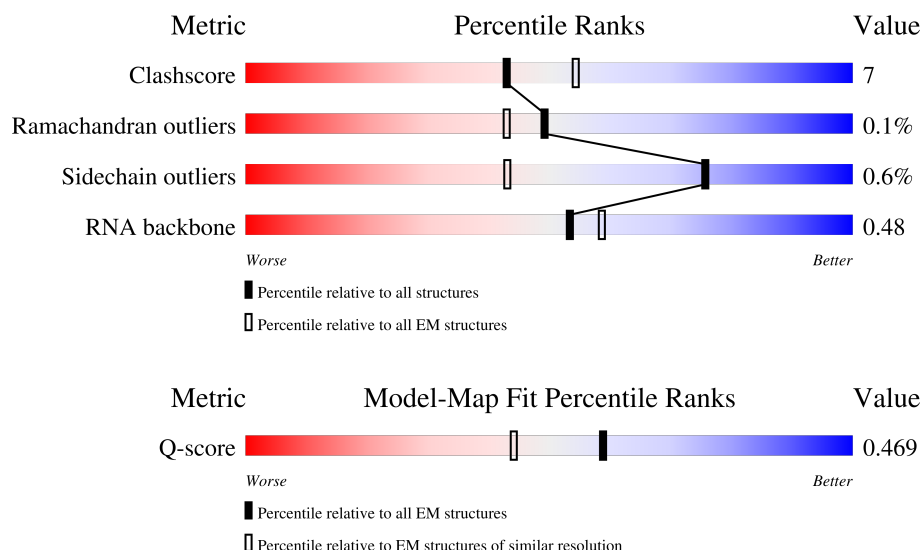
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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.



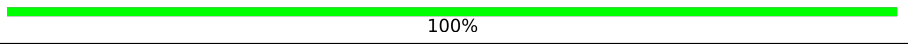
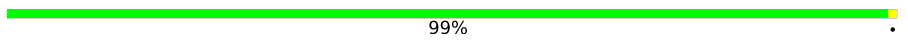
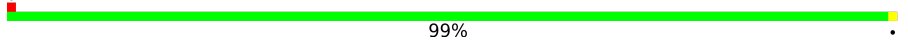
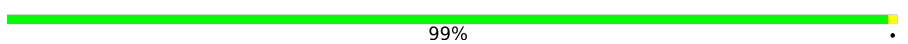
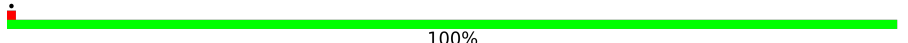
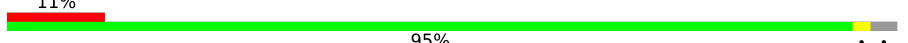
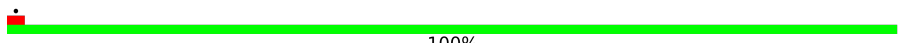
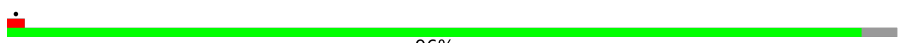
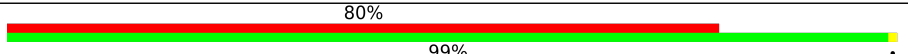
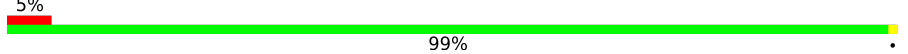
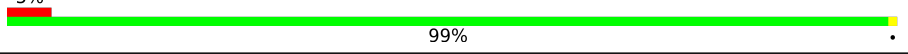
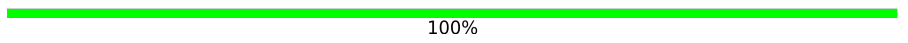
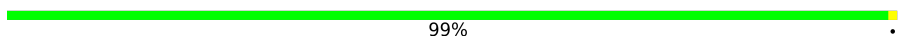
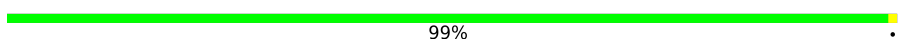
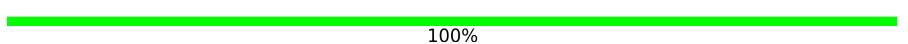
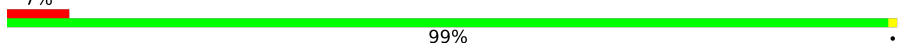
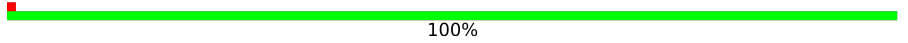
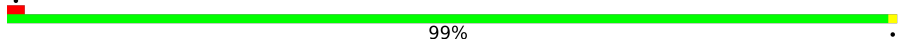
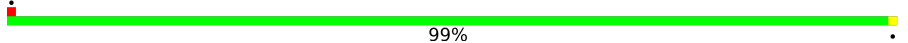
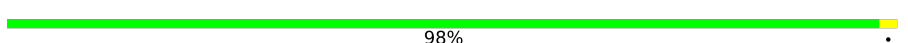
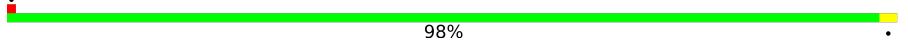
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	A18S	1869	
2	A28S	3601	
3	A58S	156	

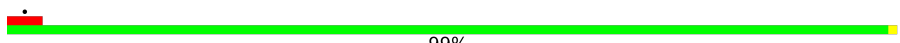
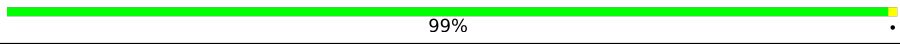
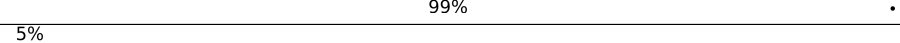
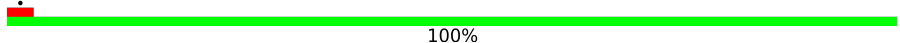
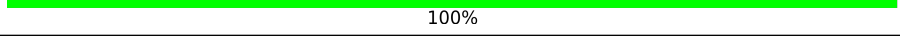
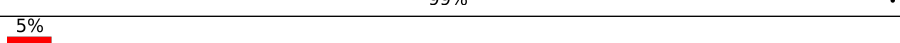
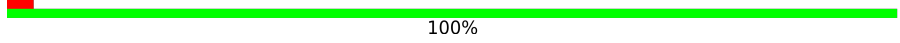
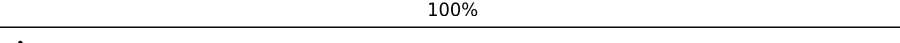
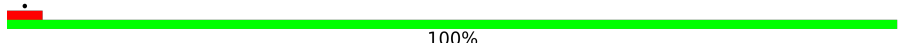
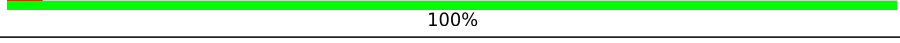
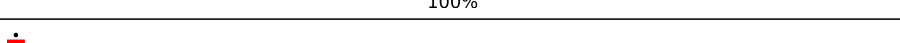
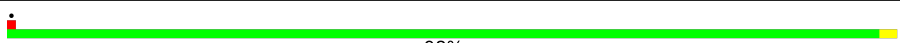
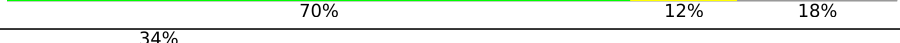
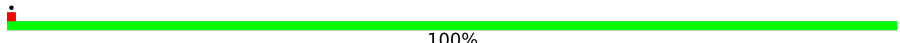
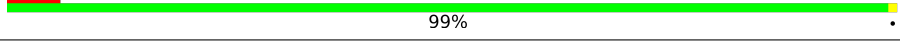
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Mol	Chain	Length	Quality of chain
4	A5S	120	
5	AL02	248	
6	AL03	394	
7	AL04	362	
8	AL05	293	
9	AL06	251	
10	AL07	225	
11	AL08	240	
12	AL09	190	
13	AL10	213	
14	AL11	170	
15	AL12	153	
16	AL13	210	
17	AL14	138	
18	AL15	203	
19	AL16	199	
20	AL17	153	
21	AL18	187	
22	AL19	180	
23	AL20	176	
24	AL21	159	
25	AL22	99	
26	AL23	131	
27	AL24	121	
28	AL25	118	

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Mol	Chain	Length	Quality of chain
29	AL26	134	 99%
30	AL27	135	 99%
31	AL28	147	 99%
32	AL29	245	 5% 42% 58%
33	AL30	98	 100%
34	AL31	107	 100%
35	AL32	128	 100%
36	AL33	109	 99%
37	AL34	114	 5% 99%
38	AL35	122	 99%
39	AL36	102	 100%
40	AL37	86	 100%
41	AL38	69	 100%
42	AL39	50	 98%
43	AL40	52	 100%
44	AL41	25	 100%
45	AL42	104	 100%
46	AL43	91	 99%
47	ALNW	124	 98%
48	ALP0	196	 96%
49	ANG	147	 7% 70% 12% 18%
50	ARAC	313	 34% 100%
51	AS00	217	 9% 100%
52	AS01	213	100%
53	AS02	221	6% 99%

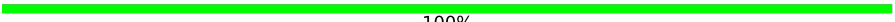
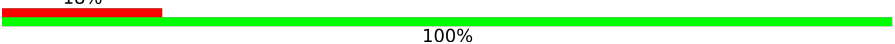
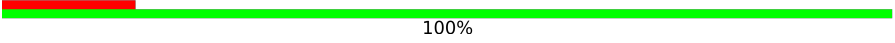
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Mol	Chain	Length	Quality of chain
54	AS03	228	
55	AS04	262	
56	AS05	191	
57	AS06	237	
58	AS07	189	
59	AS08	206	
60	AS09	185	
61	AS10	96	
62	AS11	151	
63	AS12	117	
64	AS13	149	
65	AS14	135	
66	AS15	120	
67	AS16	142	
68	AS17	132	
69	AS18	144	
70	AS19	141	
71	AS20	100	
72	AS21	83	
73	AS22	129	
74	AS23	141	
75	AS24	124	
76	AS25	75	
77	AS26	101	
78	AS27	83	

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Mol	Chain	Length	Quality of chain
79	AS28	62	 100%
80	AS29	55	 18% 100%
81	AS30	55	 15% 100%
82	ETRN	77	 8% 84% 16%
82	PTRN	77	 1% 91% 9%
83	MRNA	28	 14% 21% 64%
84	TIRN	76	 25% 79% 14% 7%

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 217108 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A18S	1691	Total	C	N	O	P	0	0
			36103	16115	6485	11813	1690		

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A28S	3557	Total	C	N	O	P	0	0
			76286	33976	13979	24774	3557		

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A58S	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A5S	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A5S	2	U	N	conflict	GB X06789.1
A5S	36	C	N	conflict	GB X06789.1
A5S	102	U	N	conflict	GB X06789.1
A5S	112	U	N	conflict	GB X06789.1
A5S	114	U	N	conflict	GB X06789.1
A5S	119	U	C	conflict	GB X06789.1
A5S	120	U	N	conflict	GB X06789.1

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AL02	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AL03	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AL04	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AL05	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AL06	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 10 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AL07	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 11 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL08	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL08	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL09	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 13 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AL10	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 14 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AL11	170	Total	C	N	O	S	0	0
			1361	861	254	240	6		

- Molecule 15 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AL12	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 16 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AL13	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL13	74	ARG	HIS	conflict	UNP G1TKB3
AL13	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 17 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AL14	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 18 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AL15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 19 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AL16	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 20 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AL17	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 21 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AL18	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL18	4	ASP	ASN	conflict	UNP G1TFE0
AL18	14	ARG	TRP	conflict	UNP G1TFE0
AL18	53	MET	LEU	conflict	UNP G1TFE0
AL18	58	ARG	TRP	conflict	UNP G1TFE0
AL18	75	ARG	GLN	conflict	UNP G1TFE0
AL18	80	ALA	PRO	conflict	UNP G1TFE0
AL18	86	VAL	ILE	conflict	UNP G1TFE0
AL18	104	ARG	HIS	conflict	UNP G1TFE0
AL18	110	ARG	CYS	conflict	UNP G1TFE0
AL18	137	VAL	GLY	conflict	UNP G1TFE0
AL18	157	GLY	ARG	conflict	UNP G1TFE0
AL18	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 22 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AL19	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL19	38	ARG	HIS	conflict	UNP G1TYL6
AL19	151	ARG	HIS	conflict	UNP G1TYL6

- Molecule 23 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AL20	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL20	1	MET	THR	conflict	UNP G1TTY7
AL20	18	PRO	-	insertion	UNP G1TTY7
AL20	19	THR	-	insertion	UNP G1TTY7
AL20	20	PRO	SER	conflict	UNP G1TTY7
AL20	22	CYS	SER	conflict	UNP G1TTY7
AL20	23	ARG	PRO	conflict	UNP G1TTY7
AL20	24	THR	ALA	conflict	UNP G1TTY7
AL20	49	SER	LEU	conflict	UNP G1TTY7
AL20	50	GLN	GLU	conflict	UNP G1TTY7
AL20	95	ARG	HIS	conflict	UNP G1TTY7
AL20	101	THR	ILE	conflict	UNP G1TTY7
AL20	102	THR	MET	conflict	UNP G1TTY7
AL20	104	GLY	SER	conflict	UNP G1TTY7
AL20	126	ILE	VAL	conflict	UNP G1TTY7
AL20	132	ILE	MET	conflict	UNP G1TTY7
AL20	135	SER	ALA	conflict	UNP G1TTY7
AL20	136	LYS	ARG	conflict	UNP G1TTY7
AL20	138	ARG	PRO	conflict	UNP G1TTY7
AL20	149	LYS	ARG	conflict	UNP G1TTY7
AL20	151	LYS	ARG	conflict	UNP G1TTY7
AL20	168	THR	TYR	conflict	UNP G1TTY7
AL20	169	THR	ALA	conflict	UNP G1TTY7
AL20	176	PHE	-	insertion	UNP G1TTY7

- Molecule 24 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AL21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 25 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AL22	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL22	18	LEU	VAL	conflict	UNP G1TSG1
AL22	32	GLY	ARG	conflict	UNP G1TSG1
AL22	36	ALA	GLU	conflict	UNP G1TSG1
AL22	39	PHE	SER	conflict	UNP G1TSG1
AL22	54	GLY	ARG	conflict	UNP G1TSG1
AL22	60	VAL	ALA	conflict	UNP G1TSG1
AL22	62	SER	THR	conflict	UNP G1TSG1
AL22	63	LEU	ILE	conflict	UNP G1TSG1
AL22	97	ARG	HIS	conflict	UNP G1TSG1
AL22	106	THR	SER	conflict	UNP G1TSG1

- Molecule 26 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AL23	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 27 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AL24	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 28 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AL25	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AL26	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 30 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AL27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 31 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AL28	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 32 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AL29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AL30	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AL31	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 35 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AL32	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL32	3	ALA	SER	conflict	UNP G1TUN8
AL32	13	VAL	ILE	conflict	UNP G1TUN8
AL32	16	ARG	TRP	conflict	UNP G1TUN8
AL32	81	ASN	SER	conflict	UNP G1TUN8
AL32	98	GLU	LYS	conflict	UNP G1TUN8
AL32	108	ARG	CYS	conflict	UNP G1TUN8
AL32	115	ALA	VAL	conflict	UNP G1TUN8

- Molecule 36 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AL33	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 37 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AL34	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AL35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 39 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AL36	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 40 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AL37	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 41 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AL38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL38	24	LYS	ASN	conflict	UNP G1U001

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AL39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 43 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AL40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 44 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AL41	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 45 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AL42	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 46 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AL43	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 47 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	ALNW	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 48 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	ALP0	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 49 is a protein called Angiogenin.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	ANG	120	Total	C	N	O	S	0	0
			955	591	186	171	7		

- Molecule 50 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 51 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AS00	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 52 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AS01	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 53 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AS02	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 54 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AS03	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 55 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AS04	262	Total	C	N	O	S	0	0
			2075	1323	386	358	8		

- Molecule 56 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AS05	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 57 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AS06	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 58 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AS07	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 59 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS08	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS08	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 60 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AS09	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 61 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AS10	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 62 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AS11	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 63 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AS12	99	Total	C	N	O	S	0	0
			758	475	139	137	7		

- Molecule 64 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AS13	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 65 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AS14	135	Total	C	N	O	S	0	0
			1004	614	196	188	6		

- Molecule 66 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AS15	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 67 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AS16	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 68 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AS17	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AS18	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 70 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AS19	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS19	119	GLY	TRP	conflict	UNP G1TN62

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

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AS20	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 72 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AS21	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS21	3	ASN	SER	conflict	UNP G1TM82

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Chain	Residue	Modelled	Actual	Comment	Reference
AS21	4	ASP	ASN	conflict	UNP G1TM82
AS21	33	GLN	PRO	conflict	UNP G1TM82
AS21	50	PHE	SER	conflict	UNP G1TM82
AS21	75	ALA	SER	conflict	UNP G1TM82
AS21	76	ASP	HIS	conflict	UNP G1TM82
AS21	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 73 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AS22	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AS23	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 75 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AS24	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 76 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AS25	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 77 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AS26	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS26	28	ARG	CYS	conflict	UNP G1TFE8

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Chain	Residue	Modelled	Actual	Comment	Reference
AS26	56	ALA	VAL	conflict	UNP G1TFE8

- Molecule 78 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AS27	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 79 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	AS28	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 80 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	AS29	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 81 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AS30	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 82 is a RNA chain called tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	ETRN	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
82	PTRN	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 83 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	MRNA	10	Total	C	N	O	P	0	0
			207	93	33	71	10		

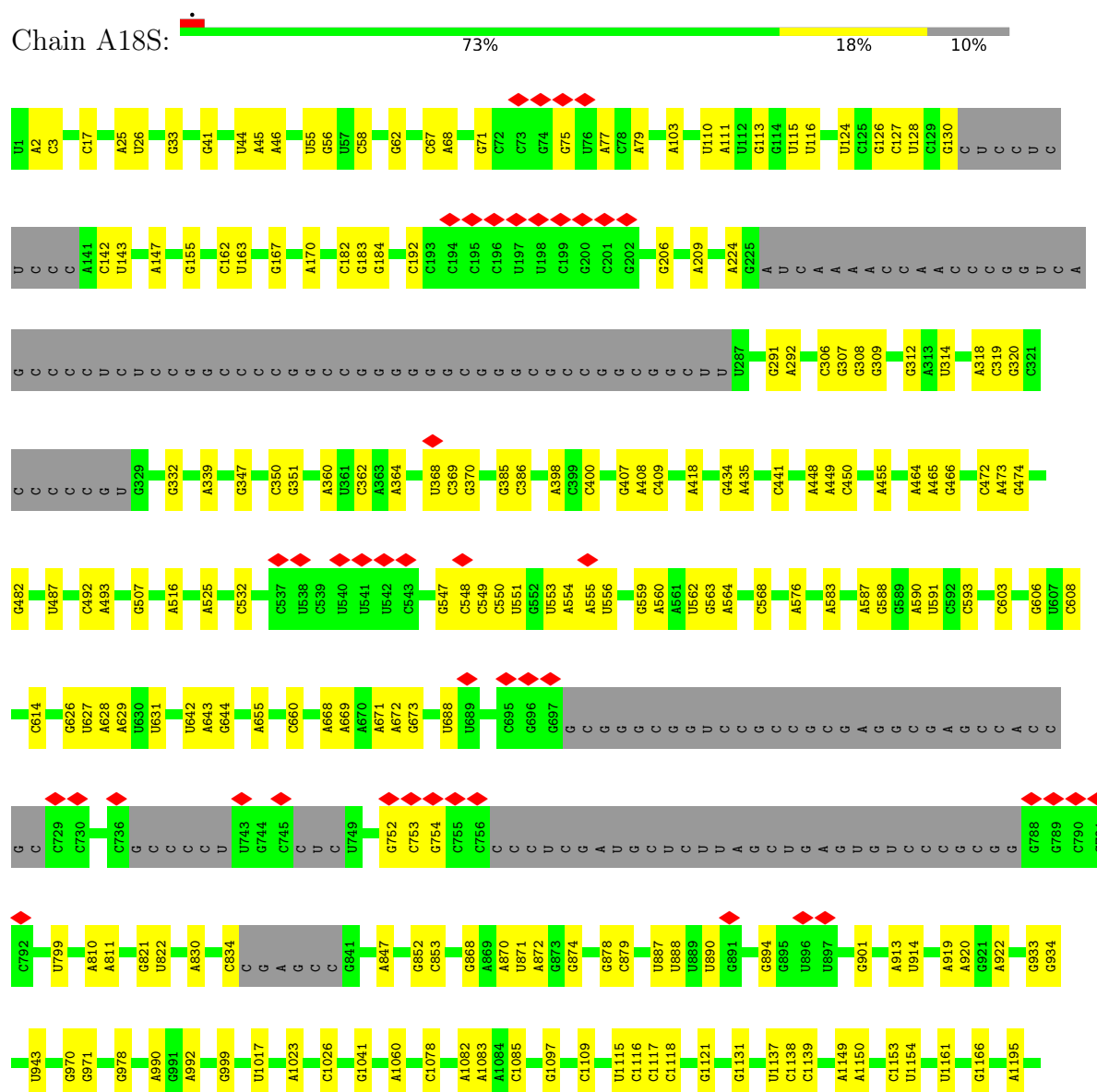
- Molecule 84 is a RNA chain called tRNA^AAla.

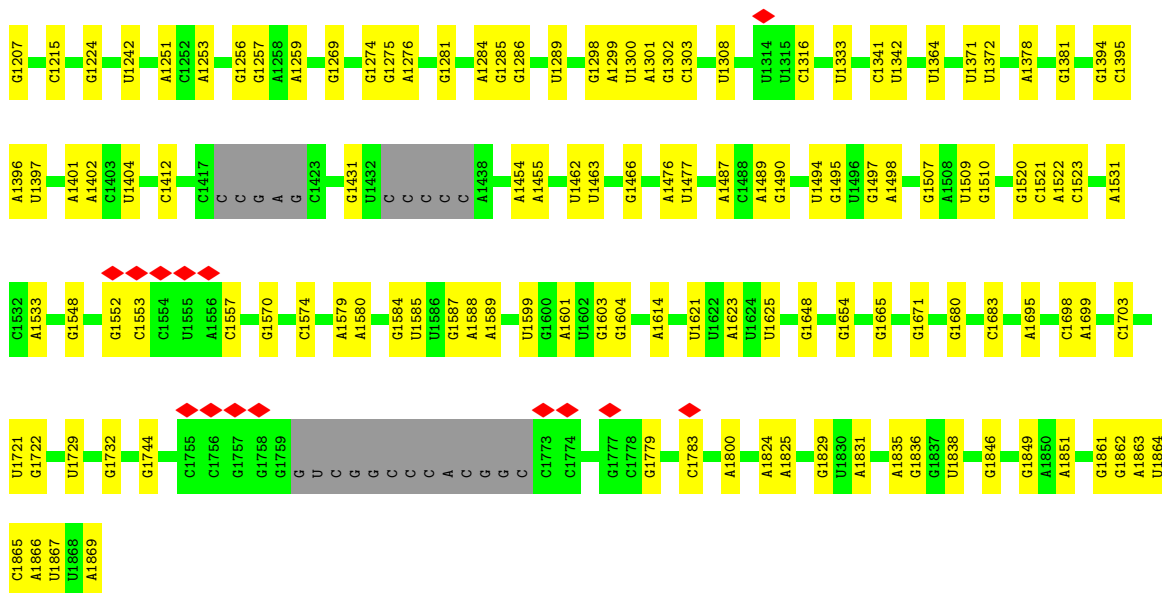
Mol	Chain	Residues	Atoms					AltConf	Trace
84	TIRN	71	Total	C	N	O	P	0	0
			1514	673	265	505	71		

3 Residue-property plots [i](#)

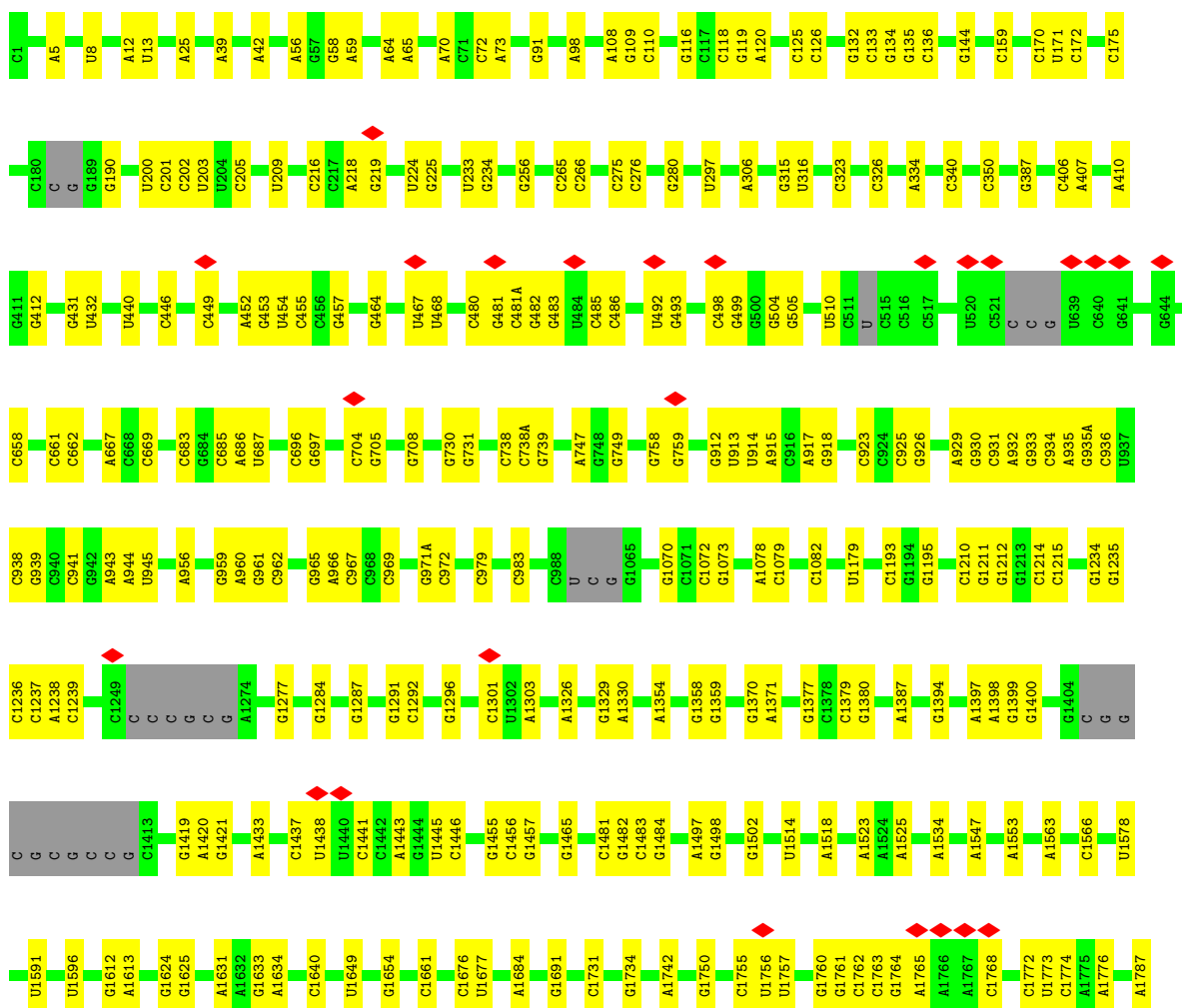
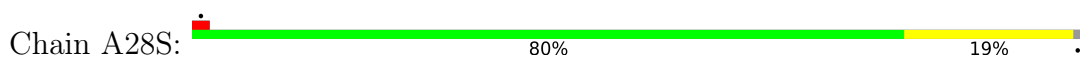
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

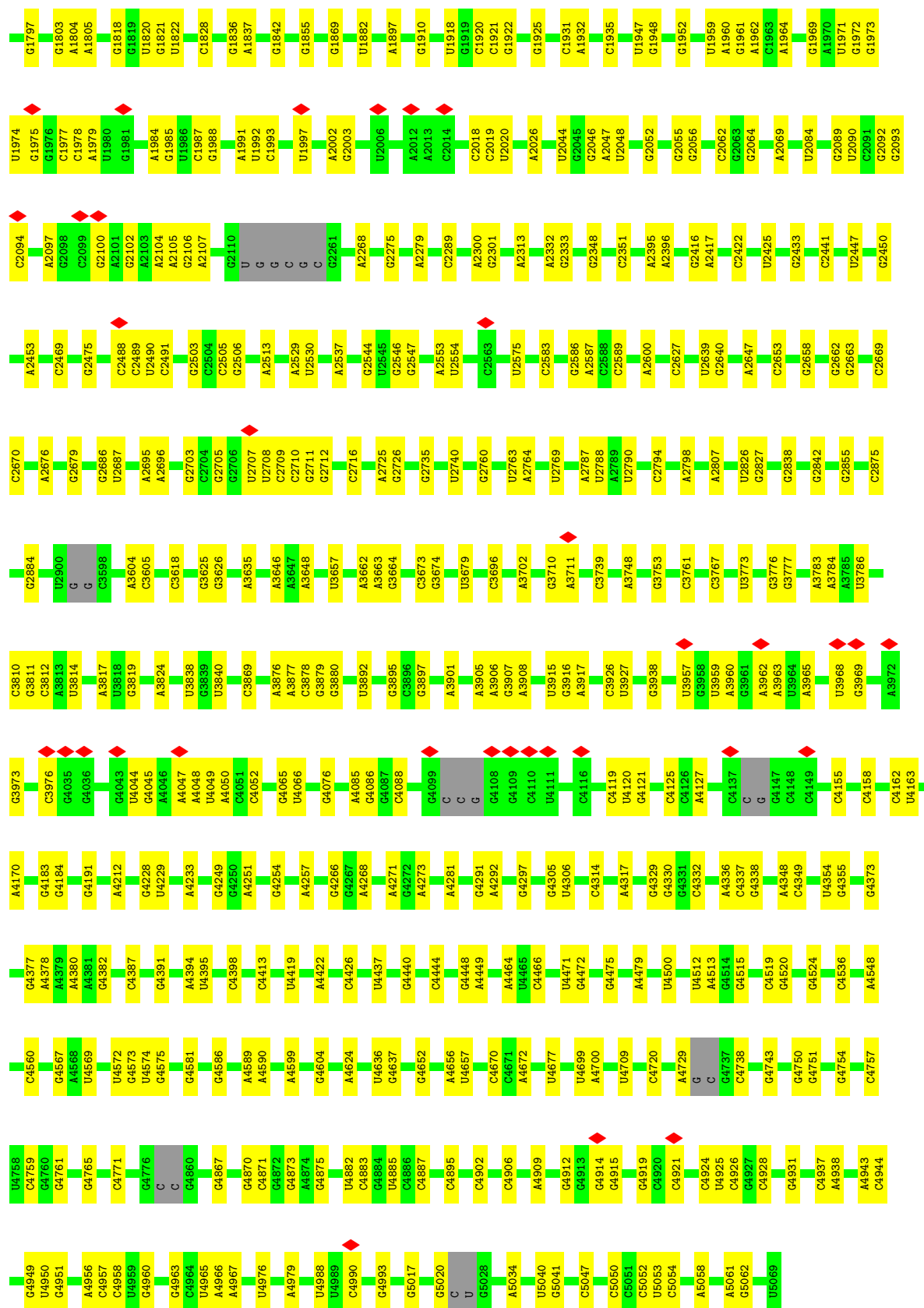
• Molecule 1: 18S rRNA





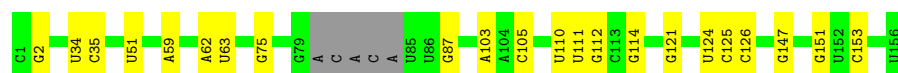
• Molecule 2: 28S rRNA





- Molecule 3: 5.8S rRNA

Chain A58S:  83% 14%



- Molecule 4: 5S rRNA

Chain A5S:  82% 18%

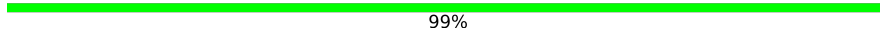


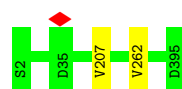
- Molecule 5: 60S ribosomal protein L8

Chain AL02:  100%

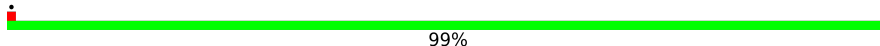


- Molecule 6: 60S ribosomal protein L3

Chain AL03:  99%

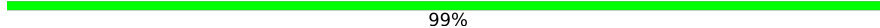


- Molecule 7: 60S ribosomal protein L4

Chain AL04:  99%



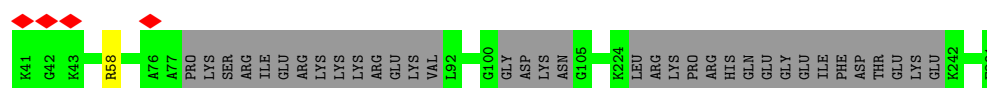
- Molecule 8: 60S ribosomal protein L5

Chain AL05:  99%

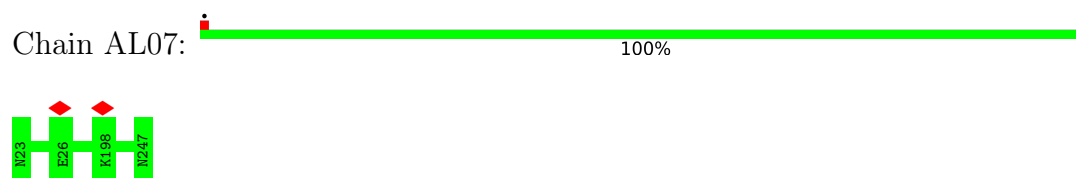


- Molecule 9: 60S ribosomal protein L6

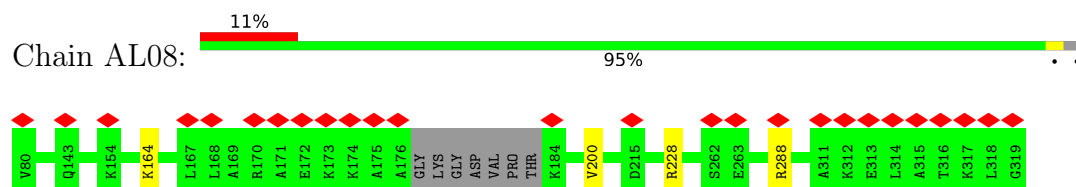
Chain AL06:  86% 14%



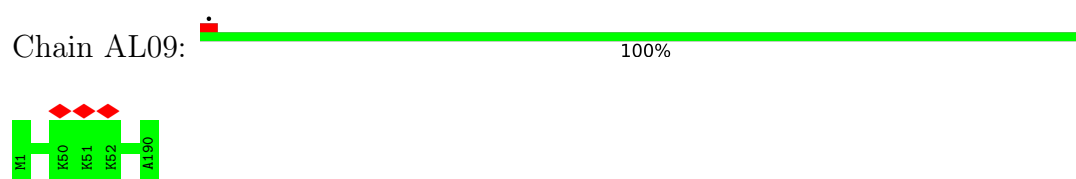
- Molecule 10: 60S ribosomal protein L7



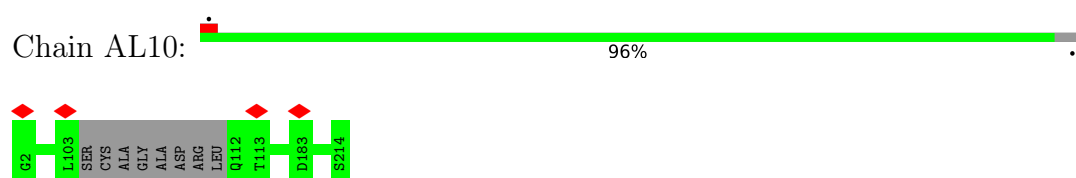
- Molecule 11: Large ribosomal subunit protein eL8



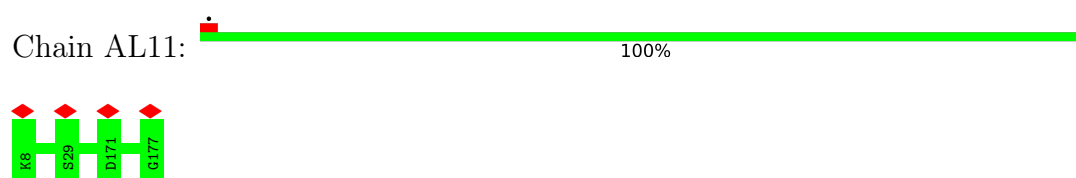
- Molecule 12: 60S ribosomal protein L9



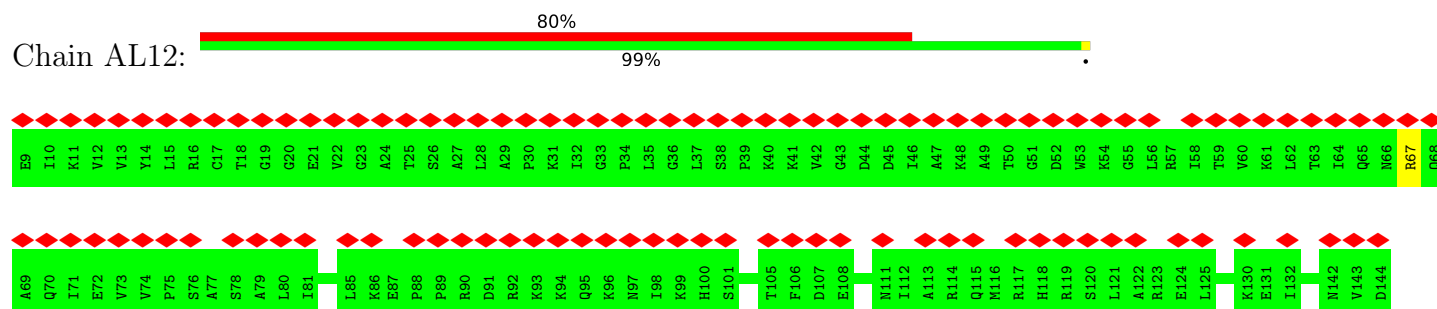
- Molecule 13: Ribosomal protein L10

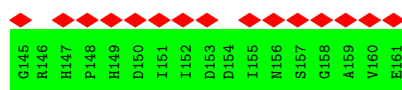


- Molecule 14: 60S ribosomal protein L11

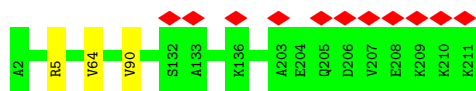


- Molecule 15: uL11

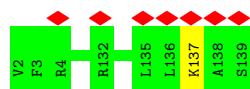




- Molecule 16: Large ribosomal subunit protein eL13



- Molecule 17: 60S ribosomal protein L14



- Molecule 18: 60S ribosomal protein L15



There are no outlier residues recorded for this chain.

- Molecule 19: Large ribosomal subunit protein uL13



- Molecule 20: 60S ribosomal protein L17



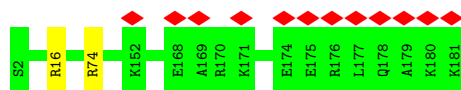
- Molecule 21: Large ribosomal subunit protein eL18



There are no outlier residues recorded for this chain.

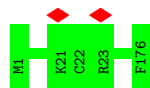
- Molecule 22: 60S ribosomal protein L19





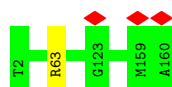
- Molecule 23: 60S ribosomal protein L18a

Chain AL20: 100%



- Molecule 24: 60S ribosomal protein L21

Chain AL21: 99%



- Molecule 25: Large ribosomal subunit protein eL22

Chain AL22: 99%



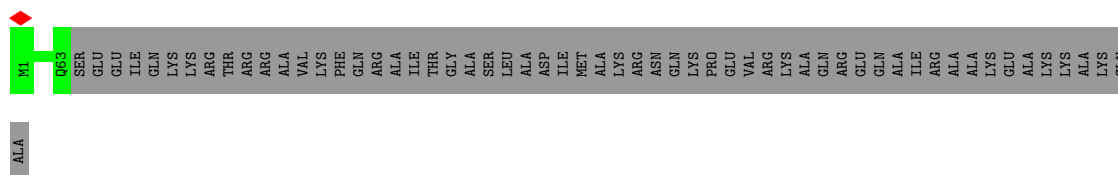
- Molecule 26: 60S ribosomal protein L23

Chain AL23: 98%



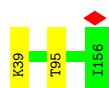
- Molecule 27: Ribosomal protein L24

Chain AL24: 52% 48%

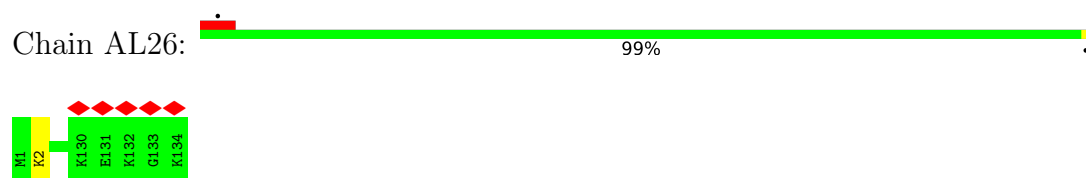


- Molecule 28: Large ribosomal subunit protein uL23

Chain AL25: 98%



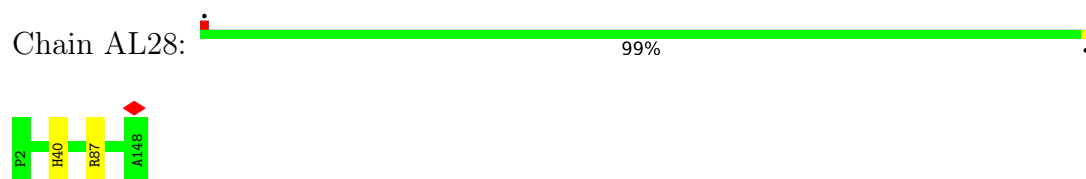
- Molecule 29: 60S ribosomal protein L26



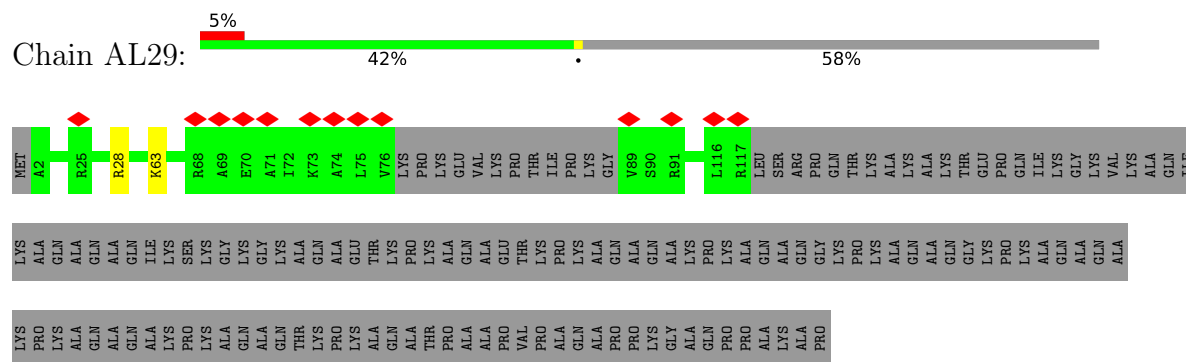
- Molecule 30: 60S ribosomal protein L27



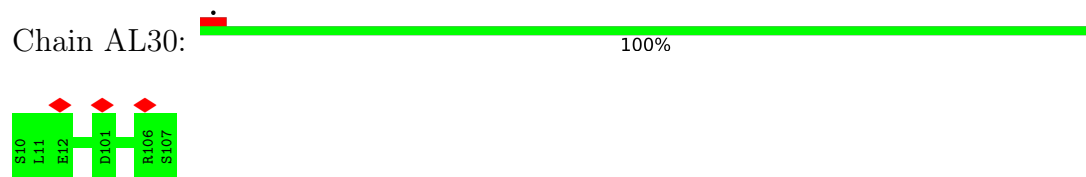
- Molecule 31: 60S ribosomal protein L27a



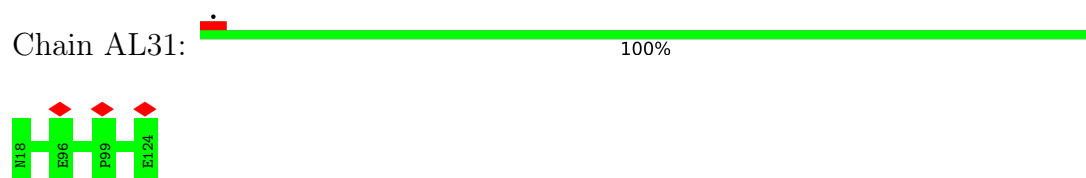
- Molecule 32: Large ribosomal subunit protein eL29



- Molecule 33: 60S ribosomal protein L30



- Molecule 34: 60S ribosomal protein L31



- Molecule 35: Large ribosomal subunit protein eL32

Chain AL32:  100%

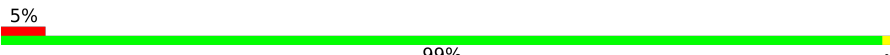


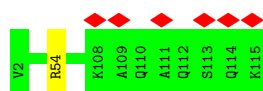
- Molecule 36: 60S ribosomal protein L35a

Chain AL33:  99%



- Molecule 37: 60S ribosomal protein L34

Chain AL34:  99%



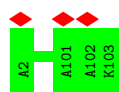
- Molecule 38: 60S ribosomal protein L35

Chain AL35:  99%



- Molecule 39: 60S ribosomal protein L36

Chain AL36:  100%



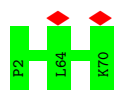
- Molecule 40: 60S ribosomal protein L37

Chain AL37:  100%

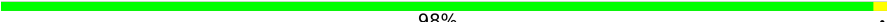
There are no outlier residues recorded for this chain.

- Molecule 41: Large ribosomal subunit protein eL38

Chain AL38:  100%



- Molecule 42: 60S ribosomal protein L39

Chain AL39:  98%



- Molecule 43: Large ribosomal subunit protein eL40

Chain AL40:  100%



- Molecule 44: eL41

Chain AL41:  100%



- Molecule 45: eL42

Chain AL42:  100%

There are no outlier residues recorded for this chain.

- Molecule 46: 60S ribosomal protein L37a

Chain AL43:  99%

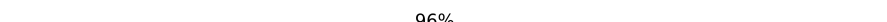


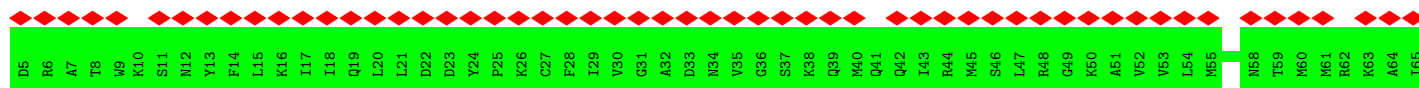
- Molecule 47: 60S ribosomal protein L28

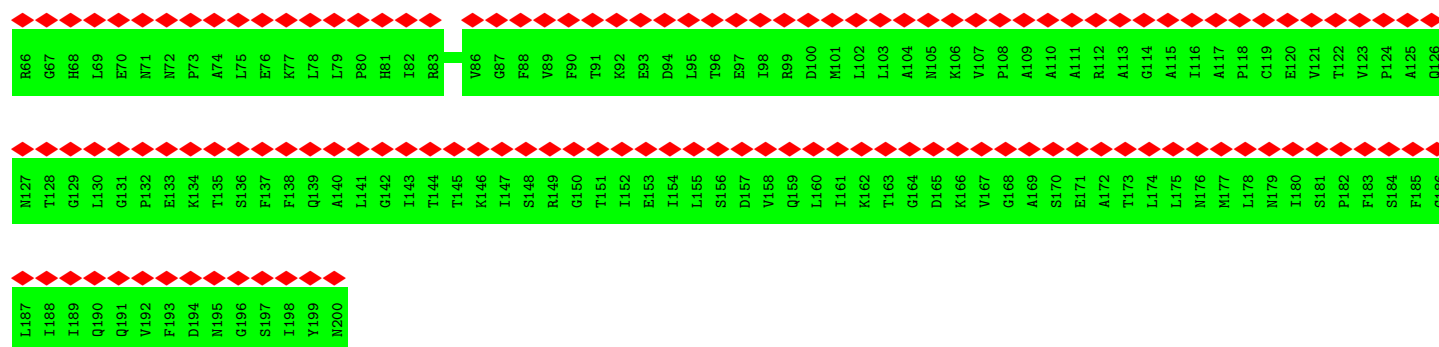
Chain ALNW:  98%



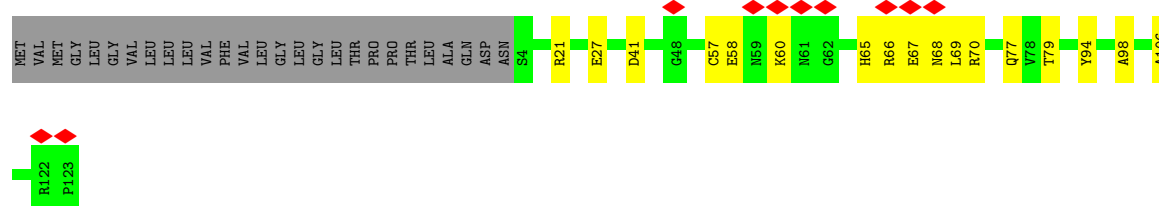
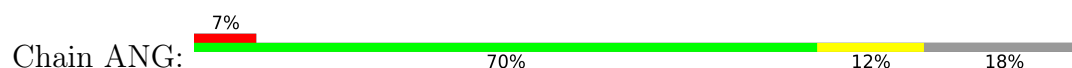
- Molecule 48: 60S acidic ribosomal protein P0

Chain ALP0:  96%
100%

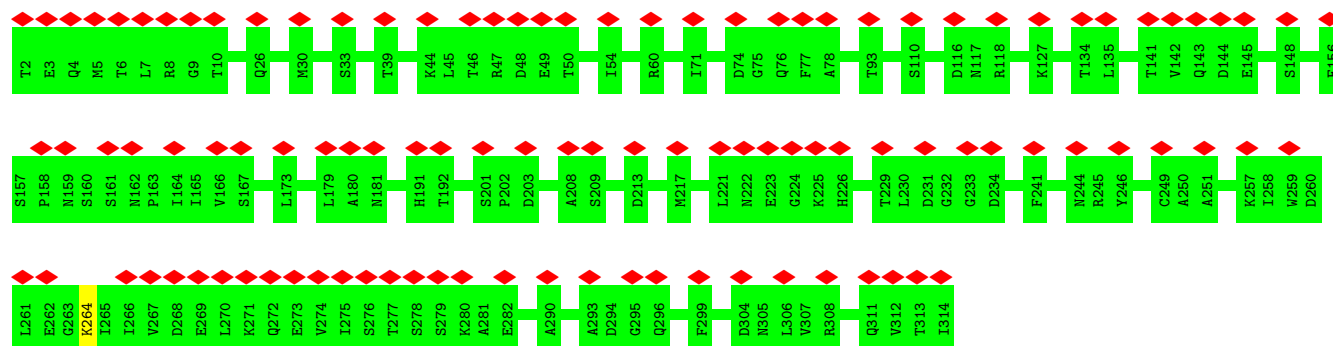
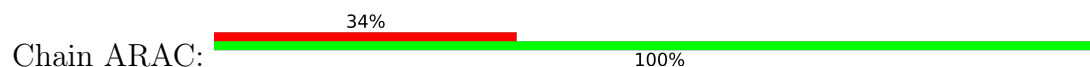




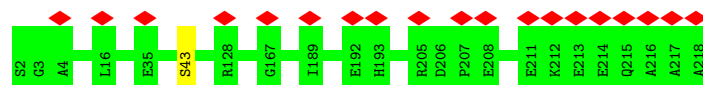
• Molecule 49: Angiogenin



• Molecule 50: Receptor of activated protein C kinase 1

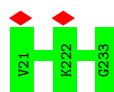


• Molecule 51: 40S_SA_C domain-containing protein



• Molecule 52: 40S ribosomal protein S3a

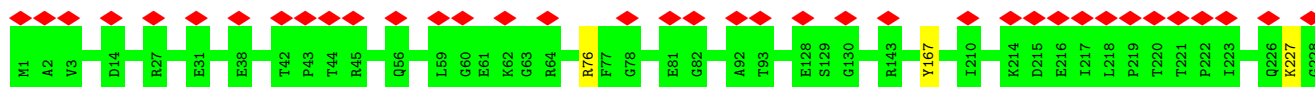




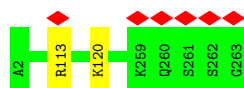
- Molecule 53: 40S ribosomal protein S2



- Molecule 54: 40S ribosomal protein S3



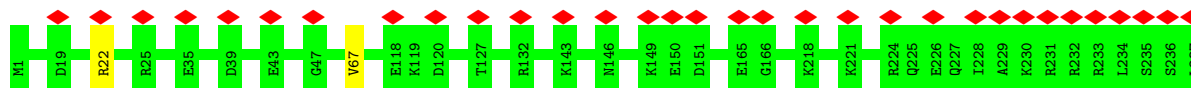
- Molecule 55: 40S ribosomal protein S4



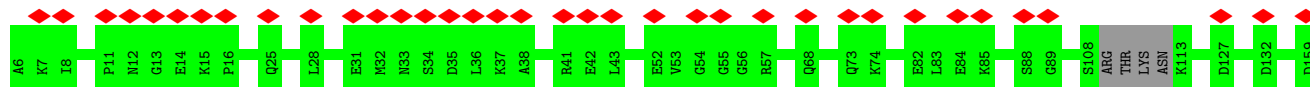
- Molecule 56: Ribosomal protein S5

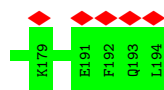


- Molecule 57: 40S ribosomal protein S6

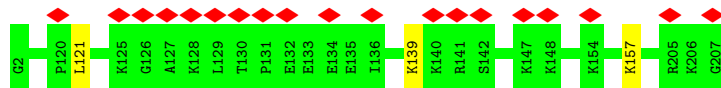


- Molecule 58: Small ribosomal subunit protein eS7

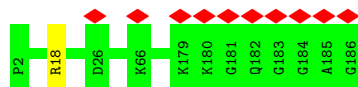




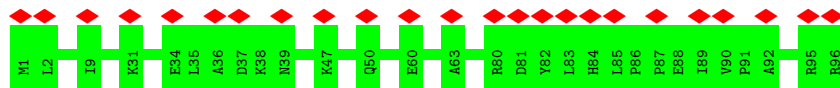
- Molecule 59: 40S ribosomal protein S8



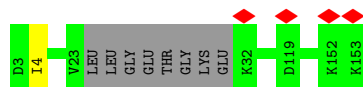
- Molecule 60: 40S ribosomal protein S9



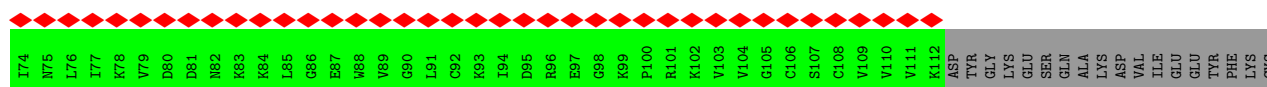
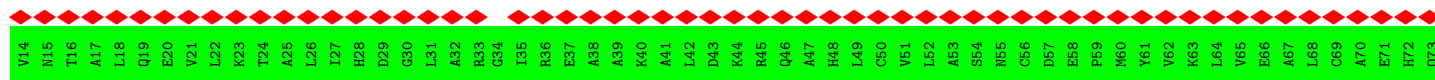
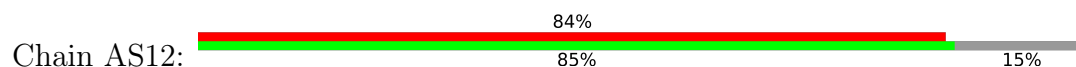
- Molecule 61: 40S ribosomal protein S10



- Molecule 62: 40S ribosomal protein S11

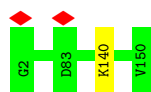


- Molecule 63: 40S ribosomal protein S12

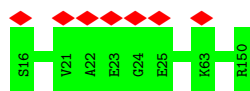


- Molecule 64: 40S ribosomal protein S13

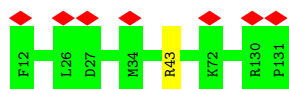




- Molecule 65: Small ribosomal subunit protein uS11



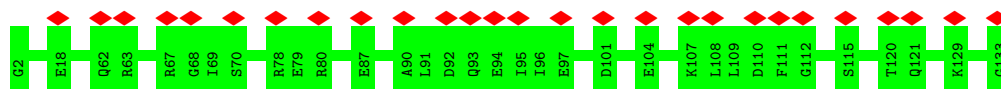
- Molecule 66: 40S ribosomal protein S15



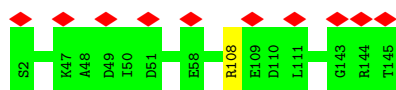
- Molecule 67: Small ribosomal subunit protein uS9



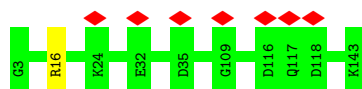
- Molecule 68: 40S ribosomal protein S17



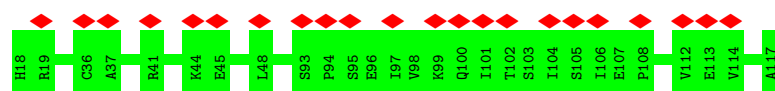
- Molecule 69: 40S ribosomal protein S18



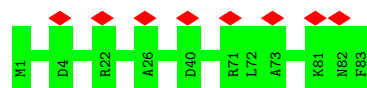
- Molecule 70: Small ribosomal subunit protein eS19



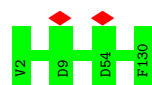
- Molecule 71: 40S ribosomal protein S20



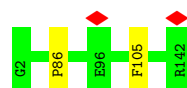
- Molecule 72: eS21



- Molecule 73: 40S ribosomal protein S15a



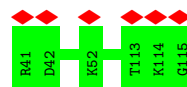
- Molecule 74: 40S ribosomal protein S23



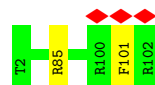
- Molecule 75: 40S ribosomal protein S24



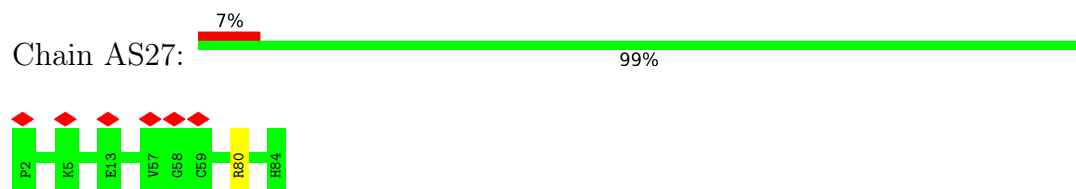
- Molecule 76: 40S ribosomal protein S25



- Molecule 77: eS26



- Molecule 78: 40S ribosomal protein S27

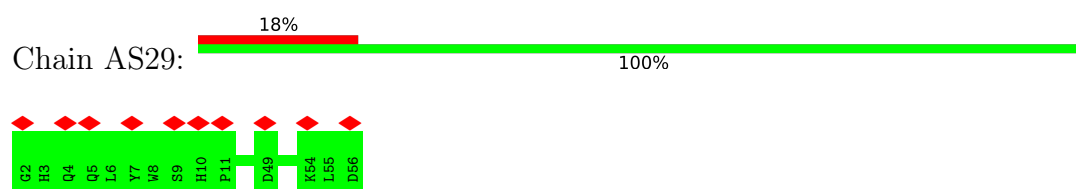


- Molecule 79: 40S ribosomal protein S28

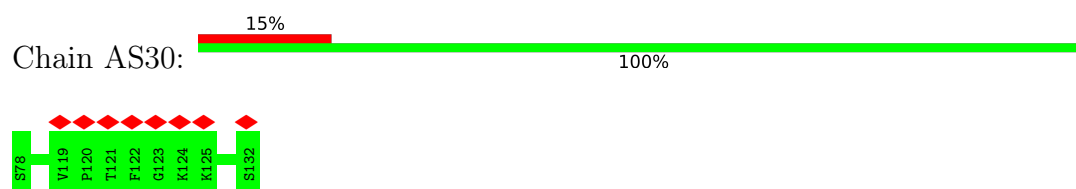


There are no outlier residues recorded for this chain.

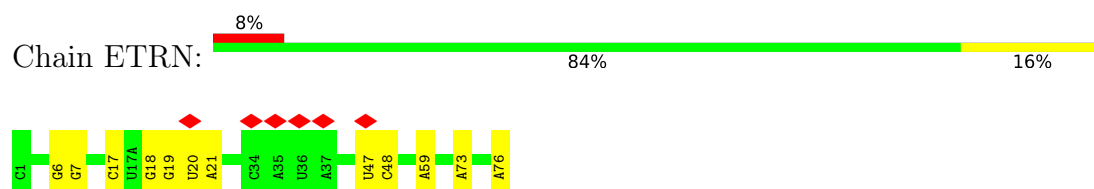
- Molecule 80: 40S ribosomal protein S29



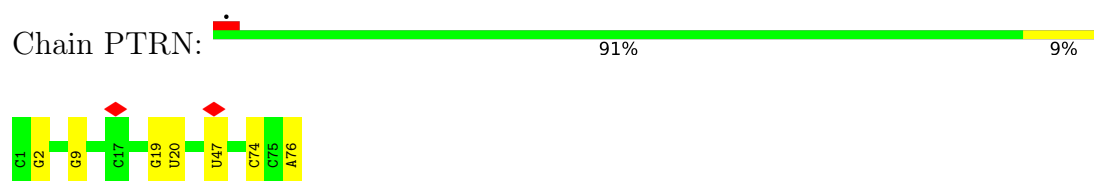
- Molecule 81: 40S ribosomal protein S30



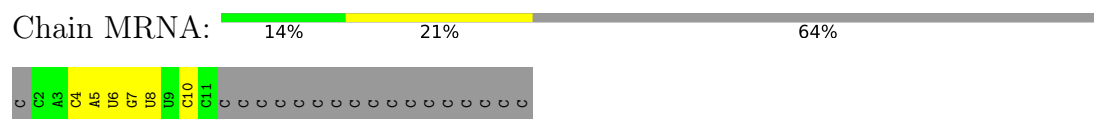
- Molecule 82: tRNA^{fMet}



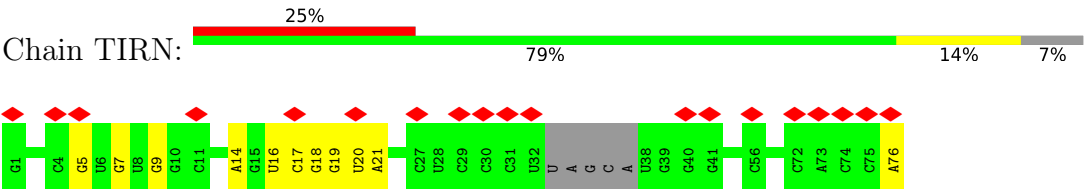
- Molecule 82: tRNA^{fMet}



- Molecule 83: mRNA



- Molecule 84: tRNA^{Ala}



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17593	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	25.784	Depositor
Minimum map value	-9.737	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.045	Depositor
Recommended contour level	3.2	Depositor
Map size ($\text{\AA}$)	528.96, 528.96, 528.96	wwPDB
Map dimensions	608, 608, 608	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.87000006, 0.87000006, 0.87000006	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	A18S	0.30	0/40369	0.31	0/62910
2	A28S	0.39	0/85337	0.33	0/133088
3	A58S	0.39	0/3581	0.31	0/5577
4	A5S	0.35	0/2858	0.27	0/4455
5	AL02	0.42	0/1936	0.56	0/2596
6	AL03	0.39	0/3240	0.54	0/4339
7	AL04	0.38	0/2937	0.55	2/3946 (0.1%)
8	AL05	0.30	0/2437	0.47	0/3264
9	AL06	0.29	0/1762	0.49	0/2362
10	AL07	0.35	0/1911	0.46	0/2549
11	AL08	0.34	0/1910	0.56	1/2569 (0.0%)
12	AL09	0.33	0/1535	0.53	0/2063
13	AL10	0.36	0/1702	0.47	0/2272
14	AL11	0.28	0/1384	0.50	0/1850
15	AL12	0.24	0/1174	0.59	0/1582
16	AL13	0.34	0/1733	0.58	1/2316 (0.0%)
17	AL14	0.31	0/1158	0.49	0/1547
18	AL15	0.44	0/1746	0.53	0/2338
19	AL16	0.38	0/1662	0.55	1/2222 (0.0%)
20	AL17	0.41	0/1268	0.55	1/1700 (0.1%)
21	AL18	0.38	0/1539	0.55	0/2054
22	AL19	0.36	0/1524	0.55	0/2013
23	AL20	0.37	0/1501	0.51	0/2012
24	AL21	0.35	0/1326	0.49	0/1770
25	AL22	0.26	0/823	0.56	0/1104
26	AL23	0.38	0/993	0.52	0/1332
27	AL24	0.36	0/541	0.60	0/720
28	AL25	0.34	0/984	0.48	0/1323
29	AL26	0.34	0/1132	0.53	0/1504
30	AL27	0.30	0/1130	0.50	0/1507
31	AL28	0.42	0/1191	0.51	0/1590
32	AL29	0.30	0/861	0.48	0/1138
33	AL30	0.33	0/771	0.42	0/1034
34	AL31	0.38	0/903	0.55	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AL32	0.41	0/1071	0.58	0/1429
36	AL33	0.40	0/895	0.60	1/1198 (0.1%)
37	AL34	0.35	0/916	0.51	0/1220
38	AL35	0.33	0/1021	0.51	0/1348
39	AL36	0.29	0/841	0.48	0/1112
40	AL37	0.43	0/720	0.59	0/952
41	AL38	0.29	0/575	0.49	0/761
42	AL39	0.42	0/459	0.53	0/608
43	AL40	0.32	0/435	0.52	0/575
44	AL41	0.31	0/240	0.54	0/305
45	AL42	0.36	0/864	0.54	0/1140
46	AL43	0.38	0/718	0.54	0/953
47	ALNW	0.36	0/1010	0.51	0/1354
48	ALP0	0.22	0/1530	0.52	0/2064
49	ANG	0.39	0/979	0.70	2/1322 (0.2%)
50	ARAC	0.21	0/2493	0.50	0/3394
51	AS00	0.28	0/1747	0.54	2/2374 (0.1%)
52	AS01	0.28	0/1756	0.55	0/2350
53	AS02	0.29	0/1753	0.53	0/2369
54	AS03	0.26	0/1796	0.53	0/2417
55	AS04	0.26	0/2117	0.51	0/2847
56	AS05	0.28	0/1492	0.53	0/2005
57	AS06	0.24	0/1946	0.50	1/2590 (0.0%)
58	AS07	0.25	0/1510	0.51	0/2022
59	AS08	0.29	0/1715	0.56	0/2287
60	AS09	0.25	0/1550	0.52	0/2069
61	AS10	0.24	0/834	0.52	0/1125
62	AS11	0.31	0/1195	0.47	0/1597
63	AS12	0.26	0/765	0.59	0/1029
64	AS13	0.29	0/1226	0.48	0/1649
65	AS14	0.30	0/1017	0.50	0/1365
66	AS15	0.22	0/1017	0.53	0/1358
67	AS16	0.26	0/1146	0.51	0/1534
68	AS17	0.25	0/1082	0.57	0/1452
69	AS18	0.26	0/1208	0.56	0/1618
70	AS19	0.25	0/1115	0.50	0/1493
71	AS20	0.24	0/805	0.54	0/1081
72	AS21	0.24	0/643	0.46	0/860
73	AS22	0.31	0/1051	0.49	0/1406
74	AS23	0.33	0/1116	0.55	0/1490
75	AS24	0.22	0/1028	0.44	0/1366
76	AS25	0.24	0/604	0.54	0/810
77	AS26	0.32	0/828	0.66	1/1109 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	AS27	0.23	0/665	0.52	0/891
79	AS28	0.25	0/490	0.53	0/656
80	AS29	0.24	0/470	0.49	0/623
81	AS30	0.24	0/447	0.51	0/587
82	ETRN	0.20	0/1832	0.30	0/2855
82	PTRN	0.25	0/1832	0.29	0/2855
83	MRNA	0.26	0/229	0.49	0/353
84	TIRN	0.14	0/1688	0.26	0/2628
All	All	0.34	0/233341	0.41	13/342717 (0.0%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AL13	90	VAL	N-CA-C	-6.62	106.06	112.29
7	AL04	49	ARG	CA-C-N	6.34	130.32	120.68
7	AL04	49	ARG	C-N-CA	6.34	130.32	120.68
19	AL16	145	VAL	N-CA-C	-6.30	107.72	113.71
57	AS06	67	VAL	N-CA-C	-6.16	107.25	113.47
51	AS00	43	SER	CA-C-N	6.09	133.17	121.54
51	AS00	43	SER	C-N-CA	6.09	133.17	121.54
11	AL08	200	VAL	N-CA-C	-6.00	106.65	111.81
49	ANG	65	HIS	CA-C-N	5.95	132.90	121.54
49	ANG	65	HIS	C-N-CA	5.95	132.90	121.54
36	AL33	18	LEU	N-CA-C	-5.10	108.09	114.56
20	AL17	92	LEU	N-CA-C	-5.07	107.64	113.88
77	AS26	101	PHE	N-CA-C	-5.06	108.13	114.56

There are no chirality outliers.

There are no planarity outliers.

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	A18S	36103	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A28S	76286	0	0	0	0
3	A58S	3208	0	0	0	0
4	A5S	2558	0	1296	6	0
5	AL02	1898	0	0	0	0
6	AL03	3172	0	0	0	0
7	AL04	2883	0	0	0	0
8	AL05	2391	0	0	0	0
9	AL06	1729	0	0	0	0
10	AL07	1875	0	0	0	0
11	AL08	1879	0	0	0	0
12	AL09	1516	0	0	0	0
13	AL10	1664	0	0	0	0
14	AL11	1361	0	0	0	0
15	AL12	1160	0	0	0	0
16	AL13	1702	0	0	0	0
17	AL14	1137	0	0	0	0
18	AL15	1701	0	0	0	0
19	AL16	1630	0	0	0	0
20	AL17	1242	0	0	0	0
21	AL18	1515	0	0	0	0
22	AL19	1508	0	0	0	0
23	AL20	1462	0	0	0	0
24	AL21	1298	0	0	0	0
25	AL22	809	0	0	0	0
26	AL23	979	0	0	0	0
27	AL24	528	0	0	0	0
28	AL25	967	0	0	0	0
29	AL26	1115	0	0	0	0
30	AL27	1107	0	0	0	0
31	AL28	1162	0	0	0	0
32	AL29	848	0	0	0	0
33	AL30	761	0	0	0	0
34	AL31	888	0	0	0	0
35	AL32	1053	0	0	0	0
36	AL33	876	0	0	0	0
37	AL34	906	0	0	0	0
38	AL35	1013	0	0	0	0
39	AL36	830	0	0	0	0
40	AL37	705	0	0	0	0
41	AL38	569	0	0	0	0
42	AL39	447	0	0	0	0
43	AL40	429	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	AL41	239	0	0	0	0
45	AL42	851	0	0	0	0
46	AL43	708	0	0	0	0
47	ALNW	994	0	0	0	0
48	ALP0	1507	0	0	0	0
49	ANG	955	0	922	8	0
50	ARAC	2436	0	0	0	0
51	AS00	1710	0	0	0	0
52	AS01	1729	0	0	0	0
53	AS02	1716	0	0	0	0
54	AS03	1768	0	0	0	0
55	AS04	2075	0	0	0	0
56	AS05	1471	0	0	0	0
57	AS06	1923	0	0	0	0
58	AS07	1488	0	0	0	0
59	AS08	1686	0	0	0	0
60	AS09	1525	0	0	0	0
61	AS10	810	0	0	0	0
62	AS11	1175	0	0	0	0
63	AS12	758	0	0	0	0
64	AS13	1202	0	0	0	0
65	AS14	1004	0	0	0	0
66	AS15	997	0	0	0	0
67	AS16	1128	0	0	0	0
68	AS17	1068	0	0	0	0
69	AS18	1190	0	0	0	0
70	AS19	1097	0	0	0	0
71	AS20	795	0	0	0	0
72	AS21	636	0	0	0	0
73	AS22	1034	0	0	0	0
74	AS23	1098	0	0	0	0
75	AS24	1011	0	0	0	0
76	AS25	598	0	0	0	0
77	AS26	814	0	0	0	0
78	AS27	651	0	0	0	0
79	AS28	488	0	0	0	0
80	AS29	459	0	0	0	0
81	AS30	443	0	0	0	0
82	ETRN	1640	0	0	0	0
82	PTRN	1640	0	0	0	0
83	MRNA	207	0	0	0	0
84	TIRN	1514	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	217108	0	2218	14	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 7.

All (14) 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)
49:ANG:58:GLU:HG2	49:ANG:60:LYS:H	1.64	0.62
4:A5S:23:A:N3	4:A5S:118:C:O2'	2.37	0.57
49:ANG:41:ASP:OD2	49:ANG:41:ASP:N	2.39	0.55
49:ANG:21:ARG:HD2	49:ANG:98:ALA:HB2	1.89	0.54
4:A5S:35:U:O2	4:A5S:45:U:O2'	2.29	0.51
4:A5S:75:G:N2	4:A5S:100:A:OP2	2.35	0.50
49:ANG:21:ARG:HH12	49:ANG:77:GLN:HB3	1.76	0.49
49:ANG:27:GLU:OE2	49:ANG:94:TYR:N	2.45	0.49
4:A5S:4:U:H2'	4:A5S:5:A:H8	1.82	0.45
49:ANG:21:ARG:NH2	49:ANG:79:THR:OG1	2.50	0.45
4:A5S:38:U:N3	4:A5S:41:G:OP2	2.39	0.43
49:ANG:69:LEU:HD23	49:ANG:106:ALA:HB2	2.01	0.42
49:ANG:57:CYS:HA	49:ANG:70:ARG:HD3	2.03	0.40
4:A5S:58:A:H2'	4:A5S:59:G:C8	2.56	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	
5	AL02	246/248 (99%)	225 (92%)	21 (8%)	0	100	100
6	AL03	392/394 (100%)	373 (95%)	19 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	AL04	360/362 (99%)	341 (95%)	19 (5%)	0	100	100
8	AL05	291/293 (99%)	276 (95%)	15 (5%)	0	100	100
9	AL06	208/251 (83%)	199 (96%)	9 (4%)	0	100	100
10	AL07	223/225 (99%)	217 (97%)	6 (3%)	0	100	100
11	AL08	229/240 (95%)	220 (96%)	9 (4%)	0	100	100
12	AL09	188/190 (99%)	178 (95%)	10 (5%)	0	100	100
13	AL10	201/213 (94%)	191 (95%)	10 (5%)	0	100	100
14	AL11	168/170 (99%)	159 (95%)	9 (5%)	0	100	100
15	AL12	151/153 (99%)	139 (92%)	12 (8%)	0	100	100
16	AL13	208/210 (99%)	194 (93%)	12 (6%)	2 (1%)	12	41
17	AL14	136/138 (99%)	126 (93%)	10 (7%)	0	100	100
18	AL15	201/203 (99%)	188 (94%)	13 (6%)	0	100	100
19	AL16	197/199 (99%)	190 (96%)	7 (4%)	0	100	100
20	AL17	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
21	AL18	185/187 (99%)	172 (93%)	13 (7%)	0	100	100
22	AL19	178/180 (99%)	174 (98%)	4 (2%)	0	100	100
23	AL20	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
24	AL21	157/159 (99%)	146 (93%)	11 (7%)	0	100	100
25	AL22	97/99 (98%)	91 (94%)	6 (6%)	0	100	100
26	AL23	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
27	AL24	61/121 (50%)	58 (95%)	3 (5%)	0	100	100
28	AL25	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
29	AL26	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
30	AL27	133/135 (98%)	125 (94%)	8 (6%)	0	100	100
31	AL28	145/147 (99%)	134 (92%)	10 (7%)	1 (1%)	18	49
32	AL29	100/245 (41%)	94 (94%)	6 (6%)	0	100	100
33	AL30	96/98 (98%)	96 (100%)	0	0	100	100
34	AL31	105/107 (98%)	96 (91%)	9 (9%)	0	100	100
35	AL32	126/128 (98%)	118 (94%)	8 (6%)	0	100	100
36	AL33	107/109 (98%)	99 (92%)	8 (8%)	0	100	100
37	AL34	112/114 (98%)	109 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	AL35	120/122 (98%)	116 (97%)	3 (2%)	1 (1%)	16	47
39	AL36	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
40	AL37	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
41	AL38	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
42	AL39	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
43	AL40	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
44	AL41	23/25 (92%)	23 (100%)	0	0	100	100
45	AL42	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
46	AL43	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
47	ALNW	122/124 (98%)	116 (95%)	6 (5%)	0	100	100
48	ALP0	194/196 (99%)	182 (94%)	12 (6%)	0	100	100
49	ANG	118/147 (80%)	108 (92%)	9 (8%)	1 (1%)	16	47
50	ARAC	311/313 (99%)	288 (93%)	23 (7%)	0	100	100
51	AS00	215/217 (99%)	194 (90%)	21 (10%)	0	100	100
52	AS01	211/213 (99%)	193 (92%)	18 (8%)	0	100	100
53	AS02	219/221 (99%)	213 (97%)	6 (3%)	0	100	100
54	AS03	226/228 (99%)	218 (96%)	8 (4%)	0	100	100
55	AS04	260/262 (99%)	243 (94%)	17 (6%)	0	100	100
56	AS05	181/191 (95%)	168 (93%)	13 (7%)	0	100	100
57	AS06	235/237 (99%)	223 (95%)	12 (5%)	0	100	100
58	AS07	181/189 (96%)	176 (97%)	5 (3%)	0	100	100
59	AS08	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
60	AS09	183/185 (99%)	176 (96%)	7 (4%)	0	100	100
61	AS10	94/96 (98%)	88 (94%)	6 (6%)	0	100	100
62	AS11	139/151 (92%)	131 (94%)	8 (6%)	0	100	100
63	AS12	97/117 (83%)	85 (88%)	12 (12%)	0	100	100
64	AS13	147/149 (99%)	140 (95%)	7 (5%)	0	100	100
65	AS14	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
66	AS15	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
67	AS16	140/142 (99%)	131 (94%)	9 (6%)	0	100	100
68	AS17	130/132 (98%)	120 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	AS18	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
70	AS19	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
71	AS20	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
72	AS21	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
73	AS22	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
74	AS23	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	18	49
75	AS24	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
76	AS25	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
77	AS26	99/101 (98%)	92 (93%)	7 (7%)	0	100	100
78	AS27	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
79	AS28	60/62 (97%)	56 (93%)	4 (7%)	0	100	100
80	AS29	53/55 (96%)	49 (92%)	4 (8%)	0	100	100
81	AS30	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
All	All	11511/11995 (96%)	10881 (94%)	624 (5%)	6 (0%)	49	78

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
49	ANG	66	ARG
16	AL13	64	VAL
38	AL35	89	ARG
31	AL28	40	HIS
16	AL13	5	ARG
74	AS23	86	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	
5	AL02	190/190 (100%)	189 (100%)	1 (0%)	81	85
6	AL03	342/342 (100%)	340 (99%)	2 (1%)	78	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	AL04	302/302 (100%)	301 (100%)	1 (0%)	86	87
8	AL05	247/247 (100%)	245 (99%)	2 (1%)	73	81
9	AL06	190/223 (85%)	189 (100%)	1 (0%)	81	85
10	AL07	196/196 (100%)	196 (100%)	0	100	100
11	AL08	200/205 (98%)	197 (98%)	3 (2%)	57	75
12	AL09	169/169 (100%)	169 (100%)	0	100	100
13	AL10	175/180 (97%)	175 (100%)	0	100	100
14	AL11	143/143 (100%)	143 (100%)	0	100	100
15	AL12	126/126 (100%)	125 (99%)	1 (1%)	73	81
16	AL13	175/175 (100%)	175 (100%)	0	100	100
17	AL14	117/117 (100%)	116 (99%)	1 (1%)	70	80
18	AL15	171/171 (100%)	171 (100%)	0	100	100
19	AL16	171/171 (100%)	171 (100%)	0	100	100
20	AL17	134/134 (100%)	134 (100%)	0	100	100
21	AL18	164/164 (100%)	164 (100%)	0	100	100
22	AL19	159/159 (100%)	157 (99%)	2 (1%)	61	77
23	AL20	157/157 (100%)	157 (100%)	0	100	100
24	AL21	139/139 (100%)	138 (99%)	1 (1%)	76	82
25	AL22	89/89 (100%)	88 (99%)	1 (1%)	65	78
26	AL23	101/101 (100%)	99 (98%)	2 (2%)	48	72
27	AL24	55/100 (55%)	55 (100%)	0	100	100
28	AL25	106/106 (100%)	104 (98%)	2 (2%)	50	73
29	AL26	124/124 (100%)	123 (99%)	1 (1%)	73	81
30	AL27	117/117 (100%)	115 (98%)	2 (2%)	53	74
31	AL28	119/119 (100%)	118 (99%)	1 (1%)	73	81
32	AL29	84/184 (46%)	82 (98%)	2 (2%)	43	69
33	AL30	84/84 (100%)	84 (100%)	0	100	100
34	AL31	98/98 (100%)	98 (100%)	0	100	100
35	AL32	114/114 (100%)	114 (100%)	0	100	100
36	AL33	88/88 (100%)	88 (100%)	0	100	100
37	AL34	98/98 (100%)	97 (99%)	1 (1%)	68	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	AL35	109/109 (100%)	109 (100%)	0	100	100
39	AL36	86/86 (100%)	86 (100%)	0	100	100
40	AL37	73/73 (100%)	73 (100%)	0	100	100
41	AL38	64/64 (100%)	64 (100%)	0	100	100
42	AL39	47/47 (100%)	46 (98%)	1 (2%)	47	71
43	AL40	48/48 (100%)	48 (100%)	0	100	100
44	AL41	24/24 (100%)	24 (100%)	0	100	100
45	AL42	92/92 (100%)	92 (100%)	0	100	100
46	AL43	74/74 (100%)	73 (99%)	1 (1%)	59	76
47	ALNW	108/108 (100%)	106 (98%)	2 (2%)	50	73
48	ALP0	164/164 (100%)	164 (100%)	0	100	100
49	ANG	105/129 (81%)	103 (98%)	2 (2%)	50	73
50	ARAC	272/272 (100%)	271 (100%)	1 (0%)	84	86
51	AS00	180/181 (99%)	180 (100%)	0	100	100
52	AS01	194/194 (100%)	194 (100%)	0	100	100
53	AS02	187/187 (100%)	185 (99%)	2 (1%)	65	78
54	AS03	190/190 (100%)	187 (98%)	3 (2%)	55	75
55	AS04	224/224 (100%)	222 (99%)	2 (1%)	70	80
56	AS05	158/161 (98%)	157 (99%)	1 (1%)	78	83
57	AS06	207/207 (100%)	206 (100%)	1 (0%)	81	85
58	AS07	165/169 (98%)	165 (100%)	0	100	100
59	AS08	178/178 (100%)	175 (98%)	3 (2%)	53	74
60	AS09	161/161 (100%)	160 (99%)	1 (1%)	78	83
61	AS10	87/87 (100%)	87 (100%)	0	100	100
62	AS11	130/136 (96%)	129 (99%)	1 (1%)	73	81
63	AS12	83/99 (84%)	83 (100%)	0	100	100
64	AS13	130/130 (100%)	129 (99%)	1 (1%)	73	81
65	AS14	104/105 (99%)	104 (100%)	0	100	100
66	AS15	109/109 (100%)	108 (99%)	1 (1%)	70	80
67	AS16	117/117 (100%)	116 (99%)	1 (1%)	70	80
68	AS17	119/119 (100%)	119 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	AS18	125/125 (100%)	124 (99%)	1 (1%)	73	81
70	AS19	111/111 (100%)	110 (99%)	1 (1%)	70	80
71	AS20	92/92 (100%)	92 (100%)	0	100	100
72	AS21	67/67 (100%)	67 (100%)	0	100	100
73	AS22	112/112 (100%)	112 (100%)	0	100	100
74	AS23	113/113 (100%)	112 (99%)	1 (1%)	70	80
75	AS24	107/107 (100%)	106 (99%)	1 (1%)	70	80
76	AS25	66/66 (100%)	66 (100%)	0	100	100
77	AS26	88/88 (100%)	87 (99%)	1 (1%)	65	78
78	AS27	75/75 (100%)	74 (99%)	1 (1%)	61	77
79	AS28	55/55 (100%)	55 (100%)	0	100	100
80	AS29	48/48 (100%)	48 (100%)	0	100	100
81	AS30	46/46 (100%)	46 (100%)	0	100	100
All	All	10038/10281 (98%)	9981 (99%)	57 (1%)	76	83

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	AL02	242	ARG
6	AL03	207	VAL
6	AL03	262	VAL
7	AL04	188	ARG
8	AL05	126	THR
8	AL05	235	MET
9	AL06	58	ARG
11	AL08	164	LYS
11	AL08	228	ARG
11	AL08	288	ARG
15	AL12	67	ARG
17	AL14	137	LYS
22	AL19	16	ARG
22	AL19	74	ARG
24	AL21	63	ARG
25	AL22	83	LEU
26	AL23	18	LEU
26	AL23	48	ARG
28	AL25	39	LYS

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Mol	Chain	Res	Type
28	AL25	95	THR
29	AL26	2	LYS
30	AL27	67	LYS
30	AL27	78	ASN
31	AL28	87	ARG
32	AL29	28	ARG
32	AL29	63	LYS
37	AL34	54	ARG
42	AL39	46	ARG
46	AL43	17	ARG
47	ALNW	71	ARG
47	ALNW	107	ARG
49	ANG	67	GLU
49	ANG	68	ASN
50	ARAC	264	LYS
53	AS02	121	ARG
53	AS02	275	LYS
54	AS03	76	ARG
54	AS03	167	TYR
54	AS03	227	LYS
55	AS04	113	ARG
55	AS04	120	LYS
56	AS05	122	ARG
57	AS06	22	ARG
59	AS08	121	LEU
59	AS08	139	LYS
59	AS08	157	LYS
60	AS09	18	ARG
62	AS11	4	ILE
64	AS13	140	LYS
66	AS15	43	ARG
67	AS16	67	ASP
69	AS18	108	ARG
70	AS19	16	ARG
74	AS23	105	PHE
75	AS24	51	THR
77	AS26	85	ARG
78	AS27	80	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	A18S	1679/1869 (89%)	322 (19%)	11 (0%)
2	A28S	3534/3601 (98%)	681 (19%)	33 (0%)
3	A58S	149/156 (95%)	21 (14%)	1 (0%)
4	A5S	119/120 (99%)	11 (9%)	0
82	ETRN	76/77 (98%)	12 (15%)	0
82	PTRN	76/77 (98%)	7 (9%)	0
83	MRNA	9/28 (32%)	5 (55%)	1 (11%)
84	TIRN	69/76 (90%)	11 (15%)	0
All	All	5711/6004 (95%)	1070 (18%)	46 (0%)

All (1070) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A18S	2	A
1	A18S	3	C
1	A18S	17	C
1	A18S	25	A
1	A18S	26	U
1	A18S	33	G
1	A18S	41	G
1	A18S	44	U
1	A18S	45	A
1	A18S	46	A
1	A18S	55	U
1	A18S	56	G
1	A18S	58	C
1	A18S	62	G
1	A18S	67	C
1	A18S	68	A
1	A18S	71	G
1	A18S	75	G
1	A18S	77	A
1	A18S	79	A
1	A18S	103	A
1	A18S	111	A
1	A18S	113	G
1	A18S	115	U
1	A18S	116	U
1	A18S	124	U
1	A18S	126	G
1	A18S	127	C

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Mol	Chain	Res	Type
1	A18S	128	U
1	A18S	130	G
1	A18S	142	C
1	A18S	143	U
1	A18S	147	A
1	A18S	155	G
1	A18S	162	C
1	A18S	163	U
1	A18S	167	G
1	A18S	170	A
1	A18S	182	C
1	A18S	183	G
1	A18S	184	G
1	A18S	192	C
1	A18S	206	G
1	A18S	209	A
1	A18S	224	A
1	A18S	291	G
1	A18S	292	A
1	A18S	306	C
1	A18S	307	G
1	A18S	308	G
1	A18S	309	G
1	A18S	312	G
1	A18S	314	U
1	A18S	318	A
1	A18S	319	C
1	A18S	320	G
1	A18S	332	G
1	A18S	339	A
1	A18S	347	G
1	A18S	350	C
1	A18S	351	G
1	A18S	360	A
1	A18S	362	C
1	A18S	364	A
1	A18S	368	U
1	A18S	369	C
1	A18S	370	G
1	A18S	385	G
1	A18S	386	C
1	A18S	398	A

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Mol	Chain	Res	Type
1	A18S	400	C
1	A18S	407	G
1	A18S	408	A
1	A18S	409	C
1	A18S	418	A
1	A18S	435	A
1	A18S	441	C
1	A18S	448	A
1	A18S	449	A
1	A18S	450	C
1	A18S	455	A
1	A18S	464	A
1	A18S	465	A
1	A18S	466	G
1	A18S	472	C
1	A18S	473	A
1	A18S	474	G
1	A18S	482	G
1	A18S	487	U
1	A18S	492	C
1	A18S	493	A
1	A18S	507	G
1	A18S	516	A
1	A18S	525	A
1	A18S	532	C
1	A18S	547	G
1	A18S	548	C
1	A18S	549	C
1	A18S	550	C
1	A18S	551	U
1	A18S	554	A
1	A18S	555	A
1	A18S	556	U
1	A18S	559	G
1	A18S	560	A
1	A18S	562	U
1	A18S	563	G
1	A18S	564	A
1	A18S	568	C
1	A18S	576	A
1	A18S	583	A
1	A18S	587	A

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Mol	Chain	Res	Type
1	A18S	588	G
1	A18S	590	A
1	A18S	591	U
1	A18S	593	C
1	A18S	603	C
1	A18S	606	G
1	A18S	608	C
1	A18S	614	C
1	A18S	626	G
1	A18S	627	U
1	A18S	628	A
1	A18S	629	A
1	A18S	631	U
1	A18S	643	A
1	A18S	644	G
1	A18S	655	A
1	A18S	660	C
1	A18S	668	A
1	A18S	669	A
1	A18S	671	A
1	A18S	672	A
1	A18S	673	G
1	A18S	688	U
1	A18S	752	G
1	A18S	753	C
1	A18S	754	G
1	A18S	799	U
1	A18S	810	A
1	A18S	811	A
1	A18S	821	G
1	A18S	822	U
1	A18S	830	A
1	A18S	834	C
1	A18S	847	A
1	A18S	852	G
1	A18S	853	C
1	A18S	868	G
1	A18S	870	A
1	A18S	871	U
1	A18S	872	A
1	A18S	874	G
1	A18S	878	G

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Mol	Chain	Res	Type
1	A18S	879	C
1	A18S	887	U
1	A18S	888	U
1	A18S	890	U
1	A18S	894	G
1	A18S	901	G
1	A18S	913	A
1	A18S	914	U
1	A18S	919	A
1	A18S	920	A
1	A18S	922	A
1	A18S	933	G
1	A18S	934	G
1	A18S	943	U
1	A18S	970	G
1	A18S	971	G
1	A18S	978	G
1	A18S	990	A
1	A18S	992	A
1	A18S	999	G
1	A18S	1017	U
1	A18S	1023	A
1	A18S	1026	C
1	A18S	1041	G
1	A18S	1060	A
1	A18S	1078	C
1	A18S	1082	A
1	A18S	1083	A
1	A18S	1085	C
1	A18S	1097	G
1	A18S	1109	C
1	A18S	1115	U
1	A18S	1116	C
1	A18S	1117	C
1	A18S	1118	C
1	A18S	1121	G
1	A18S	1131	G
1	A18S	1138	C
1	A18S	1139	C
1	A18S	1149	A
1	A18S	1150	A
1	A18S	1153	C

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Mol	Chain	Res	Type
1	A18S	1154	U
1	A18S	1161	U
1	A18S	1166	G
1	A18S	1195	A
1	A18S	1207	G
1	A18S	1215	C
1	A18S	1224	G
1	A18S	1242	U
1	A18S	1251	A
1	A18S	1253	A
1	A18S	1256	G
1	A18S	1257	G
1	A18S	1259	A
1	A18S	1269	G
1	A18S	1274	G
1	A18S	1275	G
1	A18S	1276	A
1	A18S	1281	G
1	A18S	1284	A
1	A18S	1285	G
1	A18S	1286	G
1	A18S	1289	U
1	A18S	1298	G
1	A18S	1299	A
1	A18S	1300	U
1	A18S	1301	A
1	A18S	1302	G
1	A18S	1303	C
1	A18S	1308	U
1	A18S	1316	C
1	A18S	1333	U
1	A18S	1341	C
1	A18S	1342	U
1	A18S	1364	U
1	A18S	1371	U
1	A18S	1372	U
1	A18S	1378	A
1	A18S	1381	G
1	A18S	1395	C
1	A18S	1396	A
1	A18S	1397	U
1	A18S	1401	A

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Mol	Chain	Res	Type
1	A18S	1402	A
1	A18S	1404	U
1	A18S	1412	C
1	A18S	1431	G
1	A18S	1454	A
1	A18S	1455	A
1	A18S	1462	U
1	A18S	1463	U
1	A18S	1466	G
1	A18S	1476	A
1	A18S	1477	U
1	A18S	1487	A
1	A18S	1489	A
1	A18S	1490	G
1	A18S	1494	U
1	A18S	1495	G
1	A18S	1497	G
1	A18S	1498	A
1	A18S	1507	G
1	A18S	1509	U
1	A18S	1510	G
1	A18S	1520	G
1	A18S	1521	C
1	A18S	1522	A
1	A18S	1523	C
1	A18S	1531	A
1	A18S	1533	A
1	A18S	1548	G
1	A18S	1552	G
1	A18S	1553	C
1	A18S	1557	C
1	A18S	1570	G
1	A18S	1574	C
1	A18S	1579	A
1	A18S	1580	A
1	A18S	1584	G
1	A18S	1585	U
1	A18S	1587	G
1	A18S	1588	A
1	A18S	1589	A
1	A18S	1599	U
1	A18S	1601	A

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Mol	Chain	Res	Type
1	A18S	1603	G
1	A18S	1604	G
1	A18S	1614	A
1	A18S	1621	U
1	A18S	1623	A
1	A18S	1625	U
1	A18S	1648	G
1	A18S	1654	G
1	A18S	1665	G
1	A18S	1671	G
1	A18S	1680	G
1	A18S	1683	C
1	A18S	1695	A
1	A18S	1698	C
1	A18S	1699	A
1	A18S	1703	C
1	A18S	1721	U
1	A18S	1722	G
1	A18S	1729	U
1	A18S	1732	G
1	A18S	1744	G
1	A18S	1779	G
1	A18S	1783	C
1	A18S	1800	A
1	A18S	1824	A
1	A18S	1825	A
1	A18S	1829	G
1	A18S	1831	A
1	A18S	1835	A
1	A18S	1836	G
1	A18S	1838	U
1	A18S	1846	G
1	A18S	1849	G
1	A18S	1851	A
1	A18S	1861	G
1	A18S	1862	G
1	A18S	1863	A
1	A18S	1864	U
1	A18S	1865	C
1	A18S	1866	A
1	A18S	1867	U
1	A18S	1869	A

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Mol	Chain	Res	Type
2	A28S	5	A
2	A28S	8	U
2	A28S	12	A
2	A28S	13	U
2	A28S	25	A
2	A28S	39	A
2	A28S	42	A
2	A28S	56	A
2	A28S	58	G
2	A28S	59	A
2	A28S	64	A
2	A28S	65	A
2	A28S	70	A
2	A28S	72	C
2	A28S	73	A
2	A28S	91	G
2	A28S	98	A
2	A28S	108	A
2	A28S	109	G
2	A28S	110	C
2	A28S	116	G
2	A28S	118	C
2	A28S	119	G
2	A28S	120	A
2	A28S	126	C
2	A28S	132	G
2	A28S	133	C
2	A28S	134	G
2	A28S	135	G
2	A28S	136	C
2	A28S	144	G
2	A28S	159	C
2	A28S	170	C
2	A28S	171	U
2	A28S	172	C
2	A28S	175	C
2	A28S	190	G
2	A28S	200	U
2	A28S	201	C
2	A28S	202	C
2	A28S	203	U
2	A28S	205	C

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Mol	Chain	Res	Type
2	A28S	209	U
2	A28S	216	C
2	A28S	218	A
2	A28S	219	G
2	A28S	224	U
2	A28S	225	G
2	A28S	233	U
2	A28S	234	G
2	A28S	256	G
2	A28S	265	C
2	A28S	266	C
2	A28S	276	C
2	A28S	280	G
2	A28S	297	U
2	A28S	306	A
2	A28S	315	G
2	A28S	316	U
2	A28S	323	C
2	A28S	326	C
2	A28S	334	A
2	A28S	340	C
2	A28S	350	C
2	A28S	387	G
2	A28S	406	C
2	A28S	407	A
2	A28S	410	A
2	A28S	412	G
2	A28S	431	G
2	A28S	432	U
2	A28S	440	U
2	A28S	446	C
2	A28S	449	C
2	A28S	452	A
2	A28S	453	G
2	A28S	454	U
2	A28S	455	C
2	A28S	457	G
2	A28S	464	G
2	A28S	467	U
2	A28S	468	U
2	A28S	481	G
2	A28S	481(A)	C

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Mol	Chain	Res	Type
2	A28S	482	G
2	A28S	483	G
2	A28S	485	C
2	A28S	486	C
2	A28S	492	U
2	A28S	493	G
2	A28S	498	C
2	A28S	499	G
2	A28S	505	G
2	A28S	510	U
2	A28S	658	C
2	A28S	661	C
2	A28S	662	C
2	A28S	667	A
2	A28S	669	C
2	A28S	683	C
2	A28S	685	C
2	A28S	686	A
2	A28S	687	U
2	A28S	696	C
2	A28S	697	G
2	A28S	704	C
2	A28S	705	G
2	A28S	708	G
2	A28S	730	G
2	A28S	731	G
2	A28S	738	C
2	A28S	738(A)	C
2	A28S	739	G
2	A28S	747	A
2	A28S	749	G
2	A28S	758	G
2	A28S	759	G
2	A28S	912	G
2	A28S	913	U
2	A28S	914	U
2	A28S	915	A
2	A28S	917	A
2	A28S	918	G
2	A28S	923	C
2	A28S	925	C
2	A28S	926	G

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Mol	Chain	Res	Type
2	A28S	929	A
2	A28S	931	C
2	A28S	932	A
2	A28S	933	G
2	A28S	934	C
2	A28S	935	A
2	A28S	935(A)	G
2	A28S	936	C
2	A28S	938	C
2	A28S	939	G
2	A28S	941	C
2	A28S	943	A
2	A28S	944	A
2	A28S	945	U
2	A28S	956	A
2	A28S	959	G
2	A28S	960	A
2	A28S	961	G
2	A28S	962	C
2	A28S	965	G
2	A28S	966	A
2	A28S	967	C
2	A28S	969	C
2	A28S	972	C
2	A28S	979	C
2	A28S	983	C
2	A28S	1070	G
2	A28S	1072	C
2	A28S	1073	G
2	A28S	1078	A
2	A28S	1079	C
2	A28S	1082	C
2	A28S	1179	U
2	A28S	1193	C
2	A28S	1195	G
2	A28S	1210	C
2	A28S	1211	G
2	A28S	1212	G
2	A28S	1214	C
2	A28S	1215	C
2	A28S	1234	G
2	A28S	1235	G

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Mol	Chain	Res	Type
2	A28S	1236	C
2	A28S	1237	C
2	A28S	1238	A
2	A28S	1239	C
2	A28S	1277	G
2	A28S	1284	G
2	A28S	1287	G
2	A28S	1292	C
2	A28S	1296	G
2	A28S	1301	C
2	A28S	1303	A
2	A28S	1326	A
2	A28S	1330	A
2	A28S	1354	A
2	A28S	1358	G
2	A28S	1359	G
2	A28S	1370	G
2	A28S	1371	A
2	A28S	1377	G
2	A28S	1379	C
2	A28S	1380	G
2	A28S	1387	A
2	A28S	1394	G
2	A28S	1397	A
2	A28S	1398	A
2	A28S	1399	G
2	A28S	1400	G
2	A28S	1419	G
2	A28S	1420	A
2	A28S	1421	G
2	A28S	1433	A
2	A28S	1437	C
2	A28S	1438	U
2	A28S	1441	C
2	A28S	1443	A
2	A28S	1445	U
2	A28S	1446	C
2	A28S	1456	C
2	A28S	1457	G
2	A28S	1465	G
2	A28S	1481	C
2	A28S	1482	G

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Mol	Chain	Res	Type
2	A28S	1483	C
2	A28S	1484	G
2	A28S	1497	A
2	A28S	1498	G
2	A28S	1502	G
2	A28S	1514	U
2	A28S	1518	A
2	A28S	1523	A
2	A28S	1525	A
2	A28S	1534	A
2	A28S	1547	A
2	A28S	1553	A
2	A28S	1563	A
2	A28S	1566	C
2	A28S	1578	U
2	A28S	1591	U
2	A28S	1596	U
2	A28S	1612	G
2	A28S	1613	A
2	A28S	1624	G
2	A28S	1625	G
2	A28S	1631	A
2	A28S	1633	G
2	A28S	1634	A
2	A28S	1640	C
2	A28S	1649	U
2	A28S	1654	G
2	A28S	1661	C
2	A28S	1676	C
2	A28S	1677	U
2	A28S	1684	A
2	A28S	1691	G
2	A28S	1731	C
2	A28S	1734	G
2	A28S	1742	A
2	A28S	1750	G
2	A28S	1755	C
2	A28S	1756	U
2	A28S	1757	U
2	A28S	1760	G
2	A28S	1761	G
2	A28S	1762	C

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Mol	Chain	Res	Type
2	A28S	1763	C
2	A28S	1764	G
2	A28S	1765	A
2	A28S	1768	C
2	A28S	1772	C
2	A28S	1773	U
2	A28S	1774	C
2	A28S	1776	A
2	A28S	1787	A
2	A28S	1797	G
2	A28S	1803	G
2	A28S	1804	A
2	A28S	1805	A
2	A28S	1818	G
2	A28S	1820	U
2	A28S	1821	G
2	A28S	1822	U
2	A28S	1828	C
2	A28S	1836	G
2	A28S	1837	A
2	A28S	1842	G
2	A28S	1855	G
2	A28S	1869	G
2	A28S	1882	U
2	A28S	1897	A
2	A28S	1910	G
2	A28S	1918	U
2	A28S	1920	C
2	A28S	1921	C
2	A28S	1922	G
2	A28S	1925	G
2	A28S	1931	C
2	A28S	1932	A
2	A28S	1935	C
2	A28S	1947	U
2	A28S	1948	G
2	A28S	1952	G
2	A28S	1959	U
2	A28S	1960	A
2	A28S	1961	G
2	A28S	1962	A
2	A28S	1964	A

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Mol	Chain	Res	Type
2	A28S	1969	G
2	A28S	1971	U
2	A28S	1972	G
2	A28S	1973	G
2	A28S	1974	U
2	A28S	1975	G
2	A28S	1977	C
2	A28S	1978	C
2	A28S	1979	A
2	A28S	1984	A
2	A28S	1985	G
2	A28S	1987	C
2	A28S	1988	G
2	A28S	1991	A
2	A28S	1992	U
2	A28S	1993	C
2	A28S	1997	U
2	A28S	2002	A
2	A28S	2003	G
2	A28S	2018	C
2	A28S	2019	C
2	A28S	2020	U
2	A28S	2026	A
2	A28S	2044	U
2	A28S	2046	G
2	A28S	2047	A
2	A28S	2048	U
2	A28S	2052	G
2	A28S	2055	G
2	A28S	2056	G
2	A28S	2062	C
2	A28S	2064	G
2	A28S	2069	A
2	A28S	2084	U
2	A28S	2089	G
2	A28S	2090	U
2	A28S	2092	G
2	A28S	2093	G
2	A28S	2094	C
2	A28S	2097	A
2	A28S	2100	G
2	A28S	2102	G

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Mol	Chain	Res	Type
2	A28S	2104	A
2	A28S	2105	A
2	A28S	2106	G
2	A28S	2107	A
2	A28S	2268	A
2	A28S	2275	G
2	A28S	2279	A
2	A28S	2289	C
2	A28S	2300	A
2	A28S	2301	G
2	A28S	2313	A
2	A28S	2332	A
2	A28S	2333	G
2	A28S	2348	G
2	A28S	2351	C
2	A28S	2395	A
2	A28S	2396	A
2	A28S	2416	G
2	A28S	2417	A
2	A28S	2422	C
2	A28S	2425	U
2	A28S	2433	G
2	A28S	2441	C
2	A28S	2447	U
2	A28S	2450	G
2	A28S	2453	A
2	A28S	2469	C
2	A28S	2475	G
2	A28S	2488	C
2	A28S	2489	C
2	A28S	2490	U
2	A28S	2491	C
2	A28S	2503	G
2	A28S	2505	C
2	A28S	2506	G
2	A28S	2513	A
2	A28S	2529	A
2	A28S	2530	U
2	A28S	2537	A
2	A28S	2544	G
2	A28S	2546	G
2	A28S	2547	G

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Mol	Chain	Res	Type
2	A28S	2553	A
2	A28S	2554	U
2	A28S	2575	U
2	A28S	2583	C
2	A28S	2586	G
2	A28S	2587	A
2	A28S	2589	C
2	A28S	2600	A
2	A28S	2627	C
2	A28S	2640	G
2	A28S	2647	A
2	A28S	2653	C
2	A28S	2658	G
2	A28S	2662	G
2	A28S	2663	G
2	A28S	2669	C
2	A28S	2670	C
2	A28S	2676	A
2	A28S	2679	G
2	A28S	2686	G
2	A28S	2687	U
2	A28S	2695	A
2	A28S	2696	A
2	A28S	2703	G
2	A28S	2705	G
2	A28S	2707	U
2	A28S	2708	U
2	A28S	2709	C
2	A28S	2710	C
2	A28S	2711	G
2	A28S	2712	G
2	A28S	2716	C
2	A28S	2725	A
2	A28S	2726	G
2	A28S	2735	G
2	A28S	2740	U
2	A28S	2760	G
2	A28S	2763	U
2	A28S	2764	A
2	A28S	2769	U
2	A28S	2787	A
2	A28S	2788	U

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Mol	Chain	Res	Type
2	A28S	2790	U
2	A28S	2794	C
2	A28S	2798	A
2	A28S	2807	A
2	A28S	2826	U
2	A28S	2827	G
2	A28S	2838	G
2	A28S	2842	G
2	A28S	2855	G
2	A28S	2875	C
2	A28S	2884	G
2	A28S	3604	A
2	A28S	3605	C
2	A28S	3618	C
2	A28S	3625	G
2	A28S	3626	G
2	A28S	3635	A
2	A28S	3646	A
2	A28S	3648	A
2	A28S	3657	U
2	A28S	3662	A
2	A28S	3663	A
2	A28S	3664	G
2	A28S	3673	C
2	A28S	3674	G
2	A28S	3679	U
2	A28S	3696	C
2	A28S	3702	A
2	A28S	3710	G
2	A28S	3711	A
2	A28S	3739	C
2	A28S	3748	A
2	A28S	3753	G
2	A28S	3761	C
2	A28S	3767	C
2	A28S	3773	U
2	A28S	3776	G
2	A28S	3777	G
2	A28S	3783	A
2	A28S	3784	A
2	A28S	3786	U
2	A28S	3810	C

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Mol	Chain	Res	Type
2	A28S	3811	G
2	A28S	3812	C
2	A28S	3814	U
2	A28S	3817	A
2	A28S	3819	G
2	A28S	3824	A
2	A28S	3838	U
2	A28S	3840	U
2	A28S	3869	C
2	A28S	3876	A
2	A28S	3877	A
2	A28S	3878	C
2	A28S	3879	G
2	A28S	3880	G
2	A28S	3892	U
2	A28S	3895	G
2	A28S	3897	G
2	A28S	3901	A
2	A28S	3905	A
2	A28S	3906	A
2	A28S	3907	G
2	A28S	3908	A
2	A28S	3915	U
2	A28S	3916	G
2	A28S	3917	A
2	A28S	3926	C
2	A28S	3927	U
2	A28S	3938	G
2	A28S	3957	U
2	A28S	3959	U
2	A28S	3960	A
2	A28S	3962	A
2	A28S	3963	A
2	A28S	3965	A
2	A28S	3969	G
2	A28S	3973	G
2	A28S	3976	C
2	A28S	4044	U
2	A28S	4045	G
2	A28S	4047	A
2	A28S	4048	A
2	A28S	4049	U

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Mol	Chain	Res	Type
2	A28S	4050	A
2	A28S	4052	C
2	A28S	4065	G
2	A28S	4066	U
2	A28S	4076	G
2	A28S	4085	A
2	A28S	4086	G
2	A28S	4088	C
2	A28S	4119	C
2	A28S	4120	U
2	A28S	4121	G
2	A28S	4125	C
2	A28S	4127	A
2	A28S	4155	C
2	A28S	4158	C
2	A28S	4162	C
2	A28S	4163	U
2	A28S	4170	A
2	A28S	4183	G
2	A28S	4184	G
2	A28S	4191	G
2	A28S	4212	A
2	A28S	4228	G
2	A28S	4229	U
2	A28S	4233	A
2	A28S	4249	G
2	A28S	4251	A
2	A28S	4254	G
2	A28S	4257	A
2	A28S	4266	G
2	A28S	4268	A
2	A28S	4271	A
2	A28S	4273	A
2	A28S	4281	A
2	A28S	4291	G
2	A28S	4292	A
2	A28S	4297	G
2	A28S	4305	G
2	A28S	4306	U
2	A28S	4314	C
2	A28S	4317	A
2	A28S	4329	G

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Mol	Chain	Res	Type
2	A28S	4330	G
2	A28S	4332	C
2	A28S	4336	A
2	A28S	4337	C
2	A28S	4338	G
2	A28S	4348	A
2	A28S	4349	C
2	A28S	4354	U
2	A28S	4355	G
2	A28S	4373	G
2	A28S	4377	G
2	A28S	4378	A
2	A28S	4380	A
2	A28S	4382	G
2	A28S	4387	C
2	A28S	4391	G
2	A28S	4394	A
2	A28S	4395	U
2	A28S	4398	C
2	A28S	4413	C
2	A28S	4419	U
2	A28S	4422	A
2	A28S	4426	C
2	A28S	4437	U
2	A28S	4440	G
2	A28S	4444	C
2	A28S	4448	G
2	A28S	4449	A
2	A28S	4464	A
2	A28S	4466	C
2	A28S	4471	U
2	A28S	4472	G
2	A28S	4475	G
2	A28S	4479	A
2	A28S	4500	U
2	A28S	4512	U
2	A28S	4513	A
2	A28S	4515	G
2	A28S	4519	C
2	A28S	4520	G
2	A28S	4524	G
2	A28S	4536	C

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Mol	Chain	Res	Type
2	A28S	4548	A
2	A28S	4560	C
2	A28S	4567	G
2	A28S	4569	U
2	A28S	4572	U
2	A28S	4573	G
2	A28S	4574	U
2	A28S	4575	G
2	A28S	4581	G
2	A28S	4586	G
2	A28S	4589	A
2	A28S	4590	A
2	A28S	4599	A
2	A28S	4604	G
2	A28S	4624	A
2	A28S	4636	U
2	A28S	4637	G
2	A28S	4652	G
2	A28S	4656	A
2	A28S	4657	U
2	A28S	4670	C
2	A28S	4672	A
2	A28S	4677	U
2	A28S	4700	A
2	A28S	4709	U
2	A28S	4720	C
2	A28S	4729	A
2	A28S	4738	C
2	A28S	4743	G
2	A28S	4750	G
2	A28S	4751	G
2	A28S	4754	G
2	A28S	4757	C
2	A28S	4759	C
2	A28S	4761	G
2	A28S	4765	G
2	A28S	4771	C
2	A28S	4867	G
2	A28S	4870	G
2	A28S	4871	C
2	A28S	4873	G
2	A28S	4875	G

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Mol	Chain	Res	Type
2	A28S	4882	U
2	A28S	4883	C
2	A28S	4885	U
2	A28S	4887	C
2	A28S	4895	C
2	A28S	4902	C
2	A28S	4906	C
2	A28S	4909	A
2	A28S	4912	G
2	A28S	4914	G
2	A28S	4915	G
2	A28S	4919	G
2	A28S	4921	C
2	A28S	4924	C
2	A28S	4925	U
2	A28S	4926	C
2	A28S	4928	C
2	A28S	4931	G
2	A28S	4937	C
2	A28S	4938	A
2	A28S	4943	A
2	A28S	4944	C
2	A28S	4949	G
2	A28S	4950	U
2	A28S	4951	G
2	A28S	4956	A
2	A28S	4957	C
2	A28S	4958	C
2	A28S	4960	G
2	A28S	4963	G
2	A28S	4965	U
2	A28S	4966	A
2	A28S	4967	A
2	A28S	4976	U
2	A28S	4979	A
2	A28S	4988	U
2	A28S	4990	C
2	A28S	4993	G
2	A28S	5017	G
2	A28S	5020	G
2	A28S	5034	A
2	A28S	5040	U

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Mol	Chain	Res	Type
2	A28S	5041	G
2	A28S	5047	C
2	A28S	5050	C
2	A28S	5052	C
2	A28S	5053	U
2	A28S	5054	C
2	A28S	5058	A
2	A28S	5061	A
2	A28S	5062	G
3	A58S	2	G
3	A58S	34	U
3	A58S	35	C
3	A58S	51	U
3	A58S	59	A
3	A58S	62	A
3	A58S	63	U
3	A58S	75	G
3	A58S	87	G
3	A58S	103	A
3	A58S	105	C
3	A58S	110	U
3	A58S	111	U
3	A58S	112	G
3	A58S	114	G
3	A58S	121	G
3	A58S	125	C
3	A58S	126	C
3	A58S	147	G
3	A58S	151	G
3	A58S	153	C
4	A5S	7	G
4	A5S	33	U
4	A5S	53	U
4	A5S	54	A
4	A5S	64	G
4	A5S	74	A
4	A5S	97	G
4	A5S	100	A
4	A5S	110	G
4	A5S	117	G
4	A5S	120	U
82	ETRN	6	G

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Mol	Chain	Res	Type
82	ETRN	7	G
82	ETRN	17	C
82	ETRN	18	G
82	ETRN	19	G
82	ETRN	20	U
82	ETRN	21	A
82	ETRN	47	U
82	ETRN	48	C
82	ETRN	59	A
82	ETRN	73	A
82	ETRN	76	A
83	MRNA	4	C
83	MRNA	5	A
83	MRNA	7	G
83	MRNA	8	U
83	MRNA	10	C
82	PTRN	2	G
82	PTRN	9	G
82	PTRN	19	G
82	PTRN	20	U
82	PTRN	47	U
82	PTRN	74	C
82	PTRN	76	A
84	TIRN	5	G
84	TIRN	7	G
84	TIRN	9	G
84	TIRN	14	A
84	TIRN	16	U
84	TIRN	17	C
84	TIRN	18	G
84	TIRN	19	G
84	TIRN	20	U
84	TIRN	21	A
84	TIRN	76	A

All (46) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A18S	110	U
1	A18S	291	G
1	A18S	434	G
1	A18S	465	A

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Mol	Chain	Res	Type
1	A18S	553	U
1	A18S	642	U
1	A18S	752	G
1	A18S	1137	U
1	A18S	1394	G
1	A18S	1395	C
1	A18S	1489	A
2	A28S	12	A
2	A28S	125	C
2	A28S	275	C
2	A28S	406	C
2	A28S	480	C
2	A28S	485	C
2	A28S	492	U
2	A28S	504	G
2	A28S	696	C
2	A28S	930	G
2	A28S	971(A)	G
2	A28S	1211	G
2	A28S	1236	C
2	A28S	1238	A
2	A28S	1291	G
2	A28S	1329	G
2	A28S	1370	G
2	A28S	1445	U
2	A28S	1455	G
2	A28S	1633	G
2	A28S	1804	A
2	A28S	2046	G
2	A28S	2089	G
2	A28S	2546	G
2	A28S	2639	U
2	A28S	2695	A
2	A28S	3959	U
2	A28S	3968	U
2	A28S	4119	C
2	A28S	4378	A
2	A28S	4448	G
2	A28S	4699	U
2	A28S	4925	U
3	A58S	124	U
83	MRNA	6	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	A28S	12

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A28S	1219:G	O3'	1233:G	P	18.84
1	A28S	3976:C	O3'	4035:G	P	14.96
1	A28S	1364:U	O3'	1368:A	P	13.66
1	A28S	1696:C	O3'	1720:C	P	13.07
1	A28S	1438:U	O3'	1440:U	P	11.61
1	A28S	1180:C	O3'	1183:C	P	8.36
1	A28S	1100:U	O3'	1168:G	P	5.90
1	A28S	760:G	O3'	904:C	P	5.88
1	A28S	1239:C	O3'	1244:G	P	4.92
1	A28S	500:G	O3'	504:G	P	4.75
1	A28S	4740:G	O3'	4743:G	P	3.35
1	A28S	4899:G	O3'	4902:C	P	3.21

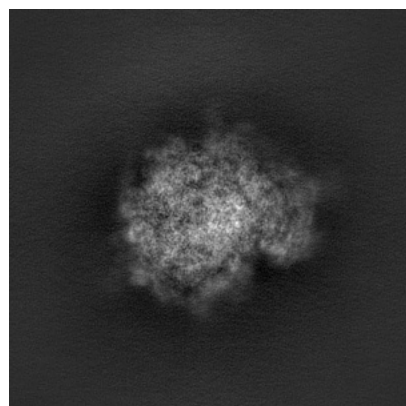
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44463. These allow visual inspection of the internal detail of the map and identification of artifacts.

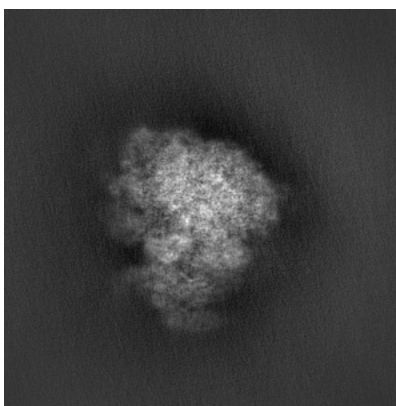
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

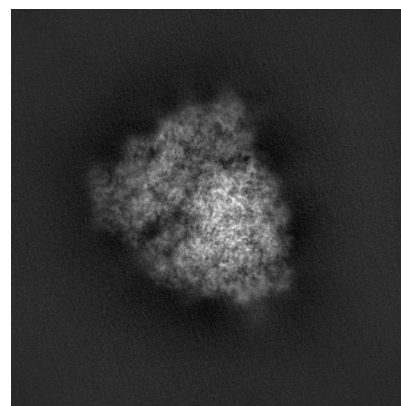
6.1.1 Primary map



X

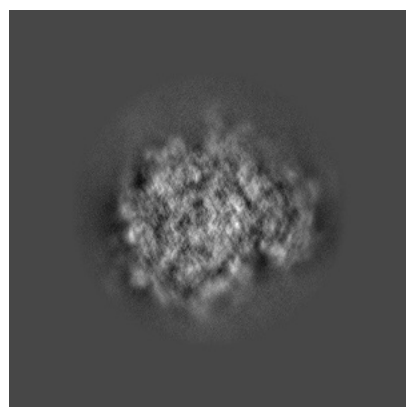


Y

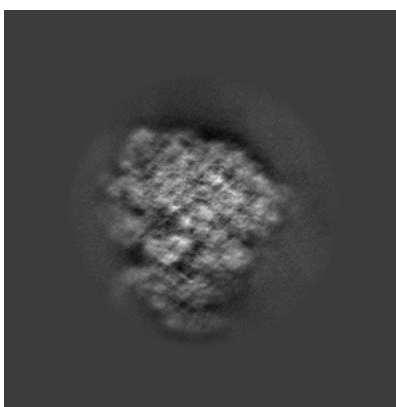


Z

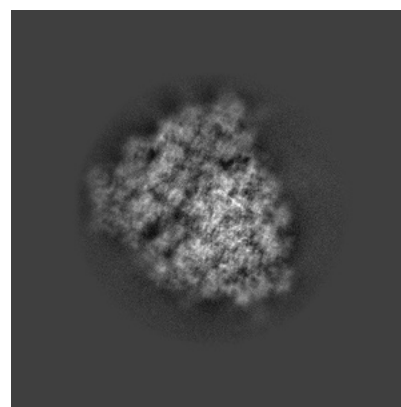
6.1.2 Raw map



X



Y

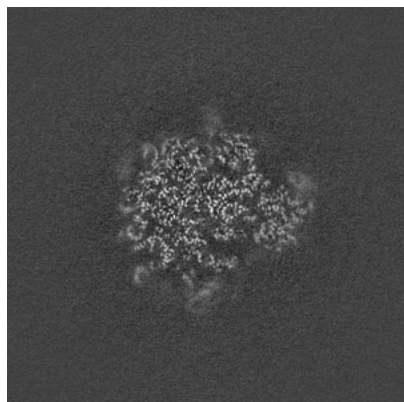


Z

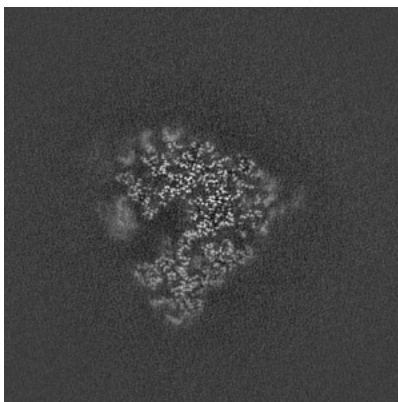
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

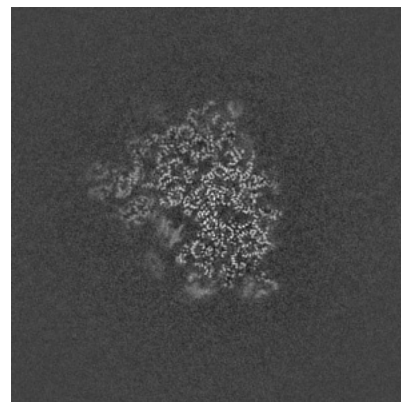
6.2.1 Primary map



X Index: 304

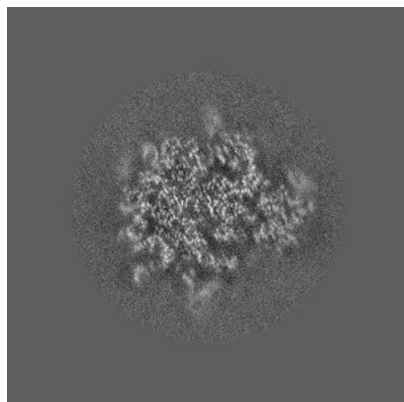


Y Index: 304

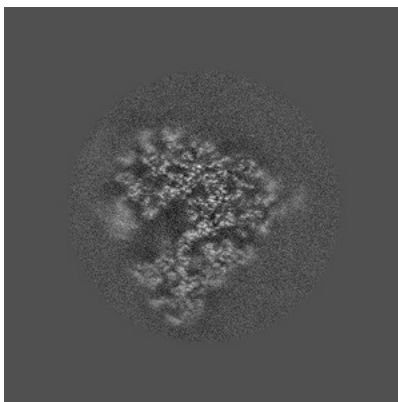


Z Index: 304

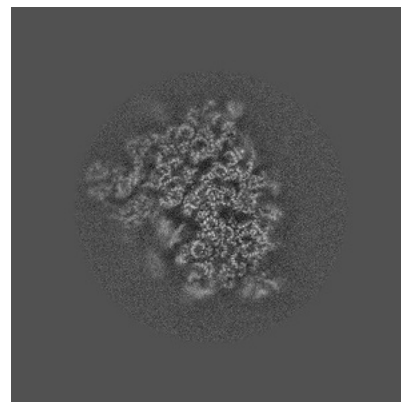
6.2.2 Raw map



X Index: 304



Y Index: 304

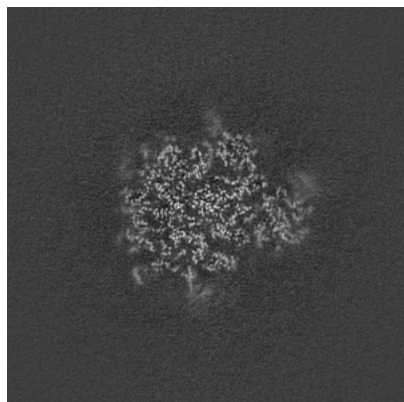


Z Index: 304

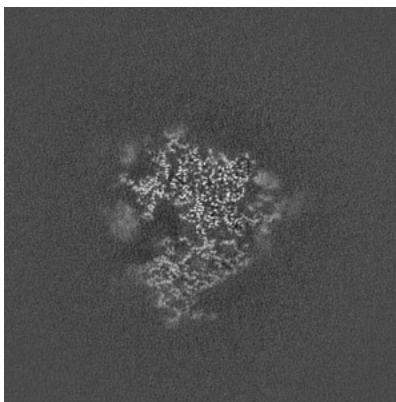
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

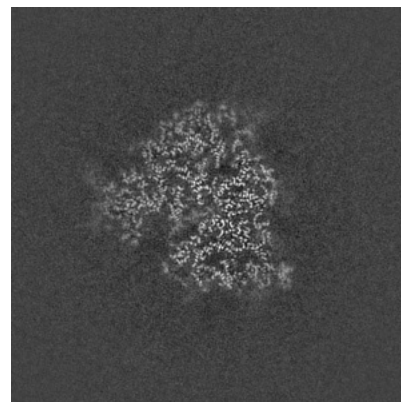
6.3.1 Primary map



X Index: 308

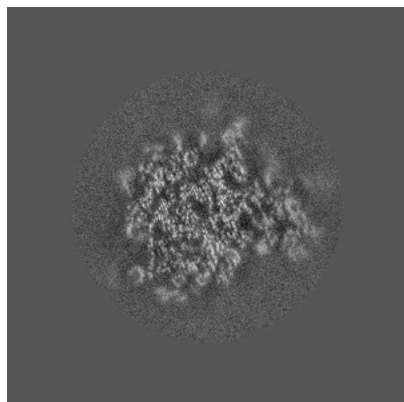


Y Index: 312

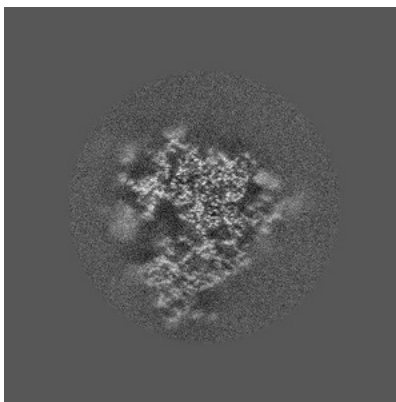


Z Index: 277

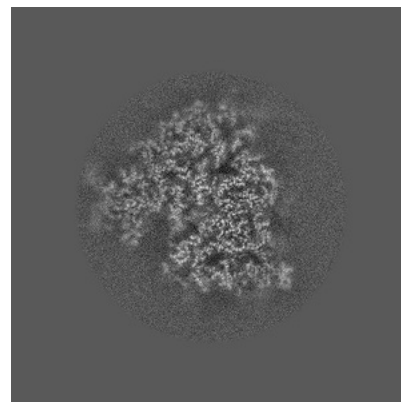
6.3.2 Raw map



X Index: 325



Y Index: 312

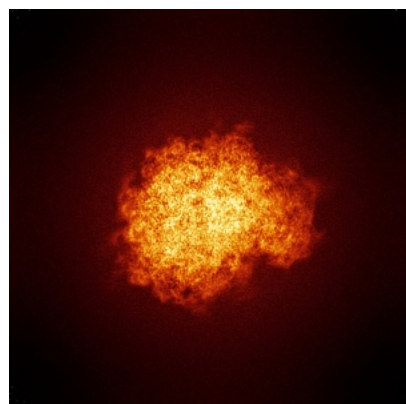


Z Index: 277

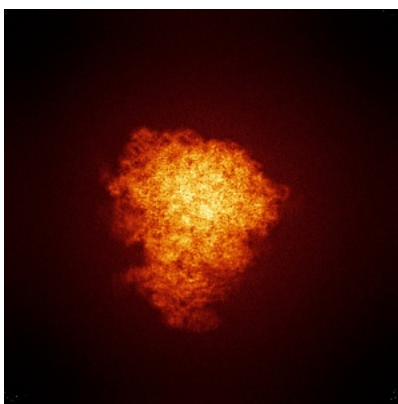
The images above show the largest variance slices of the map in three orthogonal directions.

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

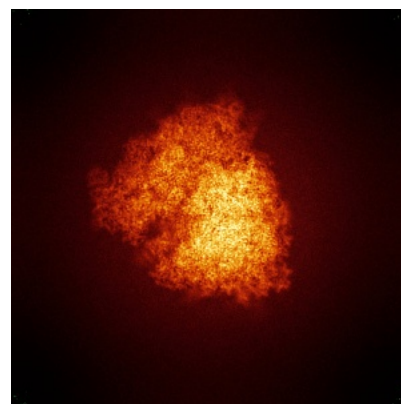
6.4.1 Primary map



X

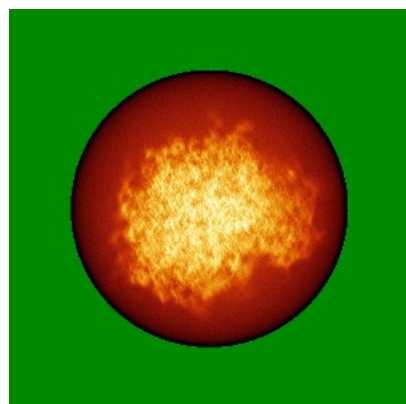


Y

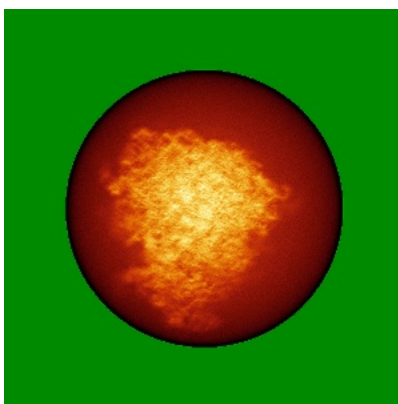


Z

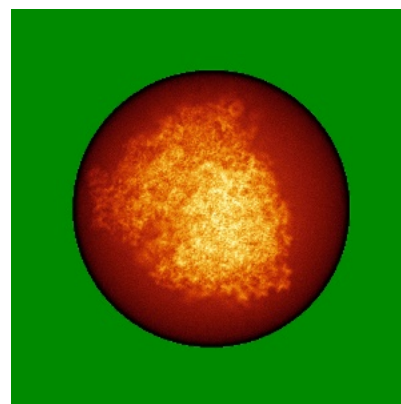
6.4.2 Raw map



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](#)

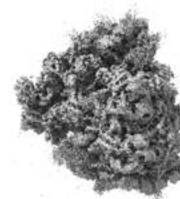
6.5.1 Primary map



X



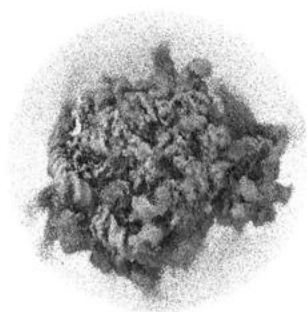
Y



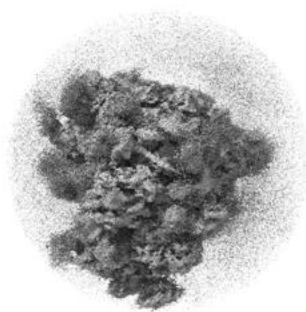
Z

The images above show the 3D surface view of the map at the recommended contour level 3.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

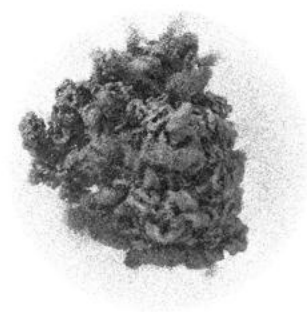
6.5.2 Raw map



X



Y



Z

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.

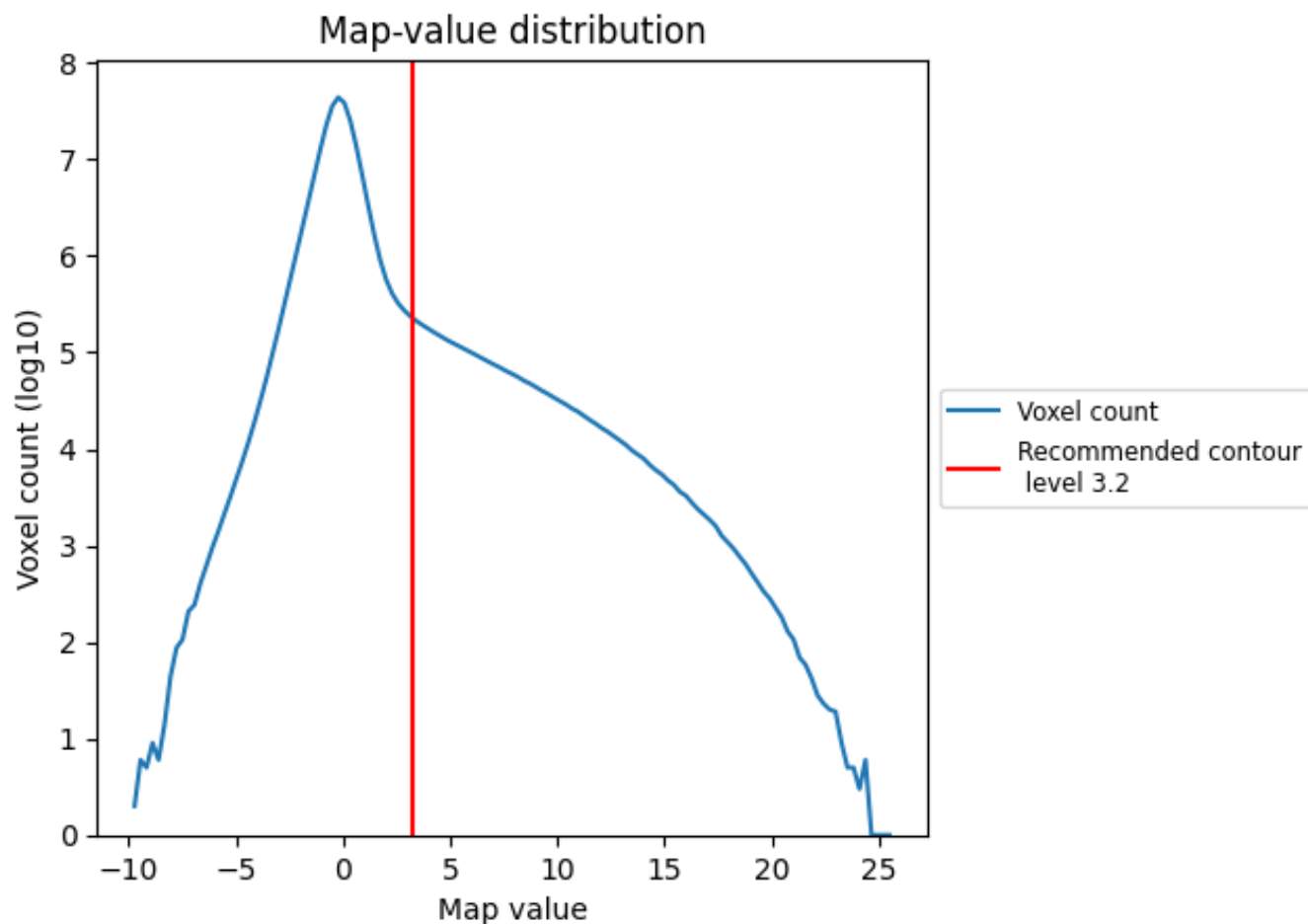
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

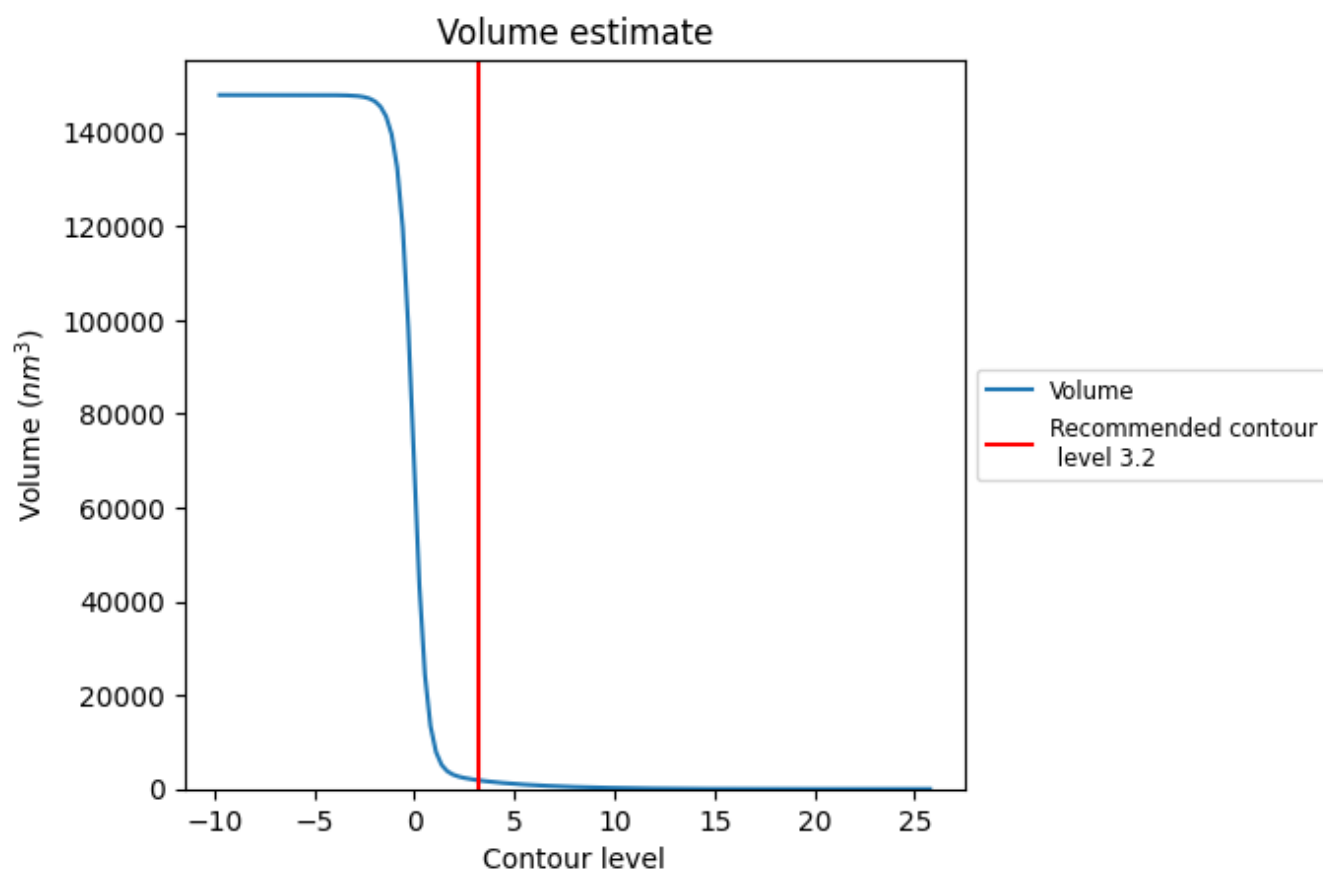
This section contains the results of statistical analysis of the map.

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.

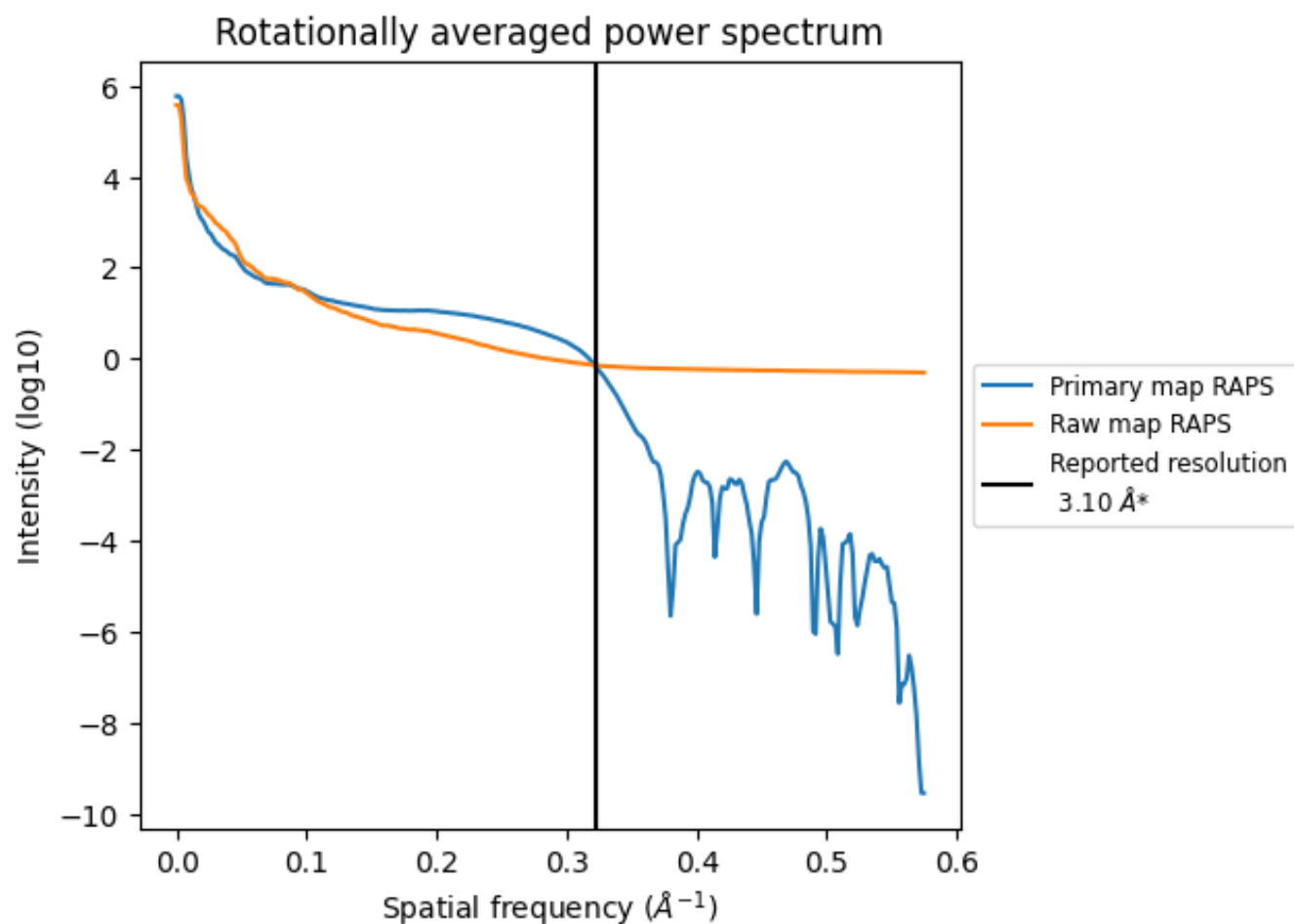
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1856 nm³; this corresponds to an approximate mass of 1676 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 ⓘ

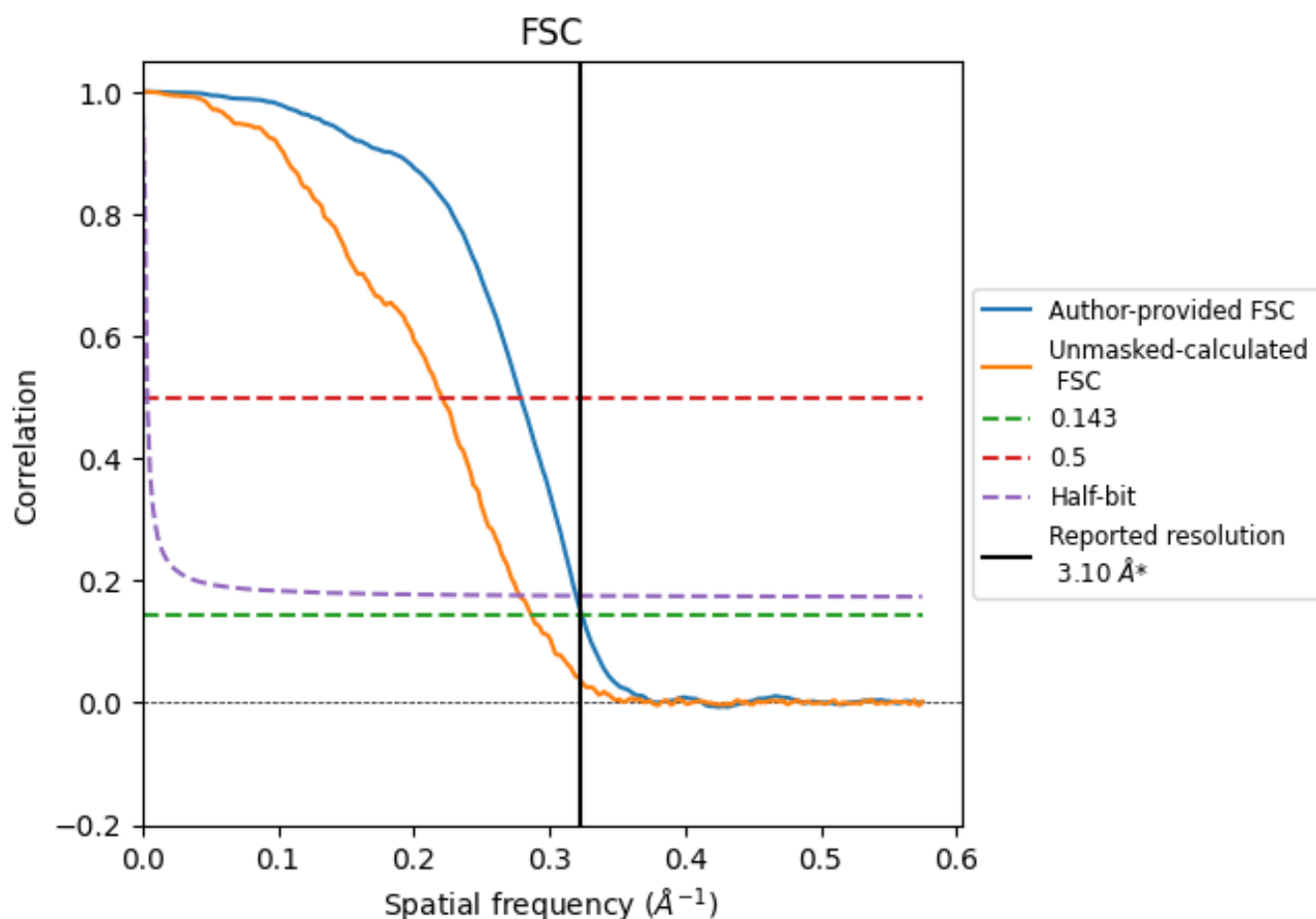


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.59	3.13
Unmasked-calculated*	3.48	4.53	3.60

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.48 differs from the reported value 3.1 by more than 10 %

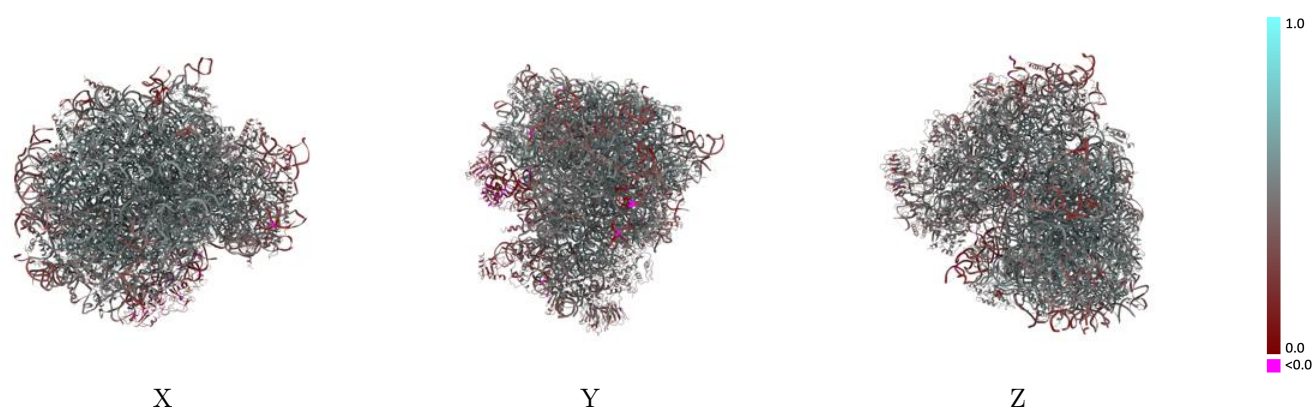
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44463 and PDB model 9BDN. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay [i](#)

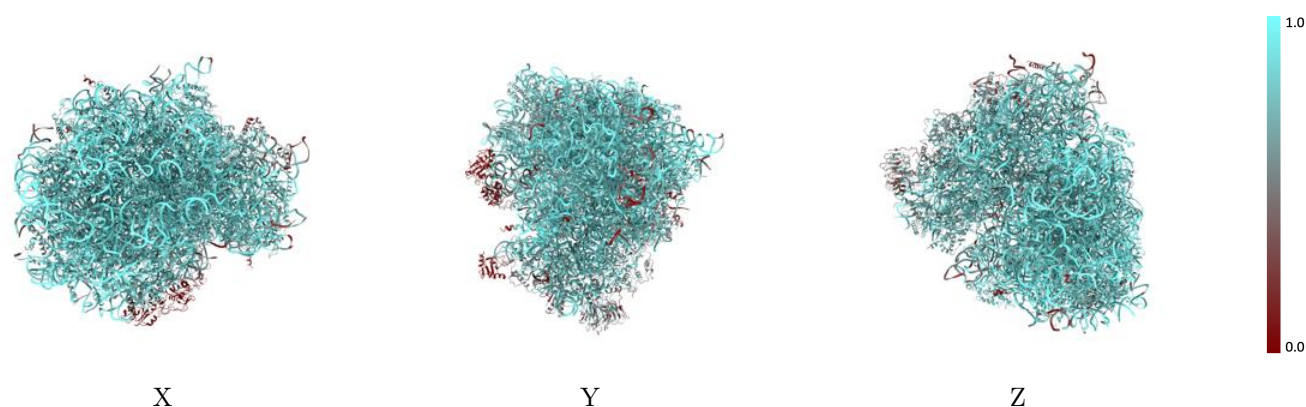
This section was not generated.

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



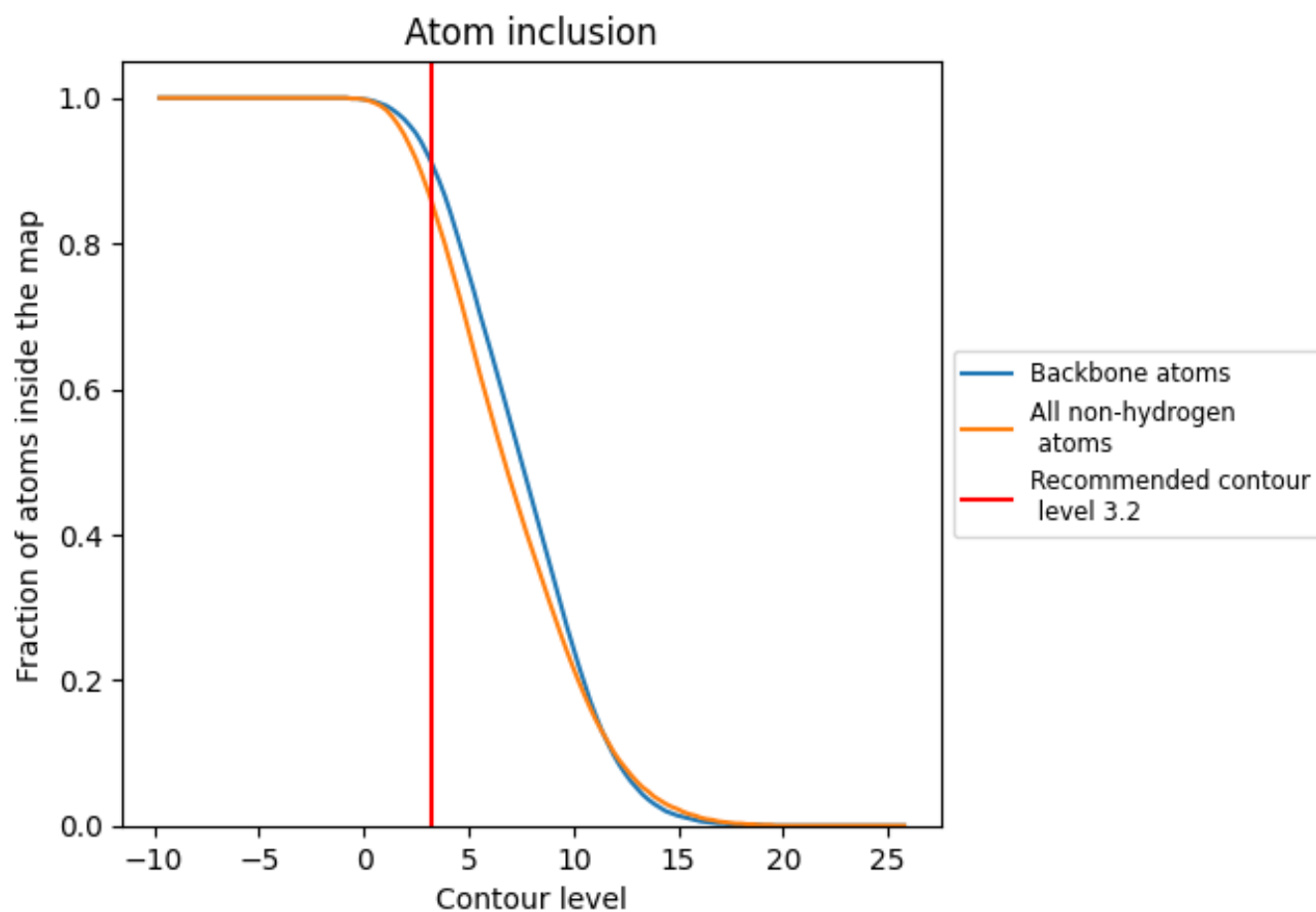
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 86% 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 (3.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8610	 0.4690
A18S	 0.9170	 0.4570
A28S	 0.9480	 0.4820
A58S	 0.9720	 0.4980
A5S	 0.9880	 0.5150
AL02	 0.8920	 0.5430
AL03	 0.8660	 0.5200
AL04	 0.8610	 0.5240
AL05	 0.8520	 0.4720
AL06	 0.8090	 0.4810
AL07	 0.8520	 0.5210
AL08	 0.7430	 0.4610
AL09	 0.8020	 0.4840
AL10	 0.8530	 0.5070
AL11	 0.8240	 0.4770
AL12	 0.1690	 0.1740
AL13	 0.8120	 0.4860
AL14	 0.8250	 0.4840
AL15	 0.9080	 0.5410
AL16	 0.8540	 0.5120
AL17	 0.8850	 0.5310
AL18	 0.8660	 0.5340
AL19	 0.8130	 0.4860
AL20	 0.8710	 0.5220
AL21	 0.8490	 0.5220
AL22	 0.8010	 0.4530
AL23	 0.8630	 0.5320
AL24	 0.8450	 0.5210
AL25	 0.8610	 0.5180
AL26	 0.8440	 0.5000
AL27	 0.8390	 0.4900
AL28	 0.9010	 0.5370
AL29	 0.7260	 0.4730
AL30	 0.8230	 0.4870
AL31	 0.8480	 0.5040



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Chain	Atom inclusion	Q-score
AL32	 0.8670	 0.5320
AL33	 0.8920	 0.5470
AL34	 0.8550	 0.5120
AL35	 0.8240	 0.4950
AL36	 0.8410	 0.4720
AL37	 0.9260	 0.5450
AL38	 0.7500	 0.4640
AL39	 0.8830	 0.5200
AL40	 0.8480	 0.5080
AL41	 0.7520	 0.5200
AL42	 0.8680	 0.5270
AL43	 0.8630	 0.5160
ALNW	 0.8700	 0.5200
ALP0	 0.0570	 0.2190
ANG	 0.7370	 0.4500
ARAC	 0.4980	 0.3640
AS00	 0.6800	 0.4390
AS01	 0.7770	 0.4700
AS02	 0.7430	 0.4680
AS03	 0.6180	 0.4130
AS04	 0.7540	 0.4590
AS05	 0.7630	 0.4470
AS06	 0.6740	 0.3930
AS07	 0.5930	 0.4090
AS08	 0.7550	 0.4630
AS09	 0.7710	 0.4560
AS10	 0.5910	 0.3640
AS11	 0.7750	 0.5020
AS12	 0.0640	 0.2450
AS13	 0.8100	 0.4820
AS14	 0.8050	 0.4760
AS15	 0.7030	 0.4050
AS16	 0.7250	 0.4440
AS17	 0.6140	 0.4260
AS18	 0.7510	 0.4350
AS19	 0.7350	 0.4180
AS20	 0.6060	 0.4120
AS21	 0.6780	 0.4440
AS22	 0.8190	 0.4870
AS23	 0.7920	 0.4990
AS24	 0.7490	 0.4190
AS25	 0.7080	 0.4220

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Chain	Atom inclusion	Q-score
AS26	 0.8360	 0.4920
AS27	 0.7470	 0.4390
AS28	 0.7870	 0.4670
AS29	 0.7080	 0.4280
AS30	 0.6710	 0.4190
ETRNL	 0.7900	 0.3010
MRNA	 0.7780	 0.4330
PTRN	 0.9050	 0.4450
TIRN	 0.5520	 0.1510