



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 06:13 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 wwPDB EM Validation Summary 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:

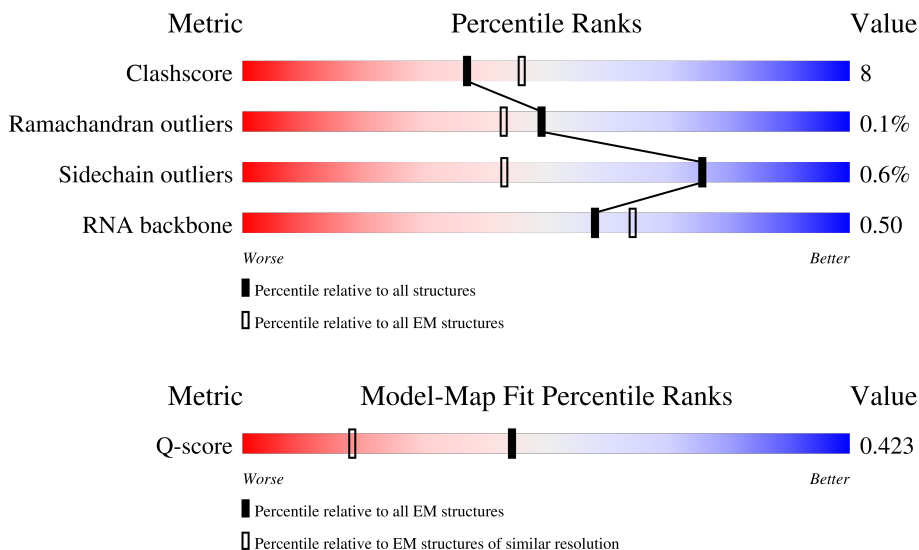
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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



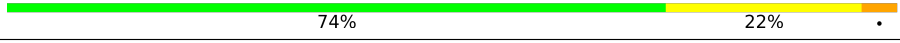
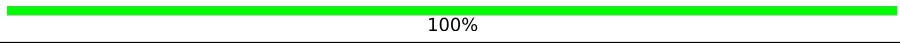
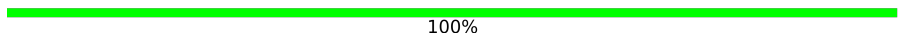
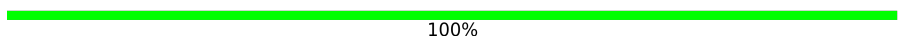
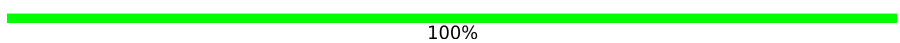

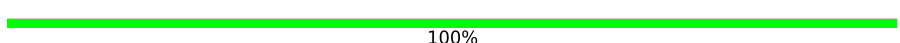
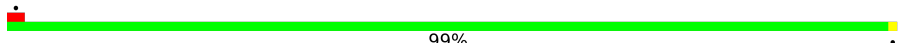
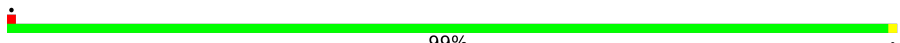
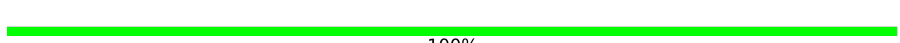


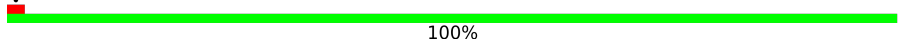
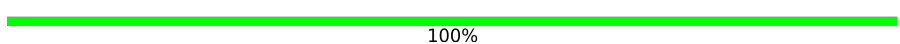
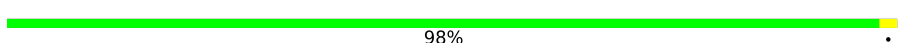
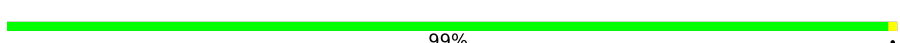
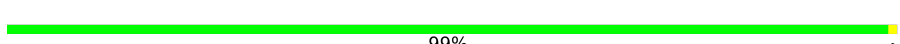
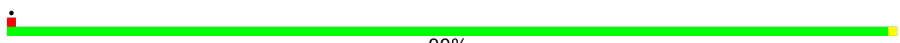





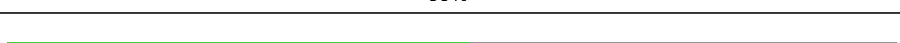
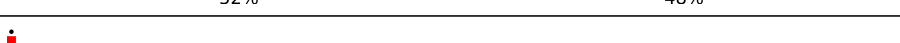
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	79% 21%
2	A28S	3552	78% 22%
3	A58S	151	80% 20%

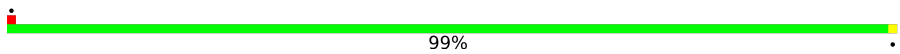
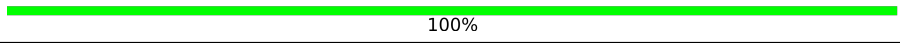
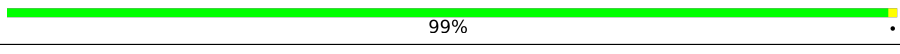
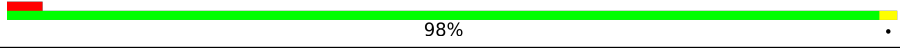
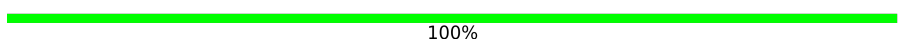
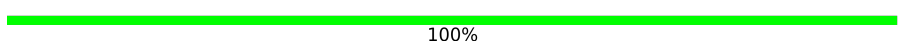
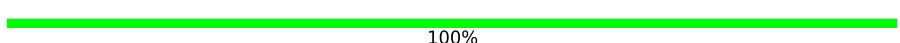
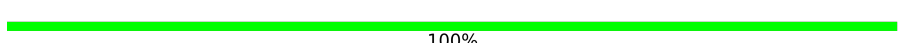
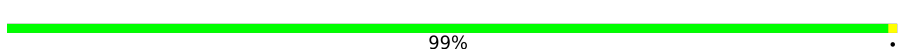
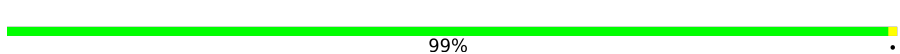

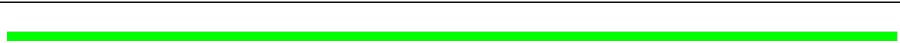
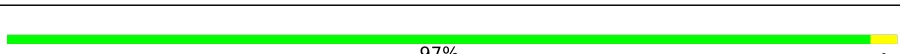
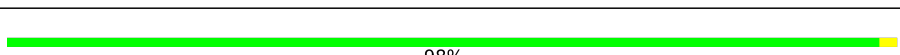
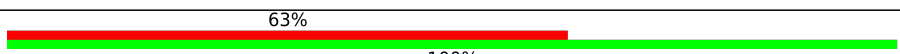
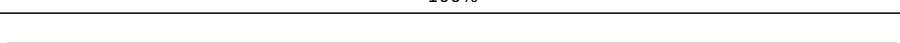
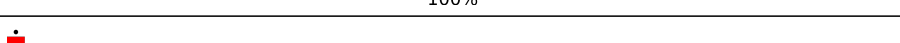
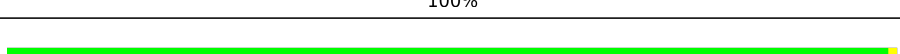
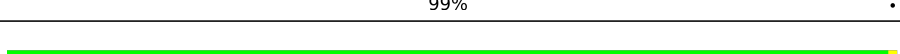
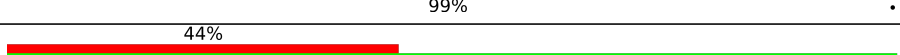
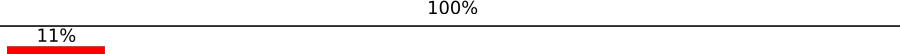
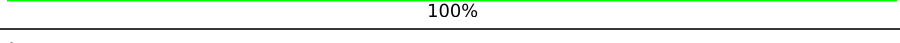
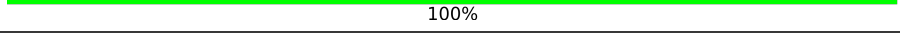
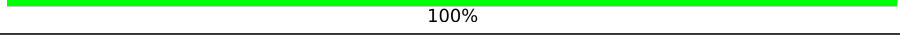
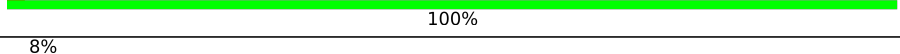
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Mol	Chain	Length	Quality of chain
4	A5S	120	 74% 22%
5	AL02	248	 100%
6	AL03	394	 100%
7	AL04	362	 100%
8	AL05	293	 100%
9	AL06	251	 85% 14%
10	AL07	225	 100%
11	AL08	233	 99%
12	AL09	190	 99%
13	AL10	205	 100%
14	AL11	170	 100%
15	AL12	153	 24% 25% 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%

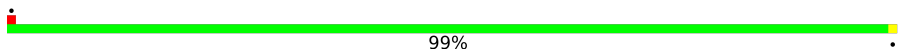
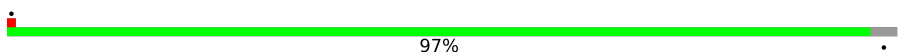
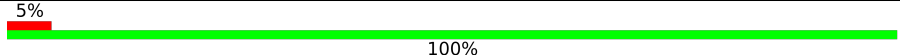
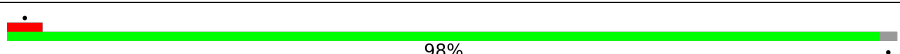
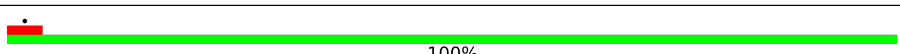
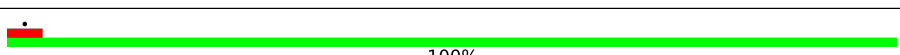
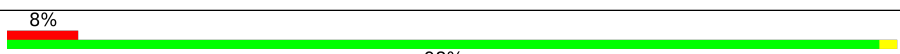
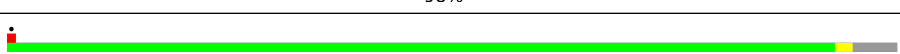
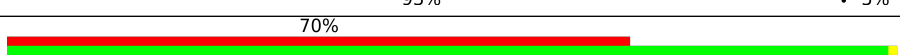
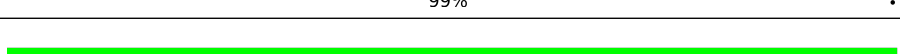
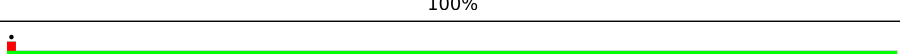
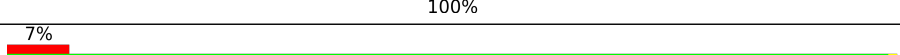
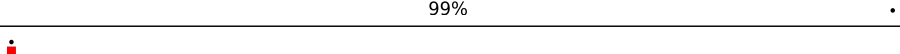
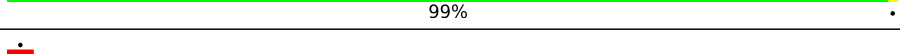
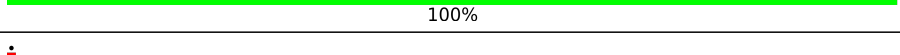
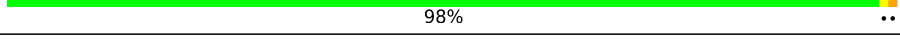
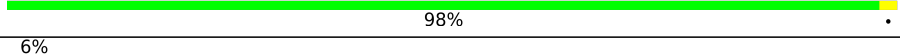
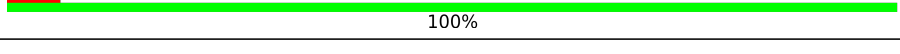
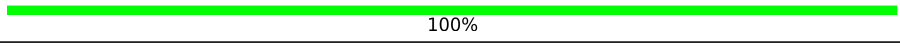
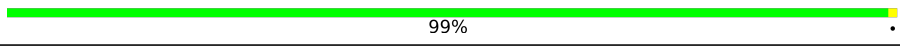
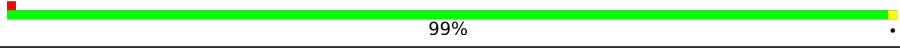
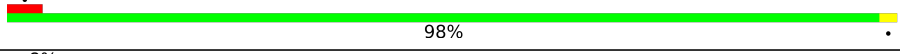
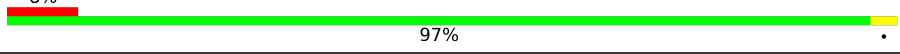
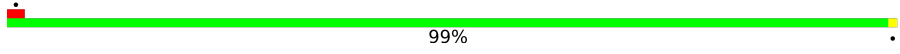
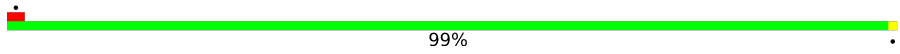
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Mol	Chain	Length	Quality of chain
29	AL26	134	 99%
30	AL27	135	 100%
31	AL28	147	 99%
32	AL29	104	 98%
33	AL30	98	 100%
34	AL31	107	 100%
35	AL32	128	 100%
36	AL33	109	 100%
37	AL34	114	 99%
38	AL35	122	 99%
39	AL36	102	 100%
40	AL37	86	 100%
41	AL38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

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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	 5% 98%
80	AS30	55	 5% 98%
81	AS31	68	 82% 99%
82	ETRN	77	 84% 16%
82	PTRN	77	 21% 79% 17%
83	GR1	40	 25% 72%
83	GR2	40	 28% 72%
84	MRNA	28	 25% 11% 64%

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
			Total	C	N	O	P		
1	A18S	1691	36103	16115	6485	11813	1690	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A28S	3552	76187	33931	13966	24738	3552	0	0

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

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

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

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

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
			Total	C	N	O	S		
5	AL02	248	1898	1189	389	314	6	0	0

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

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

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

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

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

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

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

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

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

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

- Molecule 11 is a protein called eL8.

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

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

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

- Molecule 13 is a protein called Ribosomal protein L10.

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

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
			Total	C	N	O	S		
14	AL11	170	1361	860	254	241	6	0	0

- Molecule 15 is a protein called uL11.

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

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

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

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
			Total	C	N	O	S		
17	AL14	138	1137	727	221	182	7	0	0

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

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

- Molecule 19 is a protein called uL13.

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

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

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

- Molecule 21 is a protein called eL18.

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

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

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

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
			Total	C	N	O	S		
23	AL20	176	1462	930	285	236	11	0	0

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

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

- Molecule 25 is a protein called eL22.

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

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

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

- Molecule 27 is a protein called Ribosomal protein L24.

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

- Molecule 28 is a protein called uL23.

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

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

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

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

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

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

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

- Molecule 32 is a protein called eL29.

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

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

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

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

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

- Molecule 35 is a protein called 60S ribosomal protein L32.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 41 is a protein called eL38.

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

- 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
			Total	C	N	O	S		
49	ARAC	313	2436	1535	424	465	12	0	0

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

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

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

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

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

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

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
			Total	C	N	O	S		
53	AS03	228	1768	1126	318	316	8	0	0

- 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
			Total	C	N	O	S		
60	AS10	96	810	530	143	131	6	0	0

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

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

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

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

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

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

- Molecule 64 is a protein called uS11.

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

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

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

- Molecule 66 is a protein called uS9.

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

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

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

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

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

- Molecule 69 is a protein called eS19.

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

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

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

- Molecule 71 is a protein called eS21.

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

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
			Total	C	N	O	S		
72	AS22	129	1034	659	193	176	6	0	0

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

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

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

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

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

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

- Molecule 76 is a protein called eS26.

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

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
			Total	C	N	O	S		
77	AS27	83	651	408	121	115	7	0	0

- 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		

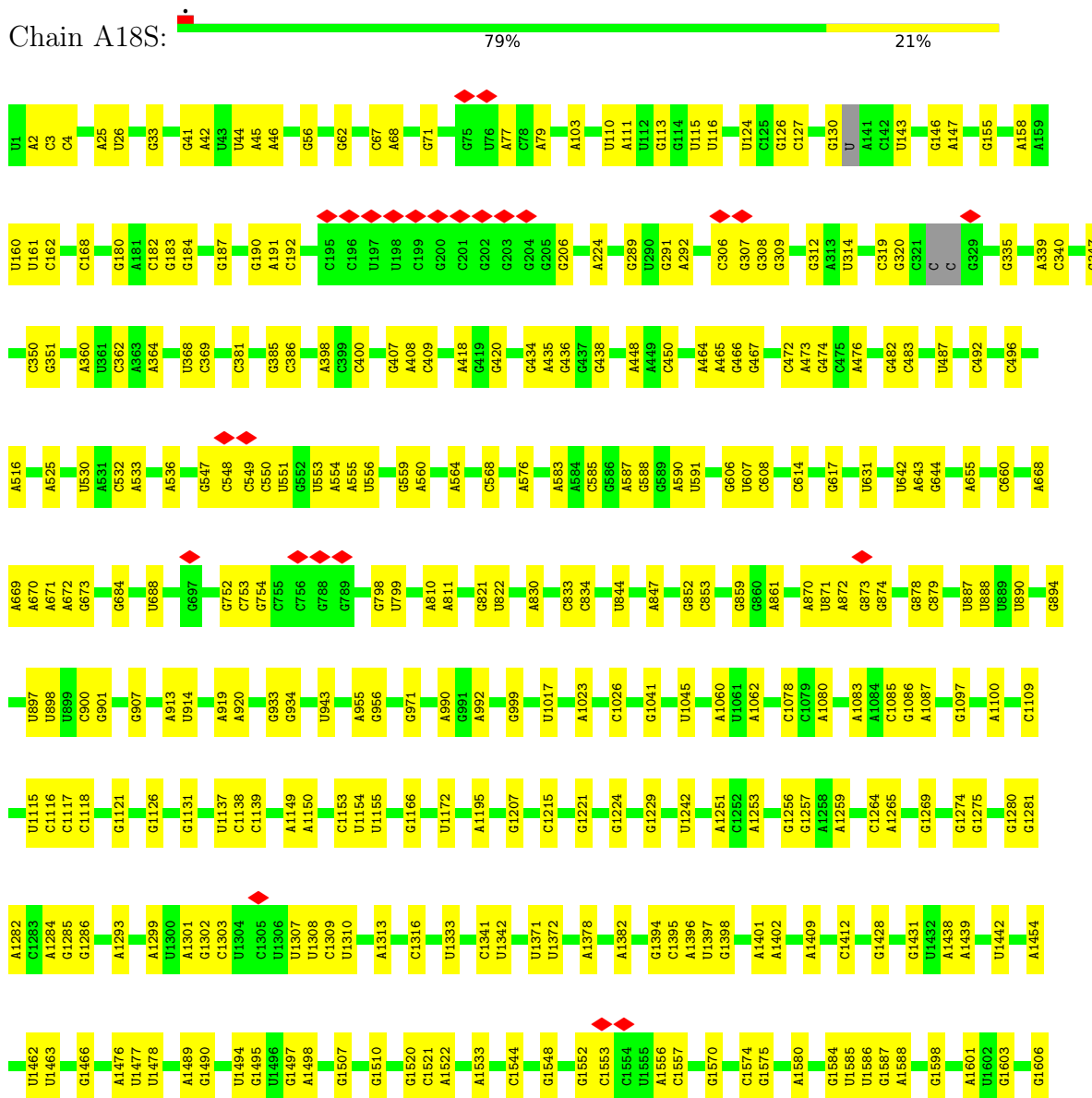
- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

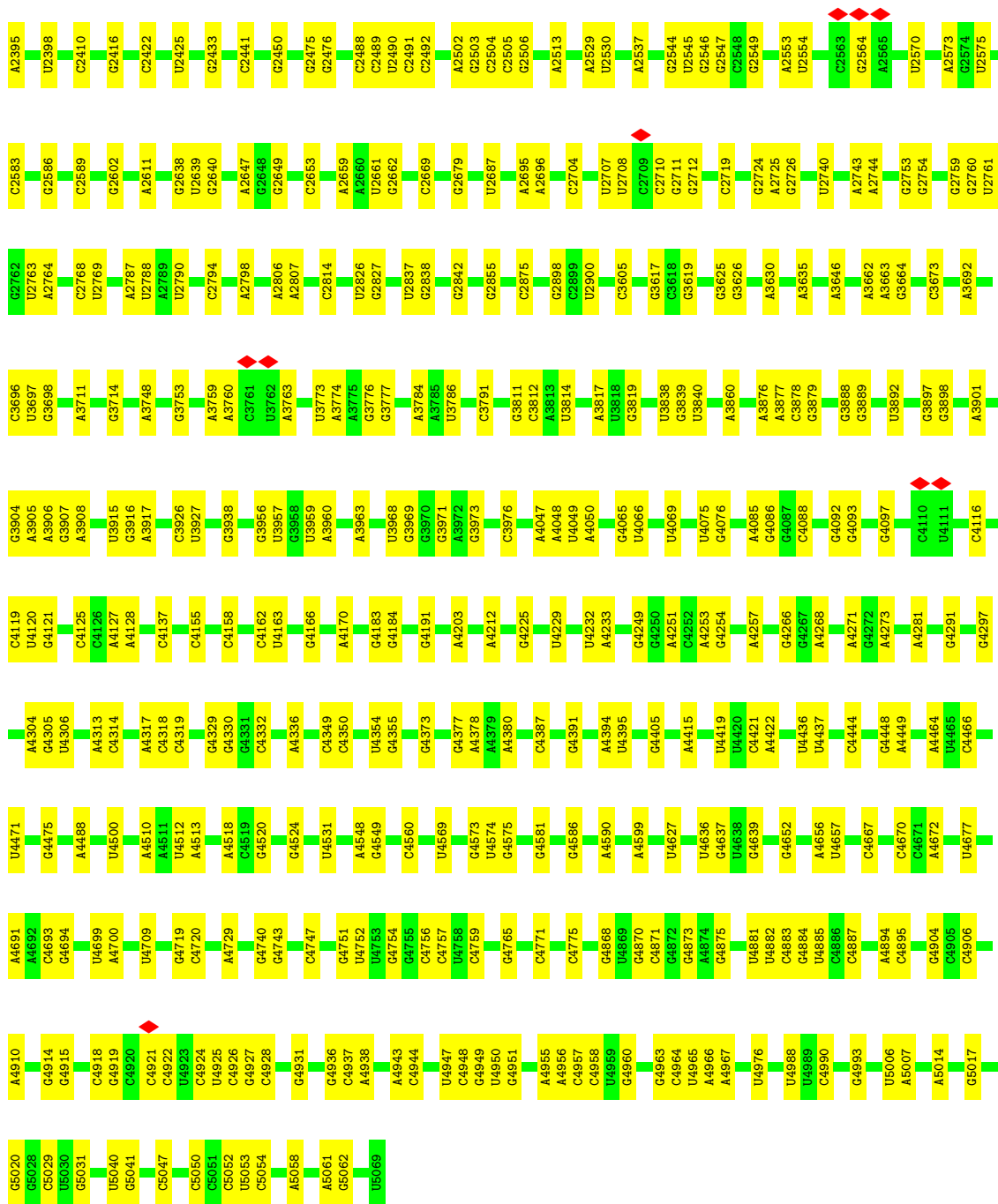
Mol	Chain	Residues	Atoms		AltConf
85	AL34	1	Total 1	Zn 1	0
85	AL37	1	Total 1	Zn 1	0
85	AL40	1	Total 1	Zn 1	0
85	AL42	1	Total 1	Zn 1	0
85	AL43	1	Total 1	Zn 1	0
85	AS26	1	Total 1	Zn 1	0

3 Residue-property plots [i](#)

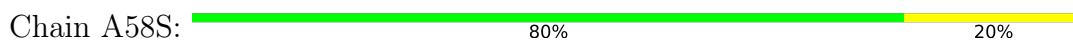
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 18S rRNA

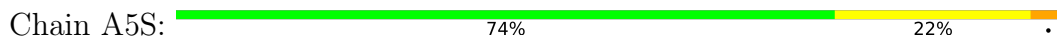




• Molecule 3: 5.8S rRNA

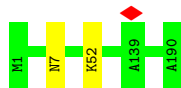


• Molecule 4: 5S rRNA

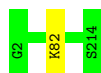




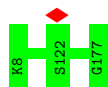
• Molecule 12: 60S ribosomal protein L9



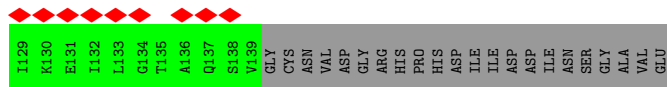
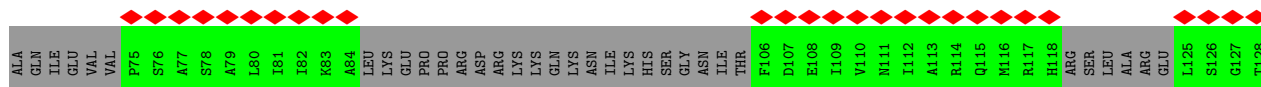
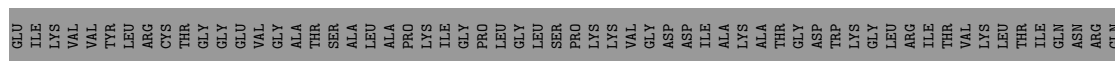
• Molecule 13: Ribosomal protein L10



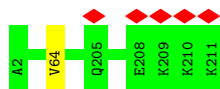
• Molecule 14: 60S ribosomal protein L11



• Molecule 15: uL11



• Molecule 16: 60S ribosomal protein L13



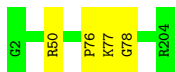
• Molecule 17: 60S ribosomal protein L14



There are no outlier residues recorded for this chain.

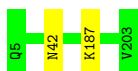
- Molecule 18: 60S ribosomal protein L15

Chain AL15:  98%



- Molecule 19: uL13

Chain AL16:  99%



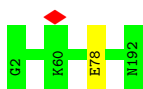
- Molecule 20: 60S ribosomal protein L17

Chain AL17:  99%



- Molecule 21: eL18

Chain AL18:  99%



- Molecule 22: 60S ribosomal protein L19

Chain AL19:  99%



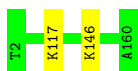
- Molecule 23: eL20

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.

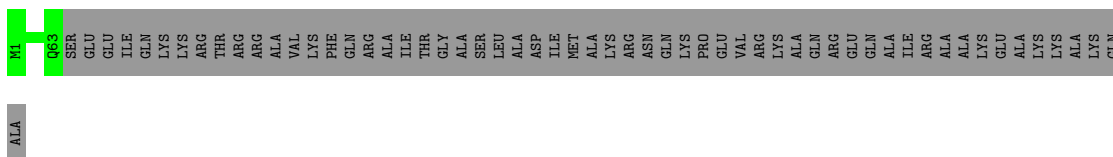
- Molecule 26: 60S ribosomal protein L23

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.

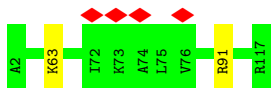
- Molecule 31: 60S ribosomal protein L27a

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.

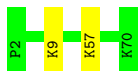
- Molecule 40: 60S ribosomal protein L37

Chain AL37:  100%

There are no outlier residues recorded for this chain.

- Molecule 41: eL38

Chain AL38:  97%



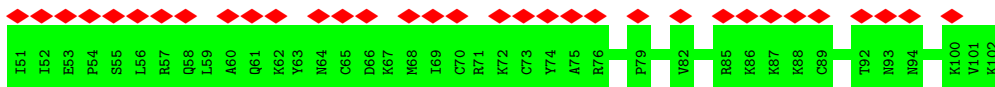
- Molecule 42: 60S ribosomal protein L39

Chain AL39:  98%



- Molecule 43: eL40

Chain AL40:  63%
100%



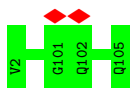
- Molecule 44: eL41

Chain AL41:  100%

There are no outlier residues recorded for this chain.

- Molecule 45: eL42

Chain AL42:  100%



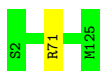
- Molecule 46: 60S ribosomal protein L37a

Chain AL43:  99%

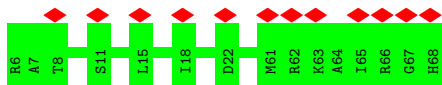


- Molecule 47: 60S ribosomal protein L28

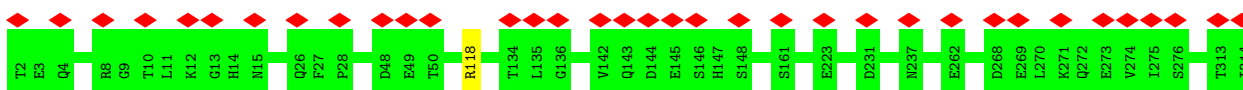
Chain ALNW:  99%



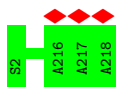
- Molecule 48: 60S acidic ribosomal protein P0



- Molecule 49: Receptor of activated protein C kinase 1



- Molecule 50: 40S_SA_C domain-containing protein

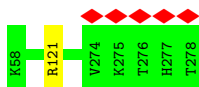


- Molecule 51: 40S ribosomal protein S3a



There are no outlier residues recorded for this chain.

- Molecule 52: 40S ribosomal protein S2



- Molecule 53: 40S ribosomal protein S3

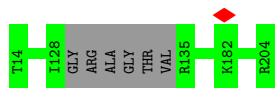


- Molecule 54: 40S ribosomal protein S4

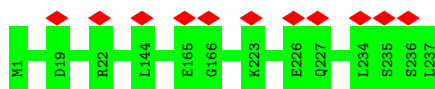




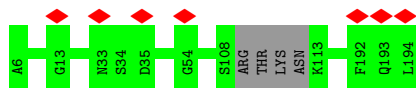
- Molecule 55: Ribosomal protein S5



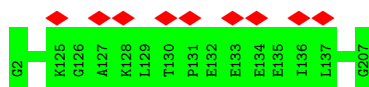
- Molecule 56: 40S ribosomal protein S6



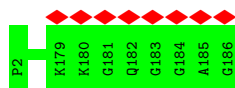
- Molecule 57: eS7



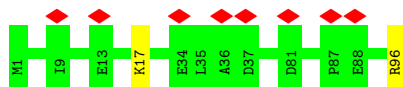
- Molecule 58: 40S ribosomal protein S8



- Molecule 59: 40S ribosomal protein S9

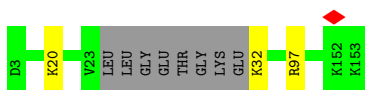


- Molecule 60: 40S ribosomal protein S10

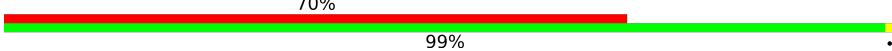


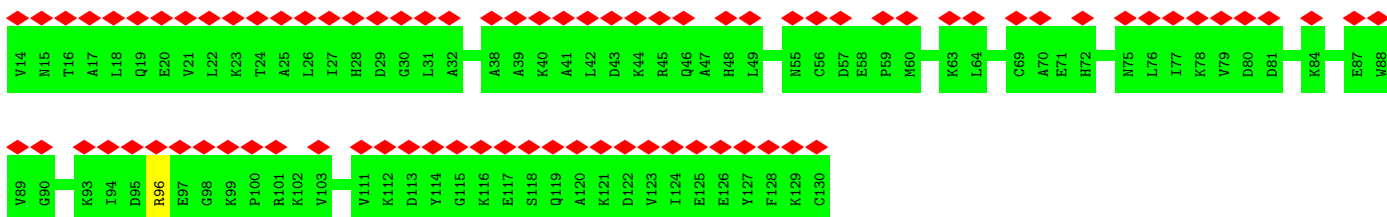
- Molecule 61: 40S ribosomal protein S11

Chain AS11:  93% • 5%



- Molecule 62: 40S ribosomal protein S12

Chain AS12:  70% 99%



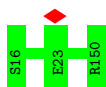
- Molecule 63: 40S ribosomal protein S13

Chain AS13:  100%

There are no outlier residues recorded for this chain.

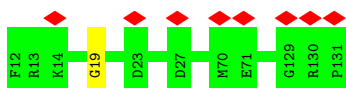
- Molecule 64: uS11

Chain AS14:  100%



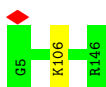
- Molecule 65: 40S ribosomal protein S15

Chain AS15:  7% 99%



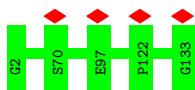
- Molecule 66: uS9

Chain AS16:  99%

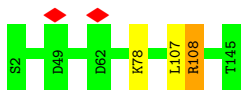


- Molecule 67: 40S ribosomal protein S17

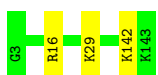
Chain AS17:  100%



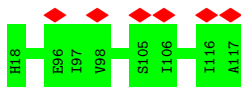
- Molecule 68: 40S ribosomal protein S18



- Molecule 69: eS19



- Molecule 70: 40S ribosomal protein S20



- Molecule 71: eS21

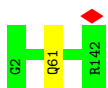


There are no outlier residues recorded for this chain.

- Molecule 72: 40S ribosomal protein S15a

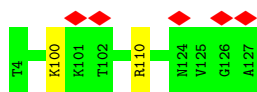


- Molecule 73: 40S ribosomal protein S23



- Molecule 74: 40S ribosomal protein S24





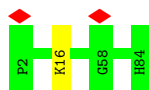
- Molecule 75: 40S ribosomal protein S25



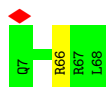
- Molecule 76: eS26



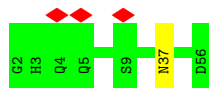
- Molecule 77: 40S ribosomal protein S27



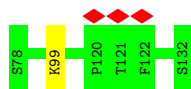
- Molecule 78: 40S ribosomal protein S28



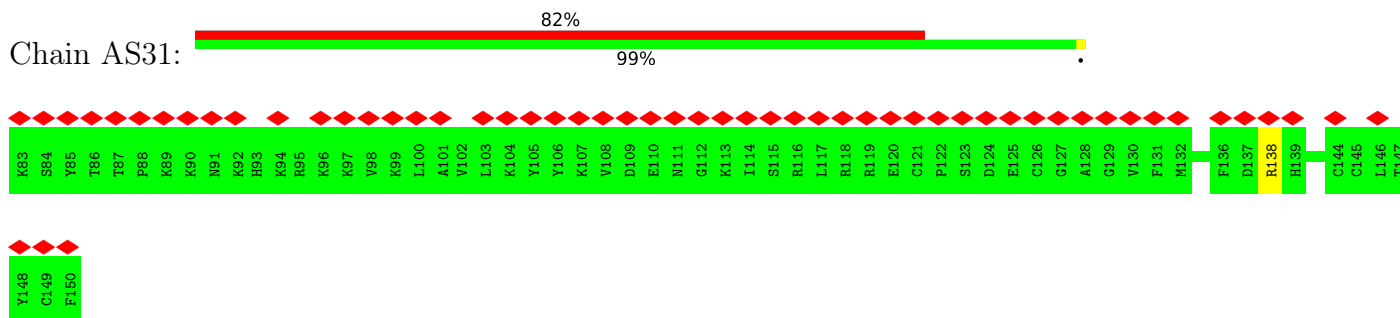
- Molecule 79: 40S ribosomal protein S29



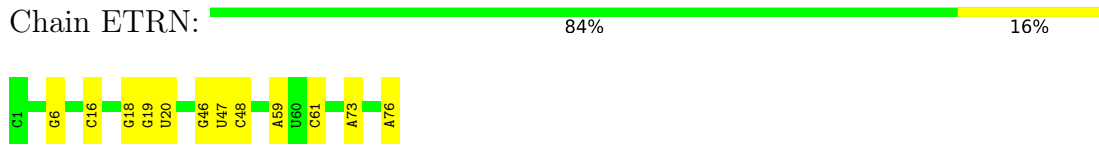
- Molecule 80: 40S ribosomal protein S30



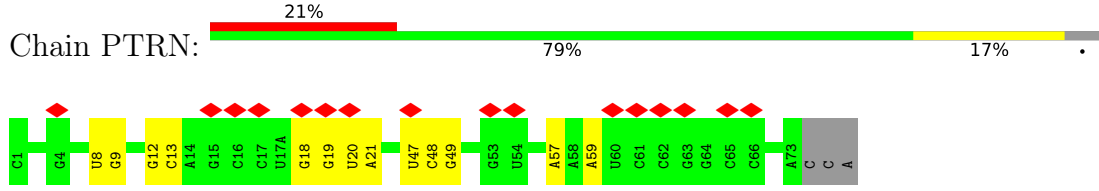
- Molecule 81: 40S ribosomal protein S27a



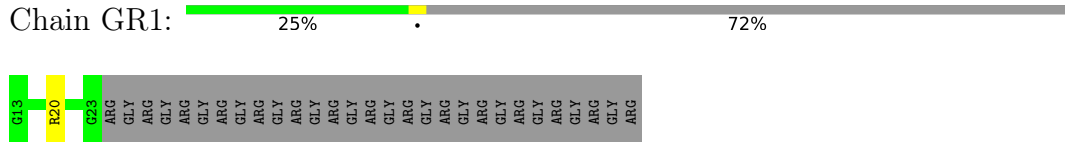
- Molecule 82: tRNA^{fMet} bound to E-site



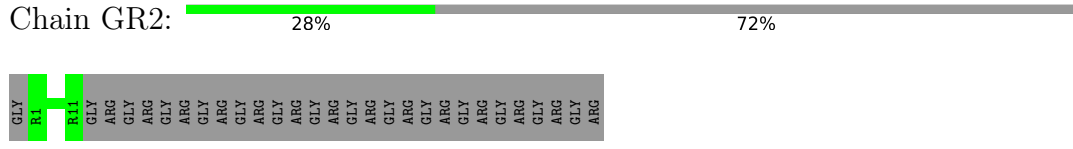
- Molecule 82: tRNA^{fMet} bound to E-site



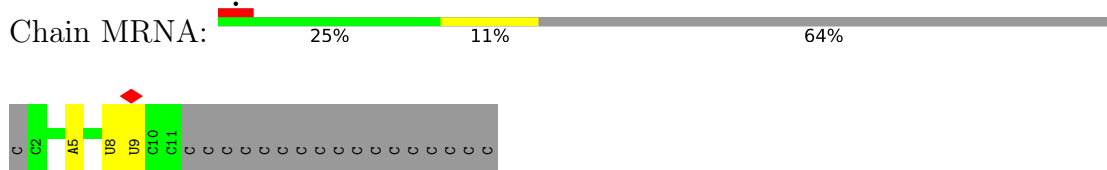
- Molecule 83: GR20, ALS/FTD dipeptide repeat protein



- Molecule 83: GR20, ALS/FTD dipeptide repeat protein



- Molecule 84: mRNA



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 (\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 (\AA)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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.

The worst 5 of 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

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.

The worst 5 of 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

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AL02	246/248 (99%)	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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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

5 of 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

5.3.2 Protein sidechains [i](#)

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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	AL39	46	ARG
75	AS25	104	ARG
53	AS03	227	LYS
75	AS25	57	LYS
79	AS29	37	ASN

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%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
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%)

5 of 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

5 of 72 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A28S	3904	G
82	PTRN	19	G
2	A28S	3968	U
2	A28S	4719	G
2	A28S	480	C

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
32	AL29	1
48	ALP0	1
11	AL08	1
3	A58S	1
13	AL10	1

The worst 5 of 38 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

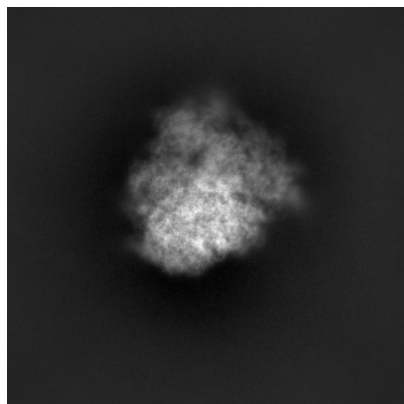
6 Map visualisation [i](#)

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.

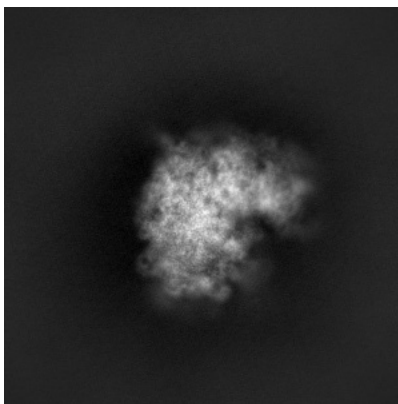
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

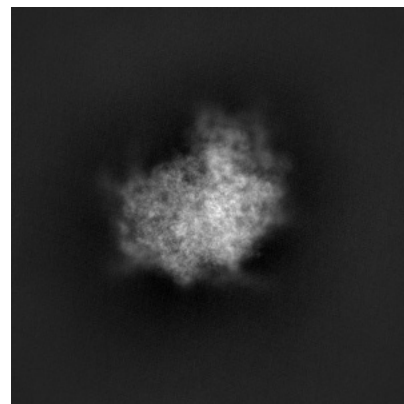
6.1.1 Primary map



X

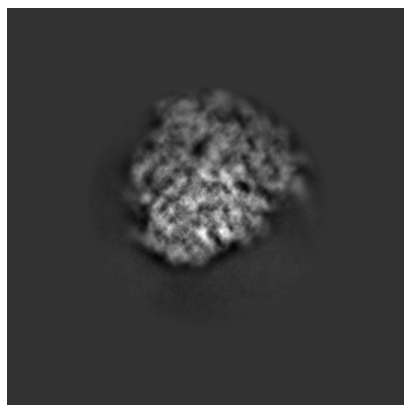


Y

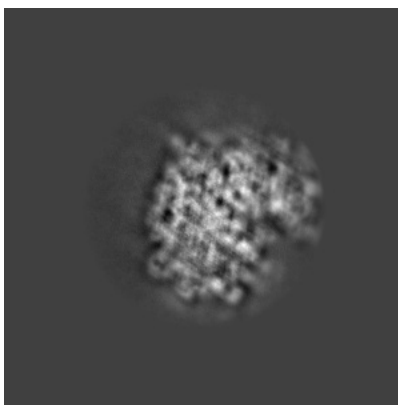


Z

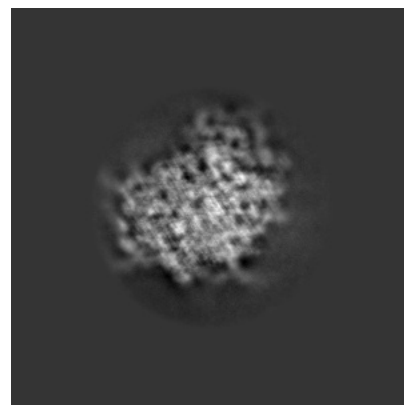
6.1.2 Raw map



X



Y

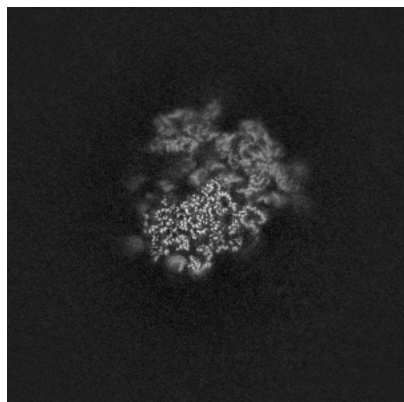


Z

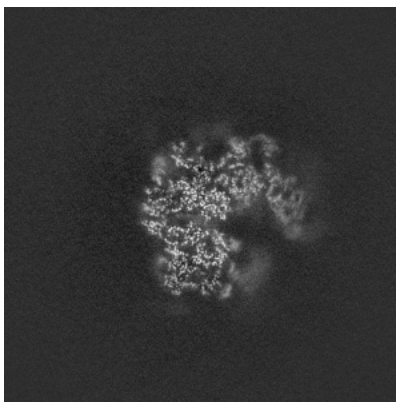
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

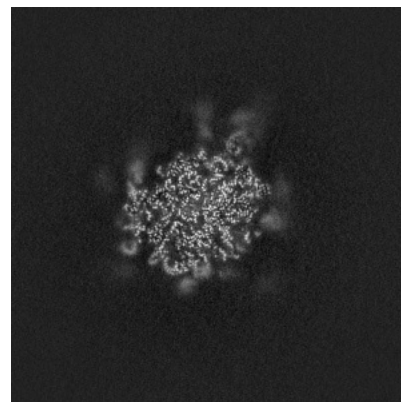
6.2.1 Primary map



X Index: 360

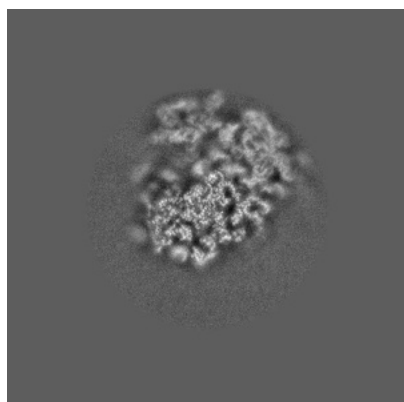


Y Index: 360

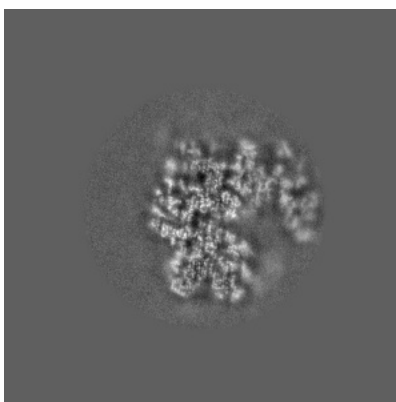


Z Index: 360

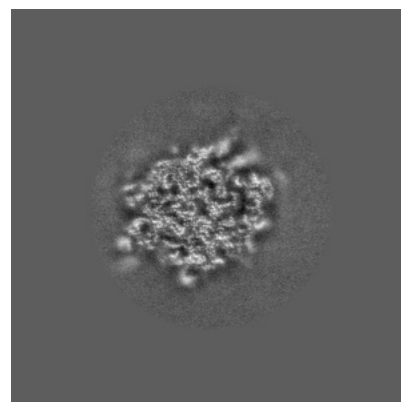
6.2.2 Raw map



X Index: 360



Y Index: 360

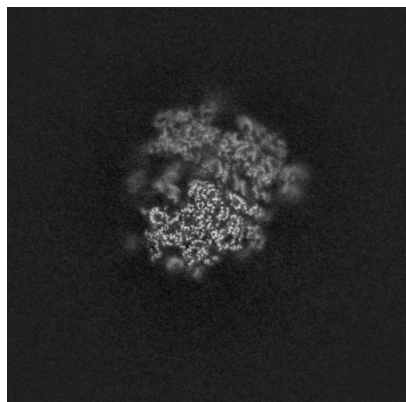


Z Index: 360

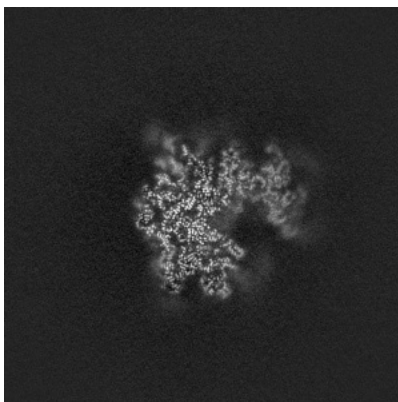
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

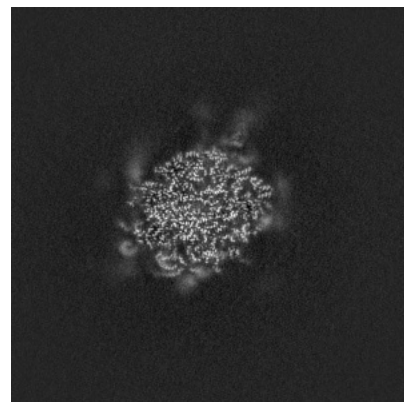
6.3.1 Primary map



X Index: 371

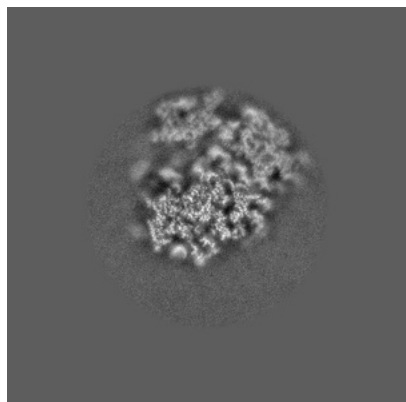


Y Index: 347

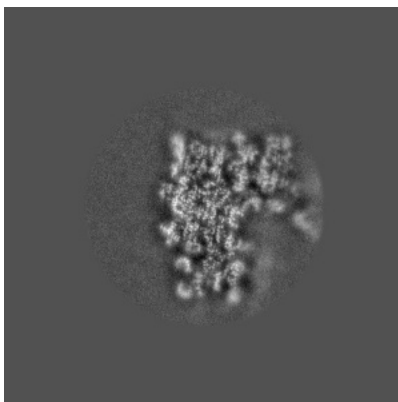


Z Index: 351

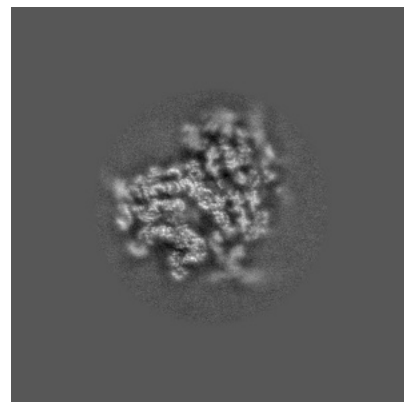
6.3.2 Raw map



X Index: 364



Y Index: 389

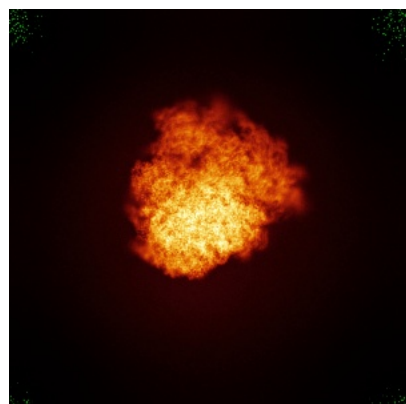


Z Index: 412

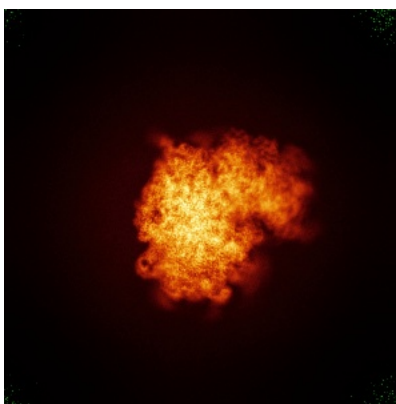
The images above show the largest variance slices of the map in three orthogonal directions.

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

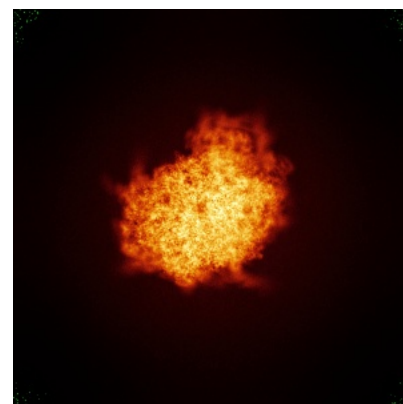
6.4.1 Primary map



X

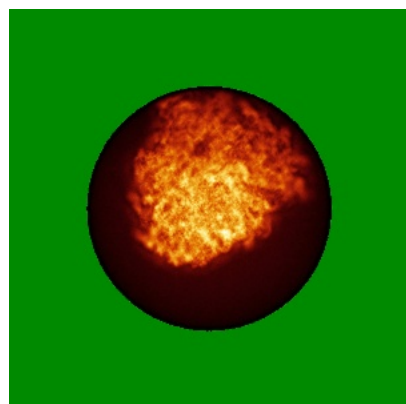


Y

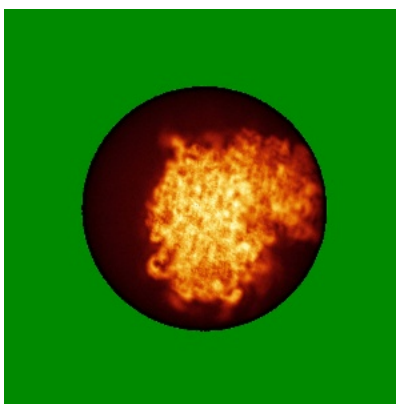


Z

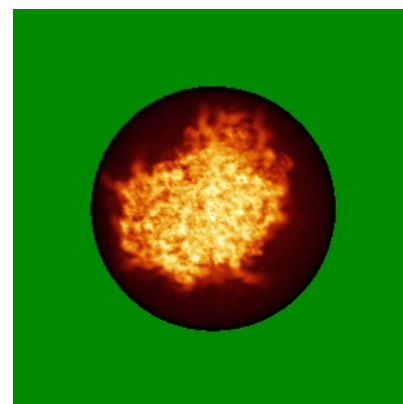
6.4.2 Raw map



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](#)

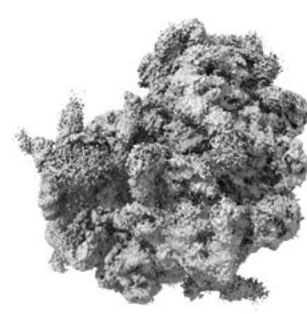
6.5.1 Primary map



X



Y



Z

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.

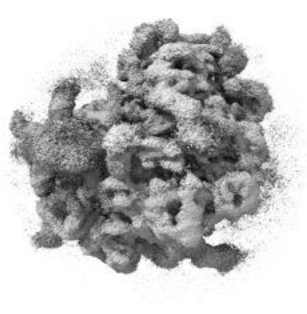
6.5.2 Raw map



X



Y



Z

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

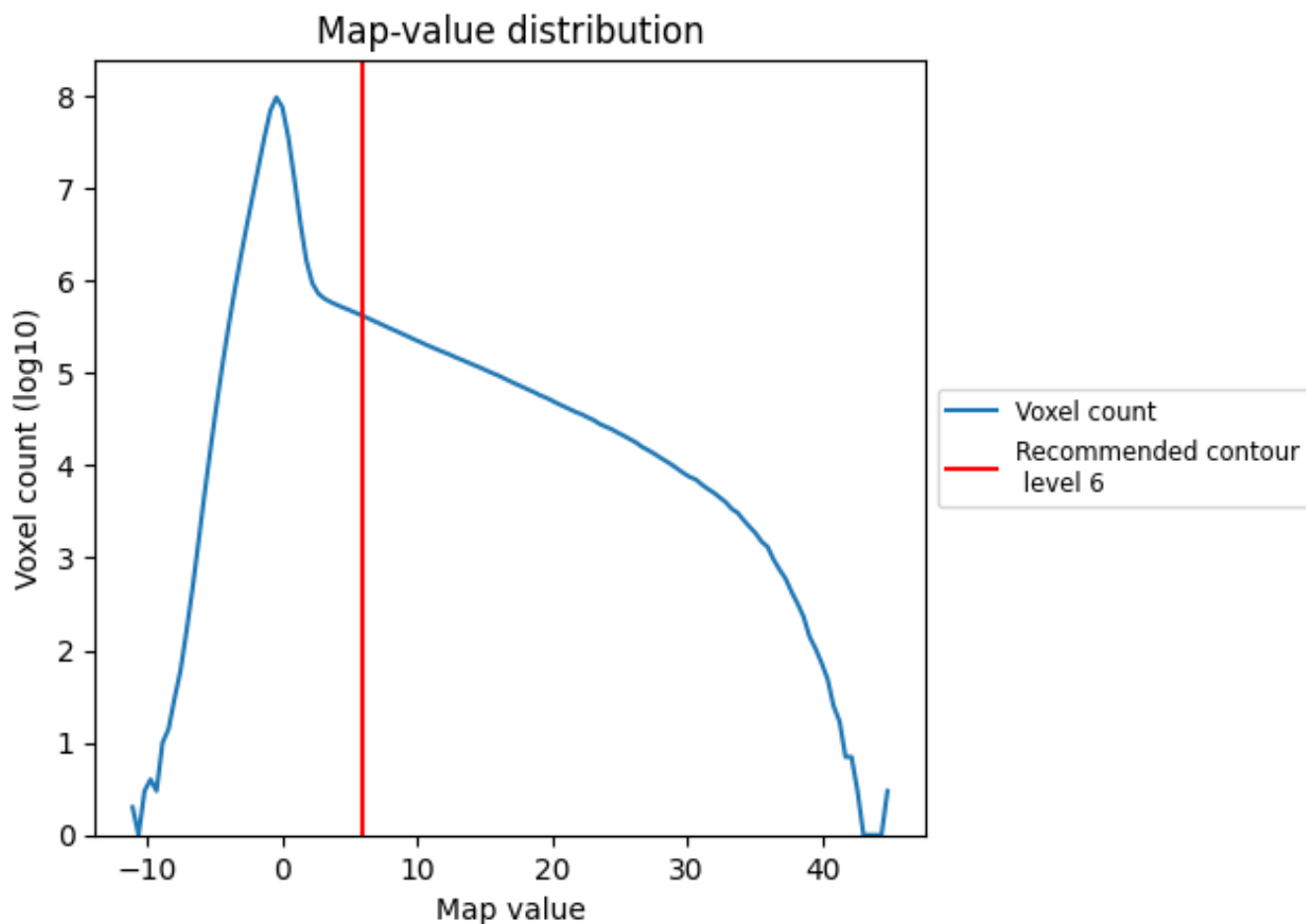
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

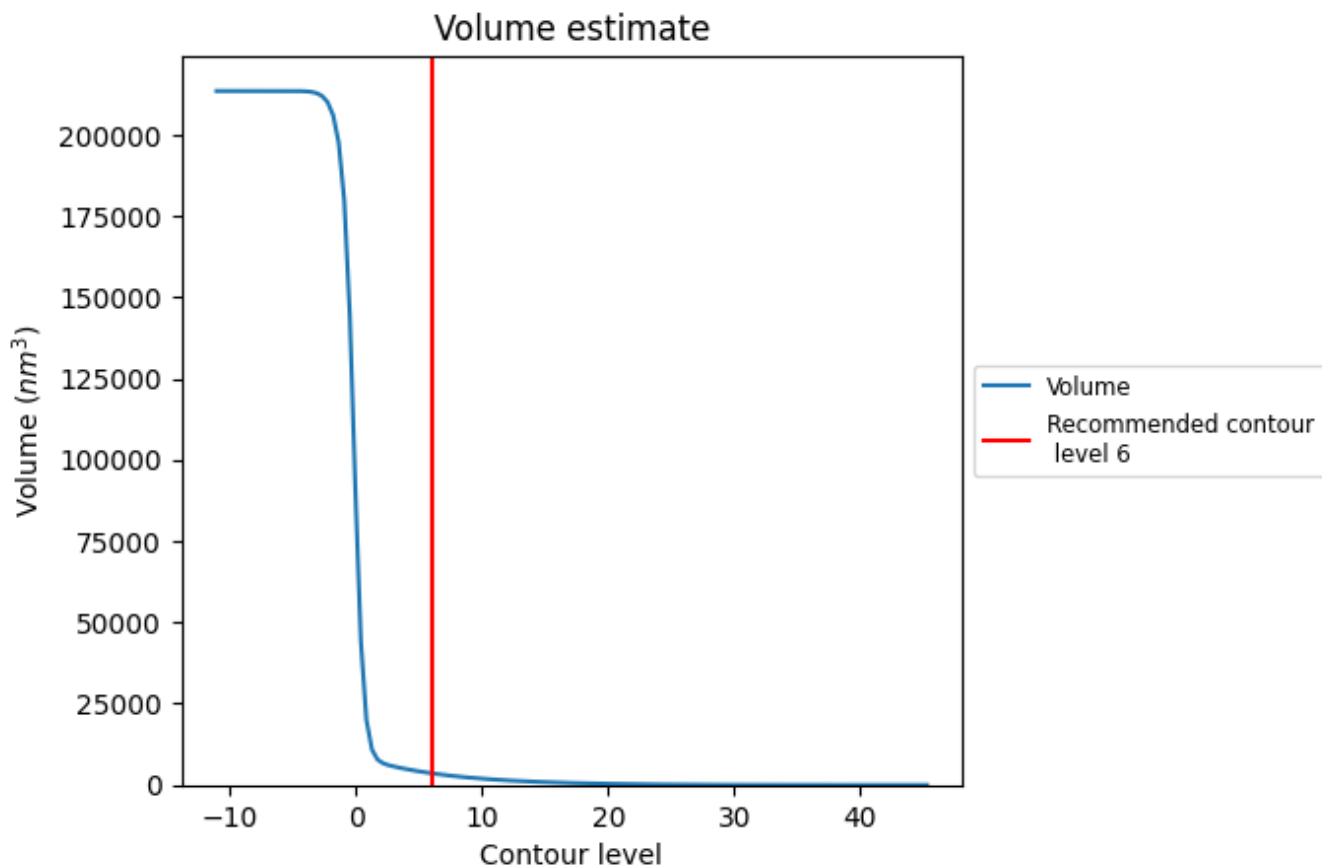
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

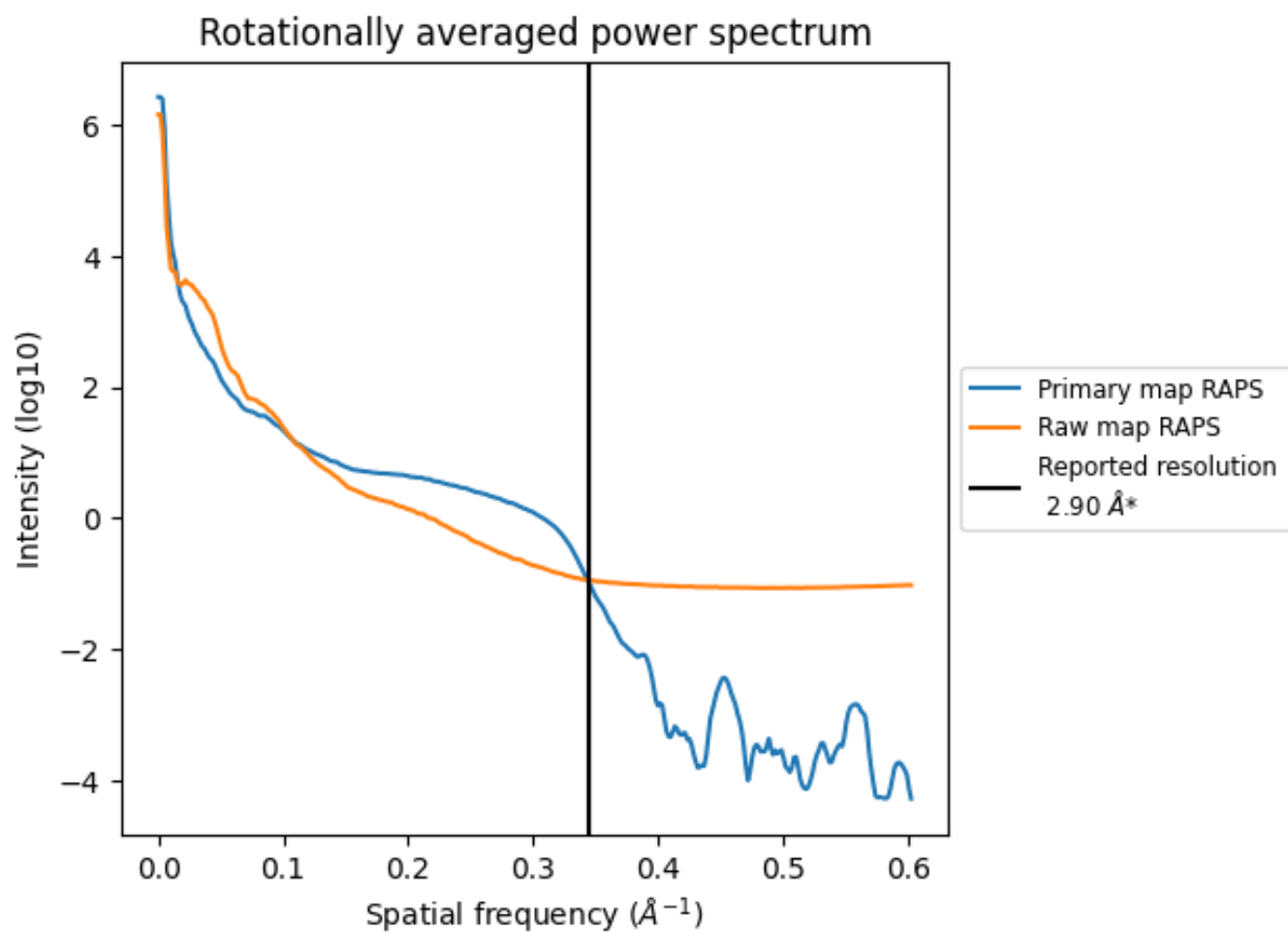
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 3588 nm^3 ; 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 i

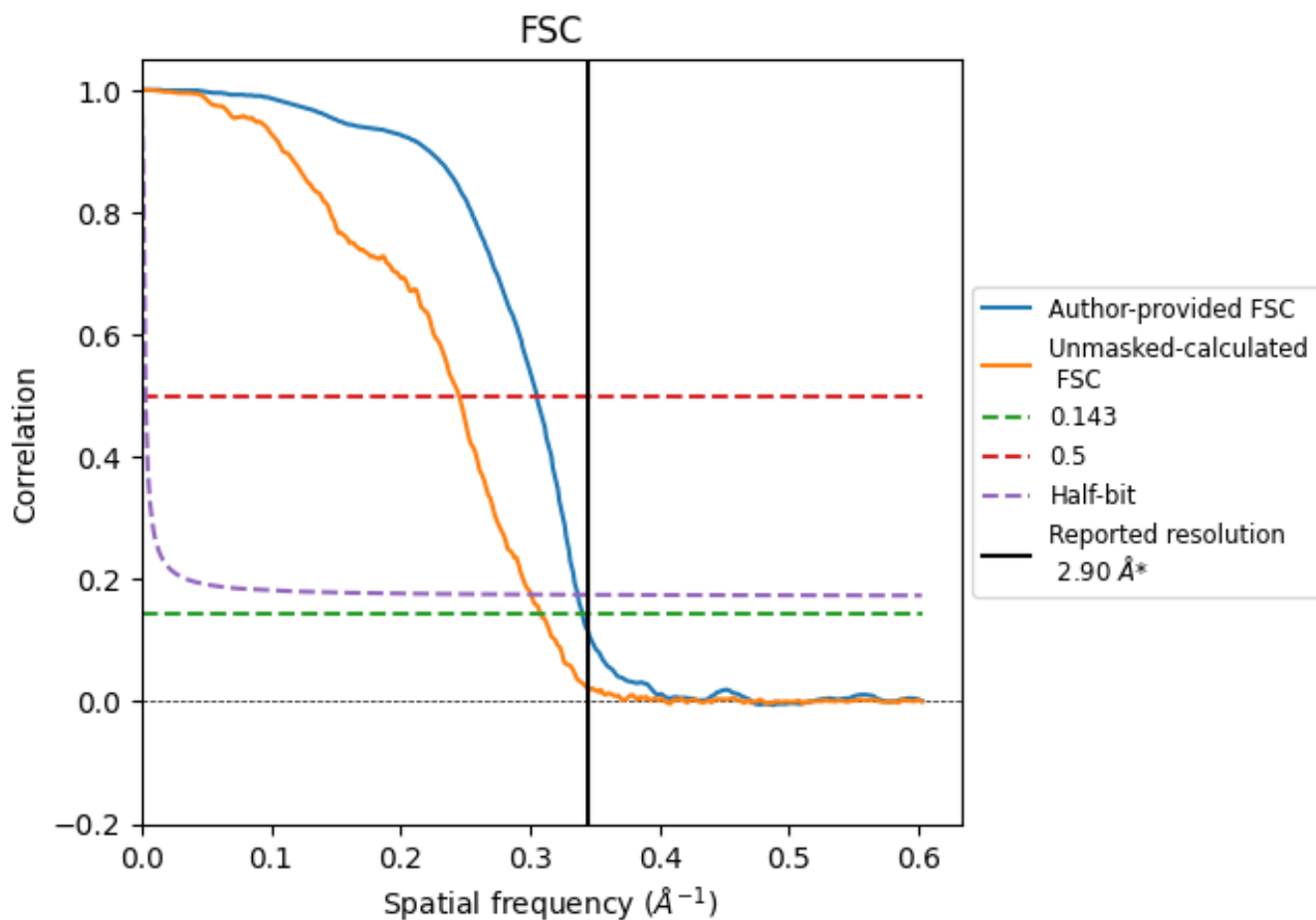


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 Å⁻¹

8.2 Resolution estimates [i](#)

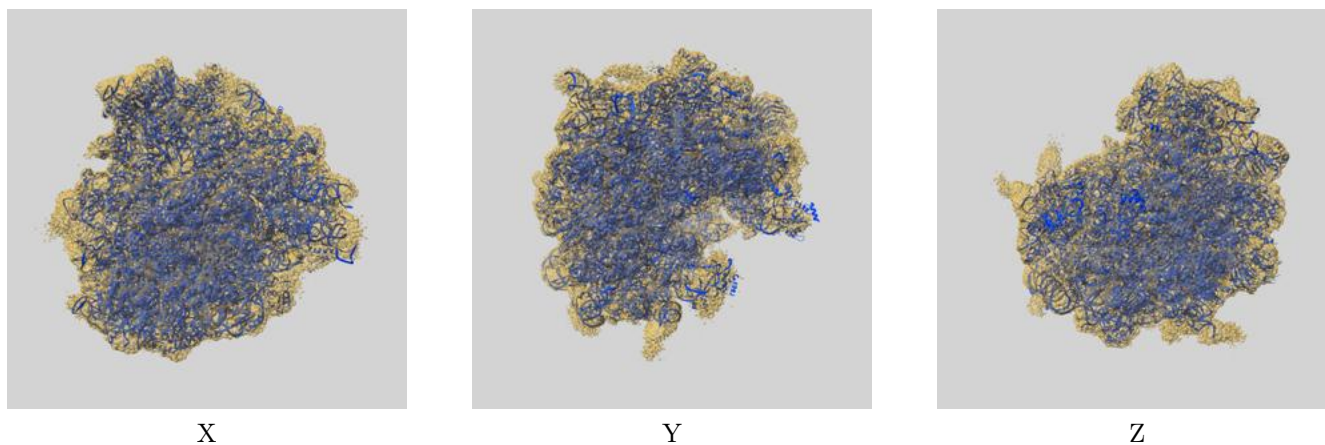
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.94	3.28	2.97
Unmasked-calculated*	3.25	4.08	3.32

*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](#)

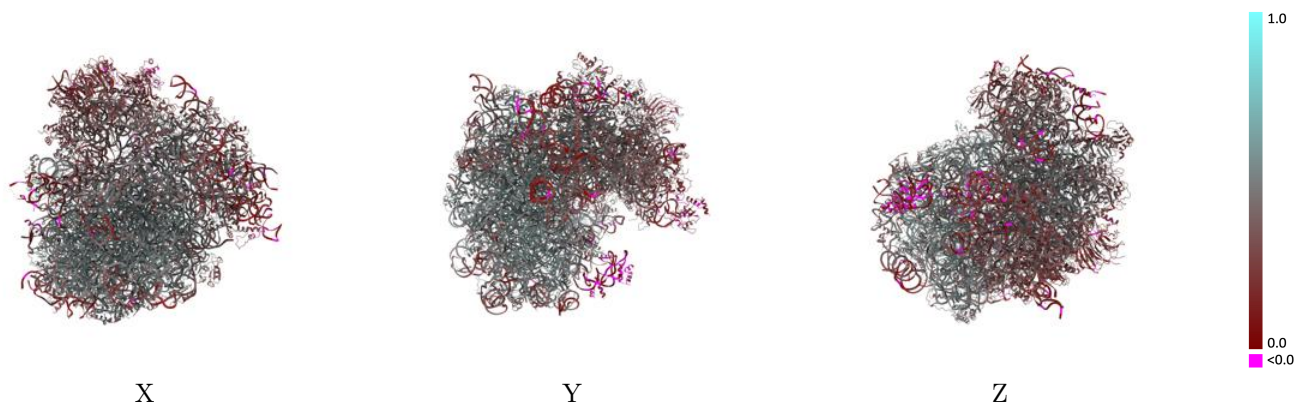
This section contains information regarding the fit between EMDB map EMD-26036 and PDB model 7TOR. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



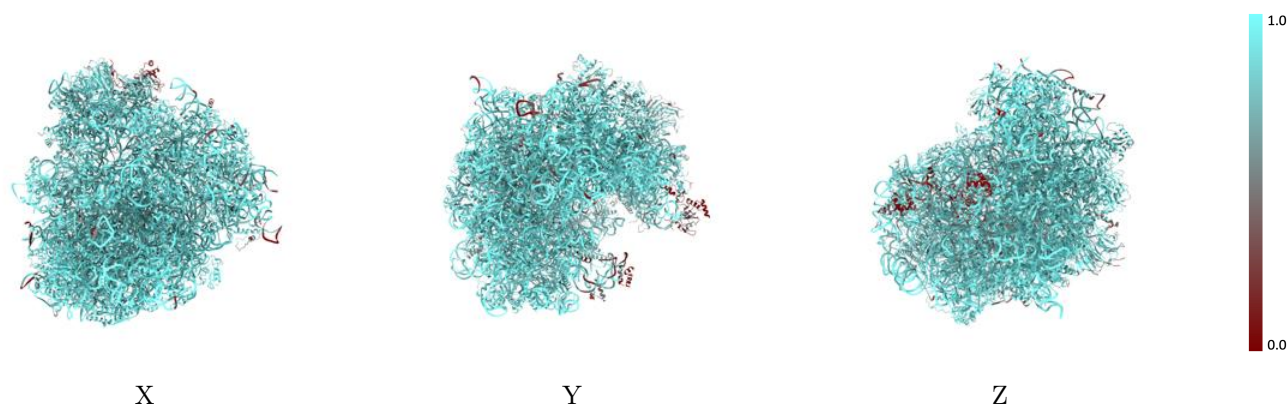
The images above show the 3D surface view of the map at the recommended contour level 6.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



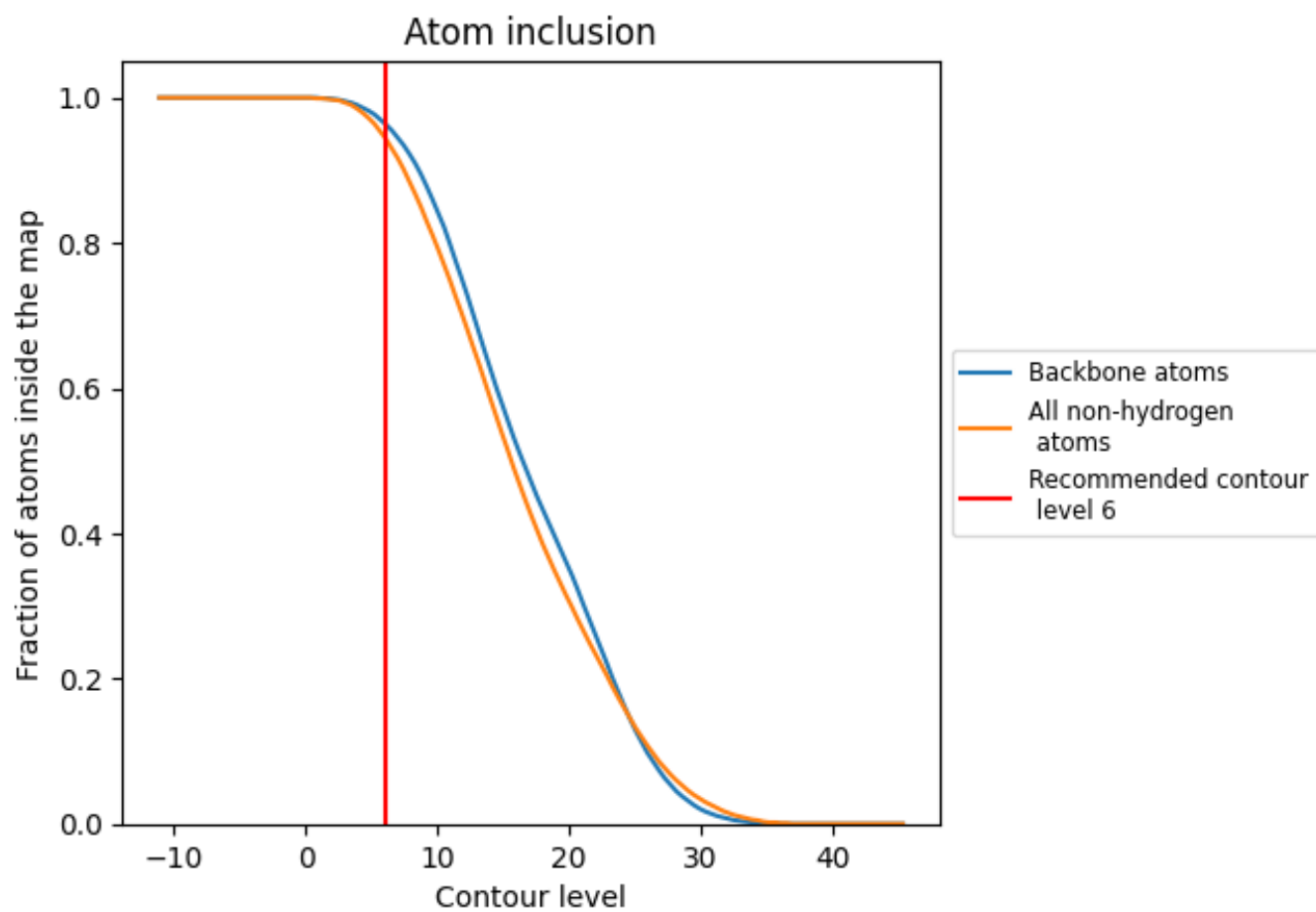
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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