



Full wwPDB EM Validation Report ⓘ

Nov 28, 2022 – 03:05 PM EST

PDB ID : 7TOQ
EMDB ID : EMD-26035
Title : Mammalian 80S ribosome bound with the ALS/FTD-associated dipeptide repeat protein poly-PR
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 : 3.10 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

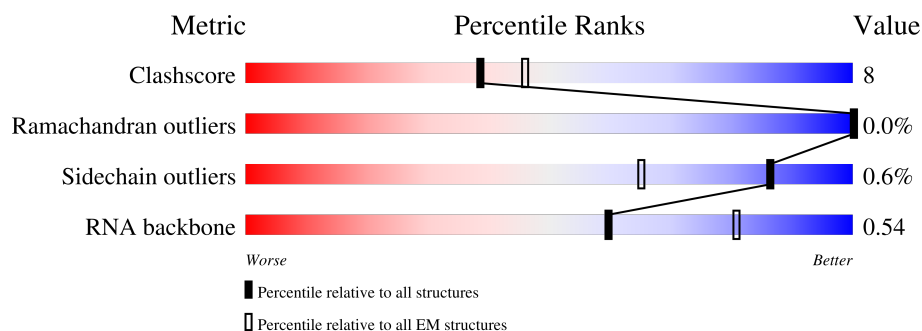
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



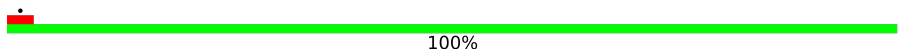

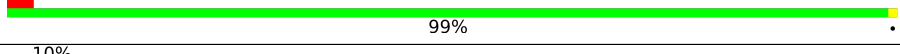
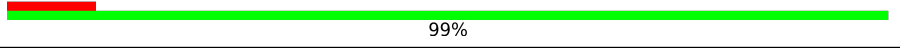
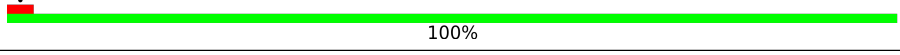
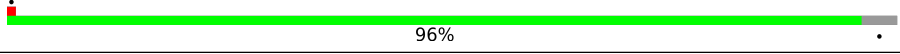
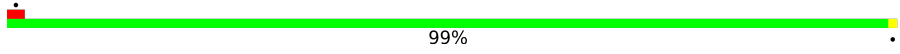

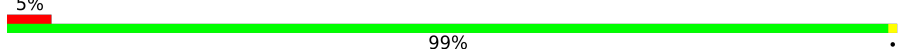
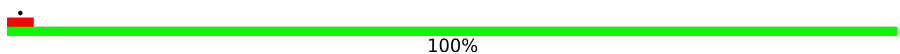
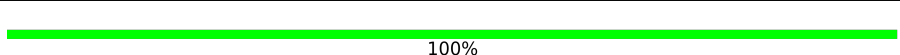
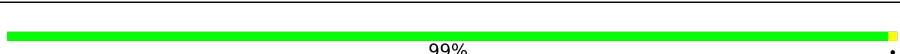
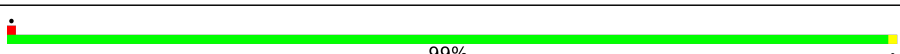
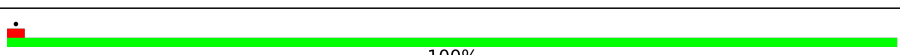
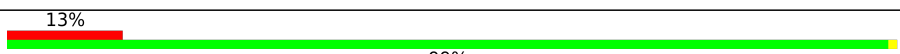
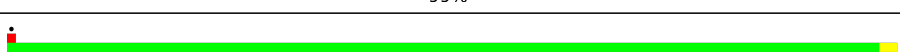
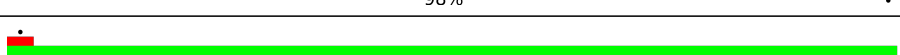
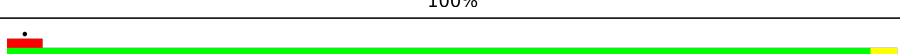
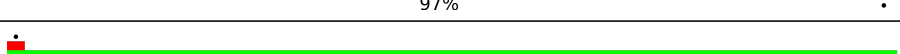
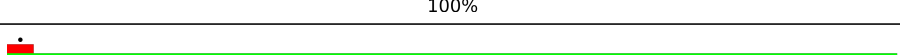
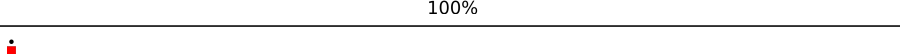
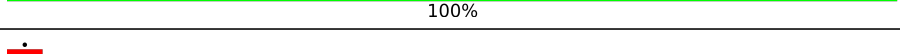
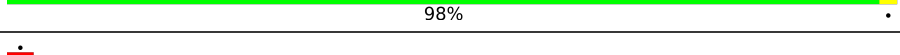
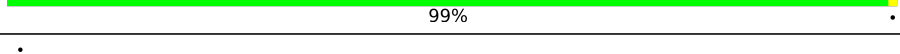
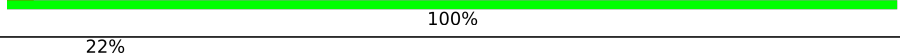
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	<div> <div>14%</div> <div>74%</div> <div>24%</div> <div>.</div> </div>
2	A25S	3649	<div> <div>78%</div> <div>21%</div> <div>.</div> </div>
3	A58S	156	<div> <div>78%</div> <div>21%</div> <div>.</div> </div>
4	A5S	120	<div> <div>71%</div> <div>24%</div> <div>5%</div> </div>
5	AL02	244	<div> <div>100%</div> </div>
6	AL03	394	<div> <div>100%</div> </div>
7	AL04	362	<div> <div>100%</div> </div>

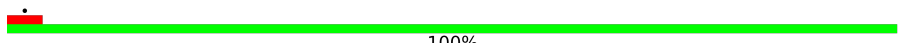
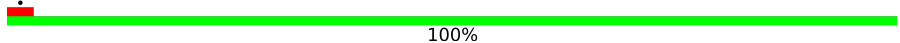
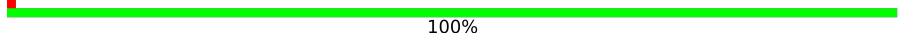
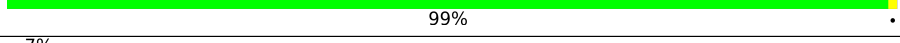
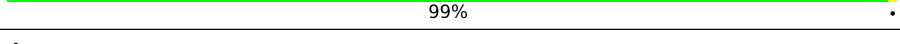
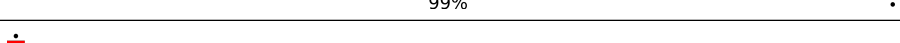
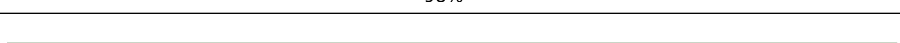

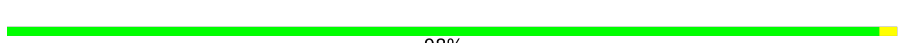
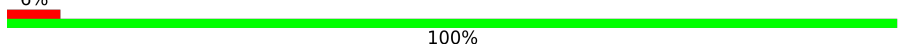
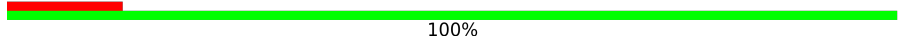
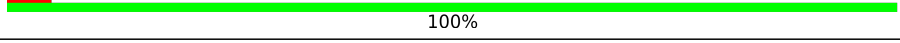
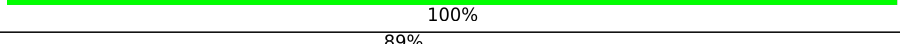
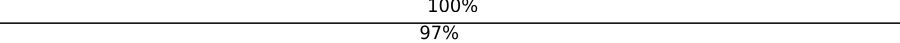
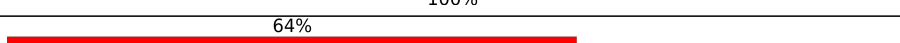



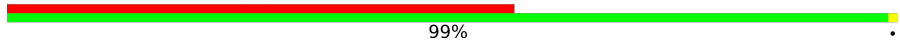
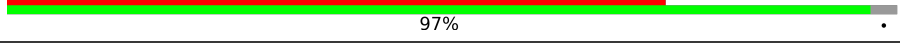
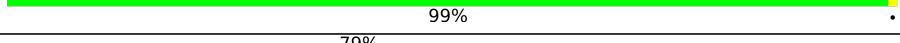
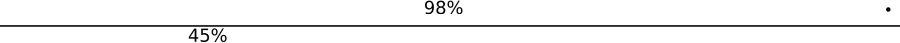
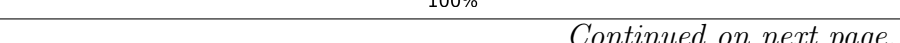



Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	AL05	293	 100%
9	AL06	251	 85% 14%
10	AL07	225	 99%
11	AL08	241	 10% 99%
12	AL09	190	 100%
13	AL10	213	 96%
14	AL11	169	 99%
15	AL12	163	 21% 23% 77%
16	AL13	210	 5% 99%
17	AL14	138	 100%
18	AL15	203	 100%
19	AL16	199	 99%
20	AL17	153	 99%
21	AL18	187	 100%
22	AL19	180	 13% 99%
23	AL20	175	 98%
24	AL21	159	 100%
25	AL22	99	 97%
26	AL23	131	 100%
27	AL24	63	 100%
28	AL25	119	 100%
29	AL26	134	 98%
30	AL27	135	 99%
31	AL28	147	 100%
32	AL29	103	 22% 100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	AL30	94	 100%
34	AL31	107	 100%
35	AL32	128	 100%
36	AL33	109	 99%
37	AL34	114	 99%
38	AL35	122	 99%
39	AL36	102	 98%
40	AL37	86	 100%
41	AL38	69	 99%
42	AL39	50	 98%
43	AL40	52	 100%
44	AL41	23	 100%
45	AL42	104	 100%
46	AL43	91	 100%
47	ALP0	27	 89%
48	ARAC	313	 97%
49	AS00	217	 64%
50	AS01	213	 29%
51	AS02	221	 43%
52	AS03	228	 80%
53	AS04	262	 98%
54	AS05	262	 57%
55	AS06	237	 74%
56	AS07	191	 97%
57	AS08	237	 68%
57	AS08	206	 79%
57	AS08	206	45%
57	AS08	206	100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
58	AS09	185	41% 100%
59	AS10	96	86% 99%
60	AS11	151	45% 93% 5%
61	AS12	117	98% 100%
62	AS13	149	45% 99%
63	AS14	136	24% 99%
64	AS15	120	26% 99%
65	AS16	142	77% 99%
66	AS17	132	75% 97%
67	AS18	144	55% 98%
68	AS19	141	71% 99%
69	AS20	100	73% 99%
70	AS21	83	71% 100%
71	AS22	129	47% 99%
72	AS23	141	28% 99%
73	AS24	124	67% 99%
74	AS25	75	87% 100%
75	AS26	101	26% 99%
76	AS27	83	49% 99%
77	AS28	62	52% 100%
78	AS29	55	33% 100%
79	AS30	55	69% 95% 5%
80	AS31	68	94% 97%
81	EL28	125	98%
82	MRNA	10	70% 70% 30%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
83	PR	40	<div><div><div></div><div></div><div></div></div><div>40%45%52%</div></div>
84	PTRN	77	<div><div><div></div><div></div><div></div></div><div>70%29%</div></div>

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 213639 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	1690	Total	C	N	O	P	0	0
			36079	16105	6479	11806	1689		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A25S	3649	Total	C	N	O	P	0	0
			78238	34842	14321	25427	3648		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A58S	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AL02	244	Total	C	N	O	S	0	0
			1868	1171	382	309	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
			3148	2007	591	537	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 uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AL07	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 11 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL08	241	Total	C	N	O	S	0	0
			1934	1233	371	326	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	204	Total	C	N	O	S	0	0
			1654	1050	319	272	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AL11	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 15 is a protein called 60S ribosomal protein L12.

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 eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AL13	210	Total	C	N	O	S	0	0
			1703	1065	354	280	4		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL13	52	SER	ALA	conflict	UNP G1TKB3
AL13	55	LEU	ILE	conflict	UNP G1TKB3
AL13	74	ARG	HIS	conflict	UNP G1TKB3
AL13	190	ARG	HIS	conflict	UNP G1TKB3

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

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

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

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

- Molecule 19 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AL16	199	Total	C	N	O	S	0	0
			1638	1056	321	256	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	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- 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	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- 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
			808	518	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	119	Total	C	N	O	S	0	0
			976	624	183	168	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	103	Total	C	N	O	S	0	0
			841	522	188	128	3		

- Molecule 33 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AL30	94	Total	C	N	O	S	0	0
			732	465	130	131	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 eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AL39	50	Total	C	N	O	S	0	0
			444	281	98	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	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- 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 acidic ribosomal protein P0.

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

- Molecule 48 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 49 is a protein called 40S_SA_C domain-containing protein.

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

- Molecule 50 is a protein called 40S ribosomal protein S3a.

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

- Molecule 51 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	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 52 is a protein called 40S ribosomal protein S3.

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

- Molecule 53 is a protein called 40S ribosomal protein S4.

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

- Molecule 54 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AS05	185	Total	C	N	O	S	0	0
			1470	921	277	266	6		

- Molecule 55 is a protein called 40S ribosomal protein S6.

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

- Molecule 56 is a protein called eS7.

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

- Molecule 57 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	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 58 is a protein called 40S ribosomal protein S9.

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

- Molecule 59 is a protein called 40S ribosomal protein S10.

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

- Molecule 60 is a protein called 40S ribosomal protein S11.

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

- Molecule 61 is a protein called 40S ribosomal protein S12.

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

- Molecule 62 is a protein called 40S ribosomal protein S13.

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

- Molecule 63 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AS14	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 64 is a protein called 40S ribosomal protein S15.

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

- Molecule 65 is a protein called uS9.

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

- Molecule 66 is a protein called 40S ribosomal protein S17.

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

- Molecule 67 is a protein called 40S ribosomal protein S18.

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

- Molecule 68 is a protein called eS19.

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

- Molecule 69 is a protein called 40S ribosomal protein S20.

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

- Molecule 70 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	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 71 is a protein called 40S ribosomal protein S15a.

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

- Molecule 72 is a protein called 40S ribosomal protein S23.

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

- Molecule 73 is a protein called 40S ribosomal protein S24.

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

- Molecule 74 is a protein called 40S ribosomal protein S25.

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

- Molecule 75 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	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 76 is a protein called 40S ribosomal protein S27.

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

- Molecule 77 is a protein called 40S ribosomal protein S28.

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

- Molecule 78 is a protein called 40S ribosomal protein S29.

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

- Molecule 79 is a protein called 40S ribosomal protein S30.

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

- Molecule 80 is a protein called 40S ribosomal protein S27a.

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

- Molecule 81 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	EL28	125	Total	C	N	O	S	0	0
			1001	621	206	168	6		

- Molecule 82 is a RNA chain called RNA (5'-R(*CP*AP*CP*AP*UP*GP*UP*UP*CP*C)-3').

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

- Molecule 83 is a protein called PR20, ALS/FTD dipeptide repeat protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	PR	19	Total	C	N	O	0	0
			126	73	34	19		

- Molecule 84 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	PTRN	77	Total	C	N	O	P	0	1
			1622	725	295	527	75		

- Molecule 85 is ZINC ION (three-letter code: ZN) (formula: Zn).

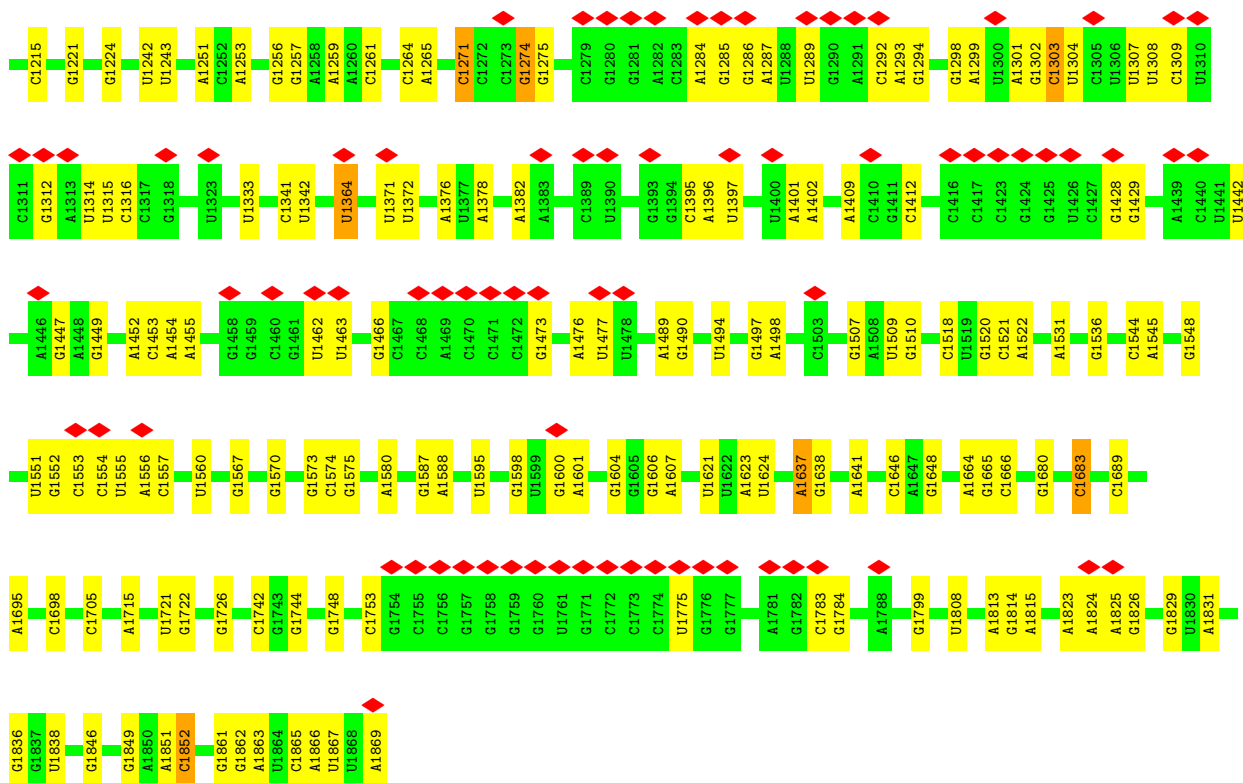
Mol	Chain	Residues	Atoms		AltConf
85	AL37	1	Total	Zn	0
			1	1	
85	AL40	1	Total	Zn	0
			1	1	
85	AL42	1	Total	Zn	0
			1	1	
85	AL43	1	Total	Zn	0
			1	1	

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.

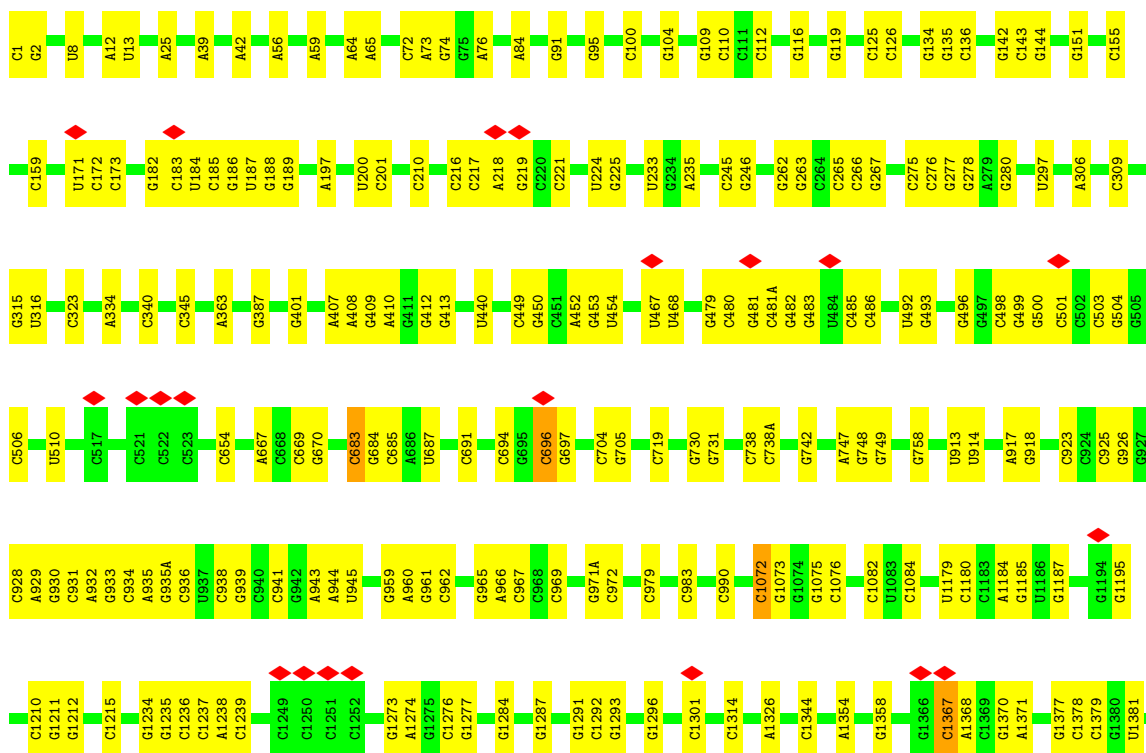
• Molecule 1: 18S rRNA



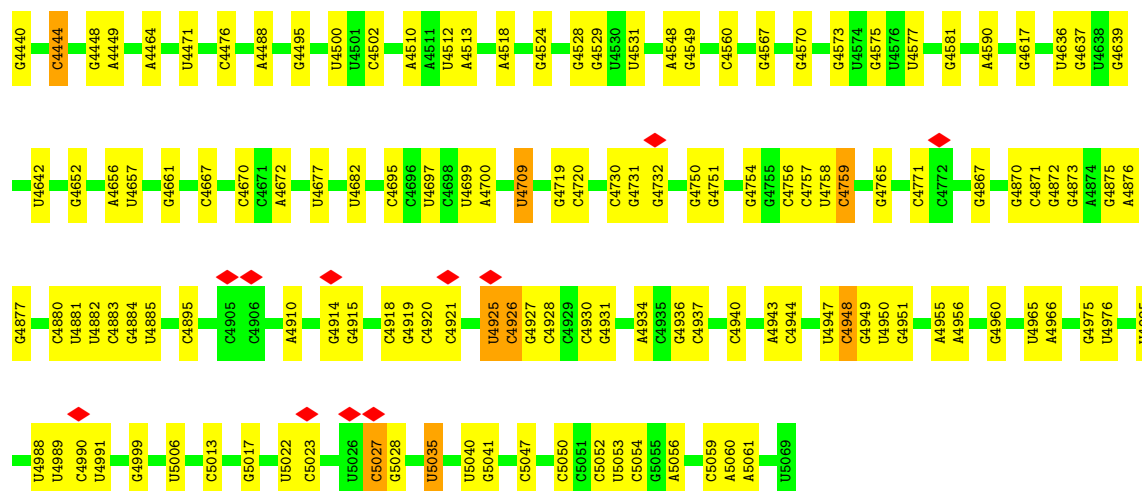


• Molecule 2: 28S rRNA

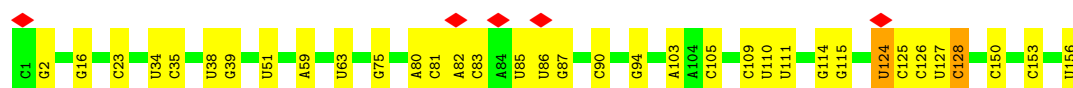
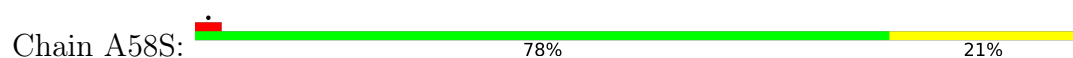
Chain A25S: 78% 21%



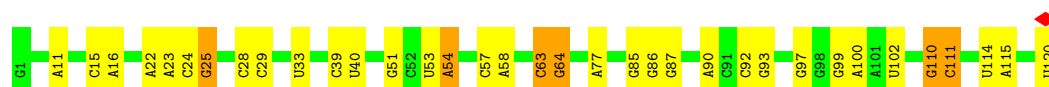
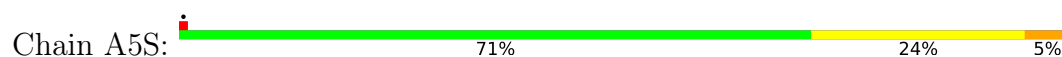




• Molecule 3: 5.8S rRNA



• Molecule 4: 5S rRNA



• Molecule 5: uL2



• Molecule 6: 60S ribosomal protein L3



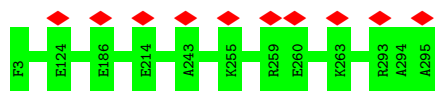
• Molecule 7: 60S ribosomal protein L4





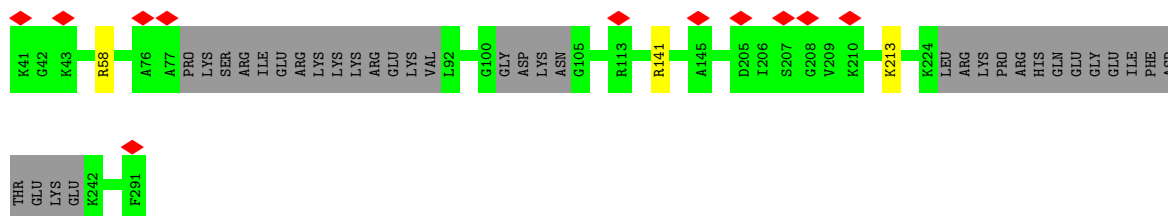
- Molecule 8: 60S ribosomal protein L5

Chain AL05: 100%



- Molecule 9: 60S ribosomal protein L6

Chain AL06: 85% 14%



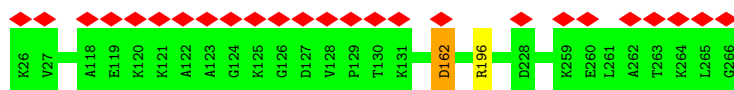
- Molecule 10: uL30

Chain AL07: 99%



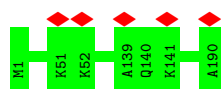
- Molecule 11: eL8

Chain AL08: 10% 99%



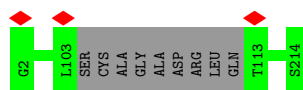
- Molecule 12: 60S ribosomal protein L9

Chain AL09: 100%



- Molecule 13: Ribosomal protein L10

Chain AL10: 96%



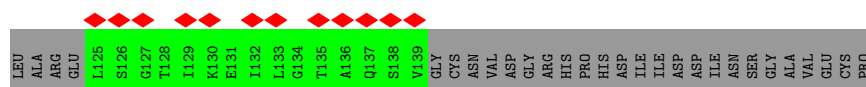
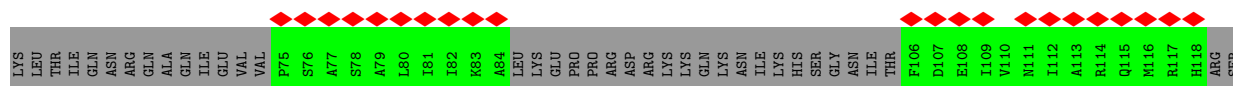
- Molecule 14: 60S ribosomal protein L11

Chain AL11: 99%



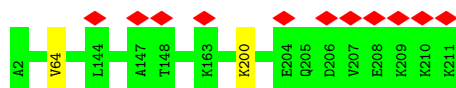
- Molecule 15: 60S ribosomal protein L12

Chain AL12: 21%
23% 77%



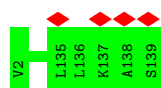
- Molecule 16: eL13

Chain AL13: 5%
99%



- Molecule 17: 60S ribosomal protein L14

Chain AL14: 100%



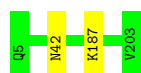
- Molecule 18: 60S ribosomal protein L15

Chain AL15: 100%

There are no outlier residues recorded for this chain.

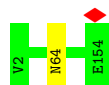
- Molecule 19: uL13

Chain AL16: 99%



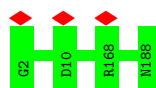
- Molecule 20: 60S ribosomal protein L17

Chain AL17: 99%



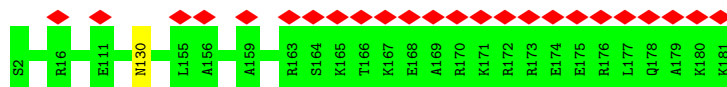
- Molecule 21: eL18

Chain AL18: 100%



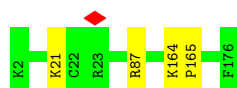
- Molecule 22: 60S ribosomal protein L19

Chain AL19: 13% 99%



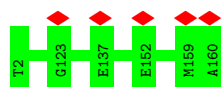
- Molecule 23: eL20

Chain AL20: 98%



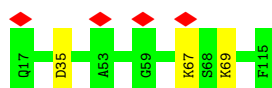
- Molecule 24: 60S ribosomal protein L21

Chain AL21: 100%



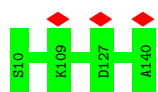
- Molecule 25: eL22

Chain AL22: 97%



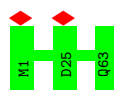
- Molecule 26: 60S ribosomal protein L23

Chain AL23:  100%



- Molecule 27: Ribosomal protein L24

Chain AL24:  100%



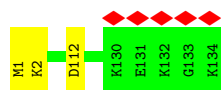
- Molecule 28: uL23

Chain AL25:  100%



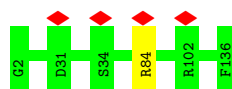
- Molecule 29: 60S ribosomal protein L26

Chain AL26:  98%



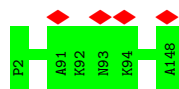
- Molecule 30: 60S ribosomal protein L27

Chain AL27:  99%



- Molecule 31: 60S ribosomal protein L27a

Chain AL28:  100%



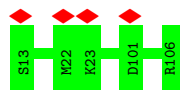
- Molecule 32: eL29

Chain AL29:  22% 100%



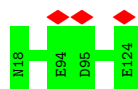
• Molecule 33: eL30

Chain AL30:  100%



• Molecule 34: 60S ribosomal protein L31

Chain AL31:  100%



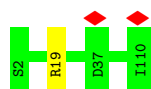
• Molecule 35: 60S ribosomal protein L32

Chain AL32:  100%



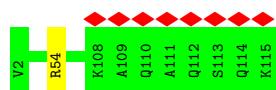
• Molecule 36: 60S ribosomal protein L35a

Chain AL33:  99%



• Molecule 37: 60S ribosomal protein L34

Chain AL34:  99%



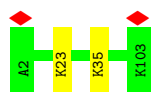
• Molecule 38: 60S ribosomal protein L35

Chain AL35:  99%



• Molecule 39: 60S ribosomal protein L36

Chain AL36:  98%



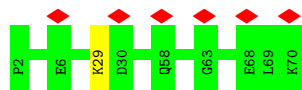
- Molecule 40: 60S ribosomal protein L37

Chain AL37:  100%

There are no outlier residues recorded for this chain.

- Molecule 41: eL38

Chain AL38:  99%



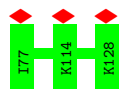
- Molecule 42: eL39

Chain AL39:  98%



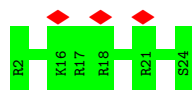
- Molecule 43: eL40

Chain AL40:  100%



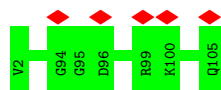
- Molecule 44: eL41

Chain AL41:  100%



- Molecule 45: eL42

Chain AL42:  100%



- Molecule 46: 60S ribosomal protein L37a

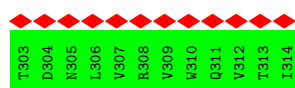
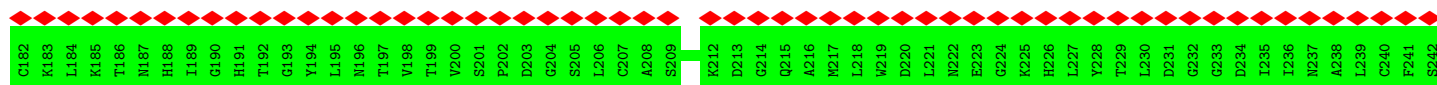
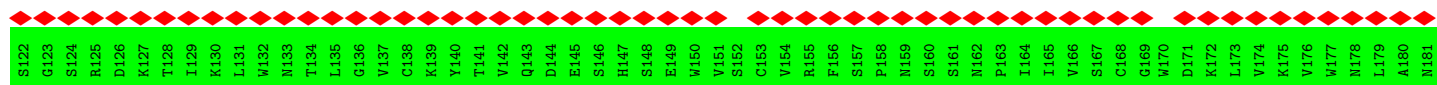
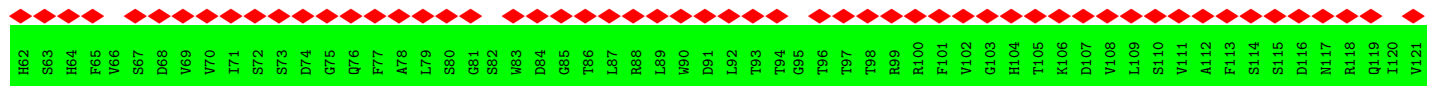
Chain AL43:  100%



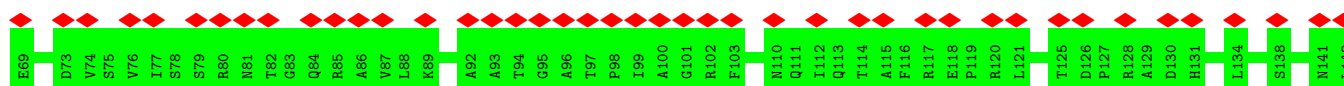
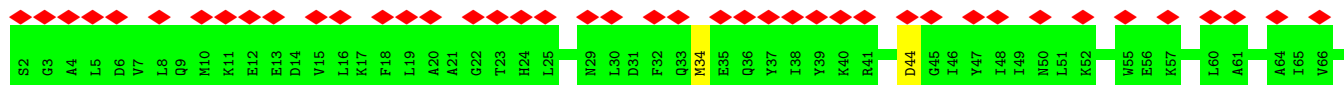
- Molecule 47: 60S acidic ribosomal protein P0

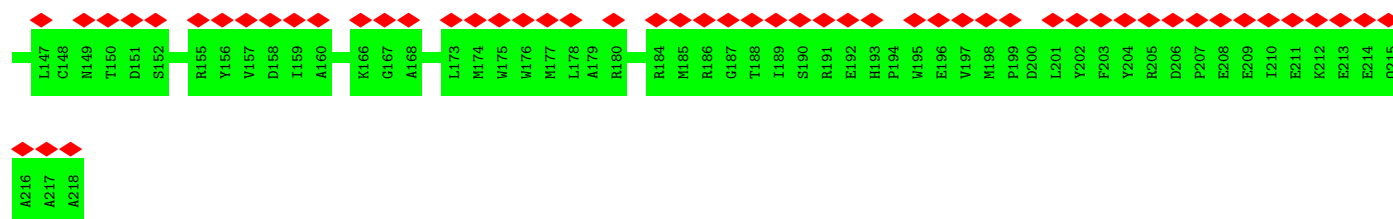


- Molecule 48: Receptor of activated protein C kinase 1



- Molecule 49: 40S_SA_C domain-containing protein





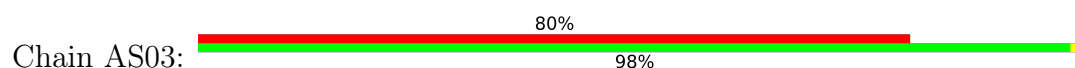
- Molecule 50: 40S ribosomal protein S3a

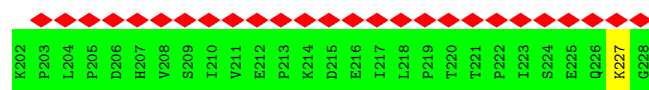


- Molecule 51: 40S ribosomal protein S2



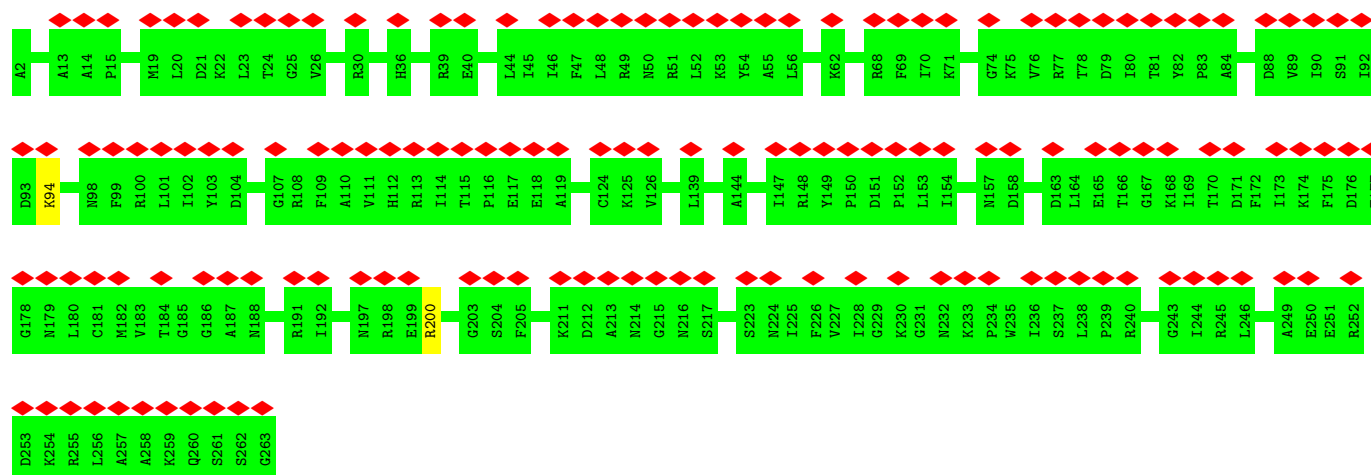
- Molecule 52: 40S ribosomal protein S3





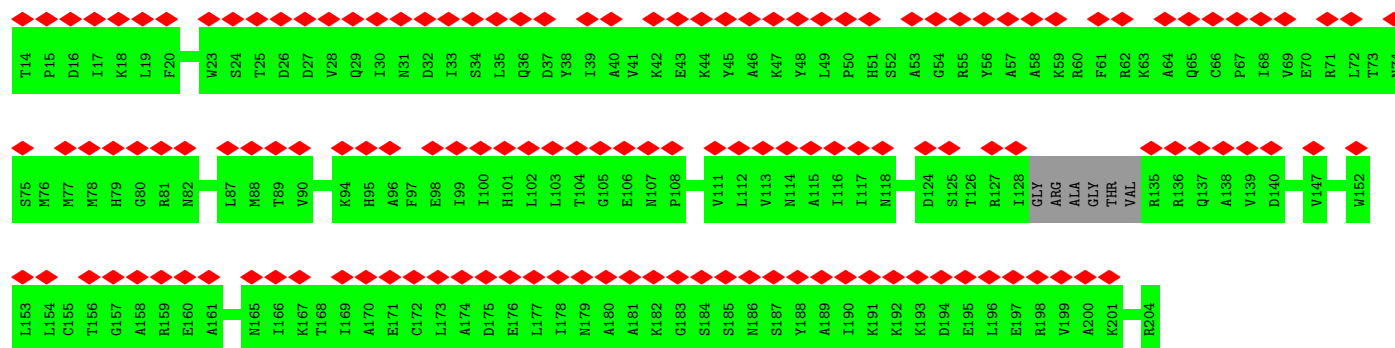
• Molecule 53: 40S ribosomal protein S4

Chain AS04: 57% 99%



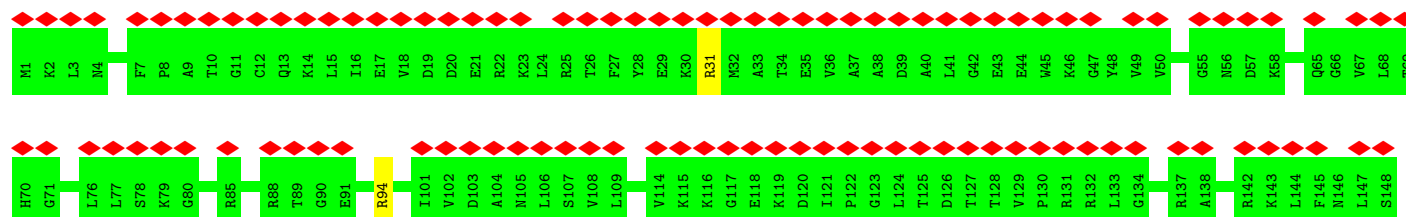
• Molecule 54: Ribosomal protein S5

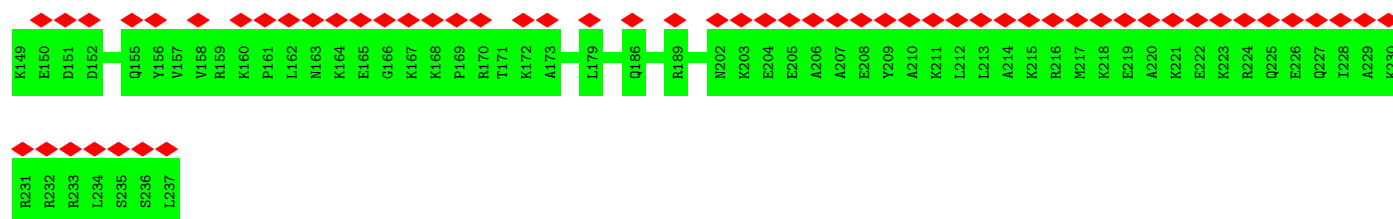
Chain AS05: 74% 97%



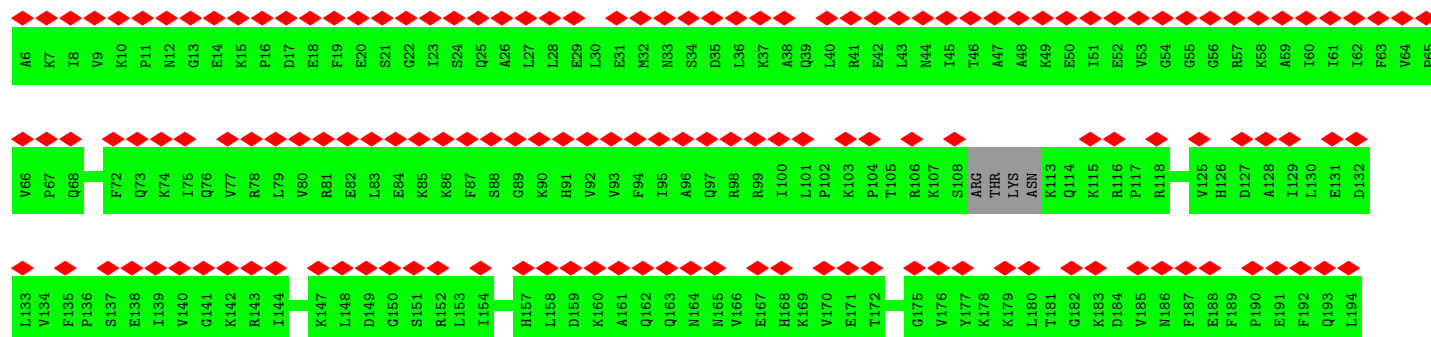
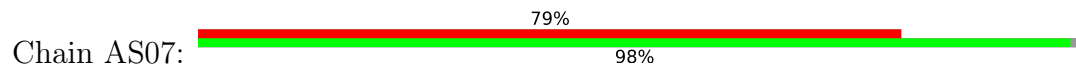
• Molecule 55: 40S ribosomal protein S6

Chain AS06: 68% 99%

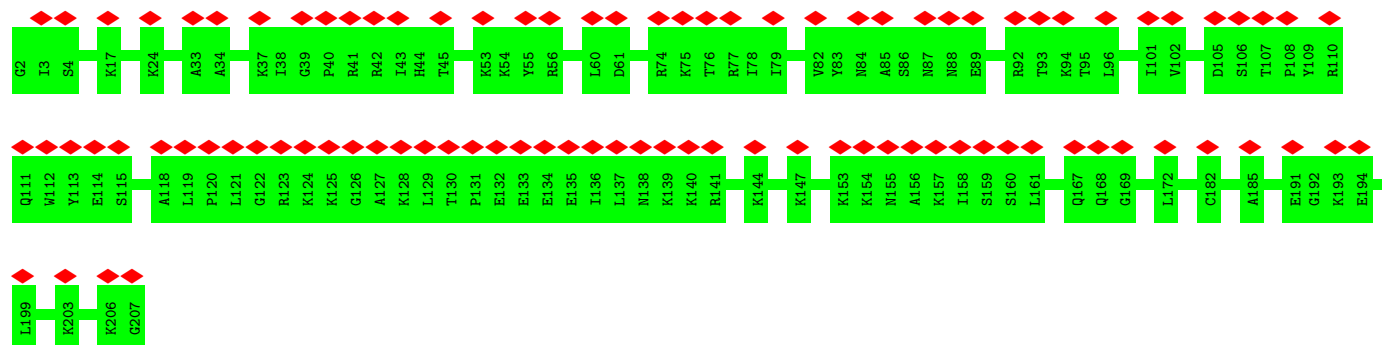




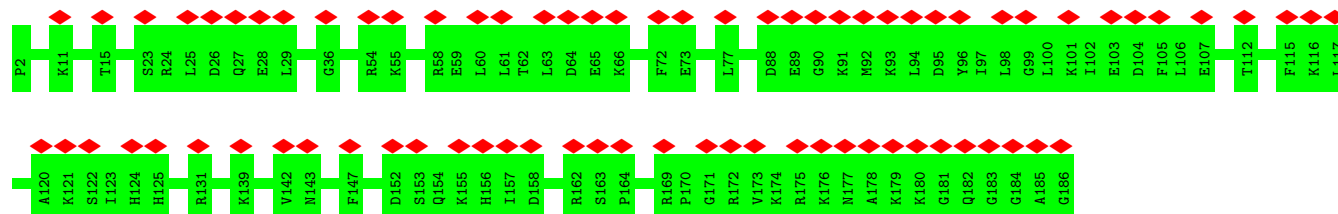
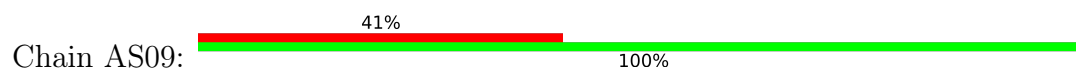
• Molecule 56: eS7



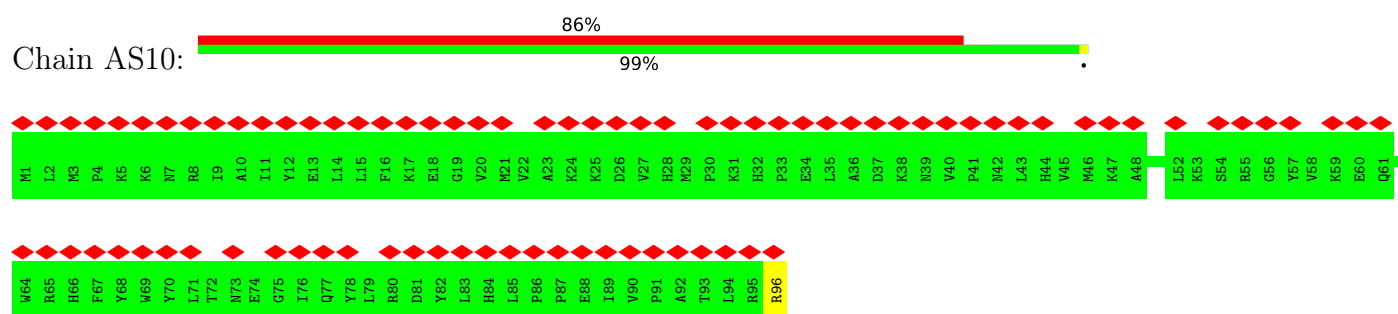
• Molecule 57: 40S ribosomal protein S8



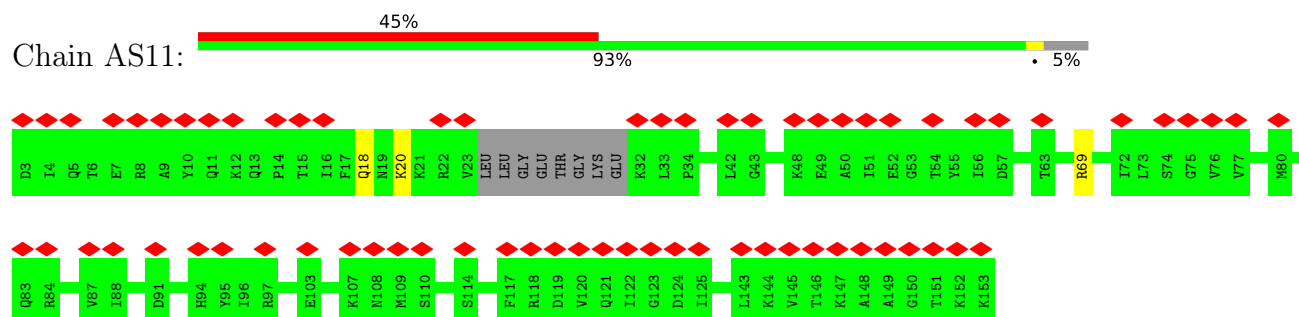
• Molecule 58: 40S ribosomal protein S9



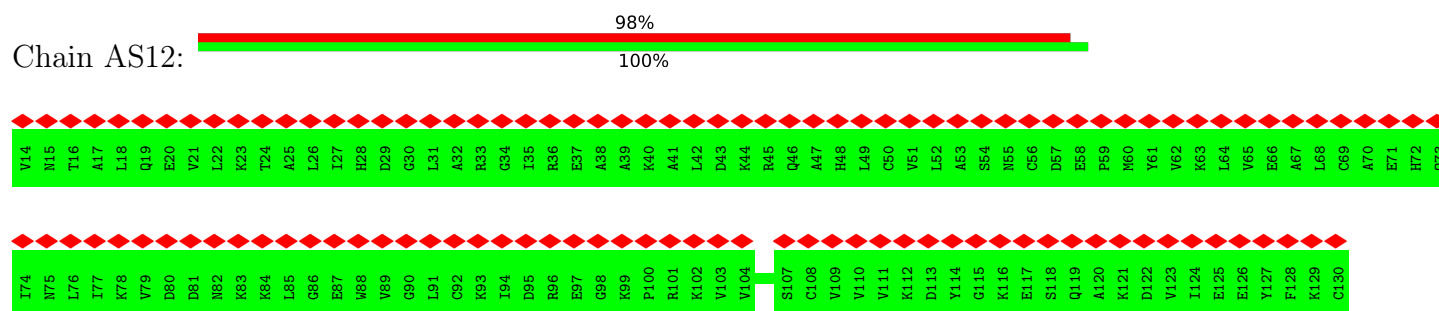
• Molecule 59: 40S ribosomal protein S10



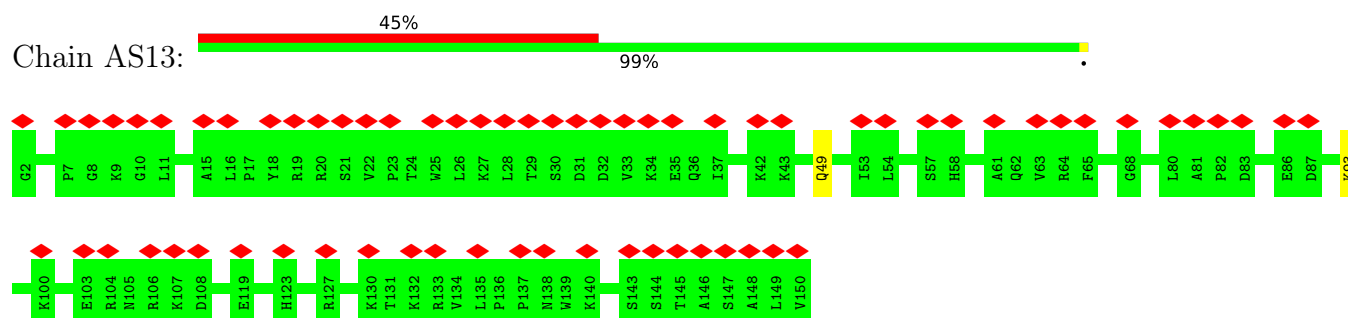
• Molecule 60: 40S ribosomal protein S11



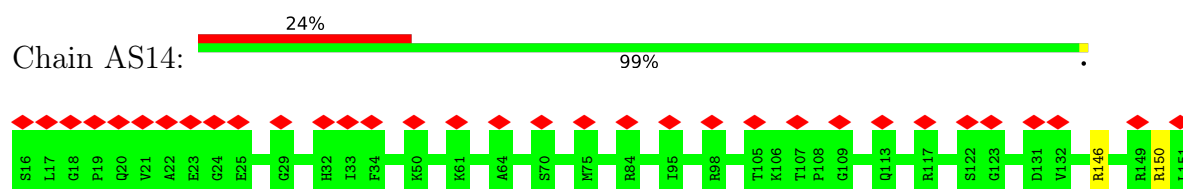
• Molecule 61: 40S ribosomal protein S12



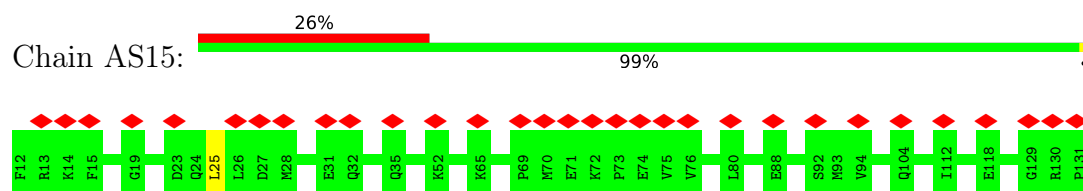
• Molecule 62: 40S ribosomal protein S13



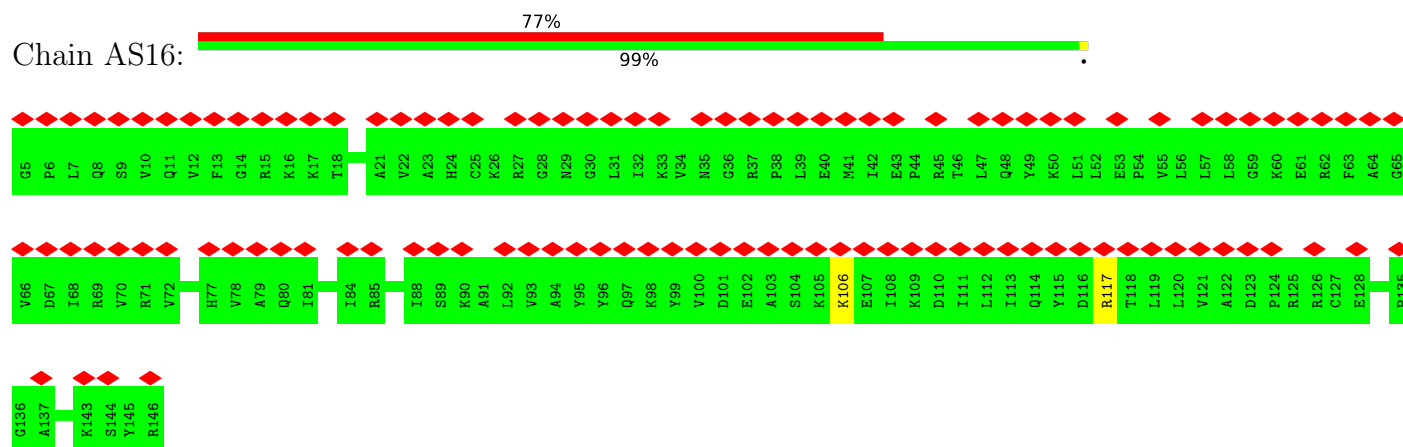
• Molecule 63: 40S ribosomal protein S14



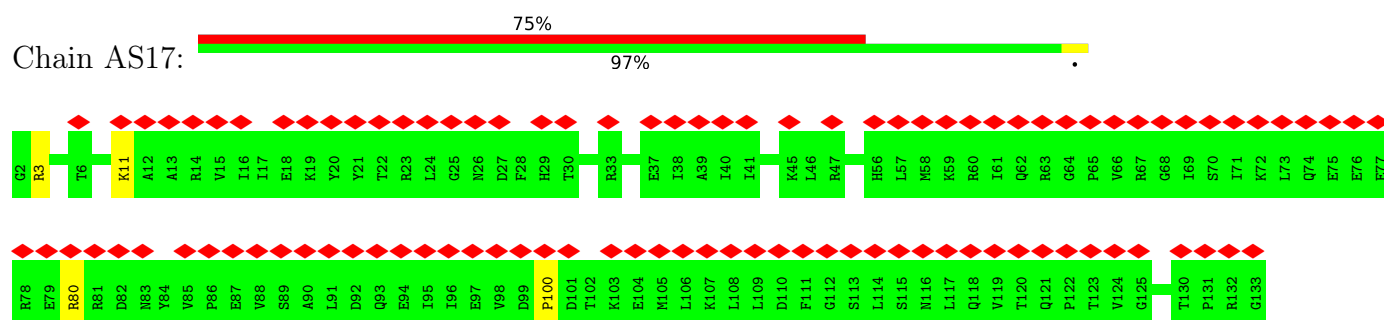
- Molecule 64: 40S ribosomal protein S15



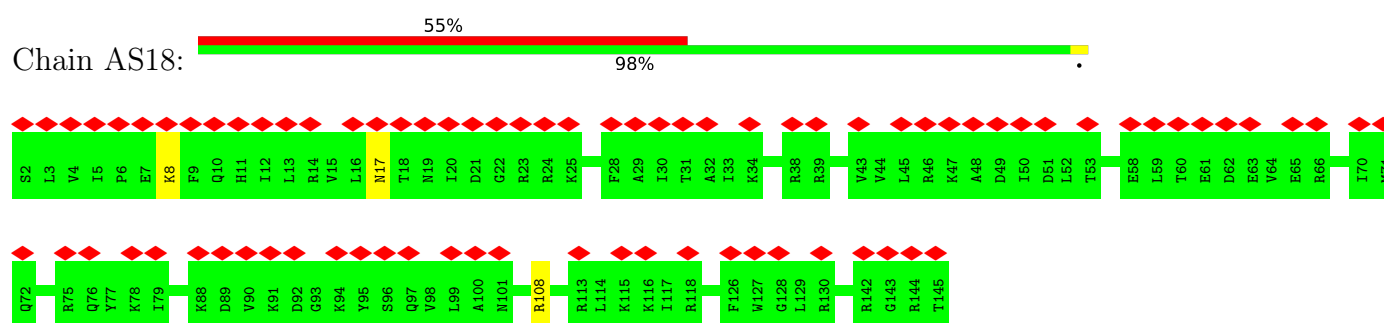
- Molecule 65: uS9



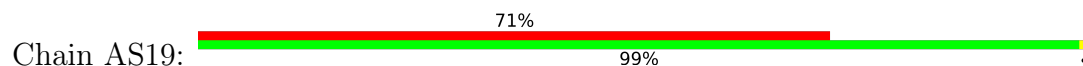
- Molecule 66: 40S ribosomal protein S17

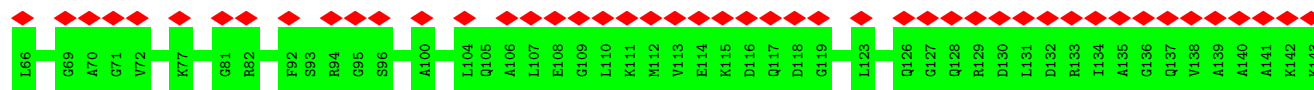
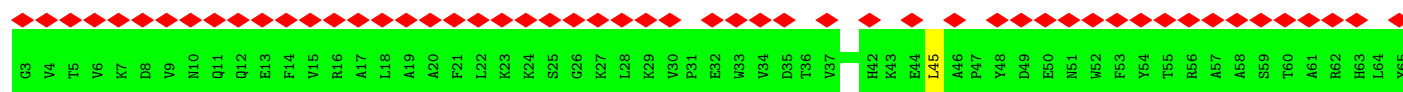


- Molecule 67: 40S ribosomal protein S18

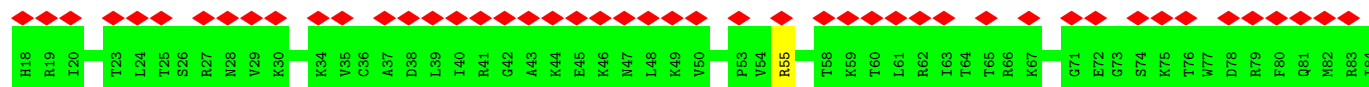
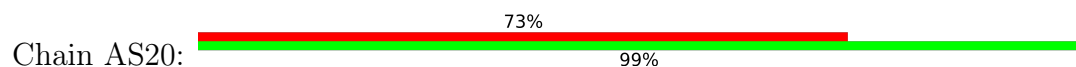


- Molecule 68: eS19

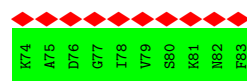
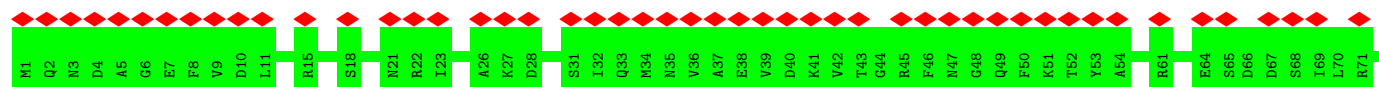




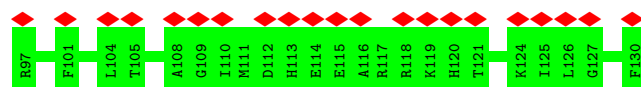
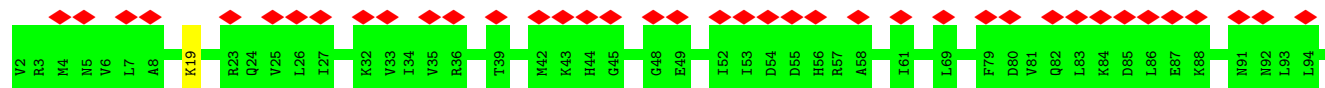
• Molecule 69: 40S ribosomal protein S20



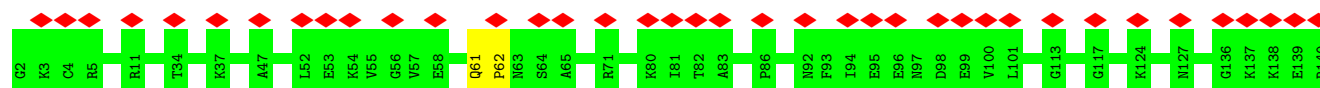
• Molecule 70: eS21



• Molecule 71: 40S ribosomal protein S15a



• Molecule 72: 40S ribosomal protein S23





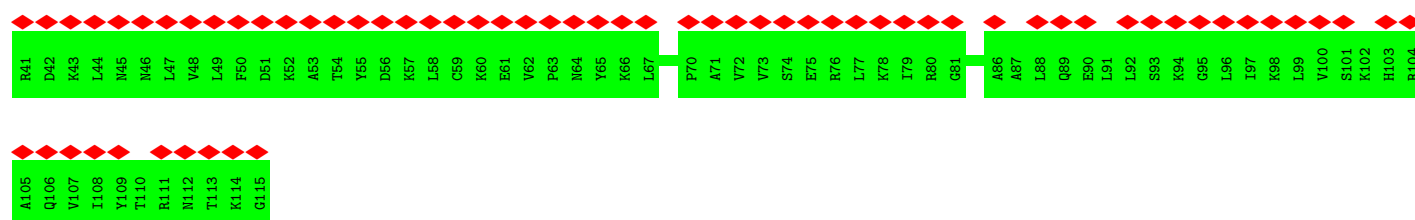
- Molecule 73: 40S ribosomal protein S24

Chain AS24: 67%
99%



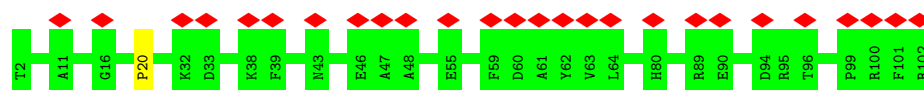
- Molecule 74: 40S ribosomal protein S25

Chain AS25: 87%
100%



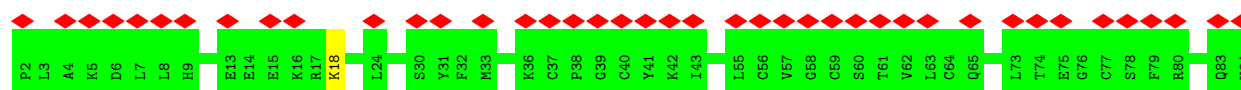
- Molecule 75: eS26

Chain AS26: 26%
99%



- Molecule 76: 40S ribosomal protein S27

Chain AS27: 49%
99%



Chain AS29:

Chain AS30:

Chain AS31:

Chain EL28:

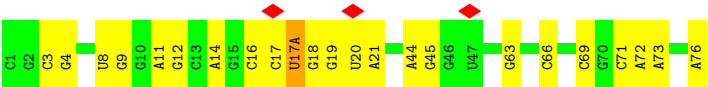
- Molecule 82: RNA (5'-R(*CP*AP*CP*AP*UP*GP*UP*UP*CP*C)-3')

Chain MRNA:

- Molecule 83: PR20, ALS/FTD dipeptide repeat protein

Chain PR:

Chain PTRN:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63475	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	17.840	Depositor
Minimum map value	-5.436	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.774	Depositor
Recommended contour level	3.0	Depositor
Map size (\AA)	528.96, 528.96, 528.96	wwPDB
Map dimensions	608, 608, 608	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.87000006, 0.87000006, 0.87000006	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	0.22	0/40343	0.89	71/62871 (0.1%)
2	A25S	0.21	0/87519	0.86	91/136513 (0.1%)
3	A58S	0.21	0/3701	0.84	2/5766 (0.0%)
4	A5S	0.19	0/2858	0.80	0/4455
5	AL02	0.26	0/1906	0.52	0/2556
6	AL03	0.26	0/3216	0.48	0/4311
7	AL04	0.24	0/2937	0.45	0/3946
8	AL05	0.25	0/2437	0.44	0/3264
9	AL06	0.24	0/1762	0.46	0/2362
10	AL07	0.29	0/1905	0.50	1/2539 (0.0%)
11	AL08	0.25	0/1967	0.48	1/2647 (0.0%)
12	AL09	0.27	0/1535	0.54	0/2063
13	AL10	0.26	0/1691	0.47	0/2256
14	AL11	0.27	0/1376	0.51	0/1841
15	AL12	0.21	0/285	0.33	0/379
16	AL13	0.25	0/1734	0.48	0/2317
17	AL14	0.27	0/1158	0.54	0/1547
18	AL15	0.24	0/1746	0.45	0/2338
19	AL16	0.26	0/1671	0.47	0/2234
20	AL17	0.25	0/1268	0.47	0/1700
21	AL18	0.24	0/1530	0.47	0/2041
22	AL19	0.25	0/1524	0.50	0/2013
23	AL20	0.26	0/1493	0.53	0/2002
24	AL21	0.27	0/1326	0.51	0/1770
25	AL22	0.30	0/822	0.67	1/1103 (0.1%)
26	AL23	0.28	0/993	0.60	0/1332
27	AL24	0.28	0/541	0.56	0/720
28	AL25	0.25	0/993	0.54	0/1334
29	AL26	0.25	0/1132	0.50	1/1504 (0.1%)
30	AL27	0.28	0/1130	0.52	0/1507
31	AL28	0.25	0/1191	0.47	0/1590
32	AL29	0.24	0/854	0.47	0/1128

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AL30	0.27	0/742	0.53	0/996
34	AL31	0.26	0/903	0.49	0/1216
35	AL32	0.27	0/1071	0.52	0/1429
36	AL33	0.27	0/895	0.53	0/1198
37	AL34	0.25	0/916	0.51	0/1220
38	AL35	0.26	0/1021	0.52	0/1348
39	AL36	0.25	0/841	0.50	0/1112
40	AL37	0.25	0/720	0.49	0/952
41	AL38	0.27	0/575	0.64	1/761 (0.1%)
42	AL39	0.23	0/454	0.45	0/599
43	AL40	0.33	0/435	0.63	0/575
44	AL41	0.22	0/223	0.50	0/284
45	AL42	0.29	0/864	0.55	0/1140
46	AL43	0.26	0/718	0.54	0/953
47	ALP0	0.26	0/233	0.42	0/308
48	ARAC	0.24	0/2493	0.46	0/3394
49	AS00	0.25	0/1747	0.50	1/2374 (0.0%)
50	AS01	0.26	0/1756	0.52	0/2350
51	AS02	0.26	0/1753	0.55	0/2369
52	AS03	0.29	0/1796	0.54	0/2417
53	AS04	0.26	0/2118	0.49	0/2849
54	AS05	0.25	0/1491	0.46	0/2004
55	AS06	0.25	0/1946	0.47	0/2590
56	AS07	0.24	0/1510	0.47	0/2022
57	AS08	0.25	0/1715	0.49	0/2287
58	AS09	0.25	0/1550	0.47	0/2069
59	AS10	0.25	0/834	0.47	0/1125
60	AS11	0.26	0/1195	0.50	0/1597
61	AS12	0.24	0/918	0.46	0/1233
62	AS13	0.23	0/1226	0.46	0/1649
63	AS14	0.26	0/1029	0.55	0/1380
64	AS15	0.25	0/1017	0.52	1/1358 (0.1%)
65	AS16	0.24	0/1146	0.48	0/1534
66	AS17	0.28	0/1082	0.53	1/1452 (0.1%)
67	AS18	0.28	0/1208	0.54	0/1618
68	AS19	0.25	0/1115	0.50	1/1493 (0.1%)
69	AS20	0.24	0/805	0.54	1/1081 (0.1%)
70	AS21	0.27	0/643	0.54	0/860
71	AS22	0.25	0/1051	0.52	0/1406
72	AS23	0.28	0/1116	0.52	0/1490
73	AS24	0.25	0/1028	0.49	0/1366
74	AS25	0.24	0/604	0.52	0/810
75	AS26	0.26	0/828	0.48	1/1109 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AS27	0.26	0/665	0.54	0/891
77	AS28	0.24	0/490	0.49	0/656
78	AS29	0.25	0/470	0.46	0/623
79	AS30	0.24	0/447	0.43	0/587
80	AS31	0.24	0/567	0.45	0/753
81	EL28	0.26	0/1017	0.57	0/1364
82	MRNA	0.14	0/229	0.76	0/353
83	PR	0.41	0/130	1.06	2/171 (1.2%)
84	PTRN	0.24	0/1810	0.96	4/2817 (0.1%)
All	All	0.23	0/229700	0.76	181/337541 (0.1%)

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
6	AL03	0	1
11	AL08	0	1
23	AL20	0	1
72	AS23	0	1
83	PR	0	1
All	All	0	5

There are no bond length outliers.

All (181) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A18S	1022	U	C2-N1-C1'	10.22	129.97	117.70
1	A18S	1078	C	N1-C2-O2	9.12	124.37	118.90
2	A25S	4420	U	C2-N1-C1'	8.95	128.44	117.70
2	A25S	4420	U	N1-C2-O2	8.61	128.83	122.80
1	A18S	1453	C	N1-C2-O2	8.24	123.84	118.90
1	A18S	1453	C	C2-N1-C1'	7.95	127.54	118.80
1	A18S	174	C	N3-C2-O2	-7.94	116.34	121.90
1	A18S	1078	C	N3-C2-O2	-7.80	116.44	121.90
2	A25S	100	C	C2-N1-C1'	7.65	127.21	118.80
2	A25S	4420	U	N3-C2-O2	-7.63	116.86	122.20
1	A18S	1078	C	C2-N1-C1'	7.59	127.15	118.80
1	A18S	853	C	N1-C2-O2	7.53	123.42	118.90
2	A25S	499	G	C4-N9-C1'	7.45	136.18	126.50
2	A25S	3772	U	C2-N1-C1'	7.39	126.57	117.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	PTRN	66	C	C2-N1-C1'	7.31	126.84	118.80
2	A25S	3771	C	N1-C2-O2	7.31	123.28	118.90
64	AS15	25	LEU	CA-CB-CG	7.27	132.03	115.30
2	A25S	3909	C	N1-C2-O2	7.24	123.24	118.90
2	A25S	694	C	N3-C2-O2	-7.19	116.86	121.90
2	A25S	1639	U	C2-N1-C1'	7.11	126.23	117.70
66	AS17	100	PRO	CA-N-CD	-7.06	101.62	111.50
2	A25S	100	C	N1-C2-O2	7.03	123.12	118.90
2	A25S	499	G	N3-C4-N9	7.02	130.21	126.00
1	A18S	1022	U	C6-N1-C1'	-6.99	111.41	121.20
83	PR	24	ARG	C-N-CD	-6.96	105.29	120.60
1	A18S	1139	C	N1-C2-O2	6.95	123.07	118.90
2	A25S	3909	C	C2-N1-C1'	6.95	126.45	118.80
2	A25S	4759	C	N1-C2-O2	6.89	123.03	118.90
1	A18S	853	C	C2-N1-C1'	6.88	126.37	118.80
1	A18S	1139	C	C2-N1-C1'	6.87	126.36	118.80
1	A18S	1022	U	N1-C2-O2	6.84	127.59	122.80
1	A18S	1123	C	N1-C2-O2	6.80	122.98	118.90
2	A25S	499	G	C8-N9-C1'	-6.77	118.20	127.00
2	A25S	3636	C	N3-C2-O2	-6.77	117.16	121.90
1	A18S	1271	C	N1-C2-O2	6.71	122.92	118.90
1	A18S	453	C	C2-N1-C1'	6.67	126.13	118.80
1	A18S	4	C	C2-N1-C1'	6.66	126.12	118.80
1	A18S	4	C	N1-C2-O2	6.62	122.87	118.90
2	A25S	3771	C	N3-C2-O2	-6.61	117.28	121.90
1	A18S	1303	C	C2-N1-C1'	6.58	126.03	118.80
1	A18S	1453	C	N3-C2-O2	-6.57	117.30	121.90
1	A18S	1123	C	N3-C2-O2	-6.55	117.32	121.90
1	A18S	1303	C	N1-C2-O2	6.48	122.79	118.90
2	A25S	4413	C	C2-N1-C1'	6.45	125.89	118.80
25	AL22	35	ASP	CB-CG-OD1	6.43	124.09	118.30
1	A18S	1117	C	N1-C2-O2	6.41	122.75	118.90
2	A25S	3772	U	N3-C2-O2	-6.34	117.76	122.20
2	A25S	4930	C	C2-N1-C1'	6.32	125.75	118.80
2	A25S	1639	U	N1-C2-O2	6.24	127.17	122.80
2	A25S	4759	C	C2-N1-C1'	6.22	125.64	118.80
2	A25S	4444	C	N1-C2-O2	6.18	122.61	118.90
2	A25S	3772	U	N1-C2-O2	6.18	127.12	122.80
2	A25S	1084	C	N1-C2-O2	6.13	122.58	118.90
1	A18S	1022	U	N3-C2-O2	-6.13	117.91	122.20
1	A18S	1117	C	C2-N1-C1'	6.13	125.54	118.80
2	A25S	2465	C	N1-C2-O2	6.12	122.58	118.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A18S	853	C	N3-C2-O2	-6.12	117.62	121.90
2	A25S	3636	C	N1-C2-O2	6.08	122.55	118.90
2	A25S	5027	C	P-O3'-C3'	6.07	126.98	119.70
2	A25S	2465	C	N3-C2-O2	-6.05	117.66	121.90
1	A18S	630	U	C2-N1-C1'	6.03	124.93	117.70
41	AL38	29	LYS	C-N-CA	6.02	136.75	121.70
2	A25S	4420	U	C6-N1-C1'	-5.98	112.83	121.20
1	A18S	1261	C	C6-N1-C2	-5.97	117.91	120.30
1	A18S	1261	C	N1-C2-O2	5.96	122.48	118.90
2	A25S	2661	U	OP1-P-O3'	5.95	118.30	105.20
1	A18S	1261	C	C2-N1-C1'	5.94	125.33	118.80
1	A18S	688	U	P-O3'-C3'	5.93	126.81	119.70
2	A25S	2661	U	P-O3'-C3'	5.88	126.75	119.70
1	A18S	1784	G	C4-N9-C1'	5.86	134.11	126.50
2	A25S	2695	A	P-O3'-C3'	5.84	126.71	119.70
29	AL26	112	ASP	CB-CG-OD1	5.84	123.56	118.30
2	A25S	4413	C	N3-C2-O2	-5.84	117.81	121.90
2	A25S	4413	C	N1-C2-O2	5.81	122.39	118.90
2	A25S	3909	C	N3-C2-O2	-5.81	117.83	121.90
2	A25S	1612	G	N3-C4-C5	-5.80	125.70	128.60
2	A25S	1639	U	N3-C2-O2	-5.79	118.14	122.20
2	A25S	1731	C	C2-N1-C1'	5.78	125.15	118.80
2	A25S	2046	G	P-O3'-C3'	5.75	126.60	119.70
1	A18S	1292	C	N1-C2-O2	5.75	122.35	118.90
1	A18S	427	U	C2-N1-C1'	5.74	124.59	117.70
2	A25S	4119	C	P-O3'-C3'	5.72	126.57	119.70
2	A25S	2089	G	P-O3'-C3'	5.71	126.56	119.70
2	A25S	3739	C	C2-N1-C1'	5.71	125.08	118.80
1	A18S	1078	C	C6-N1-C2	-5.68	118.03	120.30
2	A25S	1612	G	N3-C4-N9	5.67	129.41	126.00
2	A25S	4502	C	N1-C2-O2	5.66	122.30	118.90
1	A18S	1683	C	N1-C2-O2	5.66	122.30	118.90
1	A18S	1551	U	C2-N1-C1'	5.64	124.47	117.70
84	PTRN	66	C	N1-C2-O2	5.64	122.29	118.90
1	A18S	1453	C	C6-N1-C2	-5.63	118.05	120.30
2	A25S	2325	C	C2-N1-C1'	5.63	124.99	118.80
2	A25S	4413	C	C6-N1-C2	-5.61	118.06	120.30
1	A18S	1271	C	C2-N1-C1'	5.60	124.96	118.80
11	AL08	162	ASP	CB-CG-OD1	5.60	123.34	118.30
1	A18S	1298	G	N3-C4-C5	-5.59	125.80	128.60
2	A25S	1978	C	C2-N1-C1'	5.58	124.94	118.80
2	A25S	4880	C	C2-N1-C1'	5.58	124.94	118.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A25S	4709	U	C2-N1-C1'	5.58	124.40	117.70
1	A18S	130	G	C4-N9-C1'	5.58	133.75	126.50
2	A25S	1072	C	P-O3'-C3'	5.57	126.38	119.70
1	A18S	1057	C	C2-N1-C1'	5.55	124.91	118.80
75	AS26	20	PRO	CA-N-CD	-5.55	103.72	111.50
2	A25S	4925	U	P-O3'-C3'	5.55	126.36	119.70
2	A25S	499	G	N3-C4-C5	-5.54	125.83	128.60
1	A18S	1139	C	N3-C2-O2	-5.52	118.03	121.90
2	A25S	112	C	C2-N1-C1'	5.50	124.86	118.80
2	A25S	100	C	C6-N1-C1'	-5.48	114.23	120.80
2	A25S	3959	U	P-O3'-C3'	5.47	126.27	119.70
1	A18S	1298	G	C4-N9-C1'	5.47	133.61	126.50
2	A25S	3771	C	P-O3'-C3'	5.46	126.25	119.70
2	A25S	1978	C	N1-C2-O2	5.44	122.16	118.90
3	A58S	128	C	N1-C2-O2	5.44	122.16	118.90
1	A18S	1624	U	C2-N1-C1'	5.43	124.22	117.70
2	A25S	1686	C	N3-C2-O2	-5.42	118.10	121.90
2	A25S	1084	C	C2-N1-C1'	5.42	124.76	118.80
2	A25S	5035	U	N3-C2-O2	-5.42	118.41	122.20
3	A58S	124	U	P-O3'-C3'	5.42	126.20	119.70
1	A18S	4	C	N3-C2-O2	-5.41	118.11	121.90
2	A25S	4759	C	N3-C2-O2	-5.41	118.11	121.90
1	A18S	1261	C	N3-C2-O2	-5.40	118.12	121.90
2	A25S	100	C	N3-C2-O2	-5.40	118.12	121.90
2	A25S	3771	C	OP1-P-O3'	5.40	117.08	105.20
2	A25S	4926	C	C2-N1-C1'	5.40	124.74	118.80
84	PTRN	17(A)	U	P-O3'-C3'	5.39	126.17	119.70
1	A18S	1364	U	N1-C2-O2	5.38	126.57	122.80
2	A25S	1612	G	C4-N9-C1'	5.38	133.49	126.50
83	PR	24	ARG	C-N-CA	5.38	144.58	122.00
2	A25S	4948	C	C2-N1-C1'	5.37	124.70	118.80
1	A18S	1298	G	N3-C4-N9	5.36	129.22	126.00
2	A25S	683	C	N1-C2-O2	5.36	122.12	118.90
1	A18S	630	U	N1-C2-O2	5.35	126.55	122.80
1	A18S	1453	C	C6-N1-C1'	-5.34	114.39	120.80
2	A25S	3909	C	C6-N1-C2	-5.33	118.17	120.30
1	A18S	914	U	C2-N1-C1'	5.32	124.09	117.70
1	A18S	1057	C	C6-N1-C2	-5.32	118.17	120.30
2	A25S	4444	C	N3-C2-O2	-5.31	118.18	121.90
2	A25S	155	C	N3-C2-O2	-5.30	118.19	121.90
2	A25S	4758	U	C2-N1-C1'	5.29	124.05	117.70
2	A25S	2627	C	C2-N1-C1'	5.29	124.61	118.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A25S	1367	C	C2-N1-C1'	5.28	124.61	118.80
2	A25S	1367	C	N1-C2-O2	5.28	122.07	118.90
84	PTRN	66	C	C6-N1-C1'	-5.28	114.47	120.80
1	A18S	1852	C	C2-N1-C1'	5.25	124.57	118.80
1	A18S	1303	C	N3-C2-O2	-5.24	118.23	121.90
69	AS20	55	ARG	C-N-CA	5.24	134.79	121.70
10	AL07	179	ARG	NE-CZ-NH1	-5.23	117.68	120.30
1	A18S	1022	U	C5-C6-N1	5.23	125.31	122.70
2	A25S	1210	C	C2-N1-C1'	5.23	124.55	118.80
2	A25S	1848	C	C2-N1-C1'	5.20	124.52	118.80
1	A18S	1271	C	N3-C2-O2	-5.20	118.26	121.90
2	A25S	4232	U	P-O3'-C3'	5.19	125.92	119.70
1	A18S	630	U	N3-C2-O2	-5.19	118.57	122.20
1	A18S	1784	G	C8-N9-C1'	-5.17	120.27	127.00
1	A18S	659	G	C4-N9-C1'	5.17	133.22	126.50
1	A18S	43	U	C2-N1-C1'	5.16	123.90	117.70
1	A18S	130	G	N3-C4-C5	-5.16	126.02	128.60
1	A18S	1551	U	N1-C2-O2	5.16	126.41	122.80
2	A25S	1686	C	N1-C2-O2	5.16	121.99	118.90
68	AS19	45	LEU	C-N-CA	5.16	134.59	121.70
1	A18S	356	C	C2-N1-C1'	5.14	124.45	118.80
2	A25S	696	C	P-O3'-C3'	5.13	125.86	119.70
2	A25S	2491	C	C2-N1-C1'	5.12	124.43	118.80
1	A18S	1637	A	P-O3'-C3'	5.12	125.84	119.70
2	A25S	4286	C	C2-N1-C1'	5.10	124.41	118.80
2	A25S	2528	G	C4-N9-C1'	5.10	133.13	126.50
1	A18S	1518	C	C2-N1-C1'	5.10	124.41	118.80
1	A18S	1689	C	C2-N1-C1'	5.09	124.40	118.80
2	A25S	4926	C	N1-C2-O2	5.08	121.95	118.90
1	A18S	183	G	C4-N9-C1'	5.07	133.09	126.50
1	A18S	1274	G	C4-N9-C1'	5.07	133.08	126.50
2	A25S	1847	C	C2-N1-C1'	5.06	124.37	118.80
2	A25S	1792	U	C2-N1-C1'	5.06	123.77	117.70
2	A25S	499	G	C6-C5-N7	-5.06	127.37	130.40
2	A25S	4925	U	OP2-P-O3'	5.06	116.32	105.20
49	AS00	44	ASP	CB-CG-OD1	5.05	122.85	118.30
1	A18S	1683	C	C2-N1-C1'	5.04	124.35	118.80
2	A25S	2627	C	N1-C2-O2	5.04	121.92	118.90
2	A25S	1180	C	C2-N1-C1'	5.04	124.34	118.80
2	A25S	4413	C	O4'-C1'-N1	5.01	112.21	108.20
1	A18S	914	U	N1-C2-O2	5.00	126.30	122.80

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	AL03	261	ARG	Peptide
11	AL08	162	ASP	Peptide
23	AL20	164	LYS	Peptide
72	AS23	61	GLN	Peptide
83	PR	24	ARG	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	36079	0	0	0	0
2	A25S	78238	0	0	0	0
3	A58S	3314	0	0	0	0
4	A5S	2558	0	1296	17	0
5	AL02	1868	0	0	0	0
6	AL03	3148	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	1870	0	0	0	0
11	AL08	1934	0	0	0	0
12	AL09	1516	0	0	0	0
13	AL10	1654	0	0	0	0
14	AL11	1353	0	0	0	0
15	AL12	285	0	0	0	0
16	AL13	1703	0	0	0	0
17	AL14	1137	0	0	0	0
18	AL15	1701	0	0	0	0
19	AL16	1638	0	0	0	0
20	AL17	1242	0	0	0	0
21	AL18	1506	0	0	0	0
22	AL19	1508	0	0	0	0
23	AL20	1454	0	0	0	0
24	AL21	1298	0	0	0	0
25	AL22	808	0	0	0	0
26	AL23	979	0	0	0	0
27	AL24	528	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	AL25	976	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	841	0	0	0	0
33	AL30	732	0	0	0	0
34	AL31	888	0	0	0	0
35	AL32	1053	0	0	0	0
36	AL33	876	0	0	0	0
37	AL34	906	0	0	0	0
38	AL35	1013	0	0	0	0
39	AL36	830	0	0	0	0
40	AL37	705	0	0	0	0
41	AL38	569	0	0	0	0
42	AL39	444	0	0	0	0
43	AL40	429	0	0	0	0
44	AL41	222	0	0	0	0
45	AL42	851	0	0	0	0
46	AL43	708	0	0	0	0
47	ALP0	230	0	0	0	0
48	ARAC	2436	0	0	0	0
49	AS00	1710	0	0	0	0
50	AS01	1729	0	0	0	0
51	AS02	1716	0	0	0	0
52	AS03	1768	0	0	0	0
53	AS04	2076	0	0	0	0
54	AS05	1470	0	0	0	0
55	AS06	1923	0	0	0	0
56	AS07	1488	0	0	0	0
57	AS08	1686	0	0	0	0
58	AS09	1525	0	0	0	0
59	AS10	810	0	0	0	0
60	AS11	1175	0	0	0	0
61	AS12	908	0	0	0	0
62	AS13	1202	0	0	0	0
63	AS14	1016	0	0	0	0
64	AS15	997	0	0	0	0
65	AS16	1128	0	0	0	0
66	AS17	1068	0	0	0	0
67	AS18	1190	0	0	0	0
68	AS19	1097	0	0	0	0
69	AS20	795	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	AS21	636	0	0	0	0
71	AS22	1034	0	0	0	0
72	AS23	1098	0	0	0	0
73	AS24	1011	0	0	0	0
74	AS25	598	0	0	0	0
75	AS26	814	0	0	0	0
76	AS27	651	0	0	0	0
77	AS28	488	0	0	0	0
78	AS29	459	0	0	0	0
79	AS30	443	0	0	0	0
80	AS31	555	0	0	0	0
81	EL28	1001	0	0	0	0
82	MRNA	207	0	0	0	0
83	PR	126	0	104	0	0
84	PTRN	1622	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
All	All	213639	0	1400	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	1.57	0.70
4:A5S:77:A:H62	4:A5S:99:G:H21	1.44	0.64
4:A5S:92:C:H2'	4:A5S:93:G:H8	1.66	0.59
4:A5S:63:C:H5'	4:A5S:64:G:H5''	1.86	0.56
4:A5S:28:C:O2'	4:A5S:54:A:N1	2.39	0.55
4:A5S:114:U:H2'	4:A5S:115:A:C8	2.45	0.51
4:A5S:114:U:H2'	4:A5S:115:A:H8	1.77	0.49
4:A5S:57:C:H2'	4:A5S:58:A:H8	1.79	0.47
4:A5S:77:A:H62	4:A5S:99:G:N2	2.12	0.46
4:A5S:92:C:H2'	4:A5S:93:G:C8	2.50	0.46
4:A5S:85:G:H2'	4:A5S:86:G:H8	1.81	0.45
4:A5S:87:G:N2	4:A5S:90:A:OP2	2.46	0.45
4:A5S:110:G:H2'	4:A5S:111:C:C6	2.53	0.43
4:A5S:24:C:H2'	4:A5S:25:G:O4'	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A5S:15:C:H2'	4:A5S:16:A:H8	1.86	0.41
4:A5S:29:C:H1'	4:A5S:51:G:H1	1.86	0.41
4:A5S:23:A:H2'	4:A5S:24:C:C6	2.56	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	242/244 (99%)	227 (94%)	15 (6%)	0	100	100
6	AL03	392/394 (100%)	377 (96%)	15 (4%)	0	100	100
7	AL04	360/362 (99%)	348 (97%)	12 (3%)	0	100	100
8	AL05	291/293 (99%)	282 (97%)	9 (3%)	0	100	100
9	AL06	208/251 (83%)	201 (97%)	7 (3%)	0	100	100
10	AL07	223/225 (99%)	218 (98%)	5 (2%)	0	100	100
11	AL08	239/241 (99%)	223 (93%)	16 (7%)	0	100	100
12	AL09	188/190 (99%)	178 (95%)	10 (5%)	0	100	100
13	AL10	200/213 (94%)	191 (96%)	9 (4%)	0	100	100
14	AL11	167/169 (99%)	154 (92%)	13 (8%)	0	100	100
15	AL12	32/163 (20%)	32 (100%)	0	0	100	100
16	AL13	208/210 (99%)	193 (93%)	14 (7%)	1 (0%)	29	64
17	AL14	136/138 (99%)	126 (93%)	10 (7%)	0	100	100
18	AL15	201/203 (99%)	194 (96%)	7 (4%)	0	100	100
19	AL16	197/199 (99%)	193 (98%)	4 (2%)	0	100	100
20	AL17	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
21	AL18	185/187 (99%)	178 (96%)	7 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	AL19	178/180 (99%)	173 (97%)	5 (3%)	0	100	100
23	AL20	173/175 (99%)	164 (95%)	8 (5%)	1 (1%)	25	59
24	AL21	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
25	AL22	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
26	AL23	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
27	AL24	61/63 (97%)	61 (100%)	0	0	100	100
28	AL25	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
29	AL26	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
30	AL27	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
31	AL28	145/147 (99%)	135 (93%)	10 (7%)	0	100	100
32	AL29	99/103 (96%)	96 (97%)	3 (3%)	0	100	100
33	AL30	92/94 (98%)	92 (100%)	0	0	100	100
34	AL31	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
35	AL32	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
36	AL33	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
37	AL34	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
38	AL35	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
39	AL36	100/102 (98%)	93 (93%)	7 (7%)	0	100	100
40	AL37	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
41	AL38	67/69 (97%)	59 (88%)	8 (12%)	0	100	100
42	AL39	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
43	AL40	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
44	AL41	21/23 (91%)	21 (100%)	0	0	100	100
45	AL42	102/104 (98%)	94 (92%)	8 (8%)	0	100	100
46	AL43	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
47	ALP0	23/27 (85%)	23 (100%)	0	0	100	100
48	ARAC	311/313 (99%)	296 (95%)	15 (5%)	0	100	100
49	AS00	215/217 (99%)	204 (95%)	11 (5%)	0	100	100
50	AS01	211/213 (99%)	202 (96%)	9 (4%)	0	100	100
51	AS02	219/221 (99%)	215 (98%)	4 (2%)	0	100	100
52	AS03	226/228 (99%)	221 (98%)	5 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	AS04	260/262 (99%)	248 (95%)	12 (5%)	0	100	100
54	AS05	181/191 (95%)	170 (94%)	11 (6%)	0	100	100
55	AS06	235/237 (99%)	233 (99%)	2 (1%)	0	100	100
56	AS07	181/189 (96%)	175 (97%)	6 (3%)	0	100	100
57	AS08	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
58	AS09	183/185 (99%)	179 (98%)	4 (2%)	0	100	100
59	AS10	94/96 (98%)	89 (95%)	5 (5%)	0	100	100
60	AS11	139/151 (92%)	131 (94%)	8 (6%)	0	100	100
61	AS12	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
62	AS13	147/149 (99%)	146 (99%)	1 (1%)	0	100	100
63	AS14	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
64	AS15	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
65	AS16	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
66	AS17	130/132 (98%)	124 (95%)	6 (5%)	0	100	100
67	AS18	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
68	AS19	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
69	AS20	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
70	AS21	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
71	AS22	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
72	AS23	139/141 (99%)	133 (96%)	5 (4%)	1 (1%)	22	57
73	AS24	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
74	AS25	73/75 (97%)	73 (100%)	0	0	100	100
75	AS26	99/101 (98%)	94 (95%)	5 (5%)	0	100	100
76	AS27	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
77	AS28	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
78	AS29	53/55 (96%)	51 (96%)	2 (4%)	0	100	100
79	AS30	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
80	AS31	66/68 (97%)	60 (91%)	6 (9%)	0	100	100
81	EL28	123/125 (98%)	111 (90%)	12 (10%)	0	100	100
83	PR	17/40 (42%)	12 (71%)	5 (29%)	0	100	100
All	All	11203/11589 (97%)	10726 (96%)	474 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
72	AS23	62	PRO
16	AL13	64	VAL
23	AL20	165	PRO

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	187/187 (100%)	186 (100%)	1 (0%)	88	94
6	AL03	336/342 (98%)	336 (100%)	0	100	100
7	AL04	302/302 (100%)	301 (100%)	1 (0%)	92	96
8	AL05	247/247 (100%)	247 (100%)	0	100	100
9	AL06	190/223 (85%)	187 (98%)	3 (2%)	62	84
10	AL07	194/195 (100%)	193 (100%)	1 (0%)	88	94
11	AL08	206/206 (100%)	205 (100%)	1 (0%)	88	94
12	AL09	169/169 (100%)	169 (100%)	0	100	100
13	AL10	174/180 (97%)	174 (100%)	0	100	100
14	AL11	142/142 (100%)	140 (99%)	2 (1%)	67	86
15	AL12	31/136 (23%)	31 (100%)	0	100	100
16	AL13	176/176 (100%)	175 (99%)	1 (1%)	86	94
17	AL14	117/117 (100%)	117 (100%)	0	100	100
18	AL15	171/171 (100%)	171 (100%)	0	100	100
19	AL16	171/171 (100%)	169 (99%)	2 (1%)	71	88
20	AL17	134/134 (100%)	133 (99%)	1 (1%)	84	93
21	AL18	163/163 (100%)	163 (100%)	0	100	100
22	AL19	159/159 (100%)	158 (99%)	1 (1%)	86	94
23	AL20	156/156 (100%)	154 (99%)	2 (1%)	69	87
24	AL21	139/139 (100%)	139 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	AL22	89/89 (100%)	87 (98%)	2 (2%)	52	78
26	AL23	101/101 (100%)	101 (100%)	0	100	100
27	AL24	55/55 (100%)	55 (100%)	0	100	100
28	AL25	107/107 (100%)	107 (100%)	0	100	100
29	AL26	124/124 (100%)	122 (98%)	2 (2%)	62	84
30	AL27	117/117 (100%)	116 (99%)	1 (1%)	78	91
31	AL28	119/119 (100%)	119 (100%)	0	100	100
32	AL29	83/83 (100%)	83 (100%)	0	100	100
33	AL30	79/79 (100%)	79 (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%)	87 (99%)	1 (1%)	73	89
37	AL34	98/98 (100%)	97 (99%)	1 (1%)	76	90
38	AL35	109/109 (100%)	108 (99%)	1 (1%)	78	91
39	AL36	86/86 (100%)	84 (98%)	2 (2%)	50	77
40	AL37	73/73 (100%)	73 (100%)	0	100	100
41	AL38	64/64 (100%)	64 (100%)	0	100	100
42	AL39	47/47 (100%)	46 (98%)	1 (2%)	53	79
43	AL40	48/48 (100%)	48 (100%)	0	100	100
44	AL41	22/22 (100%)	22 (100%)	0	100	100
45	AL42	92/92 (100%)	92 (100%)	0	100	100
46	AL43	74/74 (100%)	74 (100%)	0	100	100
47	ALP0	24/24 (100%)	24 (100%)	0	100	100
48	ARAC	272/272 (100%)	272 (100%)	0	100	100
49	AS00	180/181 (99%)	179 (99%)	1 (1%)	86	94
50	AS01	194/194 (100%)	194 (100%)	0	100	100
51	AS02	187/187 (100%)	186 (100%)	1 (0%)	88	94
52	AS03	190/190 (100%)	186 (98%)	4 (2%)	53	79
53	AS04	224/224 (100%)	222 (99%)	2 (1%)	78	91
54	AS05	157/161 (98%)	157 (100%)	0	100	100
55	AS06	207/207 (100%)	205 (99%)	2 (1%)	76	90

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	AS07	165/169 (98%)	165 (100%)	0	100	100
57	AS08	178/178 (100%)	178 (100%)	0	100	100
58	AS09	161/161 (100%)	161 (100%)	0	100	100
59	AS10	87/87 (100%)	86 (99%)	1 (1%)	73	89
60	AS11	130/136 (96%)	127 (98%)	3 (2%)	50	77
61	AS12	99/99 (100%)	99 (100%)	0	100	100
62	AS13	130/130 (100%)	128 (98%)	2 (2%)	65	85
63	AS14	106/106 (100%)	104 (98%)	2 (2%)	57	81
64	AS15	109/109 (100%)	109 (100%)	0	100	100
65	AS16	117/117 (100%)	115 (98%)	2 (2%)	60	83
66	AS17	119/119 (100%)	116 (98%)	3 (2%)	47	75
67	AS18	125/125 (100%)	122 (98%)	3 (2%)	49	76
68	AS19	111/111 (100%)	111 (100%)	0	100	100
69	AS20	92/92 (100%)	92 (100%)	0	100	100
70	AS21	67/67 (100%)	67 (100%)	0	100	100
71	AS22	112/112 (100%)	111 (99%)	1 (1%)	78	91
72	AS23	113/113 (100%)	113 (100%)	0	100	100
73	AS24	107/107 (100%)	106 (99%)	1 (1%)	78	91
74	AS25	66/66 (100%)	66 (100%)	0	100	100
75	AS26	88/88 (100%)	88 (100%)	0	100	100
76	AS27	75/75 (100%)	74 (99%)	1 (1%)	69	87
77	AS28	55/55 (100%)	55 (100%)	0	100	100
78	AS29	48/48 (100%)	48 (100%)	0	100	100
79	AS30	46/46 (100%)	43 (94%)	3 (6%)	17	47
80	AS31	61/61 (100%)	59 (97%)	2 (3%)	38	69
81	EL28	109/109 (100%)	107 (98%)	2 (2%)	59	82
83	PR	10/40 (25%)	10 (100%)	0	100	100
All	All	9772/9968 (98%)	9709 (99%)	63 (1%)	86	94

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	AL02	193	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	AL04	188	ARG
9	AL06	58	ARG
9	AL06	141	ARG
9	AL06	213	LYS
10	AL07	183	LYS
11	AL08	196	ARG
14	AL11	12	MET
14	AL11	63	ARG
16	AL13	200	LYS
19	AL16	42	ASN
19	AL16	187	LYS
20	AL17	64	ASN
22	AL19	130	ASN
23	AL20	21	LYS
23	AL20	87	ARG
25	AL22	67	LYS
25	AL22	69	LYS
29	AL26	1	MET
29	AL26	2	LYS
30	AL27	84	ARG
36	AL33	19	ARG
37	AL34	54	ARG
38	AL35	32	ARG
39	AL36	23	LYS
39	AL36	35	LYS
42	AL39	46	ARG
49	AS00	34	MET
51	AS02	68	ARG
52	AS03	76	ARG
52	AS03	173	ARG
52	AS03	197	LYS
52	AS03	227	LYS
53	AS04	94	LYS
53	AS04	200	ARG
55	AS06	31	ARG
55	AS06	94	ARG
59	AS10	96	ARG
60	AS11	18	GLN
60	AS11	20	LYS
60	AS11	69	ARG
62	AS13	49	GLN
62	AS13	93	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
63	AS14	146	ARG
63	AS14	150	ARG
65	AS16	106	LYS
65	AS16	117	ARG
66	AS17	3	ARG
66	AS17	11	LYS
66	AS17	80	ARG
67	AS18	8	LYS
67	AS18	17	ASN
67	AS18	108	ARG
71	AS22	19	LYS
73	AS24	113	ARG
76	AS27	18	LYS
79	AS30	81	ARG
79	AS30	99	LYS
79	AS30	104	ARG
80	AS31	104	LYS
80	AS31	138	ARG
81	EL28	31	ASN
81	EL28	71	ARG

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

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A18S	1680/1698 (98%)	399 (23%)	17 (1%)
2	A25S	3632/3649 (99%)	752 (20%)	63 (1%)
3	A58S	155/156 (99%)	34 (21%)	1 (0%)
4	A5S	119/120 (99%)	16 (13%)	0
82	MRNA	9/10 (90%)	3 (33%)	0
84	PTRN	74/77 (96%)	21 (28%)	1 (1%)
All	All	5669/5710 (99%)	1225 (21%)	82 (1%)

All (1225) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A18S	2	A
1	A18S	3	C
1	A18S	4	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A18S	17	C
1	A18S	20	G
1	A18S	25	A
1	A18S	26	U
1	A18S	33	G
1	A18S	39	A
1	A18S	41	G
1	A18S	42	A
1	A18S	44	U
1	A18S	45	A
1	A18S	46	A
1	A18S	54	A
1	A18S	56	G
1	A18S	62	G
1	A18S	67	C
1	A18S	68	A
1	A18S	69	C
1	A18S	71	G
1	A18S	74	G
1	A18S	77	A
1	A18S	79	A
1	A18S	93	U
1	A18S	103	A
1	A18S	111	A
1	A18S	113	G
1	A18S	114	G
1	A18S	115	U
1	A18S	118	C
1	A18S	124	U
1	A18S	126	G
1	A18S	127	C
1	A18S	129	C
1	A18S	130	G
1	A18S	141	A
1	A18S	142	C
1	A18S	143	U
1	A18S	146	G
1	A18S	155	G
1	A18S	158	A
1	A18S	162	C
1	A18S	170	A
1	A18S	171	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A18S	180	G
1	A18S	183	G
1	A18S	184	G
1	A18S	185	G
1	A18S	187	G
1	A18S	188	C
1	A18S	189	U
1	A18S	190	G
1	A18S	191	A
1	A18S	192	C
1	A18S	215	G
1	A18S	291	G
1	A18S	292	A
1	A18S	294	U
1	A18S	302	A
1	A18S	305	U
1	A18S	306	C
1	A18S	307	G
1	A18S	308	G
1	A18S	309	G
1	A18S	310	C
1	A18S	312	G
1	A18S	313	A
1	A18S	317	C
1	A18S	319	C
1	A18S	335	G
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	370	G
1	A18S	381	C
1	A18S	383	G
1	A18S	385	G
1	A18S	386	C
1	A18S	389	A
1	A18S	395	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A18S	398	A
1	A18S	399	C
1	A18S	400	C
1	A18S	407	G
1	A18S	408	A
1	A18S	409	C
1	A18S	417	C
1	A18S	418	A
1	A18S	420	G
1	A18S	421	G
1	A18S	435	A
1	A18S	438	G
1	A18S	448	A
1	A18S	450	C
1	A18S	451	G
1	A18S	464	A
1	A18S	465	A
1	A18S	466	G
1	A18S	472	C
1	A18S	473	A
1	A18S	474	G
1	A18S	476	A
1	A18S	482	G
1	A18S	487	U
1	A18S	492	C
1	A18S	500	A
1	A18S	507	G
1	A18S	516	A
1	A18S	518	G
1	A18S	521	A
1	A18S	525	A
1	A18S	530	U
1	A18S	532	C
1	A18S	533	A
1	A18S	536	A
1	A18S	541	U
1	A18S	542	U
1	A18S	544	G
1	A18S	547	G
1	A18S	548	C
1	A18S	550	C
1	A18S	551	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	574	A
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	605	A
1	A18S	606	G
1	A18S	608	C
1	A18S	614	C
1	A18S	617	G
1	A18S	621	C
1	A18S	626	A
1	A18S	628	A
1	A18S	634	A
1	A18S	643	A
1	A18S	644	G
1	A18S	658	U
1	A18S	660	C
1	A18S	664	A
1	A18S	668	A
1	A18S	669	A
1	A18S	670	A
1	A18S	671	A
1	A18S	672	A
1	A18S	673	G
1	A18S	678	U
1	A18S	684	G
1	A18S	688	U
1	A18S	689	U
1	A18S	799	U
1	A18S	811	A
1	A18S	812	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A18S	821	G
1	A18S	822	U
1	A18S	827	A
1	A18S	829	C
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	861	A
1	A18S	865	A
1	A18S	868	G
1	A18S	869	A
1	A18S	870	A
1	A18S	871	U
1	A18S	872	A
1	A18S	873	G
1	A18S	875	A
1	A18S	878	G
1	A18S	887	U
1	A18S	888	U
1	A18S	890	U
1	A18S	892	U
1	A18S	896	U
1	A18S	897	U
1	A18S	899	U
1	A18S	901	G
1	A18S	902	G
1	A18S	903	A
1	A18S	909	G
1	A18S	913	A
1	A18S	914	U
1	A18S	920	A
1	A18S	922	A
1	A18S	933	G
1	A18S	943	U
1	A18S	955	A
1	A18S	963	A
1	A18S	970	G
1	A18S	971	G
1	A18S	978	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A18S	990	A
1	A18S	992	A
1	A18S	999	G
1	A18S	1021	U
1	A18S	1023	A
1	A18S	1024	A
1	A18S	1040	G
1	A18S	1041	G
1	A18S	1045	U
1	A18S	1058	A
1	A18S	1062	A
1	A18S	1078	C
1	A18S	1082	A
1	A18S	1083	A
1	A18S	1085	C
1	A18S	1087	A
1	A18S	1089	G
1	A18S	1097	G
1	A18S	1100	A
1	A18S	1109	C
1	A18S	1113	A
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	1133	A
1	A18S	1138	C
1	A18S	1139	C
1	A18S	1153	C
1	A18S	1154	U
1	A18S	1155	U
1	A18S	1195	A
1	A18S	1211	G
1	A18S	1215	C
1	A18S	1221	G
1	A18S	1224	G
1	A18S	1242	U
1	A18S	1243	U
1	A18S	1251	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	1271	C
1	A18S	1274	G
1	A18S	1275	G
1	A18S	1284	A
1	A18S	1285	G
1	A18S	1286	G
1	A18S	1287	A
1	A18S	1289	U
1	A18S	1293	A
1	A18S	1294	G
1	A18S	1299	A
1	A18S	1301	A
1	A18S	1302	G
1	A18S	1303	C
1	A18S	1304	U
1	A18S	1307	U
1	A18S	1308	U
1	A18S	1309	C
1	A18S	1312	G
1	A18S	1314	U
1	A18S	1315	U
1	A18S	1316	C
1	A18S	1333	U
1	A18S	1341	C
1	A18S	1342	U
1	A18S	1364	U
1	A18S	1371	U
1	A18S	1372	U
1	A18S	1376	A
1	A18S	1378	A
1	A18S	1382	A
1	A18S	1395	C
1	A18S	1396	A
1	A18S	1397	U
1	A18S	1401	A
1	A18S	1402	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A18S	1409	A
1	A18S	1412	C
1	A18S	1428	G
1	A18S	1429	G
1	A18S	1442	U
1	A18S	1447	G
1	A18S	1449	G
1	A18S	1452	A
1	A18S	1454	A
1	A18S	1455	A
1	A18S	1462	U
1	A18S	1463	U
1	A18S	1466	G
1	A18S	1473	G
1	A18S	1476	A
1	A18S	1477	U
1	A18S	1489	A
1	A18S	1490	G
1	A18S	1494	U
1	A18S	1497	G
1	A18S	1498	A
1	A18S	1507	G
1	A18S	1509	U
1	A18S	1510	G
1	A18S	1521	C
1	A18S	1522	A
1	A18S	1531	A
1	A18S	1536	G
1	A18S	1544	C
1	A18S	1545	A
1	A18S	1548	G
1	A18S	1552	G
1	A18S	1553	C
1	A18S	1554	C
1	A18S	1555	U
1	A18S	1556	A
1	A18S	1557	C
1	A18S	1560	U
1	A18S	1567	G
1	A18S	1570	G
1	A18S	1573	G
1	A18S	1574	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A18S	1575	G
1	A18S	1580	A
1	A18S	1587	G
1	A18S	1588	A
1	A18S	1595	U
1	A18S	1598	G
1	A18S	1600	G
1	A18S	1601	A
1	A18S	1604	G
1	A18S	1606	G
1	A18S	1607	A
1	A18S	1621	U
1	A18S	1623	A
1	A18S	1637	A
1	A18S	1638	G
1	A18S	1641	A
1	A18S	1646	C
1	A18S	1648	G
1	A18S	1664	A
1	A18S	1665	G
1	A18S	1666	C
1	A18S	1680	G
1	A18S	1683	C
1	A18S	1695	A
1	A18S	1698	C
1	A18S	1705	C
1	A18S	1715	A
1	A18S	1721	U
1	A18S	1722	G
1	A18S	1726	G
1	A18S	1742	C
1	A18S	1744	G
1	A18S	1748	G
1	A18S	1753	C
1	A18S	1775	U
1	A18S	1783	C
1	A18S	1799	G
1	A18S	1808	U
1	A18S	1813	A
1	A18S	1814	G
1	A18S	1815	A
1	A18S	1823	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A18S	1824	A
1	A18S	1825	A
1	A18S	1826	G
1	A18S	1829	G
1	A18S	1831	A
1	A18S	1836	G
1	A18S	1838	U
1	A18S	1846	G
1	A18S	1849	G
1	A18S	1851	A
1	A18S	1852	C
1	A18S	1861	G
1	A18S	1862	G
1	A18S	1863	A
1	A18S	1865	C
1	A18S	1866	A
1	A18S	1867	U
1	A18S	1869	A
2	A25S	2	G
2	A25S	8	U
2	A25S	12	A
2	A25S	13	U
2	A25S	25	A
2	A25S	39	A
2	A25S	42	A
2	A25S	56	A
2	A25S	59	A
2	A25S	64	A
2	A25S	65	A
2	A25S	72	C
2	A25S	73	A
2	A25S	74	G
2	A25S	76	A
2	A25S	84	A
2	A25S	91	G
2	A25S	95	G
2	A25S	104	G
2	A25S	109	G
2	A25S	110	C
2	A25S	116	G
2	A25S	119	G
2	A25S	126	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	134	G
2	A25S	135	G
2	A25S	136	C
2	A25S	142	G
2	A25S	143	C
2	A25S	144	G
2	A25S	151	G
2	A25S	159	C
2	A25S	171	U
2	A25S	172	C
2	A25S	173	C
2	A25S	182	G
2	A25S	183	C
2	A25S	184	U
2	A25S	185	C
2	A25S	187	U
2	A25S	188	G
2	A25S	189	G
2	A25S	197	A
2	A25S	200	U
2	A25S	201	C
2	A25S	210	C
2	A25S	216	C
2	A25S	217	C
2	A25S	218	A
2	A25S	219	G
2	A25S	221	C
2	A25S	224	U
2	A25S	225	G
2	A25S	233	U
2	A25S	235	A
2	A25S	246	G
2	A25S	262	G
2	A25S	263	G
2	A25S	265	C
2	A25S	266	C
2	A25S	267	G
2	A25S	276	C
2	A25S	277	G
2	A25S	278	G
2	A25S	280	G
2	A25S	297	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	306	A
2	A25S	309	C
2	A25S	315	G
2	A25S	316	U
2	A25S	323	C
2	A25S	334	A
2	A25S	340	C
2	A25S	345	C
2	A25S	363	A
2	A25S	387	G
2	A25S	401	G
2	A25S	407	A
2	A25S	408	A
2	A25S	409	G
2	A25S	410	A
2	A25S	412	G
2	A25S	413	G
2	A25S	440	U
2	A25S	449	C
2	A25S	450	G
2	A25S	452	A
2	A25S	453	G
2	A25S	454	U
2	A25S	467	U
2	A25S	468	U
2	A25S	479	G
2	A25S	481	G
2	A25S	481(A)	C
2	A25S	482	G
2	A25S	483	G
2	A25S	485	C
2	A25S	486	C
2	A25S	492	U
2	A25S	493	G
2	A25S	496	G
2	A25S	498	C
2	A25S	500	G
2	A25S	501	C
2	A25S	503	C
2	A25S	504	G
2	A25S	506	C
2	A25S	510	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	654	C
2	A25S	667	A
2	A25S	669	C
2	A25S	670	G
2	A25S	683	C
2	A25S	684	G
2	A25S	685	C
2	A25S	687	U
2	A25S	691	C
2	A25S	696	C
2	A25S	697	G
2	A25S	704	C
2	A25S	705	G
2	A25S	719	C
2	A25S	730	G
2	A25S	731	G
2	A25S	738	C
2	A25S	738(A)	C
2	A25S	742	G
2	A25S	747	A
2	A25S	748	G
2	A25S	749	G
2	A25S	758	G
2	A25S	913	U
2	A25S	914	U
2	A25S	917	A
2	A25S	918	G
2	A25S	923	C
2	A25S	925	C
2	A25S	926	G
2	A25S	928	C
2	A25S	929	A
2	A25S	931	C
2	A25S	932	A
2	A25S	933	G
2	A25S	934	C
2	A25S	935	A
2	A25S	935(A)	G
2	A25S	936	C
2	A25S	938	C
2	A25S	939	G
2	A25S	941	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	943	A
2	A25S	944	A
2	A25S	945	U
2	A25S	959	G
2	A25S	960	A
2	A25S	961	G
2	A25S	962	C
2	A25S	965	G
2	A25S	966	A
2	A25S	967	C
2	A25S	969	C
2	A25S	972	C
2	A25S	979	C
2	A25S	983	C
2	A25S	990	C
2	A25S	1072	C
2	A25S	1073	G
2	A25S	1075	G
2	A25S	1076	C
2	A25S	1082	C
2	A25S	1179	U
2	A25S	1184	A
2	A25S	1185	G
2	A25S	1187	G
2	A25S	1195	G
2	A25S	1211	G
2	A25S	1212	G
2	A25S	1215	C
2	A25S	1234	G
2	A25S	1235	G
2	A25S	1236	C
2	A25S	1237	C
2	A25S	1238	A
2	A25S	1239	C
2	A25S	1273	G
2	A25S	1274	A
2	A25S	1276	C
2	A25S	1277	G
2	A25S	1284	G
2	A25S	1287	G
2	A25S	1292	C
2	A25S	1293	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	1296	G
2	A25S	1301	C
2	A25S	1314	C
2	A25S	1326	A
2	A25S	1344	C
2	A25S	1354	A
2	A25S	1358	G
2	A25S	1367	C
2	A25S	1368	A
2	A25S	1370	G
2	A25S	1371	A
2	A25S	1377	G
2	A25S	1378	C
2	A25S	1379	C
2	A25S	1381	U
2	A25S	1387	A
2	A25S	1390	G
2	A25S	1394	G
2	A25S	1397	A
2	A25S	1399	G
2	A25S	1408	G
2	A25S	1409	C
2	A25S	1410	U
2	A25S	1411	C
2	A25S	1419	G
2	A25S	1420	A
2	A25S	1429	C
2	A25S	1434	G
2	A25S	1445	U
2	A25S	1446	C
2	A25S	1448	G
2	A25S	1456	C
2	A25S	1457	G
2	A25S	1458	C
2	A25S	1465	G
2	A25S	1475	G
2	A25S	1482	G
2	A25S	1483	C
2	A25S	1497	A
2	A25S	1498	G
2	A25S	1501	C
2	A25S	1502	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	1516	G
2	A25S	1518	A
2	A25S	1523	A
2	A25S	1525	A
2	A25S	1534	A
2	A25S	1547	A
2	A25S	1553	A
2	A25S	1562	G
2	A25S	1564	A
2	A25S	1566	C
2	A25S	1574	G
2	A25S	1577	G
2	A25S	1578	U
2	A25S	1591	U
2	A25S	1596	U
2	A25S	1602	U
2	A25S	1612	G
2	A25S	1613	A
2	A25S	1624	G
2	A25S	1625	G
2	A25S	1631	A
2	A25S	1633	G
2	A25S	1634	A
2	A25S	1638	A
2	A25S	1641	G
2	A25S	1650	A
2	A25S	1654	G
2	A25S	1661	C
2	A25S	1676	C
2	A25S	1677	U
2	A25S	1691	G
2	A25S	1721	G
2	A25S	1724	G
2	A25S	1725	U
2	A25S	1731	C
2	A25S	1734	G
2	A25S	1741	G
2	A25S	1742	A
2	A25S	1750	G
2	A25S	1753	G
2	A25S	1755	C
2	A25S	1756	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	1761	G
2	A25S	1764	G
2	A25S	1768	C
2	A25S	1772	C
2	A25S	1773	U
2	A25S	1776	A
2	A25S	1777	C
2	A25S	1781	U
2	A25S	1787	A
2	A25S	1800	U
2	A25S	1801	A
2	A25S	1803	G
2	A25S	1804	A
2	A25S	1805	A
2	A25S	1809	C
2	A25S	1812	C
2	A25S	1815	G
2	A25S	1819	G
2	A25S	1821	G
2	A25S	1822	U
2	A25S	1828	C
2	A25S	1835	G
2	A25S	1836	G
2	A25S	1837	A
2	A25S	1842	G
2	A25S	1848	C
2	A25S	1855	G
2	A25S	1869	G
2	A25S	1881	C
2	A25S	1882	U
2	A25S	1889	U
2	A25S	1890	G
2	A25S	1897	A
2	A25S	1910	G
2	A25S	1916	G
2	A25S	1917	A
2	A25S	1918	U
2	A25S	1920	C
2	A25S	1921	C
2	A25S	1922	G
2	A25S	1930	U
2	A25S	1931	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	1932	A
2	A25S	1935	C
2	A25S	1938	C
2	A25S	1957	U
2	A25S	1958	A
2	A25S	1959	U
2	A25S	1960	A
2	A25S	1961	G
2	A25S	1962	A
2	A25S	1964	A
2	A25S	1975	G
2	A25S	1977	C
2	A25S	1980	U
2	A25S	1983	A
2	A25S	1984	A
2	A25S	1987	C
2	A25S	1991	A
2	A25S	1997	U
2	A25S	2001	G
2	A25S	2002	A
2	A25S	2003	G
2	A25S	2004	U
2	A25S	2007	G
2	A25S	2008	U
2	A25S	2011	C
2	A25S	2020	U
2	A25S	2026	A
2	A25S	2034	G
2	A25S	2044	U
2	A25S	2047	A
2	A25S	2048	U
2	A25S	2055	G
2	A25S	2056	G
2	A25S	2062	C
2	A25S	2069	A
2	A25S	2084	C
2	A25S	2085	G
2	A25S	2089	G
2	A25S	2090	U
2	A25S	2092	G
2	A25S	2093	G
2	A25S	2094	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	2095	A
2	A25S	2097	A
2	A25S	2098	G
2	A25S	2100	G
2	A25S	2101	A
2	A25S	2102	G
2	A25S	2104	A
2	A25S	2105	A
2	A25S	2107	A
2	A25S	2108	G
2	A25S	2110	G
2	A25S	2259	G
2	A25S	2260	C
2	A25S	2262	G
2	A25S	2266	C
2	A25S	2267	U
2	A25S	2268	A
2	A25S	2269	C
2	A25S	2270	G
2	A25S	2279	A
2	A25S	2289	C
2	A25S	2300	A
2	A25S	2301	G
2	A25S	2306	G
2	A25S	2313	A
2	A25S	2316	G
2	A25S	2322	G
2	A25S	2331	G
2	A25S	2333	G
2	A25S	2348	G
2	A25S	2351	C
2	A25S	2360	A
2	A25S	2395	A
2	A25S	2396	A
2	A25S	2410	C
2	A25S	2417	A
2	A25S	2422	C
2	A25S	2425	U
2	A25S	2433	G
2	A25S	2441	C
2	A25S	2450	G
2	A25S	2463	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	2488	C
2	A25S	2489	C
2	A25S	2491	C
2	A25S	2503	G
2	A25S	2504	C
2	A25S	2505	C
2	A25S	2506	G
2	A25S	2507	A
2	A25S	2513	A
2	A25S	2530	U
2	A25S	2537	A
2	A25S	2544	G
2	A25S	2546	G
2	A25S	2547	G
2	A25S	2549	G
2	A25S	2553	A
2	A25S	2554	U
2	A25S	2571	C
2	A25S	2572	C
2	A25S	2575	U
2	A25S	2581	A
2	A25S	2583	C
2	A25S	2586	G
2	A25S	2587	A
2	A25S	2589	C
2	A25S	2620	G
2	A25S	2627	C
2	A25S	2640	G
2	A25S	2661	U
2	A25S	2662	G
2	A25S	2669	C
2	A25S	2676	A
2	A25S	2679	G
2	A25S	2686	G
2	A25S	2687	U
2	A25S	2694	G
2	A25S	2695	A
2	A25S	2696	A
2	A25S	2708	U
2	A25S	2710	C
2	A25S	2711	G
2	A25S	2712	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	2716	C
2	A25S	2721	G
2	A25S	2724	G
2	A25S	2725	A
2	A25S	2726	G
2	A25S	2740	U
2	A25S	2743	A
2	A25S	2753	G
2	A25S	2754	G
2	A25S	2758	G
2	A25S	2760	G
2	A25S	2762	G
2	A25S	2767	U
2	A25S	2768	C
2	A25S	2769	U
2	A25S	2770	C
2	A25S	2787	A
2	A25S	2788	U
2	A25S	2790	U
2	A25S	2794	C
2	A25S	2798	A
2	A25S	2814	C
2	A25S	2826	U
2	A25S	2827	G
2	A25S	2828	U
2	A25S	2842	G
2	A25S	2855	G
2	A25S	2857	A
2	A25S	2867	C
2	A25S	2898	G
2	A25S	2904	U
2	A25S	2905	C
2	A25S	3593	C
2	A25S	3595	U
2	A25S	3596	A
2	A25S	3597	G
2	A25S	3602	C
2	A25S	3605	C
2	A25S	3616	U
2	A25S	3617	G
2	A25S	3625	G
2	A25S	3626	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	3630	A
2	A25S	3635	A
2	A25S	3649	A
2	A25S	3662	A
2	A25S	3664	G
2	A25S	3673	C
2	A25S	3710	G
2	A25S	3711	A
2	A25S	3748	A
2	A25S	3760	A
2	A25S	3772	U
2	A25S	3773	U
2	A25S	3774	A
2	A25S	3777	G
2	A25S	3778	U
2	A25S	3784	A
2	A25S	3786	U
2	A25S	3791	C
2	A25S	3810	C
2	A25S	3812	C
2	A25S	3814	U
2	A25S	3817	A
2	A25S	3819	G
2	A25S	3822	U
2	A25S	3838	U
2	A25S	3840	U
2	A25S	3843	C
2	A25S	3860	A
2	A25S	3867	A
2	A25S	3869	C
2	A25S	3876	A
2	A25S	3877	A
2	A25S	3878	C
2	A25S	3879	G
2	A25S	3889	G
2	A25S	3892	U
2	A25S	3897	G
2	A25S	3898	G
2	A25S	3899	G
2	A25S	3901	A
2	A25S	3905	A
2	A25S	3906	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	3907	G
2	A25S	3908	A
2	A25S	3915	U
2	A25S	3926	C
2	A25S	3938	G
2	A25S	3959	U
2	A25S	3960	A
2	A25S	3963	A
2	A25S	3965	A
2	A25S	3969	G
2	A25S	3971	G
2	A25S	3973	G
2	A25S	3976	C
2	A25S	4047	A
2	A25S	4048	A
2	A25S	4049	U
2	A25S	4050	A
2	A25S	4065	G
2	A25S	4066	U
2	A25S	4076	G
2	A25S	4084	G
2	A25S	4085	A
2	A25S	4086	G
2	A25S	4088	C
2	A25S	4094	G
2	A25S	4096	C
2	A25S	4097	G
2	A25S	4099	G
2	A25S	4104	G
2	A25S	4107	G
2	A25S	4108	G
2	A25S	4109	G
2	A25S	4115	G
2	A25S	4116	C
2	A25S	4117	U
2	A25S	4119	C
2	A25S	4120	U
2	A25S	4121	G
2	A25S	4125	C
2	A25S	4127	A
2	A25S	4128	A
2	A25S	4142	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	4143	G
2	A25S	4144	C
2	A25S	4145	C
2	A25S	4158	C
2	A25S	4162	C
2	A25S	4166	G
2	A25S	4171	C
2	A25S	4172	A
2	A25S	4173	G
2	A25S	4183	G
2	A25S	4184	G
2	A25S	4191	G
2	A25S	4203	A
2	A25S	4212	A
2	A25S	4225	G
2	A25S	4229	U
2	A25S	4233	A
2	A25S	4234	A
2	A25S	4241	C
2	A25S	4243	C
2	A25S	4249	G
2	A25S	4251	A
2	A25S	4254	G
2	A25S	4255	A
2	A25S	4268	A
2	A25S	4271	A
2	A25S	4273	A
2	A25S	4291	G
2	A25S	4297	G
2	A25S	4304	A
2	A25S	4305	G
2	A25S	4306	U
2	A25S	4313	A
2	A25S	4314	C
2	A25S	4317	A
2	A25S	4318	C
2	A25S	4319	C
2	A25S	4329	G
2	A25S	4330	G
2	A25S	4332	C
2	A25S	4339	A
2	A25S	4349	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	4350	C
2	A25S	4354	U
2	A25S	4355	G
2	A25S	4376	A
2	A25S	4377	G
2	A25S	4378	A
2	A25S	4379	A
2	A25S	4387	C
2	A25S	4393	G
2	A25S	4394	A
2	A25S	4419	U
2	A25S	4421	C
2	A25S	4422	A
2	A25S	4426	C
2	A25S	4436	U
2	A25S	4437	U
2	A25S	4440	G
2	A25S	4444	C
2	A25S	4448	G
2	A25S	4449	A
2	A25S	4464	A
2	A25S	4471	U
2	A25S	4476	C
2	A25S	4488	A
2	A25S	4495	G
2	A25S	4500	U
2	A25S	4510	A
2	A25S	4512	U
2	A25S	4513	A
2	A25S	4518	A
2	A25S	4524	G
2	A25S	4528	G
2	A25S	4529	G
2	A25S	4531	U
2	A25S	4548	A
2	A25S	4549	G
2	A25S	4560	C
2	A25S	4567	G
2	A25S	4570	G
2	A25S	4573	G
2	A25S	4575	G
2	A25S	4577	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	4581	G
2	A25S	4590	A
2	A25S	4617	G
2	A25S	4636	U
2	A25S	4637	G
2	A25S	4639	G
2	A25S	4642	U
2	A25S	4652	G
2	A25S	4656	A
2	A25S	4657	U
2	A25S	4661	G
2	A25S	4667	C
2	A25S	4670	C
2	A25S	4672	A
2	A25S	4677	U
2	A25S	4682	U
2	A25S	4695	C
2	A25S	4697	U
2	A25S	4700	A
2	A25S	4709	U
2	A25S	4719	G
2	A25S	4720	C
2	A25S	4730	C
2	A25S	4731	G
2	A25S	4732	G
2	A25S	4750	G
2	A25S	4751	G
2	A25S	4754	G
2	A25S	4756	C
2	A25S	4757	C
2	A25S	4759	C
2	A25S	4765	G
2	A25S	4771	C
2	A25S	4867	G
2	A25S	4870	G
2	A25S	4871	C
2	A25S	4872	G
2	A25S	4873	G
2	A25S	4875	G
2	A25S	4876	A
2	A25S	4877	G
2	A25S	4881	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	4882	U
2	A25S	4883	C
2	A25S	4885	U
2	A25S	4895	C
2	A25S	4910	A
2	A25S	4914	G
2	A25S	4915	G
2	A25S	4918	C
2	A25S	4919	G
2	A25S	4920	C
2	A25S	4921	C
2	A25S	4925	U
2	A25S	4926	C
2	A25S	4927	G
2	A25S	4928	C
2	A25S	4931	G
2	A25S	4934	A
2	A25S	4937	C
2	A25S	4940	C
2	A25S	4943	A
2	A25S	4944	C
2	A25S	4947	U
2	A25S	4948	C
2	A25S	4949	G
2	A25S	4950	U
2	A25S	4951	G
2	A25S	4955	A
2	A25S	4956	A
2	A25S	4960	G
2	A25S	4965	U
2	A25S	4966	A
2	A25S	4975	G
2	A25S	4976	U
2	A25S	4985	U
2	A25S	4988	U
2	A25S	4989	U
2	A25S	4990	C
2	A25S	4991	U
2	A25S	4999	G
2	A25S	5006	U
2	A25S	5013	C
2	A25S	5017	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	5023	C
2	A25S	5027	C
2	A25S	5028	G
2	A25S	5035	U
2	A25S	5040	U
2	A25S	5041	G
2	A25S	5047	C
2	A25S	5050	C
2	A25S	5052	C
2	A25S	5053	U
2	A25S	5054	C
2	A25S	5056	A
2	A25S	5060	A
2	A25S	5061	A
3	A58S	2	G
3	A58S	16	G
3	A58S	23	C
3	A58S	34	U
3	A58S	35	C
3	A58S	38	U
3	A58S	39	G
3	A58S	51	U
3	A58S	59	A
3	A58S	63	U
3	A58S	75	G
3	A58S	80	A
3	A58S	81	C
3	A58S	82	A
3	A58S	83	C
3	A58S	85	U
3	A58S	86	U
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	115	G
3	A58S	125	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	A58S	126	C
3	A58S	127	U
3	A58S	128	C
3	A58S	150	C
3	A58S	153	C
3	A58S	156	U
4	A5S	11	A
4	A5S	22	A
4	A5S	25	G
4	A5S	33	U
4	A5S	39	C
4	A5S	40	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	102	U
4	A5S	110	G
4	A5S	111	C
4	A5S	120	U
82	MRNA	4	C
82	MRNA	5	A
82	MRNA	8	U
84	PTRN	3	C
84	PTRN	4	G
84	PTRN	8	U
84	PTRN	9	G
84	PTRN	11	A
84	PTRN	12	G
84	PTRN	14	A
84	PTRN	16	C
84	PTRN	17	C
84	PTRN	18	G
84	PTRN	19	G
84	PTRN	20	U
84	PTRN	21	A
84	PTRN	44	A
84	PTRN	45	G
84	PTRN	63	G
84	PTRN	69	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
84	PTRN	71	C
84	PTRN	72	A
84	PTRN	73	A
84	PTRN	76	A

All (82) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A18S	110	U
1	A18S	140	U
1	A18S	182	C
1	A18S	434	G
1	A18S	465	A
1	A18S	532	C
1	A18S	553	U
1	A18S	642	U
1	A18S	688	U
1	A18S	798	G
1	A18S	870	A
1	A18S	902	G
1	A18S	1137	U
1	A18S	1395	C
1	A18S	1520	G
1	A18S	1637	A
1	A18S	1664	A
2	A25S	1	C
2	A25S	12	A
2	A25S	125	C
2	A25S	186	G
2	A25S	187	U
2	A25S	218	A
2	A25S	245	C
2	A25S	265	C
2	A25S	275	C
2	A25S	449	C
2	A25S	480	C
2	A25S	485	C
2	A25S	492	U
2	A25S	696	C
2	A25S	930	G
2	A25S	959	G
2	A25S	966	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	971(A)	G
2	A25S	1072	C
2	A25S	1211	G
2	A25S	1236	C
2	A25S	1238	A
2	A25S	1291	G
2	A25S	1445	U
2	A25S	1455	G
2	A25S	1633	G
2	A25S	1804	A
2	A25S	1818	G
2	A25S	1835	G
2	A25S	1979	A
2	A25S	1983	A
2	A25S	2046	G
2	A25S	2083	C
2	A25S	2089	G
2	A25S	2265	G
2	A25S	2266	C
2	A25S	2502	G
2	A25S	2639	U
2	A25S	2661	U
2	A25S	2695	A
2	A25S	3625	G
2	A25S	3771	C
2	A25S	3876	A
2	A25S	3888	G
2	A25S	3959	U
2	A25S	3968	U
2	A25S	4119	C
2	A25S	4170	A
2	A25S	4232	U
2	A25S	4354	U
2	A25S	4448	G
2	A25S	4528	G
2	A25S	4656	A
2	A25S	4699	U
2	A25S	4719	G
2	A25S	4884	G
2	A25S	4925	U
2	A25S	4936	G
2	A25S	4947	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A25S	5022	U
2	A25S	5027	C
2	A25S	5059	C
2	A25S	5060	A
3	A58S	124	U
84	PTRN	17(A)	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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	A25S	17
1	A18S	9

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
32	AL29	1
47	ALP0	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A25S	2113:G	O3'	2258:C	P	41.34
1	AL29	76:VAL	C	90:SER	N	39.54
1	A25S	1252:C	O3'	1271:G	P	36.22
1	A25S	1219:G	O3'	1233:G	P	22.39
1	ALP0	22:ASP	C	59:THR	N	20.66
1	A18S	697:G	O3'	729:C	P	18.54
1	A18S	1761:U	O3'	1771:G	P	18.45
1	A25S	4776:G	O3'	4859:C	P	18.31
1	A25S	990:C	O3'	1064:G	P	17.93
1	A25S	2910:G	O3'	3584:C	P	17.51
1	A25S	523:C	O3'	638:G	P	17.49
1	A25S	1436:C	O3'	1443:A	P	16.72
1	A18S	834:C	O3'	841:G	P	15.73
1	A18S	323:C	O3'	329:G	P	15.70
1	A18S	1417:C	O3'	1423:C	P	15.17
1	A18S	130:G	O3'	140:U	P	15.02
1	A25S	760:G	O3'	904:C	P	14.92
1	A25S	3976:C	O3'	4035:G	P	14.35
1	A25S	1696:C	O3'	1720:C	P	12.93
1	A25S	1180:C	O3'	1183:C	P	9.21
1	A25S	512:U	O3'	515:C	P	8.52
1	A18S	225:G	O3'	287:U	P	7.49
1	A18S	736:C	O3'	743:U	P	6.45
1	A25S	1100:U	O3'	1168:G	P	5.64
1	A25S	1239:C	O3'	1244:G	P	5.57
1	A18S	1432:U	O3'	1438:A	P	5.08
1	A25S	4740:G	O3'	4743:G	P	4.64
1	A25S	4899:G	O3'	4902:C	P	3.52

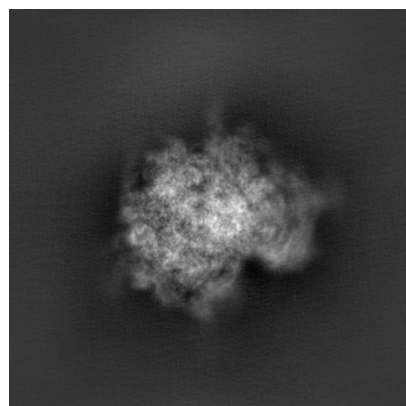
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26035. These allow visual inspection of the internal detail of the map and identification of artifacts.

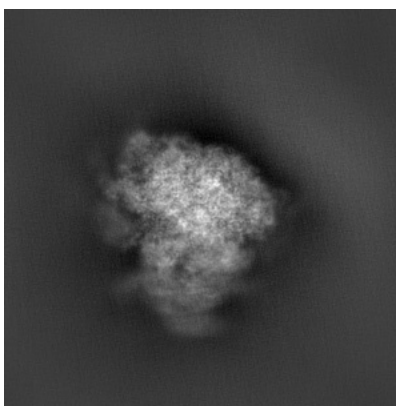
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

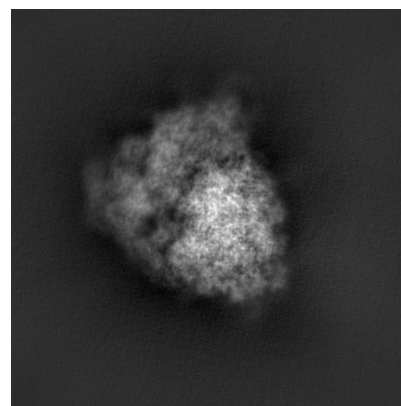
6.1.1 Primary map



X

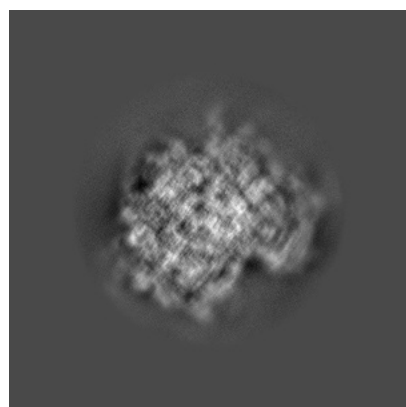


Y

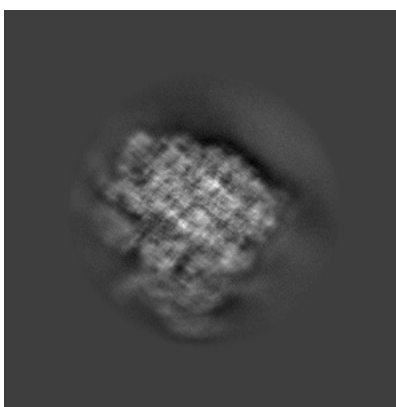


Z

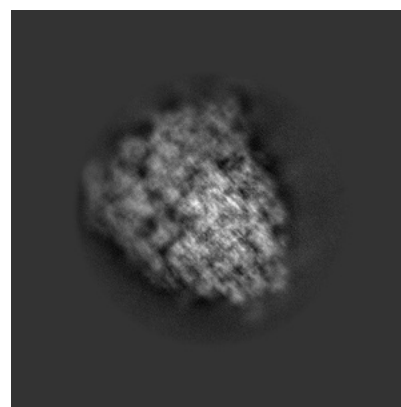
6.1.2 Raw map



X



Y

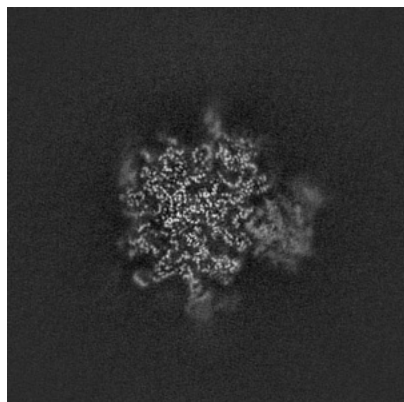


Z

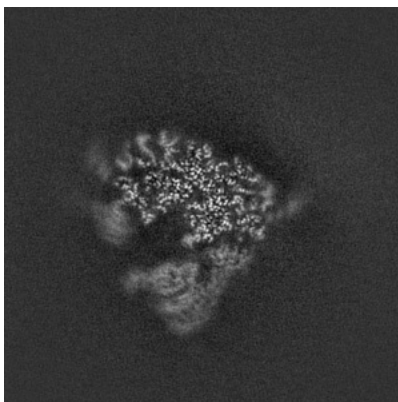
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

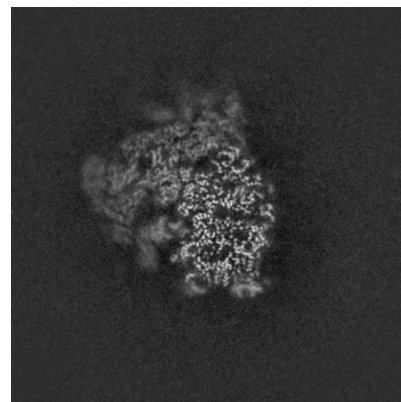
6.2.1 Primary map



X Index: 304

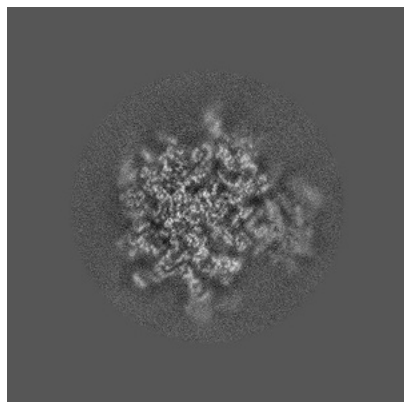


Y Index: 304

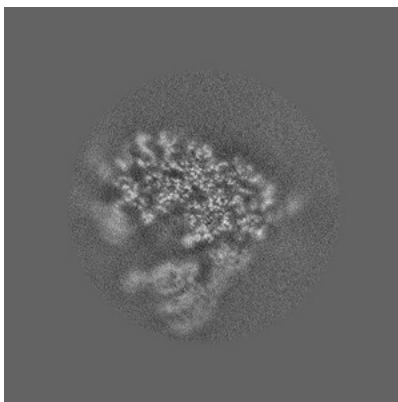


Z Index: 304

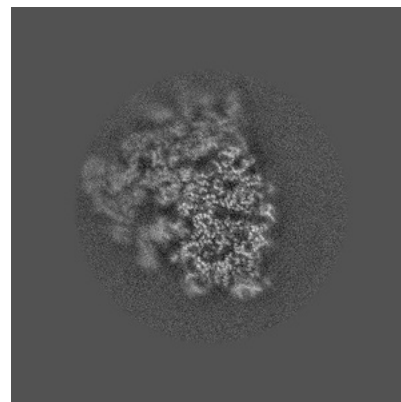
6.2.2 Raw map



X Index: 304



Y Index: 304

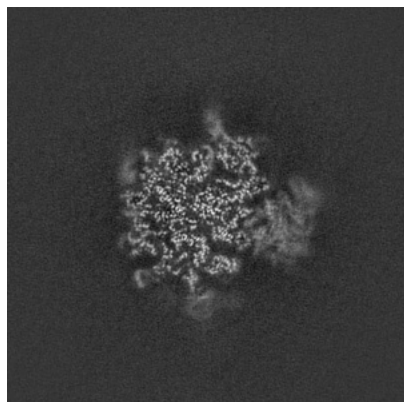


Z Index: 304

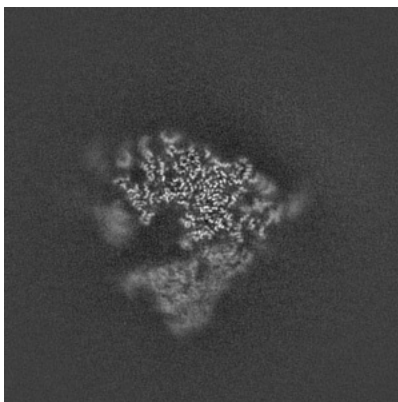
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

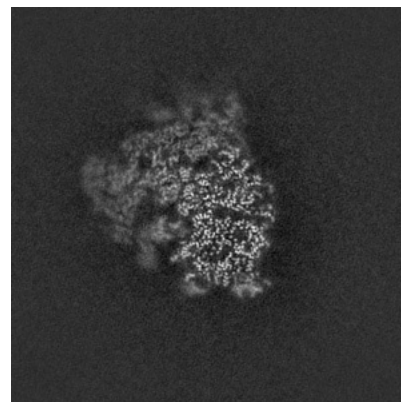
6.3.1 Primary map



X Index: 301

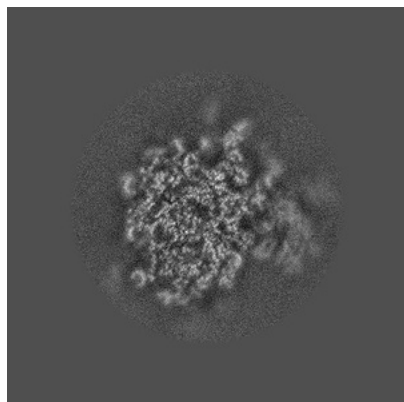


Y Index: 309

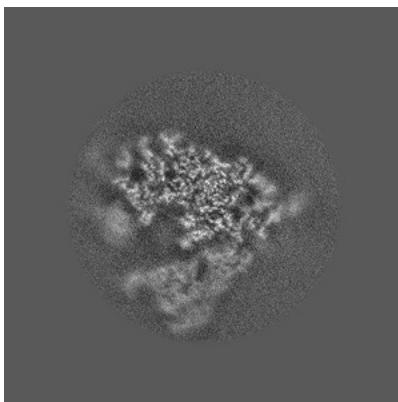


Z Index: 303

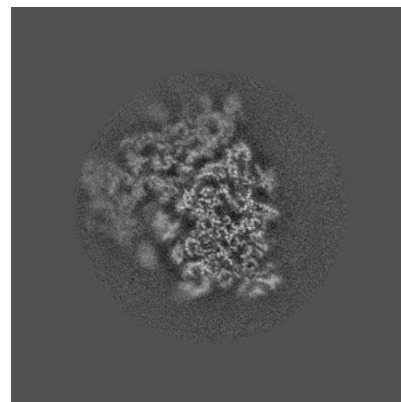
6.3.2 Raw map



X Index: 319



Y Index: 309

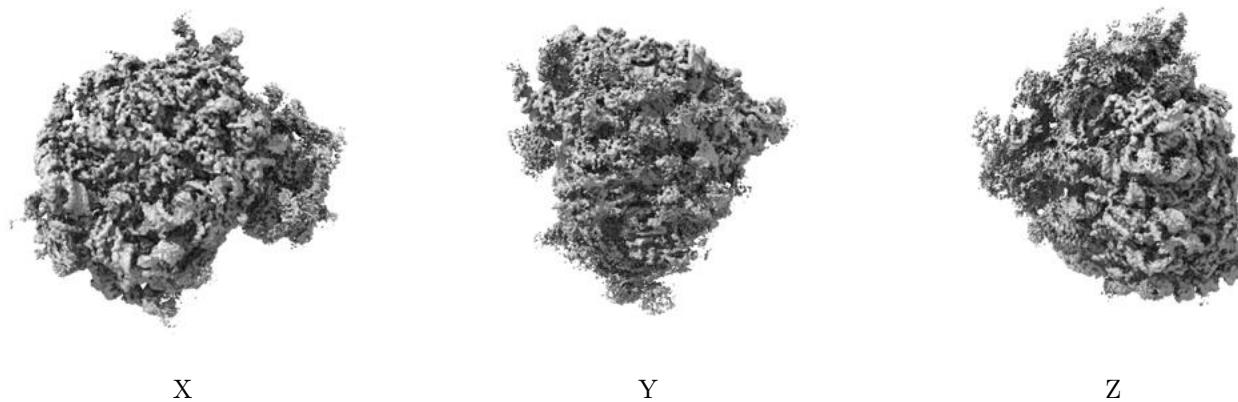


Z Index: 295

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

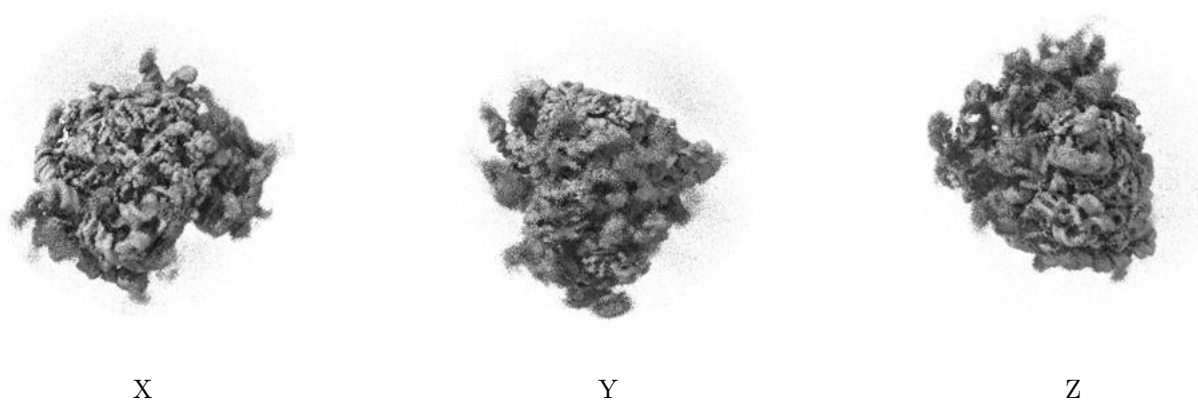
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

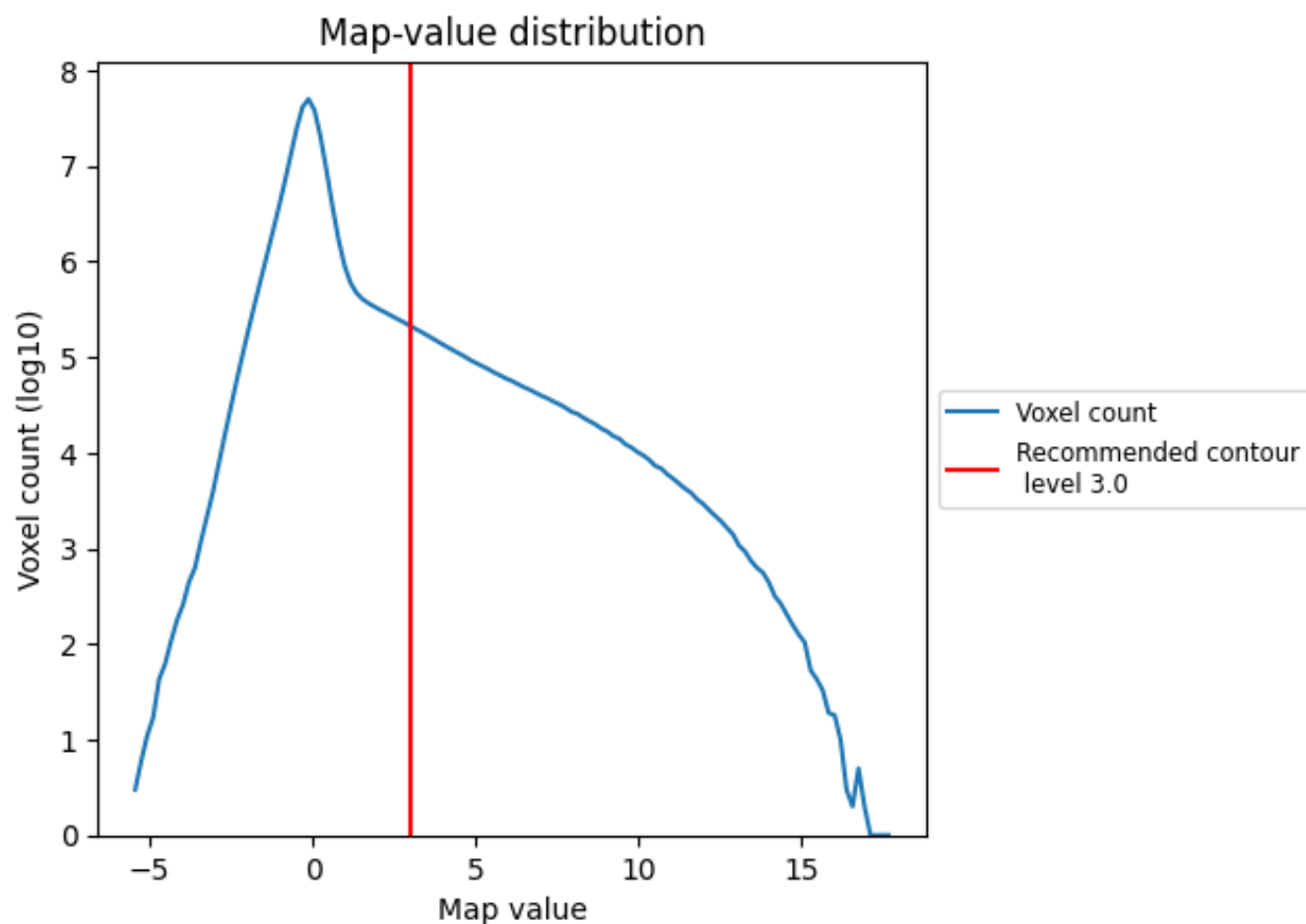
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

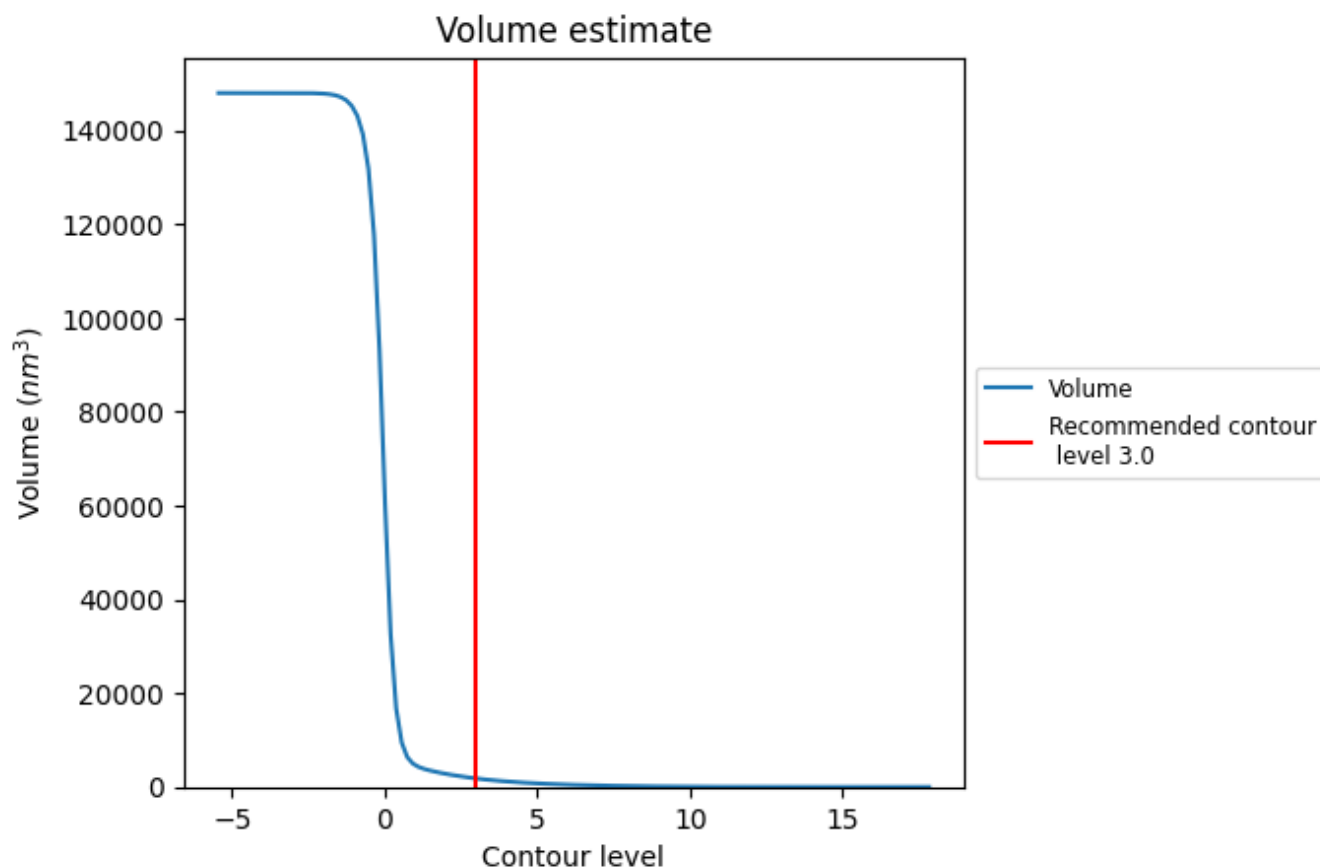
This section contains the results of statistical analysis of the map.

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.

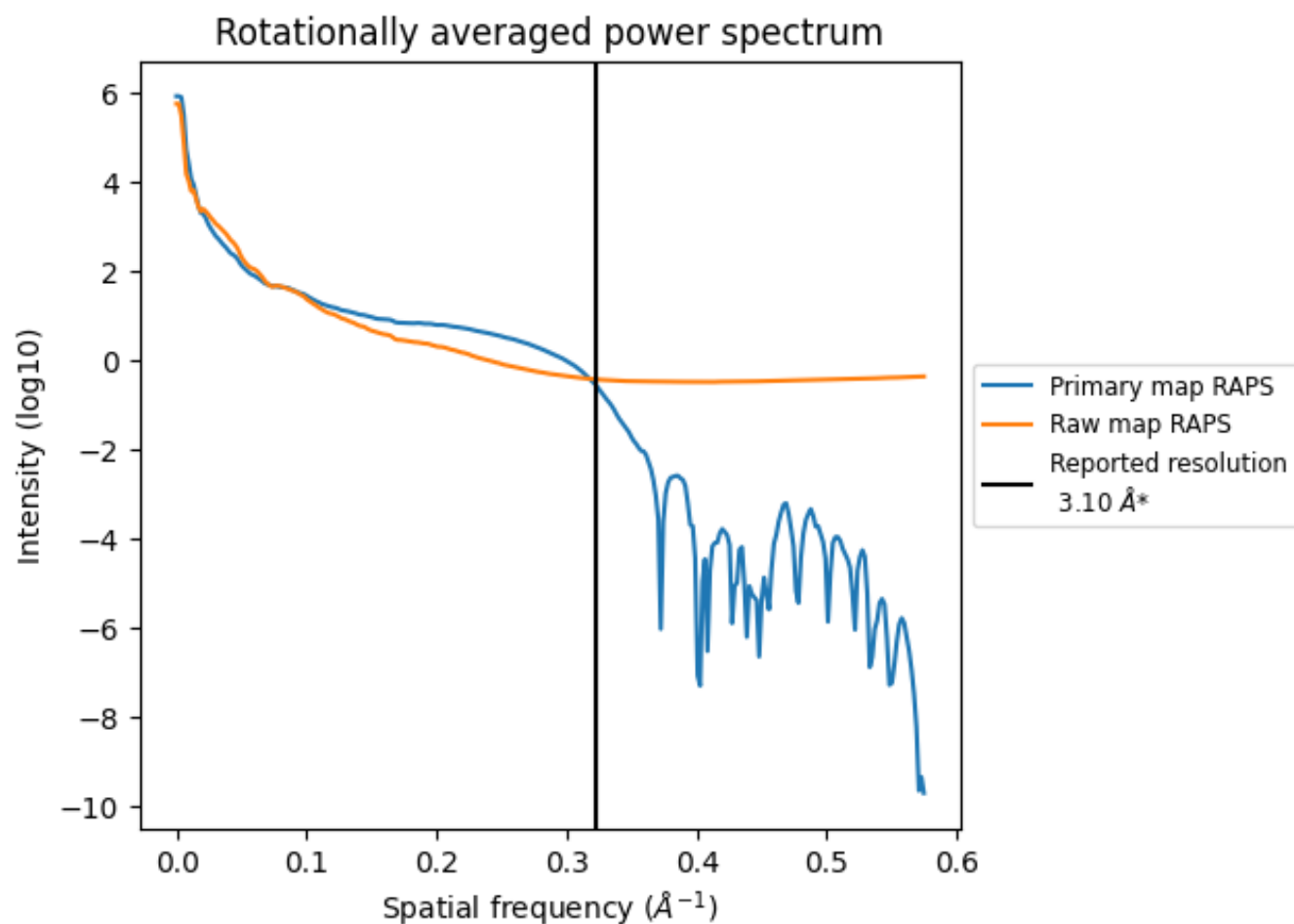
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1816 nm^3 ; this corresponds to an approximate mass of 1641 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

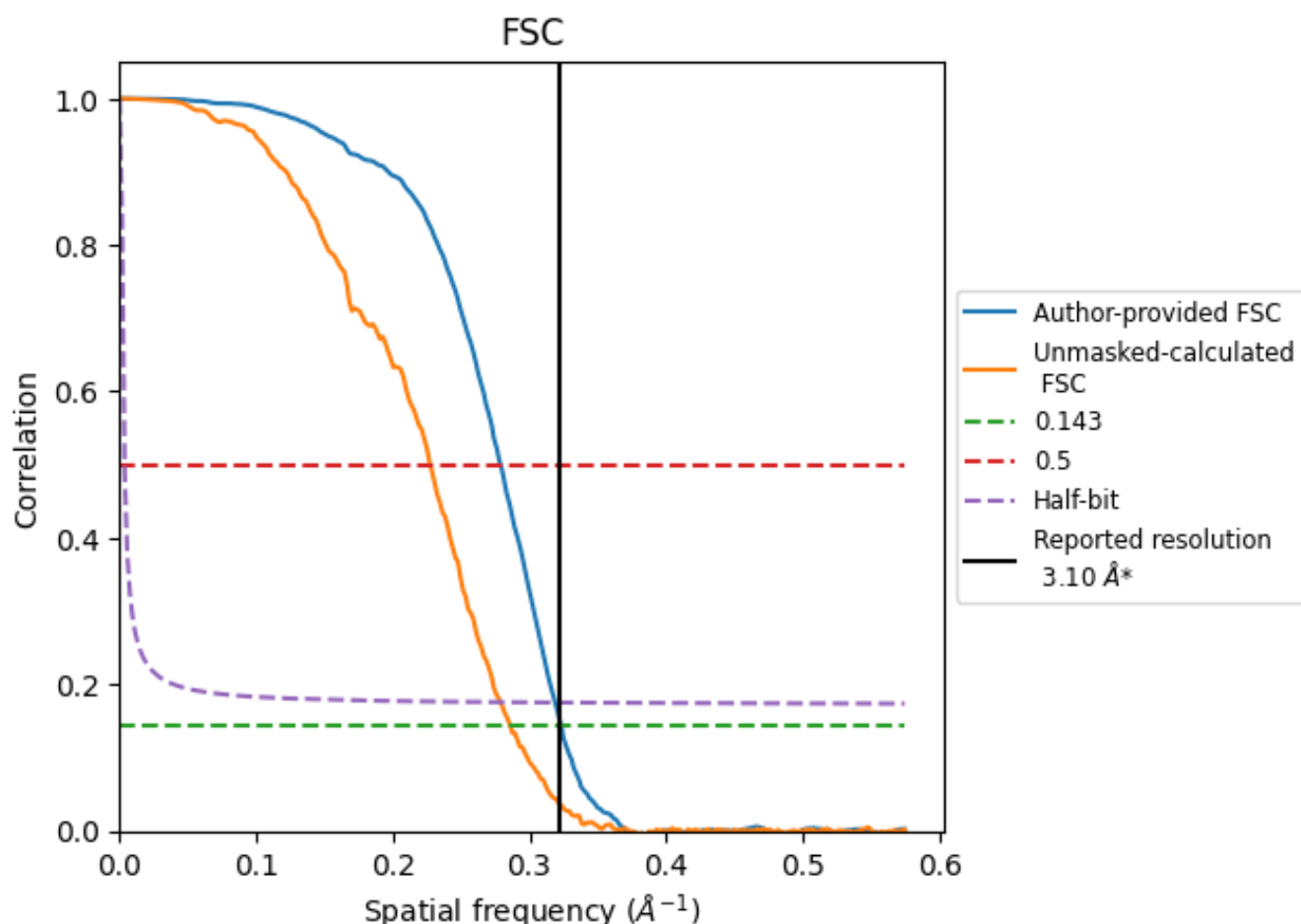


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

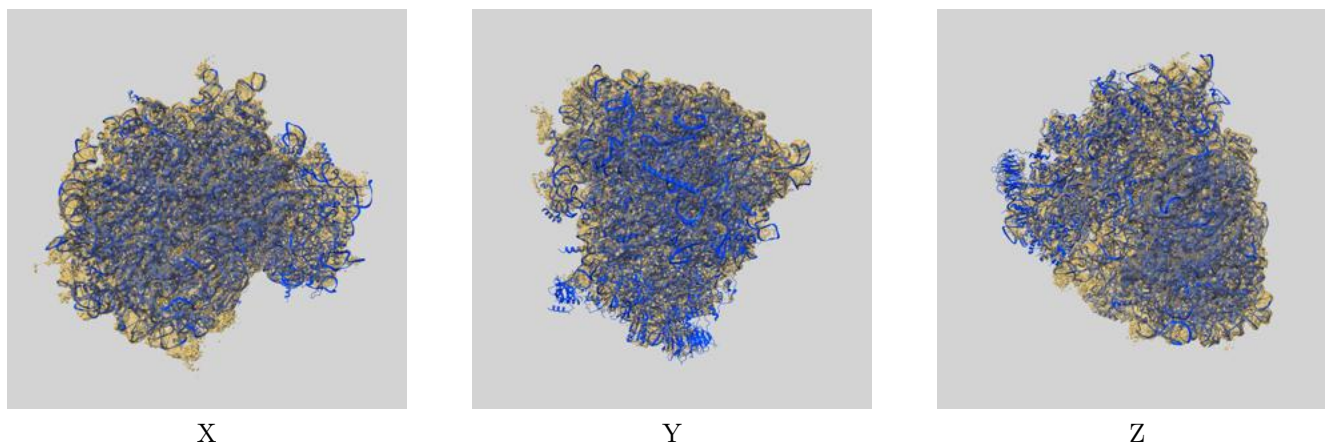
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.59	3.14
Unmasked-calculated*	3.50	4.40	3.59

*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 3.50 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

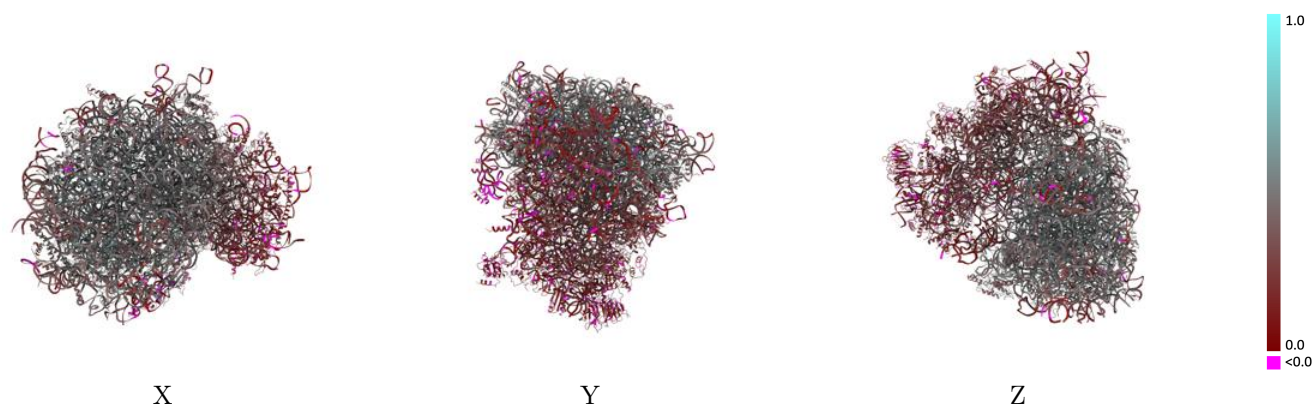
This section contains information regarding the fit between EMDB map EMD-26035 and PDB model 7TOQ. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



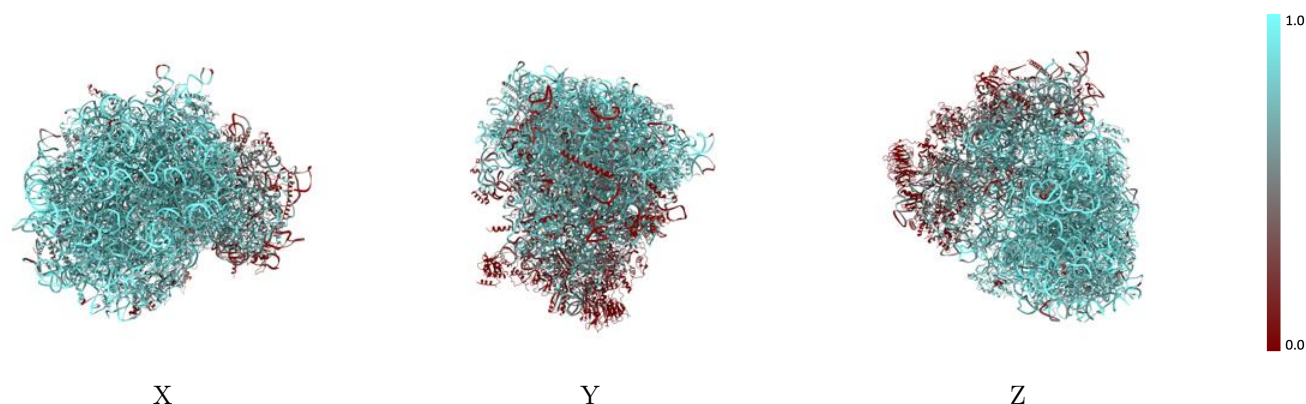
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



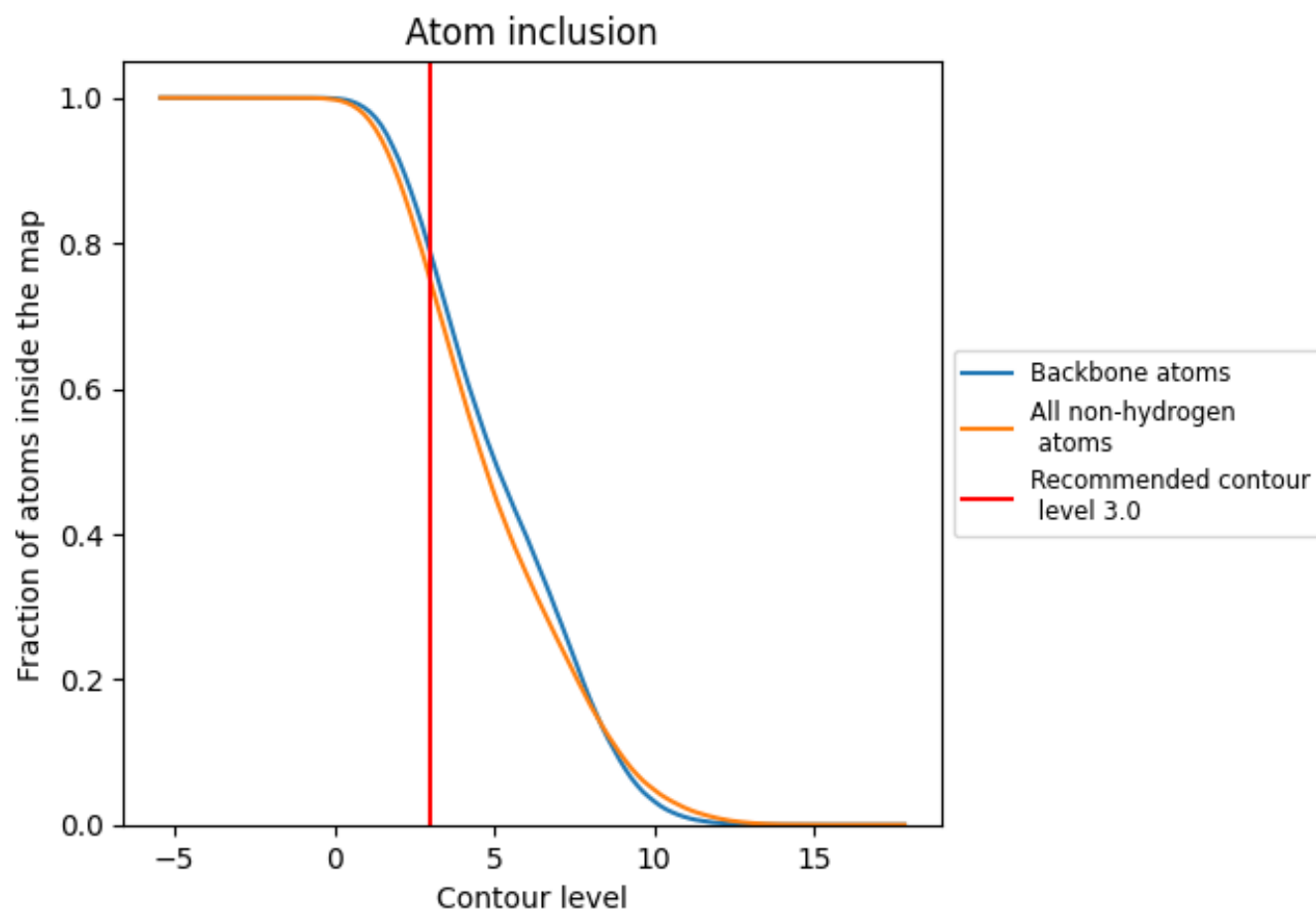
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.0).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7497	 0.3620
A18S	 0.7410	 0.2510
A25S	 0.9160	 0.4220
A58S	 0.9339	 0.4450
A5S	 0.9793	 0.4660
AL02	 0.8417	 0.4920
AL03	 0.8139	 0.4620
AL04	 0.8068	 0.4690
AL05	 0.7809	 0.4110
AL06	 0.7487	 0.4170
AL07	 0.7880	 0.4670
AL08	 0.7112	 0.4080
AL09	 0.7876	 0.4410
AL10	 0.8155	 0.4680
AL11	 0.7485	 0.3980
AL12	 0.0996	 0.0220
AL13	 0.7731	 0.4460
AL14	 0.8062	 0.4460
AL15	 0.8698	 0.4920
AL16	 0.8048	 0.4700
AL17	 0.8400	 0.4810
AL18	 0.8115	 0.4870
AL19	 0.7252	 0.4110
AL20	 0.8143	 0.4720
AL21	 0.7854	 0.4620
AL22	 0.7494	 0.3890
AL23	 0.7774	 0.4710
AL24	 0.8075	 0.4520
AL25	 0.7998	 0.4570
AL26	 0.7718	 0.4480
AL27	 0.7838	 0.4240
AL28	 0.8449	 0.4880
AL29	 0.6733	 0.4030
AL30	 0.7636	 0.4130
AL31	 0.7771	 0.4460



















Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
AL32	 0.8033	 0.4850
AL33	 0.8337	 0.4980
AL34	 0.7940	 0.4670
AL35	 0.7783	 0.4370
AL36	 0.7940	 0.4200
AL37	 0.8871	 0.4910
AL38	 0.6804	 0.4050
AL39	 0.8392	 0.4720
AL40	 0.8173	 0.4580
AL41	 0.6567	 0.3980
AL42	 0.7797	 0.4600
AL43	 0.7547	 0.4380
ALP0	 0.1802	 0.0950
ARAC	 0.0535	 0.1440
AS00	 0.3158	 0.2500
AS01	 0.5444	 0.2870
AS02	 0.4412	 0.2510
AS03	 0.1954	 0.1870
AS04	 0.3748	 0.1990
AS05	 0.2250	 0.1850
AS06	 0.2895	 0.1970
AS07	 0.1985	 0.2350
AS08	 0.4511	 0.2450
AS09	 0.4956	 0.1910
AS10	 0.1747	 0.1910
AS11	 0.4833	 0.2630
AS12	 0.0101	 0.1480
AS13	 0.4846	 0.3110
AS14	 0.6059	 0.2770
AS15	 0.5513	 0.2340
AS16	 0.2289	 0.1650
AS17	 0.2235	 0.1830
AS18	 0.3755	 0.2190
AS19	 0.2315	 0.2020
AS20	 0.2403	 0.1800
AS21	 0.3006	 0.2420
AS22	 0.4079	 0.2910
AS23	 0.5481	 0.2880
AS24	 0.3170	 0.1660
AS25	 0.1252	 0.2210
AS26	 0.5723	 0.3040
AS27	 0.4100	 0.2780

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
AS28	 0.3404	 0.2250
AS29	 0.5079	 0.2000
AS30	 0.2676	 0.2250
AS31	 0.0833	 0.1560
EL28	 0.8112	 0.4630
MRNA	 0.2077	 0.1550
PR	 0.1724	 0.3490
PTRN	 0.8453	 0.2670