



wwPDB EM Validation Summary Report ⓘ

Feb 11, 2025 – 12:16 AM EST

PDB ID : 8UTI
EMDB ID : EMD-42540
Title : Eukaryotic 80S ribosome with Reh1 and A/P site tRNA
Authors : Yelland, J.N.; Taylor, D.W.; Johnson, A.W.
Deposited on : 2023-10-31
Resolution : 3.13 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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

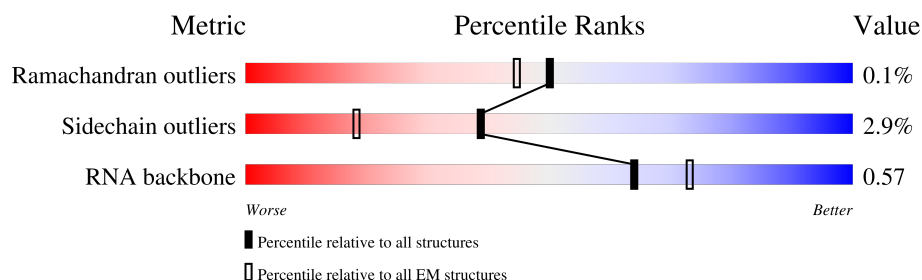
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.13 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.



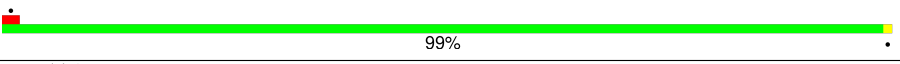
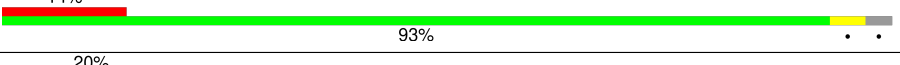
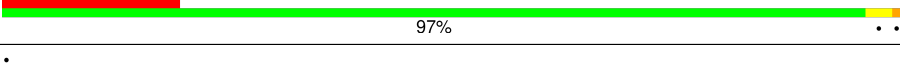
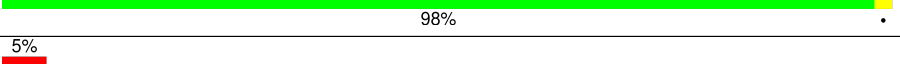
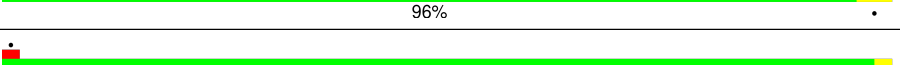
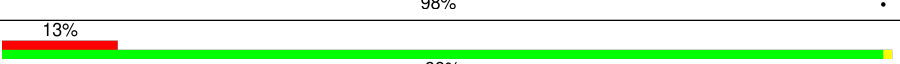
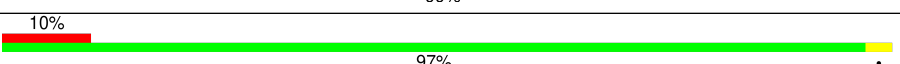
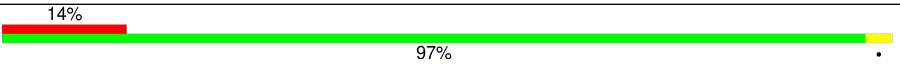
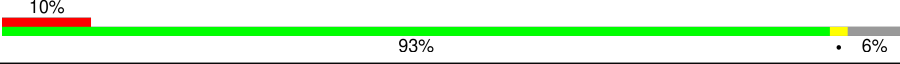
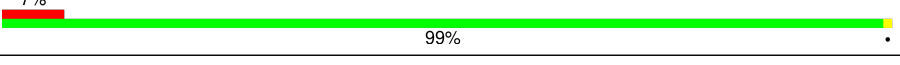
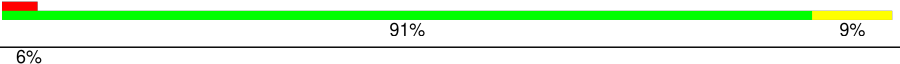
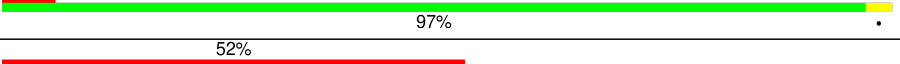
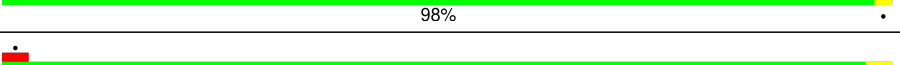
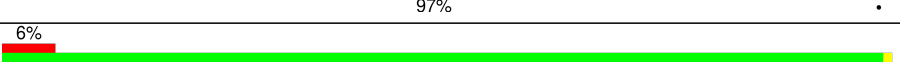
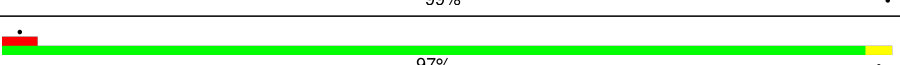
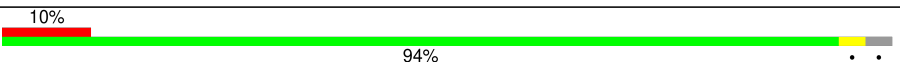
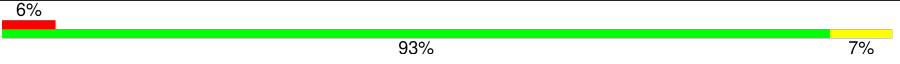
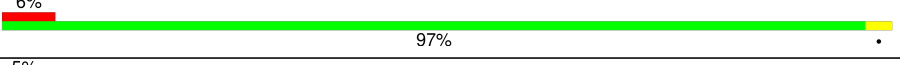
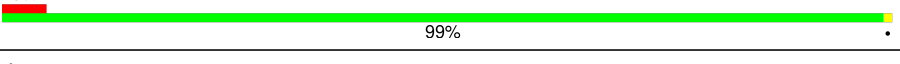
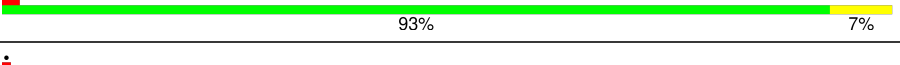
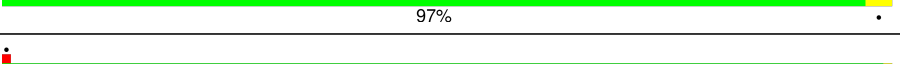
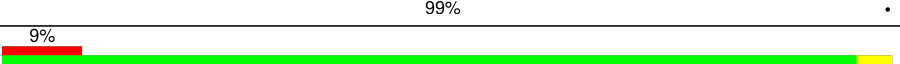
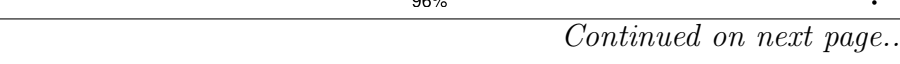


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A	3394	
2	B	121	
3	C	158	
4	D	10	
5	m	76	
6	n	75	
7	z	588	
8	E	1800	

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Mol	Chain	Length	Quality of chain
9	SP	206	
10	SQ	232	
11	SE	117	
12	SR	216	
13	SA	222	
14	SS	258	
15	SB	206	
16	ST	228	
17	SU	184	
18	SV	198	
19	SW	184	
20	SC	92	
21	SX	142	
22	SD	121	
23	SY	150	
24	SZ	127	
25	SF	141	
26	SG	125	
27	SH	145	
28	SI	143	
29	SJ	100	
30	Sa	87	
31	Sb	129	
32	Sc	144	
33	Sd	134	

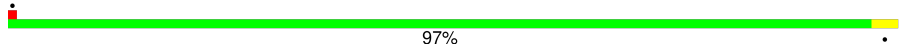
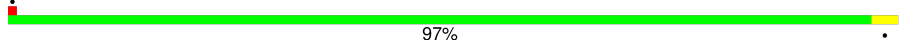
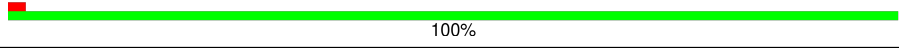
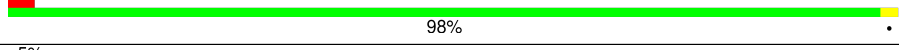
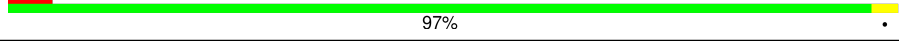
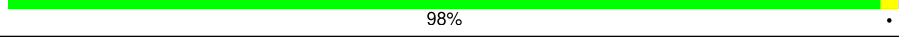
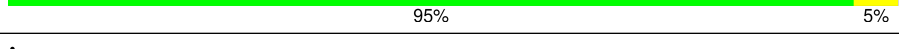
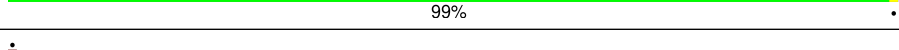
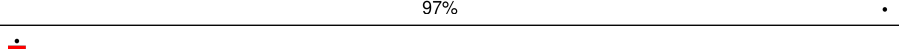
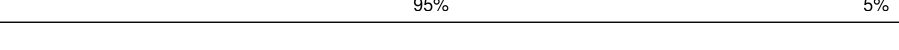
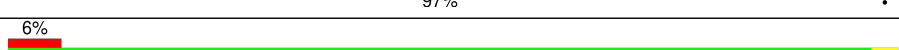
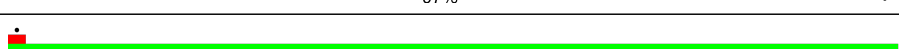

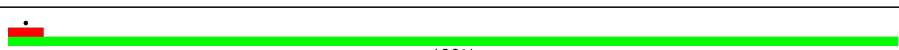
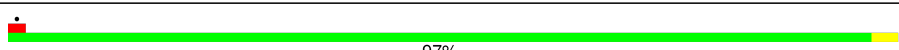
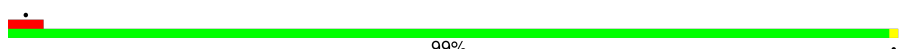

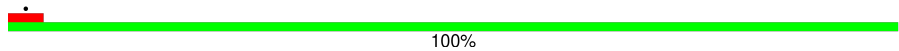

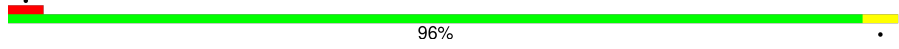
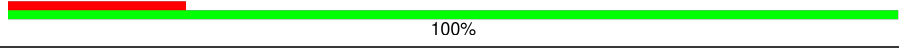
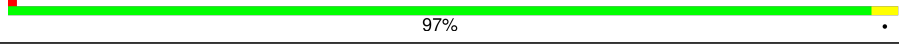
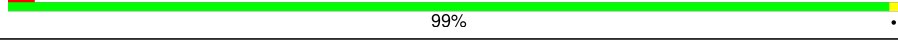

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Mol	Chain	Length	Quality of chain
34	Se	97	 5% 96%
35	Sf	81	 10% 98%
36	SM	53	 100%
37	Sg	57	 12% 100%
38	SN	73	 51% 99%
39	SO	312	 15% 96%
40	SL	63	 22% 97%
41	AA	108	 19% 85% 12%
42	LD	251	 98%
43	LE	386	 97%
44	LF	361	 96%
45	LG	294	 100%
46	LH	175	 93% 5%
47	LI	222	 97%
48	LJ	233	 6% 98%
49	LK	191	 96%
50	LL	218	 96%
51	LM	169	 5% 96%
52	LN	193	 98%
53	LO	136	 99%
54	LP	203	 98%
55	LQ	197	 98%
56	LR	183	 99%
57	LS	185	 97%
58	LT	188	 5% 98%

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Mol	Chain	Length	Quality of chain
59	LU	171	 97%
60	LV	159	 97%
61	LW	100	 100%
62	LX	136	 98%
63	LY	65	 5% 97%
64	LZ	121	 98%
65	La	125	 95% 5%
66	Lb	135	 99%
67	Lc	148	 97%
68	Ld	58	 95% 5%
69	Le	96	 97%
70	Lf	109	 6% 97%
71	Lg	127	 100%
72	Lh	106	 99%
73	Li	112	 100%
74	Lj	119	 97%
75	Lk	99	 99%
76	Ll	81	 96%
77	Lm	77	 100%
78	Ln	50	 100%
79	Lo	52	 96%
80	Lp	25	 20% 100%
81	Lq	103	 97%
82	Lr	91	 99%

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 196410 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3044	Total	C	N	O	P	0	0
			65120	29088	11753	21235	3044		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	493	U	G	conflict	GB 2313943860

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a RNA chain called Messenger RNA (5'-R(P*AP*AP*UP*AP*AP*UP*GP*AP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	10	Total	C	N	O	P	0	0
			218	98	44	66	10		

- Molecule 5 is a RNA chain called A site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	m	76	Total	C	N	O	P	0	0
			1611	721	281	534	75		

- Molecule 6 is a RNA chain called P site initiator tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	n	75	Total	C	N	O	P	0	0
			1607	716	297	519	75		

- Molecule 7 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1 (N-terminal 3xFLAG tag).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	z	57	Total	C	N	O	S	0	0
			480	295	96	86	3		

- Molecule 8 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	1597	Total	C	N	O	P	0	0
			34053	15224	6049	11183	1597		

- Molecule 9 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SP	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 10 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SQ	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 11 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SE	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 12 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SR	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 13 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SA	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 14 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SS	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 15 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SB	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 16 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	ST	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 17 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	SU	184	Total	C	N	O	0	0
			1473	946	263	264		

- Molecule 18 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SV	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 19 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SW	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 20 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SC	92	Total	C	N	O	S	0	0
			754	489	122	141	2		

- Molecule 21 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SX	142	Total	C	N	O	S	0	0
			1142	733	217	189	3		

- Molecule 22 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SD	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 23 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SY	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 24 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SZ	127	Total	C	N	O	S	0	0
			923	568	185	167	3		

- Molecule 25 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	SF	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 26 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SG	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

- Molecule 27 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SH	145	Total	C	N	O	S	0	0
			1188	741	237	208	2		

- Molecule 28 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SI	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 29 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SJ	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 30 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Sa	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 31 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Sb	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 32 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sc	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 33 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Sd	134	Total	C	N	O	0	0
			1032	651	195	186		

- Molecule 34 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Se	97	Total	C	N	O	S	0	0
			765	473	160	127	5		

- Molecule 35 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Sf	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 36 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	SM	53	Total	C	N	O	S	0	0
			443	275	92	72	4		

- Molecule 37 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Sg	57	Total	C	N	O	S	0	0
			451	284	93	73	1		

- Molecule 38 is a protein called 40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	SN	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SN	97	ALA	LYS	conflict	UNP A0A6A5PU37

- Molecule 39 is a protein called 40S ribosomal protein ASC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	SO	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	SL	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 41 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AA	95	Total	C	N	O	S	0	0
			737	466	139	132			

- Molecule 42 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LD	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 43 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LE	386	Total	C	N	O	S	0	0
			3079	1954	584	533	8		

- Molecule 44 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LF	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 45 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LG	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 46 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LH	167	Total	C	N	O	S	0	0
			1307	843	234	230			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	120	LYS	ASN	conflict	UNP P05739

- Molecule 47 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LI	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 48 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LJ	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 49 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LK	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 50 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LL	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 51 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LM	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 52 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LN	193	Total	C	N	O		0	0
			1543	962	315	266			

- Molecule 53 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LO	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 54 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LP	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 55 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LQ	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 56 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LR	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 57 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LS	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 58 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LT	188	Total	C	N	O		0	0
			1515	932	323	260			

- Molecule 59 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LU	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LV	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 61 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LW	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 62 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LX	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 63 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LY	65	Total	C	N	O	S	0	0
			528	339	104	84	1		

- Molecule 64 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	LZ	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 65 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	La	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 66 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Lb	135	Total	C	N	O		0	0
			1080	701	199	180			

- Molecule 67 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Lc	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 68 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ld	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 69 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Le	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 70 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Lf	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 71 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lg	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 72 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Lh	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 73 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Li	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 74 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Lj	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 75 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Lk	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 76 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ll	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 77 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Lm	77	Total	C	N	O		0	0
			612	391	115	106			

- Molecule 78 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Ln	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 79 is a protein called 60S ribosomal protein L40-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Lo	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 80 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Lp	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

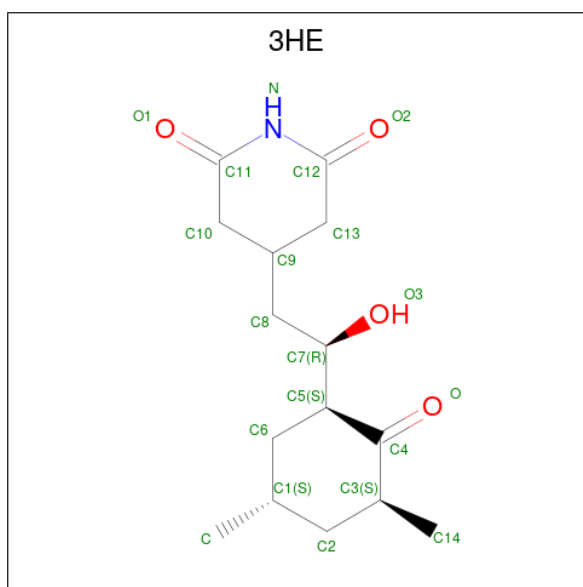
- Molecule 81 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Lq	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 82 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Lr	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 83 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (three-letter code: 3HE) (formula: C₁₅H₂₃NO₄).

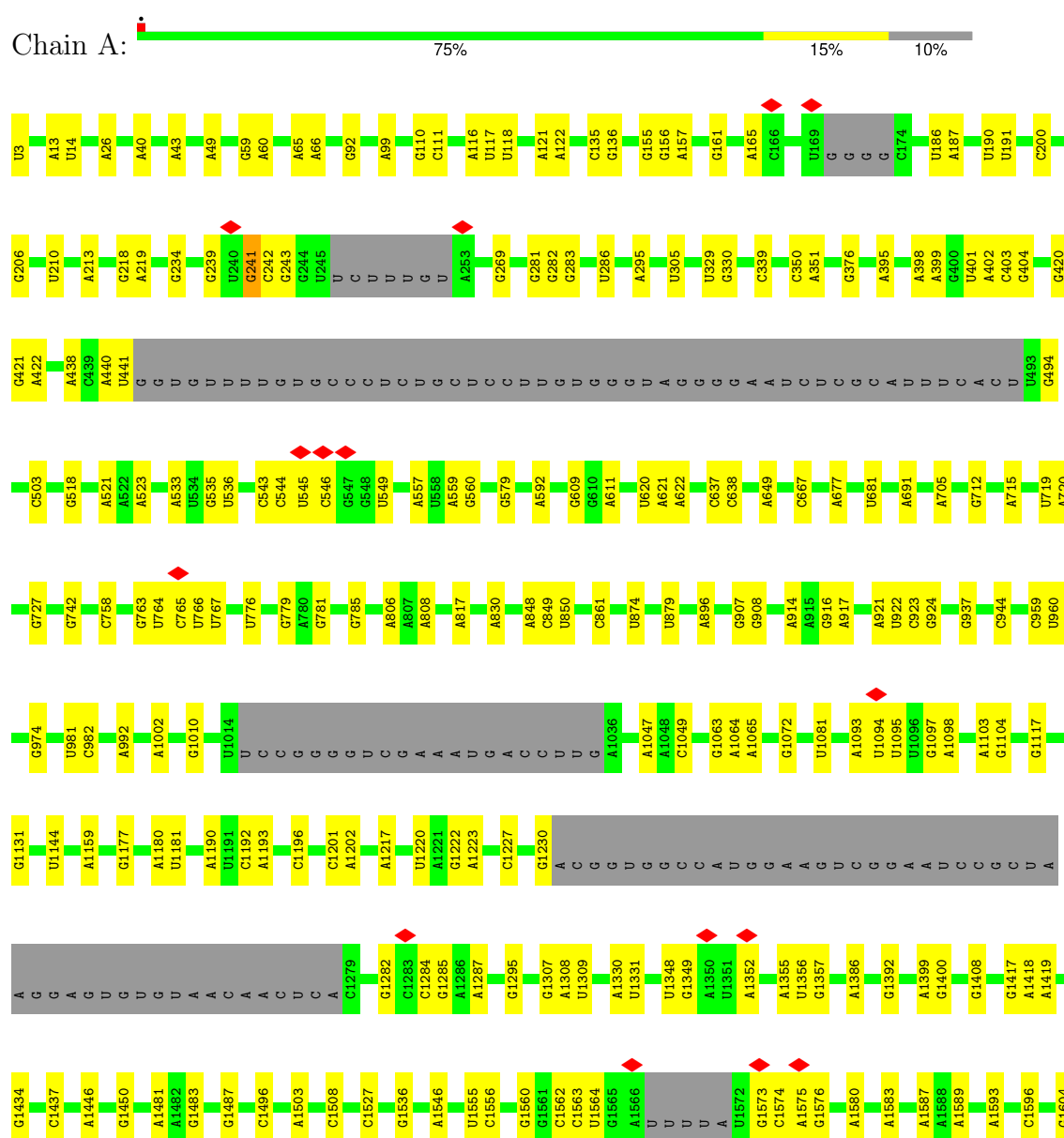


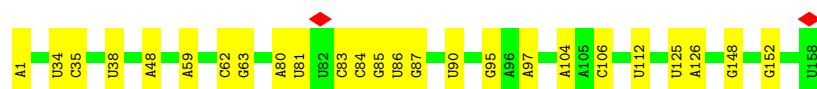
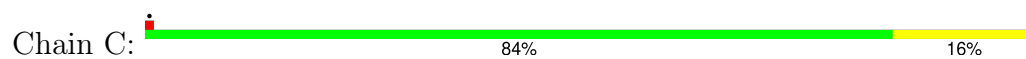
Mol	Chain	Residues	Atoms				AltConf
83	A	1	Total	C	N	O	0
			20	15	1	4	

3 Residue-property plots

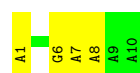
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S rRNA





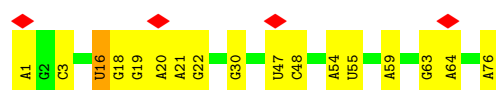
- Molecule 4: Messenger RNA (5'-R(P*AP*AP*UP*AP*AP*UP*GP*AP*AP*AP*A)-3')



- Molecule 5: A site tRNA



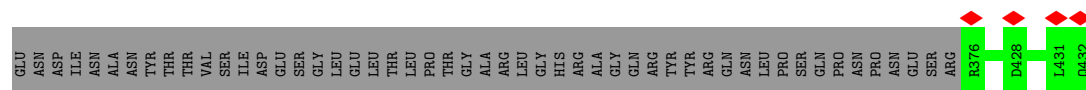
- Molecule 6: P site initiator tRNA



- Molecule 7: Cytoplasmic 60S subunit biogenesis factor REH1 (N-terminal 3xFLAG tag)

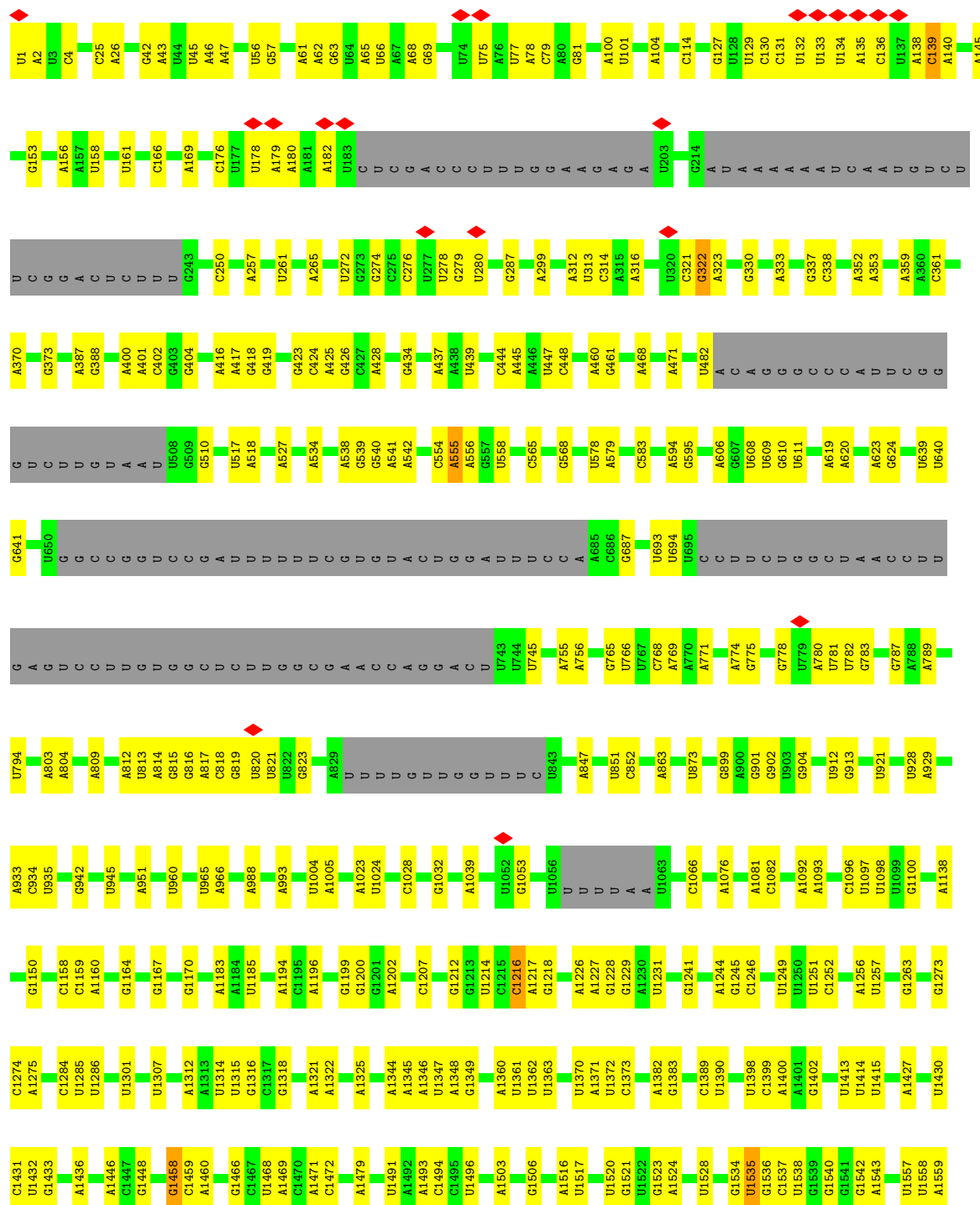


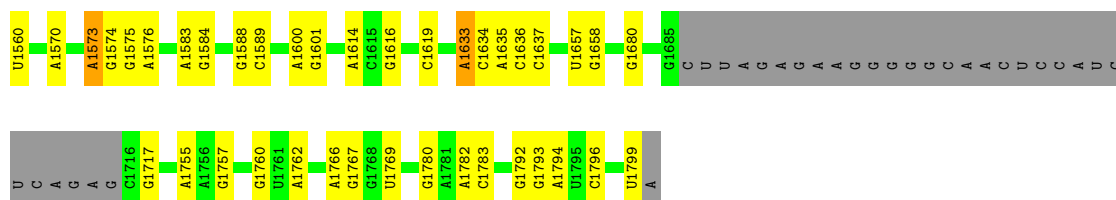
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• Molecule 8: 18S rRNA

Chain E: 68% 20% 11%





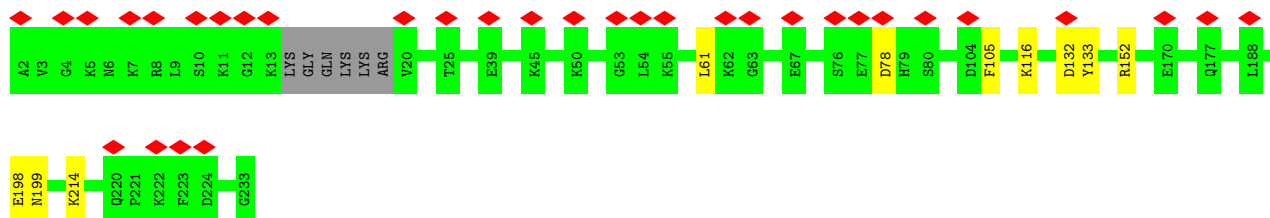
- Molecule 9: 40S ribosomal protein S0-A

Chain SP: 99%



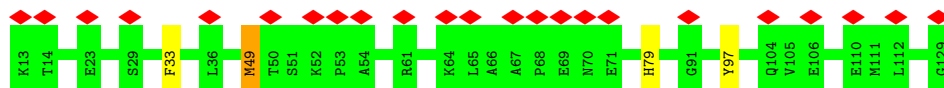
- Molecule 10: 40S ribosomal protein S1-A

Chain SQ: 93%



- Molecule 11: 40S ribosomal protein S15

Chain SE: 97%



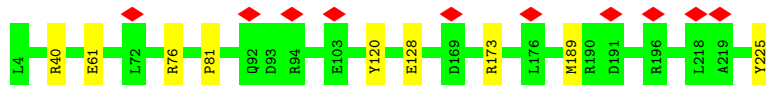
- Molecule 12: 40S ribosomal protein S2

Chain SR: 98%



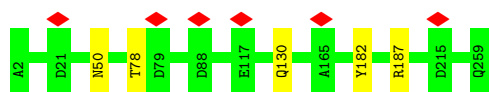
- Molecule 13: 40S ribosomal protein S3

Chain SA: 96%



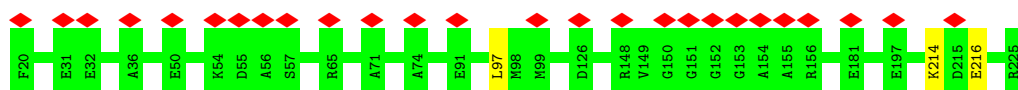
- Molecule 14: 40S ribosomal protein S4-A

Chain SS:  98%



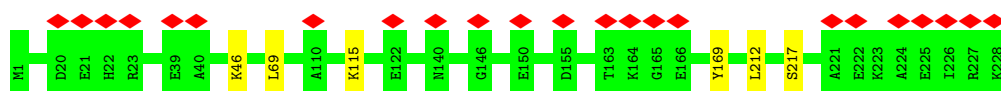
- Molecule 15: 40S ribosomal protein S5

Chain SB:  99%



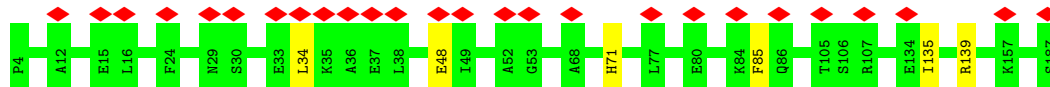
- Molecule 16: 40S ribosomal protein S6-A

Chain ST:  97%



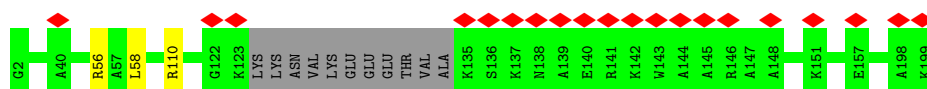
- Molecule 17: 40S ribosomal protein S7-A

Chain SU:  97%



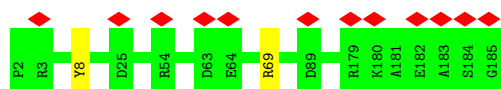
- Molecule 18: 40S ribosomal protein S8-A

Chain SV:  93% 6%



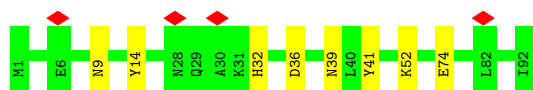
- Molecule 19: 40S ribosomal protein S9-A

Chain SW:  99%

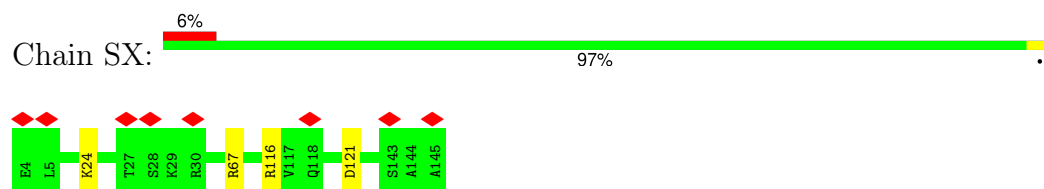


- Molecule 20: 40S ribosomal protein S10-A

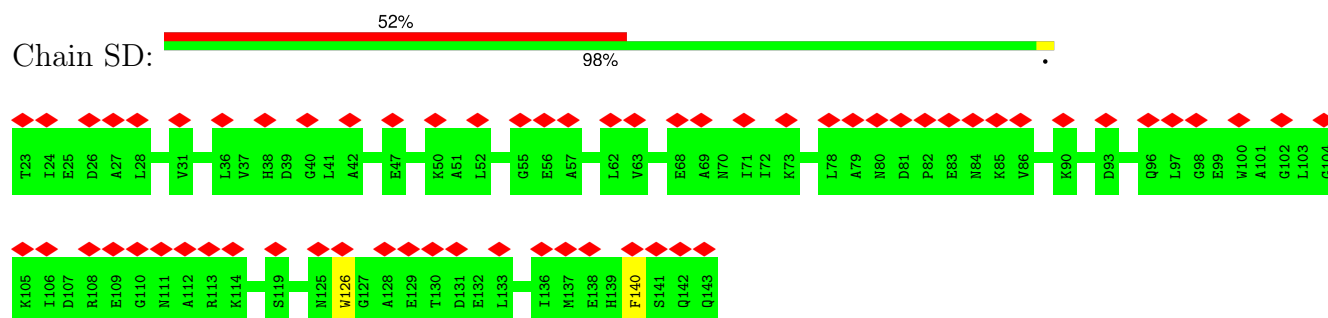
Chain SC:  91% 9%



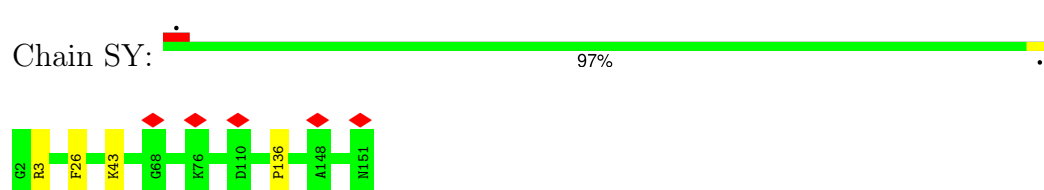
- Molecule 21: 40S ribosomal protein S11-A



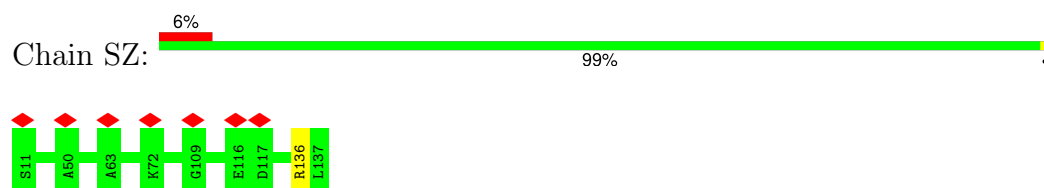
- Molecule 22: 40S ribosomal protein S12



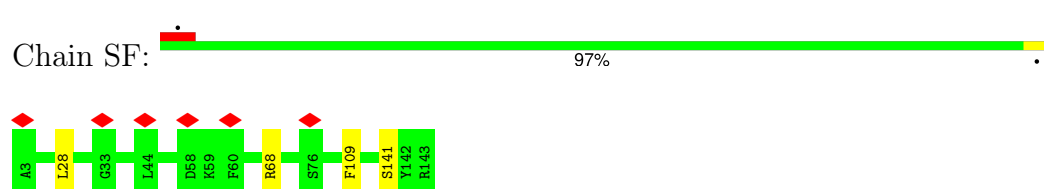
- Molecule 23: 40S ribosomal protein S13



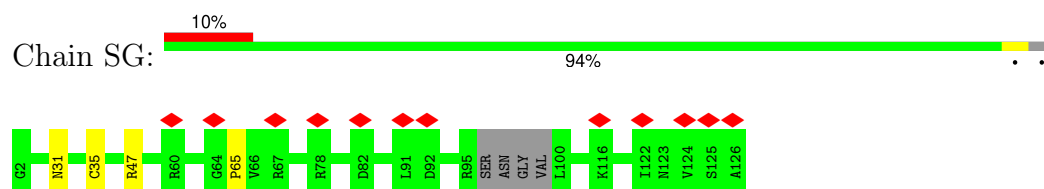
- Molecule 24: 40S ribosomal protein S14-B



- Molecule 25: 40S ribosomal protein S16-A



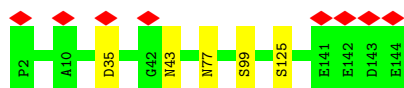
- Molecule 26: 40S ribosomal protein S17-B



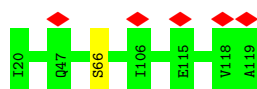
- Molecule 27: 40S ribosomal protein S18-A



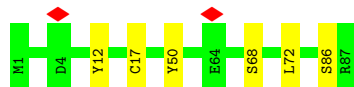
- Molecule 28: 40S ribosomal protein S19-A



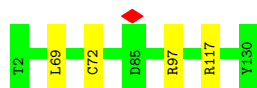
- Molecule 29: 40S ribosomal protein S20



- Molecule 30: 40S ribosomal protein S21-A



- Molecule 31: 40S ribosomal protein S22-A



- Molecule 32: 40S ribosomal protein S23-A



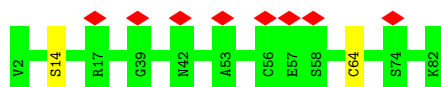
- Molecule 33: 40S ribosomal protein S24-A



- Molecule 34: 40S ribosomal protein S26-B



- Molecule 35: 40S ribosomal protein S27-A

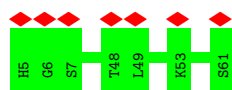


- Molecule 36: 40S ribosomal protein S29-A

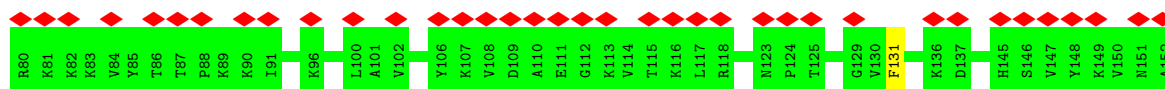


There are no outlier residues recorded for this chain.

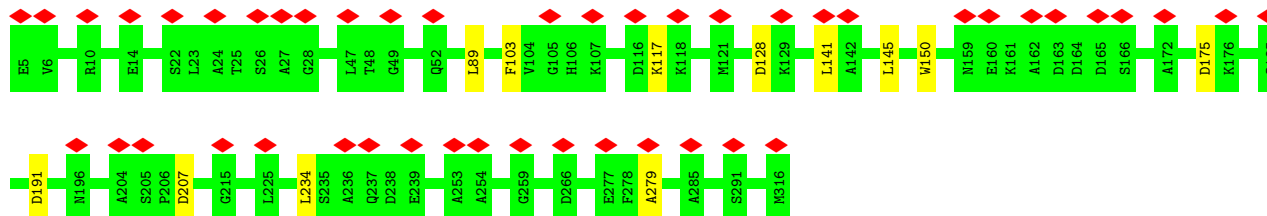
- Molecule 37: 40S ribosomal protein S30-A



- Molecule 38: 40S ribosomal protein S31

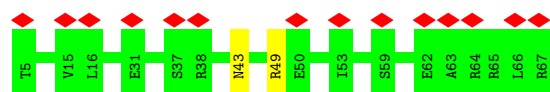


- Molecule 39: 40S ribosomal protein ASC1

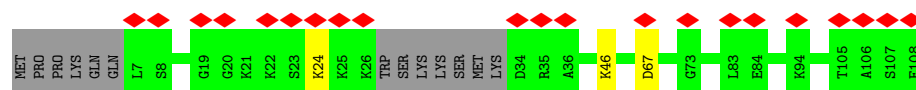
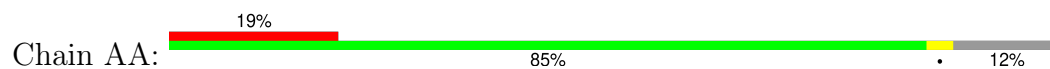


- Molecule 40: 40S ribosomal protein S28-A





- Molecule 41: 40S ribosomal protein S25-A



- Molecule 42: 60S ribosomal protein L2-A



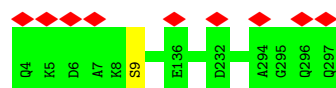
- Molecule 43: 60S ribosomal protein L3



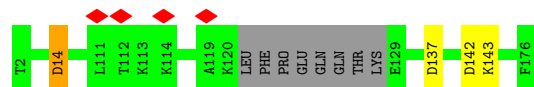
- Molecule 44: 60S ribosomal protein L4-A



- Molecule 45: 60S ribosomal protein L5

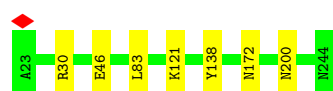


- Molecule 46: 60S ribosomal protein L6-B



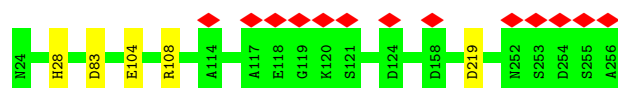
- Molecule 47: 60S ribosomal protein L7-A

Chain LI:  97%



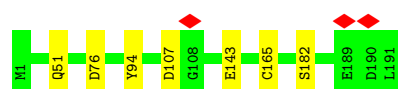
- Molecule 48: 60S ribosomal protein L8-A

Chain LJ:  98%



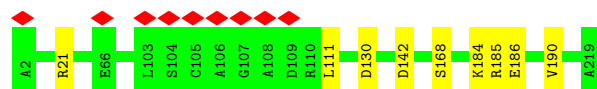
- Molecule 49: 60S ribosomal protein L9-A

Chain LK:  96%



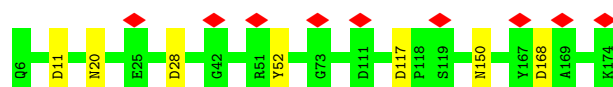
- Molecule 50: 60S ribosomal protein L10

Chain LL:  96%



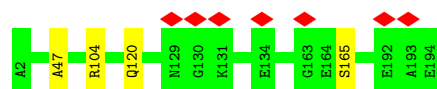
- Molecule 51: 60S ribosomal protein L11-B

Chain LM:  96%



- Molecule 52: 60S ribosomal protein L13-A

Chain LN:  98%



- Molecule 53: 60S ribosomal protein L14-A

Chain LO:  99%



- Molecule 54: 60S ribosomal protein L15-A

Chain LP:  98%



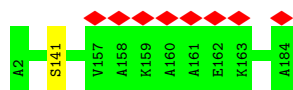
- Molecule 55: 60S ribosomal protein L16-A

Chain LQ:  98%



- Molecule 56: 60S ribosomal protein L17-A

Chain LR:  99%



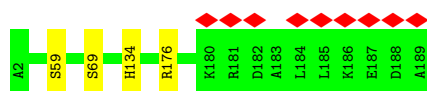
- Molecule 57: 60S ribosomal protein L18-A

Chain LS:  97%



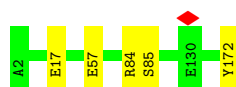
- Molecule 58: 60S ribosomal protein L19-A

Chain LT:  5% 98%



- Molecule 59: 60S ribosomal protein L20-A

Chain LU:  97%



- Molecule 60: 60S ribosomal protein L21-A

Chain LV:  97%



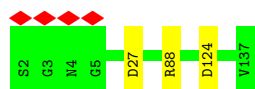
- Molecule 61: 60S ribosomal protein L22-A

Chain LW: 100%



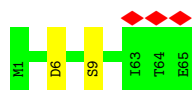
- Molecule 62: 60S ribosomal protein L23-A

Chain LX: 98%



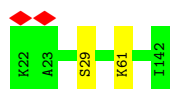
- Molecule 63: 60S ribosomal protein L24-A

Chain LY: 97%



- Molecule 64: 60S ribosomal protein L25

Chain LZ: 98%



- Molecule 65: 60S ribosomal protein L26-A

Chain La: 95%



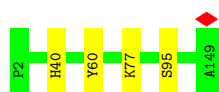
- Molecule 66: 60S ribosomal protein L27-A

Chain Lb: 99%



- Molecule 67: 60S ribosomal protein L28

Chain Lc:  97%



- Molecule 68: 60S ribosomal protein L29

Chain Ld:  95%



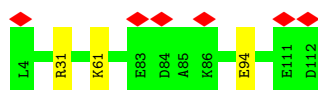
- Molecule 69: 60S ribosomal protein L30

Chain Le:  97%



- Molecule 70: 60S ribosomal protein L31-A

Chain Lf:  97%



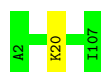
- Molecule 71: 60S ribosomal protein L32

Chain Lg:  100%



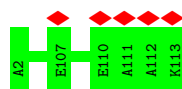
- Molecule 72: 60S ribosomal protein L33-A

Chain Lh:  99%



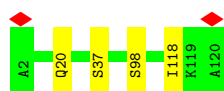
- Molecule 73: 60S ribosomal protein L34-A

Chain Li:  100%



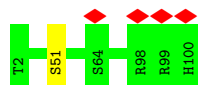
- Molecule 74: 60S ribosomal protein L35-A

Chain Lj:  97%



- Molecule 75: 60S ribosomal protein L36-A

Chain Lk:  99%



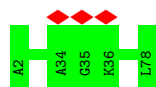
- Molecule 76: 60S ribosomal protein L37-A

Chain Ll:  96%



- Molecule 77: 60S ribosomal protein L38

Chain Lm:  100%



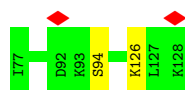
- Molecule 78: 60S ribosomal protein L39

Chain Ln:  100%

There are no outlier residues recorded for this chain.

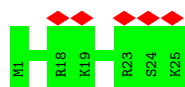
- Molecule 79: 60S ribosomal protein L40-A

Chain Lo:  96%



- Molecule 80: 60S ribosomal protein L41-A

Chain Lp:  20% 100%



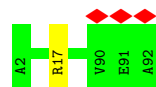
- Molecule 81: 60S ribosomal protein L42-A

Chain Lq:  97% .



- Molecule 82: 60S ribosomal protein L43-A

Chain Lr:  99% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32746	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.644	Depositor
Minimum map value	-0.339	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.0875	Depositor
Map size (Å)	524.88, 524.88, 524.88	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.81, 0.81, 0.81	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 3HE

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	A	0.65	0/72889	0.81	18/113624 (0.0%)
2	B	0.51	0/2883	0.78	1/4491 (0.0%)
3	C	0.68	0/3746	0.80	1/5832 (0.0%)
4	D	0.86	1/245 (0.4%)	0.91	0/378
5	m	0.41	0/1799	0.87	0/2801
6	n	1.04	1/1797 (0.1%)	1.05	8/2801 (0.3%)
7	z	0.31	0/483	0.55	0/640
8	E	0.48	0/38089	0.82	18/59339 (0.0%)
9	SP	0.31	0/1644	0.54	0/2249
10	SQ	0.31	0/1823	0.60	2/2447 (0.1%)
11	SE	0.31	0/936	0.65	2/1259 (0.2%)
12	SR	0.31	0/1656	0.55	0/2251
13	SA	0.32	0/1754	0.61	1/2361 (0.0%)
14	SS	0.31	0/2097	0.56	0/2823
15	SB	0.28	0/1625	0.59	1/2197 (0.0%)
16	ST	0.30	0/1839	0.56	0/2460
17	SU	0.29	0/1498	0.57	1/2019 (0.0%)
18	SV	0.33	0/1501	0.58	0/2006
19	SW	0.31	0/1504	0.58	0/2016
20	SC	0.38	0/772	0.63	0/1044
21	SX	0.35	0/1168	0.58	0/1575
22	SD	0.27	0/883	0.56	0/1199
23	SY	0.32	0/1215	0.58	1/1638 (0.1%)
24	SZ	0.30	0/934	0.60	0/1257
25	SF	0.31	0/1125	0.61	1/1510 (0.1%)
26	SG	0.31	0/957	0.60	1/1283 (0.1%)
27	SH	0.29	0/1207	0.59	0/1623
28	SI	0.31	0/1130	0.57	0/1517
29	SJ	0.32	0/807	0.58	0/1091
30	Sa	0.32	0/682	0.62	1/921 (0.1%)
31	Sb	0.32	0/1038	0.56	0/1395
32	Sc	0.31	0/1139	0.53	0/1518

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Sd	0.31	0/1046	0.55	0/1401
34	Se	0.31	0/778	0.61	0/1042
35	Sf	0.30	0/620	0.54	0/838
36	SM	0.35	0/453	0.58	0/602
37	Sg	0.29	0/459	0.60	0/611
38	SN	0.29	0/567	0.55	0/764
39	SO	0.27	0/2436	0.57	1/3318 (0.0%)
40	SL	0.30	0/493	0.67	0/663
41	AA	0.29	0/744	0.60	0/991
42	LD	0.40	0/1933	0.59	0/2598
43	LE	0.39	0/3150	0.56	0/4236
44	LF	0.36	0/2801	0.54	0/3792
45	LG	0.32	0/2400	0.52	0/3239
46	LH	0.37	0/1329	0.54	1/1794 (0.1%)
47	LI	0.36	0/1821	0.50	0/2451
48	LJ	0.35	0/1836	0.52	0/2481
49	LK	0.36	0/1529	0.57	0/2060
50	LL	0.34	0/1801	0.57	0/2416
51	LM	0.32	0/1367	0.61	0/1834
52	LN	0.35	0/1568	0.58	0/2106
53	LO	0.34	0/1068	0.54	0/1438
54	LP	0.41	0/1757	0.61	1/2354 (0.0%)
55	LQ	0.38	0/1585	0.53	0/2128
56	LR	0.38	0/1439	0.56	0/1938
57	LS	0.34	0/1465	0.57	0/1965
58	LT	0.35	0/1532	0.56	0/2043
59	LU	0.37	0/1473	0.57	0/1980
60	LV	0.35	0/1296	0.55	0/1739
61	LW	0.37	0/812	0.58	0/1099
62	LX	0.38	0/1018	0.55	0/1369
63	LY	0.38	0/540	0.56	0/717
64	LZ	0.40	0/979	0.54	0/1321
65	La	0.38	0/995	0.55	0/1329
66	Lb	0.40	0/1106	0.53	0/1485
67	Lc	0.36	0/1200	0.54	0/1607
68	Ld	0.31	0/473	0.59	1/629 (0.2%)
69	Le	0.36	0/745	0.51	0/1001
70	Lf	0.37	0/890	0.56	0/1196
71	Lg	0.35	0/1038	0.54	0/1390
72	Lh	0.43	0/868	0.58	0/1168
73	Li	0.39	0/890	0.59	0/1189
74	Lj	0.35	0/978	0.56	0/1301
75	Lk	0.31	0/772	0.61	0/1026

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Ll	0.39	0/660	0.57	0/875
77	Lm	0.33	0/618	0.58	0/826
78	Ln	0.35	0/443	0.61	0/588
79	Lo	0.32	0/416	0.60	0/553
80	Lp	0.28	0/230	0.70	0/296
81	Lq	0.36	0/836	0.57	0/1104
82	Lr	0.38	0/701	0.58	0/934
All	All	0.51	2/210819 (0.0%)	0.73	61/309390 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
27	SH	0	1
42	LD	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	n	16	U	O3'-P	40.42	2.09	1.61
4	D	1	A	OP3-P	-10.86	1.48	1.61

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	n	16	U	P-O3'-C3'	-25.13	89.55	119.70
6	n	16	U	OP1-P-O3'	-12.38	77.95	105.20
1	A	2094	C	N3-C2-O2	-11.01	114.19	121.90
6	n	16	U	C5-C4-O4	9.42	131.55	125.90
6	n	16	U	OP2-P-O3'	9.32	125.71	105.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
42	LD	192	LYS	Peptide
27	SH	144	ARG	Sidechain

5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
7	z	55/588 (9%)	51 (93%)	4 (7%)	0	100	100
9	SP	204/206 (99%)	195 (96%)	9 (4%)	0	100	100
10	SQ	222/232 (96%)	209 (94%)	13 (6%)	0	100	100
11	SE	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
12	SR	214/216 (99%)	203 (95%)	11 (5%)	0	100	100
13	SA	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
14	SS	256/258 (99%)	237 (93%)	19 (7%)	0	100	100
15	SB	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
16	ST	226/228 (99%)	216 (96%)	10 (4%)	0	100	100
17	SU	182/184 (99%)	176 (97%)	5 (3%)	1 (0%)	25	55
18	SV	183/198 (92%)	172 (94%)	11 (6%)	0	100	100
19	SW	182/184 (99%)	176 (97%)	6 (3%)	0	100	100
20	SC	90/92 (98%)	85 (94%)	5 (6%)	0	100	100
21	SX	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
22	SD	119/121 (98%)	106 (89%)	13 (11%)	0	100	100
23	SY	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
24	SZ	125/127 (98%)	119 (95%)	6 (5%)	0	100	100
25	SF	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
26	SG	117/125 (94%)	114 (97%)	3 (3%)	0	100	100
27	SH	143/145 (99%)	137 (96%)	6 (4%)	0	100	100
28	SI	141/143 (99%)	139 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	SJ	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
30	Sa	85/87 (98%)	81 (95%)	4 (5%)	0	100	100
31	Sb	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
32	Sc	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
33	Sd	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
34	Se	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
35	Sf	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
36	SM	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
37	Sg	55/57 (96%)	52 (94%)	3 (6%)	0	100	100
38	SN	71/73 (97%)	59 (83%)	12 (17%)	0	100	100
39	SO	310/312 (99%)	282 (91%)	27 (9%)	1 (0%)	37	65
40	SL	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
41	AA	91/108 (84%)	82 (90%)	9 (10%)	0	100	100
42	LD	249/251 (99%)	235 (94%)	14 (6%)	0	100	100
43	LE	384/386 (100%)	365 (95%)	19 (5%)	0	100	100
44	LF	359/361 (99%)	346 (96%)	13 (4%)	0	100	100
45	LG	292/294 (99%)	284 (97%)	8 (3%)	0	100	100
46	LH	163/175 (93%)	154 (94%)	9 (6%)	0	100	100
47	LI	220/222 (99%)	211 (96%)	9 (4%)	0	100	100
48	LJ	231/233 (99%)	219 (95%)	12 (5%)	0	100	100
49	LK	189/191 (99%)	180 (95%)	9 (5%)	0	100	100
50	LL	216/218 (99%)	205 (95%)	11 (5%)	0	100	100
51	LM	167/169 (99%)	160 (96%)	7 (4%)	0	100	100
52	LN	191/193 (99%)	180 (94%)	10 (5%)	1 (0%)	25	55
53	LO	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
54	LP	201/203 (99%)	192 (96%)	9 (4%)	0	100	100
55	LQ	195/197 (99%)	191 (98%)	4 (2%)	0	100	100
56	LR	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
57	LS	183/185 (99%)	172 (94%)	10 (6%)	1 (0%)	25	55
58	LT	186/188 (99%)	182 (98%)	4 (2%)	0	100	100
59	LU	169/171 (99%)	161 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	LV	157/159 (99%)	155 (99%)	2 (1%)	0	100	100
61	LW	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
62	LX	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
63	LY	63/65 (97%)	63 (100%)	0	0	100	100
64	LZ	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
65	La	123/125 (98%)	123 (100%)	0	0	100	100
66	Lb	133/135 (98%)	129 (97%)	4 (3%)	0	100	100
67	Lc	146/148 (99%)	135 (92%)	10 (7%)	1 (1%)	19	48
68	Ld	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
69	Le	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
70	Lf	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
71	Lg	125/127 (98%)	116 (93%)	9 (7%)	0	100	100
72	Lh	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
73	Li	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
74	Lj	117/119 (98%)	114 (97%)	2 (2%)	1 (1%)	14	43
75	Lk	97/99 (98%)	91 (94%)	6 (6%)	0	100	100
76	Ll	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
77	Lm	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
78	Ln	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
79	Lo	50/52 (96%)	50 (100%)	0	0	100	100
80	Lp	23/25 (92%)	23 (100%)	0	0	100	100
81	Lq	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
82	Lr	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
All	All	10980/11713 (94%)	10497 (96%)	477 (4%)	6 (0%)	50	77

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	SU	135	ILE
39	SO	279	ALA
52	LN	47	ALA
67	Lc	40	HIS
74	Lj	118	ILE

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	
7	z	52/523 (10%)	52 (100%)	0	100	100
9	SP	170/173 (98%)	168 (99%)	2 (1%)	67	81
10	SQ	200/205 (98%)	192 (96%)	8 (4%)	27	54
11	SE	95/98 (97%)	91 (96%)	4 (4%)	25	52
12	SR	175/175 (100%)	171 (98%)	4 (2%)	45	67
13	SA	182/182 (100%)	174 (96%)	8 (4%)	24	50
14	SS	220/220 (100%)	215 (98%)	5 (2%)	45	67
15	SB	172/173 (99%)	170 (99%)	2 (1%)	67	81
16	ST	189/195 (97%)	183 (97%)	6 (3%)	34	60
17	SU	163/165 (99%)	159 (98%)	4 (2%)	42	66
18	SV	148/159 (93%)	145 (98%)	3 (2%)	50	71
19	SW	156/157 (99%)	154 (99%)	2 (1%)	65	80
20	SC	78/85 (92%)	70 (90%)	8 (10%)	6	20
21	SX	126/127 (99%)	122 (97%)	4 (3%)	34	60
22	SD	88/98 (90%)	86 (98%)	2 (2%)	45	67
23	SY	127/127 (100%)	124 (98%)	3 (2%)	44	67
24	SZ	90/96 (94%)	89 (99%)	1 (1%)	70	83
25	SF	117/117 (100%)	114 (97%)	3 (3%)	41	65
26	SG	101/113 (89%)	98 (97%)	3 (3%)	36	61
27	SH	127/128 (99%)	118 (93%)	9 (7%)	12	35
28	SI	115/115 (100%)	110 (96%)	5 (4%)	25	51
29	SJ	93/93 (100%)	92 (99%)	1 (1%)	70	83
30	Sa	71/74 (96%)	66 (93%)	5 (7%)	12	35
31	Sb	110/110 (100%)	106 (96%)	4 (4%)	30	57
32	Sc	119/119 (100%)	117 (98%)	2 (2%)	56	75
33	Sd	102/112 (91%)	97 (95%)	5 (5%)	21	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Se	82/83 (99%)	78 (95%)	4 (5%)	21	47
35	Sf	70/70 (100%)	68 (97%)	2 (3%)	37	62
36	SM	47/47 (100%)	47 (100%)	0	100	100
37	Sg	48/49 (98%)	48 (100%)	0	100	100
38	SN	56/63 (89%)	55 (98%)	1 (2%)	54	74
39	SO	250/257 (97%)	240 (96%)	10 (4%)	27	54
40	SL	55/56 (98%)	53 (96%)	2 (4%)	30	57
41	AA	76/89 (85%)	73 (96%)	3 (4%)	27	54
42	LD	190/193 (98%)	185 (97%)	5 (3%)	41	65
43	LE	321/322 (100%)	308 (96%)	13 (4%)	27	54
44	LF	288/288 (100%)	275 (96%)	13 (4%)	23	50
45	LG	241/243 (99%)	240 (100%)	1 (0%)	89	94
46	LH	139/154 (90%)	135 (97%)	4 (3%)	37	62
47	LI	186/186 (100%)	179 (96%)	7 (4%)	28	55
48	LJ	187/191 (98%)	182 (97%)	5 (3%)	40	64
49	LK	168/171 (98%)	161 (96%)	7 (4%)	25	52
50	LL	185/185 (100%)	176 (95%)	9 (5%)	21	47
51	LM	145/147 (99%)	138 (95%)	7 (5%)	21	48
52	LN	154/154 (100%)	151 (98%)	3 (2%)	52	72
53	LO	107/107 (100%)	105 (98%)	2 (2%)	52	72
54	LP	175/175 (100%)	172 (98%)	3 (2%)	56	75
55	LQ	160/160 (100%)	157 (98%)	3 (2%)	52	72
56	LR	138/145 (95%)	137 (99%)	1 (1%)	81	89
57	LS	150/150 (100%)	146 (97%)	4 (3%)	40	64
58	LT	152/153 (99%)	148 (97%)	4 (3%)	41	65
59	LU	155/155 (100%)	150 (97%)	5 (3%)	34	60
60	LV	135/136 (99%)	130 (96%)	5 (4%)	29	56
61	LW	87/87 (100%)	87 (100%)	0	100	100
62	LX	104/104 (100%)	101 (97%)	3 (3%)	37	62
63	LY	54/57 (95%)	52 (96%)	2 (4%)	29	56
64	LZ	104/105 (99%)	102 (98%)	2 (2%)	52	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
65	La	108/108 (100%)	102 (94%)	6 (6%)	17	42
66	Lb	112/115 (97%)	110 (98%)	2 (2%)	54	74
67	Lc	117/118 (99%)	114 (97%)	3 (3%)	41	65
68	Ld	46/46 (100%)	44 (96%)	2 (4%)	25	51
69	Le	81/81 (100%)	78 (96%)	3 (4%)	29	56
70	Lf	92/96 (96%)	89 (97%)	3 (3%)	33	59
71	Lg	108/109 (99%)	108 (100%)	0	100	100
72	Lh	90/90 (100%)	89 (99%)	1 (1%)	70	83
73	Li	95/95 (100%)	95 (100%)	0	100	100
74	Lj	104/104 (100%)	101 (97%)	3 (3%)	37	62
75	Lk	80/81 (99%)	79 (99%)	1 (1%)	65	80
76	Ll	67/67 (100%)	64 (96%)	3 (4%)	23	50
77	Lm	68/68 (100%)	68 (100%)	0	100	100
78	Ln	45/45 (100%)	45 (100%)	0	100	100
79	Lo	45/47 (96%)	43 (96%)	2 (4%)	24	50
80	Lp	22/23 (96%)	22 (100%)	0	100	100
81	Lq	87/88 (99%)	84 (97%)	3 (3%)	32	59
82	Lr	71/71 (100%)	70 (99%)	1 (1%)	62	79
All	All	9233/9873 (94%)	8967 (97%)	266 (3%)	39	62

5 of 266 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
64	LZ	29	SER
65	La	74	TYR
79	Lo	94	SER
32	Sc	107	PHE
31	Sb	97	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
57	LS	145	ASN
79	Lo	109	ASN
60	LV	112	ASN

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Mol	Chain	Res	Type
70	Lf	17	HIS
23	SY	138	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3033/3394 (89%)	481 (15%)	25 (0%)
2	B	120/121 (99%)	11 (9%)	2 (1%)
3	C	157/158 (99%)	24 (15%)	1 (0%)
4	D	9/10 (90%)	3 (33%)	1 (11%)
5	m	75/76 (98%)	26 (34%)	0
6	n	74/75 (98%)	16 (21%)	0
8	E	1588/1800 (88%)	352 (22%)	48 (3%)
All	All	5056/5634 (89%)	913 (18%)	77 (1%)

5 of 913 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	14	U
1	A	26	A
1	A	40	A
1	A	43	A

5 of 77 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	E	1217	A
8	E	1535	U
8	E	1245	G
8	E	1344	A
8	E	1633	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
83	3HE	A	3401	-	21,21,21	0.53	0	23,30,30	0.90	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
83	3HE	A	3401	-	-	6/8/36/36	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

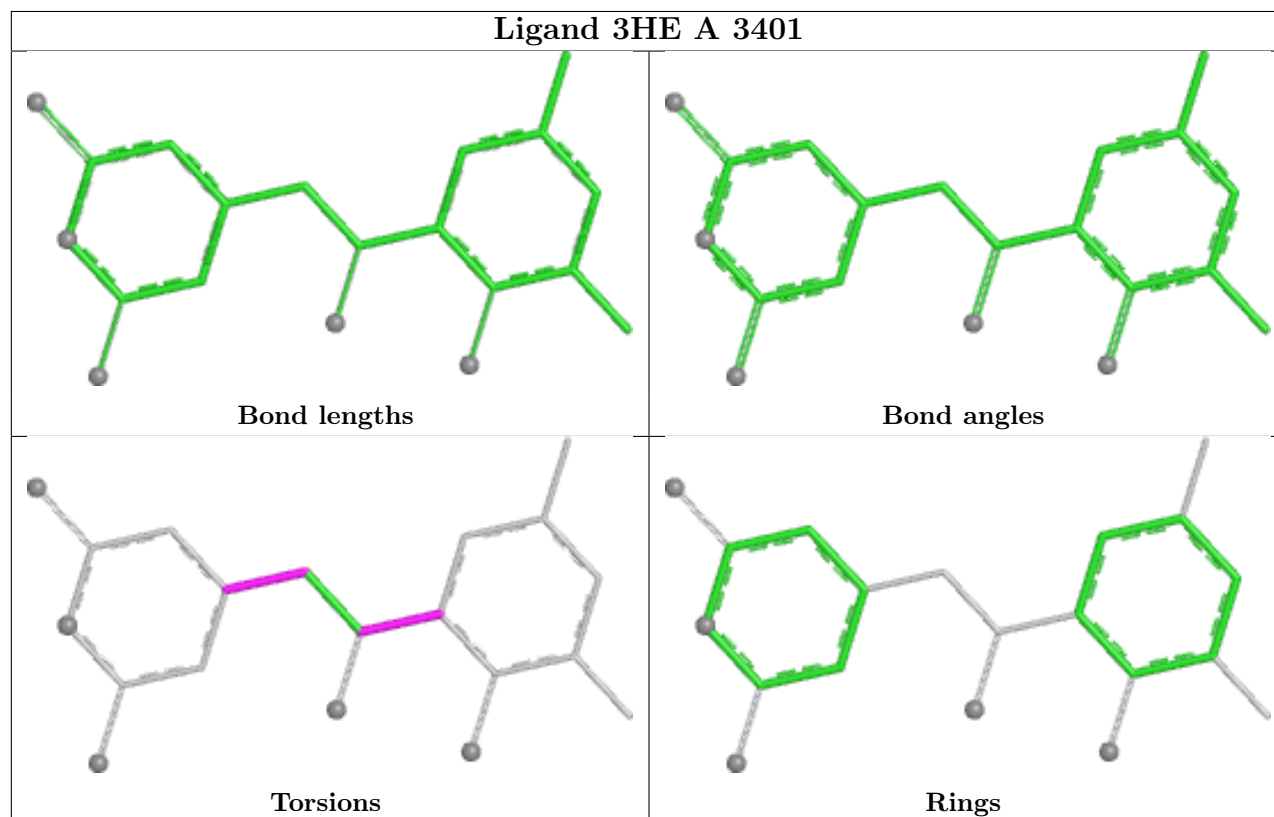
Mol	Chain	Res	Type	Atoms
83	A	3401	3HE	C4-C5-C7-C8
83	A	3401	3HE	C4-C5-C7-O3
83	A	3401	3HE	C6-C5-C7-C8
83	A	3401	3HE	C6-C5-C7-O3
83	A	3401	3HE	C7-C8-C9-C13

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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
6	n	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	n	16:U	O3'	18:G	P	2.09

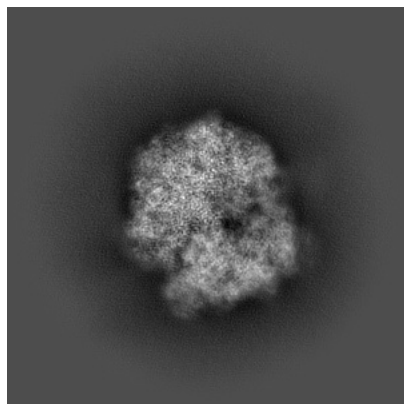
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42540. These allow visual inspection of the internal detail of the map and identification of artifacts.

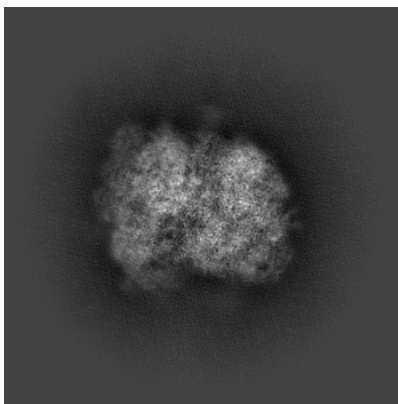
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

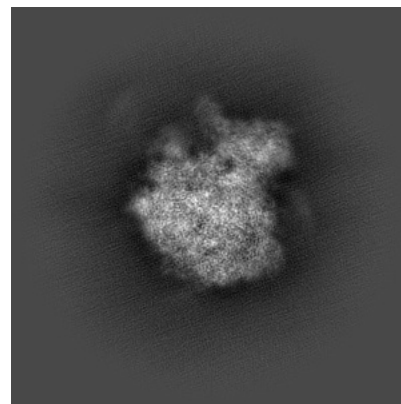
6.1.1 Primary map



X

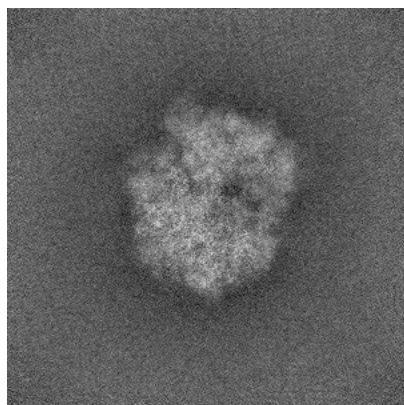


Y

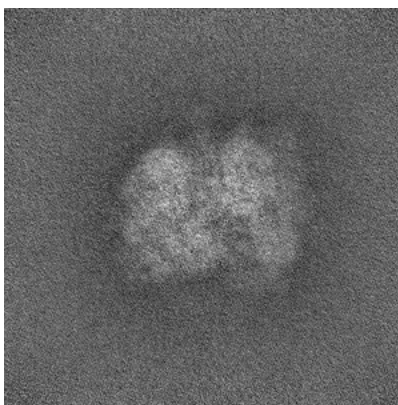


Z

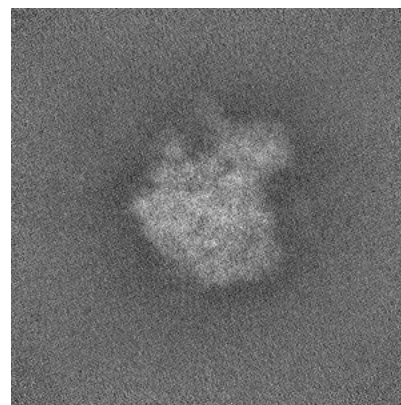
6.1.2 Raw map



X



Y

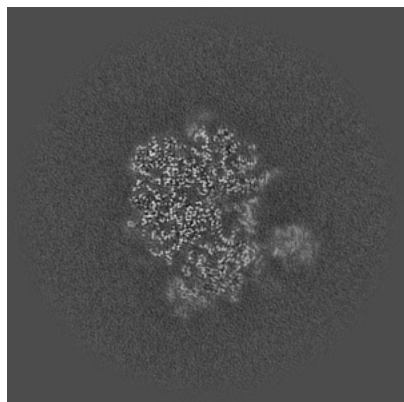


Z

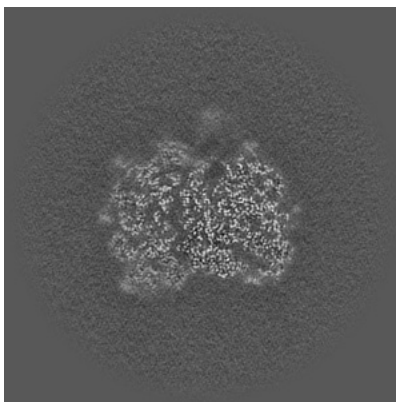
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

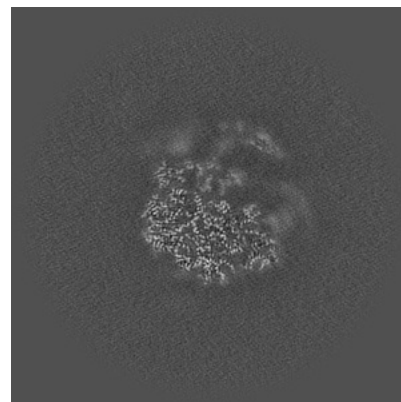
6.2.1 Primary map



X Index: 324

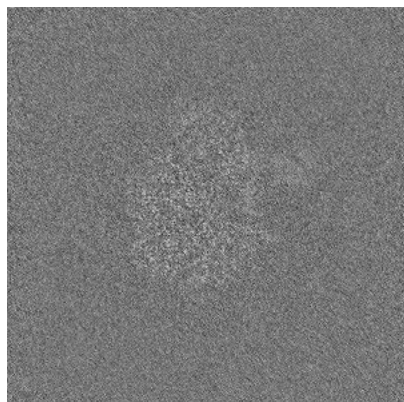


Y Index: 324

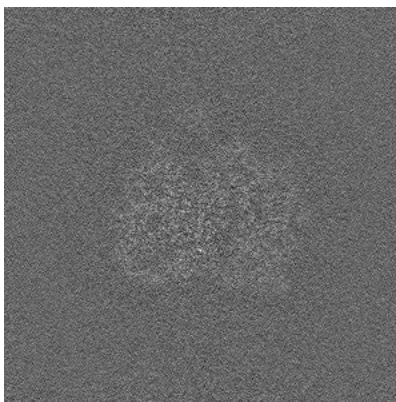


Z Index: 324

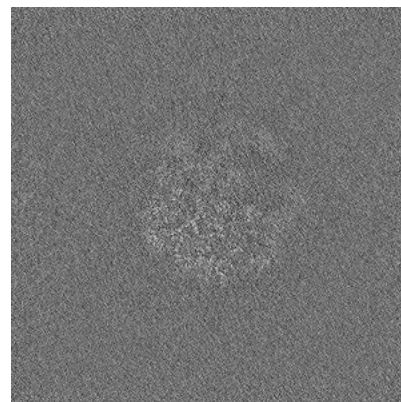
6.2.2 Raw map



X Index: 324



Y Index: 324

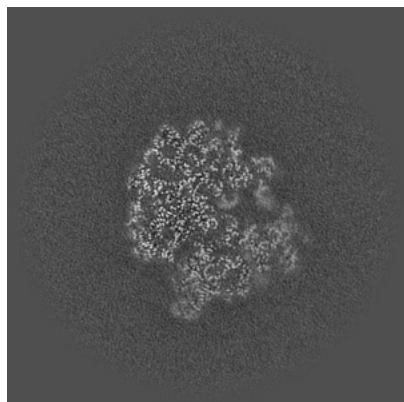


Z Index: 324

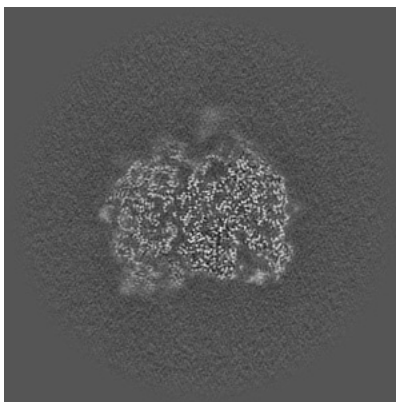
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

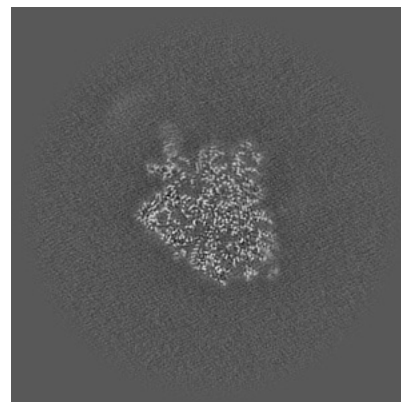
6.3.1 Primary map



X Index: 343

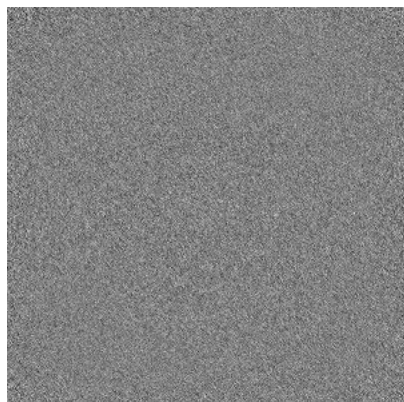


Y Index: 319

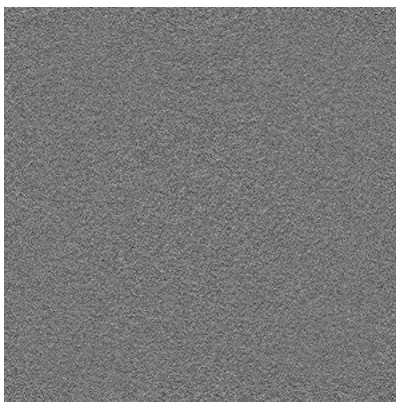


Z Index: 367

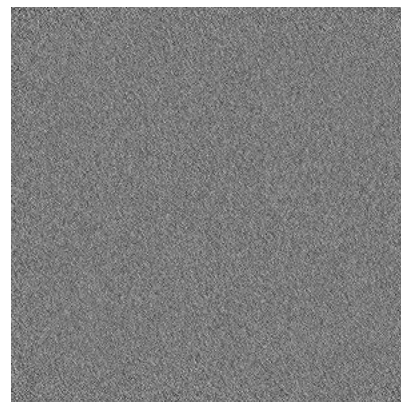
6.3.2 Raw map



X Index: 0



Y Index: 0

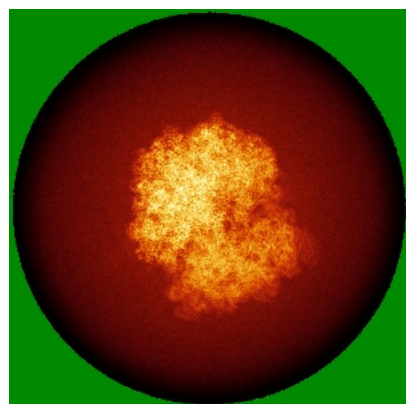


Z Index: 0

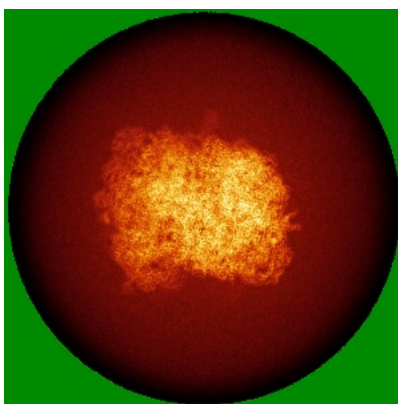
The images above show the largest variance slices of the map in three orthogonal directions.

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

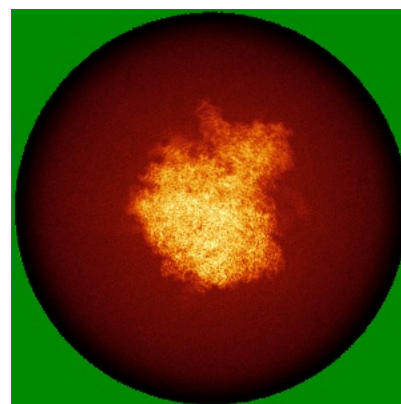
6.4.1 Primary map



X

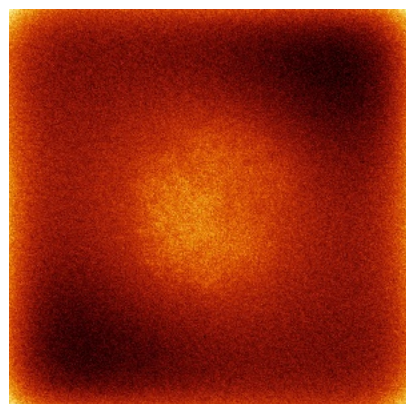


Y

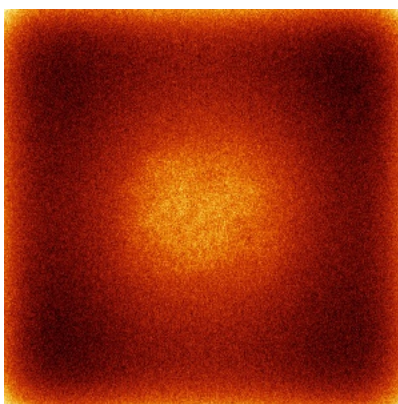


Z

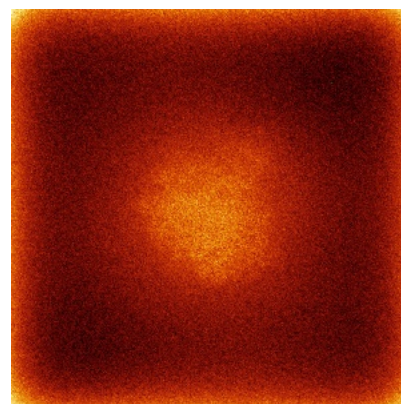
6.4.2 Raw map



X



Y

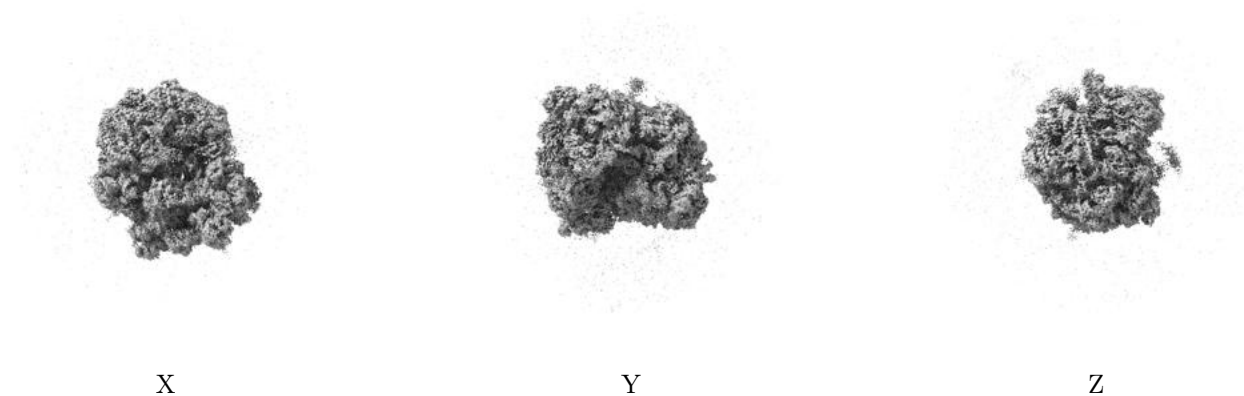


Z

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

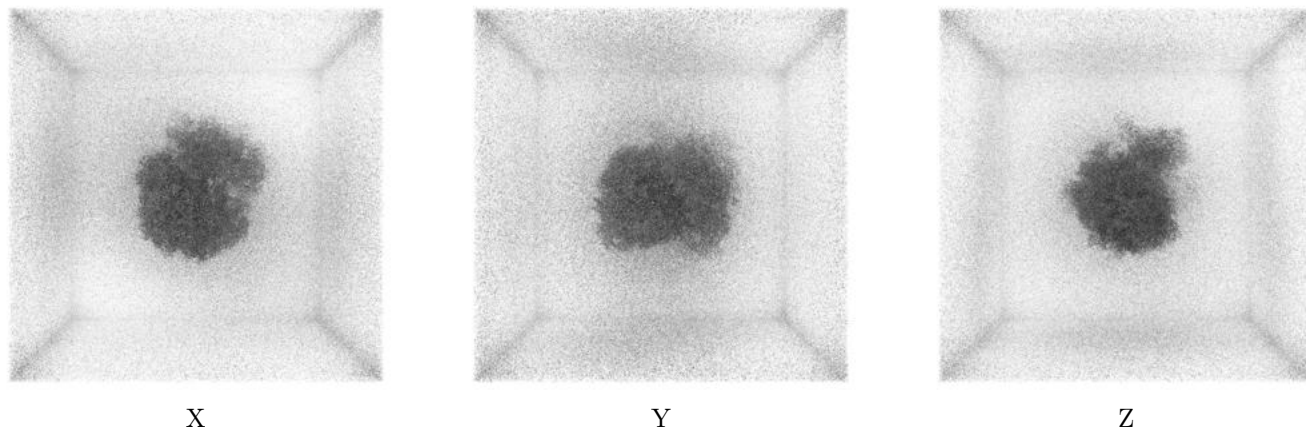
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0875. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

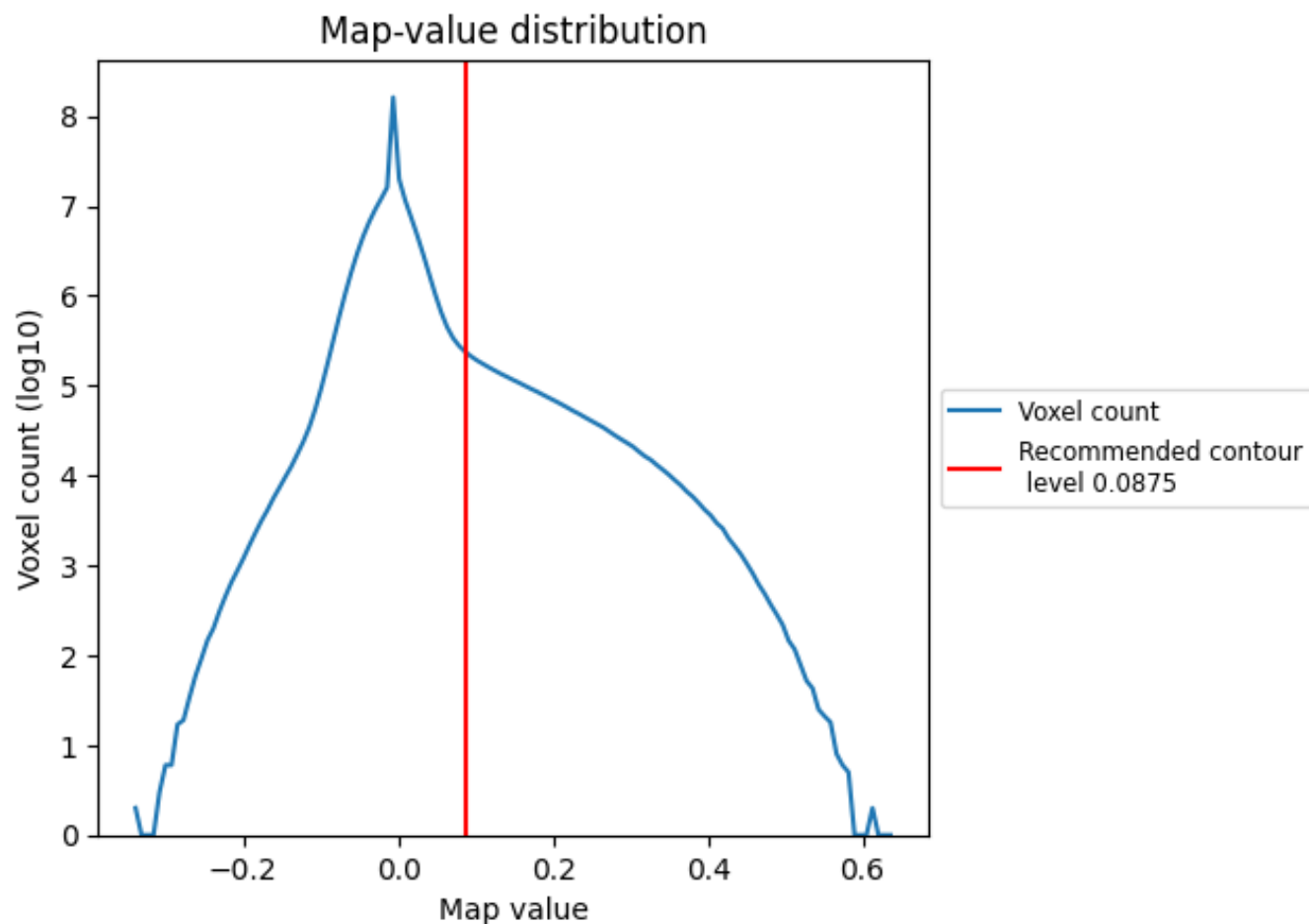
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

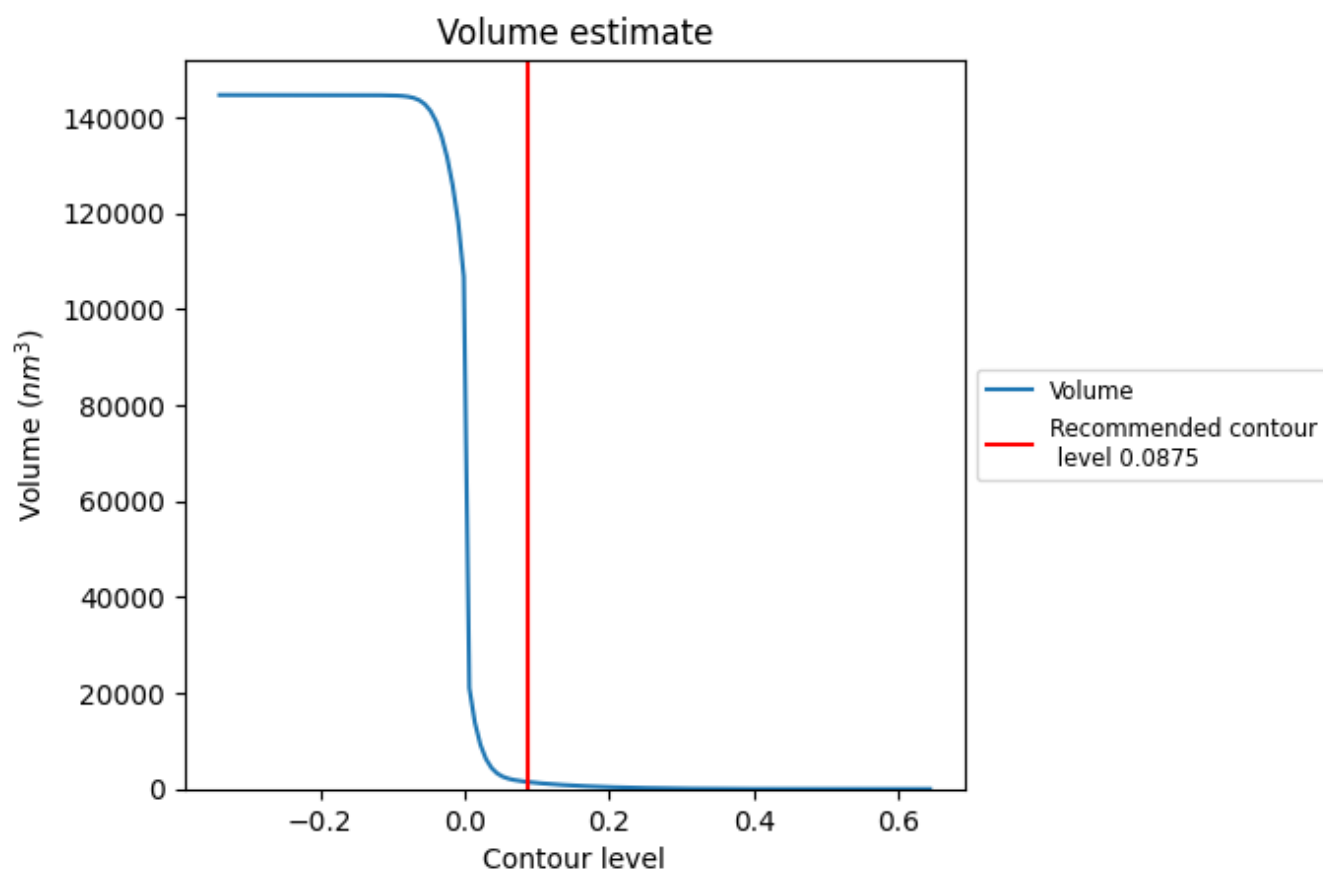
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

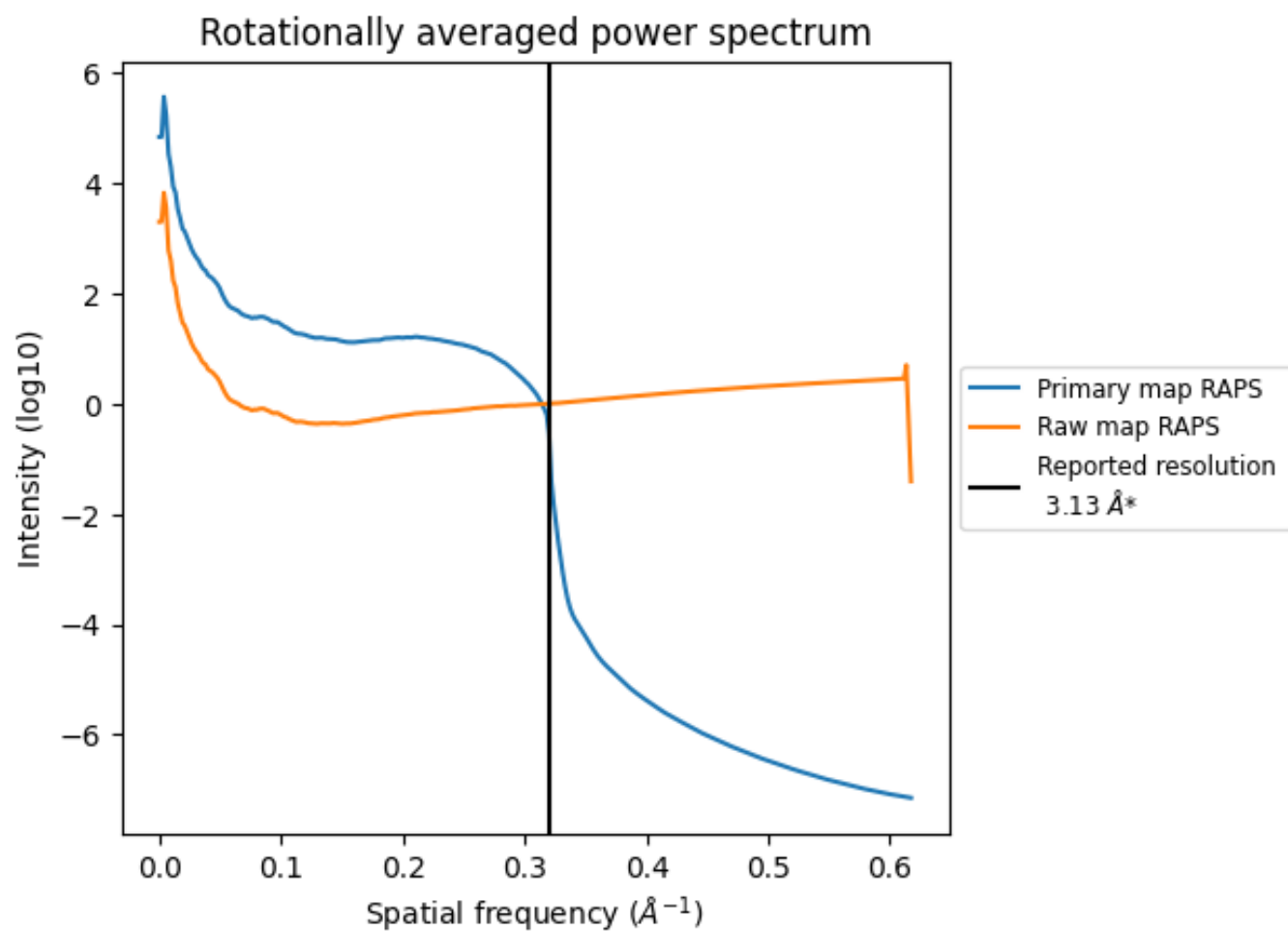
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1452 nm^3 ; this corresponds to an approximate mass of 1312 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 ⓘ

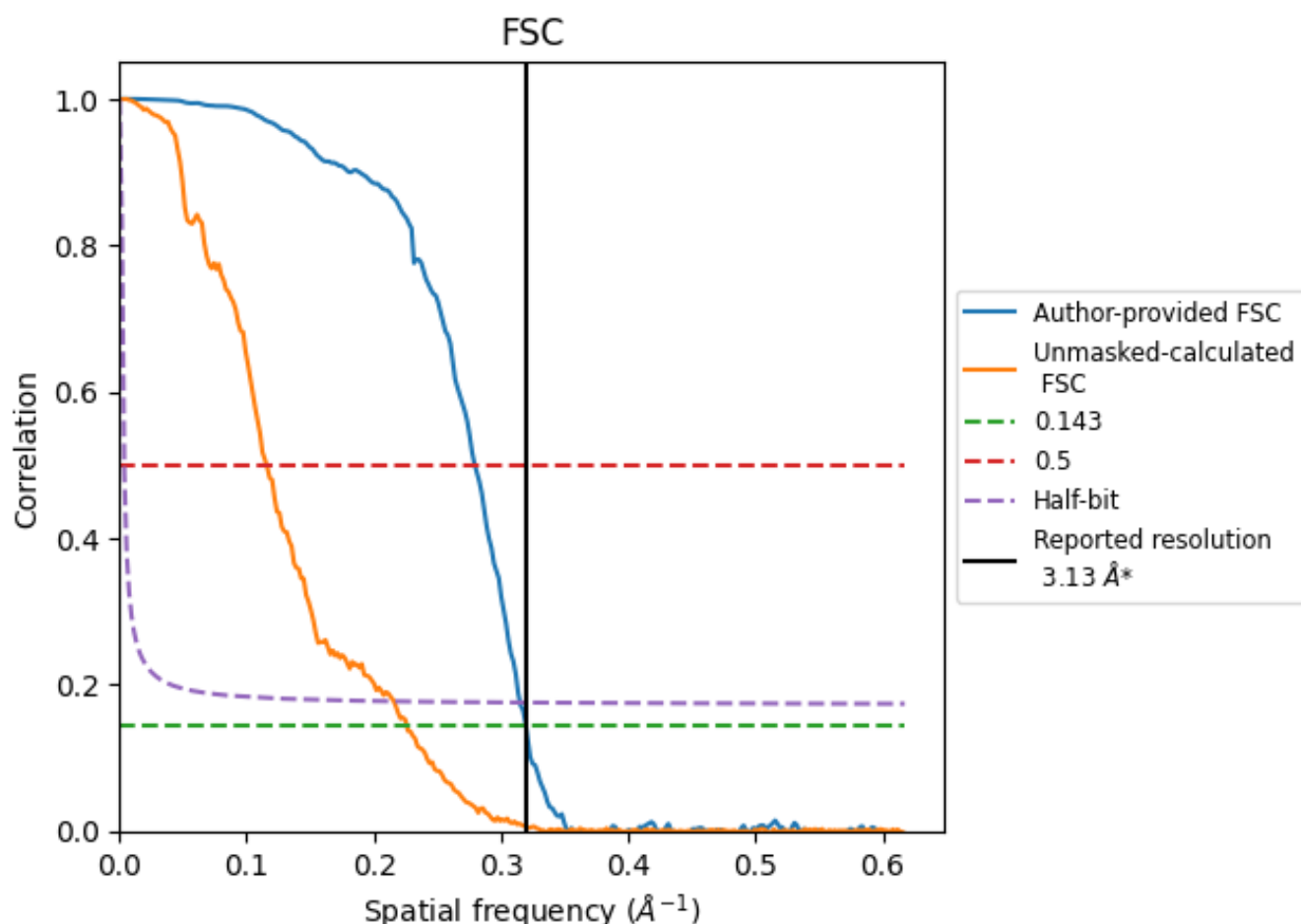


*Reported resolution corresponds to spatial frequency of 0.319 \AA^{-1}

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 0.319 Å⁻¹

8.2 Resolution estimates [i](#)

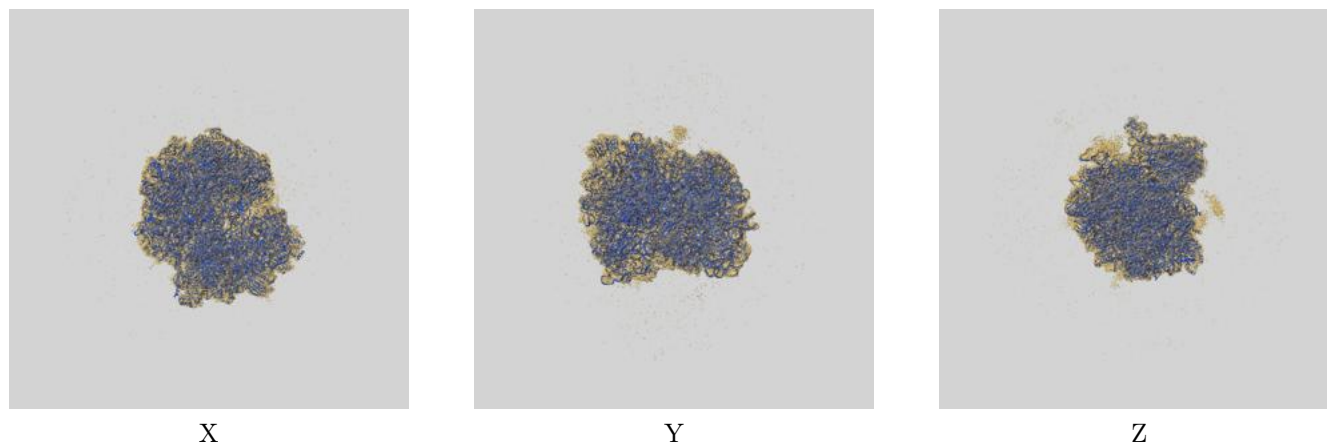
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.13	-	-
Author-provided FSC curve	3.13	3.58	3.18
Unmasked-calculated*	4.43	8.65	4.64

*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 4.43 differs from the reported value 3.13 by more than 10 %

9 Map-model fit [i](#)

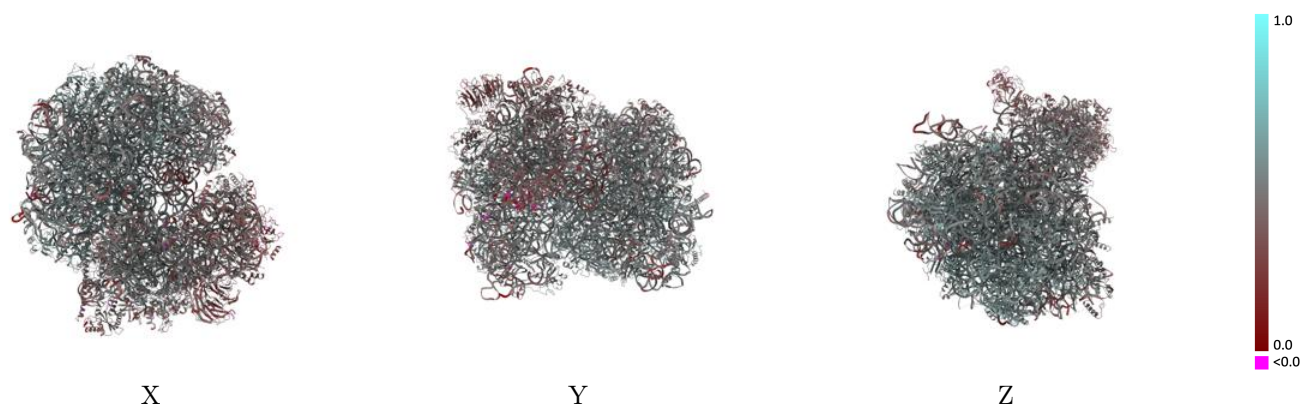
This section contains information regarding the fit between EMDB map EMD-42540 and PDB model 8UTI. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

9.1 Map-model overlay [i](#)



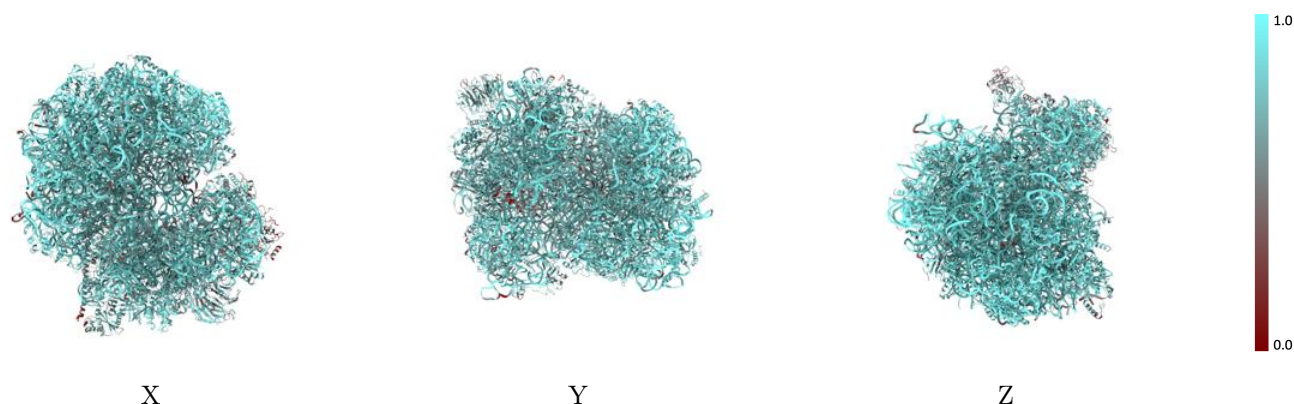
The images above show the 3D surface view of the map at the recommended contour level 0.0875 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



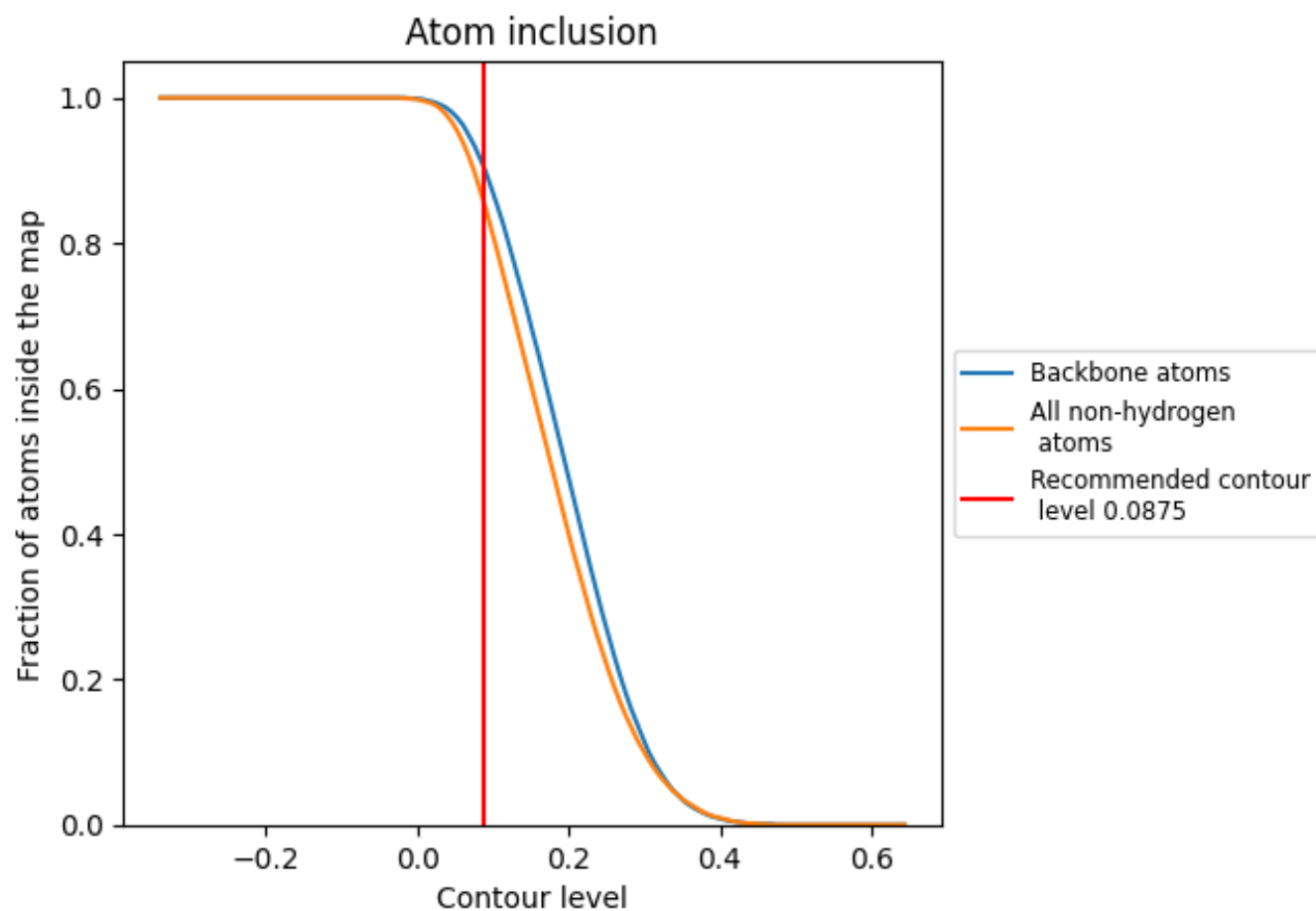
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0875).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.0875) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8580	 0.4810
A	 0.9250	 0.4990
AA	 0.5730	 0.3440
B	 0.9480	 0.4690
C	 0.9420	 0.5120
D	 0.9170	 0.4830
E	 0.8910	 0.4470
LD	 0.8340	 0.5510
LE	 0.8820	 0.5420
LF	 0.8910	 0.5430
LG	 0.8490	 0.4550
LH	 0.8340	 0.5030
LI	 0.8460	 0.5170
LJ	 0.8180	 0.4930
LK	 0.8410	 0.5070
LL	 0.7780	 0.4980
LM	 0.7640	 0.4450
LN	 0.8370	 0.5180
LO	 0.8570	 0.5070
LP	 0.8580	 0.5400
LQ	 0.8430	 0.5240
LR	 0.8630	 0.5460
LS	 0.8670	 0.5340
LT	 0.8100	 0.5170
LU	 0.8490	 0.5230
LV	 0.8330	 0.5180
LW	 0.8500	 0.4980
LX	 0.7900	 0.5450
LY	 0.8380	 0.5400
LZ	 0.8810	 0.5490
La	 0.9110	 0.5600
Lb	 0.8810	 0.5270
Lc	 0.8850	 0.5400
Ld	 0.8070	 0.5000
Le	 0.8660	 0.5270















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Chain	Atom inclusion	Q-score
Lf	 0.8600	 0.5300
Lg	 0.8640	 0.5590
Lh	 0.8790	 0.5540
Li	 0.8400	 0.5340
Lj	 0.8620	 0.5310
Lk	 0.8090	 0.4730
Ll	 0.9260	 0.5630
Lm	 0.8260	 0.5100
Ln	 0.9060	 0.5600
Lo	 0.8280	 0.5260
Lp	 0.5960	 0.4980
Lq	 0.8470	 0.5240
Lr	 0.7980	 0.5510
SA	 0.7110	 0.4400
SB	 0.6490	 0.3890
SC	 0.7370	 0.3860
SD	 0.3920	 0.2300
SE	 0.6700	 0.3770
SF	 0.7390	 0.4160
SG	 0.7120	 0.3930
SH	 0.7380	 0.4320
SI	 0.7500	 0.4180
SJ	 0.7330	 0.4360
SL	 0.6260	 0.4000
SM	 0.8490	 0.4800
SN	 0.4050	 0.2600
SO	 0.6690	 0.3330
SP	 0.8040	 0.4460
SQ	 0.6750	 0.4260
SR	 0.7800	 0.4980
SS	 0.7850	 0.4950
ST	 0.7160	 0.4400
SU	 0.6940	 0.4050
SV	 0.7330	 0.4860
SW	 0.7650	 0.4650
SX	 0.7730	 0.5030
SY	 0.7600	 0.4710
SZ	 0.7280	 0.4470
Sa	 0.8070	 0.4830
Sb	 0.8030	 0.5150
Sc	 0.7500	 0.5300
Sd	 0.7690	 0.4610

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Chain	Atom inclusion	Q-score
Se	 0.7800	 0.4750
Sf	 0.7290	 0.4490
Sg	 0.6760	 0.4620
m	 0.8110	 0.3900
n	 0.8080	 0.3820
z	 0.7260	 0.5160