



wwPDB EM Validation Summary 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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

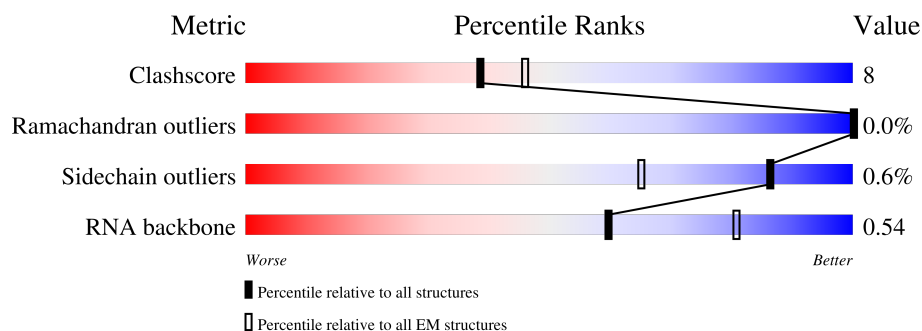
1 Overall quality at a glance

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.



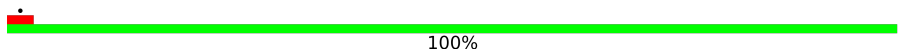

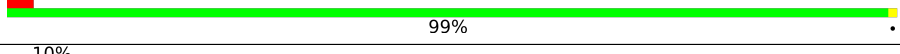
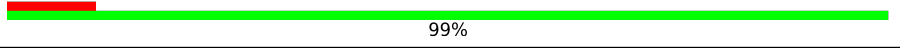
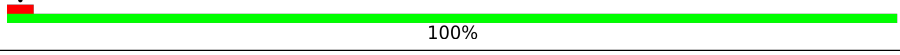
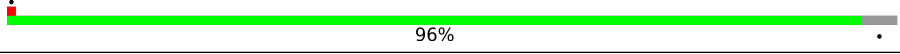
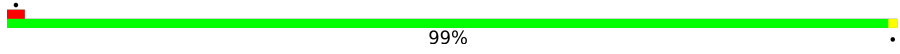

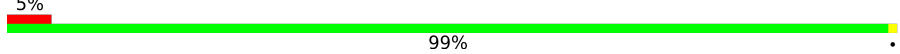
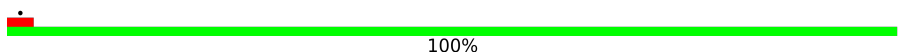
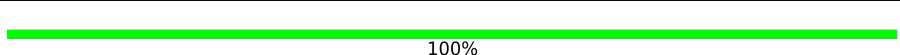
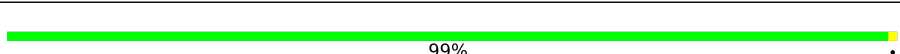
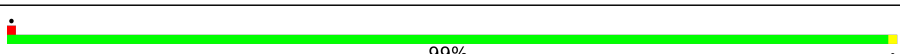
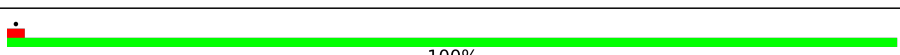
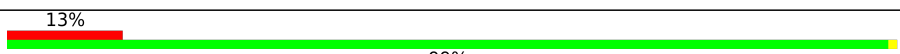
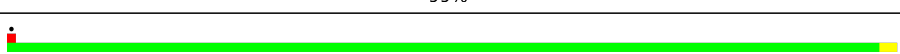
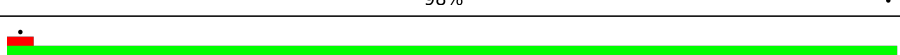
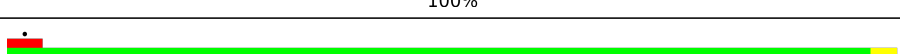
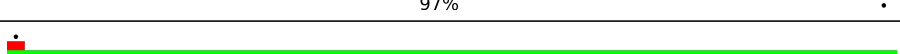
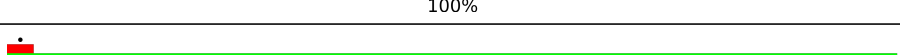
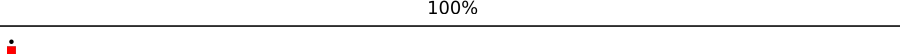
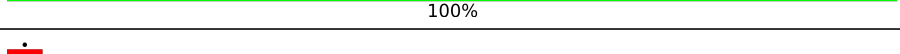
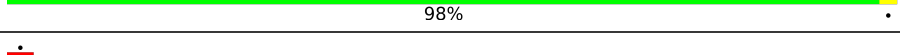
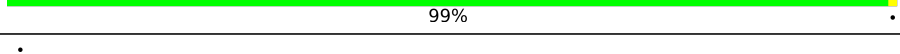
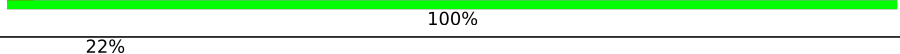
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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>

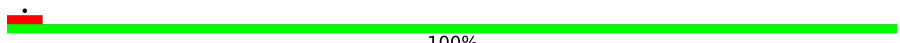
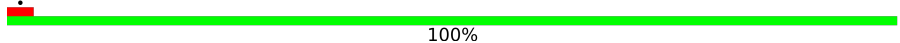
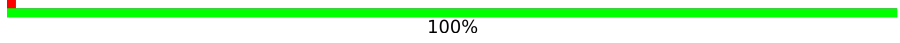
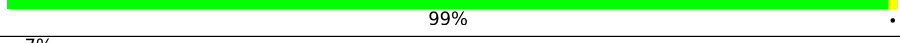
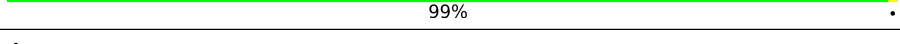
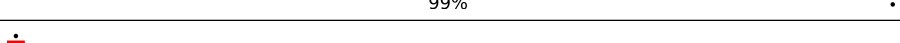
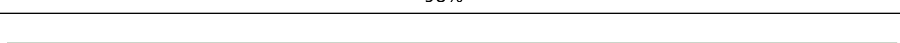

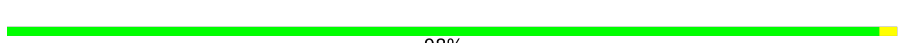
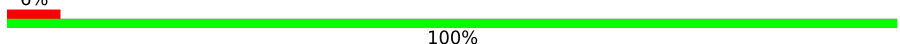
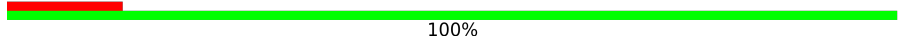
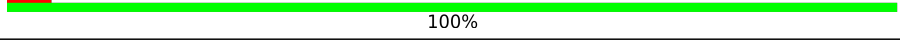
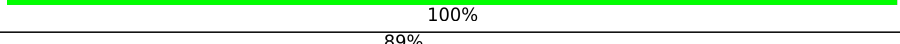
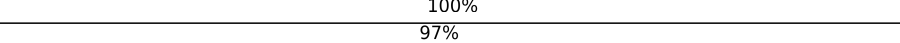
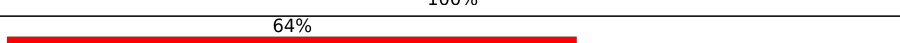



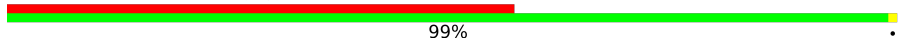
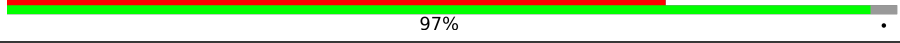
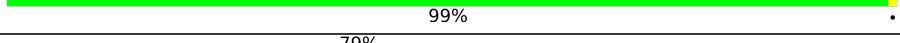
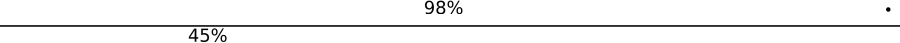
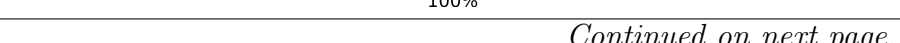


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Mol	Chain	Length	Quality of chain
8	AL05	293	 100%
9	AL06	251	 85%14%
10	AL07	225	 99%
11	AL08	241	 10%99%
12	AL09	190	 100%
13	AL10	213	 96%
14	AL11	169	 99%
15	AL12	163	 21%23%77%
16	AL13	210	 5%99%
17	AL14	138	 100%
18	AL15	203	 100%
19	AL16	199	 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%

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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	 57%
54	AS05	191	 74%
55	AS06	237	 68%
56	AS07	189	 79%
57	AS08	206	 45%

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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%

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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).

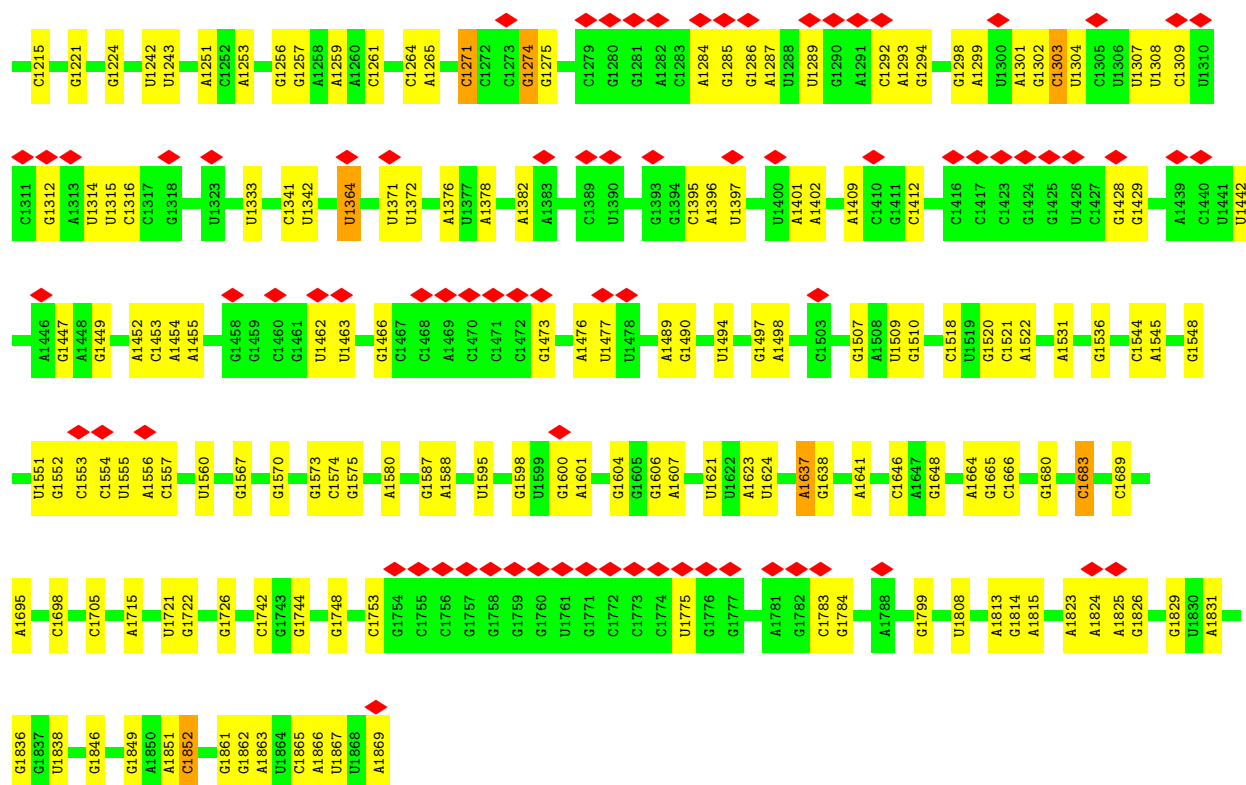
Mol	Chain	Residues	Atoms		AltConf
85	AL37	1	Total	Zn	0
			1	1	
85	AL40	1	Total	Zn	0
			1	1	
85	AL42	1	Total	Zn	0
			1	1	
85	AL43	1	Total	Zn	0
			1	1	

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.

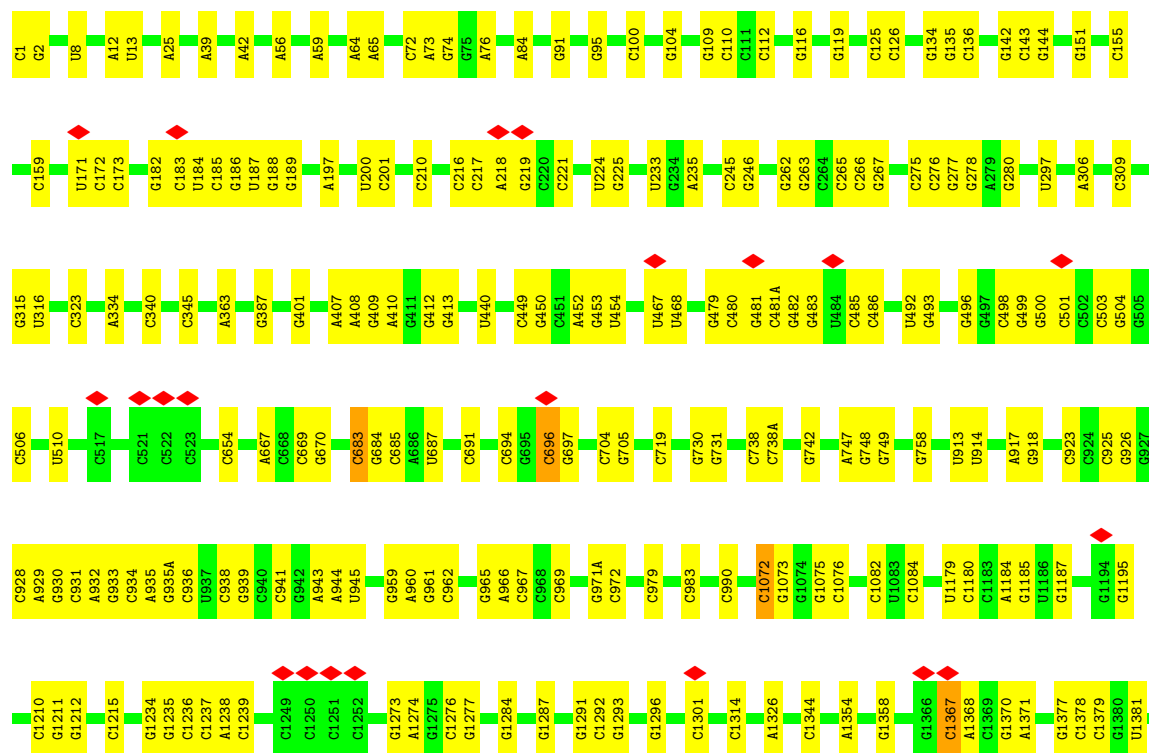
• Molecule 1: 18S rRNA



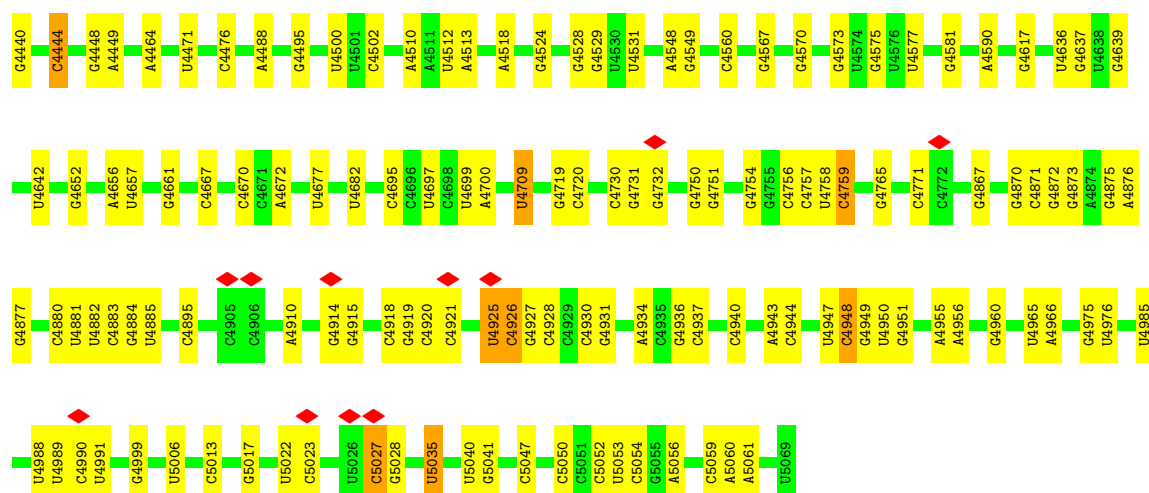


• Molecule 2: 28S rRNA

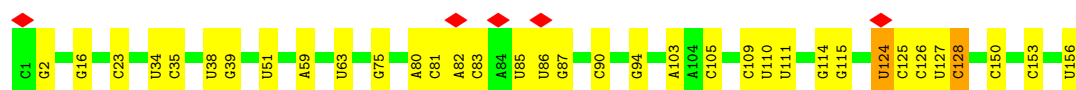
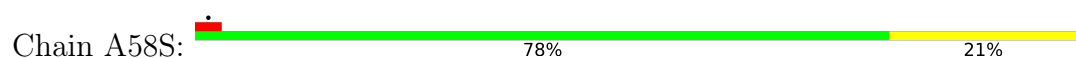
Chain A25S: 78% 21%



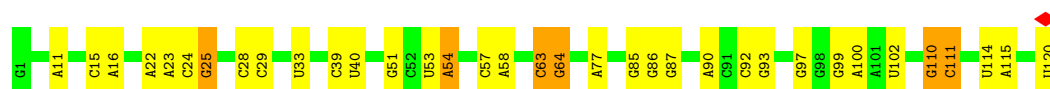
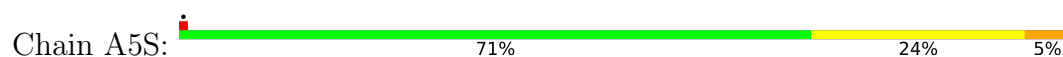
U4111	C4112	G4115	C4116	U4117	U4118	C4119	U4120	C4121	C4125	C4126	A4127	A4128	C4140	C4141	C4142	C4143	C4144	C4145	C4158	C4162	C4166	A4170	C4171	A4172	C4173	G4183	G4184	C4191	A4203	A4212	G4225	U4229	U4232	A4233	A4234	C4241	U4242	C4243	G4249	G4250	G4251	G4254							
C3926	G3938	U3959	A3960	G3961	A3962	A3963	U3964	A3965	U3968	G3969	G3970	G3971	A3972	G3973	C3976	G4035	C4041	G4042	G4043	U4044	A4047	U4048	U4049	A4050	G4065	U4066	C4076	G4084	A4085	U4086	G4087	C4088	G4094	G4095	C4096	G4097	A4098	C4099	C4100	C4101	C4102	C4103	C4104	A4105	G4106	G4107	G4108	G4109	C4110
U3773	A3774	G3777	U3778	A3784	U3785	U3786	C3791	C3810	G3811	C3812	A3813	U3814	A3817	U3818	G3819	U3822	U3838	G3839	U3840	C3843	A3860	A3867	G3868	C3869	A3876	A3877	C3878	G3879	G3888	G3889	U3892	G3897	G3898	G3899	G3900	A3901	A3905	A3906	C3907	A3908	C3909	U3915	C3771	U3772					
C3867	G3898	U3903	U3904	C3905	U3908	C3909	G3910	C3954	G3955	G3956	C3957	C3958	G3959	G3960	C3962	C3965	U3616	G3617	G3625	G3626	A3630	A3635	C3636	A3649	A3662	A3663	G3664	C3673	G3710	A3711	C3739	A3748	A3760	C3771	U3772														
U2687	G2694	A2695	A2696	U2707	U2708	C2709	C2710	C2711	C2712	C2716	C2721	G2724	A2725	G2726	U2740	C2743	G2753	G2754	U2758	U2759	G2760	U2761	G2762	U2767	C2768	C2770	A2787	U2788	A2789	U2790	C2794	A2798	C2814	U2826	C2827	U2828	G2842	G2855	C2856	A2857									
C2491	G2502	C2503	C2504	C2505	G2506	A2507	A2513	G2528	A2529	U2530	A2537	G2544	U2545	G2546	G2547	G2548	G2549	A2553	U2554	C2563	C2571	C2572	U2575	A2581	A2582	C2583	G2586	A2587	C2588	G2620	C2627	U2639	G2640	U2661	G2662	C2669	A2676	G2679	G2686										
G2262	G2265	C2266	U2267	A2268	C2269	G2270	A2279	C2289	A2300	G2301	G2306	A2313	G2316	G2322	C2325	G2331	A2332	G2333	G2348	C2351	A2360	A2395	A2396	C2410	A2417	C2422	U2425	G2433	C2441	G2450	G2463	C2464	C2465	C2488	C2489	U2490													
A2002	G2003	U2004	G2007	U2008	A2009	A2010	C2011	A2012	U2020	A2026	G2034	U2044	G2045	G2046	A2047	U2048	C2083	C2084	G2085	G2089	U2090	C2091	G2092	G2093	C2094	A2095	G2096	A2097	G2098	C2099	G2100	A2101	A2102	A2103	A2104	A2105	G2106	A2107	G2108	A2109	G2110	G2259	C2260	G2261					
C1881	U1882	U1889	G1890	A1897	G1910	G1916	A1917	U1918	G1919	G1920	C1921	U1930	C1931	A1932	C1935	C1938	U1957	A1958	U1959	A1960	G1961	A1962	C1963	A1964	G1965	C1966	A1967	G1975	G1976	C1977	G1978	A1979	U1980	G1981	G1982	A1983	A1984	C1987	G1988	G1989	A1990	U1991	U1992	U1997	G2001				
U1754	C1755	U1756	G1761	C1762	C1763	G1764	A1765	A1766	A1767	C1768	G1769	A1770	U1771	C1772	U1773	A1776	C1777	U1781	A1787	U1792	U1800	A1801	A1802	G1803	A1804	A1805	C1809	G1812	G1815	G1818	G1819	U1820	G1821	U1822	C1828	G1835	G1836	A1837	G1842	C1847	C1848	G1855	G1869						
A1563	A1564	A1565	A1566	G1574	G1577	U1578	U1591	U1596	U1602	A1612	A1613	G1624	G1625	A1631	A1632	A1633	A1634	A1638	U1639	G1640	G1641	A1650	G1654	C1661	C1676	U1677	C1686	G1691	G1721	G1724	U1725	C1731	G1734	G1741	A1742	G1750	G1753												
A1387	G1390	G1394	A1397	A1398	G1399	G1408	C1409	U1410	C1411	G1419	A1420	C1429	G1434	U1445	C1446	C1447	G1448	G1455	C1456	G1457	C1458	G1465	G1475	G1482	C1483	A1497	G1498	C1501	G1502	G1516	G1517	A1518	A1523	A1524	A1525	A1534	A1547	A1553	G1562										



• Molecule 3: 5.8S rRNA



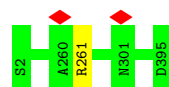
• Molecule 4: 5S rRNA



• Molecule 5: uL2



• Molecule 6: 60S ribosomal protein L3



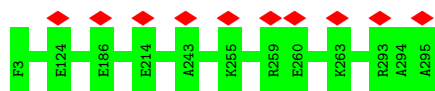
• Molecule 7: 60S ribosomal protein L4





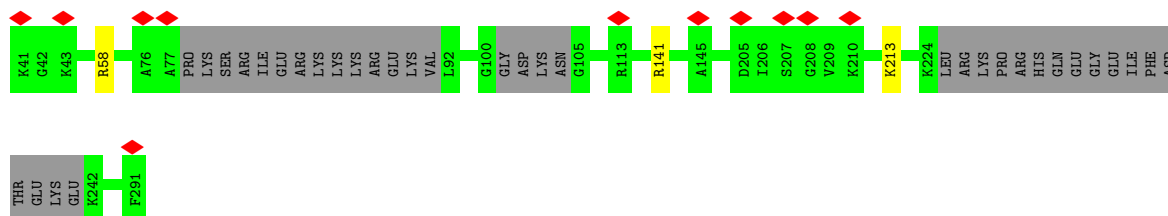
- Molecule 8: 60S ribosomal protein L5

Chain AL05: 100%



- Molecule 9: 60S ribosomal protein L6

Chain AL06: 85% 14%



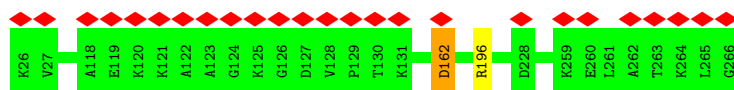
- Molecule 10: uL30

Chain AL07: 99%



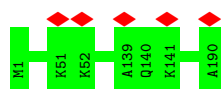
- Molecule 11: eL8

Chain AL08: 10% 99%



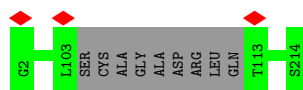
- Molecule 12: 60S ribosomal protein L9

Chain AL09: 100%



- Molecule 13: Ribosomal protein L10

Chain AL10: 96%



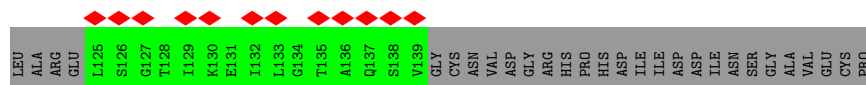
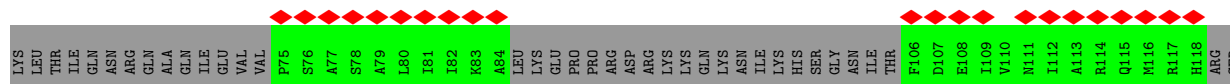
- Molecule 14: 60S ribosomal protein L11

Chain AL11: 99%



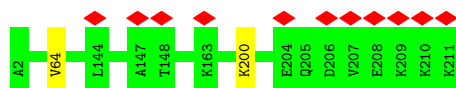
- Molecule 15: 60S ribosomal protein L12

Chain AL12: 21% 23% 77%



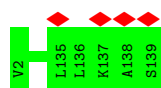
- Molecule 16: eL13

Chain AL13: 5% 99%



- Molecule 17: 60S ribosomal protein L14

Chain AL14: 100%



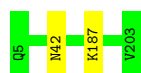
- Molecule 18: 60S ribosomal protein L15

Chain AL15: 100%

There are no outlier residues recorded for this chain.

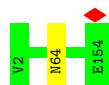
- Molecule 19: uL13

Chain AL16: 99%



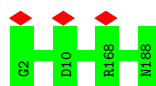
- Molecule 20: 60S ribosomal protein L17

Chain AL17: 99%



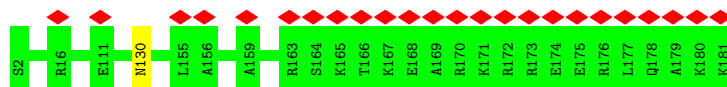
- Molecule 21: eL18

Chain AL18: 100%



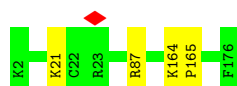
- Molecule 22: 60S ribosomal protein L19

Chain AL19: 13% 99%



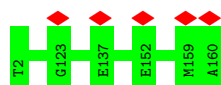
- Molecule 23: eL20

Chain AL20: 98%



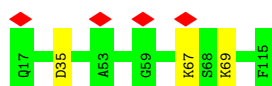
- Molecule 24: 60S ribosomal protein L21

Chain AL21: 100%



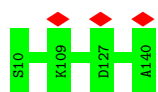
- Molecule 25: eL22

Chain AL22: 97%



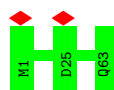
- Molecule 26: 60S ribosomal protein L23

Chain AL23:  100%



- Molecule 27: Ribosomal protein L24

Chain AL24:  100%



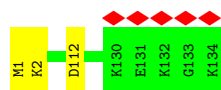
- Molecule 28: uL23

Chain AL25:  100%



- Molecule 29: 60S ribosomal protein L26

Chain AL26:  98%



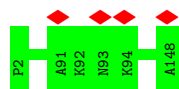
- Molecule 30: 60S ribosomal protein L27

Chain AL27:  99%



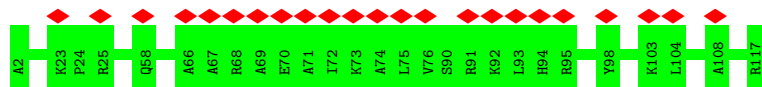
- Molecule 31: 60S ribosomal protein L27a

Chain AL28:  100%



- Molecule 32: eL29

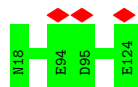
Chain AL29:  22%  100%



• Molecule 33: eL30

Chain AL30:  100%

• Molecule 34: 60S ribosomal protein L31

Chain AL31:  100%

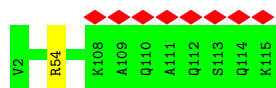
• Molecule 35: 60S ribosomal protein L32

Chain AL32:  100%

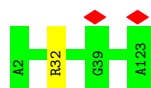
• Molecule 36: 60S ribosomal protein L35a

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%



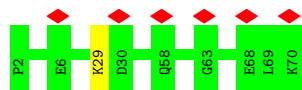
- Molecule 40: 60S ribosomal protein L37

Chain AL37: 100%

There are no outlier residues recorded for this chain.

- Molecule 41: eL38

Chain AL38: 99%



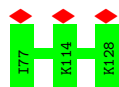
- Molecule 42: eL39

Chain AL39: 98%



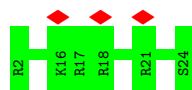
- Molecule 43: eL40

Chain AL40: 100%



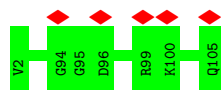
- Molecule 44: eL41

Chain AL41: 100%



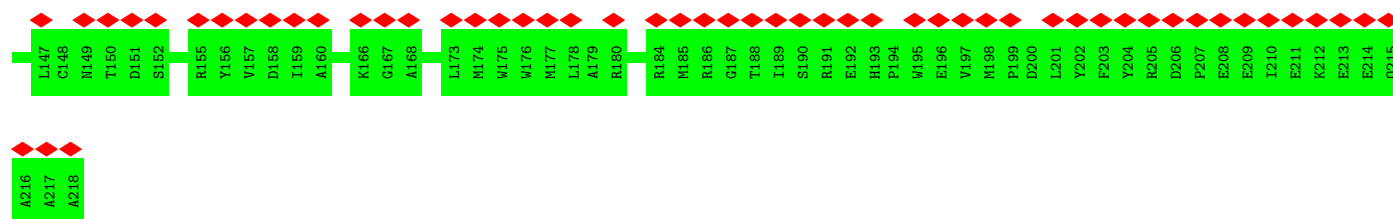
- Molecule 45: eL42

Chain AL42: 100%

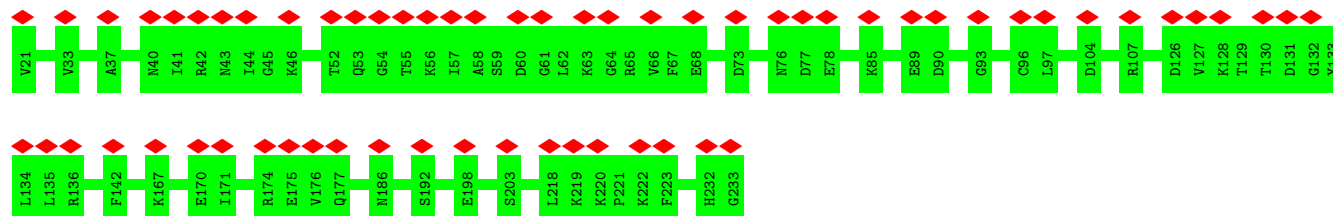


- Molecule 46: 60S ribosomal protein L37a

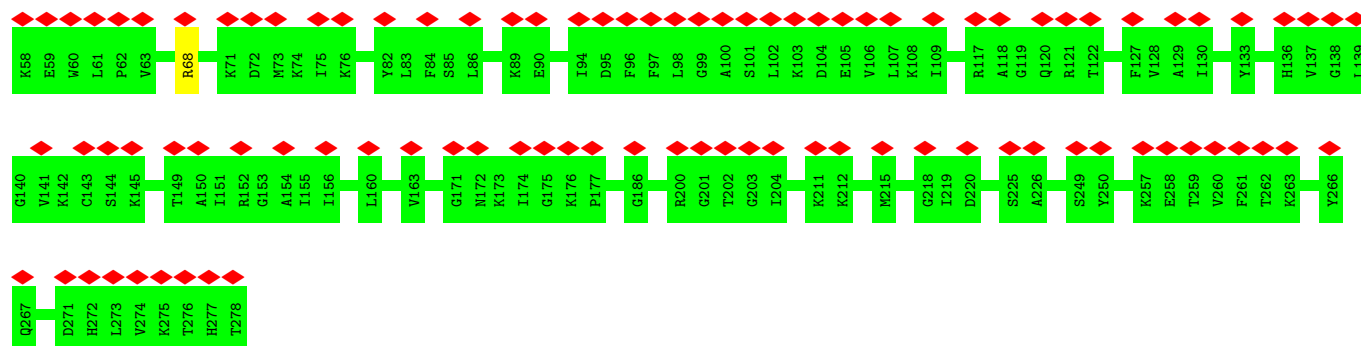
Chain AL43: 100%



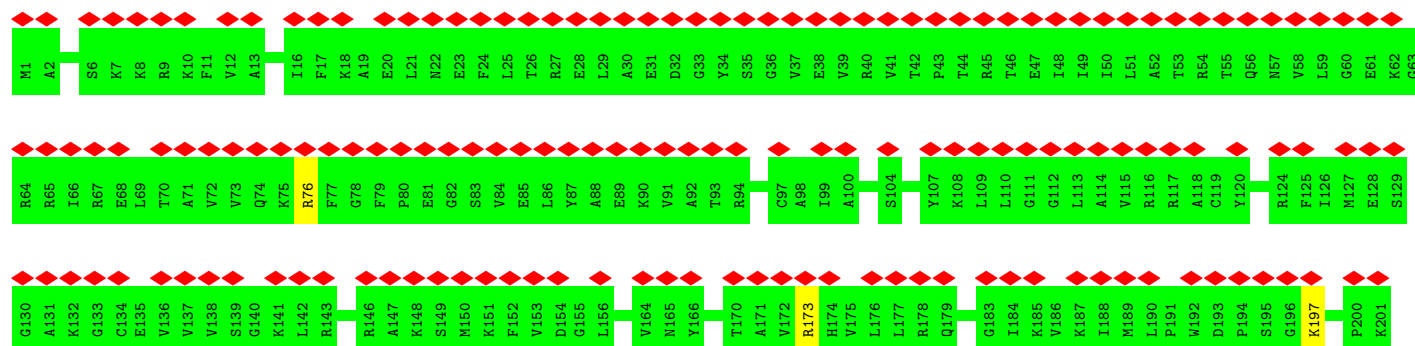
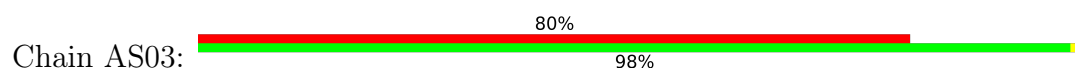
- Molecule 50: 40S ribosomal protein S3a

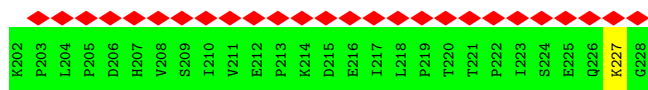


- Molecule 51: 40S ribosomal protein S2

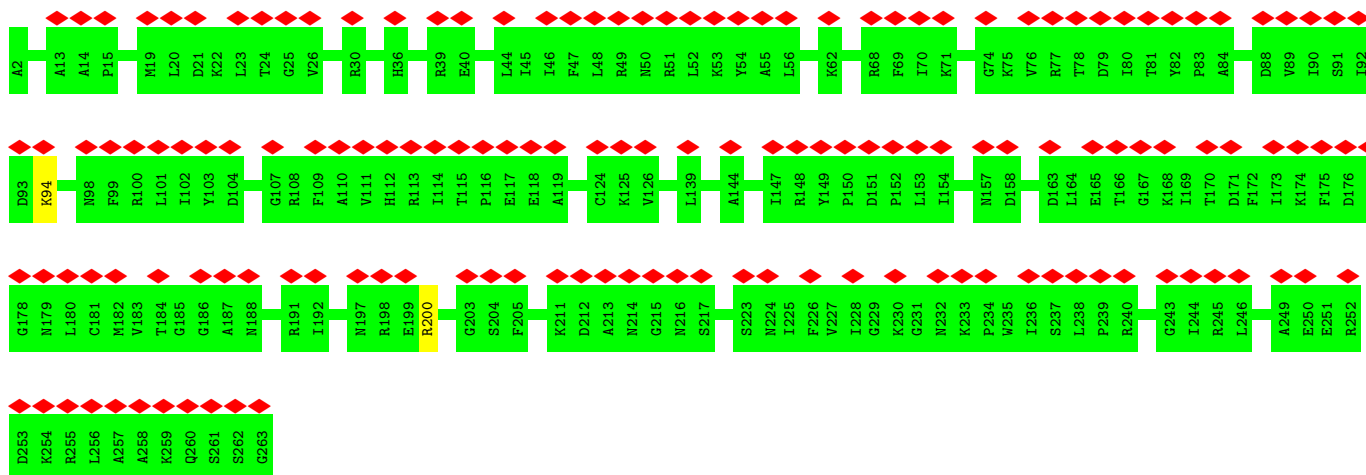


- Molecule 52: 40S ribosomal protein S3

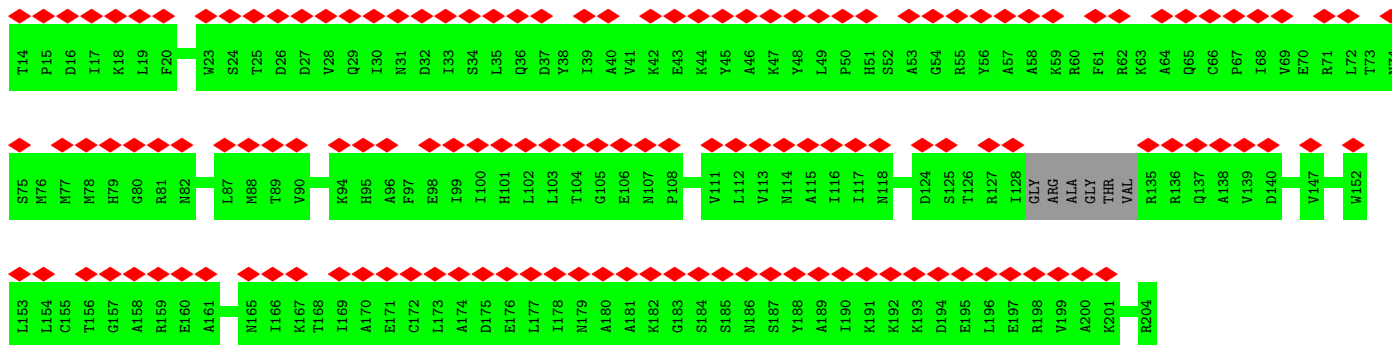
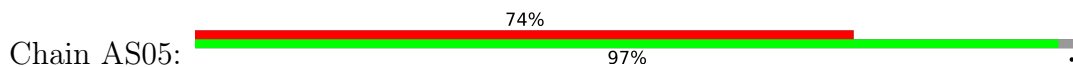




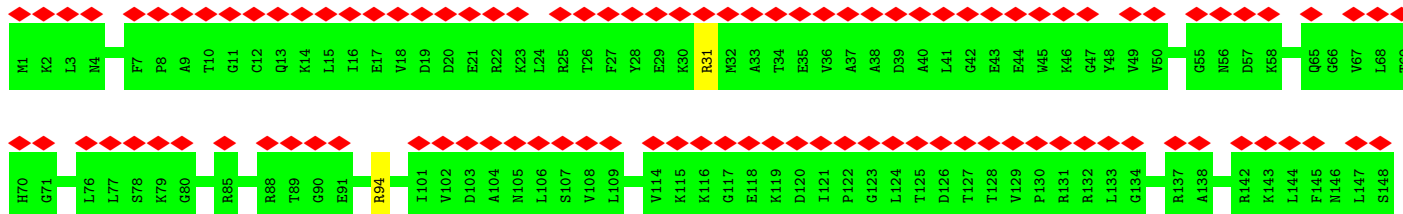
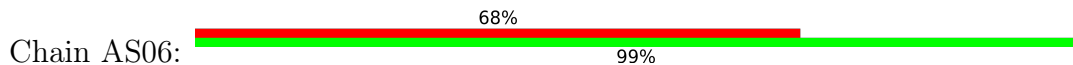
- Molecule 53: 40S ribosomal protein S4

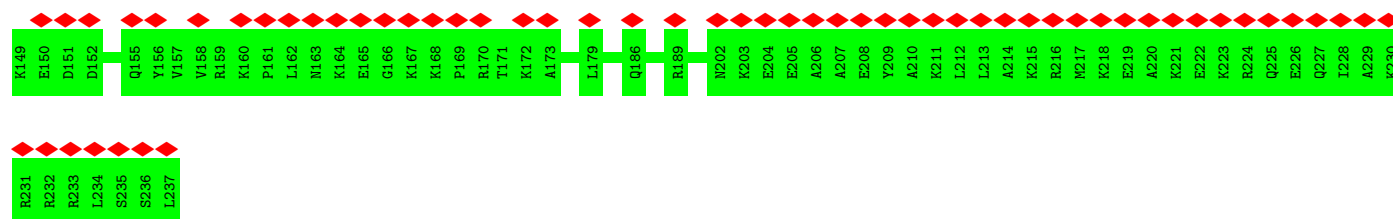


- Molecule 54: Ribosomal protein S5

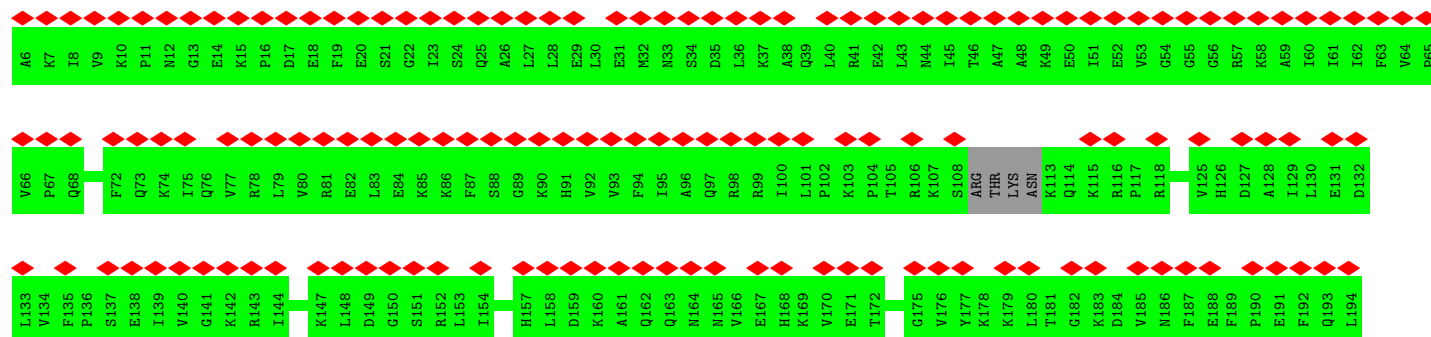
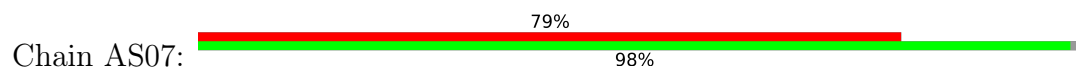


- Molecule 55: 40S ribosomal protein S6

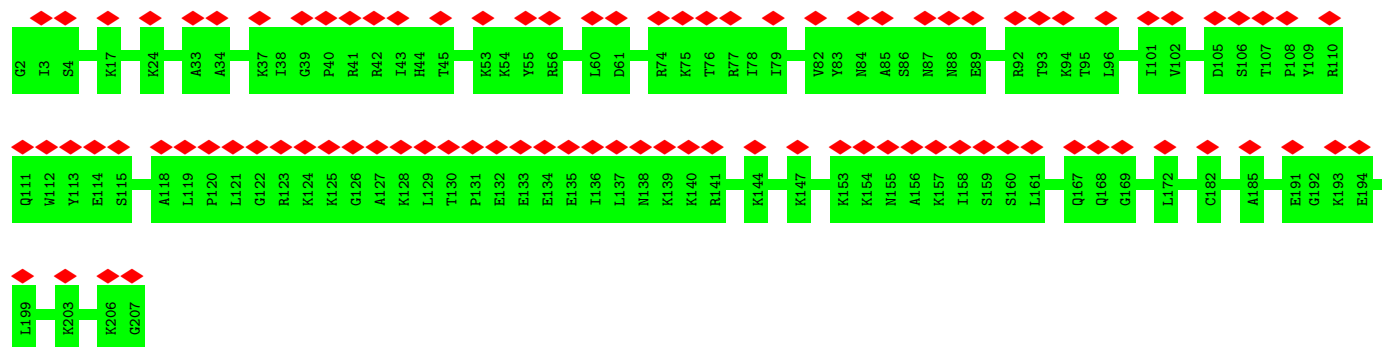




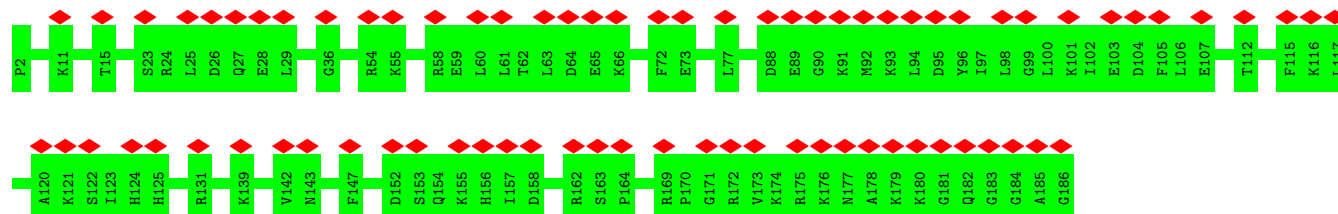
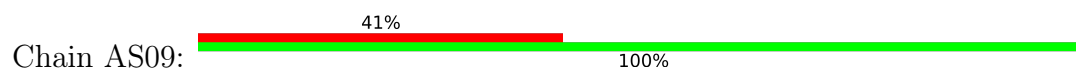
• Molecule 56: eS7



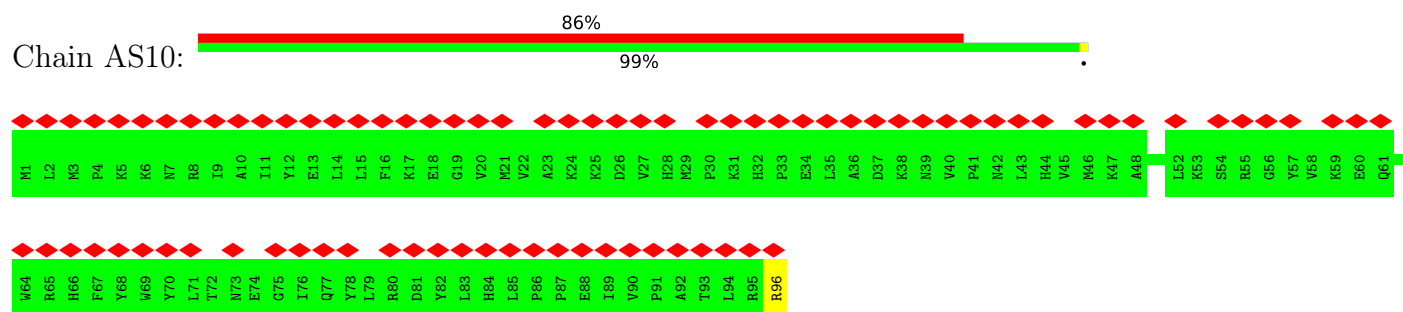
• Molecule 57: 40S ribosomal protein S8



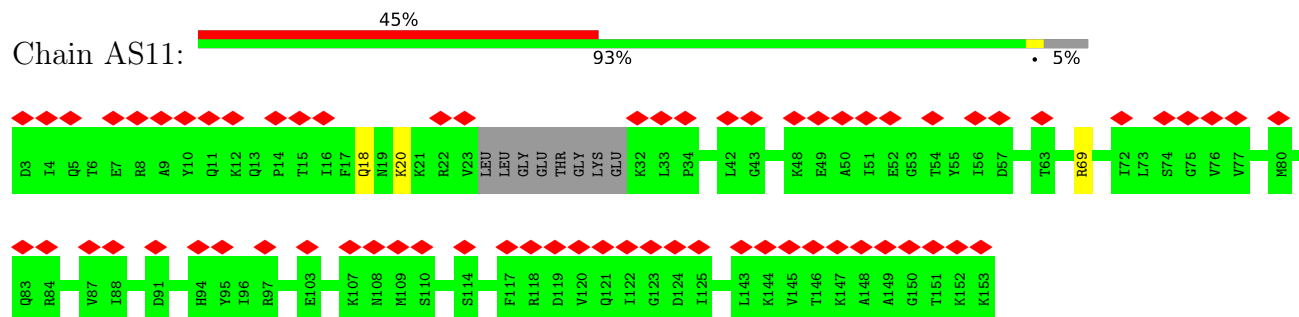
• Molecule 58: 40S ribosomal protein S9



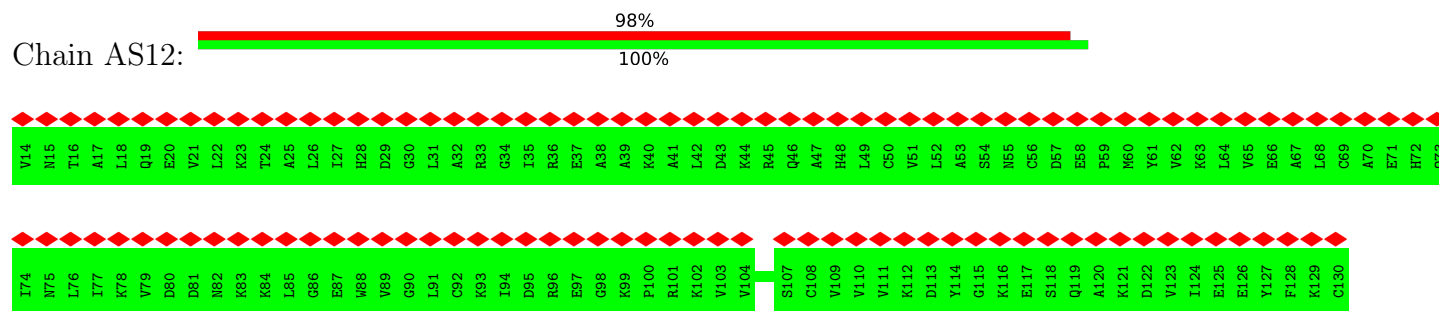
• Molecule 59: 40S ribosomal protein S10



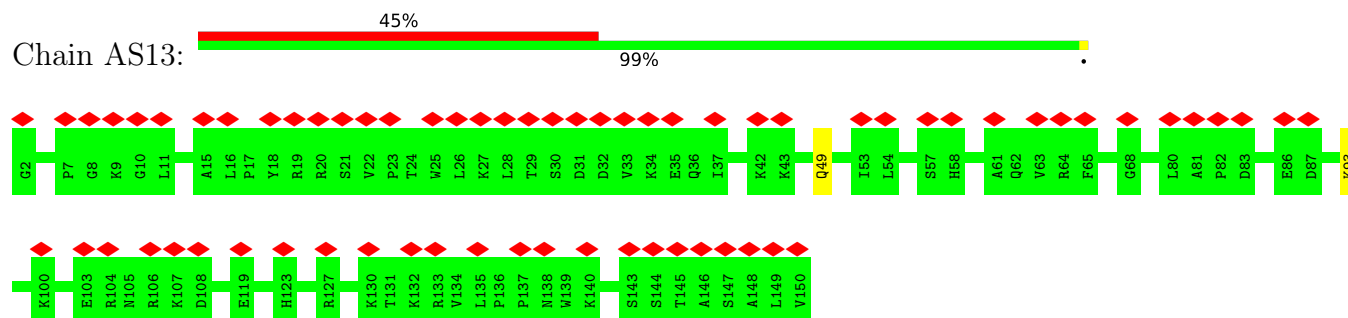
• Molecule 60: 40S ribosomal protein S11



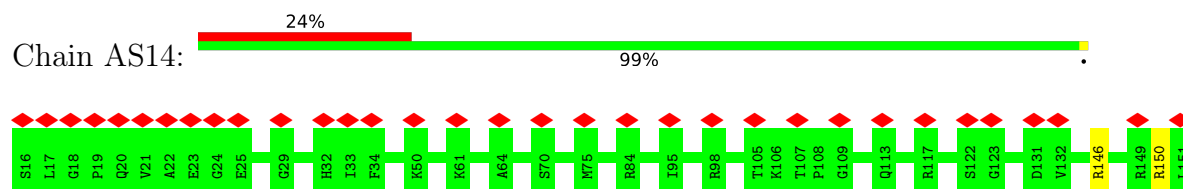
• Molecule 61: 40S ribosomal protein S12



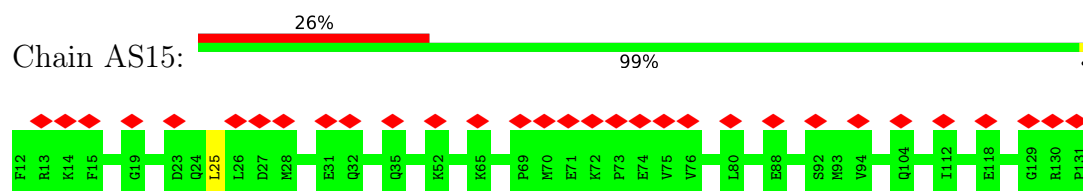
• Molecule 62: 40S ribosomal protein S13



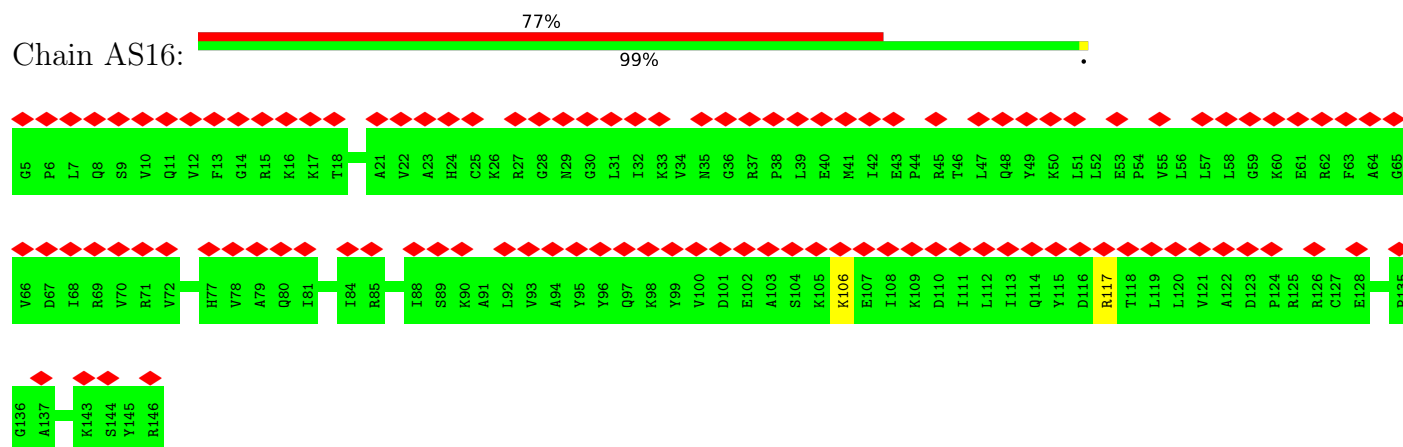
• Molecule 63: 40S ribosomal protein S14



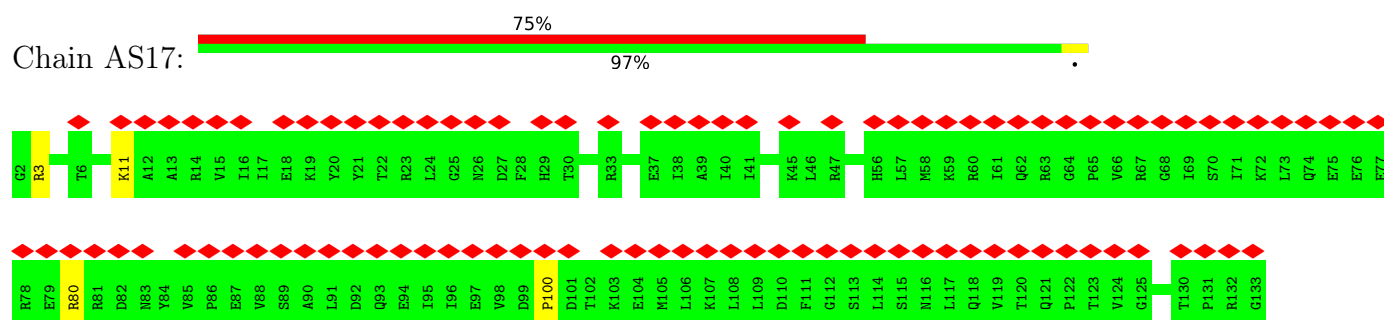
- Molecule 64: 40S ribosomal protein S15



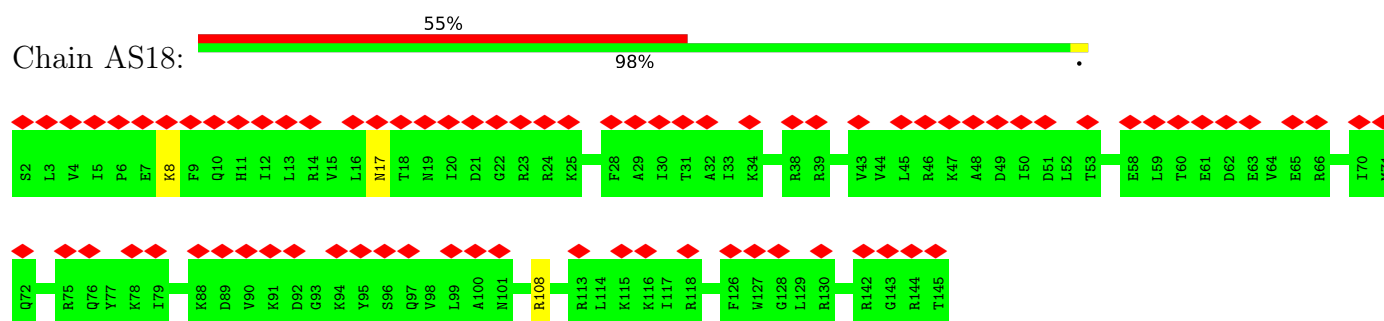
- Molecule 65: uS9



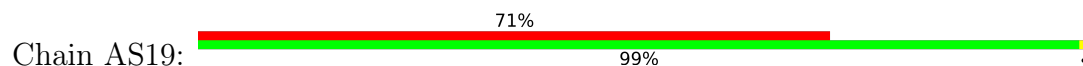
- Molecule 66: 40S ribosomal protein S17

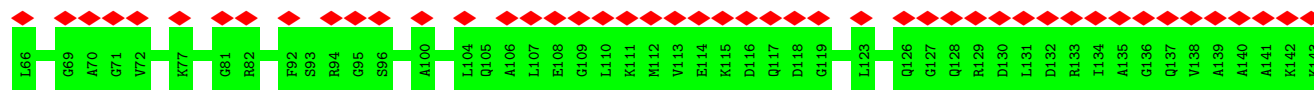
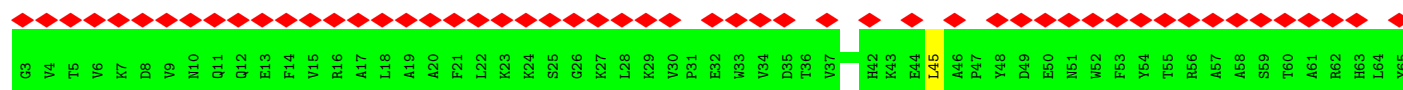


- Molecule 67: 40S ribosomal protein S18

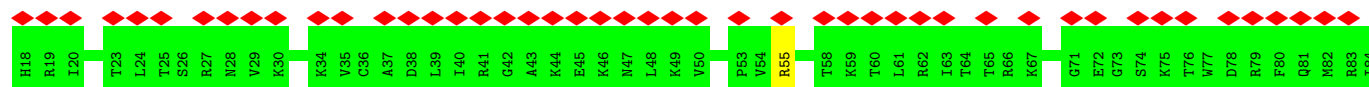
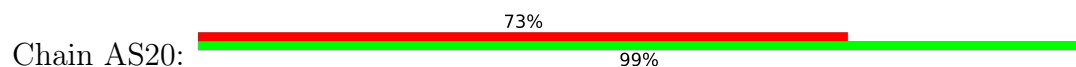


- Molecule 68: eS19

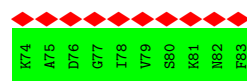
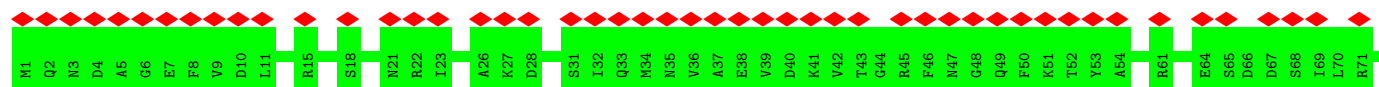




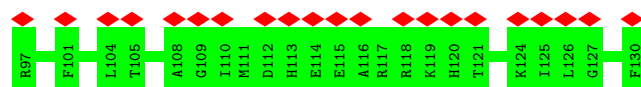
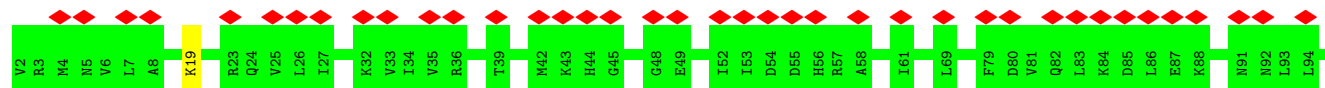
• Molecule 69: 40S ribosomal protein S20



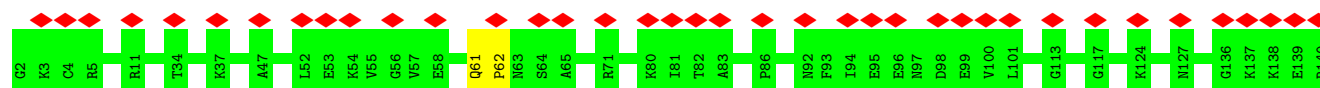
• Molecule 70: eS21



• Molecule 71: 40S ribosomal protein S15a

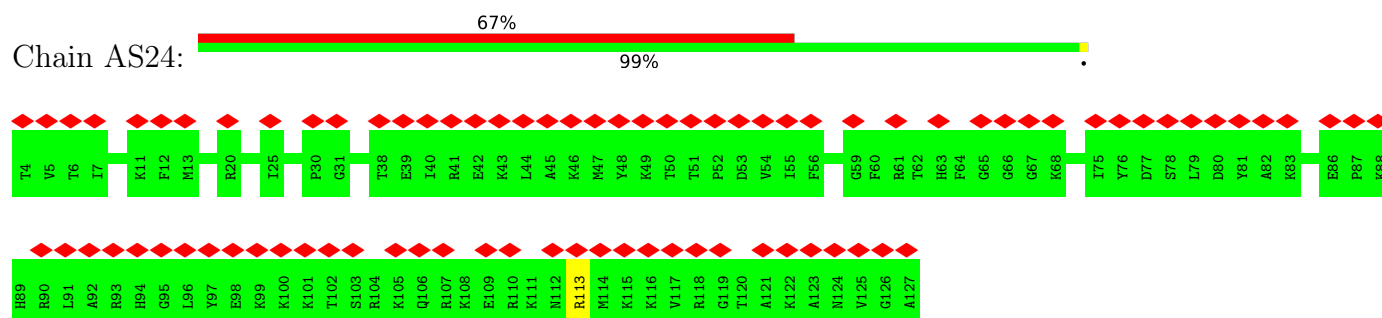


• Molecule 72: 40S ribosomal protein S23

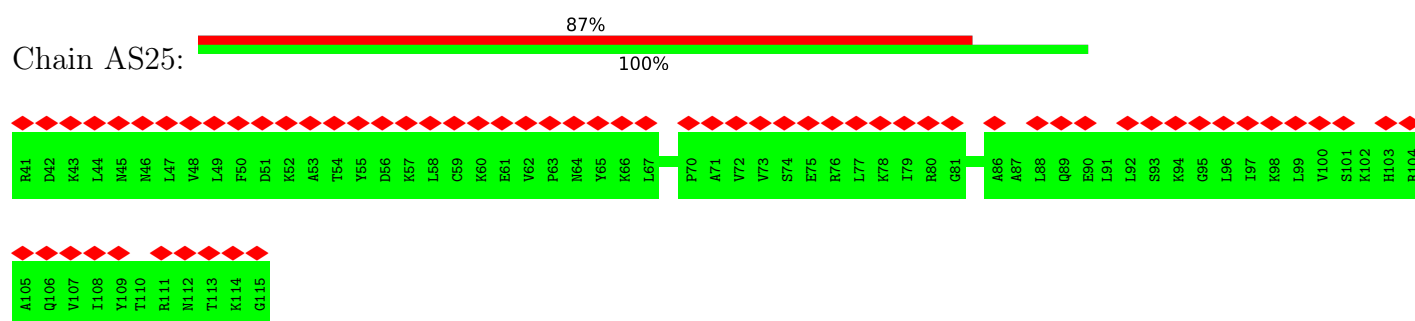




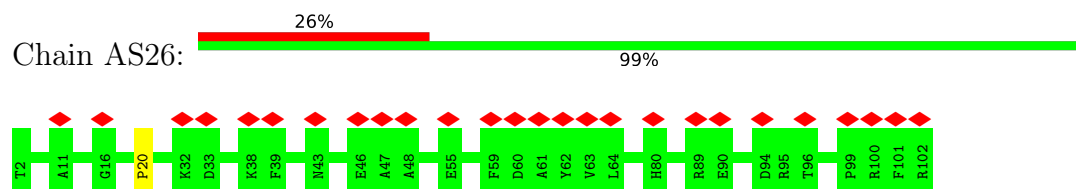
- Molecule 73: 40S ribosomal protein S24



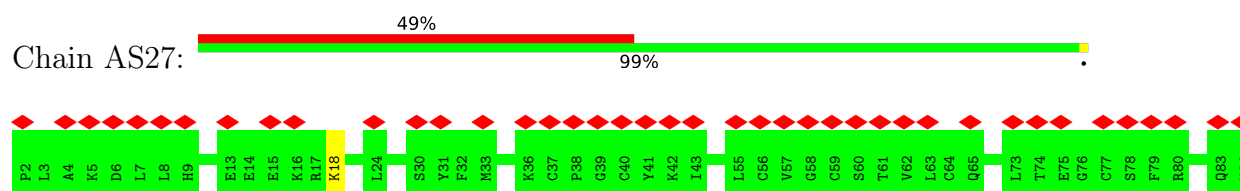
- Molecule 74: 40S ribosomal protein S25



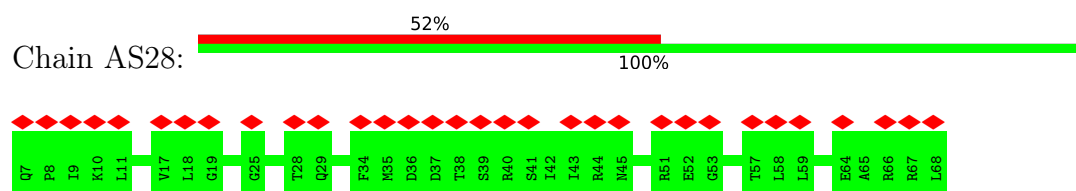
- Molecule 75: eS26



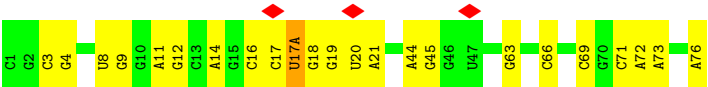
- Molecule 76: 40S ribosomal protein S27



- Molecule 77: 40S ribosomal protein S28



- Molecule 78: 40S ribosomal protein S29



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.

The worst 5 of 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

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

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Mol	Chain	Res	Type	Group
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
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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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.

The worst 5 of 17 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A5S:28:C:H1'	4:A5S:54:A:H61	1.57	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

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AL02	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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 ⓘ

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	AS02	68	ARG
76	AS27	18	LYS
55	AS06	31	ARG
73	AS24	113	ARG
80	AS31	104	LYS

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

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
84	PTRN	74/77 (96%)	21 (28%)	1 (1%)
All	All	5669/5710 (99%)	1225 (21%)	82 (1%)

5 of 1225 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A18S	2	A
1	A18S	3	C
1	A18S	4	C
1	A18S	17	C
1	A18S	20	G

5 of 82 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A25S	3625	G
2	A25S	4719	G
2	A25S	3876	A
2	A25S	4232	U
2	A25S	4947	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
32	AL29	1
47	ALP0	1

The worst 5 of 28 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

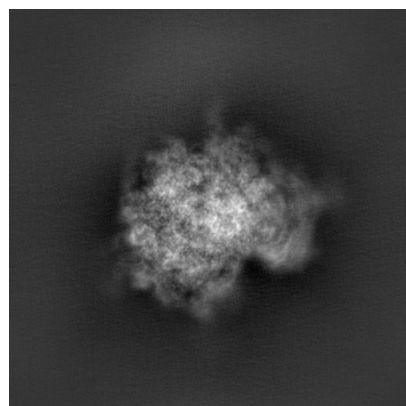
6 Map visualisation [i](#)

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.

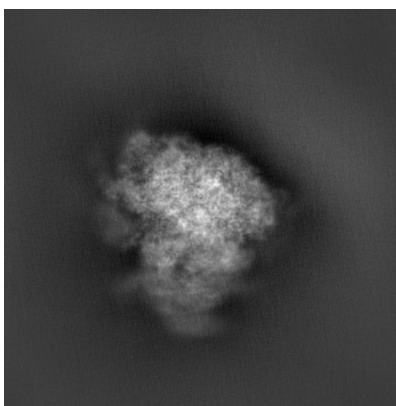
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

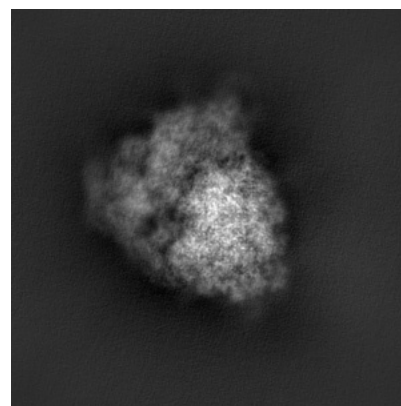
6.1.1 Primary map



X

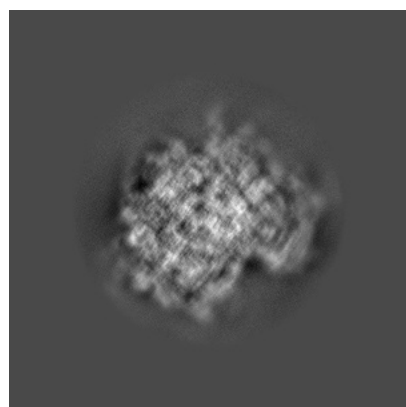


Y

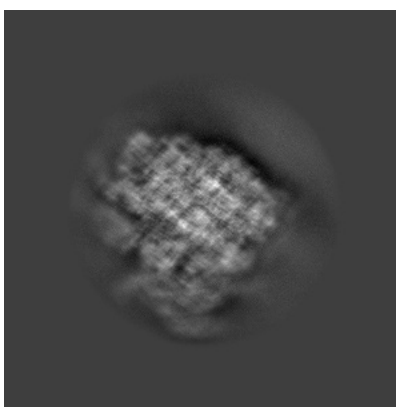


Z

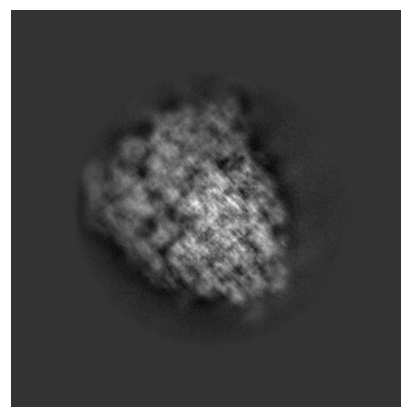
6.1.2 Raw map



X



Y

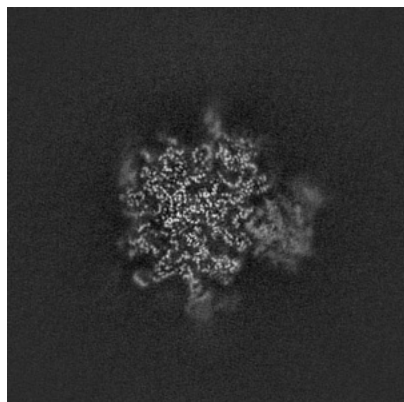


Z

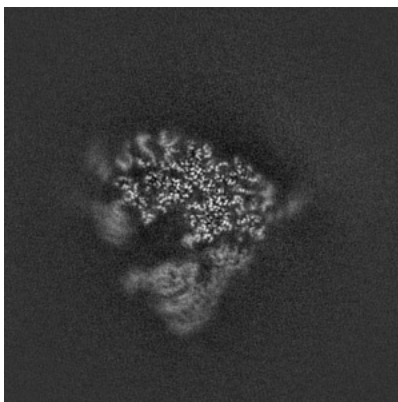
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

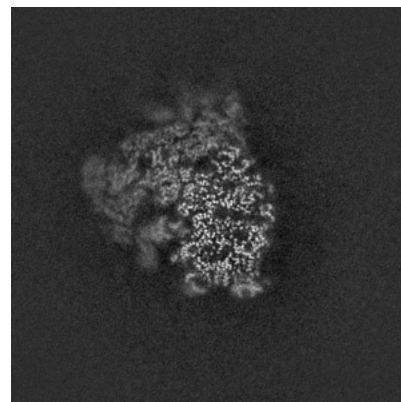
6.2.1 Primary map



X Index: 304

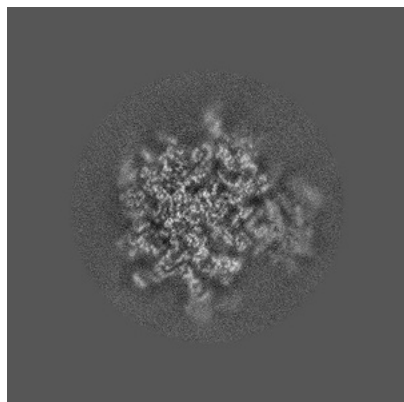


Y Index: 304

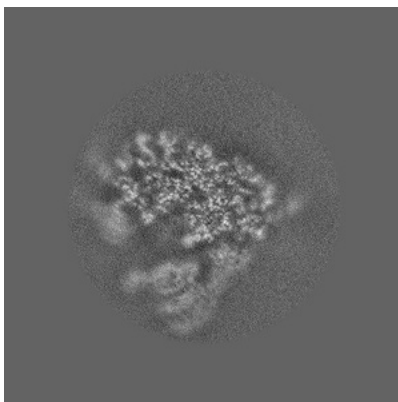


Z Index: 304

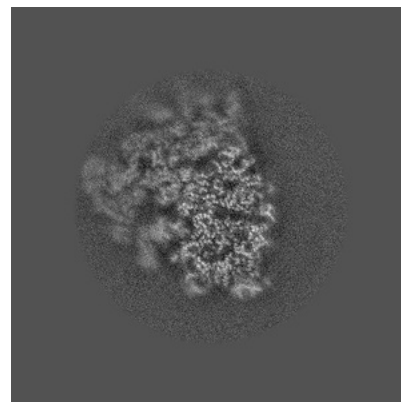
6.2.2 Raw map



X Index: 304



Y Index: 304

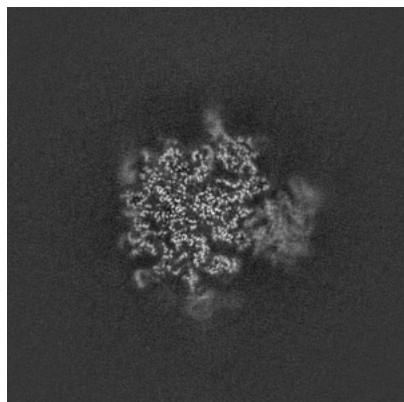


Z Index: 304

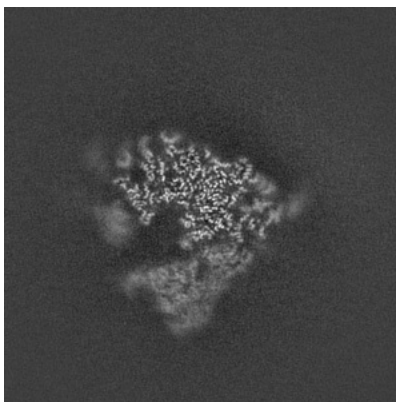
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

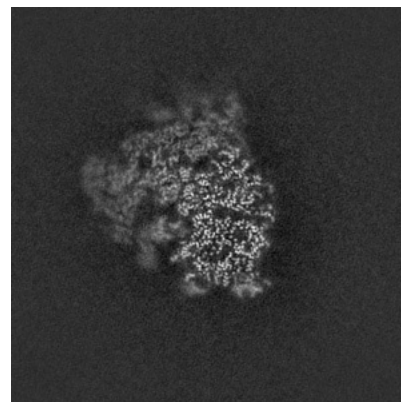
6.3.1 Primary map



X Index: 301

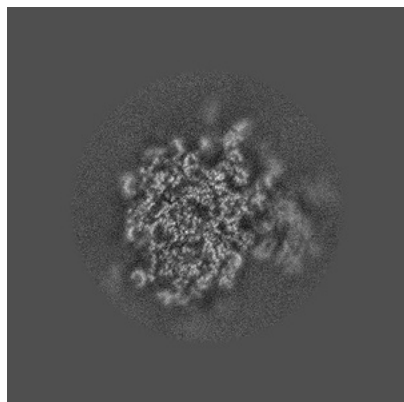


Y Index: 309

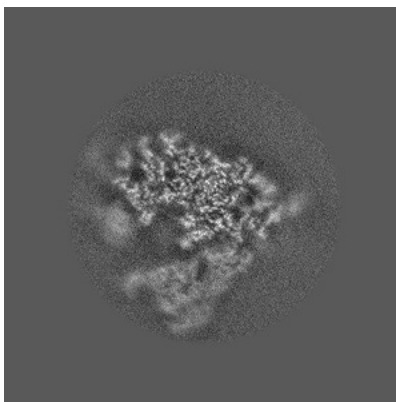


Z Index: 303

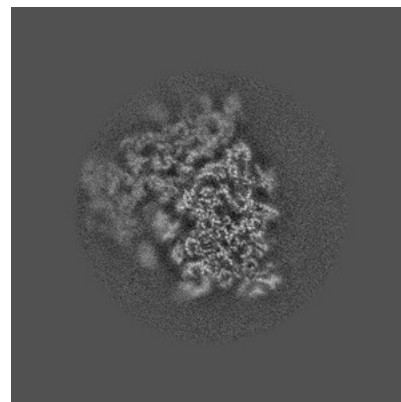
6.3.2 Raw map



X Index: 319



Y Index: 309

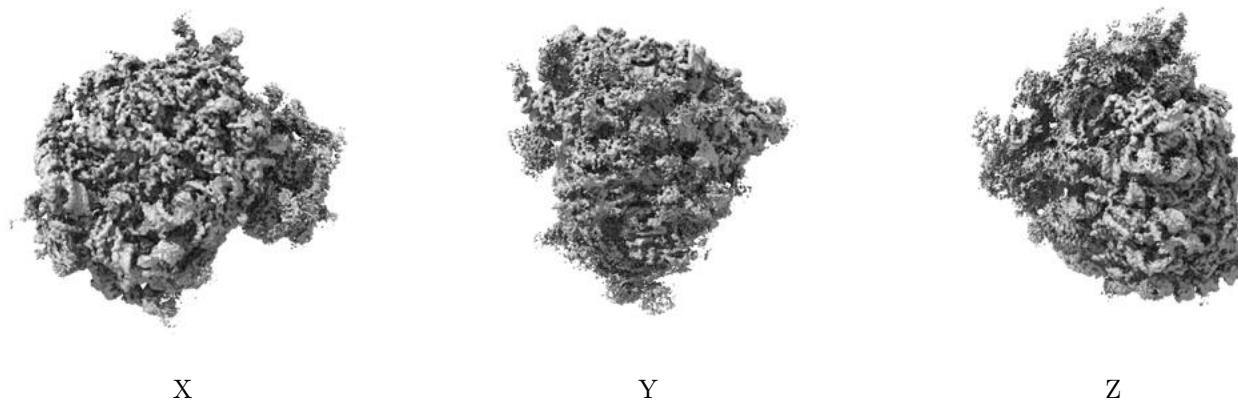


Z Index: 295

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

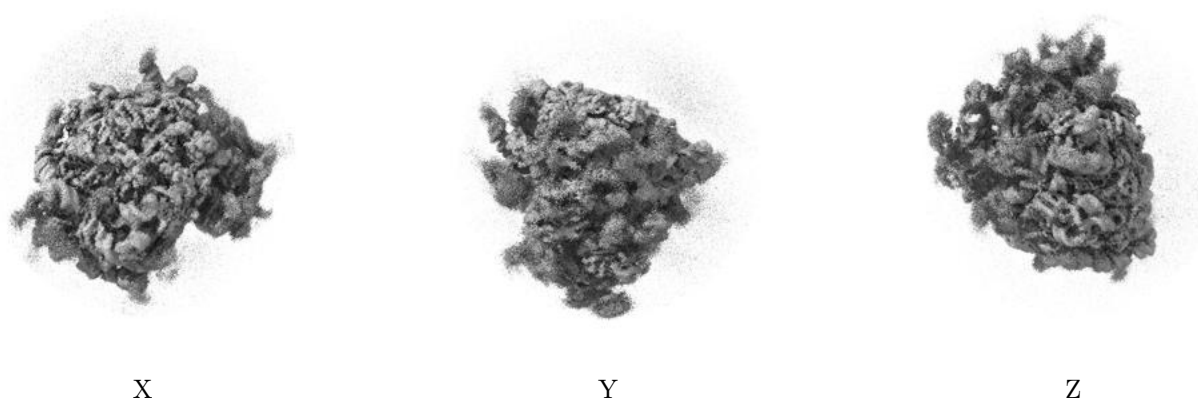
6.4 Orthogonal surface views [i](#)

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.

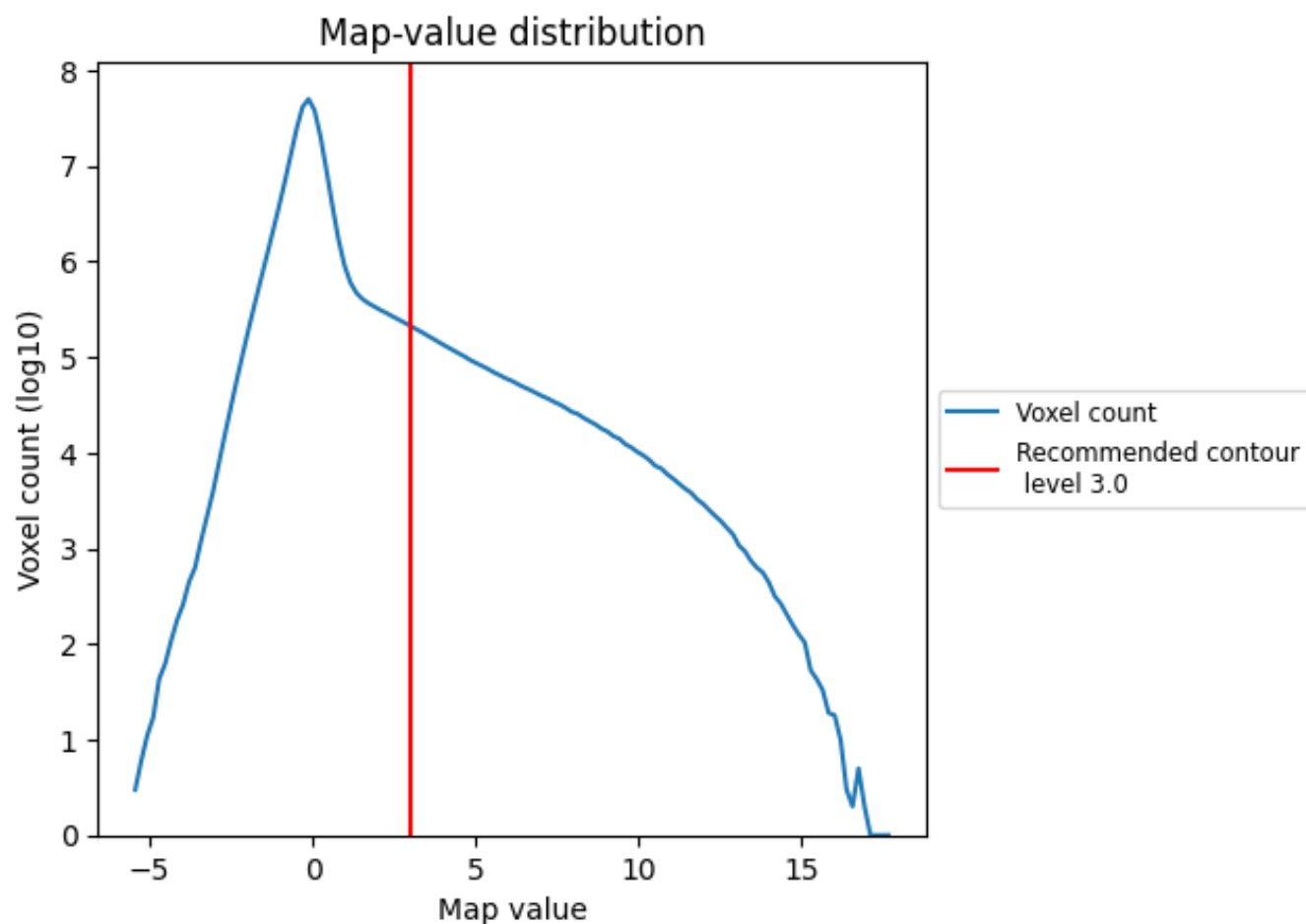
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

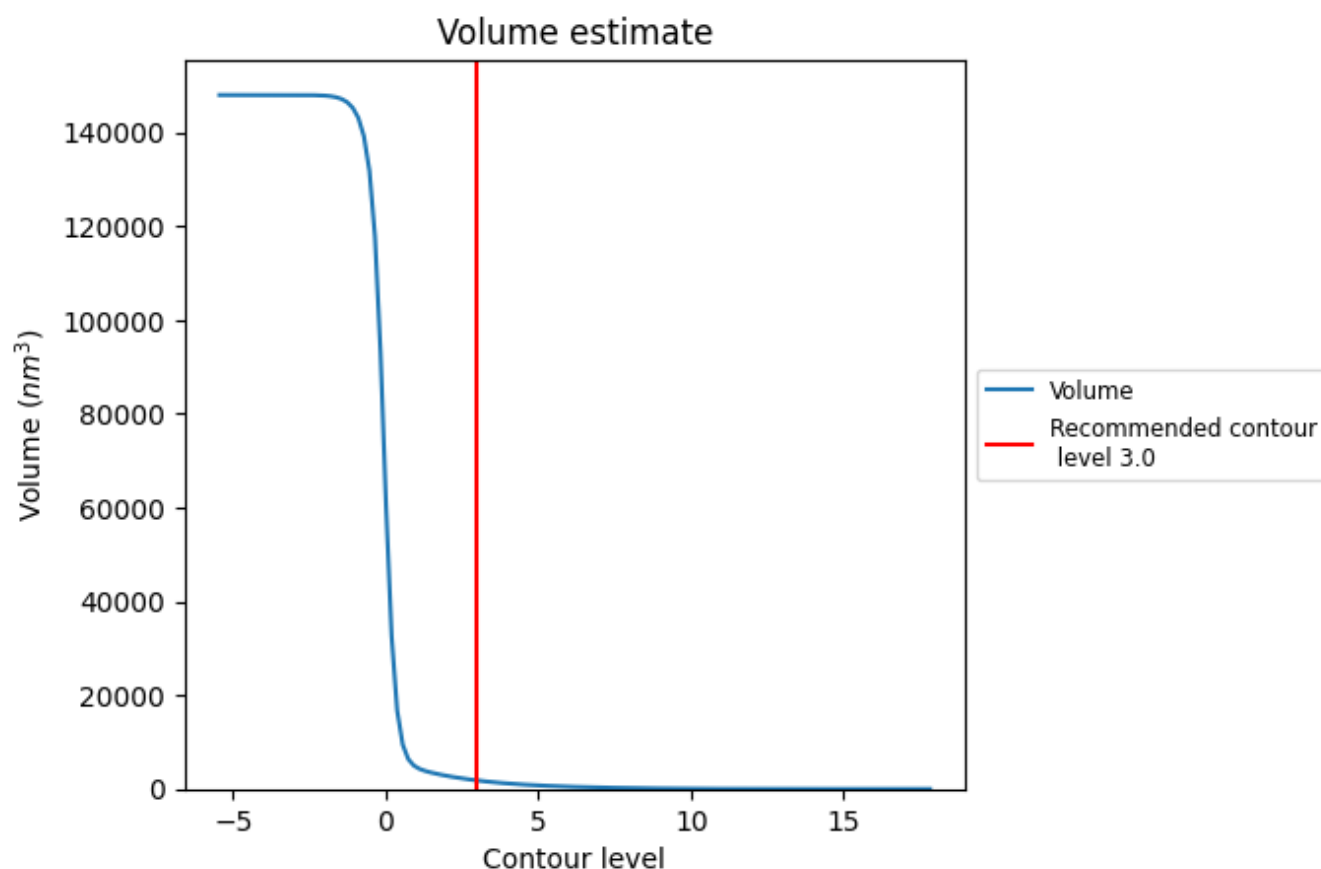
This section contains the results of statistical analysis of the map.

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.

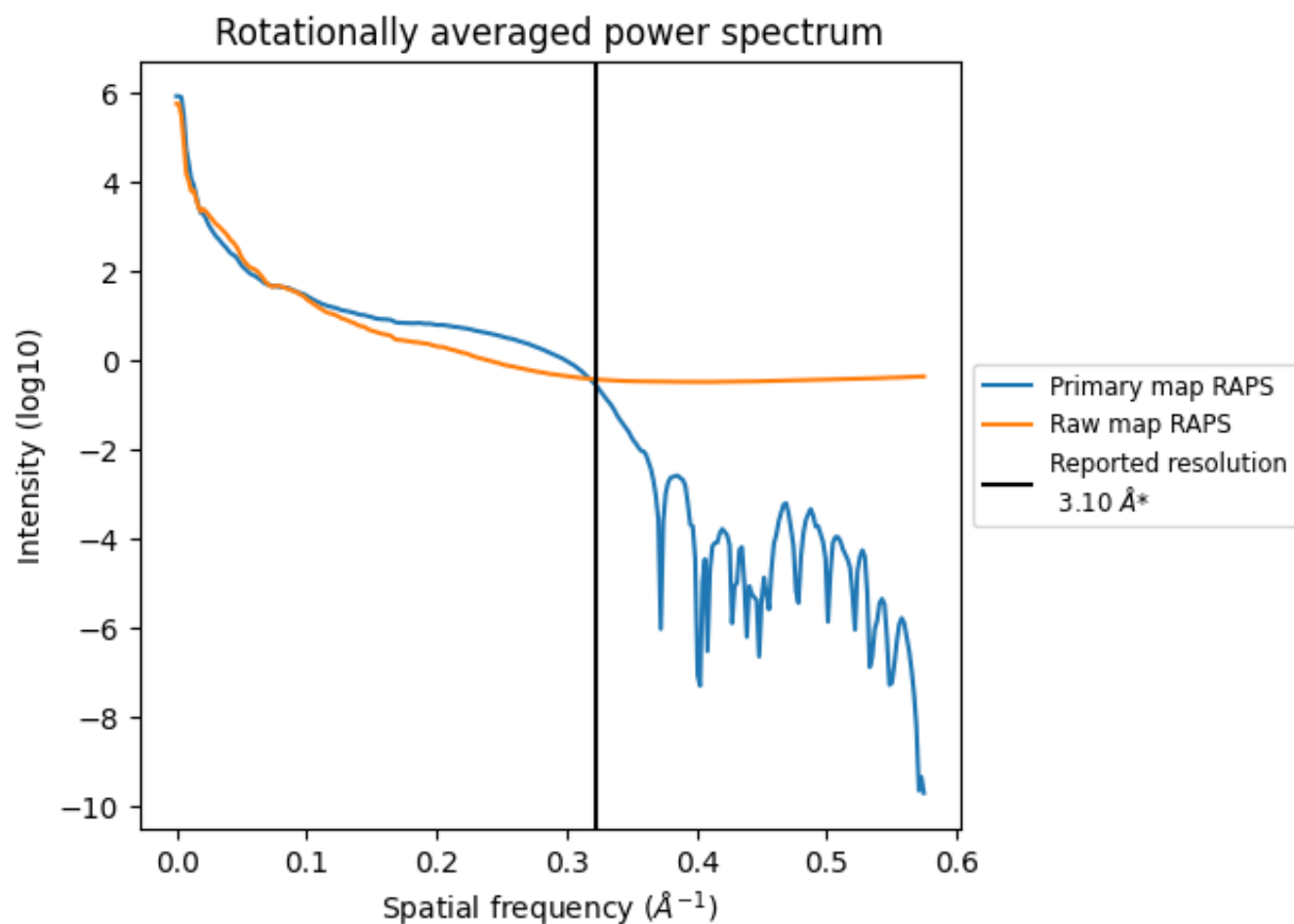
7.2 Volume estimate [i](#)



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 ⓘ

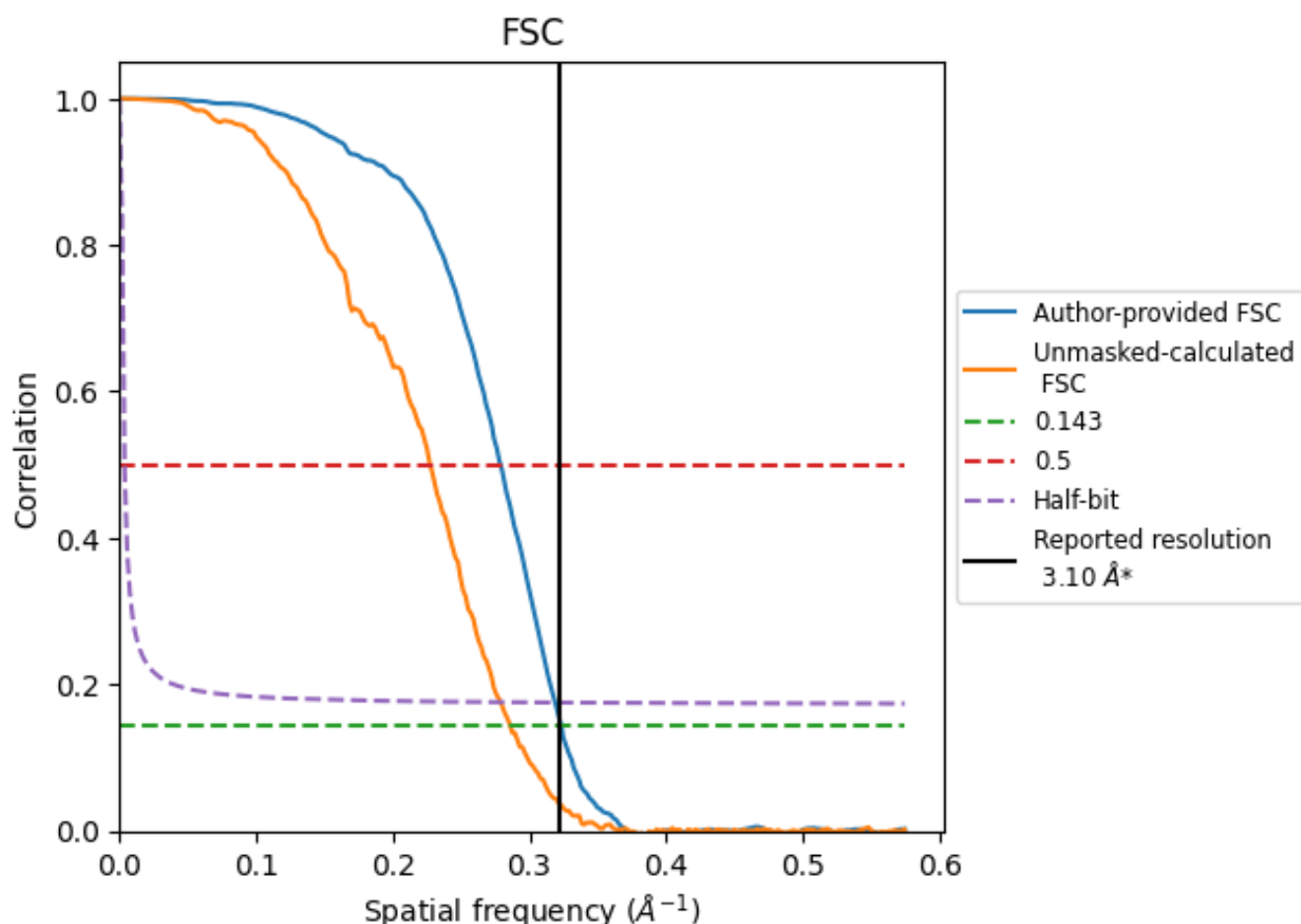


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 \AA^{-1}

8.2 Resolution estimates [i](#)

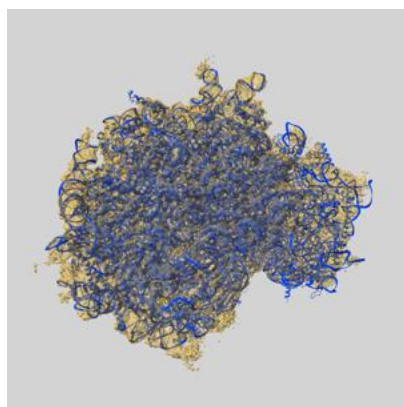
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.59	3.14
Unmasked-calculated*	3.50	4.40	3.59

*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 %

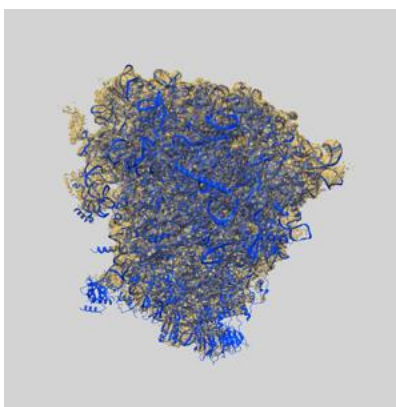
9 Map-model fit [i](#)

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](#).

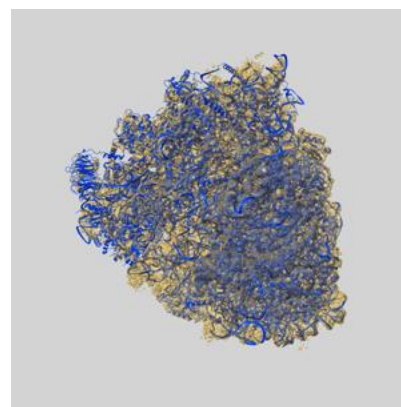
9.1 Map-model overlay [i](#)



X



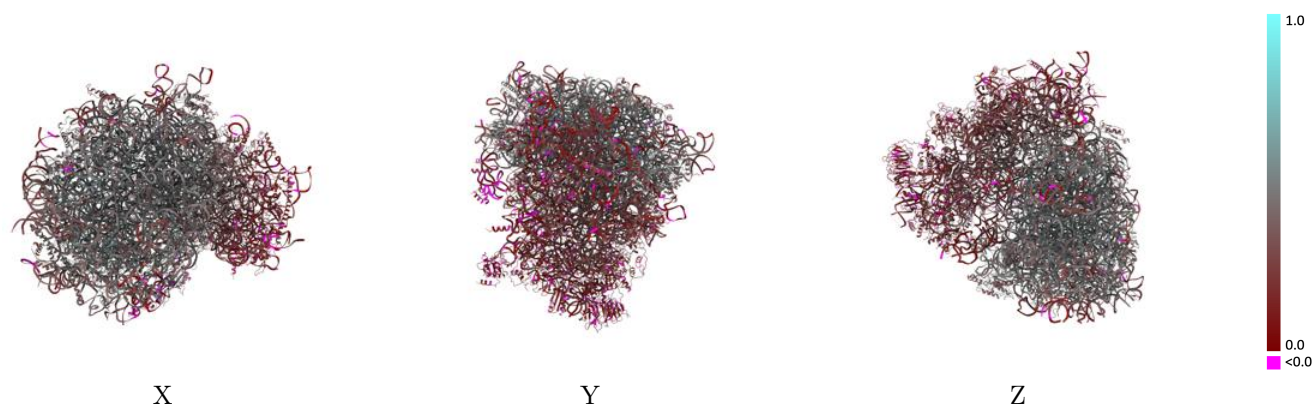
Y



Z

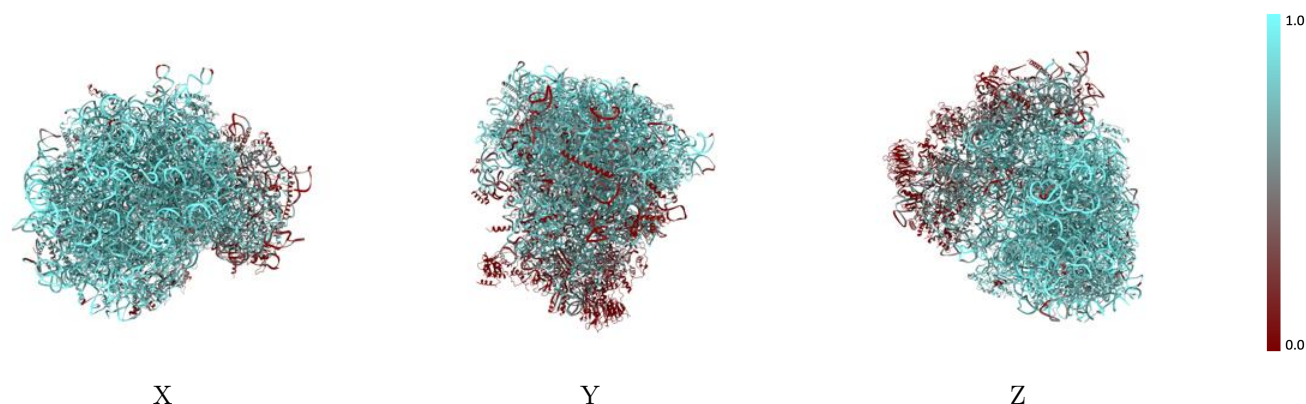
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



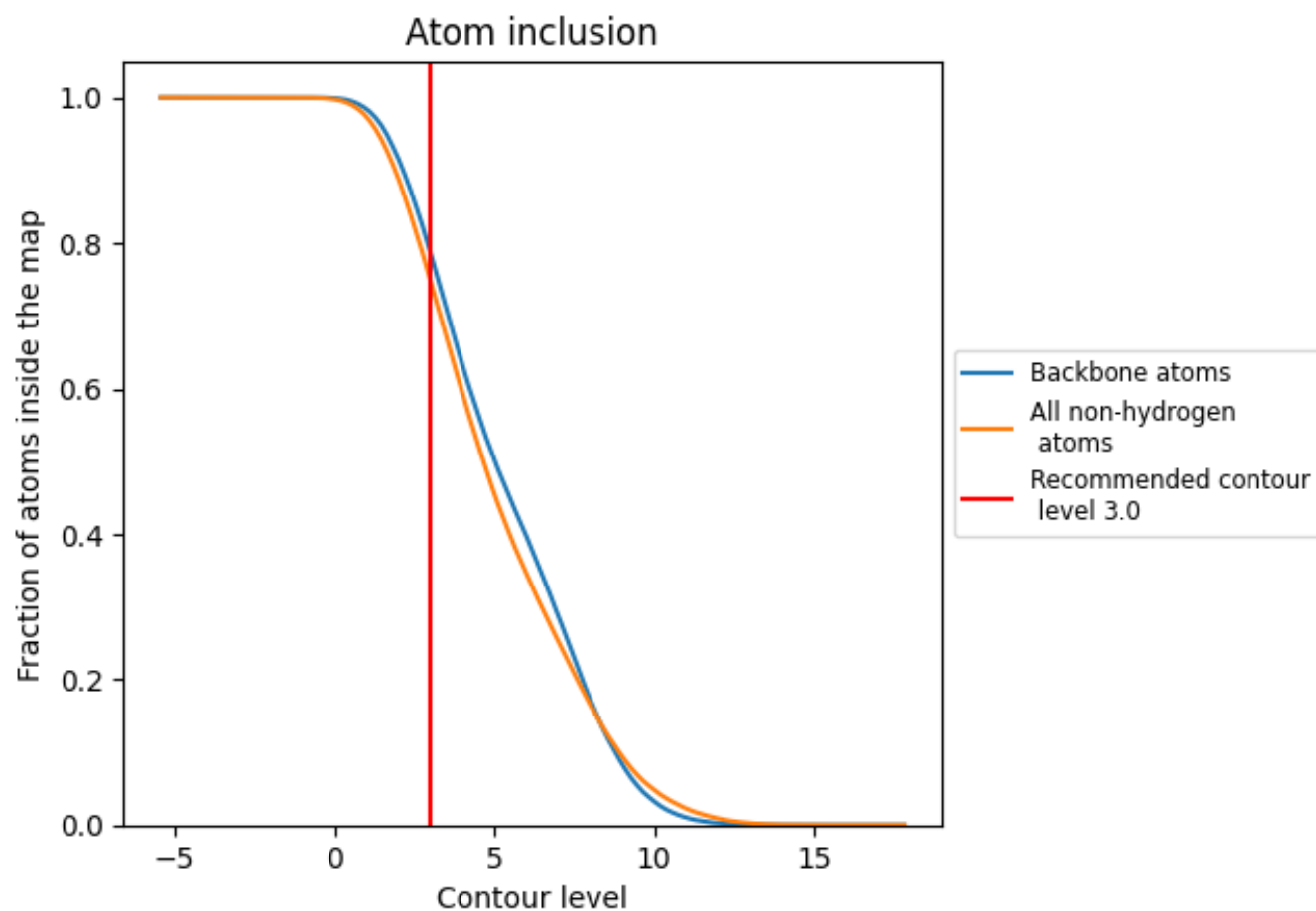
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



















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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

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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