



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 06:15 AM UTC

PDB ID : 7TOR / pdb_00007tor
EMDB ID : EMD-26036
Title : Mammalian 80S ribosome bound with the ALS/FTD-associated dipeptide repeat protein GR20
Authors : Loveland, A.B.; Svidritskiy, E.; Susorov, D.; Lee, S.; Park, A.; Zvornicanin, S.; Demo, G.; Gao, F.B.; Korostelev, A.A.
Deposited on : 2022-01-24
Resolution : 2.90 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

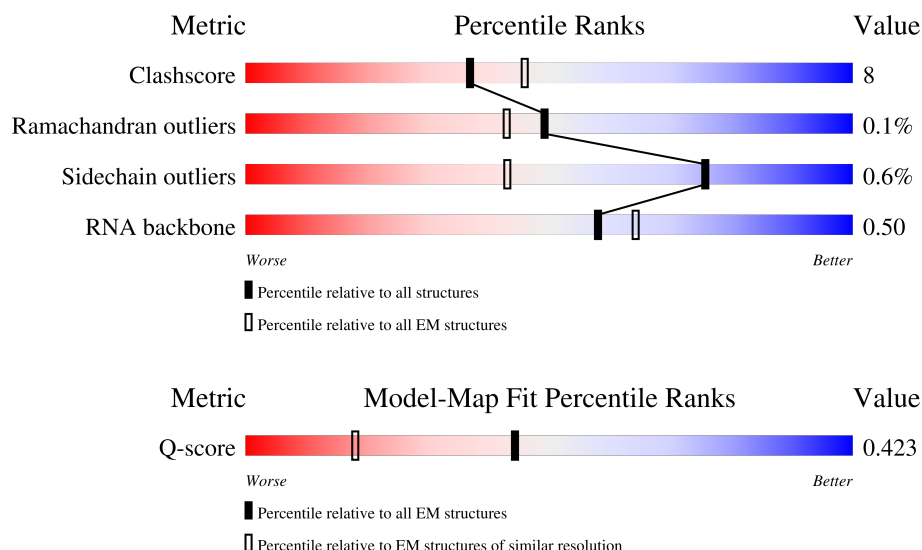
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.



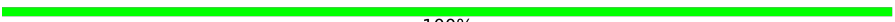
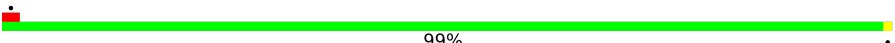
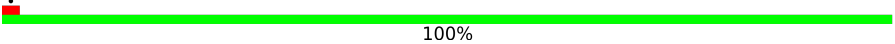
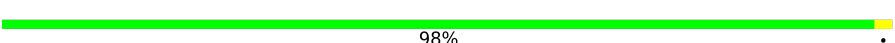
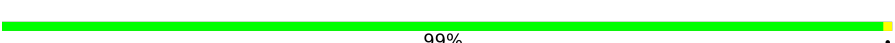
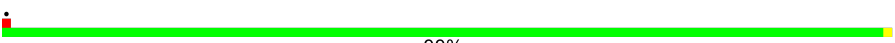
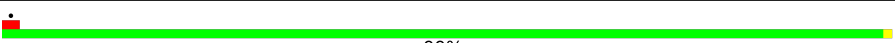
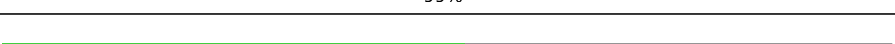
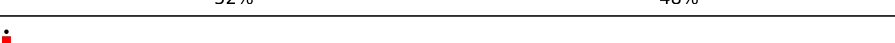
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	1698	
2	A28S	3552	
3	A58S	151	

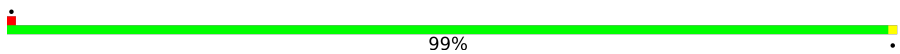
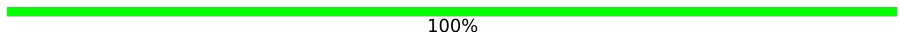
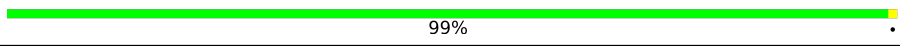
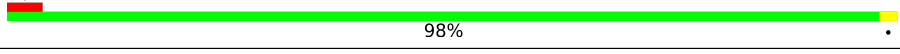
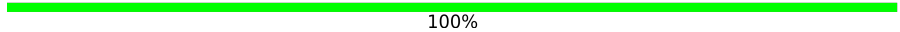
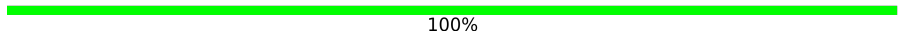
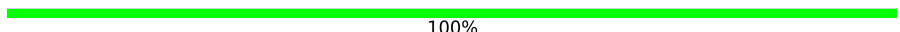
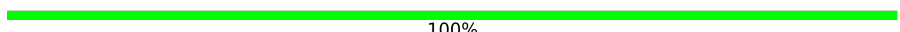
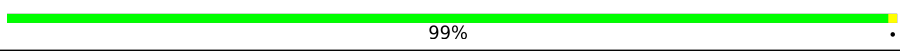
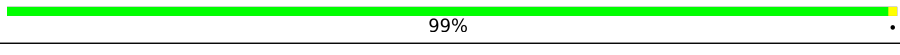
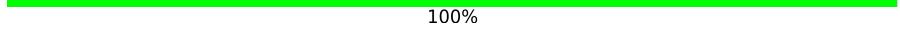
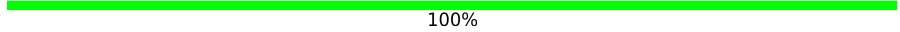
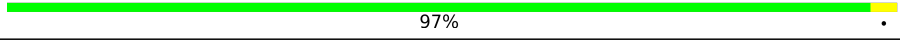
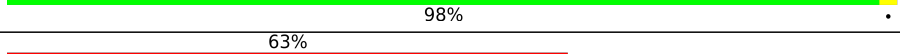
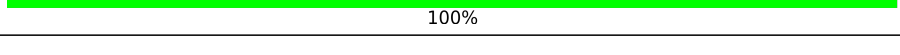
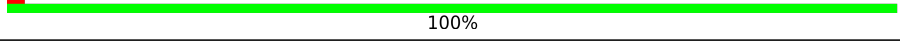
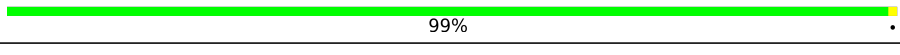
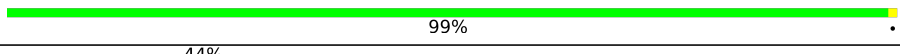
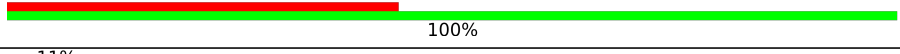
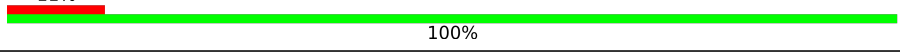
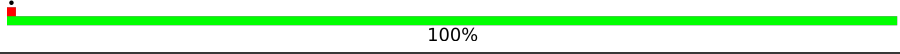
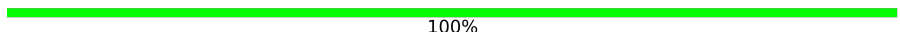
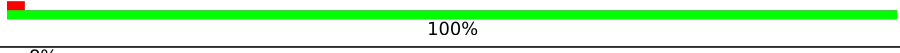
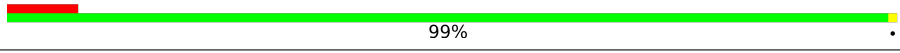
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Mol	Chain	Length	Quality of chain
4	A5S	120	 74% 22%
5	AL02	248	 100%
6	AL03	394	 100%
7	AL04	362	 100%
8	AL05	293	 100%
9	AL06	251	 85% 14%
10	AL07	225	 100%
11	AL08	233	 99%
12	AL09	190	 99%
13	AL10	205	 100%
14	AL11	170	 100%
15	AL12	153	 24% 25% 75%
16	AL13	210	 100%
17	AL14	138	 100%
18	AL15	203	 98%
19	AL16	199	 99%
20	AL17	153	 99%
21	AL18	191	 99%
22	AL19	180	 99%
23	AL20	176	 100%
24	AL21	159	 99%
25	AL22	99	 100%
26	AL23	131	 99%
27	AL24	121	 52% 48%
28	AL25	118	 100%

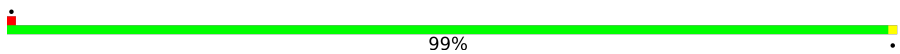
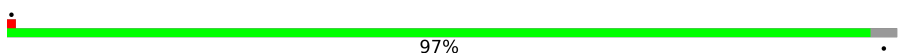
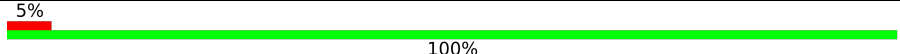
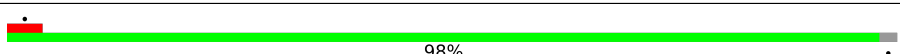
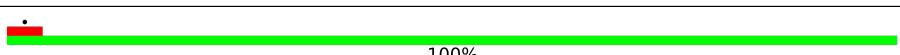
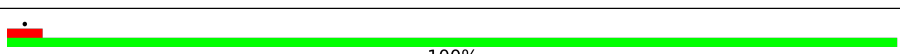
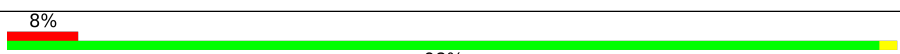
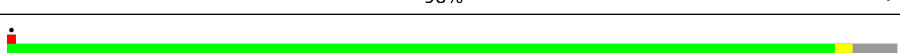
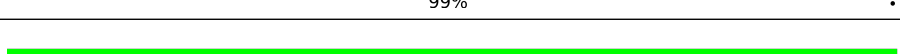
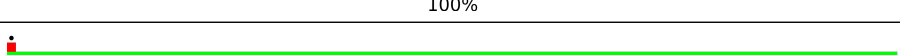
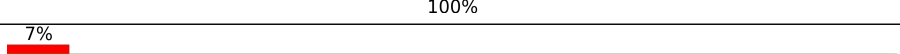
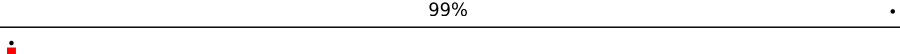
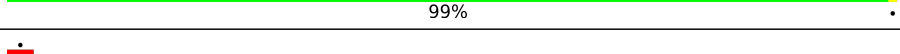
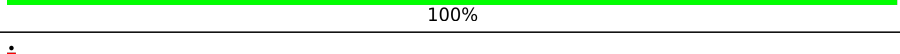
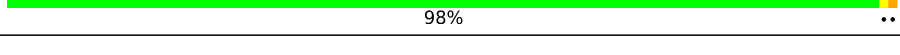
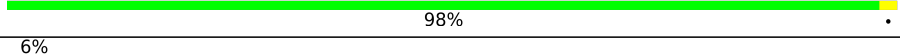
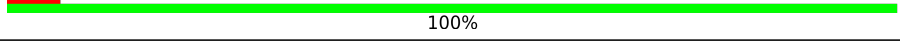
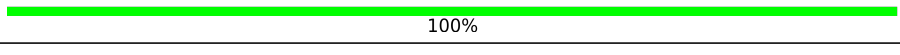
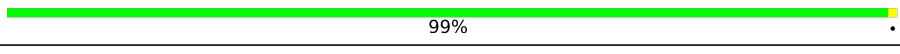
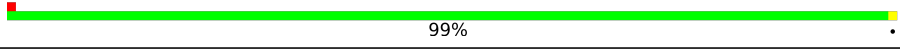
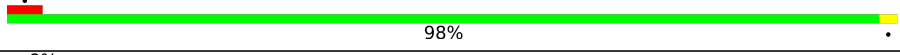
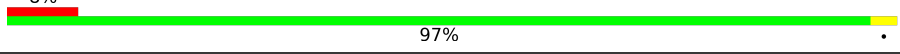
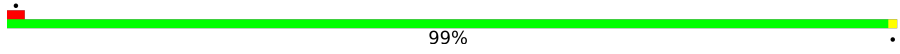
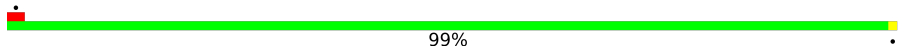
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Mol	Chain	Length	Quality of chain
29	AL26	134	 99%
30	AL27	135	 100%
31	AL28	147	 99%
32	AL29	104	 98%
33	AL30	98	 100%
34	AL31	107	 100%
35	AL32	128	 100%
36	AL33	109	 100%
37	AL34	114	 99%
38	AL35	122	 99%
39	AL36	102	 100%
40	AL37	86	 100%
41	AL38	69	 97%
42	AL39	50	 98%
43	AL40	52	 63% 100%
44	AL41	25	 100%
45	AL42	104	 100%
46	AL43	91	 99%
47	ALNW	124	 99%
48	ALP0	27	 44% 100%
49	ARAC	313	 11% 100%
50	AS00	217	 100%
51	AS01	213	 100%
52	AS02	221	 100%
53	AS03	228	 8% 99%

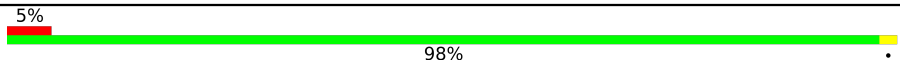
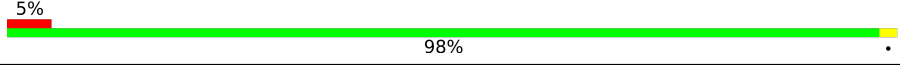
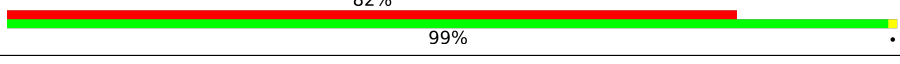
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Mol	Chain	Length	Quality of chain
54	AS04	262	 99%
55	AS05	191	 97%
56	AS06	237	 5%100%
57	AS07	189	 98%
58	AS08	206	 100%
59	AS09	185	 100%
60	AS10	96	 8%98%
61	AS11	151	 93%5%
62	AS12	117	 70%99%
63	AS13	149	 100%
64	AS14	135	 100%
65	AS15	120	 7%99%
66	AS16	142	 99%
67	AS17	132	 100%
68	AS18	144	 98%
69	AS19	141	 98%
70	AS20	100	 6%100%
71	AS21	83	 100%
72	AS22	129	 99%
73	AS23	141	 99%
74	AS24	124	 98%
75	AS25	75	 8%97%
76	AS26	101	 99%
77	AS27	83	 99%
78	AS28	62	 98%

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Mol	Chain	Length	Quality of chain
79	AS29	55	
80	AS30	55	
81	AS31	68	
82	ETRN	77	
82	PTRN	77	
83	GR1	40	
83	GR2	40	
84	MRNA	28	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 213154 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	3552	Total	C	N	O	P	0	0
			76187	33931	13966	24738	3552		

- 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 eL8.

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

- 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		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL10	?	-	LEU	deletion	UNP B7NZQ2
AL10	?	-	SER	deletion	UNP B7NZQ2
AL10	?	-	CYS	deletion	UNP B7NZQ2
AL10	?	-	ALA	deletion	UNP B7NZQ2
AL10	?	-	GLY	deletion	UNP B7NZQ2
AL10	?	-	ALA	deletion	UNP B7NZQ2
AL10	?	-	ASP	deletion	UNP B7NZQ2
AL10	?	-	ARG	deletion	UNP B7NZQ2

- 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	860	254	241	6		

- Molecule 15 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AL12	38	Total	C	N	O	S	0	0
			285	180	51	53	1		

- Molecule 16 is a protein called 60S ribosomal protein L13.

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

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL13	46	ILE	-	insertion	UNP G1TPV0
AL13	47	ALA	-	insertion	UNP G1TPV0
AL13	48	PRO	-	insertion	UNP G1TPV0
AL13	49	ARG	-	insertion	UNP G1TPV0
AL13	50	PRO	-	insertion	UNP G1TPV0
AL13	51	ALA	-	insertion	UNP G1TPV0
AL13	52	ALA	-	insertion	UNP G1TPV0
AL13	53	GLY	-	insertion	UNP G1TPV0
AL13	54	PRO	-	insertion	UNP G1TPV0

- 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 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 eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AL18	191	Total	C	N	O	S	0	3
			1522	947	320	251	4		

- 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 eL20.

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

- 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 eL22.

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

- 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 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 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 60S ribosomal protein L32.

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

- 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 eL38.

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

- 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 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
			989	615	201	167	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	ALP0	27	Total	C	N	O	S	0	0
			230	149	44	35	2		

- Molecule 49 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 50 is a protein called 40S_SA_C domain-containing protein.

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

- Molecule 51 is a protein called 40S ribosomal protein S3a.

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

- Molecule 52 is a protein called 40S ribosomal protein S2.

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

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS02	73	MET	VAL	conflict	UNP G1TUT9
AS02	101	SER	ALA	conflict	UNP G1TUT9
AS02	119	GLY	ALA	conflict	UNP G1TUT9
AS02	194	ARG	HIS	conflict	UNP G1TUT9
AS02	215	MET	LEU	conflict	UNP G1TUT9
AS02	227	ARG	TRP	conflict	UNP G1TUT9
AS02	228	GLY	SER	conflict	UNP G1TUT9

- Molecule 53 is a protein called 40S ribosomal protein S3.

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

- Molecule 54 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AS04	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 55 is a protein called Ribosomal protein S5.

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

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AS06	237	Total	C	N	O	S	0	0
			1922	1199	387	329	7		

- Molecule 57 is a protein called eS7.

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

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	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 59 is a protein called 40S ribosomal protein S9.

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

- Molecule 60 is a protein called 40S ribosomal protein S10.

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

- Molecule 61 is a protein called 40S ribosomal protein S11.

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

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AS12	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 63 is a protein called 40S ribosomal protein S13.

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

- Molecule 64 is a protein called uS11.

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

- Molecule 65 is a protein called 40S ribosomal protein S15.

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

- Molecule 66 is a protein called uS9.

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

- Molecule 67 is a protein called 40S ribosomal protein S17.

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

- Molecule 68 is a protein called 40S ribosomal protein S18.

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

- Molecule 69 is a protein called eS19.

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

- Molecule 70 is a protein called 40S ribosomal protein S20.

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

- Molecule 71 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	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
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 72 is a protein called 40S ribosomal protein S15a.

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

- Molecule 73 is a protein called 40S ribosomal protein S23.

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

- Molecule 74 is a protein called 40S ribosomal protein S24.

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

- Molecule 75 is a protein called 40S ribosomal protein S25.

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

- Molecule 76 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	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
AS26	56	ALA	VAL	conflict	UNP G1TFE8

- Molecule 77 is a protein called 40S ribosomal protein S27.

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

- Molecule 78 is a protein called 40S ribosomal protein S28.

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

- Molecule 79 is a protein called 40S ribosomal protein S29.

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

- Molecule 80 is a protein called 40S ribosomal protein S30.

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

- Molecule 81 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AS31	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 82 is a RNA chain called tRNA^fMet bound to E-site.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	ETRN	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
82	PTRN	74	Total	C	N	O	P	0	0
			1578	704	286	515	73		

- Molecule 83 is a protein called GR20, ALS/FTD dipeptide repeat protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	GR1	11	Total	C	N	O	0	0
			79	42	26	11		
83	GR2	11	Total	C	N	O	0	0
			50	28	11	11		

- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	MRNA	10	Total	C	N	O	P	0	0
			193	93	33	57	10		

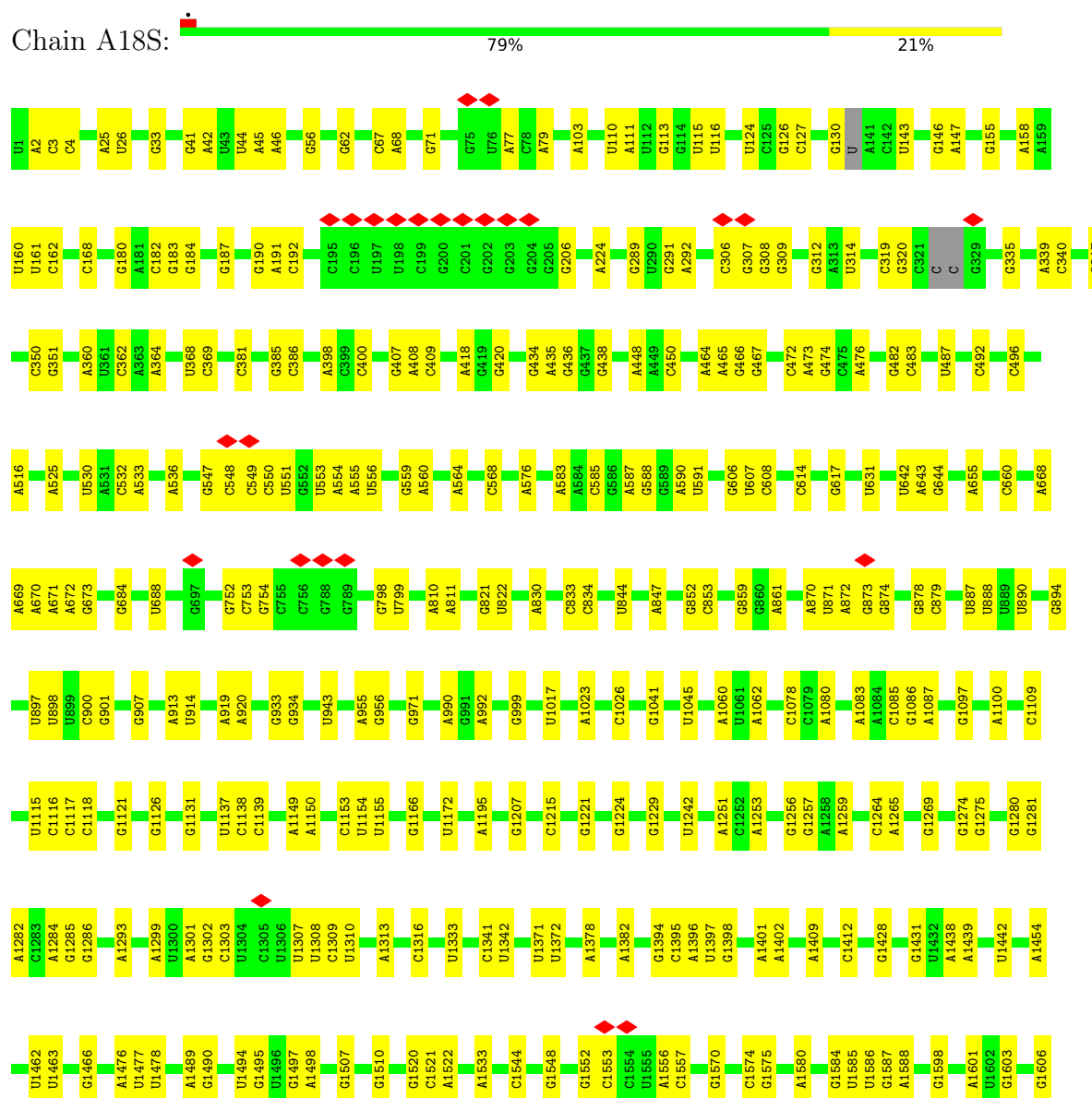
- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

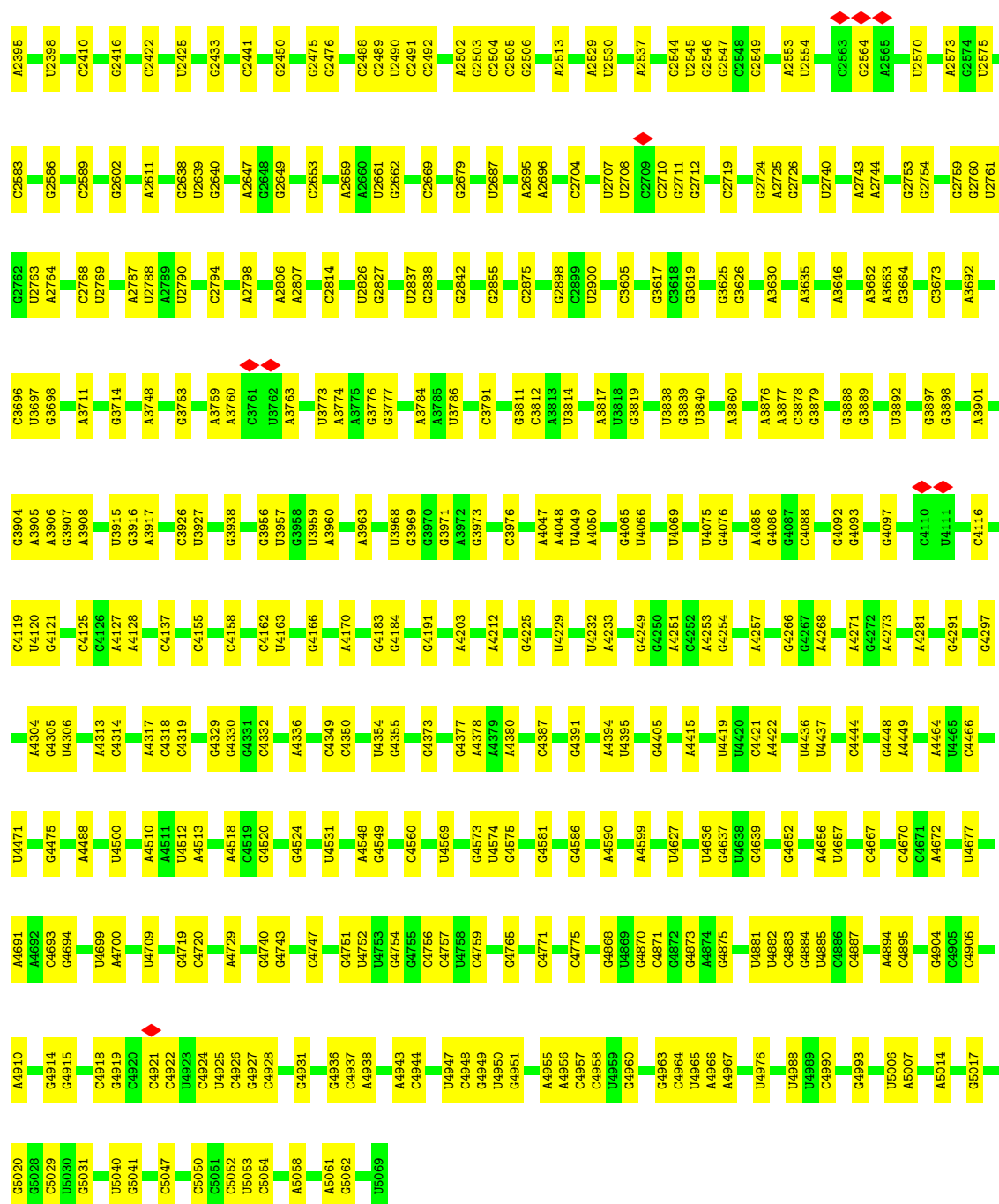
Mol	Chain	Residues	Atoms		AltConf
85	AL34	1	Total 1	Zn 1	0
85	AL37	1	Total 1	Zn 1	0
85	AL40	1	Total 1	Zn 1	0
85	AL42	1	Total 1	Zn 1	0
85	AL43	1	Total 1	Zn 1	0
85	AS26	1	Total 1	Zn 1	0

3 Residue-property plots

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

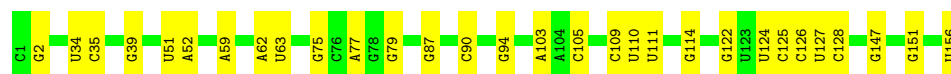
• Molecule 1: 18S rRNA





• Molecule 3: 5.8S rRNA

Chain A58S: 80% 20%

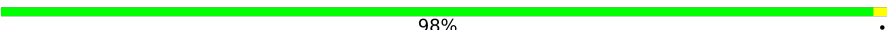


• Molecule 4: 5S rRNA

Chain A5S: 74% 22%

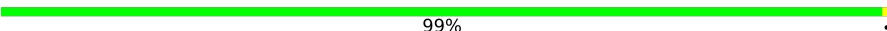
There are no outlier residues recorded for this chain.

- Molecule 18: 60S ribosomal protein L15

Chain AL15:  98%

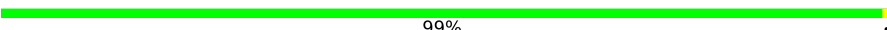


- Molecule 19: uL13

Chain AL16:  99%

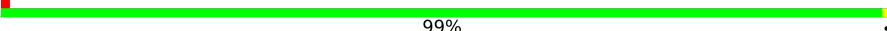


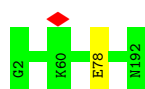
- Molecule 20: 60S ribosomal protein L17

Chain AL17:  99%

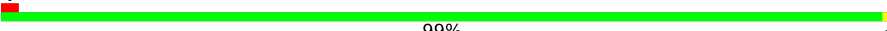


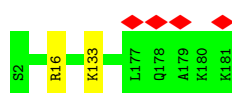
- Molecule 21: eL18

Chain AL18:  99%

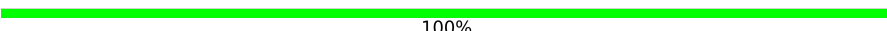


- Molecule 22: 60S ribosomal protein L19

Chain AL19:  99%

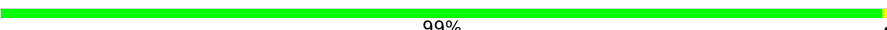


- Molecule 23: eL20

Chain AL20:  100%

There are no outlier residues recorded for this chain.

- Molecule 24: 60S ribosomal protein L21

Chain AL21:  99%



- Molecule 25: eL22

Chain AL22:  100%

There are no outlier residues recorded for this chain.

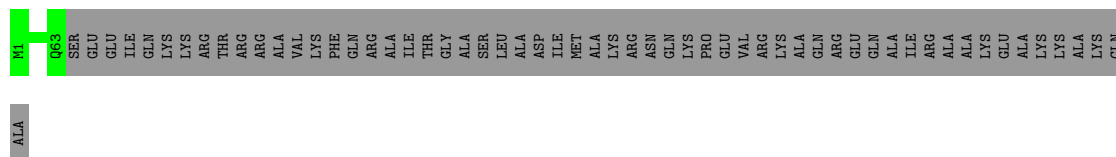
- Molecule 26: 60S ribosomal protein L23

Chain AL23:  99%



- Molecule 27: Ribosomal protein L24

Chain AL24:  52%  48%



- Molecule 28: uL23

Chain AL25:  100%



- Molecule 29: 60S ribosomal protein L26

Chain AL26:  99%



- Molecule 30: 60S ribosomal protein L27

Chain AL27:  100%

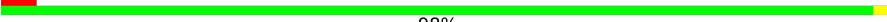
There are no outlier residues recorded for this chain.

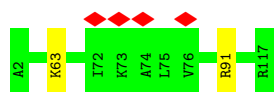
- Molecule 31: 60S ribosomal protein L27a

Chain AL28:  99%



- Molecule 32: eL29

Chain AL29:  98%



- Molecule 33: 60S ribosomal protein L30

Chain AL30:  100%

There are no outlier residues recorded for this chain.

- Molecule 34: 60S ribosomal protein L31

Chain AL31:  100%

There are no outlier residues recorded for this chain.

- Molecule 35: 60S ribosomal protein L32

Chain AL32:  100%

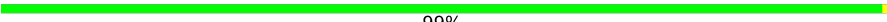
There are no outlier residues recorded for this chain.

- Molecule 36: 60S ribosomal protein L35a

Chain AL33:  100%

There are no outlier residues recorded for this chain.

- 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%

There are no outlier residues recorded for this chain.

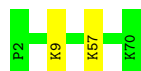
- Molecule 40: 60S ribosomal protein L37

Chain AL37:  100%

There are no outlier residues recorded for this chain.

- Molecule 41: eL38

Chain AL38:  97%



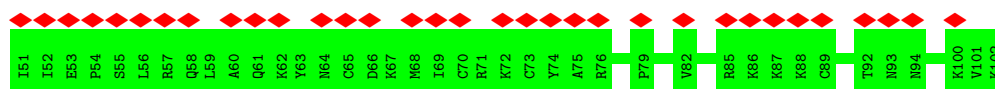
- Molecule 42: 60S ribosomal protein L39

Chain AL39:  98%



- Molecule 43: eL40

Chain AL40:  63% 100%

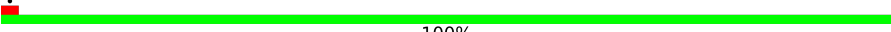


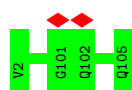
- Molecule 44: eL41

Chain AL41:  100%

There are no outlier residues recorded for this chain.

- Molecule 45: eL42

Chain AL42:  100%



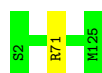
- Molecule 46: 60S ribosomal protein L37a

Chain AL43:  99%

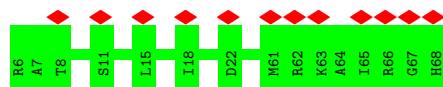


- Molecule 47: 60S ribosomal protein L28

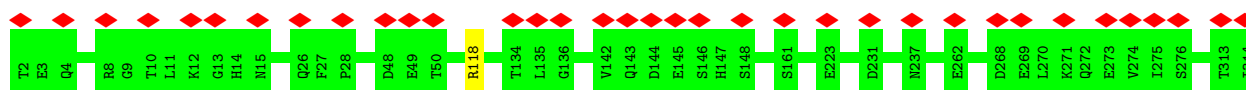
Chain ALNW:  99%



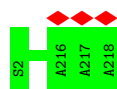
- Molecule 48: 60S acidic ribosomal protein P0



- Molecule 49: Receptor of activated protein C kinase 1



- Molecule 50: 40S_SA_C domain-containing protein

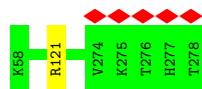


- Molecule 51: 40S ribosomal protein S3a

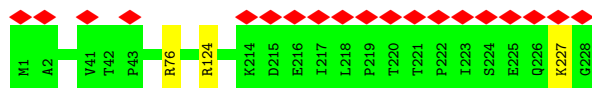


There are no outlier residues recorded for this chain.

- Molecule 52: 40S ribosomal protein S2



- Molecule 53: 40S ribosomal protein S3

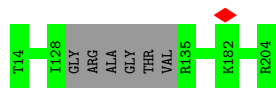


- Molecule 54: 40S ribosomal protein S4

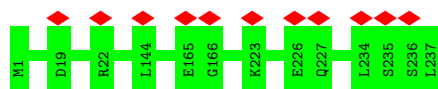




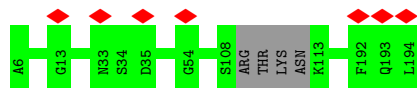
- Molecule 55: Ribosomal protein S5



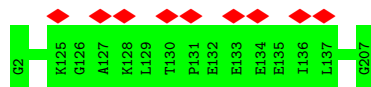
- Molecule 56: 40S ribosomal protein S6



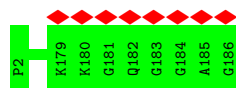
- Molecule 57: eS7



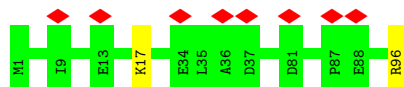
- Molecule 58: 40S ribosomal protein S8



- Molecule 59: 40S ribosomal protein S9

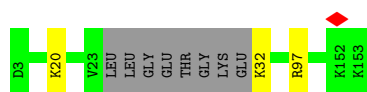


- Molecule 60: 40S ribosomal protein S10



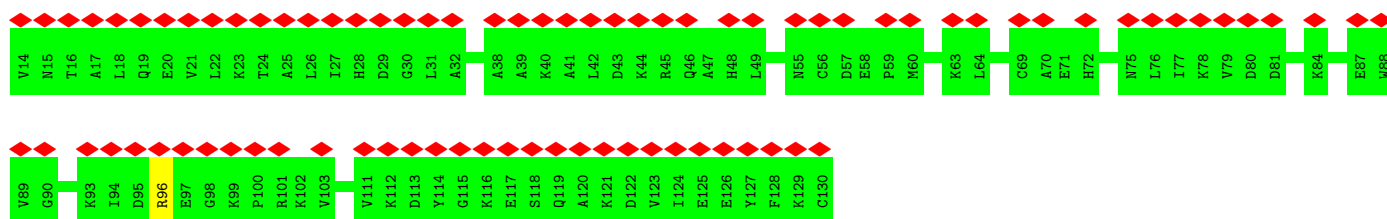
- Molecule 61: 40S ribosomal protein S11

Chain AS11:  93% • 5%



- Molecule 62: 40S ribosomal protein S12

Chain AS12:  70% 99% •



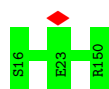
- Molecule 63: 40S ribosomal protein S13

Chain AS13:  100%

There are no outlier residues recorded for this chain.

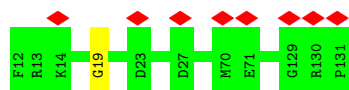
- Molecule 64: uS11

Chain AS14:  100%



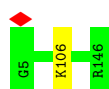
- Molecule 65: 40S ribosomal protein S15

Chain AS15:  7% 99% •



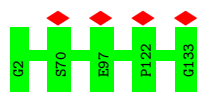
- Molecule 66: uS9

Chain AS16:  99% •



- Molecule 67: 40S ribosomal protein S17

Chain AS17:  100%



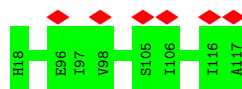
- Molecule 68: 40S ribosomal protein S18



- Molecule 69: eS19



- Molecule 70: 40S ribosomal protein S20

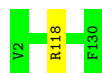


- Molecule 71: eS21

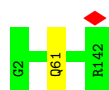


There are no outlier residues recorded for this chain.

- Molecule 72: 40S ribosomal protein S15a

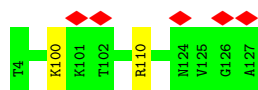


- Molecule 73: 40S ribosomal protein S23



- Molecule 74: 40S ribosomal protein S24

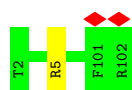




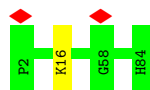
- Molecule 75: 40S ribosomal protein S25



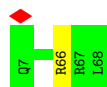
- Molecule 76: eS26



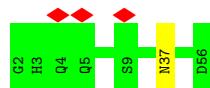
- Molecule 77: 40S ribosomal protein S27



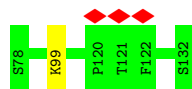
- Molecule 78: 40S ribosomal protein S28



- Molecule 79: 40S ribosomal protein S29



- Molecule 80: 40S ribosomal protein S30



- Molecule 81: 40S ribosomal protein S27a

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20284	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	45.285	Depositor
Minimum map value	-11.054	Depositor
Average map value	0.016	Depositor
Map value standard deviation	1.963	Depositor
Recommended contour level	6	Depositor
Map size ($\text{\AA}$)	597.6, 597.6, 597.6	wwPDB
Map dimensions	720, 720, 720	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.12	0/40369	0.30	0/62910
2	A28S	0.12	0/85228	0.29	0/132921
3	A58S	0.10	0/3581	0.27	0/5577
4	A5S	0.10	0/2858	0.23	0/4455
5	AL02	0.15	0/1936	0.41	0/2596
6	AL03	0.14	0/3240	0.39	0/4339
7	AL04	0.13	0/2937	0.37	0/3946
8	AL05	0.12	0/2437	0.42	0/3264
9	AL06	0.14	0/1762	0.38	0/2362
10	AL07	0.17	0/1911	0.39	0/2549
11	AL08	0.12	0/1910	0.38	0/2569
12	AL09	0.19	0/1535	0.47	0/2063
13	AL10	0.13	0/1702	0.35	0/2272
14	AL11	0.14	0/1382	0.42	0/1847
15	AL12	0.09	0/285	0.29	0/379
16	AL13	0.14	0/1733	0.39	0/2316
17	AL14	0.14	0/1158	0.42	0/1547
18	AL15	0.12	0/1746	0.42	2/2338 (0.1%)
19	AL16	0.14	0/1662	0.41	0/2222
20	AL17	0.13	0/1268	0.41	0/1700
21	AL18	0.14	0/1539	0.46	0/2046
22	AL19	0.13	0/1524	0.42	0/2013
23	AL20	0.15	0/1501	0.40	0/2012
24	AL21	0.13	0/1326	0.38	0/1770
25	AL22	0.18	0/823	0.50	0/1104
26	AL23	0.15	0/993	0.41	0/1332
27	AL24	0.12	0/541	0.39	0/720
28	AL25	0.15	0/984	0.42	0/1323
29	AL26	0.18	0/1132	0.45	0/1504
30	AL27	0.15	0/1130	0.40	0/1507
31	AL28	0.11	0/1191	0.38	0/1590
32	AL29	0.13	0/861	0.41	0/1138

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AL30	0.14	0/771	0.37	0/1034
34	AL31	0.16	0/903	0.46	0/1216
35	AL32	0.15	0/1071	0.40	0/1429
36	AL33	0.13	0/895	0.40	0/1198
37	AL34	0.13	0/916	0.43	0/1220
38	AL35	0.14	0/1021	0.44	0/1348
39	AL36	0.15	0/841	0.44	0/1112
40	AL37	0.14	0/720	0.39	0/952
41	AL38	0.20	0/575	0.46	0/761
42	AL39	0.13	0/459	0.41	0/608
43	AL40	0.13	0/435	0.40	0/575
44	AL41	0.12	0/240	0.40	0/305
45	AL42	0.14	0/864	0.41	0/1140
46	AL43	0.13	0/718	0.39	0/953
47	ALNW	0.14	0/1005	0.42	0/1347
48	ALP0	0.10	0/233	0.27	0/308
49	ARAC	0.14	0/2493	0.38	0/3394
50	AS00	0.18	0/1747	0.45	0/2374
51	AS01	0.13	0/1756	0.41	0/2350
52	AS02	0.16	0/1753	0.40	0/2369
53	AS03	0.15	0/1796	0.42	0/2417
54	AS04	0.13	0/2118	0.39	0/2849
55	AS05	0.17	0/1492	0.49	0/2005
56	AS06	0.13	0/1943	0.40	0/2586
57	AS07	0.18	0/1510	0.46	0/2022
58	AS08	0.15	0/1715	0.42	0/2287
59	AS09	0.18	0/1550	0.46	0/2069
60	AS10	0.23	0/834	0.61	0/1125
61	AS11	0.14	0/1195	0.40	0/1597
62	AS12	0.13	0/918	0.40	0/1233
63	AS13	0.14	0/1226	0.39	0/1649
64	AS14	0.17	0/1017	0.52	0/1365
65	AS15	0.17	0/1017	0.53	0/1358
66	AS16	0.17	0/1146	0.45	0/1534
67	AS17	0.15	0/1082	0.41	0/1452
68	AS18	0.23	0/1208	0.67	3/1618 (0.2%)
69	AS19	0.15	0/1115	0.43	0/1493
70	AS20	0.15	0/805	0.45	0/1081
71	AS21	0.19	0/643	0.52	0/860
72	AS22	0.17	0/1051	0.40	0/1406
73	AS23	0.14	0/1116	0.44	0/1490
74	AS24	0.17	0/1028	0.46	0/1366
75	AS25	0.18	0/604	0.47	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AS26	0.17	0/828	0.40	0/1109
77	AS27	0.15	0/665	0.41	0/891
78	AS28	0.20	0/490	0.50	0/656
79	AS29	0.16	0/470	0.48	0/623
80	AS30	0.16	0/447	0.47	0/587
81	AS31	0.12	0/567	0.36	0/753
82	ETRN	0.11	0/1832	0.24	0/2855
82	PTRN	0.10	0/1763	0.28	0/2748
83	GR1	0.41	0/78	1.70	1/97 (1.0%)
83	GR2	0.30	0/49	1.33	0/64
84	MRNA	0.12	0/215	0.41	0/318
All	All	0.13	0/229134	0.35	6/336597 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
18	AL15	0	1
73	AS23	0	1
All	All	0	2

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	AS18	107	LEU	CA-C-N	-6.14	113.47	122.86
68	AS18	107	LEU	C-N-CA	-6.14	113.47	122.86
68	AS18	108	ARG	CA-CB-CG	5.62	125.35	114.10
18	AL15	76	PRO	CA-C-N	5.21	131.48	121.54
18	AL15	76	PRO	C-N-CA	5.21	131.48	121.54
83	GR1	20	ARG	N-CA-C	5.09	117.22	111.02

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	AL15	77	LYS	Peptide
73	AS23	61	GLN	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A18S	36103	0	0	0	0
2	A28S	76187	0	0	0	0
3	A58S	3208	0	0	0	0
4	A5S	2558	0	1296	17	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	285	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	1522	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
44	AL41	239	0	0	0	0
45	AL42	851	0	0	0	0
46	AL43	708	0	0	0	0
47	ALNW	989	0	0	0	0
48	ALP0	230	0	0	0	0
49	ARAC	2436	0	0	0	0
50	AS00	1710	0	0	0	0
51	AS01	1729	0	0	0	0
52	AS02	1716	0	0	0	0
53	AS03	1768	0	0	0	0
54	AS04	2076	0	0	0	0
55	AS05	1471	0	0	0	0
56	AS06	1922	0	0	0	0
57	AS07	1488	0	0	0	0
58	AS08	1686	0	0	0	0
59	AS09	1525	0	0	0	0
60	AS10	810	0	0	0	0
61	AS11	1175	0	0	0	0
62	AS12	908	0	0	0	0
63	AS13	1202	0	0	0	0
64	AS14	1004	0	0	0	0
65	AS15	997	0	0	0	0
66	AS16	1128	0	0	0	0
67	AS17	1068	0	0	0	0
68	AS18	1190	0	0	0	0
69	AS19	1097	0	0	0	0
70	AS20	795	0	0	0	0
71	AS21	636	0	0	0	0
72	AS22	1034	0	0	0	0
73	AS23	1098	0	0	0	0
74	AS24	1011	0	0	0	0
75	AS25	598	0	0	0	0
76	AS26	814	0	0	0	0
77	AS27	651	0	0	0	0
78	AS28	488	0	0	0	0
79	AS29	459	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	AS30	443	0	0	0	0
81	AS31	555	0	0	0	0
82	ETRN	1640	0	0	0	0
82	PTRN	1578	0	0	0	0
83	GR1	79	0	82	0	0
83	GR2	50	0	29	0	0
84	MRNA	193	0	0	0	0
85	AL34	1	0	0	0	0
85	AL37	1	0	0	0	0
85	AL40	1	0	0	0	0
85	AL42	1	0	0	0	0
85	AL43	1	0	0	0	0
85	AS26	1	0	0	0	0
All	All	213154	0	1407	17	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 8.

All (17) 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)
4:A5S:28:C:H1'	4:A5S:54:A:H61	1.51	0.75
4:A5S:23:A:N3	4:A5S:118:C:O2'	2.31	0.62
4:A5S:28:C:O2'	4:A5S:54:A:N1	2.34	0.60
4:A5S:92:C:H2'	4:A5S:93:G:H8	1.69	0.58
4:A5S:63:C:H5'	4:A5S:64:G:H5''	1.88	0.56
4:A5S:24:C:O2	4:A5S:117:G:N2	2.37	0.50
4:A5S:11:A:N1	4:A5S:66:G:O2'	2.42	0.49
4:A5S:34:C:N3	4:A5S:46:C:O2'	2.46	0.49
4:A5S:57:C:H2'	4:A5S:58:A:H8	1.79	0.46
4:A5S:110:G:H2'	4:A5S:111:C:C6	2.51	0.45
4:A5S:92:C:H2'	4:A5S:93:G:C8	2.51	0.44
4:A5S:4:U:H2'	4:A5S:5:A:H8	1.82	0.43
4:A5S:24:C:H2'	4:A5S:25:G:O4'	2.19	0.43
4:A5S:114:U:H2'	4:A5S:115:A:C8	2.55	0.41
4:A5S:15:C:H2'	4:A5S:16:A:H8	1.86	0.41
4:A5S:23:A:H2'	4:A5S:24:C:C6	2.55	0.41
4:A5S:4:U:H2'	4:A5S:5:A:C8	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	233 (95%)	13 (5%)	0	100	100
6	AL03	392/394 (100%)	382 (97%)	10 (3%)	0	100	100
7	AL04	360/362 (99%)	355 (99%)	5 (1%)	0	100	100
8	AL05	291/293 (99%)	280 (96%)	10 (3%)	1 (0%)	36	65
9	AL06	208/251 (83%)	197 (95%)	11 (5%)	0	100	100
10	AL07	223/225 (99%)	219 (98%)	4 (2%)	0	100	100
11	AL08	229/233 (98%)	220 (96%)	9 (4%)	0	100	100
12	AL09	188/190 (99%)	181 (96%)	7 (4%)	0	100	100
13	AL10	201/205 (98%)	191 (95%)	10 (5%)	0	100	100
14	AL11	168/170 (99%)	164 (98%)	4 (2%)	0	100	100
15	AL12	32/153 (21%)	32 (100%)	0	0	100	100
16	AL13	208/210 (99%)	201 (97%)	6 (3%)	1 (0%)	24	54
17	AL14	136/138 (99%)	132 (97%)	4 (3%)	0	100	100
18	AL15	201/203 (99%)	191 (95%)	9 (4%)	1 (0%)	24	54
19	AL16	197/199 (99%)	193 (98%)	4 (2%)	0	100	100
20	AL17	151/153 (99%)	151 (100%)	0	0	100	100
21	AL18	178/191 (93%)	170 (96%)	7 (4%)	1 (1%)	21	51
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%)	153 (98%)	4 (2%)	0	100	100
25	AL22	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
26	AL23	129/131 (98%)	125 (97%)	4 (3%)	0	100	100
27	AL24	61/121 (50%)	59 (97%)	2 (3%)	0	100	100
28	AL25	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
29	AL26	132/134 (98%)	129 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	AL27	133/135 (98%)	129 (97%)	4 (3%)	0	100	100
31	AL28	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
32	AL29	100/104 (96%)	96 (96%)	4 (4%)	0	100	100
33	AL30	96/98 (98%)	95 (99%)	1 (1%)	0	100	100
34	AL31	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
35	AL32	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
36	AL33	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
37	AL34	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
38	AL35	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	16	44
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%)	45 (94%)	3 (6%)	0	100	100
43	AL40	50/52 (96%)	50 (100%)	0	0	100	100
44	AL41	23/25 (92%)	23 (100%)	0	0	100	100
45	AL42	102/104 (98%)	97 (95%)	5 (5%)	0	100	100
46	AL43	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
47	ALNW	122/124 (98%)	117 (96%)	5 (4%)	0	100	100
48	ALP0	23/27 (85%)	23 (100%)	0	0	100	100
49	ARAC	311/313 (99%)	294 (94%)	17 (6%)	0	100	100
50	AS00	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
51	AS01	211/213 (99%)	203 (96%)	8 (4%)	0	100	100
52	AS02	219/221 (99%)	214 (98%)	5 (2%)	0	100	100
53	AS03	226/228 (99%)	222 (98%)	4 (2%)	0	100	100
54	AS04	260/262 (99%)	252 (97%)	8 (3%)	0	100	100
55	AS05	181/191 (95%)	172 (95%)	9 (5%)	0	100	100
56	AS06	235/237 (99%)	231 (98%)	4 (2%)	0	100	100
57	AS07	181/189 (96%)	177 (98%)	4 (2%)	0	100	100
58	AS08	204/206 (99%)	195 (96%)	9 (4%)	0	100	100
59	AS09	183/185 (99%)	181 (99%)	2 (1%)	0	100	100
60	AS10	94/96 (98%)	85 (90%)	9 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	AS11	139/151 (92%)	132 (95%)	7 (5%)	0	100	100
62	AS12	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
63	AS13	147/149 (99%)	145 (99%)	2 (1%)	0	100	100
64	AS14	133/135 (98%)	126 (95%)	7 (5%)	0	100	100
65	AS15	118/120 (98%)	109 (92%)	8 (7%)	1 (1%)	16	44
66	AS16	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
67	AS17	130/132 (98%)	123 (95%)	7 (5%)	0	100	100
68	AS18	142/144 (99%)	131 (92%)	11 (8%)	0	100	100
69	AS19	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
70	AS20	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
71	AS21	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
72	AS22	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
73	AS23	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
74	AS24	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
75	AS25	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
76	AS26	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
77	AS27	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
78	AS28	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
79	AS29	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
80	AS30	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
81	AS31	66/68 (97%)	62 (94%)	4 (6%)	0	100	100
83	GR1	9/40 (22%)	6 (67%)	3 (33%)	0	100	100
83	GR2	9/40 (22%)	5 (56%)	4 (44%)	0	100	100
All	All	11198/11675 (96%)	10816 (97%)	376 (3%)	6 (0%)	49	77

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	AL18	78	GLU
38	AL35	89	ARG
18	AL15	78	GLY
8	AL05	37	VAL
16	AL13	64	VAL
65	AS15	19	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	AL02	190/190 (100%)	189 (100%)	1 (0%)	81	93
6	AL03	342/342 (100%)	341 (100%)	1 (0%)	86	96
7	AL04	302/302 (100%)	301 (100%)	1 (0%)	86	96
8	AL05	247/247 (100%)	247 (100%)	0	100	100
9	AL06	190/223 (85%)	188 (99%)	2 (1%)	65	88
10	AL07	196/196 (100%)	195 (100%)	1 (0%)	81	93
11	AL08	200/200 (100%)	197 (98%)	3 (2%)	57	84
12	AL09	169/169 (100%)	167 (99%)	2 (1%)	63	86
13	AL10	175/175 (100%)	174 (99%)	1 (1%)	78	93
14	AL11	143/143 (100%)	143 (100%)	0	100	100
15	AL12	31/126 (25%)	31 (100%)	0	100	100
16	AL13	175/175 (100%)	175 (100%)	0	100	100
17	AL14	117/117 (100%)	117 (100%)	0	100	100
18	AL15	171/171 (100%)	170 (99%)	1 (1%)	78	93
19	AL16	171/171 (100%)	169 (99%)	2 (1%)	63	86
20	AL17	134/134 (100%)	133 (99%)	1 (1%)	76	92
21	AL18	164/168 (98%)	164 (100%)	0	100	100
22	AL19	159/159 (100%)	157 (99%)	2 (1%)	61	86
23	AL20	157/157 (100%)	157 (100%)	0	100	100
24	AL21	139/139 (100%)	137 (99%)	2 (1%)	59	85
25	AL22	89/89 (100%)	89 (100%)	0	100	100
26	AL23	101/101 (100%)	100 (99%)	1 (1%)	68	89
27	AL24	55/100 (55%)	55 (100%)	0	100	100
28	AL25	106/106 (100%)	106 (100%)	0	100	100
29	AL26	124/124 (100%)	123 (99%)	1 (1%)	73	90
30	AL27	117/117 (100%)	117 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	AL28	119/119 (100%)	118 (99%)	1 (1%)	73	90
32	AL29	84/84 (100%)	82 (98%)	2 (2%)	43	75
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	89
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%)	62 (97%)	2 (3%)	35	69
42	AL39	47/47 (100%)	46 (98%)	1 (2%)	47	77
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	85
47	ALNW	107/108 (99%)	106 (99%)	1 (1%)	70	90
48	ALP0	24/24 (100%)	24 (100%)	0	100	100
49	ARAC	272/272 (100%)	271 (100%)	1 (0%)	84	94
50	AS00	180/181 (99%)	180 (100%)	0	100	100
51	AS01	194/194 (100%)	194 (100%)	0	100	100
52	AS02	187/187 (100%)	186 (100%)	1 (0%)	81	93
53	AS03	190/190 (100%)	187 (98%)	3 (2%)	55	83
54	AS04	224/224 (100%)	221 (99%)	3 (1%)	61	86
55	AS05	158/161 (98%)	158 (100%)	0	100	100
56	AS06	206/207 (100%)	206 (100%)	0	100	100
57	AS07	165/169 (98%)	165 (100%)	0	100	100
58	AS08	178/178 (100%)	178 (100%)	0	100	100
59	AS09	161/161 (100%)	161 (100%)	0	100	100
60	AS10	87/87 (100%)	85 (98%)	2 (2%)	44	76
61	AS11	130/136 (96%)	127 (98%)	3 (2%)	44	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	AS12	99/99 (100%)	98 (99%)	1 (1%)	68	89
63	AS13	130/130 (100%)	130 (100%)	0	100	100
64	AS14	104/105 (99%)	104 (100%)	0	100	100
65	AS15	109/109 (100%)	109 (100%)	0	100	100
66	AS16	117/117 (100%)	116 (99%)	1 (1%)	70	90
67	AS17	119/119 (100%)	119 (100%)	0	100	100
68	AS18	125/125 (100%)	123 (98%)	2 (2%)	55	83
69	AS19	111/111 (100%)	108 (97%)	3 (3%)	39	73
70	AS20	92/92 (100%)	92 (100%)	0	100	100
71	AS21	67/67 (100%)	67 (100%)	0	100	100
72	AS22	112/112 (100%)	111 (99%)	1 (1%)	70	90
73	AS23	113/113 (100%)	113 (100%)	0	100	100
74	AS24	107/107 (100%)	105 (98%)	2 (2%)	50	79
75	AS25	66/66 (100%)	64 (97%)	2 (3%)	36	70
76	AS26	88/88 (100%)	87 (99%)	1 (1%)	65	88
77	AS27	75/75 (100%)	74 (99%)	1 (1%)	61	86
78	AS28	55/55 (100%)	54 (98%)	1 (2%)	51	80
79	AS29	48/48 (100%)	47 (98%)	1 (2%)	47	77
80	AS30	46/46 (100%)	45 (98%)	1 (2%)	45	77
81	AS31	61/61 (100%)	60 (98%)	1 (2%)	55	83
83	GR1	5/20 (25%)	5 (100%)	0	100	100
All	All	9778/9987 (98%)	9716 (99%)	62 (1%)	76	93

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	AL02	242	ARG
6	AL03	261	ARG
7	AL04	188	ARG
9	AL06	58	ARG
9	AL06	213	LYS
10	AL07	35	LYS
11	AL08	228	ARG
11	AL08	270	LYS
11	AL08	288	ARG

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Mol	Chain	Res	Type
12	AL09	7	ASN
12	AL09	52	LYS
13	AL10	82	LYS
18	AL15	50	ARG
19	AL16	42	ASN
19	AL16	187	LYS
20	AL17	97	ASN
22	AL19	16	ARG
22	AL19	133	LYS
24	AL21	117	LYS
24	AL21	146	LYS
26	AL23	48	ARG
29	AL26	2	LYS
31	AL28	87	ARG
32	AL29	63	LYS
32	AL29	91	ARG
37	AL34	54	ARG
41	AL38	9	LYS
41	AL38	57	LYS
42	AL39	46	ARG
46	AL43	17	ARG
47	ALNW	71	ARG
49	ARAC	118	ARG
52	AS02	121	ARG
53	AS03	76	ARG
53	AS03	124	ARG
53	AS03	227	LYS
54	AS04	22	LYS
54	AS04	113	ARG
54	AS04	120	LYS
60	AS10	17	LYS
60	AS10	96	ARG
61	AS11	20	LYS
61	AS11	32	LYS
61	AS11	97	ARG
62	AS12	96	ARG
66	AS16	106	LYS
68	AS18	78	LYS
68	AS18	108	ARG
69	AS19	16	ARG
69	AS19	29	LYS
69	AS19	142	LYS

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Mol	Chain	Res	Type
72	AS22	118	ARG
74	AS24	100	LYS
74	AS24	110	ARG
75	AS25	57	LYS
75	AS25	104	ARG
76	AS26	5	ARG
77	AS27	16	LYS
78	AS28	66	ARG
79	AS29	37	ASN
80	AS30	99	LYS
81	AS31	138	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A18S	1680/1698 (98%)	351 (20%)	17 (1%)
2	A28S	3529/3552 (99%)	740 (20%)	53 (1%)
3	A58S	149/151 (98%)	29 (19%)	1 (0%)
4	A5S	119/120 (99%)	11 (9%)	0
82	ETRN	76/77 (98%)	12 (15%)	0
82	PTRN	73/77 (94%)	13 (17%)	1 (1%)
84	MRNA	9/28 (32%)	3 (33%)	0
All	All	5635/5703 (98%)	1159 (20%)	72 (1%)

All (1159) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A18S	2	A
1	A18S	3	C
1	A18S	4	C
1	A18S	25	A
1	A18S	26	U
1	A18S	33	G
1	A18S	41	G
1	A18S	42	A
1	A18S	44	U
1	A18S	45	A
1	A18S	46	A

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Mol	Chain	Res	Type
1	A18S	56	G
1	A18S	62	G
1	A18S	67	C
1	A18S	68	A
1	A18S	71	G
1	A18S	77	A
1	A18S	79	A
1	A18S	103	A
1	A18S	110	U
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
1	A18S	130	G
1	A18S	143	U
1	A18S	146	G
1	A18S	147	A
1	A18S	155	G
1	A18S	158	A
1	A18S	160	U
1	A18S	161	U
1	A18S	162	C
1	A18S	168	C
1	A18S	180	G
1	A18S	182	C
1	A18S	183	G
1	A18S	184	G
1	A18S	187	G
1	A18S	190	G
1	A18S	191	A
1	A18S	192	C
1	A18S	206	G
1	A18S	224	A
1	A18S	289	G
1	A18S	292	A
1	A18S	306	C
1	A18S	307	G
1	A18S	308	G
1	A18S	309	G

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Mol	Chain	Res	Type
1	A18S	312	G
1	A18S	314	U
1	A18S	319	C
1	A18S	320	G
1	A18S	335	G
1	A18S	339	A
1	A18S	340	C
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	381	C
1	A18S	385	G
1	A18S	386	C
1	A18S	398	A
1	A18S	400	C
1	A18S	407	G
1	A18S	408	A
1	A18S	409	C
1	A18S	418	A
1	A18S	420	G
1	A18S	435	A
1	A18S	436	G
1	A18S	438	G
1	A18S	448	A
1	A18S	450	C
1	A18S	464	A
1	A18S	465	A
1	A18S	466	G
1	A18S	467	G
1	A18S	472	C
1	A18S	473	A
1	A18S	474	G
1	A18S	476	A
1	A18S	482	G
1	A18S	483	C
1	A18S	487	U
1	A18S	492	C

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Mol	Chain	Res	Type
1	A18S	496	C
1	A18S	516	A
1	A18S	525	A
1	A18S	530	U
1	A18S	532	C
1	A18S	533	A
1	A18S	536	A
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	564	A
1	A18S	568	C
1	A18S	576	A
1	A18S	583	A
1	A18S	585	C
1	A18S	587	A
1	A18S	588	G
1	A18S	590	A
1	A18S	591	U
1	A18S	606	G
1	A18S	607	U
1	A18S	608	C
1	A18S	614	C
1	A18S	617	G
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	670	A
1	A18S	671	A
1	A18S	672	A
1	A18S	673	G

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Mol	Chain	Res	Type
1	A18S	684	G
1	A18S	688	U
1	A18S	752	G
1	A18S	753	C
1	A18S	754	G
1	A18S	798	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	833	C
1	A18S	834	C
1	A18S	844	U
1	A18S	847	A
1	A18S	852	G
1	A18S	853	C
1	A18S	859	G
1	A18S	861	A
1	A18S	870	A
1	A18S	871	U
1	A18S	872	A
1	A18S	873	G
1	A18S	874	G
1	A18S	878	G
1	A18S	879	C
1	A18S	887	U
1	A18S	888	U
1	A18S	890	U
1	A18S	894	G
1	A18S	897	U
1	A18S	898	U
1	A18S	900	C
1	A18S	901	G
1	A18S	907	G
1	A18S	913	A
1	A18S	914	U
1	A18S	919	A
1	A18S	920	A
1	A18S	933	G
1	A18S	934	G

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Mol	Chain	Res	Type
1	A18S	943	U
1	A18S	955	A
1	A18S	956	G
1	A18S	971	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	1045	U
1	A18S	1060	A
1	A18S	1062	A
1	A18S	1078	C
1	A18S	1080	A
1	A18S	1083	A
1	A18S	1085	C
1	A18S	1086	G
1	A18S	1087	A
1	A18S	1097	G
1	A18S	1100	A
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	1126	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
1	A18S	1154	U
1	A18S	1155	U
1	A18S	1166	G
1	A18S	1172	U
1	A18S	1195	A
1	A18S	1207	G
1	A18S	1215	C

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Mol	Chain	Res	Type
1	A18S	1221	G
1	A18S	1224	G
1	A18S	1229	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	1264	C
1	A18S	1265	A
1	A18S	1269	G
1	A18S	1274	G
1	A18S	1275	G
1	A18S	1280	G
1	A18S	1281	G
1	A18S	1282	A
1	A18S	1284	A
1	A18S	1285	G
1	A18S	1286	G
1	A18S	1293	A
1	A18S	1299	A
1	A18S	1301	A
1	A18S	1302	G
1	A18S	1303	C
1	A18S	1307	U
1	A18S	1308	U
1	A18S	1309	C
1	A18S	1310	U
1	A18S	1313	A
1	A18S	1316	C
1	A18S	1333	U
1	A18S	1341	C
1	A18S	1342	U
1	A18S	1371	U
1	A18S	1372	U
1	A18S	1378	A
1	A18S	1382	A
1	A18S	1394	G
1	A18S	1395	C
1	A18S	1396	A
1	A18S	1397	U

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Mol	Chain	Res	Type
1	A18S	1398	G
1	A18S	1401	A
1	A18S	1402	A
1	A18S	1409	A
1	A18S	1412	C
1	A18S	1428	G
1	A18S	1431	G
1	A18S	1438	A
1	A18S	1439	A
1	A18S	1442	U
1	A18S	1454	A
1	A18S	1462	U
1	A18S	1463	U
1	A18S	1466	G
1	A18S	1476	A
1	A18S	1477	U
1	A18S	1478	U
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	1510	G
1	A18S	1521	C
1	A18S	1522	A
1	A18S	1533	A
1	A18S	1544	C
1	A18S	1548	G
1	A18S	1552	G
1	A18S	1553	C
1	A18S	1556	A
1	A18S	1557	C
1	A18S	1570	G
1	A18S	1574	C
1	A18S	1575	G
1	A18S	1580	A
1	A18S	1584	G
1	A18S	1585	U
1	A18S	1586	U
1	A18S	1587	G

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Mol	Chain	Res	Type
1	A18S	1588	A
1	A18S	1598	G
1	A18S	1601	A
1	A18S	1603	G
1	A18S	1606	G
1	A18S	1621	U
1	A18S	1623	A
1	A18S	1637	A
1	A18S	1638	G
1	A18S	1647	A
1	A18S	1648	G
1	A18S	1649	U
1	A18S	1654	G
1	A18S	1665	G
1	A18S	1680	G
1	A18S	1683	C
1	A18S	1686	G
1	A18S	1695	A
1	A18S	1698	C
1	A18S	1699	A
1	A18S	1721	U
1	A18S	1722	G
1	A18S	1744	G
1	A18S	1745	A
1	A18S	1748	G
1	A18S	1753	C
1	A18S	1756	C
1	A18S	1779	G
1	A18S	1781	A
1	A18S	1783	C
1	A18S	1784	G
1	A18S	1785	C
1	A18S	1823	A
1	A18S	1825	A
1	A18S	1826	G
1	A18S	1836	G
1	A18S	1838	U
1	A18S	1849	G
1	A18S	1851	A
1	A18S	1861	G
1	A18S	1862	G
1	A18S	1863	A

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Mol	Chain	Res	Type
1	A18S	1865	C
1	A18S	1866	A
1	A18S	1867	U
1	A18S	1869	A
2	A28S	12	A
2	A28S	13	U
2	A28S	25	A
2	A28S	39	A
2	A28S	42	A
2	A28S	49	U
2	A28S	56	A
2	A28S	59	A
2	A28S	64	A
2	A28S	65	A
2	A28S	71	C
2	A28S	72	C
2	A28S	73	A
2	A28S	74	G
2	A28S	91	G
2	A28S	109	G
2	A28S	110	C
2	A28S	116	G
2	A28S	117	C
2	A28S	118	C
2	A28S	119	G
2	A28S	120	A
2	A28S	126	C
2	A28S	132	G
2	A28S	134	G
2	A28S	135	G
2	A28S	136	C
2	A28S	137	G
2	A28S	142	G
2	A28S	143	C
2	A28S	144	G
2	A28S	159	C
2	A28S	170	C
2	A28S	171	U
2	A28S	172	C
2	A28S	177	G
2	A28S	190	G
2	A28S	197	A

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Mol	Chain	Res	Type
2	A28S	200	U
2	A28S	201	C
2	A28S	202	C
2	A28S	207	G
2	A28S	209	U
2	A28S	210	C
2	A28S	216	C
2	A28S	218	A
2	A28S	219	G
2	A28S	220	C
2	A28S	224	U
2	A28S	233	U
2	A28S	234	G
2	A28S	246	G
2	A28S	256	G
2	A28S	258	G
2	A28S	262	G
2	A28S	264	C
2	A28S	265	C
2	A28S	266	C
2	A28S	275	C
2	A28S	276	C
2	A28S	280	G
2	A28S	297	U
2	A28S	306	A
2	A28S	309	C
2	A28S	315	G
2	A28S	316	U
2	A28S	323	C
2	A28S	334	A
2	A28S	340	C
2	A28S	350	C
2	A28S	363	A
2	A28S	387	G
2	A28S	407	A
2	A28S	412	G
2	A28S	413	G
2	A28S	431	G
2	A28S	432	U
2	A28S	440	U
2	A28S	446	C
2	A28S	449	C

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Mol	Chain	Res	Type
2	A28S	452	A
2	A28S	453	G
2	A28S	454	U
2	A28S	455	C
2	A28S	458	C
2	A28S	462	G
2	A28S	463	A
2	A28S	464	G
2	A28S	465	G
2	A28S	467	U
2	A28S	468	U
2	A28S	481	G
2	A28S	481(A)	C
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	497	G
2	A28S	498	C
2	A28S	499	G
2	A28S	505	G
2	A28S	506	C
2	A28S	510	U
2	A28S	517	C
2	A28S	520	U
2	A28S	521	C
2	A28S	647	G
2	A28S	657	C
2	A28S	658	C
2	A28S	660	G
2	A28S	662	C
2	A28S	665	C
2	A28S	666	G
2	A28S	667	A
2	A28S	668	C
2	A28S	669	C
2	A28S	672	C
2	A28S	683	C
2	A28S	685	C
2	A28S	686	A

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Mol	Chain	Res	Type
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	729	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	750	U
2	A28S	758	G
2	A28S	759	G
2	A28S	905	C
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
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	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

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Mol	Chain	Res	Type
2	A28S	965	G
2	A28S	966	A
2	A28S	967	C
2	A28S	968	C
2	A28S	969	C
2	A28S	972	C
2	A28S	979	C
2	A28S	983	C
2	A28S	1066	G
2	A28S	1072	C
2	A28S	1073	G
2	A28S	1082	C
2	A28S	1174	G
2	A28S	1179	U
2	A28S	1184	A
2	A28S	1185	G
2	A28S	1187	G
2	A28S	1195	G
2	A28S	1211	G
2	A28S	1212	G
2	A28S	1214	C
2	A28S	1215	C
2	A28S	1234	G
2	A28S	1235	G
2	A28S	1236	C
2	A28S	1237	C
2	A28S	1238	A
2	A28S	1239	C
2	A28S	1275	G
2	A28S	1277	G
2	A28S	1284	G
2	A28S	1285	U
2	A28S	1287	G
2	A28S	1292	C
2	A28S	1295	U
2	A28S	1296	G
2	A28S	1301	C
2	A28S	1303	A
2	A28S	1304	C
2	A28S	1314	C
2	A28S	1326	A
2	A28S	1330	A

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Mol	Chain	Res	Type
2	A28S	1337	A
2	A28S	1354	A
2	A28S	1358	G
2	A28S	1359	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	1416	G
2	A28S	1419	G
2	A28S	1420	A
2	A28S	1421	G
2	A28S	1429	C
2	A28S	1433	A
2	A28S	1445	U
2	A28S	1446	C
2	A28S	1456	C
2	A28S	1457	G
2	A28S	1465	G
2	A28S	1475	G
2	A28S	1478	C
2	A28S	1481	C
2	A28S	1482	G
2	A28S	1483	C
2	A28S	1484	G
2	A28S	1486	C
2	A28S	1487	G
2	A28S	1497	A
2	A28S	1498	G
2	A28S	1502	G
2	A28S	1516	G
2	A28S	1523	A
2	A28S	1525	A
2	A28S	1534	A
2	A28S	1547	A
2	A28S	1563	A
2	A28S	1566	C
2	A28S	1574	G

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Mol	Chain	Res	Type
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	1638	A
2	A28S	1641	G
2	A28S	1650	A
2	A28S	1654	G
2	A28S	1661	C
2	A28S	1676	C
2	A28S	1677	U
2	A28S	1691	G
2	A28S	1721	G
2	A28S	1740	C
2	A28S	1742	A
2	A28S	1752	G
2	A28S	1755	C
2	A28S	1756	U
2	A28S	1757	U
2	A28S	1760	G
2	A28S	1761	G
2	A28S	1764	G
2	A28S	1765	A
2	A28S	1768	C
2	A28S	1769	G
2	A28S	1772	C
2	A28S	1773	U
2	A28S	1775	A
2	A28S	1776	A
2	A28S	1777	C
2	A28S	1781	U
2	A28S	1787	A
2	A28S	1803	G
2	A28S	1804	A
2	A28S	1805	A
2	A28S	1806	G

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Mol	Chain	Res	Type
2	A28S	1812	C
2	A28S	1815	G
2	A28S	1819	G
2	A28S	1820	U
2	A28S	1821	G
2	A28S	1822	U
2	A28S	1828	C
2	A28S	1834	U
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	1892	A
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	1930	U
2	A28S	1931	C
2	A28S	1935	C
2	A28S	1938	C
2	A28S	1940	G
2	A28S	1947	U
2	A28S	1948	G
2	A28S	1951	G
2	A28S	1959	U
2	A28S	1961	G
2	A28S	1962	A
2	A28S	1964	A
2	A28S	1971	U
2	A28S	1974	U
2	A28S	1976	G
2	A28S	1983	A
2	A28S	1984	A
2	A28S	1985	G
2	A28S	1987	C
2	A28S	1991	A
2	A28S	1993	C

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Mol	Chain	Res	Type
2	A28S	1997	U
2	A28S	2001	G
2	A28S	2002	A
2	A28S	2003	G
2	A28S	2005	G
2	A28S	2011	C
2	A28S	2020	U
2	A28S	2024	G
2	A28S	2026	A
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	2090	U
2	A28S	2092	G
2	A28S	2093	G
2	A28S	2094	C
2	A28S	2095	A
2	A28S	2097	A
2	A28S	2098	G
2	A28S	2100	G
2	A28S	2102	G
2	A28S	2104	A
2	A28S	2105	A
2	A28S	2107	A
2	A28S	2108	G
2	A28S	2267	U
2	A28S	2268	A
2	A28S	2270	G
2	A28S	2275	G
2	A28S	2289	C
2	A28S	2300	A
2	A28S	2301	G
2	A28S	2306	G
2	A28S	2313	A
2	A28S	2314	G

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Mol	Chain	Res	Type
2	A28S	2316	G
2	A28S	2331	G
2	A28S	2333	G
2	A28S	2348	G
2	A28S	2351	C
2	A28S	2360	A
2	A28S	2395	A
2	A28S	2398	U
2	A28S	2410	C
2	A28S	2416	G
2	A28S	2422	C
2	A28S	2425	U
2	A28S	2433	G
2	A28S	2441	C
2	A28S	2450	G
2	A28S	2475	G
2	A28S	2476	G
2	A28S	2488	C
2	A28S	2489	C
2	A28S	2490	U
2	A28S	2491	C
2	A28S	2492	C
2	A28S	2503	G
2	A28S	2504	C
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	2545	U
2	A28S	2546	G
2	A28S	2547	G
2	A28S	2549	G
2	A28S	2553	A
2	A28S	2554	U
2	A28S	2564	G
2	A28S	2570	U
2	A28S	2573	A
2	A28S	2575	U
2	A28S	2583	C

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Mol	Chain	Res	Type
2	A28S	2586	G
2	A28S	2589	C
2	A28S	2602	G
2	A28S	2611	A
2	A28S	2638	G
2	A28S	2640	G
2	A28S	2647	A
2	A28S	2649	G
2	A28S	2653	C
2	A28S	2659	A
2	A28S	2661	U
2	A28S	2662	G
2	A28S	2669	C
2	A28S	2679	G
2	A28S	2687	U
2	A28S	2695	A
2	A28S	2696	A
2	A28S	2704	C
2	A28S	2707	U
2	A28S	2708	U
2	A28S	2710	C
2	A28S	2711	G
2	A28S	2712	G
2	A28S	2719	C
2	A28S	2724	G
2	A28S	2725	A
2	A28S	2726	G
2	A28S	2740	U
2	A28S	2743	A
2	A28S	2744	A
2	A28S	2753	G
2	A28S	2754	G
2	A28S	2759	G
2	A28S	2760	G
2	A28S	2761	U
2	A28S	2763	U
2	A28S	2764	A
2	A28S	2768	C
2	A28S	2769	U
2	A28S	2787	A
2	A28S	2788	U
2	A28S	2790	U

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Mol	Chain	Res	Type
2	A28S	2794	C
2	A28S	2798	A
2	A28S	2806	A
2	A28S	2807	A
2	A28S	2814	C
2	A28S	2826	U
2	A28S	2827	G
2	A28S	2837	U
2	A28S	2838	G
2	A28S	2842	G
2	A28S	2855	G
2	A28S	2875	C
2	A28S	2898	G
2	A28S	2900	U
2	A28S	3605	C
2	A28S	3617	G
2	A28S	3619	G
2	A28S	3625	G
2	A28S	3626	G
2	A28S	3630	A
2	A28S	3635	A
2	A28S	3646	A
2	A28S	3662	A
2	A28S	3663	A
2	A28S	3664	G
2	A28S	3673	C
2	A28S	3692	A
2	A28S	3696	C
2	A28S	3698	G
2	A28S	3711	A
2	A28S	3714	G
2	A28S	3748	A
2	A28S	3753	G
2	A28S	3759	A
2	A28S	3760	A
2	A28S	3763	A
2	A28S	3773	U
2	A28S	3774	A
2	A28S	3776	G
2	A28S	3777	G
2	A28S	3784	A
2	A28S	3786	U

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Mol	Chain	Res	Type
2	A28S	3791	C
2	A28S	3811	G
2	A28S	3812	C
2	A28S	3814	U
2	A28S	3817	A
2	A28S	3819	G
2	A28S	3838	U
2	A28S	3839	G
2	A28S	3840	U
2	A28S	3860	A
2	A28S	3876	A
2	A28S	3877	A
2	A28S	3878	C
2	A28S	3879	G
2	A28S	3889	G
2	A28S	3892	U
2	A28S	3897	G
2	A28S	3898	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	3956	G
2	A28S	3957	U
2	A28S	3959	U
2	A28S	3960	A
2	A28S	3963	A
2	A28S	3969	G
2	A28S	3971	G
2	A28S	3973	G
2	A28S	3976	C
2	A28S	4047	A
2	A28S	4048	A
2	A28S	4049	U
2	A28S	4050	A

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Mol	Chain	Res	Type
2	A28S	4065	G
2	A28S	4066	U
2	A28S	4069	U
2	A28S	4076	G
2	A28S	4085	A
2	A28S	4086	G
2	A28S	4088	C
2	A28S	4092	G
2	A28S	4093	G
2	A28S	4097	G
2	A28S	4116	C
2	A28S	4119	C
2	A28S	4120	U
2	A28S	4121	G
2	A28S	4125	C
2	A28S	4127	A
2	A28S	4128	A
2	A28S	4137	C
2	A28S	4155	C
2	A28S	4158	C
2	A28S	4162	C
2	A28S	4163	U
2	A28S	4166	G
2	A28S	4170	A
2	A28S	4183	G
2	A28S	4184	G
2	A28S	4191	G
2	A28S	4203	A
2	A28S	4212	A
2	A28S	4225	G
2	A28S	4229	U
2	A28S	4233	A
2	A28S	4249	G
2	A28S	4251	A
2	A28S	4253	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

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Mol	Chain	Res	Type
2	A28S	4291	G
2	A28S	4297	G
2	A28S	4304	A
2	A28S	4305	G
2	A28S	4306	U
2	A28S	4313	A
2	A28S	4314	C
2	A28S	4317	A
2	A28S	4318	C
2	A28S	4319	C
2	A28S	4329	G
2	A28S	4330	G
2	A28S	4332	C
2	A28S	4336	A
2	A28S	4349	C
2	A28S	4350	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	4387	C
2	A28S	4391	G
2	A28S	4394	A
2	A28S	4395	U
2	A28S	4405	G
2	A28S	4415	A
2	A28S	4419	U
2	A28S	4421	C
2	A28S	4422	A
2	A28S	4436	U
2	A28S	4437	U
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	4475	G
2	A28S	4488	A
2	A28S	4500	U

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Mol	Chain	Res	Type
2	A28S	4510	A
2	A28S	4512	U
2	A28S	4513	A
2	A28S	4518	A
2	A28S	4520	G
2	A28S	4524	G
2	A28S	4531	U
2	A28S	4548	A
2	A28S	4549	G
2	A28S	4560	C
2	A28S	4569	U
2	A28S	4573	G
2	A28S	4574	U
2	A28S	4575	G
2	A28S	4581	G
2	A28S	4586	G
2	A28S	4590	A
2	A28S	4599	A
2	A28S	4627	U
2	A28S	4636	U
2	A28S	4637	G
2	A28S	4639	G
2	A28S	4652	G
2	A28S	4656	A
2	A28S	4657	U
2	A28S	4667	C
2	A28S	4670	C
2	A28S	4672	A
2	A28S	4677	U
2	A28S	4691	A
2	A28S	4693	C
2	A28S	4694	G
2	A28S	4700	A
2	A28S	4709	U
2	A28S	4720	C
2	A28S	4729	A
2	A28S	4740	G
2	A28S	4743	G
2	A28S	4747	C
2	A28S	4751	G
2	A28S	4752	U
2	A28S	4754	G

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Mol	Chain	Res	Type
2	A28S	4756	C
2	A28S	4757	C
2	A28S	4759	C
2	A28S	4765	G
2	A28S	4771	C
2	A28S	4775	C
2	A28S	4868	G
2	A28S	4870	G
2	A28S	4871	C
2	A28S	4873	G
2	A28S	4875	G
2	A28S	4881	U
2	A28S	4882	U
2	A28S	4883	C
2	A28S	4885	U
2	A28S	4887	C
2	A28S	4894	A
2	A28S	4895	C
2	A28S	4904	G
2	A28S	4906	C
2	A28S	4910	A
2	A28S	4914	G
2	A28S	4915	G
2	A28S	4918	C
2	A28S	4919	G
2	A28S	4921	C
2	A28S	4922	C
2	A28S	4924	C
2	A28S	4925	U
2	A28S	4926	C
2	A28S	4927	G
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	4948	C
2	A28S	4949	G
2	A28S	4950	U
2	A28S	4951	G
2	A28S	4955	A

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Mol	Chain	Res	Type
2	A28S	4956	A
2	A28S	4957	C
2	A28S	4958	C
2	A28S	4960	G
2	A28S	4963	G
2	A28S	4964	C
2	A28S	4965	U
2	A28S	4966	A
2	A28S	4967	A
2	A28S	4976	U
2	A28S	4988	U
2	A28S	4990	C
2	A28S	4993	G
2	A28S	5006	U
2	A28S	5007	A
2	A28S	5014	A
2	A28S	5017	G
2	A28S	5020	G
2	A28S	5029	C
2	A28S	5031	G
2	A28S	5040	U
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	39	G
3	A58S	51	U
3	A58S	52	A
3	A58S	59	A
3	A58S	62	A
3	A58S	63	U
3	A58S	75	G
3	A58S	77	A
3	A58S	79	G

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Mol	Chain	Res	Type
3	A58S	87	G
3	A58S	90	C
3	A58S	94	G
3	A58S	103	A
3	A58S	105	C
3	A58S	109	C
3	A58S	110	U
3	A58S	111	U
3	A58S	114	G
3	A58S	122	G
3	A58S	125	C
3	A58S	126	C
3	A58S	127	U
3	A58S	128	C
3	A58S	147	G
3	A58S	151	G
3	A58S	156	U
4	A5S	22	A
4	A5S	33	U
4	A5S	53	U
4	A5S	54	A
4	A5S	63	C
4	A5S	64	G
4	A5S	97	G
4	A5S	100	A
4	A5S	110	G
4	A5S	111	C
4	A5S	120	U
82	ETRN	6	G
82	ETRN	16	C
82	ETRN	18	G
82	ETRN	19	G
82	ETRN	20	U
82	ETRN	46	G
82	ETRN	47	U
82	ETRN	48	C
82	ETRN	59	A
82	ETRN	61	C
82	ETRN	73	A
82	ETRN	76	A
84	MRNA	5	A
84	MRNA	8	U

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Mol	Chain	Res	Type
84	MRNA	9	U
82	PTRN	8	U
82	PTRN	9	G
82	PTRN	12	G
82	PTRN	13	C
82	PTRN	18	G
82	PTRN	19	G
82	PTRN	20	U
82	PTRN	21	A
82	PTRN	47	U
82	PTRN	48	C
82	PTRN	49	G
82	PTRN	57	A
82	PTRN	59	A

All (72) 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
1	A18S	532	C
1	A18S	553	U
1	A18S	642	U
1	A18S	752	G
1	A18S	870	A
1	A18S	1137	U
1	A18S	1394	G
1	A18S	1395	C
1	A18S	1396	A
1	A18S	1489	A
1	A18S	1520	G
1	A18S	1637	A
1	A18S	1664	A
2	A28S	12	A
2	A28S	48	G
2	A28S	125	C
2	A28S	142	G
2	A28S	245	C
2	A28S	275	C
2	A28S	406	C

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Mol	Chain	Res	Type
2	A28S	480	C
2	A28S	485	C
2	A28S	492	U
2	A28S	504	G
2	A28S	696	C
2	A28S	922(B)	C
2	A28S	930	G
2	A28S	966	A
2	A28S	971(A)	G
2	A28S	1072	C
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	2068	C
2	A28S	2089	G
2	A28S	2266	C
2	A28S	2502	A
2	A28S	2546	G
2	A28S	2639	U
2	A28S	2661	U
2	A28S	2695	A
2	A28S	3625	G
2	A28S	3697	U
2	A28S	3876	A
2	A28S	3888	G
2	A28S	3904	G
2	A28S	3959	U
2	A28S	3968	U
2	A28S	4075	U
2	A28S	4119	C
2	A28S	4232	U
2	A28S	4448	G
2	A28S	4699	U
2	A28S	4719	G

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Mol	Chain	Res	Type
2	A28S	4884	G
2	A28S	4925	U
2	A28S	4936	G
2	A28S	4947	U
3	A58S	124	U
82	PTRN	19	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	A28S	25
1	A18S	8

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Mol	Chain	Number of breaks
32	AL29	1
48	ALP0	1
11	AL08	1
3	A58S	1
13	AL10	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A28S	1249:C	O3'	1274:A	P	38.32
1	AL29	76:VAL	C	89:VAL	N	38.26
1	A28S	2110:G	O3'	2261:G	P	37.67
1	A28S	1219:G	O3'	1233:G	P	22.45
1	ALP0	22:ASP	C	59:THR	N	21.36
1	A18S	697:G	O3'	729:C	P	19.03
1	A28S	521:C	O3'	639:U	P	18.61
1	A18S	756:C	O3'	788:G	P	17.74
1	A28S	4099:G	O3'	4108:G	P	17.46
1	AL08	176:ALA	C	184:LYS	N	16.89
1	A18S	834:C	O3'	841:G	P	16.87
1	A28S	988:C	O3'	1065:G	P	16.85
1	A28S	1404:G	O3'	1413:C	P	16.83
1	A28S	4137:C	O3'	4147:G	P	16.07
1	A28S	180:C	O3'	189:G	P	15.88
1	A18S	1417:C	O3'	1423:C	P	15.56
1	A28S	5020:G	O3'	5028:G	P	15.38
1	A28S	2900:U	O3'	3598:C	P	15.34
1	A28S	1436:C	O3'	1443:A	P	15.31
1	A28S	1696:C	O3'	1720:C	P	15.08
1	A28S	3976:C	O3'	4035:G	P	14.42
1	A28S	4776:G	O3'	4860:G	P	13.21
1	A28S	1364:U	O3'	1368:A	P	13.04
1	A28S	4729:A	O3'	4737:G	P	13.04
1	A58S	79:G	O3'	85:U	P	11.70
1	AL10	103:LEU	C	112:GLN	N	10.47
1	A28S	1180:C	O3'	1183:C	P	8.88
1	A18S	736:C	O3'	743:U	P	8.31
1	A28S	511:C	O3'	515:C	P	8.09
1	A18S	745:C	O3'	749:U	P	7.40
1	A28S	1239:C	O3'	1244:G	P	5.72
1	A28S	1100:U	O3'	1168:G	P	5.63
1	A18S	225:G	O3'	287:U	P	4.90
1	A28S	760:G	O3'	904:C	P	4.66

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A28S	500:G	O3'	504:G	P	3.47
1	A28S	4899:G	O3'	4902:C	P	3.43
1	A28S	4740:G	O3'	4743:G	P	3.33
1	A18S	1432:U	O3'	1438:A	P	3.27

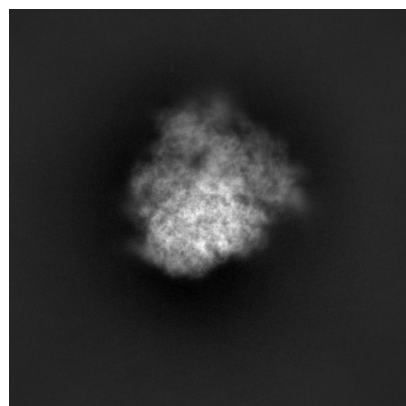
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26036. These allow visual inspection of the internal detail of the map and identification of artifacts.

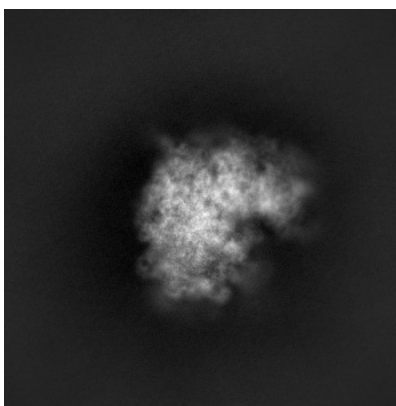
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

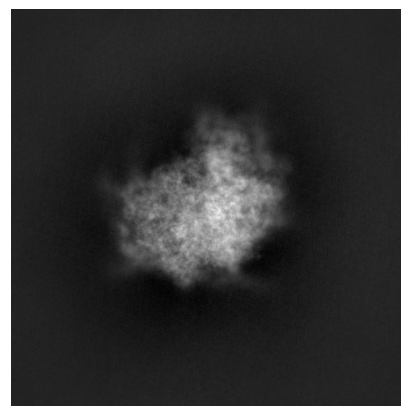
6.1.1 Primary map



X

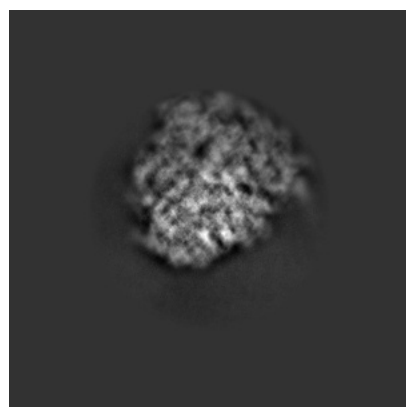


Y

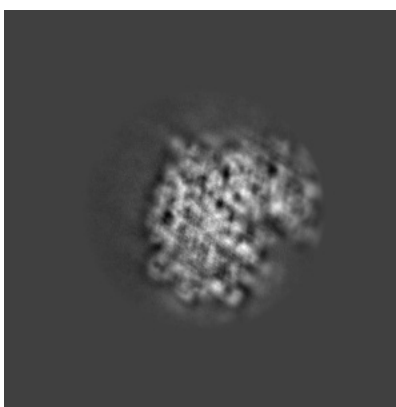


Z

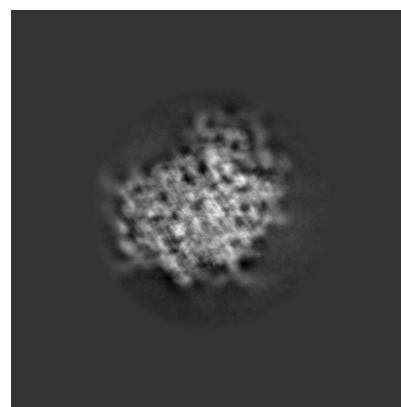
6.1.2 Raw map



X



Y

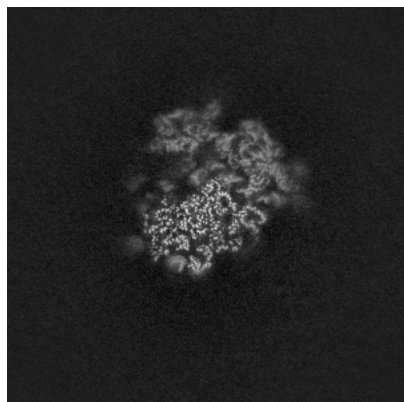


Z

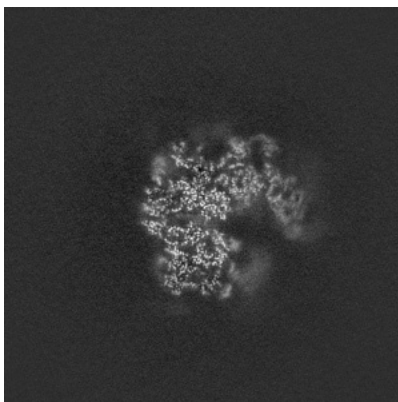
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

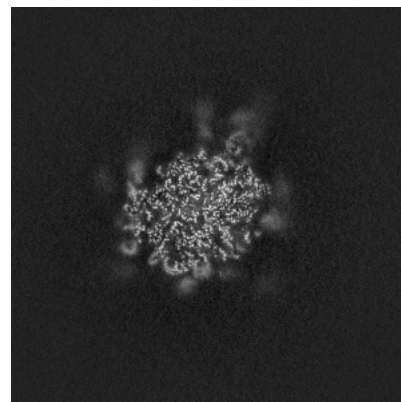
6.2.1 Primary map



X Index: 360

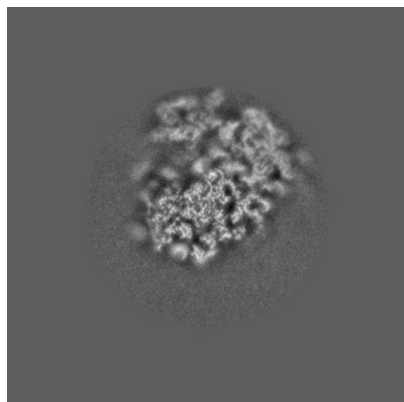


Y Index: 360

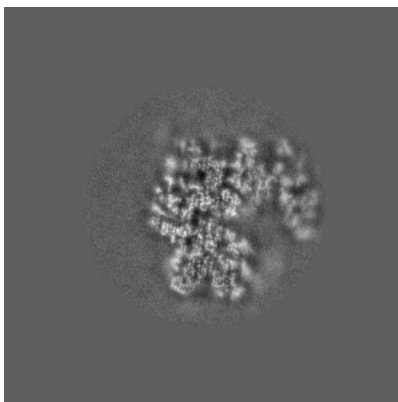


Z Index: 360

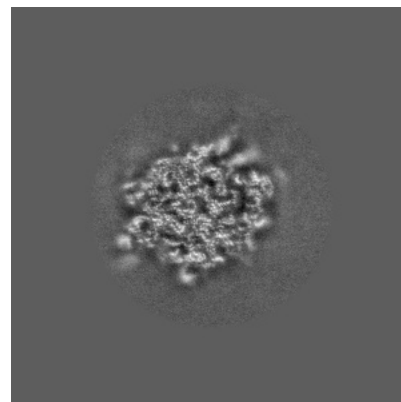
6.2.2 Raw map



X Index: 360



Y Index: 360

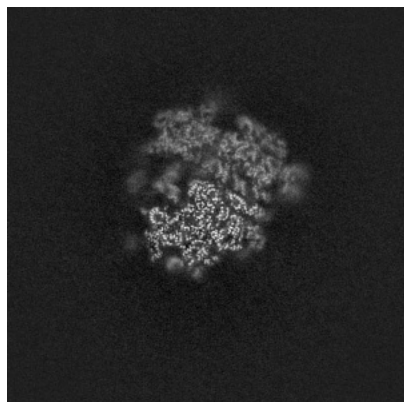


Z Index: 360

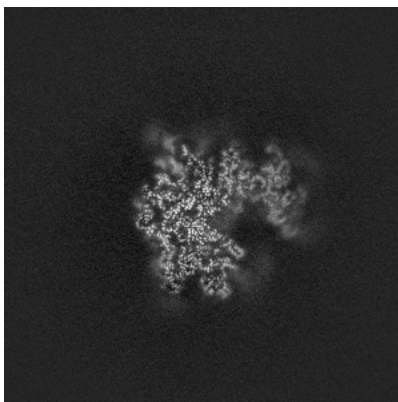
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

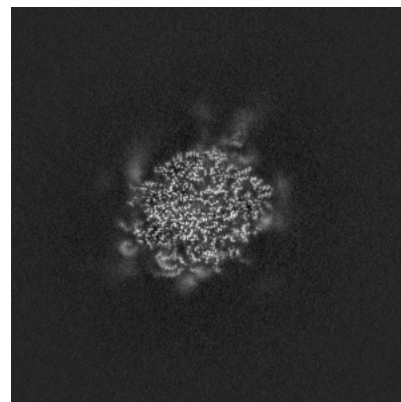
6.3.1 Primary map



X Index: 371

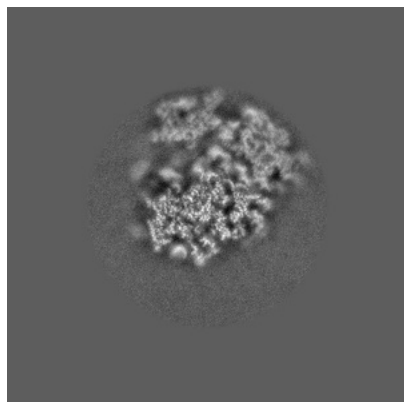


Y Index: 347

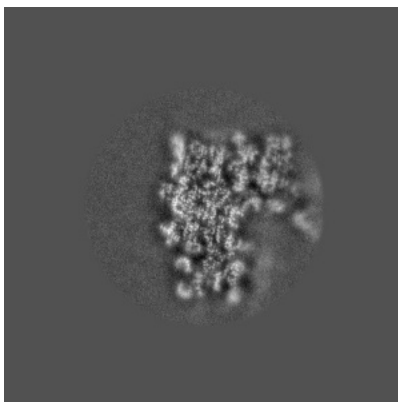


Z Index: 351

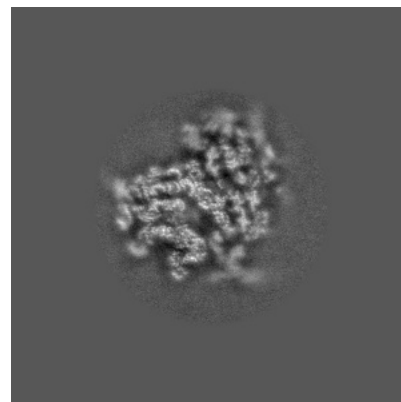
6.3.2 Raw map



X Index: 364



Y Index: 389

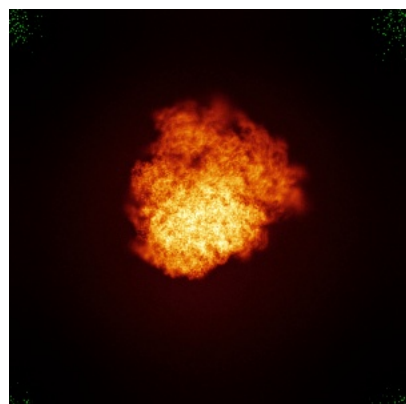


Z Index: 412

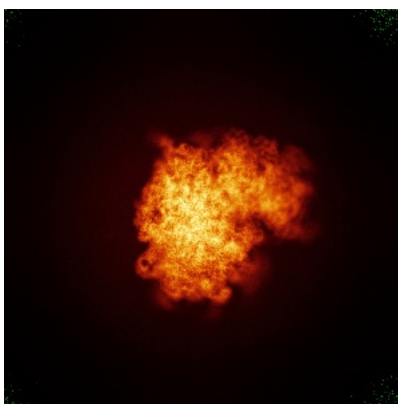
The images above show the largest variance slices of the map in three orthogonal directions.

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

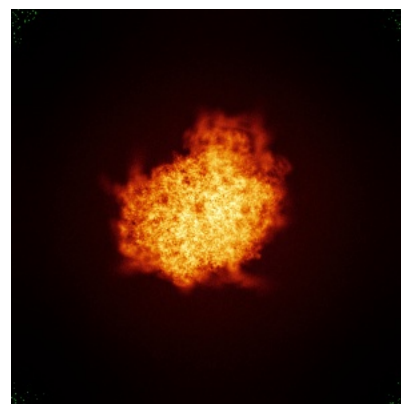
6.4.1 Primary map



X

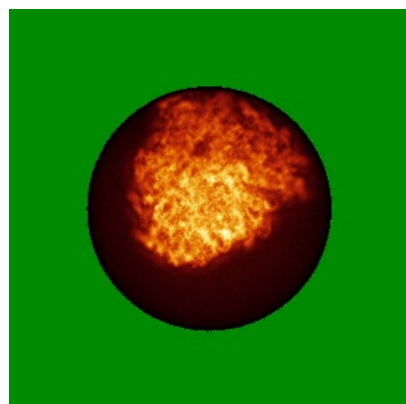


Y

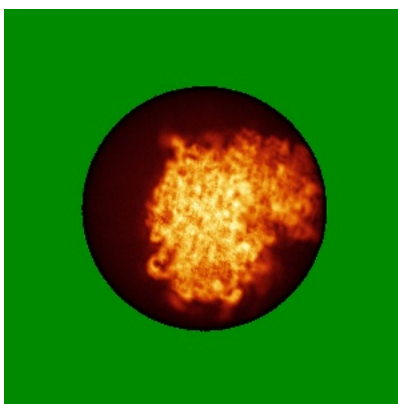


Z

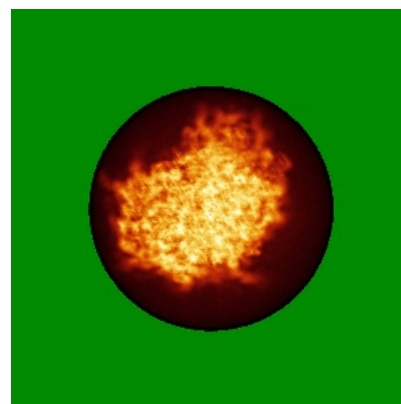
6.4.2 Raw map



X



Y

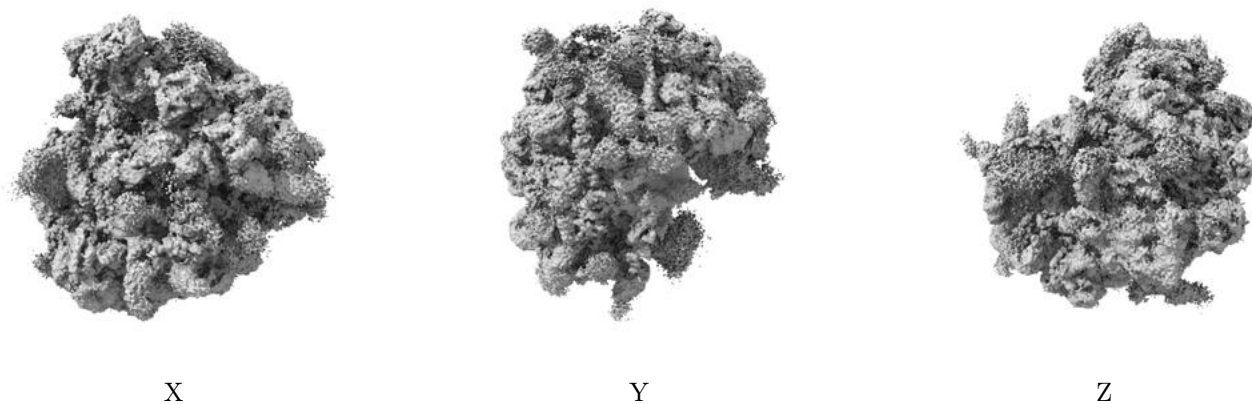


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

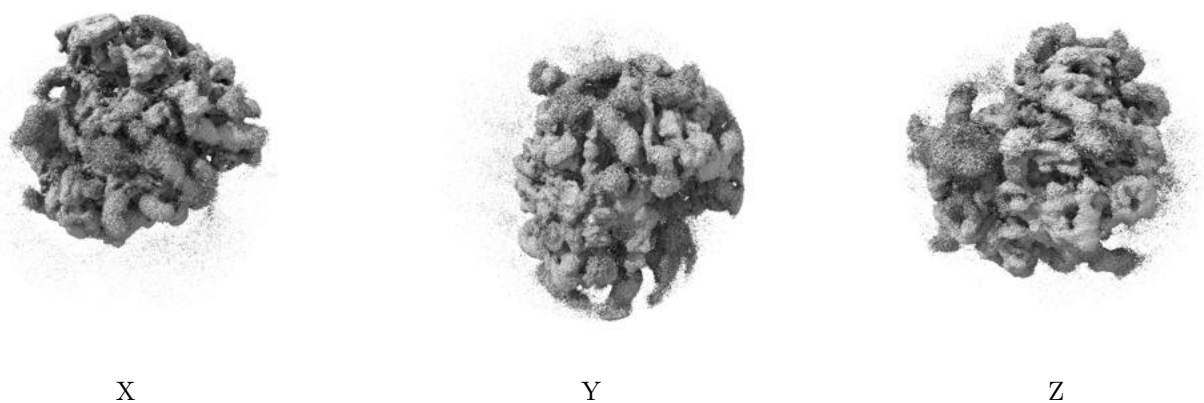
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 6.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

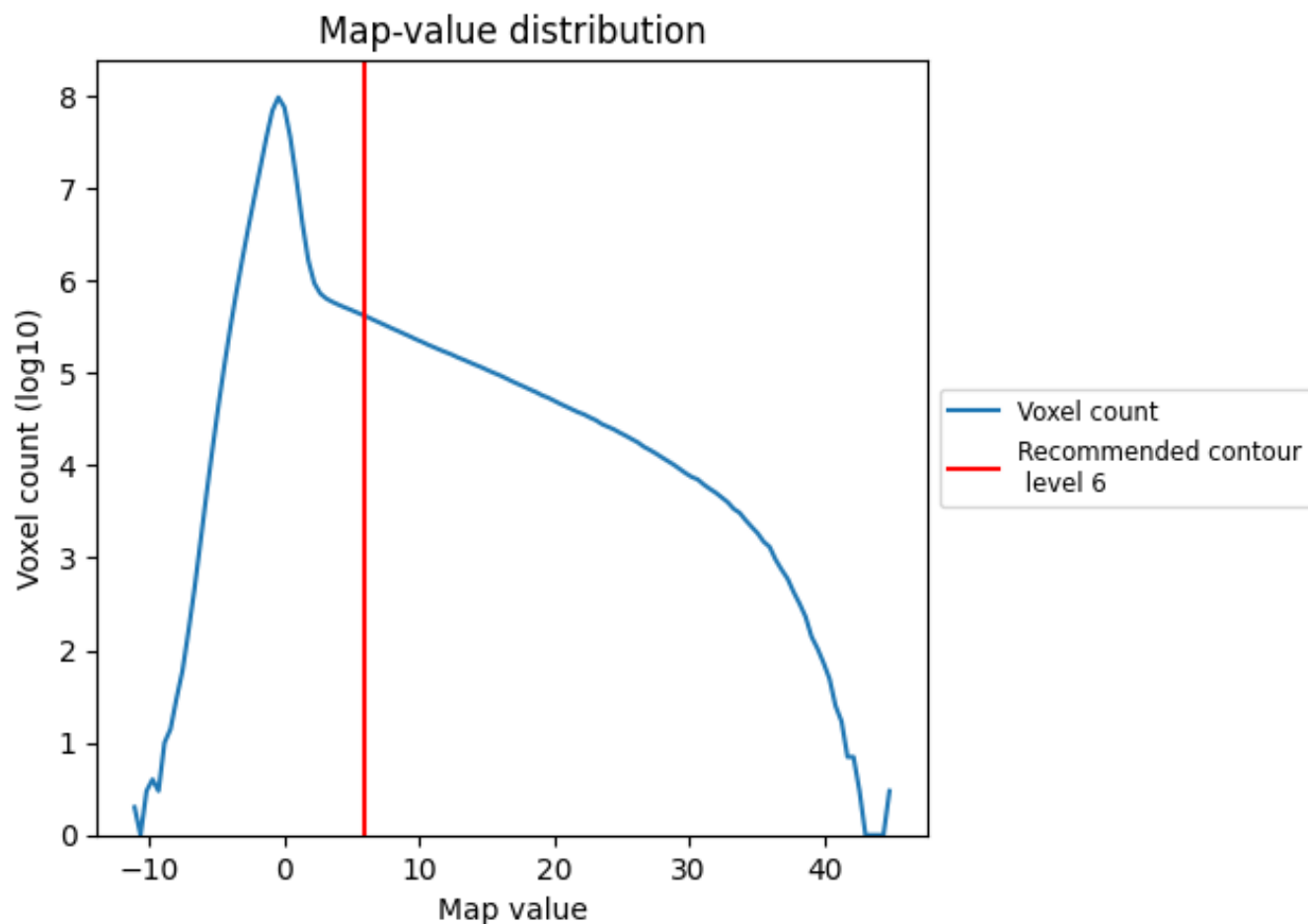
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

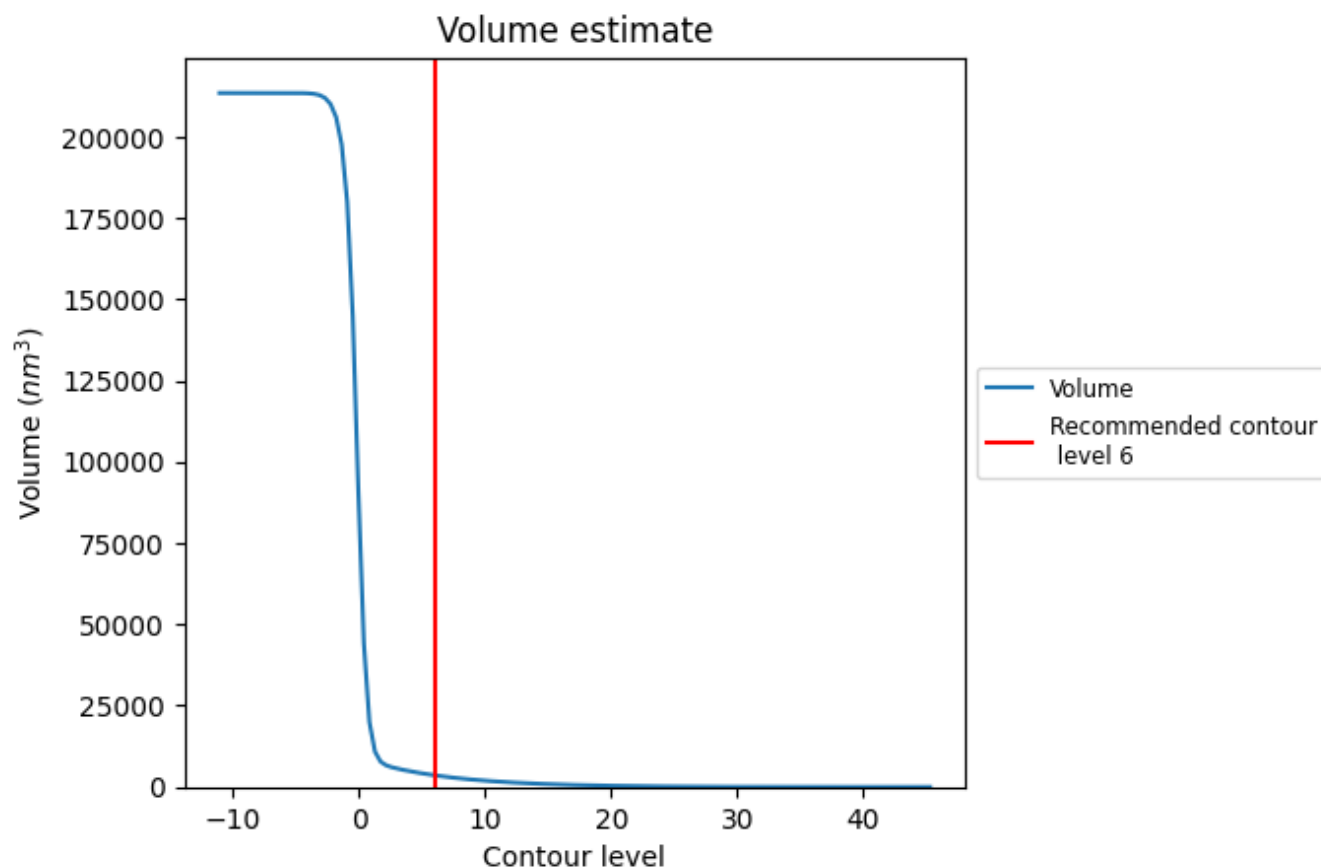
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

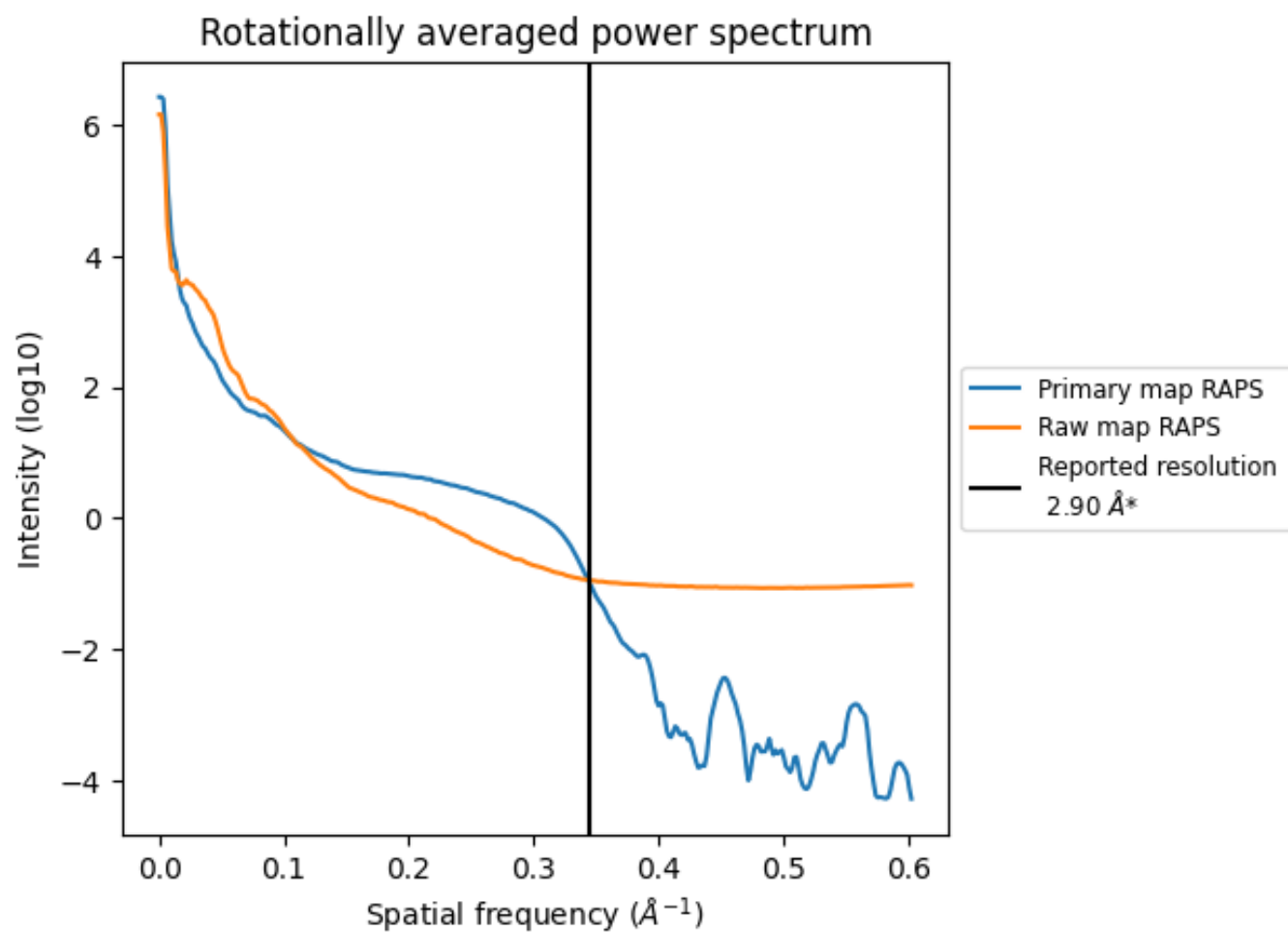
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3588 nm³; this corresponds to an approximate mass of 3241 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 ⓘ

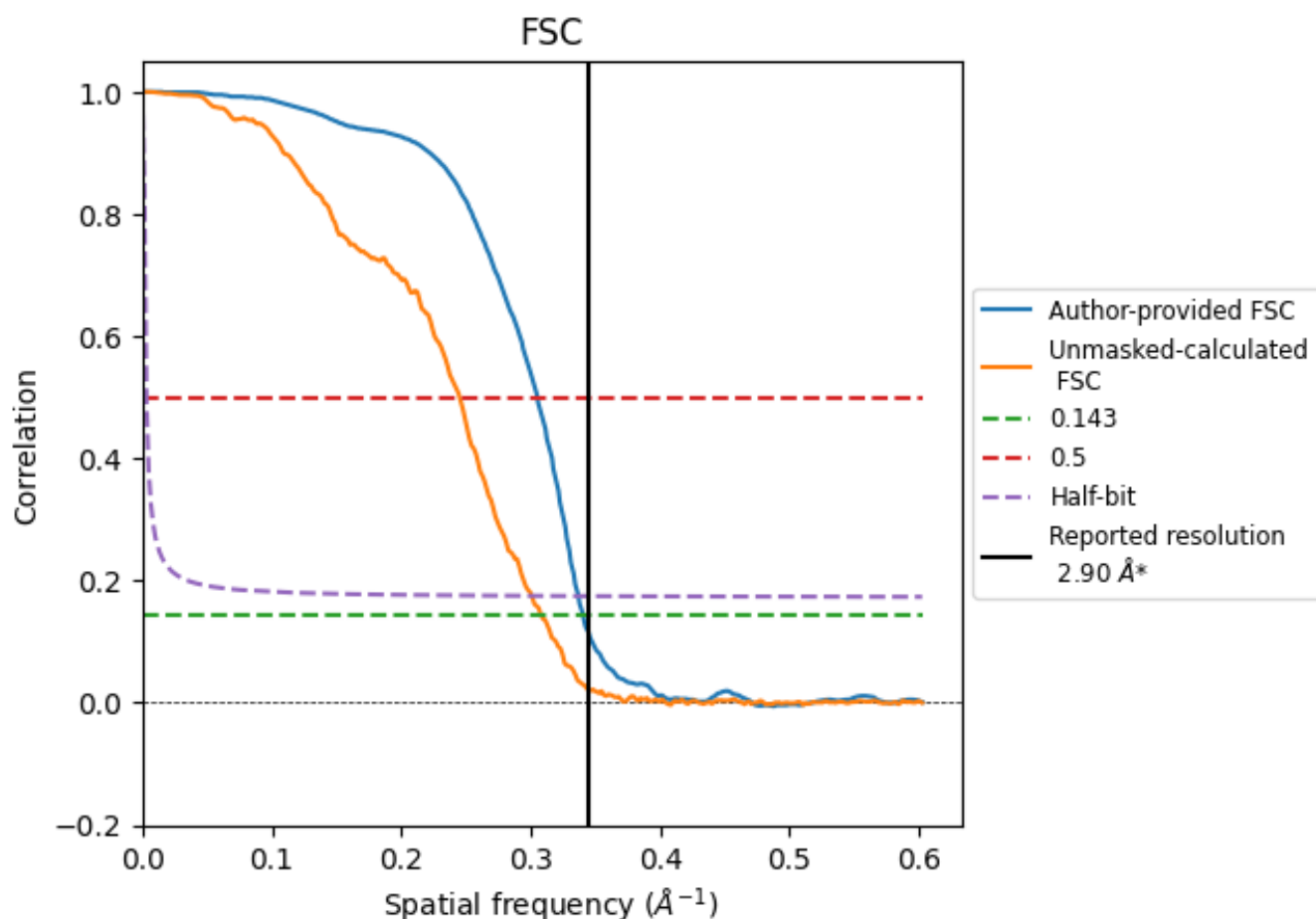


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

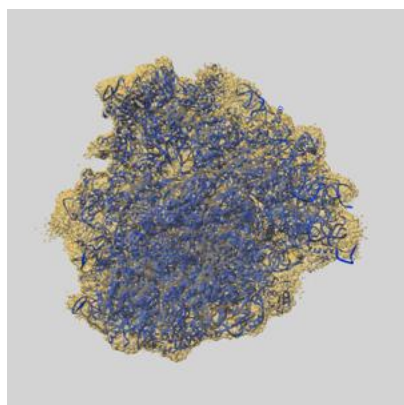
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.94	3.28	2.97
Unmasked-calculated*	3.25	4.08	3.32

*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 3.25 differs from the reported value 2.9 by more than 10 %

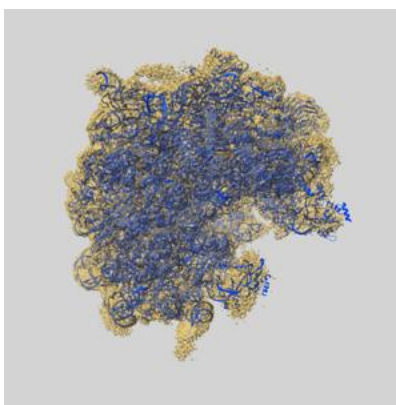
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26036 and PDB model 7TOR. Per-residue inclusion information can be found in section [3](#) on page [22](#).

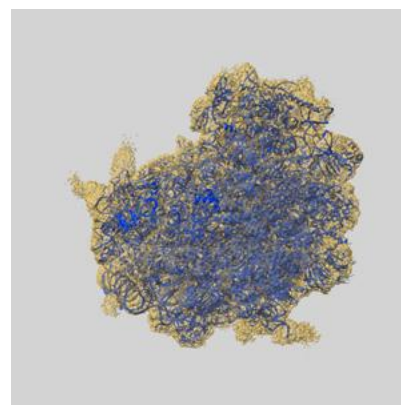
9.1 Map-model overlay [i](#)



X



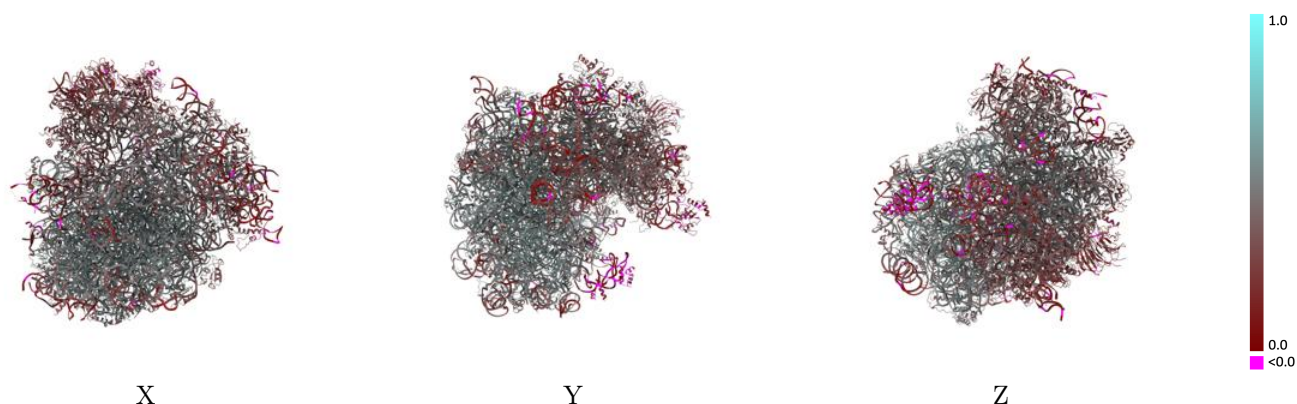
Y



Z

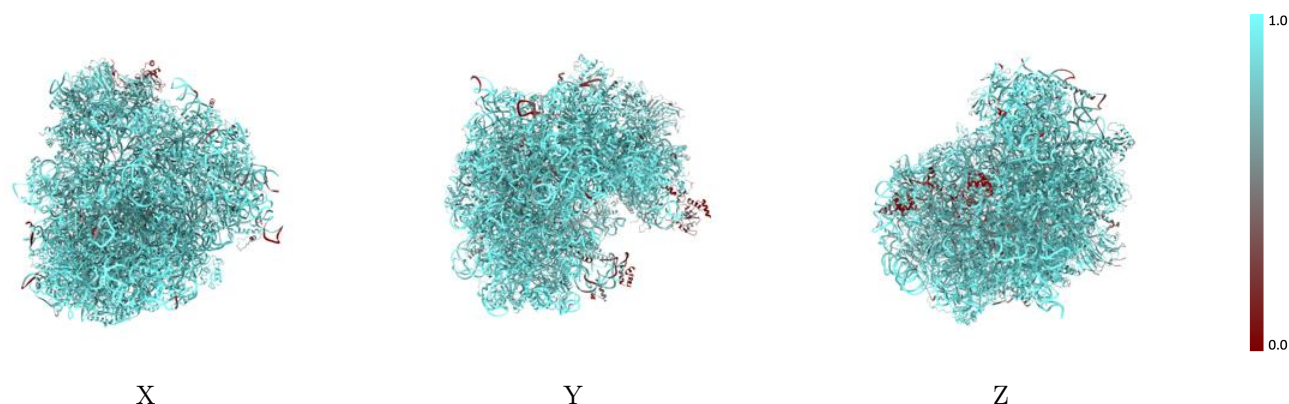
The images above show the 3D surface view of the map at the recommended contour level 6.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



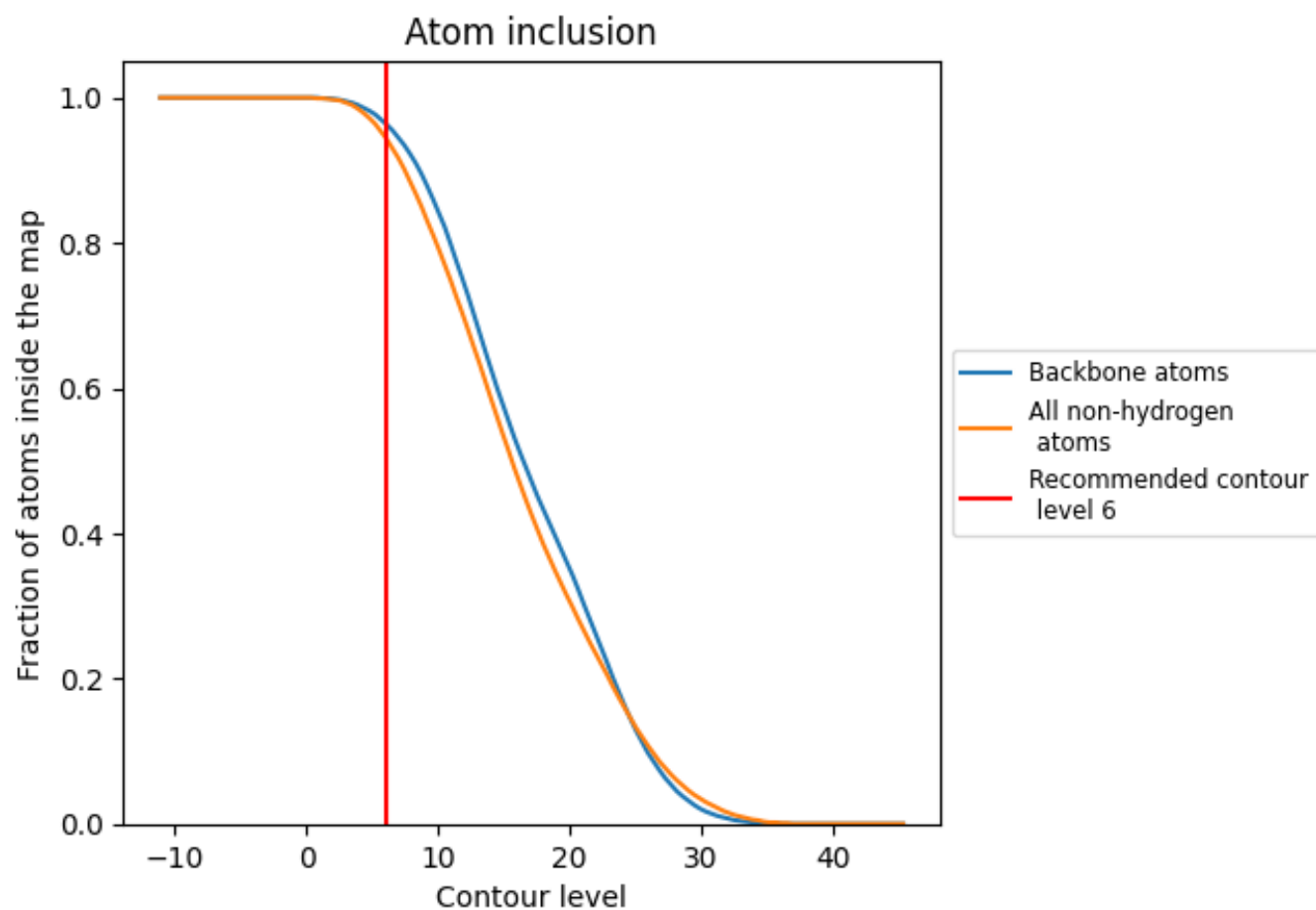
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9460	 0.4230
A18S	 0.9700	 0.3710
A28S	 0.9770	 0.4470
A58S	 0.9990	 0.4810
A5S	 0.9980	 0.5130
AL02	 0.9830	 0.5320
AL03	 0.9740	 0.5240
AL04	 0.9770	 0.5180
AL05	 0.9480	 0.4720
AL06	 0.9540	 0.4810
AL07	 0.9700	 0.5150
AL08	 0.9200	 0.4480
AL09	 0.9440	 0.4650
AL10	 0.9600	 0.4770
AL11	 0.9320	 0.4160
AL12	 0.0750	 -0.0150
AL13	 0.9410	 0.4860
AL14	 0.9620	 0.4870
AL15	 0.9870	 0.5300
AL16	 0.9710	 0.5160
AL17	 0.9790	 0.5180
AL18	 0.9680	 0.5110
AL19	 0.9310	 0.4580
AL20	 0.9740	 0.5240
AL21	 0.9680	 0.5060
AL22	 0.9580	 0.3480
AL23	 0.9770	 0.5270
AL24	 0.9690	 0.5100
AL25	 0.9690	 0.4950
AL26	 0.9640	 0.4940
AL27	 0.9730	 0.4780
AL28	 0.9820	 0.5300
AL29	 0.8900	 0.4370
AL30	 0.9660	 0.4800
AL31	 0.9720	 0.4980



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Chain	Atom inclusion	Q-score
AL32	 0.9850	 0.5360
AL33	 0.9800	 0.5480
AL34	 0.9620	 0.5020
AL35	 0.9650	 0.4820
AL36	 0.9520	 0.4610
AL37	 0.9880	 0.5290
AL38	 0.8960	 0.4340
AL39	 0.9740	 0.4910
AL40	 0.3370	 0.2340
AL41	 0.9360	 0.4620
AL42	 0.9380	 0.4820
AL43	 0.9490	 0.4950
ALNW	 0.9720	 0.5140
ALP0	 0.4600	 0.0370
ARAC	 0.7490	 0.2390
AS00	 0.9110	 0.3890
AS01	 0.9470	 0.4270
AS02	 0.8970	 0.4050
AS03	 0.8040	 0.3060
AS04	 0.9330	 0.3750
AS05	 0.9010	 0.3310
AS06	 0.8500	 0.2870
AS07	 0.8220	 0.3410
AS08	 0.8770	 0.3720
AS09	 0.9080	 0.3630
AS10	 0.8300	 0.2360
AS11	 0.9320	 0.4410
AS12	 0.2650	 0.1240
AS13	 0.9490	 0.4520
AS14	 0.9640	 0.4120
AS15	 0.8440	 0.2770
AS16	 0.8890	 0.3020
AS17	 0.8300	 0.3290
AS18	 0.8560	 0.2780
AS19	 0.9110	 0.2840
AS20	 0.8180	 0.2970
AS21	 0.9080	 0.3880
AS22	 0.9540	 0.4490
AS23	 0.9300	 0.4150
AS24	 0.8970	 0.3300
AS25	 0.8370	 0.2760
AS26	 0.9490	 0.4440

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Chain	Atom inclusion	Q-score
AS27	 0.9300	 0.3900
AS28	 0.9400	 0.3460
AS29	 0.8820	 0.2780
AS30	 0.8450	 0.3280
AS31	 0.1780	 0.1320
ETR1	 0.9750	 0.2360
GR1	 1.0000	 0.4110
GR2	 0.9200	 0.4060
MRNA	 0.8390	 0.2570
PTRN	 0.6840	 0.2340