



Full wwPDB EM Validation Report ⓘ

Oct 14, 2024 – 04:45 PM EDT

PDB ID : 8TPU
EMDB ID : EMD-41485
Title : Subtomogram averaged consensus structure of the malarial 80S ribosome in Plasmodium falciparum-infected human erythrocytes
Authors : Anton, L.; Cheng, W.; Zhu, X.; Ho, C.M.
Deposited on : 2023-08-05
Resolution : 4.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

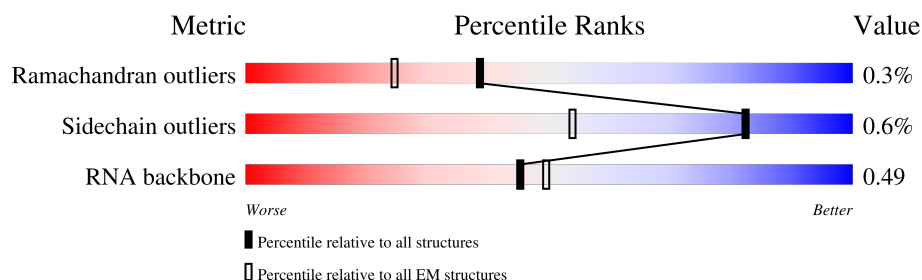
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 4.10 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)
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	S1	133	
2	S2	105	
3	S3	107	
4	S4	82	
5	S5	58	
6	S6	43	
7	S7	74	
8	SA	2087	

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Mol	Chain	Length	Quality of chain
9	SB	262	
10	SC	263	
11	SD	221	
12	SE	189	
13	SF	261	
14	SG	272	
15	SH	306	
16	SI	195	
17	SJ	194	
18	SK	130	
19	SL	218	
20	SM	144	
21	SN	118	
22	SO	137	
23	SP	151	
24	SQ	145	
25	SR	141	
26	SS	156	
27	ST	54	
28	SU	151	
29	SV	161	
30	SW	137	
31	SX	145	
32	SY	170	
33	SZ	82	

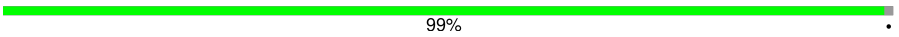
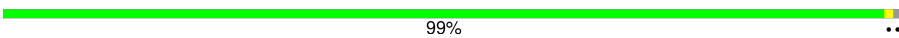


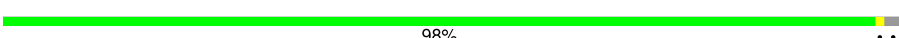

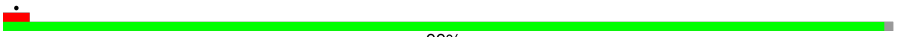



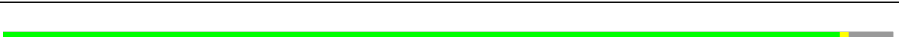

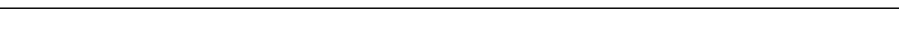
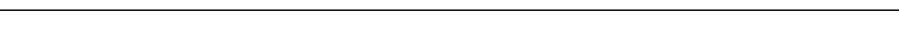
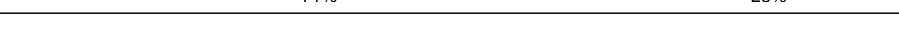
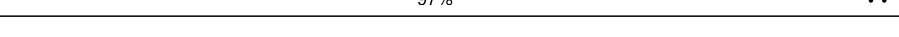
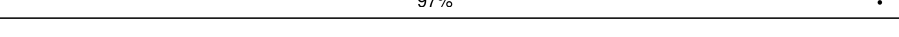
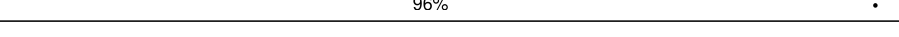

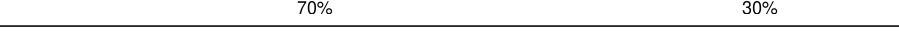

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Mol	Chain	Length	Quality of chain
34	AA	3788	
35	AC	159	
36	AB	119	
37	AL	215	
38	A1	146	
39	A2	126	
40	A4	67	
41	A6	107	
42	A7	120	
43	AN	165	
44	A8	130	
45	A9	139	
46	Aa	149	
47	Ab	112	
48	Ad	87	
49	Ae	51	
50	Af	128	
51	AP	203	
52	Ah	95	
53	Ai	103	
54	AI	221	
55	AJ	283	
56	Ac	92	
57	AK	202	
58	AM	139	

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Mol	Chain	Length	Quality of chain
59	AS	187	 99%
60	AO	148	 99%
61	AQ	219	 84%14%
62	AR	294	 85%14%
63	AW	173	 98%
64	AY	190	 53%47%
65	AT	182	 99%
66	AZ	126	 95%
67	A3	124	 95%
68	A5	257	 86%13%
69	AD	260	 94%5%
70	AE	386	 98%
71	AF	411	 94%5%
72	AG	173	 71%28%
73	AU	184	 97%
74	AH	190	 97%
75	AV	162	 96%
76	Ag	39	 92%5%
77	AX	139	 70%30%
78	A0	162	 38%62%
79	S8	323	 24%98%

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 195395 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 protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	S1	120	Total	C	N	O	S	0	0
			985	632	189	162	2		

- Molecule 2 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	S2	41	Total	C	N	O	0	0
			320	208	56	56		

- Molecule 3 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S3	95	Total	C	N	O	S	0	0
			781	478	169	128	6		

- Molecule 4 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 5 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	S5	58	Total	C	N	O	0	0
			458	285	93	80		

- Molecule 6 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	S6	43	Total	C	N	O	0	0
			346	213	75	58		

- Molecule 7 is a RNA chain called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S7	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SA	1608	Total	C	N	O	P	0	0
			34208	15346	6106	11170	1586		

- Molecule 9 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SB	210	Total	C	N	O	S	0	0
			1713	1097	301	303	12		

- Molecule 10 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SC	195	Total	C	N	O	S	0	0
			1538	990	266	273	9		

- Molecule 11 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SD	157	Total	C	N	O	S	0	0
			1228	782	225	214	7		

- Molecule 12 is a protein called 40S ribosomal protein S9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SE	185	Total	C	N	O	S	0	0
			1514	962	290	260	2		

- Molecule 13 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SF	257	Total	C	N	O	S	0	0
			2061	1320	377	356	8		

- Molecule 14 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SG	224	Total	C	N	O	S	0	0
			1757	1132	307	309	9		

- Molecule 15 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SH	204	Total	C	N	O	S	0	0
			1651	1046	316	283	6		

- Molecule 16 is a protein called 40S ribosomal protein S5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SI	180	Total	C	N	O	S	0	0
			1424	893	263	258	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SJ	188	Total	C	N	O	S	0	0
			1528	982	264	278	4		

- Molecule 18 is a protein called 40S ribosomal protein S15A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SK	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 19 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SL	171	Total	C	N	O	S	0	0
			1383	872	264	243	4		

- Molecule 20 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SM	138	Total	C	N	O	S	0	0
			1098	704	200	193	1		

- Molecule 21 is a protein called 40S ribosomal protein S20e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SN	98	Total	C	N	O	S	0	0
			772	484	135	148	5		

- Molecule 22 is a protein called 40S ribosomal protein S10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SO	79	Total	C	N	O	S	0	0
			686	450	116	118	2		

- Molecule 23 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SP	127	Total	C	N	O	S	0	0
			954	591	184	176	3		

- Molecule 24 is a protein called 40S ribosomal protein S23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SQ	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 25 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SR	98	Total	C	N	O	S	0	0
			746	474	123	145	4		

- Molecule 26 is a protein called 40S ribosomal protein S18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SS	128	Total	C	N	O	S	0	0
			1046	657	205	180	4		

- Molecule 27 is a protein called 40S ribosomal protein S29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	ST	48	Total	C	N	O	S	0	0
			405	252	85	64	4		

- Molecule 28 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SU	149	Total	C	N	O	S	0	0
			1202	769	220	210	3		

- Molecule 29 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SV	146	Total	C	N	O	S	0	0
			1206	772	227	200	7		

- Molecule 30 is a protein called 40S ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SW	95	Total	C	N	O	S	0	0
			785	498	149	135	3		

- Molecule 31 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SX	96	Total	C	N	O	S	0	0
			776	497	137	138	4		

- Molecule 32 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	SY	154	Total	C	N	O	S	0	0
			1266	811	239	214	2		

- Molecule 33 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SZ	72	Total	C	N	O	S	0	0
			557	346	102	105	4		

- Molecule 34 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AA	3193	Total	C	N	O	P	0	0
			67884	30446	12054	22223	3161		

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AC	151	Total	C	N	O	P	0	0
			3215	1444	589	1034	148		

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	118	Total	C	N	O	P	0	0
			2522	1128	461	816	117		

- Molecule 37 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AL	211	Total	C	N	O	S	0	0
			1761	1119	349	290	3		

- Molecule 38 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A2	104	Total	C	N	O	S	0	0
			828	529	150	146	3		

- Molecule 40 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 41 is a protein called 60S ribosomal protein L30e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A6	97	Total	C	N	O	S	0	0
			732	458	131	136	7		

- Molecule 42 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	A7	96	Total	C	N	O	S	0	0
			793	508	151	129	5		

- Molecule 43 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AN	147	Total	C	N	O	S	0	0
			1210	787	212	205	6		

- Molecule 44 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	A8	124	Total	C	N	O	S	0	0
			1029	655	205	162	7		

- Molecule 45 is a protein called 60S ribosomal protein L35ae, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A9	102	Total	C	N	O	S	0	0
			840	541	162	134	3		

- Molecule 46 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Aa	105	Total	C	N	O	S	0	0
			854	528	183	137	6		

- Molecule 47 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ab	95	Total	C	N	O	S	0	0
			756	477	150	129			

- Molecule 48 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ad	72	Total	C	N	O	S	0	0
			603	395	107	99	2		

- Molecule 49 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ae	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 50 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Af	51	Total	C	N	O	S	0	0
			413	255	87	66	5		

- Molecule 51 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AP	202	Total	C	N	O	S	0	0
			1682	1064	349	265	4		

- Molecule 52 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ah	84	Total	C	N	O	S	0	0
			653	414	126	106	7		

- Molecule 53 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ai	94	Total	C	N	O	S	0	0
			769	484	150	126	9		

- Molecule 54 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AI	207	Total	C	N	O	S	0	0
			1685	1096	298	286	5		

- Molecule 55 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AJ	222	Total	C	N	O	S	0	0
			1813	1174	323	309	7		

- Molecule 56 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ac	89	Total	C	N	O	S	0	0
			709	441	150	113	5		

- Molecule 57 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AK	201	Total	C	N	O	S	0	0
			1659	1064	311	276	8		

- Molecule 58 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AM	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 59 is a protein called 60S ribosomal protein L18-2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	186	Total	C	N	O	S	0	0
			1503	958	299	241	5		

- Molecule 60 is a protein called 60S ribosomal protein L27a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AO	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 61 is a protein called 60S ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AQ	189	Total	C	N	O	S	0	0
			1544	984	291	261	8		

- Molecule 62 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AR	252	Total	C	N	O	S	0	0
			2049	1301	385	357	6		

- Molecule 63 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	170	Total	C	N	O	S	0	0
			1319	824	266	222	7		

- Molecule 64 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AY	101	Total	C	N	O	S	0	0
			796	502	144	144	6		

- Molecule 65 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AT	181	Total	C	N	O	S	0	0
			1509	952	309	244	4		

- Molecule 66 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	121	Total	C	N	O	S	0	0
			1000	626	206	165	3		

- Molecule 67 is a protein called 60S ribosomal protein L35, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	A3	119	Total	C	N	O	S	0	0
			994	635	194	163	2		

- Molecule 68 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	A5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 69 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AD	247	Total	C	N	O	S	0	0
			1866	1166	374	317	9		

- Molecule 70 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AE	380	Total	C	N	O	S	0	0
			3061	1948	575	521	17		

- Molecule 71 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AF	390	Total	C	N	O	S	0	0
			3094	1962	594	527	11		

- Molecule 72 is a protein called 60S ribosomal protein L11a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AG	124	Total	C	N	O	S	0	0
			1010	636	197	171	6		

- Molecule 73 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AU	180	Total	C	N	O	S	0	0
			1497	946	289	255	7		

- Molecule 74 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AH	185	Total	C	N	O	S	0	0
			1475	950	264	255	6		

- Molecule 75 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AV	155	Total	C	N	O	S	0	0
			1275	814	241	214	6		

- Molecule 76 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ag	37	Total	C	N	O	S	0	0
			343	210	86	45	2		

- Molecule 77 is a protein called 60S ribosomal protein L22, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AX	97	Total	C	N	O	S	0	0
			824	548	135	139	2		

- Molecule 78 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	A0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

- Molecule 79 is a protein called Receptor for activated c kinase.

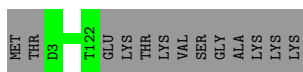
Mol	Chain	Residues	Atoms					AltConf	Trace
79	S8	317	Total	C	N	O	S	0	0
			2464	1557	419	478	10		

3 Residue-property plots [i](#)

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

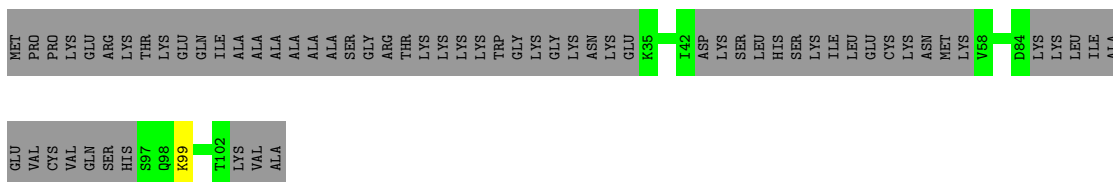
- Molecule 1: 40S ribosomal protein S24

Chain S1: 




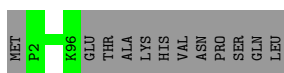
- Molecule 2: 40S ribosomal protein S25

Chain S2: 



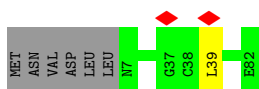
- Molecule 3: 40S ribosomal protein S26

Chain S3: 



- Molecule 4: 40S ribosomal protein S27

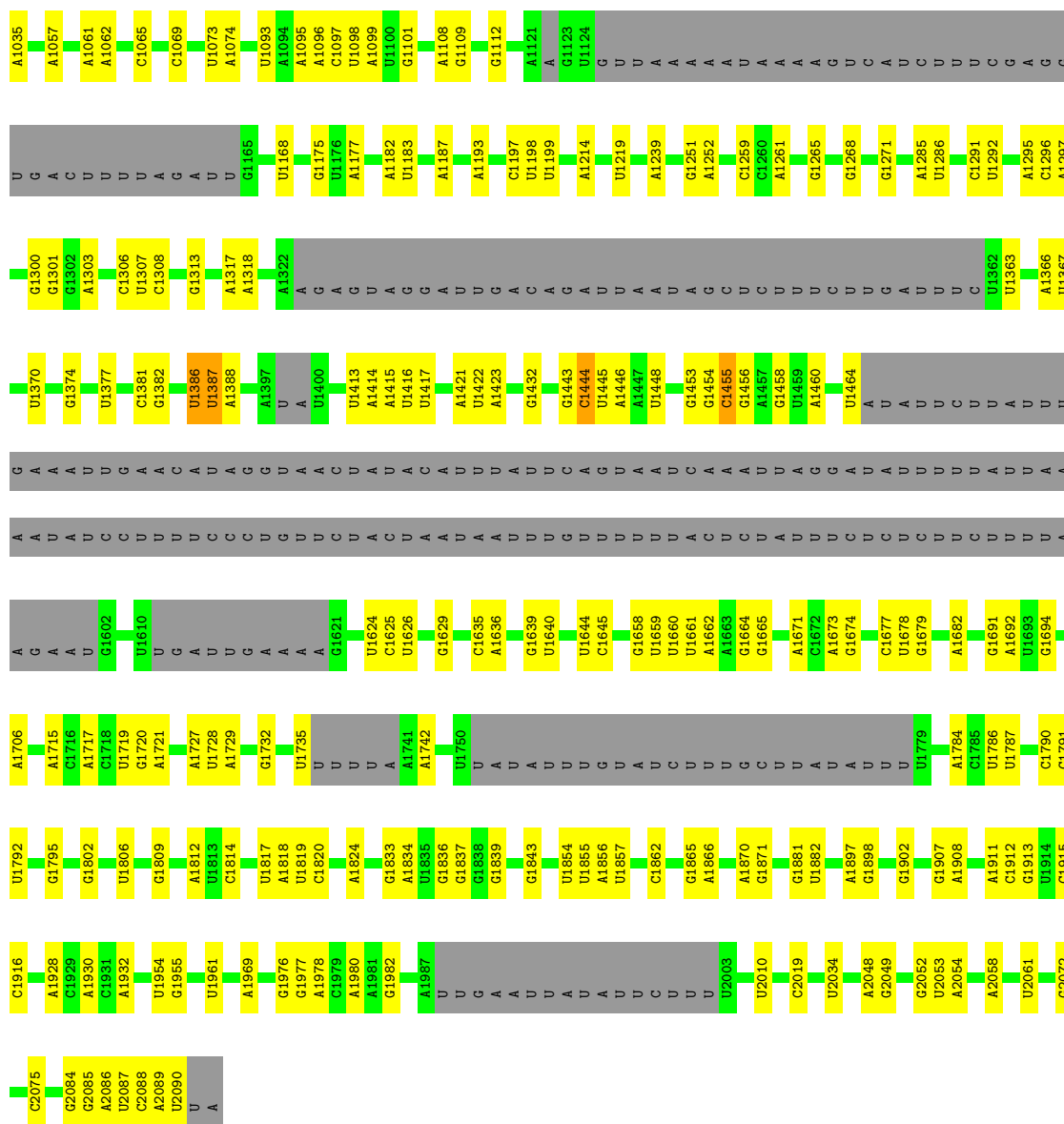
Chain S4: 



- Molecule 5: 60S ribosomal protein L41

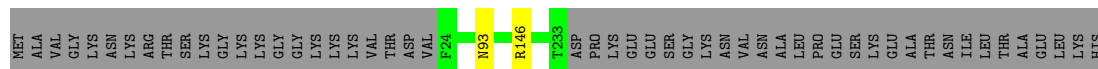
Chain S5: 





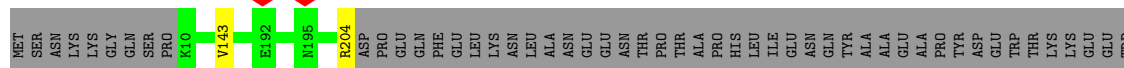
- Molecule 9: 40S ribosomal protein S3a

Chain SB: 79% 20%

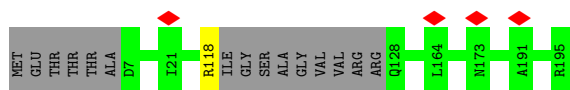


- Molecule 10: 40S ribosomal protein SA

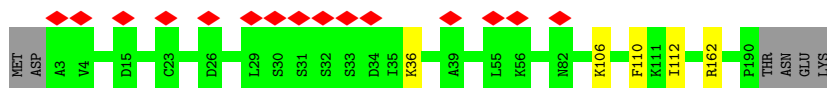
Chain SC: 73% 26%



Chain SI:  92% • 8%



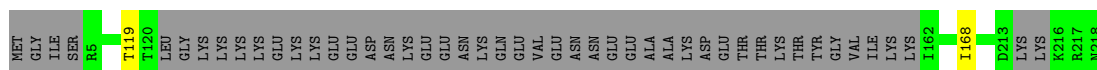
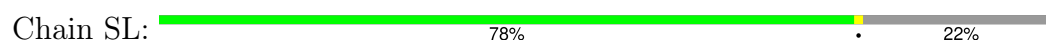
- Molecule 17: 40S ribosomal protein S7



- Molecule 18: 40S ribosomal protein S15A, putative



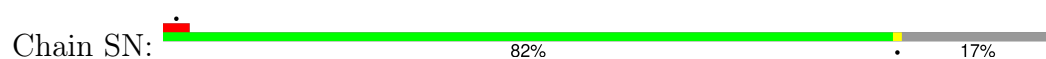
- Molecule 19: 40S ribosomal protein S8



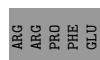
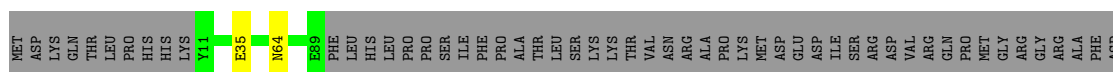
- Molecule 20: 40S ribosomal protein S16




- Molecule 21: 40S ribosomal protein S20e, putative

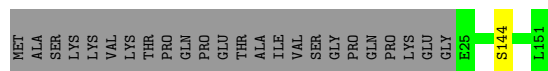


- Molecule 22: 40S ribosomal protein S10, putative



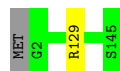
- Molecule 23: 40S ribosomal protein S11

Chain SP:  83% 16%



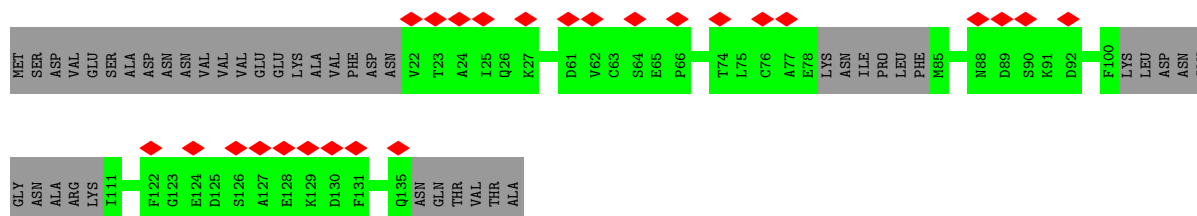
- Molecule 24: 40S ribosomal protein S23, putative

Chain SQ:  99%




- Molecule 25: 40S ribosomal protein S12

Chain SR:  18% 70% 30%



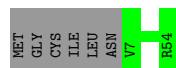
- Molecule 26: 40S ribosomal protein S18, putative

Chain SS:  80% 18%



- Molecule 27: 40S ribosomal protein S29, putative

Chain ST:  89% 11%



- Molecule 28: 40S ribosomal protein S15

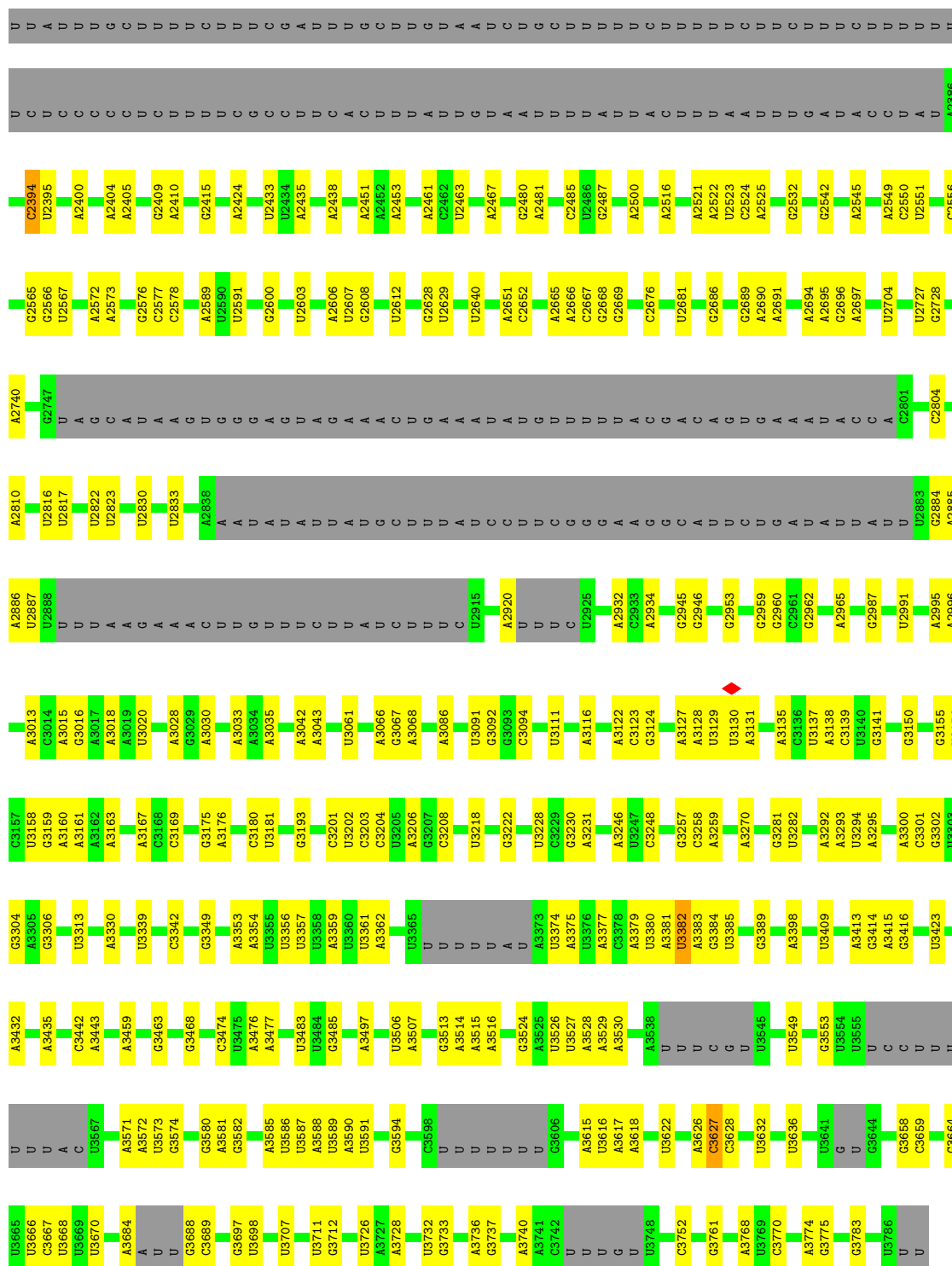
Chain SU:  99%



- Molecule 29: 40S ribosomal protein S11, putative

Chain SV:  89% 9%



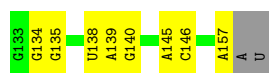


• Molecule 35: 5.8S ribosomal RNA

Chain AC:

70% 25% 5%





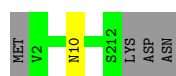
- Molecule 36: 5S ribosomal RNA

Chain AB: 83% 16%



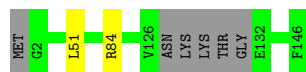
- Molecule 37: 60S ribosomal protein L13

Chain AL: 98%



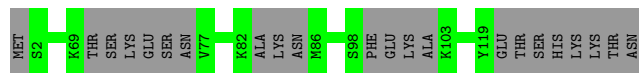
- Molecule 38: 60S ribosomal protein L27

Chain A1: 95%



- Molecule 39: 60S ribosomal protein L28

Chain A2: 83% 17%



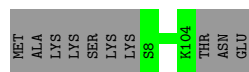
- Molecule 40: 60S ribosomal protein L29

Chain A4: 99%



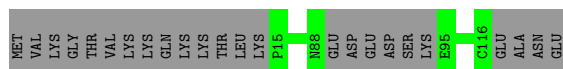
- Molecule 41: 60S ribosomal protein L30e, putative

Chain A6: 91% 9%




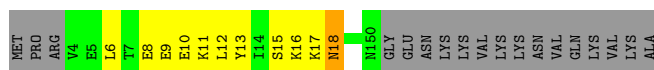
- Molecule 42: 60S ribosomal protein L31

Chain A7: 80% 20%



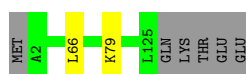
- Molecule 43: 60S ribosomal protein L14, putative

Chain AN:  82% 6% • 11%



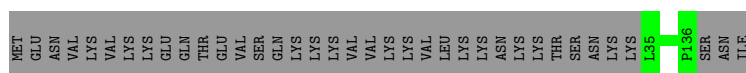
- Molecule 44: 60S ribosomal protein L32

Chain A8:  94% • 5%



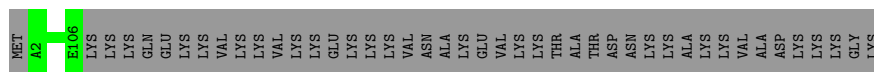
- Molecule 45: 60S ribosomal protein L35ae, putative

Chain A9:  73% 27%




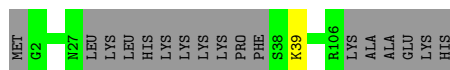
- Molecule 46: 60S ribosomal protein L34

Chain Aa:  70% 30%




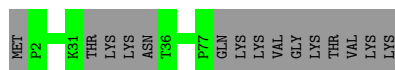
- Molecule 47: 60S ribosomal protein L36

Chain Ab:  84% • 15%




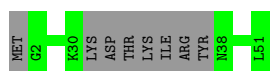
- Molecule 48: 60S ribosomal protein L38

Chain Ad:  83% 17%



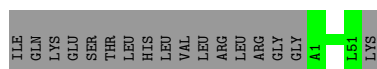
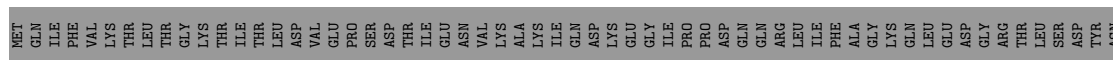
- Molecule 49: 60S ribosomal protein L39

Chain Ae:  84% 16%



- Molecule 50: Ubiquitin-60S ribosomal protein L40

Chain Af: 40% 60%



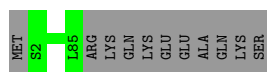
- Molecule 51: Ribosomal protein L15

Chain AP: 98%



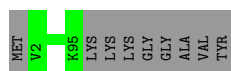
- Molecule 52: Large ribosomal subunit protein eL43

Chain Ah: 88% 12%



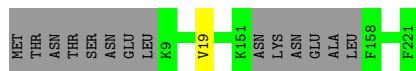
- Molecule 53: Large ribosomal subunit protein eL42

Chain Ai: 91% 9%



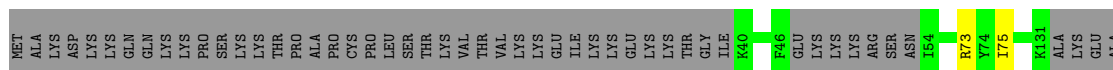
- Molecule 54: 60S ribosomal protein L6, putative

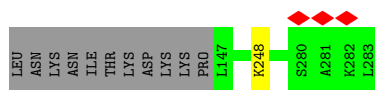
Chain AI: 93% 6%



- Molecule 55: 60S ribosomal protein L7a

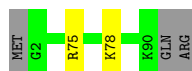
Chain AJ: 77% 22%





- Molecule 56: Ribosomal protein L37

Chain Ac: 95%



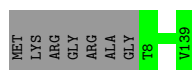
- Molecule 57: 60S ribosomal protein L13, putative

Chain AK: 100%



- Molecule 58: 60S ribosomal protein L23, putative

Chain AM: 95%



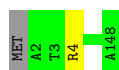
- Molecule 59: 60S ribosomal protein L18-2, putative

Chain AS: 99%



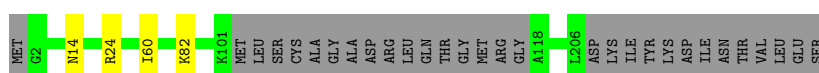
- Molecule 60: 60S ribosomal protein L27a, putative

Chain AO: 99%



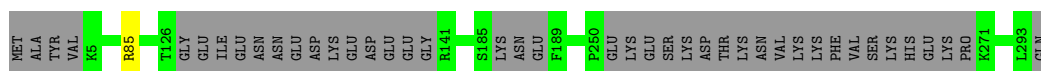
- Molecule 61: 60S ribosomal protein L10, putative

Chain AQ: 84%



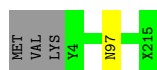
- Molecule 62: 60S ribosomal protein L5, putative

Chain AR: 85%



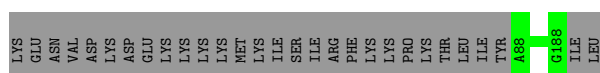
- Molecule 63: 60S ribosomal protein L17, putative

Chain AW: 98%



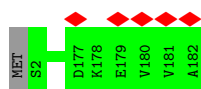
- Molecule 64: 60S ribosomal protein L23

Chain AY: 53% 47%



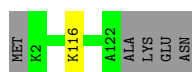
- Molecule 65: 60S ribosomal protein L19

Chain AT: 99%



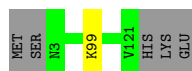
- Molecule 66: 60S ribosomal protein L26, putative

Chain AZ: 95%



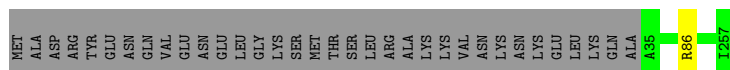
- Molecule 67: 60S ribosomal protein L35, putative

Chain A3: 95%



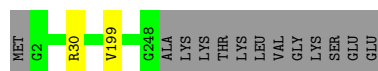
- Molecule 68: 60S ribosomal protein L7, putative

Chain A5: 86% 13%



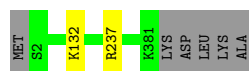
- Molecule 69: 60S ribosomal protein L2

Chain AD:  94% 5%



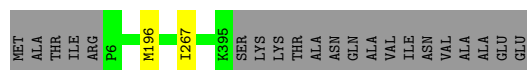
- Molecule 70: 60S ribosomal protein L3

Chain AE:  98%



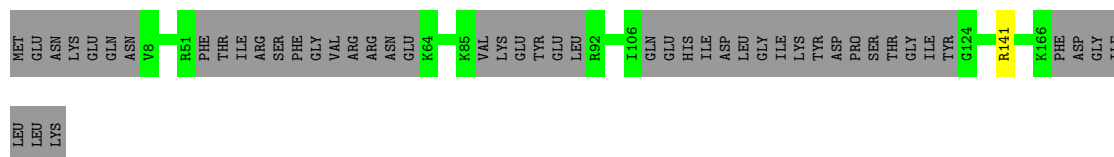
- Molecule 71: 60S ribosomal protein L4

Chain AF:  94% 5%



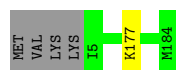
- Molecule 72: 60S ribosomal protein L11a, putative

Chain AG:  71% 28%



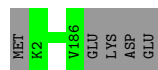
- Molecule 73: 60S ribosomal protein L18a

Chain AU:  97%



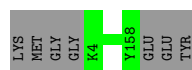
- Molecule 74: 60S ribosomal protein L6, putative

Chain AH:  97%



- Molecule 75: 60S ribosomal protein L21

Chain AV:  96%



-

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|
| MET | VAL | ALA | LYS | LYS | ASP | SER | THR | LYS | VAL | SER | LYS | LYS | LEU | LYS | LYS | VAL | VAL | LYS | THR | LYS | LYS | ILE | VAL | GLY | LEU | LYS | LYS | GLN | LYS | MET | ASN | LYS | SER | THR | LYS | GLY | I40 | Q136 | LEU | ASN | ASN |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|

- [illegible]

- [illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	3D CRYSTAL, $a=500.24002$ Å, $b=500.24002$ Å, $c=500.24002$ Å, $\alpha=90.0^\circ$, $\beta=90.0^\circ$, $\gamma=90.0^\circ$, space group=C1	Depositor
Number of subtomograms used	120226	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 ($e^-/\text{\AA}^2$)	120	Depositor
Minimum defocus (nm)	2800	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.159	Depositor
Minimum map value	-0.276	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.075	Depositor
Recommended contour level	0.16	Depositor
Map size (Å)	500.24002, 500.24002, 500.24002	wwPDB
Map dimensions	296, 296, 296	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.69, 1.69, 1.69	Depositor

5 Model quality

5.1 Standard geometry

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	S1	0.26	0/998	0.53	0/1321
2	S2	0.24	0/323	0.46	0/435
3	S3	0.26	0/793	0.60	0/1055
4	S4	0.26	0/597	0.58	1/801 (0.1%)
5	S5	0.29	0/460	0.74	1/609 (0.2%)
6	S6	0.23	0/349	0.55	0/458
7	S7	0.24	0/1754	0.85	1/2732 (0.0%)
8	SA	0.28	0/38276	0.84	30/59598 (0.1%)
9	SB	0.27	0/1737	0.52	0/2321
10	SC	0.26	0/1569	0.50	0/2129
11	SD	0.25	0/1240	0.55	1/1652 (0.1%)
12	SE	0.25	0/1538	0.55	0/2055
13	SF	0.27	0/2097	0.55	1/2819 (0.0%)
14	SG	0.28	0/1799	0.53	0/2429
15	SH	0.25	0/1668	0.56	0/2214
16	SI	0.25	0/1443	0.50	0/1936
17	SJ	0.25	0/1544	0.54	0/2064
18	SK	0.29	0/1054	0.57	0/1411
19	SL	0.26	0/1407	0.55	0/1879
20	SM	0.25	0/1113	0.54	0/1487
21	SN	0.24	0/780	0.56	0/1053
22	SO	0.27	0/705	0.51	0/950
23	SP	0.25	0/966	0.58	0/1295
24	SQ	0.27	0/1149	0.55	0/1532
25	SR	0.24	0/754	0.44	0/1013
26	SS	0.25	0/1062	0.59	0/1425
27	ST	0.24	0/412	0.54	0/544
28	SU	0.27	0/1223	0.52	0/1634
29	SV	0.27	0/1233	0.53	0/1645
30	SW	0.25	0/792	0.61	0/1053
31	SX	0.25	0/787	0.54	0/1050
32	SY	0.25	0/1294	0.52	0/1742
33	SZ	0.25	0/565	0.52	0/758
34	AA	0.36	0/75947	0.85	47/118255 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AC	0.37	0/3599	0.84	0/5603
36	AB	0.33	0/2823	0.79	0/4400
37	AL	0.27	0/1793	0.54	0/2387
38	A1	0.27	0/1151	0.55	1/1531 (0.1%)
39	A2	0.26	0/837	0.45	0/1112
40	A4	0.26	0/564	0.46	0/737
41	A6	0.27	0/740	0.54	0/990
42	A7	0.28	0/805	0.53	0/1073
43	AN	0.37	0/1226	0.61	0/1632
44	A8	0.28	0/1046	0.59	1/1389 (0.1%)
45	A9	0.31	0/860	0.58	0/1155
46	Aa	0.29	0/867	0.61	0/1156
47	Ab	0.26	0/762	0.55	0/1008
48	Ad	0.27	0/611	0.54	0/812
49	Ae	0.26	0/396	0.61	0/521
50	Af	0.27	0/418	0.58	0/556
51	AP	0.29	0/1720	0.58	0/2299
52	Ah	0.29	0/662	0.56	0/880
53	Ai	0.27	0/779	0.52	0/1021
54	AI	0.26	0/1708	0.48	0/2274
55	AJ	0.25	0/1840	0.49	0/2456
56	Ac	0.27	0/722	0.61	0/951
57	AK	0.28	0/1689	0.50	0/2260
58	AM	0.27	0/1012	0.52	0/1363
59	AS	0.28	0/1531	0.57	0/2040
60	AO	0.28	0/1199	0.52	0/1597
61	AQ	0.29	0/1579	0.53	0/2113
62	AR	0.27	0/2078	0.51	0/2776
63	AW	0.28	0/1244	0.56	0/1663
64	AY	0.27	0/805	0.49	0/1074
65	AT	0.27	0/1525	0.54	0/2016
66	AZ	0.26	0/1012	0.60	0/1339
67	A3	0.26	0/1004	0.51	0/1329
68	A5	0.29	0/1917	0.55	0/2562
69	AD	0.28	0/1901	0.56	0/2544
70	AE	0.28	0/3129	0.54	0/4195
71	AF	0.28	0/3144	0.52	1/4205 (0.0%)
72	AG	0.27	0/1020	0.57	0/1349
73	AU	0.28	0/1527	0.55	0/2043
74	AH	0.28	0/1500	0.56	0/2025
75	AV	0.29	0/1300	0.52	0/1732
76	Ag	0.25	0/348	0.69	0/448
77	AX	0.28	0/841	0.52	0/1125

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	A0	0.27	0/533	0.53	0/711
79	S8	0.25	0/2520	0.50	0/3428
All	All	0.31	0/209715	0.74	85/307234 (0.0%)

There are no bond length outliers.

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	SA	1444	C	C2-N1-C1'	9.62	129.38	118.80
34	AA	594	C	C2-N1-C1'	9.61	129.37	118.80
8	SA	415	C	N3-C2-O2	-8.93	115.65	121.90
34	AA	3382	U	C2-N1-C1'	8.92	128.41	117.70
8	SA	1635	C	N1-C2-O2	7.98	123.69	118.90
8	SA	1635	C	C2-N1-C1'	7.92	127.52	118.80
34	AA	1747	U	C2-N1-C1'	7.88	127.15	117.70
5	S5	28	GLN	N-CA-C	7.74	131.88	111.00
8	SA	1791	C	N3-C2-O2	-7.67	116.53	121.90
8	SA	1444	C	C6-N1-C1'	-7.64	111.63	120.80
8	SA	1635	C	N3-C2-O2	-7.34	116.76	121.90
34	AA	2804	C	N3-C2-O2	-7.13	116.91	121.90
34	AA	685	U	C2-N1-C1'	7.10	126.22	117.70
34	AA	3627	C	N1-C2-O2	7.09	123.15	118.90
34	AA	594	C	C6-N1-C1'	-6.90	112.53	120.80
34	AA	414	C	N1-C2-O2	6.87	123.02	118.90
8	SA	395	G	C5-C6-O6	6.85	132.71	128.60
34	AA	1747	U	N1-C2-O2	6.73	127.51	122.80
8	SA	1635	C	C6-N1-C2	-6.65	117.64	120.30
8	SA	387	C	N3-C2-O2	-6.60	117.28	121.90
8	SA	647	C	N1-C2-O2	6.54	122.83	118.90
34	AA	594	C	N1-C2-O2	6.51	122.81	118.90
34	AA	3382	U	C6-N1-C1'	-6.49	112.11	121.20
34	AA	3627	C	C2-N1-C1'	6.48	125.92	118.80
8	SA	1444	C	N1-C2-O2	6.42	122.75	118.90
34	AA	1041	U	C2-N1-C1'	6.39	125.37	117.70
44	A8	66	LEU	C-N-CA	6.28	137.41	121.70
38	A1	51	LEU	CA-CB-CG	6.26	129.71	115.30
8	SA	647	C	C2-N1-C1'	6.22	125.64	118.80
34	AA	3628	C	N3-C2-O2	-6.21	117.56	121.90
8	SA	1882	U	N3-C2-O2	-6.20	117.86	122.20
34	AA	685	U	N1-C2-O2	6.19	127.13	122.80
34	AA	200	A	N9-C4-C5	-6.11	103.36	105.80
8	SA	1069	C	C2-N1-C1'	6.07	125.47	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	SA	395	G	N1-C6-O6	-6.01	116.29	119.90
34	AA	1747	U	N3-C2-O2	-5.93	118.05	122.20
34	AA	3139	C	N1-C2-O2	5.90	122.44	118.90
8	SA	1387	U	O4'-C1'-N1	-5.89	103.48	108.20
8	SA	1809	G	C5-C6-O6	5.89	132.13	128.60
4	S4	39	LEU	CA-CB-CG	5.88	128.83	115.30
8	SA	647	C	N3-C2-O2	-5.84	117.81	121.90
8	SA	1034	U	C2-N1-C1'	5.84	124.70	117.70
34	AA	101	C	C2-N1-C1'	5.82	125.20	118.80
34	AA	1041	U	N1-C2-O2	5.75	126.83	122.80
34	AA	3139	C	C2-N1-C1'	5.73	125.10	118.80
8	SA	415	C	C6-N1-C2	-5.70	118.02	120.30
34	AA	594	C	C6-N1-C2	-5.69	118.02	120.30
34	AA	414	C	C2-N1-C1'	5.63	124.99	118.80
34	AA	768	C	C2-N1-C1'	5.60	124.96	118.80
8	SA	856	U	C2-N1-C1'	5.59	124.41	117.70
34	AA	265	U	N1-C2-O2	5.57	126.70	122.80
34	AA	1573	C	C2-N1-C1'	5.57	124.93	118.80
34	AA	685	U	N3-C2-O2	-5.55	118.31	122.20
8	SA	1455	C	OP1-P-O3'	5.53	117.38	105.20
34	AA	162	U	P-O3'-C3'	5.53	126.34	119.70
8	SA	415	C	N1-C2-O2	5.52	122.21	118.90
34	AA	494	U	C2-N1-C1'	5.51	124.32	117.70
34	AA	265	U	C2-N1-C1'	5.47	124.27	117.70
8	SA	161	U	C2-N1-C1'	5.42	124.21	117.70
34	AA	2524	C	N1-C2-O2	5.42	122.15	118.90
8	SA	1809	G	N1-C6-O6	-5.41	116.66	119.90
7	S7	72	C	C2-N3-C4	-5.39	117.20	119.90
34	AA	3627	C	C6-N1-C1'	-5.39	114.33	120.80
8	SA	1791	C	C6-N1-C2	-5.38	118.15	120.30
34	AA	1041	U	N3-C2-O2	-5.33	118.47	122.20
34	AA	1747	U	C6-N1-C1'	-5.33	113.74	121.20
34	AA	3202	U	N1-C2-O2	5.31	126.52	122.80
34	AA	2394	C	OP1-P-O3'	5.26	116.76	105.20
11	SD	143	LEU	CA-CB-CG	5.24	127.34	115.30
8	SA	1455	C	P-O3'-C3'	5.23	125.98	119.70
34	AA	2219	A	P-O3'-C3'	5.21	125.95	119.70
8	SA	1386	U	P-O3'-C3'	5.20	125.93	119.70
34	AA	3202	U	C2-N1-C1'	5.17	123.90	117.70
34	AA	2804	C	N1-C2-O2	5.16	122.00	118.90
13	SF	246	LEU	CA-CB-CG	5.08	126.98	115.30
34	AA	3628	C	C6-N1-C2	-5.06	118.28	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	594	C	N3-C2-O2	-5.06	118.36	121.90
34	AA	2524	C	C2-N1-C1'	5.03	124.33	118.80
34	AA	2556	C	C2-N1-C1'	5.02	124.33	118.80
34	AA	3382	U	N1-C2-O2	5.02	126.31	122.80
34	AA	494	U	N1-C2-O2	5.01	126.31	122.80
34	AA	414	C	N3-C2-O2	-5.01	118.39	121.90
71	AF	196	MET	CA-CB-CG	5.01	121.82	113.30
8	SA	1857	U	C2-N1-C1'	5.01	123.71	117.70
34	AA	3627	C	N3-C2-O2	-5.00	118.40	121.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

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	
1	S1	118/133 (89%)	112 (95%)	6 (5%)	0	100	100
2	S2	35/105 (33%)	33 (94%)	2 (6%)	0	100	100
3	S3	93/107 (87%)	84 (90%)	9 (10%)	0	100	100
4	S4	74/82 (90%)	60 (81%)	14 (19%)	0	100	100
5	S5	56/58 (97%)	49 (88%)	5 (9%)	2 (4%)	3	23
6	S6	41/43 (95%)	35 (85%)	6 (15%)	0	100	100
9	SB	208/262 (79%)	196 (94%)	10 (5%)	2 (1%)	13	48
10	SC	193/263 (73%)	179 (93%)	13 (7%)	1 (0%)	25	62
11	SD	149/221 (67%)	143 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	SE	183/189 (97%)	171 (93%)	12 (7%)	0	100	100
13	SF	255/261 (98%)	235 (92%)	19 (8%)	1 (0%)	30	67
14	SG	222/272 (82%)	209 (94%)	13 (6%)	0	100	100
15	SH	200/306 (65%)	187 (94%)	12 (6%)	1 (0%)	25	62
16	SI	176/195 (90%)	163 (93%)	13 (7%)	0	100	100
17	SJ	186/194 (96%)	168 (90%)	16 (9%)	2 (1%)	12	46
18	SK	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
19	SL	165/218 (76%)	147 (89%)	16 (10%)	2 (1%)	11	44
20	SM	136/144 (94%)	128 (94%)	7 (5%)	1 (1%)	19	56
21	SN	96/118 (81%)	90 (94%)	6 (6%)	0	100	100
22	SO	77/137 (56%)	71 (92%)	5 (6%)	1 (1%)	10	42
23	SP	125/151 (83%)	118 (94%)	6 (5%)	1 (1%)	16	53
24	SQ	142/145 (98%)	132 (93%)	10 (7%)	0	100	100
25	SR	92/141 (65%)	86 (94%)	6 (6%)	0	100	100
26	SS	126/156 (81%)	99 (79%)	24 (19%)	3 (2%)	5	30
27	ST	46/54 (85%)	44 (96%)	2 (4%)	0	100	100
28	SU	147/151 (97%)	141 (96%)	6 (4%)	0	100	100
29	SV	142/161 (88%)	131 (92%)	10 (7%)	1 (1%)	19	56
30	SW	91/137 (66%)	82 (90%)	7 (8%)	2 (2%)	5	32
31	SX	92/145 (63%)	83 (90%)	9 (10%)	0	100	100
32	SY	152/170 (89%)	147 (97%)	5 (3%)	0	100	100
33	SZ	70/82 (85%)	65 (93%)	4 (6%)	1 (1%)	9	40
37	AL	209/215 (97%)	200 (96%)	9 (4%)	0	100	100
38	A1	136/146 (93%)	123 (90%)	13 (10%)	0	100	100
39	A2	96/126 (76%)	93 (97%)	3 (3%)	0	100	100
40	A4	64/67 (96%)	58 (91%)	6 (9%)	0	100	100
41	A6	95/107 (89%)	89 (94%)	6 (6%)	0	100	100
42	A7	92/120 (77%)	92 (100%)	0	0	100	100
43	AN	145/165 (88%)	134 (92%)	10 (7%)	1 (1%)	19	56
44	A8	122/130 (94%)	100 (82%)	22 (18%)	0	100	100
45	A9	100/139 (72%)	87 (87%)	13 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	Aa	103/149 (69%)	95 (92%)	8 (8%)	0	100	100
47	Ab	91/112 (81%)	85 (93%)	6 (7%)	0	100	100
48	Ad	68/87 (78%)	66 (97%)	2 (3%)	0	100	100
49	Ae	39/51 (76%)	39 (100%)	0	0	100	100
50	Af	49/128 (38%)	42 (86%)	7 (14%)	0	100	100
51	AP	200/203 (98%)	179 (90%)	17 (8%)	4 (2%)	6	34
52	Ah	82/95 (86%)	76 (93%)	6 (7%)	0	100	100
53	Ai	92/103 (89%)	84 (91%)	8 (9%)	0	100	100
54	AI	203/221 (92%)	190 (94%)	12 (6%)	1 (0%)	25	62
55	AJ	216/283 (76%)	208 (96%)	7 (3%)	1 (0%)	25	62
56	Ac	87/92 (95%)	72 (83%)	15 (17%)	0	100	100
57	AK	199/202 (98%)	193 (97%)	6 (3%)	0	100	100
58	AM	130/139 (94%)	122 (94%)	8 (6%)	0	100	100
59	AS	184/187 (98%)	174 (95%)	10 (5%)	0	100	100
60	AO	145/148 (98%)	131 (90%)	14 (10%)	0	100	100
61	AQ	185/219 (84%)	166 (90%)	16 (9%)	3 (2%)	8	39
62	AR	244/294 (83%)	231 (95%)	13 (5%)	0	100	100
63	AW	149/173 (86%)	139 (93%)	10 (7%)	0	100	100
64	AY	99/190 (52%)	95 (96%)	4 (4%)	0	100	100
65	AT	179/182 (98%)	175 (98%)	4 (2%)	0	100	100
66	AZ	119/126 (94%)	114 (96%)	5 (4%)	0	100	100
67	A3	117/124 (94%)	105 (90%)	12 (10%)	0	100	100
68	A5	221/257 (86%)	206 (93%)	15 (7%)	0	100	100
69	AD	245/260 (94%)	230 (94%)	14 (6%)	1 (0%)	30	67
70	AE	378/386 (98%)	361 (96%)	17 (4%)	0	100	100
71	AF	388/411 (94%)	362 (93%)	25 (6%)	1 (0%)	37	71
72	AG	116/173 (67%)	110 (95%)	6 (5%)	0	100	100
73	AU	178/184 (97%)	172 (97%)	6 (3%)	0	100	100
74	AH	183/190 (96%)	172 (94%)	11 (6%)	0	100	100
75	AV	153/162 (94%)	143 (94%)	10 (6%)	0	100	100
76	Ag	35/39 (90%)	29 (83%)	6 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	AX	95/139 (68%)	88 (93%)	7 (7%)	0	100	100
78	A0	60/162 (37%)	57 (95%)	3 (5%)	0	100	100
79	S8	315/323 (98%)	300 (95%)	15 (5%)	0	100	100
All	All	10421/12340 (84%)	9689 (93%)	699 (7%)	33 (0%)	38	71

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	SH	148	ASP
17	SJ	112	ILE
20	SM	41	GLU
29	SV	41	VAL
30	SW	4	VAL
51	AP	79	VAL
51	AP	148	ILE
55	AJ	75	ILE
5	S5	31	ARG
9	SB	93	ASN
19	SL	168	ILE
22	SO	35	GLU
26	SS	102	ALA
51	AP	121	VAL
54	AI	19	VAL
5	S5	27	ALA
9	SB	146	ARG
26	SS	101	ILE
61	AQ	24	ARG
10	SC	143	VAL
19	SL	119	THR
51	AP	77	LYS
13	SF	195	ILE
17	SJ	110	PHE
30	SW	69	ILE
33	SZ	81	GLN
43	AN	18	ASN
61	AQ	14	ASN
61	AQ	60	ILE
69	AD	199	VAL
23	SP	144	SER
71	AF	267	ILE
26	SS	14	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	
1	S1	104/115 (90%)	104 (100%)	0	100	100
2	S2	35/88 (40%)	34 (97%)	1 (3%)	37	58
3	S3	87/98 (89%)	87 (100%)	0	100	100
4	S4	70/76 (92%)	70 (100%)	0	100	100
5	S5	47/47 (100%)	43 (92%)	4 (8%)	8	30
6	S6	36/36 (100%)	36 (100%)	0	100	100
9	SB	195/238 (82%)	195 (100%)	0	100	100
10	SC	167/227 (74%)	166 (99%)	1 (1%)	84	88
11	SD	132/188 (70%)	130 (98%)	2 (2%)	60	75
12	SE	161/167 (96%)	161 (100%)	0	100	100
13	SF	233/237 (98%)	233 (100%)	0	100	100
14	SG	191/222 (86%)	191 (100%)	0	100	100
15	SH	182/279 (65%)	181 (100%)	1 (0%)	86	90
16	SI	154/165 (93%)	153 (99%)	1 (1%)	84	88
17	SJ	177/183 (97%)	174 (98%)	3 (2%)	56	72
18	SK	115/116 (99%)	115 (100%)	0	100	100
19	SL	151/193 (78%)	151 (100%)	0	100	100
20	SM	116/122 (95%)	116 (100%)	0	100	100
21	SN	91/109 (84%)	90 (99%)	1 (1%)	70	80
22	SO	76/129 (59%)	75 (99%)	1 (1%)	65	77
23	SP	99/119 (83%)	99 (100%)	0	100	100
24	SQ	120/121 (99%)	119 (99%)	1 (1%)	79	84
25	SR	83/121 (69%)	83 (100%)	0	100	100
26	SS	114/136 (84%)	114 (100%)	0	100	100
27	ST	43/48 (90%)	43 (100%)	0	100	100
28	SU	132/133 (99%)	132 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	SV	131/144 (91%)	130 (99%)	1 (1%)	79	84
30	SW	86/127 (68%)	86 (100%)	0	100	100
31	SX	88/130 (68%)	88 (100%)	0	100	100
32	SY	137/151 (91%)	136 (99%)	1 (1%)	81	86
33	SZ	60/70 (86%)	59 (98%)	1 (2%)	56	72
37	AL	190/194 (98%)	189 (100%)	1 (0%)	86	90
38	A1	127/132 (96%)	126 (99%)	1 (1%)	79	84
39	A2	97/117 (83%)	97 (100%)	0	100	100
40	A4	60/61 (98%)	60 (100%)	0	100	100
41	A6	82/91 (90%)	82 (100%)	0	100	100
42	A7	90/112 (80%)	90 (100%)	0	100	100
43	AN	136/152 (90%)	125 (92%)	11 (8%)	9	31
44	A8	113/119 (95%)	112 (99%)	1 (1%)	75	83
45	A9	90/127 (71%)	90 (100%)	0	100	100
46	Aa	89/128 (70%)	89 (100%)	0	100	100
47	Ab	82/97 (84%)	81 (99%)	1 (1%)	67	79
48	Ad	69/83 (83%)	69 (100%)	0	100	100
49	Ae	40/48 (83%)	40 (100%)	0	100	100
50	Af	45/114 (40%)	45 (100%)	0	100	100
51	AP	177/178 (99%)	177 (100%)	0	100	100
52	Ah	70/80 (88%)	70 (100%)	0	100	100
53	Ai	86/92 (94%)	86 (100%)	0	100	100
54	AI	189/203 (93%)	189 (100%)	0	100	100
55	AJ	204/260 (78%)	202 (99%)	2 (1%)	73	81
56	Ac	74/77 (96%)	72 (97%)	2 (3%)	40	61
57	AK	181/182 (100%)	181 (100%)	0	100	100
58	AM	106/110 (96%)	106 (100%)	0	100	100
59	AS	158/159 (99%)	158 (100%)	0	100	100
60	AO	121/122 (99%)	120 (99%)	1 (1%)	79	84
61	AQ	165/190 (87%)	164 (99%)	1 (1%)	84	88
62	AR	215/254 (85%)	214 (100%)	1 (0%)	86	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	AW	128/131 (98%)	127 (99%)	1 (1%)	79	84
64	AY	90/177 (51%)	90 (100%)	0	100	100
65	AT	162/163 (99%)	162 (100%)	0	100	100
66	AZ	111/115 (96%)	110 (99%)	1 (1%)	75	83
67	A3	110/115 (96%)	109 (99%)	1 (1%)	75	83
68	A5	201/231 (87%)	200 (100%)	1 (0%)	86	90
69	AD	191/202 (95%)	190 (100%)	1 (0%)	86	90
70	AE	335/340 (98%)	333 (99%)	2 (1%)	84	88
71	AF	336/352 (96%)	336 (100%)	0	100	100
72	AG	110/155 (71%)	109 (99%)	1 (1%)	75	83
73	AU	162/166 (98%)	161 (99%)	1 (1%)	84	88
74	AH	168/173 (97%)	168 (100%)	0	100	100
75	AV	140/145 (97%)	140 (100%)	0	100	100
76	Ag	34/35 (97%)	33 (97%)	1 (3%)	37	58
77	AX	92/131 (70%)	92 (100%)	0	100	100
78	A0	53/146 (36%)	52 (98%)	1 (2%)	52	69
79	S8	281/287 (98%)	281 (100%)	0	100	100
All	All	9373/10881 (86%)	9321 (99%)	52 (1%)	82	88

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	S2	99	LYS
5	S5	28	GLN
5	S5	31	ARG
5	S5	32	PHE
5	S5	42	ARG
10	SC	204	ARG
11	SD	76	ARG
11	SD	118	ARG
15	SH	160	ARG
16	SI	118	ARG
17	SJ	36	LYS
17	SJ	106	LYS
17	SJ	162	ARG
21	SN	46	ASN

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Mol	Chain	Res	Type
22	SO	64	ASN
24	SQ	129	ARG
29	SV	70	ARG
32	SY	55	LYS
33	SZ	33	GLN
37	AL	10	ASN
38	A1	84	ARG
43	AN	6	LEU
43	AN	8	GLU
43	AN	9	GLU
43	AN	10	GLU
43	AN	11	LYS
43	AN	12	LEU
43	AN	13	TYR
43	AN	15	SER
43	AN	16	LYS
43	AN	17	LYS
43	AN	18	ASN
44	A8	79	LYS
47	Ab	39	LYS
55	AJ	73	ARG
55	AJ	248	LYS
56	Ac	75	ARG
56	Ac	78	LYS
60	AO	4	ARG
61	AQ	82	LYS
62	AR	85	ARG
63	AW	97	ASN
66	AZ	116	LYS
67	A3	99	LYS
68	A5	86	ARG
69	AD	30	ARG
70	AE	132	LYS
70	AE	237	ARG
72	AG	141	ARG
73	AU	177	LYS
76	Ag	7	ARG
78	A0	67	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	S1	15	ASN
6	S6	17	GLN
10	SC	155	HIS
11	SD	13	ASN
13	SF	142	HIS
16	SI	101	GLN
17	SJ	5	GLN
18	SK	24	GLN
18	SK	101	HIS
22	SO	17	GLN
22	SO	50	ASN
44	A8	21	GLN
51	AP	86	GLN
51	AP	117	ASN
51	AP	195	GLN
53	Ai	14	ASN
57	AK	28	ASN
61	AQ	14	ASN
63	AW	147	GLN
66	AZ	113	ASN
67	A3	62	GLN
69	AD	115	ASN
70	AE	11	HIS
70	AE	68	HIS
70	AE	342	GLN
71	AF	38	GLN
75	AV	113	ASN
78	A0	49	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	AA	3164/3788 (83%)	747 (23%)	71 (2%)
35	AC	148/159 (93%)	37 (25%)	5 (3%)
36	AB	117/119 (98%)	18 (15%)	3 (2%)
7	S7	73/74 (98%)	19 (26%)	1 (1%)
8	SA	1587/2087 (76%)	366 (23%)	27 (1%)
All	All	5089/6227 (81%)	1187 (23%)	107 (2%)

All (1187) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	S7	8	U
7	S7	10	G
7	S7	16	U
7	S7	17	U
7	S7	18	G
7	S7	19	G
7	S7	20	U
7	S7	32	U
7	S7	34	U
7	S7	37	U
7	S7	46	G
7	S7	53	A
7	S7	54	G
7	S7	56	U
7	S7	57	C
7	S7	69	U
7	S7	72	C
7	S7	73	C
7	S7	74	A
8	SA	2	A
8	SA	5	U
8	SA	26	A
8	SA	27	U
8	SA	34	G
8	SA	35	U
8	SA	42	G
8	SA	43	A
8	SA	44	U
8	SA	45	U
8	SA	47	A
8	SA	57	G
8	SA	59	G
8	SA	65	A
8	SA	71	A
8	SA	73	A
8	SA	74	U
8	SA	79	U
8	SA	82	G
8	SA	84	A
8	SA	102	A
8	SA	106	A
8	SA	107	A
8	SA	116	A

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Mol	Chain	Res	Type
8	SA	118	U
8	SA	126	A
8	SA	128	A
8	SA	129	U
8	SA	130	U
8	SA	143	A
8	SA	144	U
8	SA	151	G
8	SA	157	G
8	SA	164	C
8	SA	166	A
8	SA	168	U
8	SA	179	U
8	SA	183	C
8	SA	207	G
8	SA	208	U
8	SA	247	G
8	SA	248	G
8	SA	249	A
8	SA	251	U
8	SA	252	U
8	SA	259	A
8	SA	260	A
8	SA	262	A
8	SA	263	A
8	SA	266	A
8	SA	268	C
8	SA	271	G
8	SA	272	U
8	SA	274	A
8	SA	292	G
8	SA	305	G
8	SA	314	A
8	SA	315	C
8	SA	320	C
8	SA	322	G
8	SA	326	U
8	SA	339	A
8	SA	343	G
8	SA	344	C
8	SA	358	G
8	SA	365	A

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Mol	Chain	Res	Type
8	SA	367	C
8	SA	371	G
8	SA	375	U
8	SA	376	A
8	SA	379	G
8	SA	386	U
8	SA	395	G
8	SA	406	A
8	SA	408	U
8	SA	409	A
8	SA	410	G
8	SA	422	A
8	SA	423	A
8	SA	424	G
8	SA	429	G
8	SA	430	C
8	SA	432	G
8	SA	443	A
8	SA	445	U
8	SA	450	C
8	SA	459	A
8	SA	474	A
8	SA	475	C
8	SA	487	A
8	SA	488	U
8	SA	494	G
8	SA	509	U
8	SA	515	U
8	SA	516	G
8	SA	518	A
8	SA	526	G
8	SA	543	A
8	SA	545	A
8	SA	546	G
8	SA	548	A
8	SA	549	A
8	SA	558	G
8	SA	564	G
8	SA	565	U
8	SA	566	C
8	SA	575	G
8	SA	581	G

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Mol	Chain	Res	Type
8	SA	585	U
8	SA	601	A
8	SA	618	U
8	SA	626	A
8	SA	627	A
8	SA	628	A
8	SA	629	A
8	SA	630	C
8	SA	631	G
8	SA	641	G
8	SA	642	A
8	SA	646	U
8	SA	647	C
8	SA	653	A
8	SA	655	C
8	SA	746	U
8	SA	753	U
8	SA	754	A
8	SA	757	A
8	SA	760	C
8	SA	790	U
8	SA	791	U
8	SA	793	G
8	SA	801	G
8	SA	803	G
8	SA	804	U
8	SA	805	A
8	SA	806	A
8	SA	815	G
8	SA	816	U
8	SA	818	C
8	SA	821	A
8	SA	824	A
8	SA	830	U
8	SA	833	A
8	SA	837	A
8	SA	845	U
8	SA	846	G
8	SA	849	U
8	SA	851	A
8	SA	852	A
8	SA	856	U

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Mol	Chain	Res	Type
8	SA	857	A
8	SA	858	U
8	SA	866	A
8	SA	870	A
8	SA	875	A
8	SA	877	U
8	SA	879	A
8	SA	888	A
8	SA	908	U
8	SA	913	U
8	SA	915	G
8	SA	920	A
8	SA	924	A
8	SA	925	C
8	SA	929	U
8	SA	931	A
8	SA	941	C
8	SA	942	U
8	SA	966	C
8	SA	967	A
8	SA	973	G
8	SA	974	A
8	SA	982	A
8	SA	983	G
8	SA	984	A
8	SA	999	A
8	SA	1002	A
8	SA	1004	U
8	SA	1011	G
8	SA	1013	A
8	SA	1029	U
8	SA	1035	A
8	SA	1057	A
8	SA	1061	A
8	SA	1062	A
8	SA	1065	C
8	SA	1073	U
8	SA	1074	A
8	SA	1093	U
8	SA	1095	A
8	SA	1096	A
8	SA	1097	C

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Mol	Chain	Res	Type
8	SA	1099	A
8	SA	1101	G
8	SA	1108	A
8	SA	1109	G
8	SA	1112	G
8	SA	1168	U
8	SA	1175	G
8	SA	1177	A
8	SA	1182	A
8	SA	1183	U
8	SA	1187	A
8	SA	1193	A
8	SA	1197	C
8	SA	1198	U
8	SA	1199	U
8	SA	1214	A
8	SA	1219	U
8	SA	1239	A
8	SA	1251	G
8	SA	1252	A
8	SA	1259	C
8	SA	1261	A
8	SA	1265	G
8	SA	1268	G
8	SA	1271	G
8	SA	1285	A
8	SA	1286	U
8	SA	1291	C
8	SA	1292	U
8	SA	1295	A
8	SA	1296	C
8	SA	1297	A
8	SA	1300	G
8	SA	1301	G
8	SA	1303	A
8	SA	1307	U
8	SA	1308	C
8	SA	1313	G
8	SA	1317	A
8	SA	1318	A
8	SA	1363	U
8	SA	1366	A

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Mol	Chain	Res	Type
8	SA	1367	U
8	SA	1370	U
8	SA	1374	G
8	SA	1377	U
8	SA	1382	G
8	SA	1386	U
8	SA	1387	U
8	SA	1388	A
8	SA	1414	A
8	SA	1415	A
8	SA	1416	U
8	SA	1417	U
8	SA	1421	A
8	SA	1422	U
8	SA	1423	A
8	SA	1432	G
8	SA	1443	G
8	SA	1444	C
8	SA	1445	U
8	SA	1446	A
8	SA	1448	U
8	SA	1453	G
8	SA	1454	G
8	SA	1456	G
8	SA	1458	G
8	SA	1460	A
8	SA	1464	U
8	SA	1624	U
8	SA	1625	C
8	SA	1626	U
8	SA	1629	G
8	SA	1636	A
8	SA	1639	G
8	SA	1640	U
8	SA	1644	U
8	SA	1645	C
8	SA	1658	G
8	SA	1659	U
8	SA	1660	U
8	SA	1661	U
8	SA	1662	A
8	SA	1664	G

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Mol	Chain	Res	Type
8	SA	1665	G
8	SA	1671	A
8	SA	1673	A
8	SA	1674	G
8	SA	1677	C
8	SA	1678	U
8	SA	1679	G
8	SA	1682	A
8	SA	1691	G
8	SA	1692	A
8	SA	1694	G
8	SA	1706	A
8	SA	1715	A
8	SA	1717	A
8	SA	1719	U
8	SA	1720	G
8	SA	1721	A
8	SA	1727	A
8	SA	1728	U
8	SA	1729	A
8	SA	1732	G
8	SA	1735	U
8	SA	1742	A
8	SA	1784	A
8	SA	1787	U
8	SA	1790	C
8	SA	1792	U
8	SA	1795	G
8	SA	1802	G
8	SA	1806	U
8	SA	1812	A
8	SA	1814	C
8	SA	1817	U
8	SA	1818	A
8	SA	1819	U
8	SA	1820	C
8	SA	1824	A
8	SA	1833	G
8	SA	1834	A
8	SA	1836	G
8	SA	1837	G
8	SA	1839	G

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Mol	Chain	Res	Type
8	SA	1843	G
8	SA	1854	U
8	SA	1855	U
8	SA	1856	A
8	SA	1862	C
8	SA	1866	A
8	SA	1870	A
8	SA	1871	G
8	SA	1881	G
8	SA	1898	G
8	SA	1902	G
8	SA	1907	G
8	SA	1908	A
8	SA	1911	A
8	SA	1912	C
8	SA	1913	G
8	SA	1915	C
8	SA	1916	C
8	SA	1928	A
8	SA	1930	A
8	SA	1932	A
8	SA	1954	U
8	SA	1955	G
8	SA	1961	U
8	SA	1969	A
8	SA	1976	G
8	SA	1977	G
8	SA	1978	A
8	SA	1980	A
8	SA	1982	G
8	SA	2010	U
8	SA	2019	C
8	SA	2034	U
8	SA	2048	A
8	SA	2049	G
8	SA	2052	G
8	SA	2054	A
8	SA	2058	A
8	SA	2061	U
8	SA	2072	G
8	SA	2075	C
8	SA	2084	G

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Mol	Chain	Res	Type
8	SA	2085	G
8	SA	2086	A
8	SA	2087	U
8	SA	2088	C
8	SA	2089	A
8	SA	2090	U
34	AA	11	A
34	AA	13	G
34	AA	14	U
34	AA	15	U
34	AA	26	A
34	AA	40	A
34	AA	41	G
34	AA	43	A
34	AA	45	A
34	AA	49	U
34	AA	60	A
34	AA	62	A
34	AA	63	A
34	AA	66	A
34	AA	70	A
34	AA	72	C
34	AA	74	A
34	AA	77	A
34	AA	85	A
34	AA	110	G
34	AA	113	C
34	AA	121	U
34	AA	124	U
34	AA	130	G
34	AA	133	U
34	AA	134	G
34	AA	136	U
34	AA	137	G
34	AA	141	A
34	AA	147	C
34	AA	155	U
34	AA	163	G
34	AA	164	A
34	AA	167	U
34	AA	169	U
34	AA	174	U

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Mol	Chain	Res	Type
34	AA	179	G
34	AA	180	C
34	AA	182	U
34	AA	183	U
34	AA	185	A
34	AA	192	G
34	AA	197	G
34	AA	198	U
34	AA	199	G
34	AA	200	A
34	AA	201	G
34	AA	204	G
34	AA	207	A
34	AA	211	U
34	AA	216	C
34	AA	219	A
34	AA	226	G
34	AA	227	A
34	AA	229	A
34	AA	230	G
34	AA	232	C
34	AA	239	U
34	AA	242	U
34	AA	246	U
34	AA	250	U
34	AA	258	U
34	AA	269	A
34	AA	271	G
34	AA	276	G
34	AA	277	U
34	AA	290	G
34	AA	292	U
34	AA	293	U
34	AA	302	A
34	AA	303	A
34	AA	306	C
34	AA	307	G
34	AA	308	U
34	AA	309	G
34	AA	313	U
34	AA	323	A
34	AA	334	U

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Mol	Chain	Res	Type
34	AA	337	A
34	AA	338	U
34	AA	347	C
34	AA	352	A
34	AA	360	A
34	AA	382	A
34	AA	384	A
34	AA	386	U
34	AA	396	U
34	AA	400	C
34	AA	409	A
34	AA	411	U
34	AA	412	A
34	AA	413	C
34	AA	414	C
34	AA	431	G
34	AA	432	A
34	AA	433	A
34	AA	439	U
34	AA	440	A
34	AA	445	A
34	AA	447	A
34	AA	448	A
34	AA	449	A
34	AA	451	C
34	AA	459	G
34	AA	462	G
34	AA	463	G
34	AA	490	U
34	AA	495	U
34	AA	497	U
34	AA	501	U
34	AA	502	U
34	AA	504	A
34	AA	505	A
34	AA	506	A
34	AA	509	A
34	AA	520	U
34	AA	521	U
34	AA	522	A
34	AA	523	A
34	AA	530	U

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Mol	Chain	Res	Type
34	AA	532	C
34	AA	536	A
34	AA	537	A
34	AA	542	A
34	AA	543	U
34	AA	551	A
34	AA	573	U
34	AA	580	A
34	AA	581	C
34	AA	582	U
34	AA	583	U
34	AA	585	C
34	AA	592	C
34	AA	593	A
34	AA	598	U
34	AA	599	G
34	AA	608	A
34	AA	609	C
34	AA	610	U
34	AA	620	U
34	AA	621	C
34	AA	623	U
34	AA	625	A
34	AA	642	A
34	AA	648	U
34	AA	650	U
34	AA	652	A
34	AA	653	A
34	AA	665	U
34	AA	666	U
34	AA	667	U
34	AA	668	U
34	AA	673	U
34	AA	674	U
34	AA	675	A
34	AA	679	U
34	AA	680	U
34	AA	682	A
34	AA	683	A
34	AA	684	G
34	AA	685	U
34	AA	693	A

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Mol	Chain	Res	Type
34	AA	694	U
34	AA	697	A
34	AA	698	G
34	AA	699	U
34	AA	700	A
34	AA	704	U
34	AA	708	A
34	AA	715	U
34	AA	716	C
34	AA	720	U
34	AA	722	G
34	AA	727	A
34	AA	738	A
34	AA	755	A
34	AA	759	U
34	AA	760	A
34	AA	763	U
34	AA	765	A
34	AA	767	U
34	AA	768	C
34	AA	769	U
34	AA	771	U
34	AA	772	A
34	AA	773	A
34	AA	774	A
34	AA	778	U
34	AA	798	U
34	AA	799	A
34	AA	803	A
34	AA	806	G
34	AA	809	A
34	AA	810	U
34	AA	812	U
34	AA	813	G
34	AA	818	C
34	AA	822	A
34	AA	827	A
34	AA	830	U
34	AA	834	U
34	AA	835	G
34	AA	857	C
34	AA	858	C

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Mol	Chain	Res	Type
34	AA	859	C
34	AA	860	A
34	AA	861	C
34	AA	862	U
34	AA	863	U
34	AA	866	C
34	AA	871	A
34	AA	874	A
34	AA	885	A
34	AA	889	U
34	AA	890	G
34	AA	893	U
34	AA	896	U
34	AA	899	A
34	AA	900	G
34	AA	903	C
34	AA	904	G
34	AA	905	A
34	AA	909	U
34	AA	918	G
34	AA	925	A
34	AA	927	A
34	AA	935	A
34	AA	936	A
34	AA	939	A
34	AA	949	A
34	AA	950	G
34	AA	966	A
34	AA	968	G
34	AA	969	U
34	AA	976	G
34	AA	980	A
34	AA	984	A
34	AA	986	U
34	AA	993	U
34	AA	998	U
34	AA	999	G
34	AA	1016	A
34	AA	1026	G
34	AA	1027	G
34	AA	1028	G
34	AA	1032	A

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Mol	Chain	Res	Type
34	AA	1033	A
34	AA	1034	A
34	AA	1035	G
34	AA	1036	A
34	AA	1040	A
34	AA	1043	G
34	AA	1044	A
34	AA	1056	G
34	AA	1062	U
34	AA	1063	A
34	AA	1070	A
34	AA	1073	G
34	AA	1074	A
34	AA	1078	C
34	AA	1086	C
34	AA	1096	G
34	AA	1100	A
34	AA	1101	A
34	AA	1106	A
34	AA	1107	U
34	AA	1111	A
34	AA	1112	C
34	AA	1122	A
34	AA	1123	U
34	AA	1124	A
34	AA	1132	G
34	AA	1158	G
34	AA	1170	A
34	AA	1172	C
34	AA	1186	A
34	AA	1189	G
34	AA	1197	U
34	AA	1198	A
34	AA	1199	A
34	AA	1200	C
34	AA	1205	U
34	AA	1206	U
34	AA	1208	G
34	AA	1209	U
34	AA	1215	A
34	AA	1217	U
34	AA	1218	C

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Mol	Chain	Res	Type
34	AA	1221	A
34	AA	1222	U
34	AA	1223	U
34	AA	1225	A
34	AA	1228	A
34	AA	1229	A
34	AA	1230	A
34	AA	1231	A
34	AA	1232	U
34	AA	1233	A
34	AA	1245	G
34	AA	1259	G
34	AA	1271	A
34	AA	1279	U
34	AA	1283	C
34	AA	1287	A
34	AA	1296	U
34	AA	1305	U
34	AA	1310	A
34	AA	1317	C
34	AA	1319	U
34	AA	1320	G
34	AA	1325	C
34	AA	1327	C
34	AA	1329	U
34	AA	1334	G
34	AA	1337	G
34	AA	1344	C
34	AA	1346	U
34	AA	1420	C
34	AA	1423	G
34	AA	1432	A
34	AA	1435	G
34	AA	1436	A
34	AA	1437	U
34	AA	1441	G
34	AA	1445	A
34	AA	1453	U
34	AA	1455	C
34	AA	1458	A
34	AA	1476	A
34	AA	1481	A

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Mol	Chain	Res	Type
34	AA	1495	U
34	AA	1498	U
34	AA	1499	U
34	AA	1503	A
34	AA	1504	A
34	AA	1505	U
34	AA	1506	C
34	AA	1524	U
34	AA	1529	G
34	AA	1535	G
34	AA	1537	G
34	AA	1538	U
34	AA	1539	U
34	AA	1540	G
34	AA	1549	U
34	AA	1550	A
34	AA	1553	U
34	AA	1554	G
34	AA	1555	A
34	AA	1556	G
34	AA	1565	G
34	AA	1567	A
34	AA	1571	C
34	AA	1572	U
34	AA	1575	C
34	AA	1583	G
34	AA	1584	A
34	AA	1586	C
34	AA	1595	A
34	AA	1601	A
34	AA	1602	A
34	AA	1604	U
34	AA	1619	U
34	AA	1630	A
34	AA	1631	A
34	AA	1633	U
34	AA	1636	A
34	AA	1637	G
34	AA	1645	U
34	AA	1657	U
34	AA	1672	U
34	AA	1676	C

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Mol	Chain	Res	Type
34	AA	1682	U
34	AA	1685	G
34	AA	1691	G
34	AA	1703	U
34	AA	1704	U
34	AA	1705	A
34	AA	1706	A
34	AA	1707	A
34	AA	1725	U
34	AA	1732	A
34	AA	1736	A
34	AA	1737	A
34	AA	1739	C
34	AA	1744	U
34	AA	1748	A
34	AA	1750	U
34	AA	1762	A
34	AA	1763	G
34	AA	1767	U
34	AA	1769	U
34	AA	1771	A
34	AA	1774	U
34	AA	1781	A
34	AA	1782	U
34	AA	1783	G
34	AA	1788	C
34	AA	1793	A
34	AA	1795	A
34	AA	1797	A
34	AA	1800	U
34	AA	1801	G
34	AA	1806	C
34	AA	1812	C
34	AA	1838	U
34	AA	1842	U
34	AA	1855	U
34	AA	1856	U
34	AA	1881	C
34	AA	1882	U
34	AA	1886	A
34	AA	1898	U
34	AA	1899	U

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Mol	Chain	Res	Type
34	AA	1902	A
34	AA	1903	C
34	AA	1904	U
34	AA	1905	C
34	AA	1914	A
34	AA	1964	G
34	AA	1969	A
34	AA	1970	A
34	AA	1971	U
34	AA	1976	A
34	AA	1978	U
34	AA	1980	G
34	AA	1981	U
34	AA	1991	U
34	AA	1996	C
34	AA	1997	G
34	AA	1998	A
34	AA	2000	G
34	AA	2003	G
34	AA	2004	U
34	AA	2009	A
34	AA	2019	A
34	AA	2023	A
34	AA	2030	G
34	AA	2031	A
34	AA	2032	A
34	AA	2034	G
34	AA	2072	U
34	AA	2081	U
34	AA	2082	C
34	AA	2084	U
34	AA	2090	U
34	AA	2092	G
34	AA	2093	U
34	AA	2096	G
34	AA	2102	A
34	AA	2106	A
34	AA	2107	C
34	AA	2108	A
34	AA	2109	A
34	AA	2113	C
34	AA	2117	A

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Mol	Chain	Res	Type
34	AA	2121	C
34	AA	2125	A
34	AA	2145	A
34	AA	2146	A
34	AA	2147	A
34	AA	2148	U
34	AA	2153	A
34	AA	2154	A
34	AA	2160	G
34	AA	2161	G
34	AA	2163	A
34	AA	2174	G
34	AA	2175	C
34	AA	2176	A
34	AA	2178	A
34	AA	2180	U
34	AA	2181	A
34	AA	2219	A
34	AA	2220	U
34	AA	2221	U
34	AA	2394	C
34	AA	2395	U
34	AA	2400	A
34	AA	2404	A
34	AA	2405	A
34	AA	2409	G
34	AA	2410	A
34	AA	2415	G
34	AA	2424	A
34	AA	2433	U
34	AA	2435	A
34	AA	2438	A
34	AA	2451	A
34	AA	2453	A
34	AA	2461	A
34	AA	2463	U
34	AA	2467	A
34	AA	2480	G
34	AA	2481	A
34	AA	2485	C
34	AA	2487	G
34	AA	2500	A

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Mol	Chain	Res	Type
34	AA	2516	A
34	AA	2521	A
34	AA	2522	A
34	AA	2523	U
34	AA	2525	A
34	AA	2532	G
34	AA	2542	G
34	AA	2545	A
34	AA	2549	A
34	AA	2550	C
34	AA	2551	U
34	AA	2565	G
34	AA	2566	G
34	AA	2567	U
34	AA	2572	A
34	AA	2573	A
34	AA	2576	G
34	AA	2577	C
34	AA	2578	C
34	AA	2589	A
34	AA	2591	U
34	AA	2600	G
34	AA	2603	U
34	AA	2606	A
34	AA	2607	U
34	AA	2608	G
34	AA	2612	U
34	AA	2628	G
34	AA	2629	U
34	AA	2640	U
34	AA	2652	C
34	AA	2665	A
34	AA	2666	A
34	AA	2667	C
34	AA	2668	G
34	AA	2669	G
34	AA	2676	C
34	AA	2681	U
34	AA	2686	G
34	AA	2689	G
34	AA	2690	A
34	AA	2691	A

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Mol	Chain	Res	Type
34	AA	2694	A
34	AA	2695	A
34	AA	2696	G
34	AA	2697	A
34	AA	2704	U
34	AA	2727	U
34	AA	2728	G
34	AA	2740	A
34	AA	2810	A
34	AA	2817	U
34	AA	2823	U
34	AA	2830	U
34	AA	2833	U
34	AA	2884	G
34	AA	2885	A
34	AA	2886	A
34	AA	2887	U
34	AA	2920	A
34	AA	2932	A
34	AA	2934	A
34	AA	2945	G
34	AA	2946	G
34	AA	2953	G
34	AA	2959	G
34	AA	2960	G
34	AA	2962	G
34	AA	2965	A
34	AA	2987	G
34	AA	2991	U
34	AA	2995	A
34	AA	2996	A
34	AA	3013	A
34	AA	3015	A
34	AA	3016	G
34	AA	3018	A
34	AA	3020	U
34	AA	3028	A
34	AA	3030	A
34	AA	3033	A
34	AA	3035	A
34	AA	3042	A
34	AA	3043	A

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Mol	Chain	Res	Type
34	AA	3061	U
34	AA	3066	A
34	AA	3067	G
34	AA	3068	A
34	AA	3086	A
34	AA	3091	U
34	AA	3092	G
34	AA	3094	C
34	AA	3111	U
34	AA	3116	A
34	AA	3122	A
34	AA	3123	C
34	AA	3124	G
34	AA	3127	A
34	AA	3128	A
34	AA	3129	U
34	AA	3131	A
34	AA	3135	A
34	AA	3138	A
34	AA	3141	G
34	AA	3150	G
34	AA	3155	G
34	AA	3156	U
34	AA	3158	U
34	AA	3159	G
34	AA	3160	A
34	AA	3161	A
34	AA	3163	A
34	AA	3167	A
34	AA	3169	C
34	AA	3175	G
34	AA	3176	A
34	AA	3180	C
34	AA	3181	U
34	AA	3193	G
34	AA	3201	C
34	AA	3203	C
34	AA	3204	C
34	AA	3206	A
34	AA	3208	C
34	AA	3218	U
34	AA	3222	G

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Mol	Chain	Res	Type
34	AA	3228	U
34	AA	3230	G
34	AA	3231	A
34	AA	3246	A
34	AA	3248	C
34	AA	3257	G
34	AA	3258	C
34	AA	3259	A
34	AA	3270	A
34	AA	3281	G
34	AA	3282	U
34	AA	3292	A
34	AA	3293	A
34	AA	3294	U
34	AA	3295	A
34	AA	3300	A
34	AA	3301	C
34	AA	3302	G
34	AA	3304	G
34	AA	3306	G
34	AA	3313	U
34	AA	3330	A
34	AA	3339	U
34	AA	3342	C
34	AA	3349	G
34	AA	3353	A
34	AA	3354	A
34	AA	3356	U
34	AA	3357	U
34	AA	3359	A
34	AA	3362	A
34	AA	3374	U
34	AA	3375	A
34	AA	3377	A
34	AA	3379	A
34	AA	3380	U
34	AA	3381	A
34	AA	3382	U
34	AA	3383	A
34	AA	3384	G
34	AA	3385	U
34	AA	3389	G

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Mol	Chain	Res	Type
34	AA	3398	A
34	AA	3409	U
34	AA	3414	G
34	AA	3415	A
34	AA	3416	G
34	AA	3423	U
34	AA	3432	A
34	AA	3435	A
34	AA	3442	C
34	AA	3443	A
34	AA	3459	A
34	AA	3463	G
34	AA	3468	G
34	AA	3474	C
34	AA	3477	A
34	AA	3483	U
34	AA	3485	G
34	AA	3497	A
34	AA	3506	U
34	AA	3507	A
34	AA	3513	G
34	AA	3514	A
34	AA	3515	A
34	AA	3516	A
34	AA	3524	G
34	AA	3526	U
34	AA	3527	U
34	AA	3528	A
34	AA	3529	A
34	AA	3530	A
34	AA	3549	U
34	AA	3553	G
34	AA	3571	A
34	AA	3572	A
34	AA	3573	U
34	AA	3574	G
34	AA	3580	G
34	AA	3581	A
34	AA	3582	G
34	AA	3585	A
34	AA	3586	U
34	AA	3588	A

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Mol	Chain	Res	Type
34	AA	3589	U
34	AA	3590	A
34	AA	3591	U
34	AA	3594	G
34	AA	3615	A
34	AA	3616	U
34	AA	3617	A
34	AA	3618	A
34	AA	3622	U
34	AA	3626	A
34	AA	3627	C
34	AA	3632	U
34	AA	3636	U
34	AA	3659	C
34	AA	3664	G
34	AA	3666	U
34	AA	3668	U
34	AA	3670	U
34	AA	3684	A
34	AA	3689	C
34	AA	3697	G
34	AA	3698	U
34	AA	3707	U
34	AA	3711	U
34	AA	3712	G
34	AA	3726	U
34	AA	3728	A
34	AA	3732	U
34	AA	3733	G
34	AA	3736	A
34	AA	3737	G
34	AA	3740	A
34	AA	3752	C
34	AA	3761	G
34	AA	3768	A
34	AA	3770	C
34	AA	3774	A
34	AA	3775	G
34	AA	3783	G
35	AC	5	A
35	AC	6	C
35	AC	16	G

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Mol	Chain	Res	Type
35	AC	17	A
35	AC	27	U
35	AC	36	C
35	AC	38	G
35	AC	39	C
35	AC	42	U
35	AC	43	G
35	AC	55	A
35	AC	63	A
35	AC	66	C
35	AC	67	G
35	AC	74	A
35	AC	75	A
35	AC	76	A
35	AC	78	U
35	AC	79	G
35	AC	85	A
35	AC	90	G
35	AC	91	A
35	AC	92	A
35	AC	98	A
35	AC	103	G
35	AC	107	A
35	AC	109	U
35	AC	115	C
35	AC	116	U
35	AC	123	A
35	AC	135	G
35	AC	138	U
35	AC	139	A
35	AC	140	G
35	AC	145	A
35	AC	146	C
35	AC	157	A
36	AB	7	G
36	AB	11	A
36	AB	22	G
36	AB	23	A
36	AB	26	C
36	AB	33	U
36	AB	39	C
36	AB	40	A

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Mol	Chain	Res	Type
36	AB	52	U
36	AB	53	U
36	AB	64	A
36	AB	73	U
36	AB	74	A
36	AB	76	U
36	AB	89	G
36	AB	97	G
36	AB	100	A
36	AB	110	G

All (107) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	S7	72	C
8	SA	105	A
8	SA	246	A
8	SA	248	G
8	SA	291	A
8	SA	423	A
8	SA	525	G
8	SA	752	U
8	SA	844	G
8	SA	981	U
8	SA	998	A
8	SA	1098	U
8	SA	1182	A
8	SA	1295	A
8	SA	1306	C
8	SA	1381	C
8	SA	1386	U
8	SA	1413	U
8	SA	1414	A
8	SA	1455	C
8	SA	1786	U
8	SA	1817	U
8	SA	1818	A
8	SA	1819	U
8	SA	1865	G
8	SA	1897	A
8	SA	1976	G
8	SA	2053	U

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Mol	Chain	Res	Type
34	AA	13	G
34	AA	61	A
34	AA	62	A
34	AA	162	U
34	AA	179	G
34	AA	182	U
34	AA	215	C
34	AA	231	G
34	AA	257	U
34	AA	270	U
34	AA	289	A
34	AA	439	U
34	AA	500	A
34	AA	501	U
34	AA	504	A
34	AA	505	A
34	AA	579	C
34	AA	580	A
34	AA	581	C
34	AA	607	A
34	AA	620	U
34	AA	652	A
34	AA	674	U
34	AA	697	A
34	AA	698	G
34	AA	703	U
34	AA	715	U
34	AA	721	U
34	AA	764	G
34	AA	821	C
34	AA	859	C
34	AA	888	A
34	AA	965	A
34	AA	1197	U
34	AA	1205	U
34	AA	1217	U
34	AA	1222	U
34	AA	1224	A
34	AA	1435	G
34	AA	1538	U
34	AA	1554	G
34	AA	1574	C

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Mol	Chain	Res	Type
34	AA	1705	A
34	AA	1736	A
34	AA	1805	U
34	AA	1841	U
34	AA	1881	C
34	AA	1990	A
34	AA	1996	C
34	AA	1999	A
34	AA	2105	A
34	AA	2180	U
34	AA	2219	A
34	AA	2394	C
34	AA	2651	A
34	AA	2816	U
34	AA	2822	U
34	AA	2885	A
34	AA	2959	G
34	AA	3130	U
34	AA	3137	U
34	AA	3230	G
34	AA	3361	U
34	AA	3413	A
34	AA	3414	G
34	AA	3476	A
34	AA	3587	U
34	AA	3590	A
34	AA	3658	G
34	AA	3667	C
34	AA	3688	G
35	AC	35	A
35	AC	37	A
35	AC	134	G
35	AC	139	A
35	AC	145	A
36	AB	22	G
36	AB	39	C
36	AB	88	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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
63	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	32.78

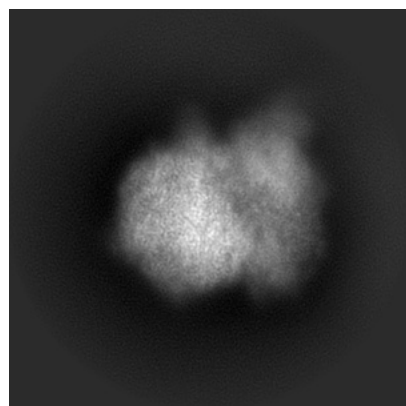
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41485. These allow visual inspection of the internal detail of the map and identification of artifacts.

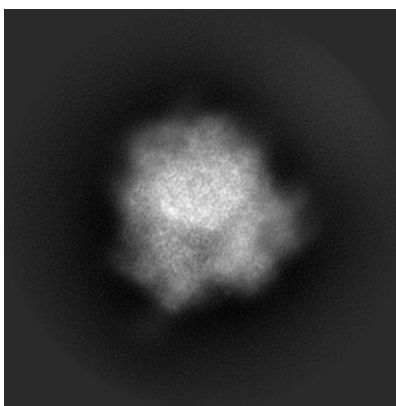
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

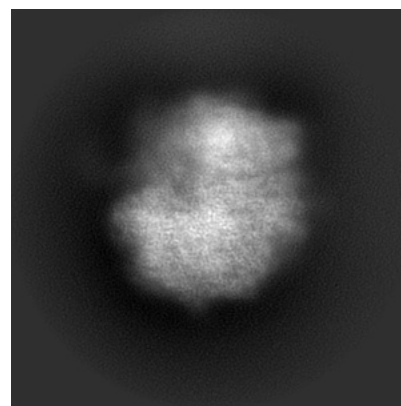
6.1.1 Primary map



X

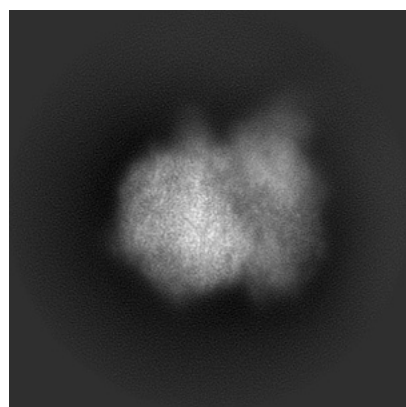


Y

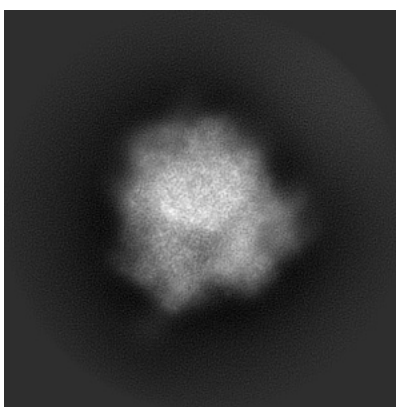


Z

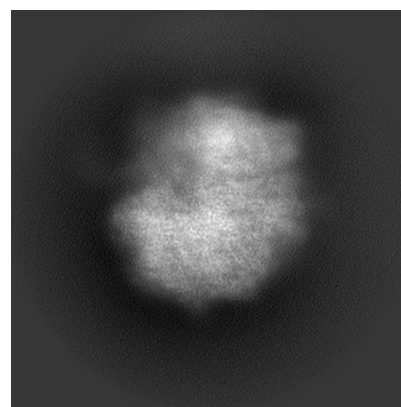
6.1.2 Raw map



X



Y

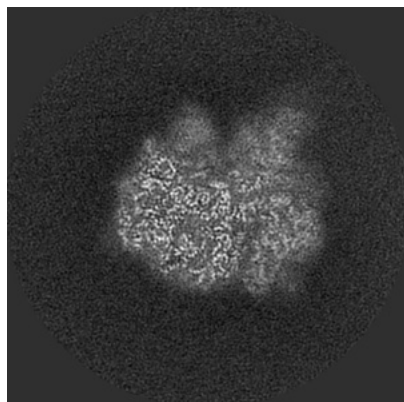


Z

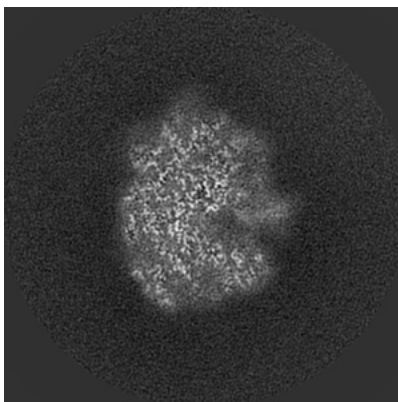
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

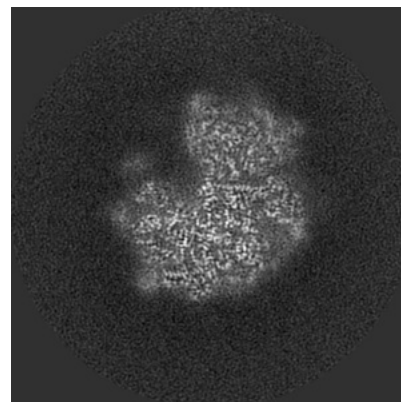
6.2.1 Primary map



X Index: 148

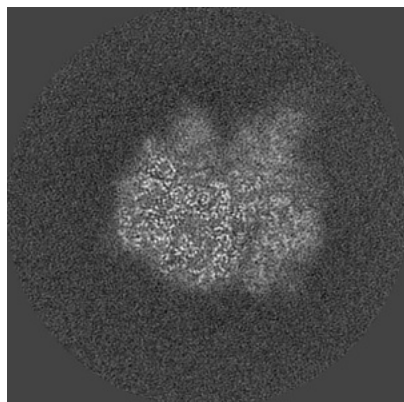


Y Index: 148

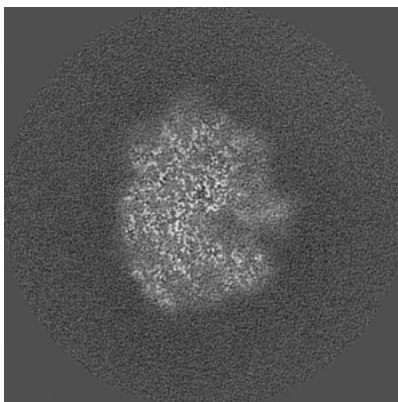


Z Index: 148

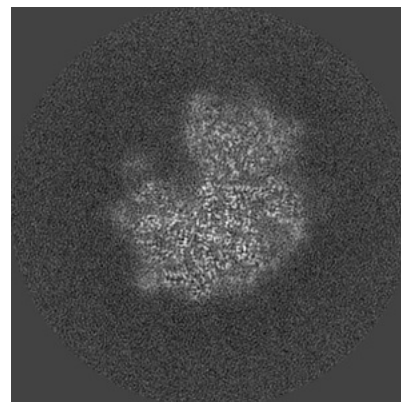
6.2.2 Raw map



X Index: 148



Y Index: 148

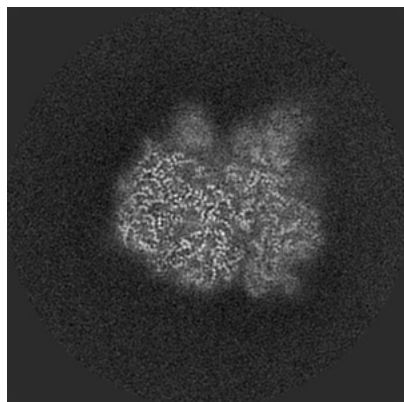


Z Index: 148

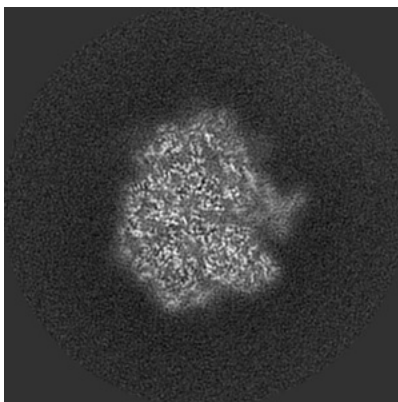
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

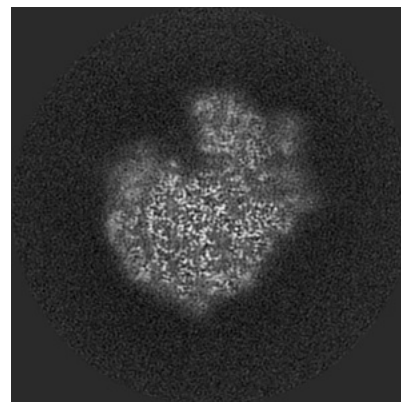
6.3.1 Primary map



X Index: 150

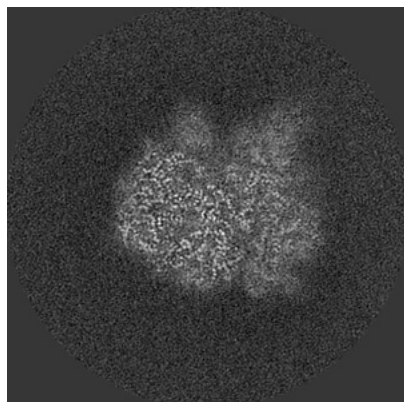


Y Index: 139

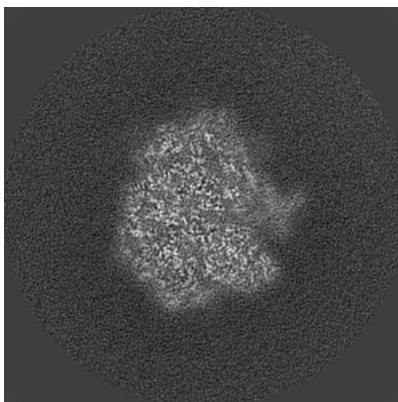


Z Index: 127

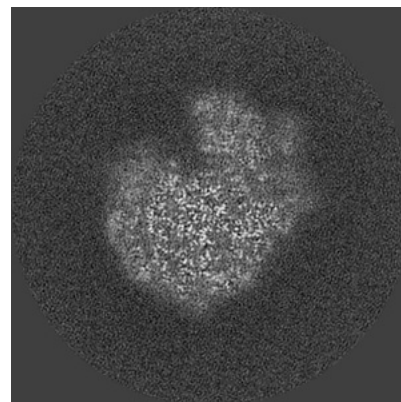
6.3.2 Raw map



X Index: 150



Y Index: 139

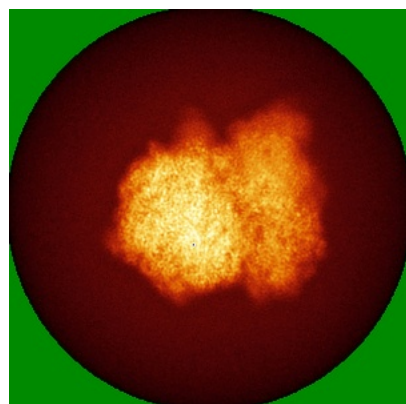


Z Index: 127

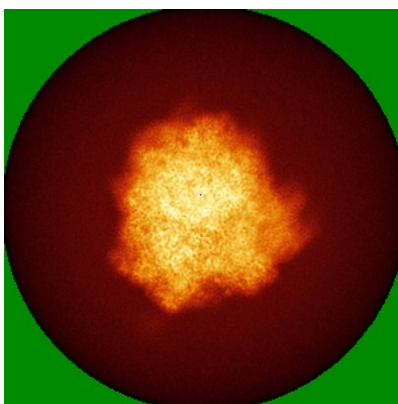
The images above show the largest variance slices of the map in three orthogonal directions.

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

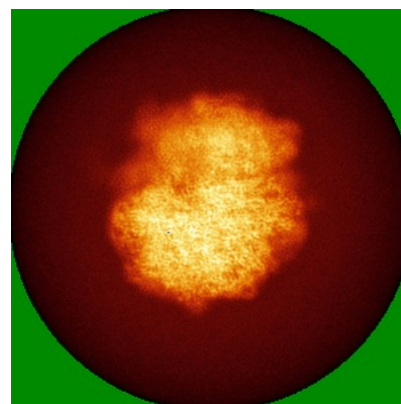
6.4.1 Primary map



X

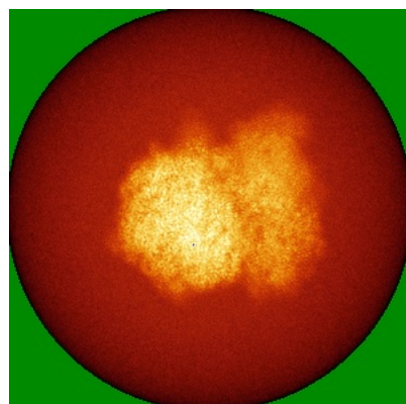


Y

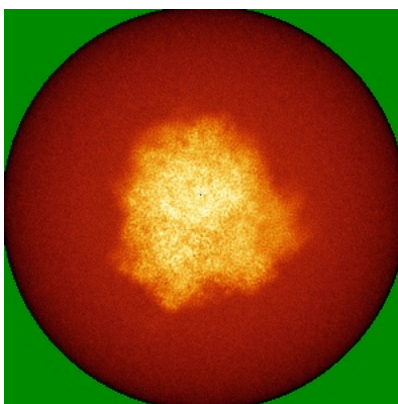


Z

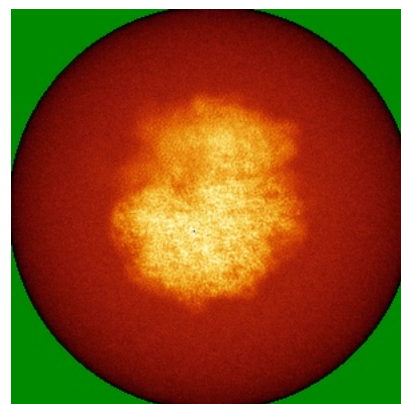
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



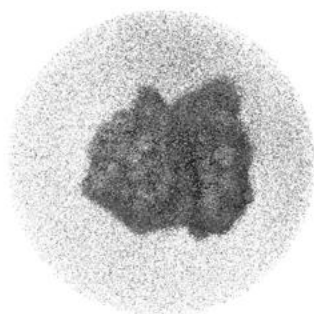
Y



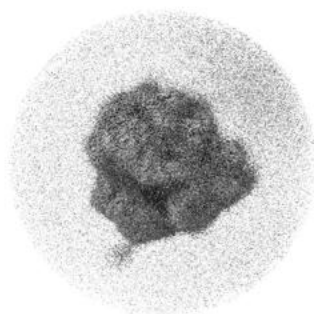
Z

The images above show the 3D surface view of the map at the recommended contour level 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

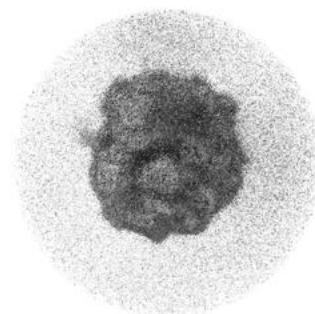
6.5.2 Raw map



X



Y



Z

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

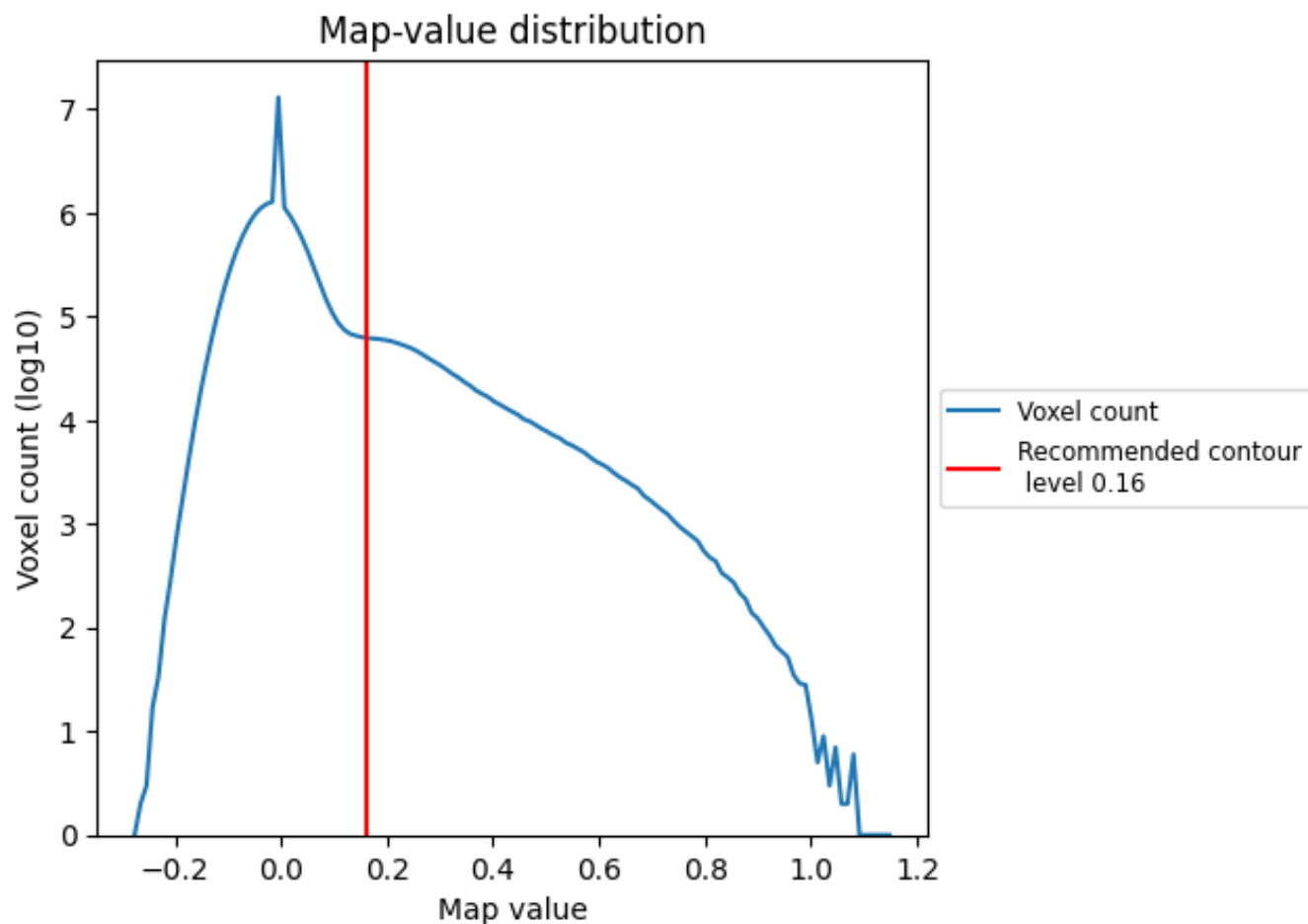
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

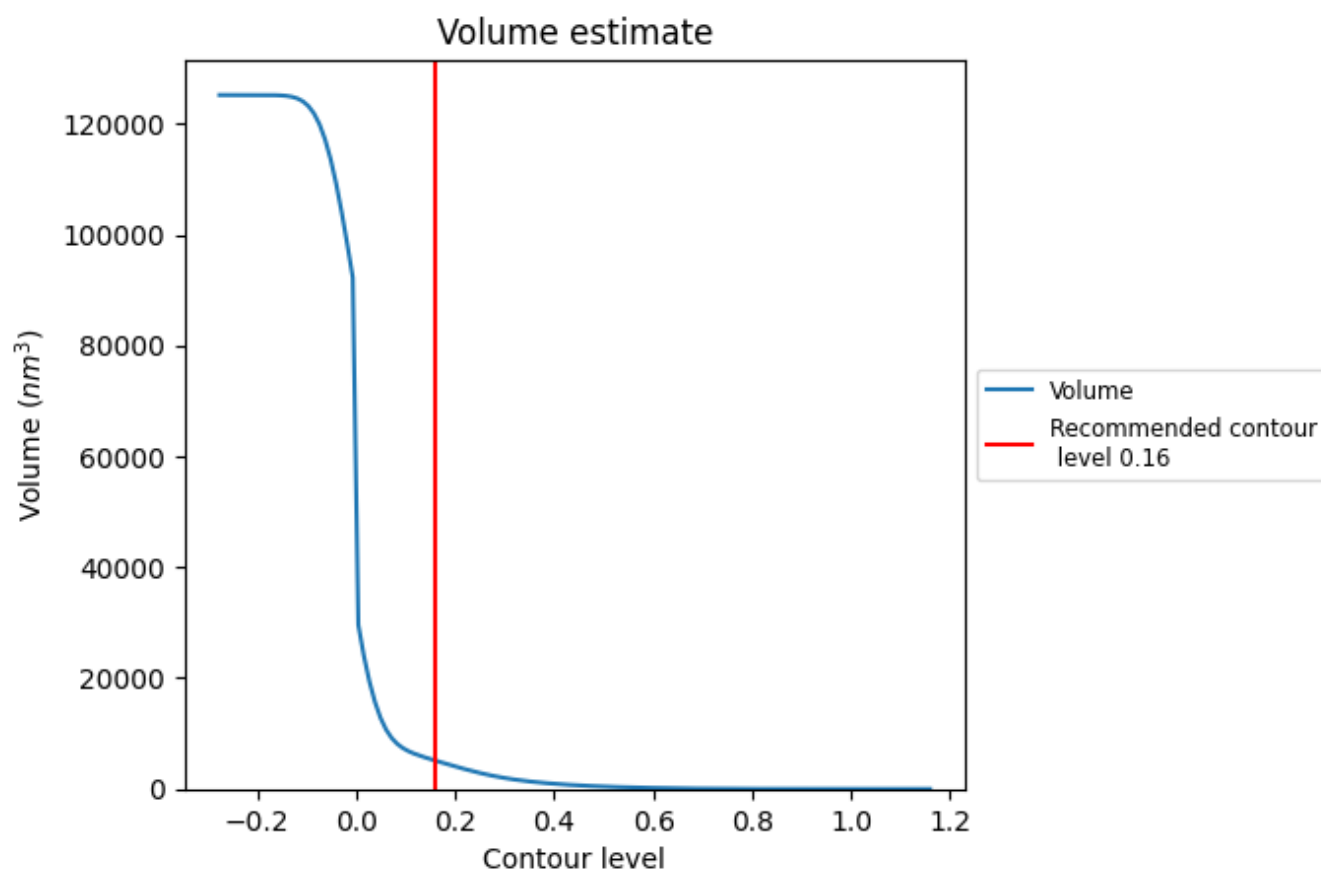
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

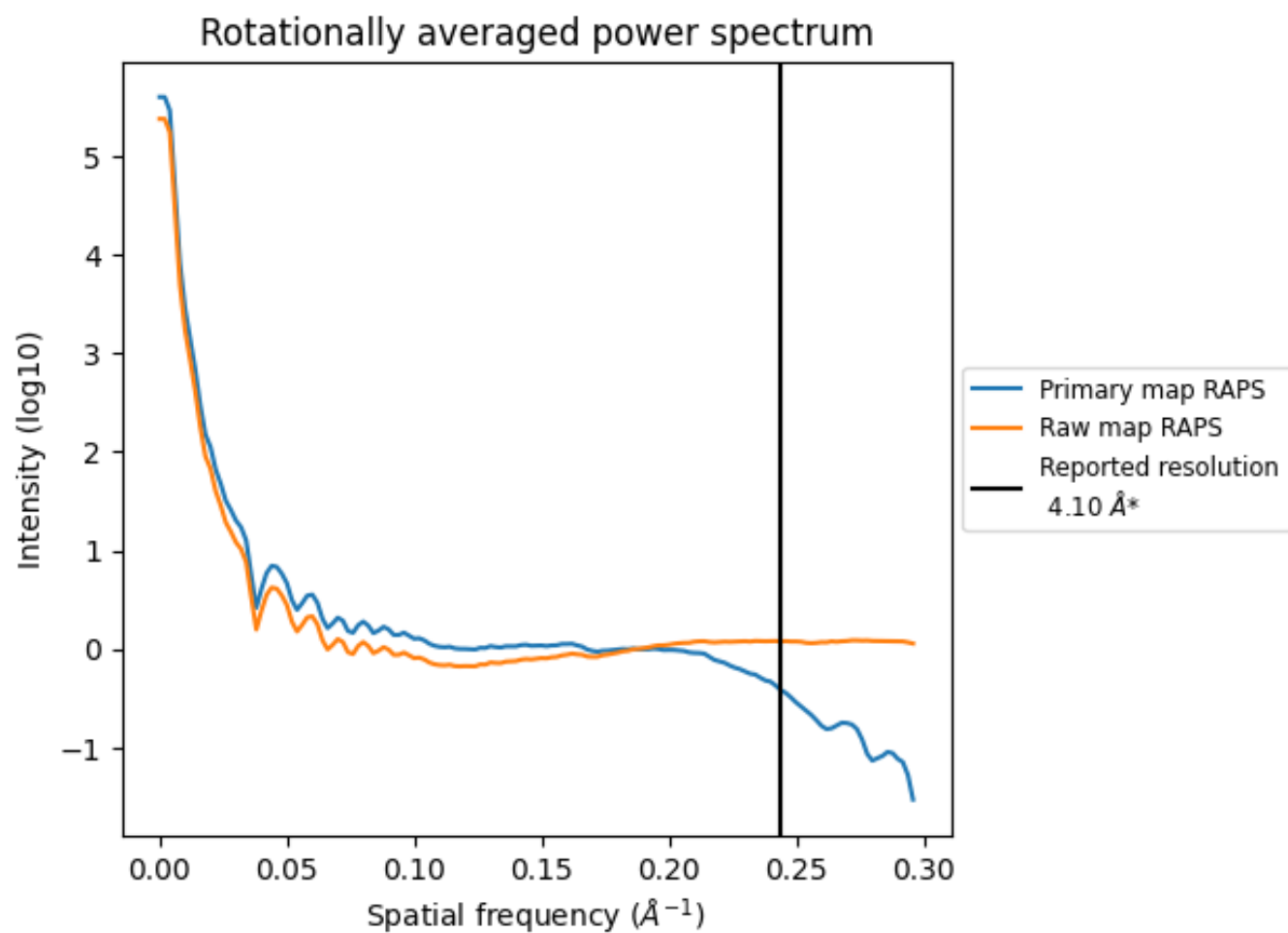
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5103 nm^3 ; this corresponds to an approximate mass of 4610 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 ⓘ

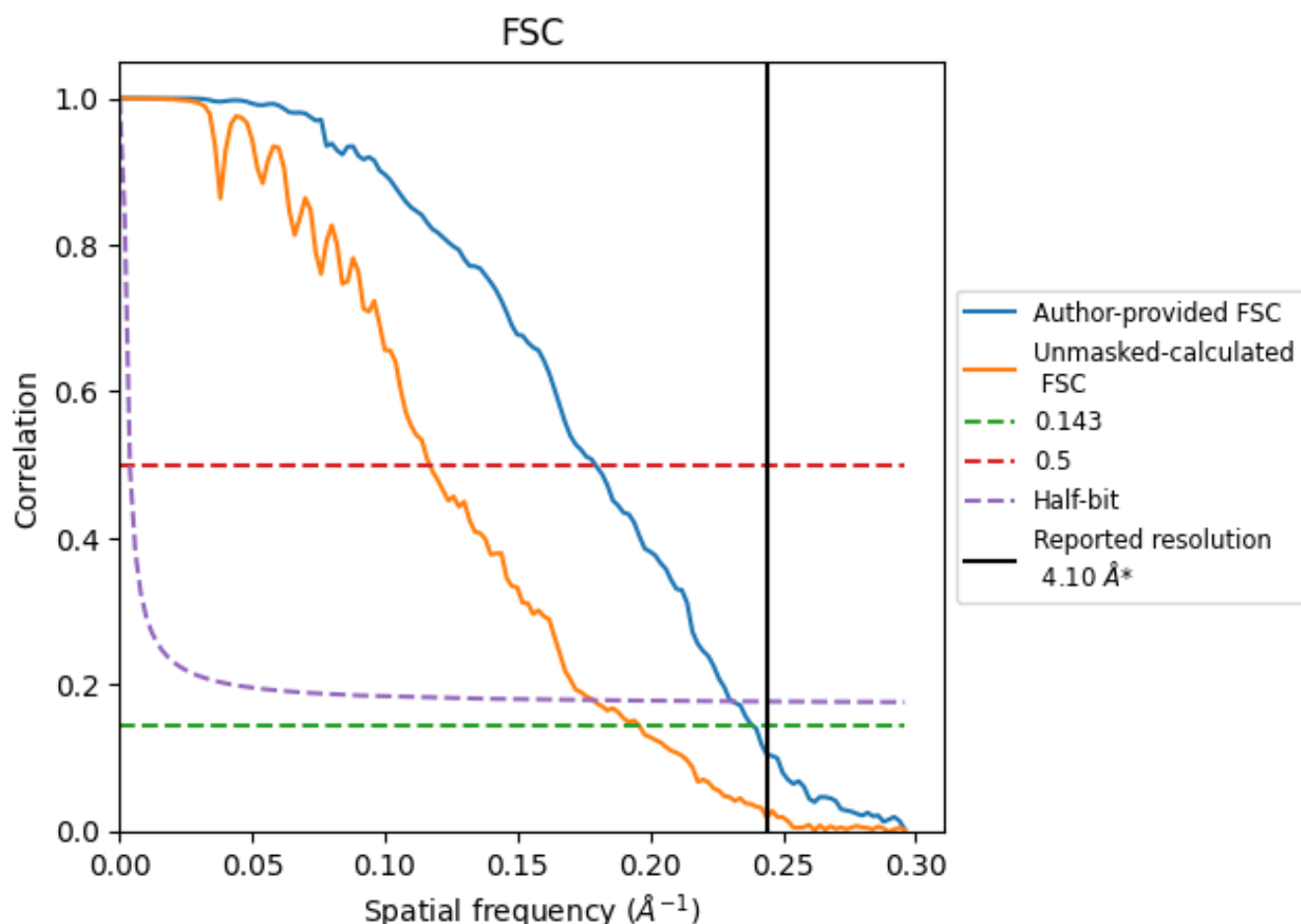


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

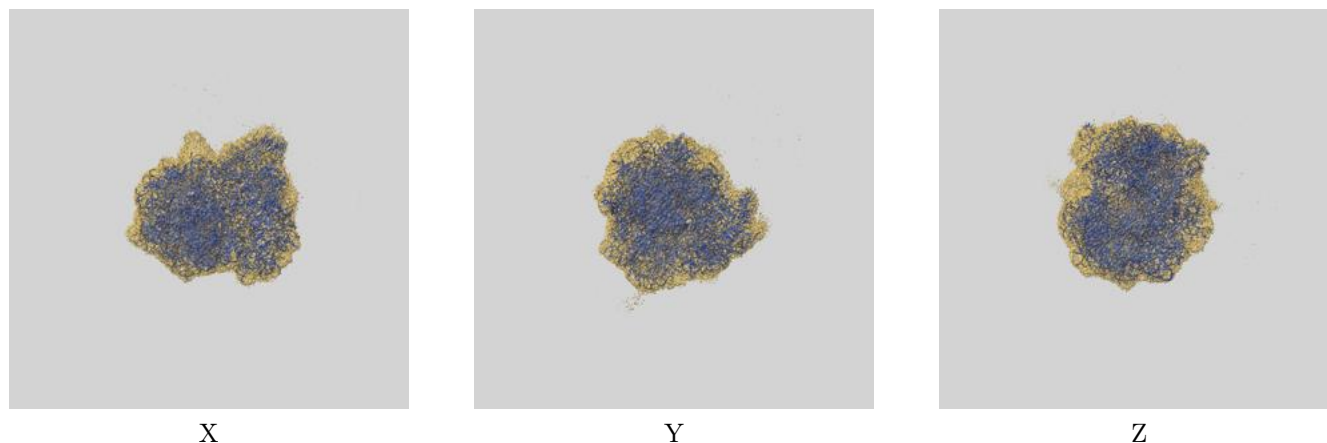
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.19	5.58	4.33
Unmasked-calculated*	5.10	8.55	5.60

*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 5.10 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

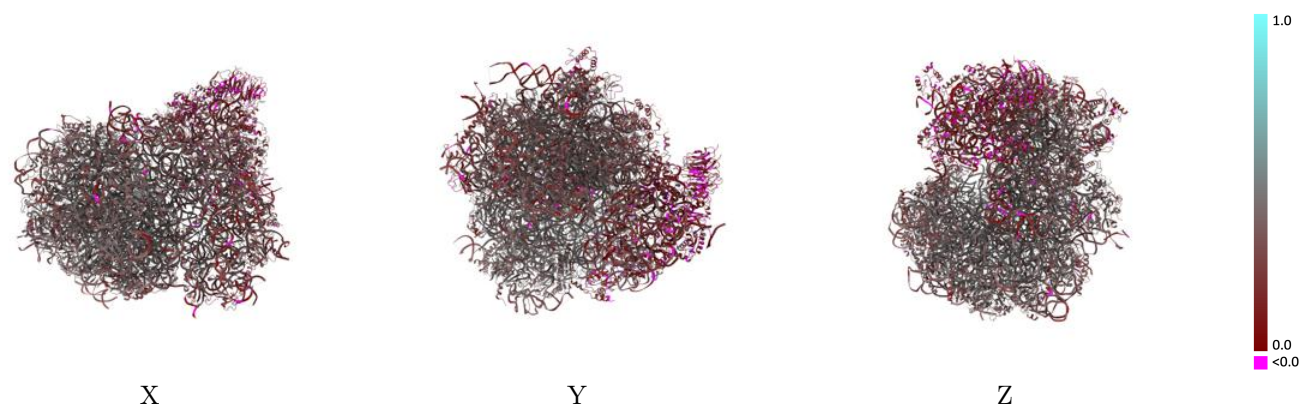
This section contains information regarding the fit between EMDB map EMD-41485 and PDB model 8TPU. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



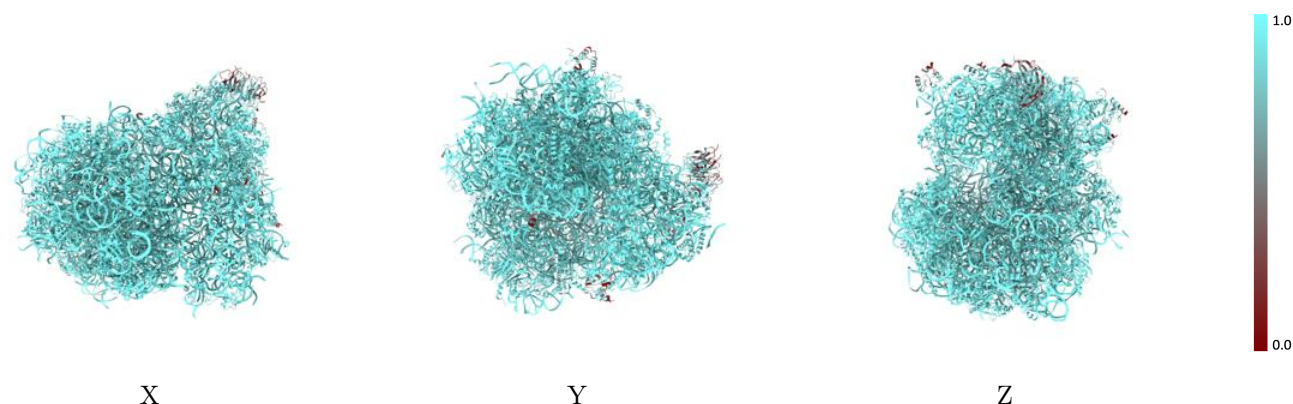
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



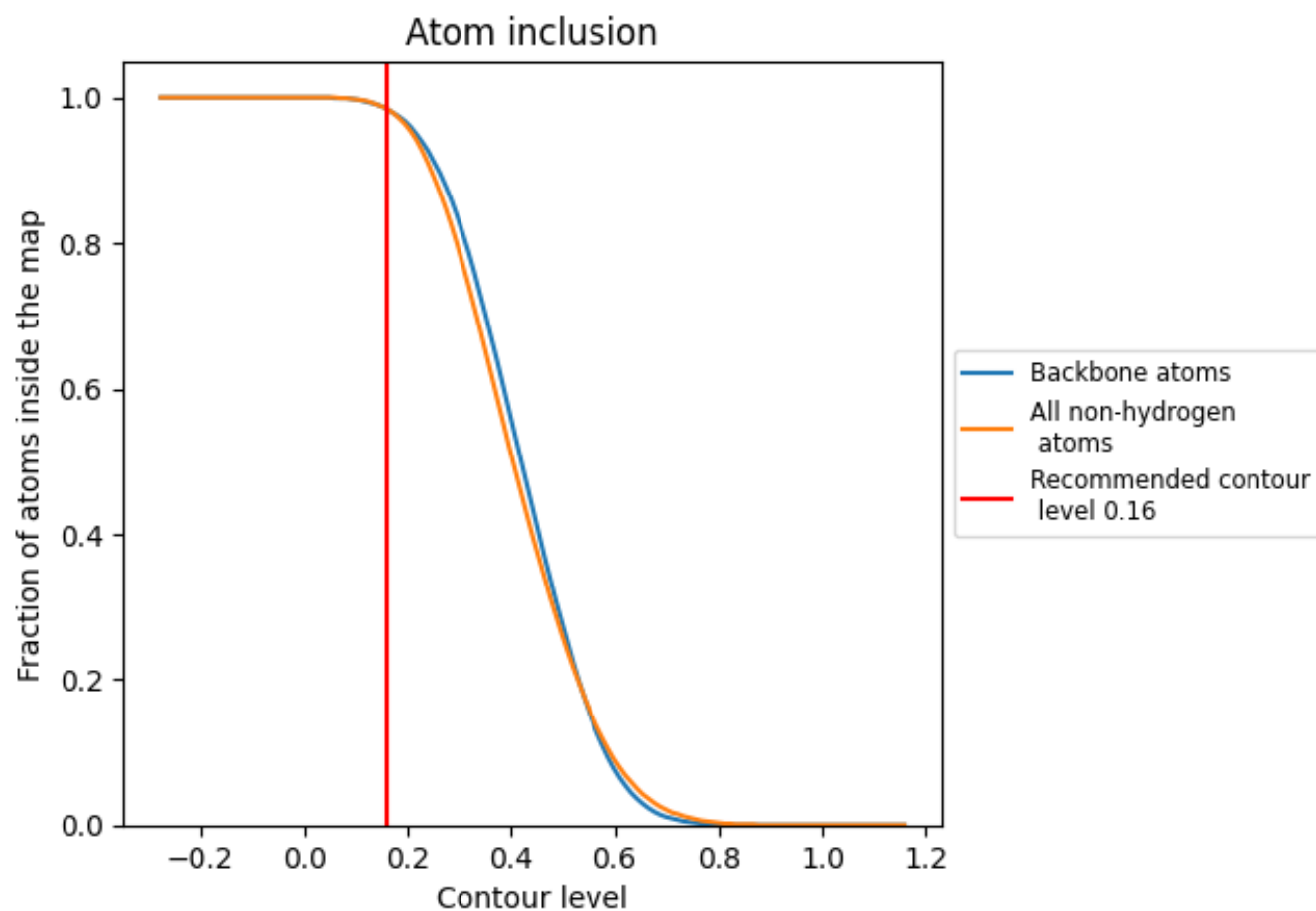
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.16).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9850	 0.3590
A0	 0.9980	 0.4070
A1	 0.9870	 0.3780
A2	 0.9960	 0.4000
A3	 0.9940	 0.3950
A4	 0.9890	 0.3650
A5	 0.9920	 0.4090
A6	 0.9900	 0.3970
A7	 0.9960	 0.4210
A8	 0.9980	 0.4200
A9	 1.0000	 0.4430
AA	 0.9980	 0.3920
AB	 1.0000	 0.3920
AC	 1.0000	 0.4030
AD	 0.9960	 0.4270
AE	 0.9910	 0.4150
AF	 0.9930	 0.4050
AG	 0.9940	 0.3640
AH	 0.9920	 0.3960
AI	 0.9880	 0.3900
AJ	 0.9550	 0.3580
AK	 0.9940	 0.4050
AL	 0.9910	 0.4040
AM	 0.9910	 0.4130
AN	 0.9950	 0.3930
AO	 0.9960	 0.4280
AP	 0.9990	 0.4220
AQ	 0.9940	 0.4030
AR	 0.9840	 0.3740
AS	 0.9980	 0.4160
AT	 0.9600	 0.3700
AU	 0.9970	 0.4200
AV	 0.9900	 0.4150
AW	 0.9960	 0.4270
AX	 0.9740	 0.3410









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Chain	Atom inclusion	Q-score
AY	 0.9950	 0.4090
AZ	 0.9990	 0.4010
Aa	 0.9990	 0.4220
Ab	 0.9990	 0.3920
Ac	 1.0000	 0.4310
Ad	 0.9920	 0.3810
Ae	 1.0000	 0.4300
Af	 1.0000	 0.4200
Ag	 1.0000	 0.3880
Ah	 0.9950	 0.4230
Ai	 0.9960	 0.4240
S1	 0.9880	 0.2920
S2	 0.9720	 0.1910
S3	 0.9930	 0.3700
S4	 0.9640	 0.3320
S5	 0.9710	 0.2180
S6	 1.0000	 0.3050
S7	 0.9840	 0.1760
S8	 0.6360	 0.1440
SA	 0.9930	 0.3110
SB	 0.9830	 0.3440
SC	 0.9580	 0.3090
SD	 0.9810	 0.2400
SE	 0.9350	 0.3160
SF	 0.9810	 0.3450
SG	 0.9840	 0.3490
SH	 0.9750	 0.2790
SI	 0.9500	 0.1480
SJ	 0.8530	 0.2900
SK	 0.9960	 0.3700
SL	 0.9910	 0.3660
SM	 0.9700	 0.1840
SN	 0.9130	 0.2260
SO	 0.9840	 0.2530
SP	 0.9860	 0.3560
SQ	 0.9960	 0.3690
SR	 0.6680	 0.1710
SS	 0.9750	 0.1940
ST	 0.9970	 0.2640
SU	 0.9940	 0.3580
SV	 0.9920	 0.4070
SW	 0.9610	 0.2440

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Chain	Atom inclusion	Q-score
SX	 0.9250	 0.1830
SY	 0.9760	 0.1850
SZ	 0.9710	 0.3450