



wwPDB EM Validation Summary Report ⓘ

Dec 26, 2024 – 08:10 AM EST

PDB ID : 6ERI
EMDB ID : EMD-3941
Title : Structure of the chloroplast ribosome with chl-RRF and hibernation-promoting factor
Authors : Perez Borema, A.; Aibara, S.; Paul, B.; Tobiasson, V.; Kimanius, D.; Forsberg, B.O.; Wallden, K.; Lindahl, E.; Amunts, A.
Deposited on : 2017-10-18
Resolution : 3.00 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
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) : 2.40

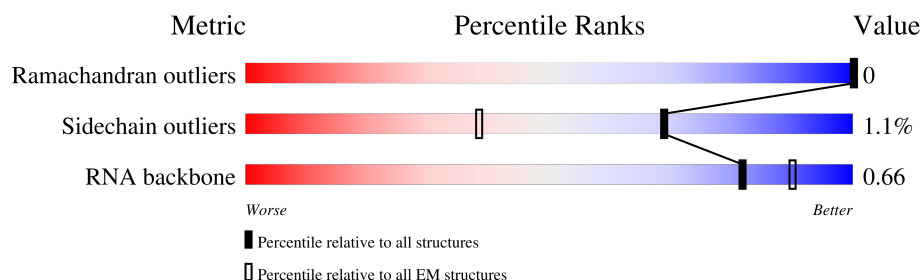
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.



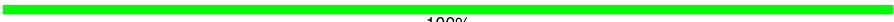













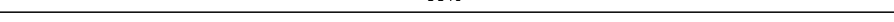
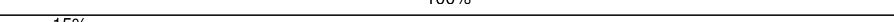
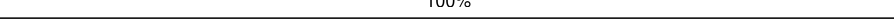
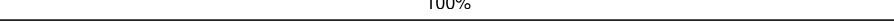
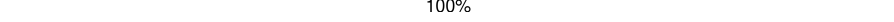
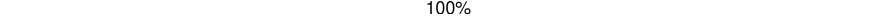
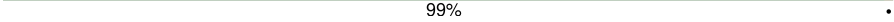

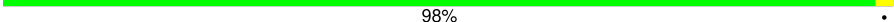


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	AA	2810	
2	AB	106	
3	AC	246	
4	AD	221	
5	AE	212	
6	AF	207	
7	AG	172	
8	AH	46	


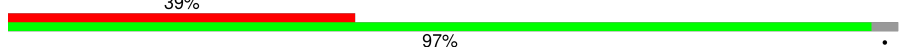
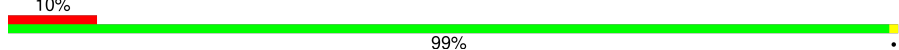
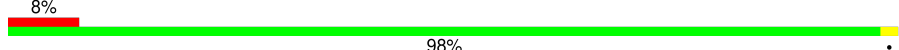

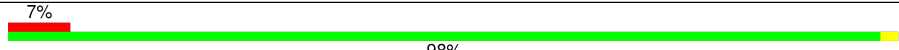
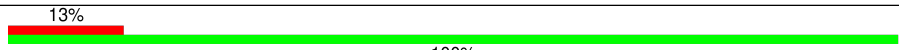
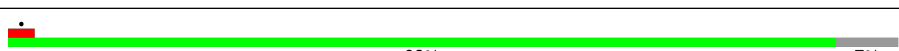
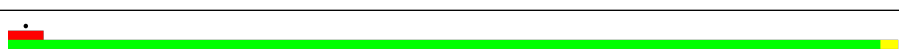
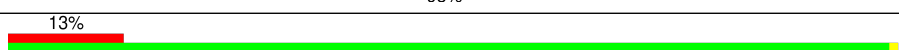
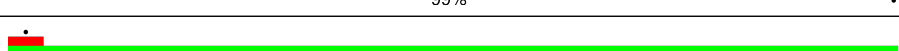
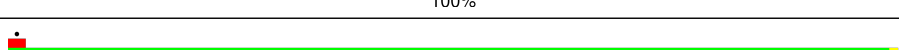
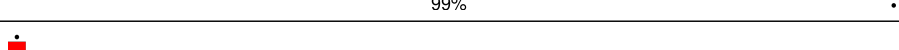
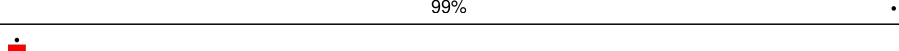
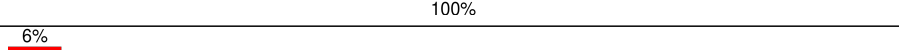
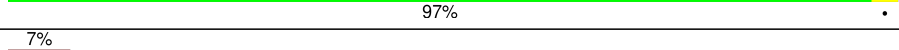
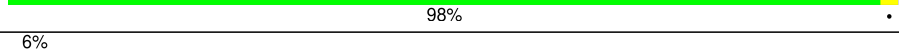
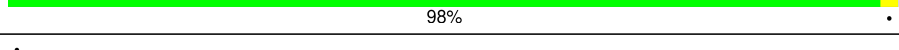
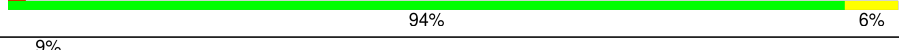
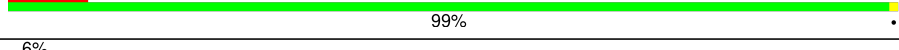
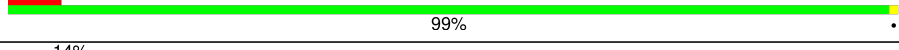
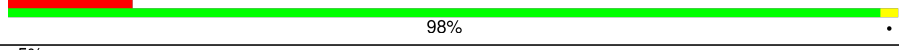
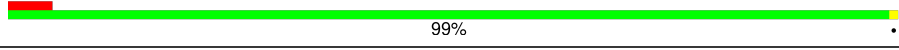
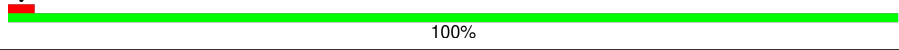
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Mol	Chain	Length	Quality of chain
9	AJ	200	 100%
10	AK	121	 98%
11	AL	184	 99%
12	AM	134	 99%
13	AN	116	 98%
14	AO	121	 98%
15	AP	118	 98%
16	AQ	115	 99%
17	AR	165	 9%
18	AS	171	 100%
19	AT	92	 100%
20	AU	127	 98%
21	AW	114	 100%
22	AX	76	 99%
23	AY	99	 100%
24	AZ	66	 15%
25	Aa	48	 100%
26	Ab	60	 100%
27	Ac	61	 100%
28	Ad	72	 99%
29	Ae	37	 100%
30	Af	47	 98%
31	Aw	49	 100%
32	Ax	118	 93% 7%
33	Az	191	 19% 100%

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Mol	Chain	Length	Quality of chain
34	BA	1481	
35	BB	215	
36	BC	217	
37	BD	200	
38	BE	158	
39	BF	113	
40	BG	151	
41	BH	134	
42	BI	141	
43	BJ	98	
44	BK	110	
45	BL	122	
46	BM	111	
47	BN	99	
48	BO	72	
49	BP	81	
50	BQ	84	
51	BR	53	
52	BS	81	
53	BT	102	
54	BU	59	
55	BV	106	
56	BW	37	
57	BY	170	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 145026 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	2696	Total	C	N	O	P	0	0
			57902	25833	10727	18646	2696		

- Molecule 2 is a RNA chain called 4.5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	106	Total	C	N	O	P	0	0
			2277	1017	423	731	106		

- Molecule 3 is a protein called 50S ribosomal protein L2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	246	Total	C	N	O	S	0	0
			1896	1175	388	327	6		

- Molecule 4 is a protein called 50S ribosomal protein L3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	221	Total	C	N	O	S	0	0
			1686	1066	308	301	11		

- Molecule 5 is a protein called 50S ribosomal protein L4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	212	Total	C	N	O	S	0	0
			1676	1061	312	300	3		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	77	SER	PRO	conflict	UNP O49937
AE	79	THR	LYS	conflict	UNP O49937
AE	130	ARG	GLY	conflict	UNP O49937

- Molecule 6 is a protein called 50S ribosomal protein L5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	171	Total	C	N	O	S	0	0
			1328	843	231	246	8		

- Molecule 7 is a protein called 50S ribosomal protein L6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	172	Total	C	N	O	S	0	0
			1343	849	246	244	4		

- Molecule 8 is a protein called 50S ribosomal protein L9, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	AH	46	Total	C	N	O	0	0
			367	241	66	60		

- Molecule 9 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AJ	200	Total	C	N	O	S	0	0
			1619	1030	300	284	5		

- Molecule 10 is a protein called 50S ribosomal protein L14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AK	120	Total	C	N	O	S	0	0
			934	582	178	169	5		

- Molecule 11 is a protein called 50S ribosomal protein L15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	184	Total	C	N	O	S	0	0
			1405	876	279	244	6		

- Molecule 12 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AM	134	Total	C	N	O	S	0	0
			1071	675	217	173	6		

- Molecule 13 is a protein called 50S ribosomal protein L17, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AN	116	Total	C	N	O	S	0	0
			944	592	193	155	4		

- Molecule 14 is a protein called 50S ribosomal protein L18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AO	121	Total	C	N	O	S	0	0
			952	592	184	171	5		

- Molecule 15 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AP	118	Total	C	N	O	S	0	0
			953	610	186	156	1		

- Molecule 16 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	115	Total	C	N	O	S	0	0
			994	631	207	154	2		

- Molecule 17 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	AR	165	Total	C	N	O	0	0
			1326	857	228	241		

- Molecule 18 is a protein called 50S ribosomal protein L22, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS	171	Total	C	N	O	S	0	0
			1388	887	256	236	9		

- Molecule 19 is a protein called 50S ribosomal protein L23, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AT	92	Total	C	N	O	S	0	0
			743	480	129	132	2		

- Molecule 20 is a protein called 50S ribosomal protein L24, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AU	127	Total	C	N	O	S	0	0
			1015	639	189	184	3		

- Molecule 21 is a protein called 50S ribosomal protein L27, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AW	114	Total	C	N	O	S	0	0
			914	573	182	159			

- Molecule 22 is a protein called 50S ribosomal protein L28, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AX	76	Total	C	N	O	S	0	0
			625	397	127	100	1		

- Molecule 23 is a protein called 50S ribosomal protein L29, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AY	99	Total	C	N	O	S	0	0
			832	520	164	145	3		

- Molecule 24 is a protein called 50S ribosomal protein L31, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AZ	66	Total	C	N	O	S	0	0
			536	338	94	102	2		

- Molecule 25 is a protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Aa	48	Total	C	N	O	S	0	0
			396	261	75	60			

- Molecule 26 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Ab	60	Total	C	N	O	S	0	0
			489	304	98	83	4		

- Molecule 27 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ac	61	Total	C	N	O	S	0	0
			471	284	108	76	3		

- Molecule 28 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ad	72	Total	C	N	O	S	0	0
			588	370	124	93	1		

- Molecule 29 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ae	37	Total	C	N	O	S	0	0
			305	186	70	45	4		

- Molecule 30 is a protein called 50S ribosomal protein 6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Af	47	Total	C	N	O	S	0	0
			375	240	72	62	1		

- Molecule 31 is a protein called 50S ribosomal protein 5 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Aw	49	Total	C	N	O	S	0	0
			423	269	92	58	4		

- Molecule 32 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ax	118	Total	C	N	O	P	0	0
			2522	1126	457	821	118		

- Molecule 33 is a protein called Ribosome-recycling factor, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Az	191	Total	C	N	O	S	0	0
			1512	939	260	308	5		

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BA	1481	Total	C	N	O	P	0	0
			31806	14180	5870	10275	1481		

- Molecule 35 is a protein called 30S ribosomal protein S2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BB	209	Total	C	N	O	S	0	0
			1639	1032	303	293	11		

- Molecule 36 is a protein called 30S ribosomal protein S3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BC	217	Total	C	N	O	S	0	0
			1745	1113	314	312	6		

- Molecule 37 is a protein called 30S ribosomal protein S4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BD	199	Total	C	N	O	S	0	0
			1633	1032	319	278	4		

- Molecule 38 is a protein called 30S ribosomal protein S5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BE	158	Total	C	N	O	S	0	0
			1189	742	230	211	6		

- Molecule 39 is a protein called 30S ribosomal protein S6 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BF	113	Total	C	N	O	S	0	0
			911	583	152	172	4		

- Molecule 40 is a protein called 30S ribosomal protein S7, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BG	151	Total	C	N	O	S	0	0
			1178	732	236	207	3		

- Molecule 41 is a protein called 30S ribosomal protein S8, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BH	124	Total	C	N	O	S	0	0
			1004	633	192	174	5		

- Molecule 42 is a protein called 30S ribosomal protein S9, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BI	141	Total	C	N	O	S	0	0
			1091	696	205	189	1		

- Molecule 43 is a protein called 30S ribosomal protein S10 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BJ	98	Total	C	N	O	S	0	0
			796	512	142	137	5		

- Molecule 44 is a protein called 30S ribosomal protein S11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BK	110	Total	C	N	O	S	0	0
			828	512	169	142	5		

- Molecule 45 is a protein called 30S ribosomal protein S12, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BL	122	Total	C	N	O	S	0	0
			959	599	197	161	2		

- Molecule 46 is a protein called 30S ribosomal protein S13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BM	111	Total	C	N	O	S	0	0
			913	562	184	162	5		

- Molecule 47 is a protein called 30S ribosomal protein S14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BN	99	Total	C	N	O	S	0	0
			824	510	174	137	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BN	73	TYR	ILE	conflict	UNP P06507

- Molecule 48 is a protein called 30S ribosomal protein S15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BO	72	Total	C	N	O	S	0	0
			606	388	117	100	1		

- Molecule 49 is a protein called 30S ribosomal protein S16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BP	81	Total	C	N	O	S	0	0
			675	431	127	115	2		

- Molecule 50 is a protein called 30S ribosomal protein S17, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BQ	84	Total	C	N	O	S	0	0
			677	423	133	117	4		

- Molecule 51 is a protein called 30S ribosomal protein S18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BR	53	Total	C	N	O	S	0	0
			440	279	87	73	1		

- Molecule 52 is a protein called 30S ribosomal protein S19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BS	81	Total	C	N	O	S	0	0
			653	421	123	107	2		

- Molecule 53 is a protein called 30S ribosomal protein S20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BT	102	Total	C	N	O	S	0	0
			818	506	168	143	1		

- Molecule 54 is a protein called 30S ribosomal protein S21, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BU	59	Total	C	N	O	S	0	0
			514	310	109	93	2		

- Molecule 55 is a protein called Ribosome-binding factor PSRP1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BV	106	Total	C	N	O	S	0	0
			836	514	164	157	1		

- Molecule 56 is a protein called 30S ribosomal protein S31, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	BW	37	Total	C	N	O	0	0
			289	179	65	45		

- Molecule 57 is a protein called bS1c.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	BY	170	Total	C	N	O	0	0
			850	510	170	170		

- Molecule 58 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	AA	247	Total	Mg	0
			247	247	
58	AB	9	Total	Mg	0
			9	9	
58	Af	1	Total	Mg	0
			1	1	
58	Aw	1	Total	Mg	0
			1	1	
58	Ax	2	Total	Mg	0
			2	2	
58	BA	82	Total	Mg	0
			82	82	
58	BN	1	Total	Mg	0
			1	1	

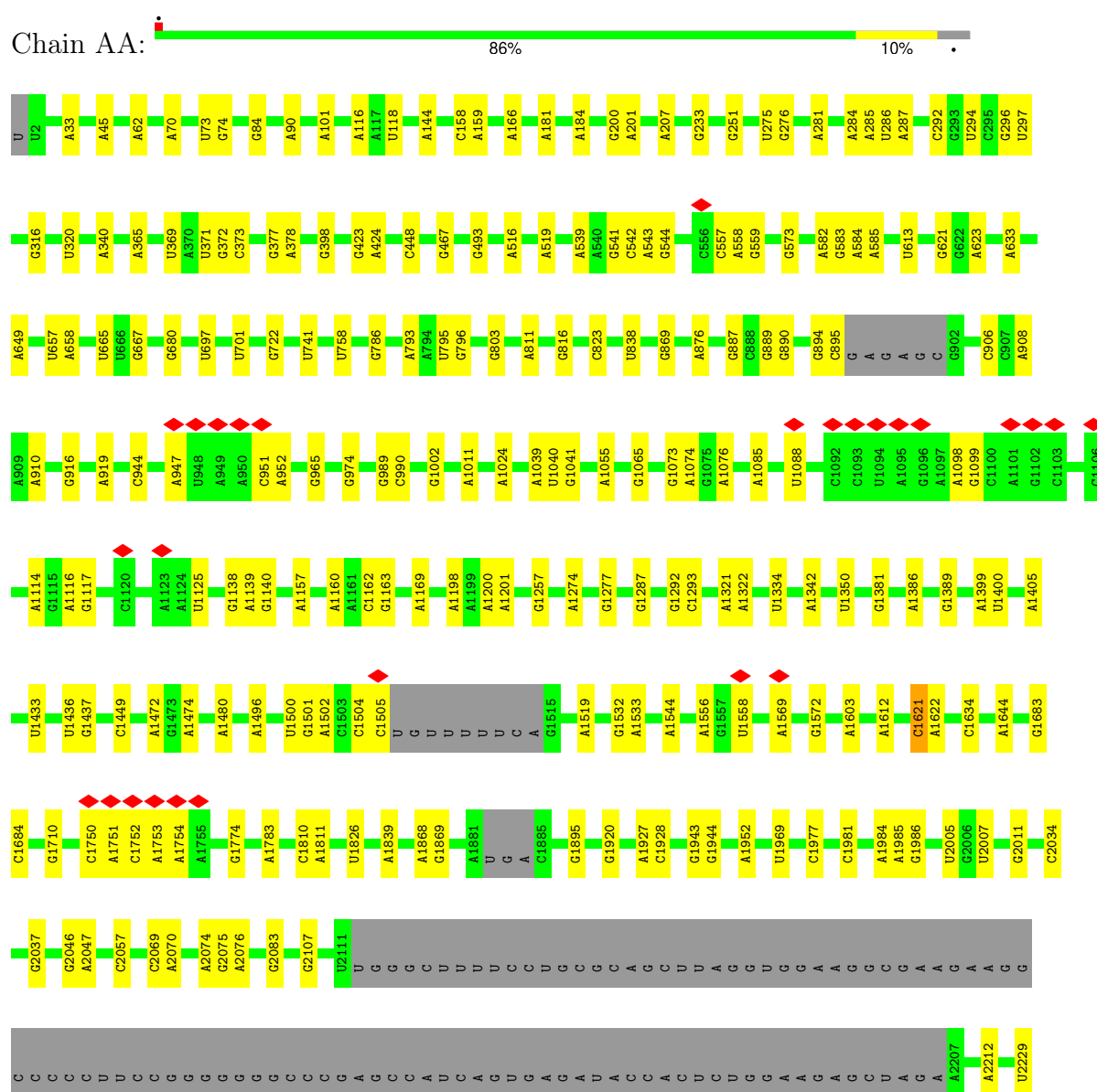
- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn).

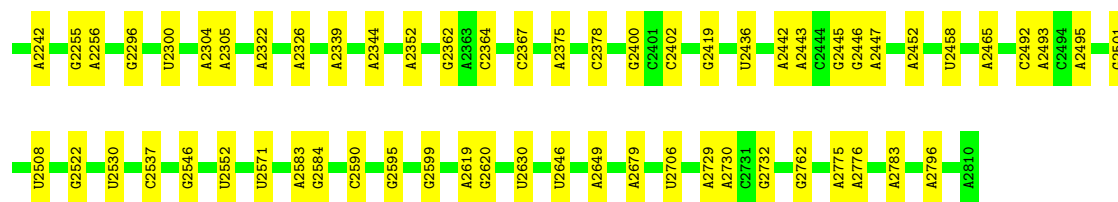
Mol	Chain	Residues	Atoms		AltConf
59	Ab	1	Total 1	Zn 1	0
59	Ae	1	Total 1	Zn 1	0

3 Residue-property plots

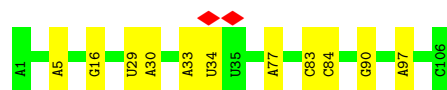
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 23S ribosomal RNA





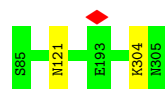
- Molecule 2: 4.5S ribosomal RNA



- Molecule 3: 50S ribosomal protein L2, chloroplastic



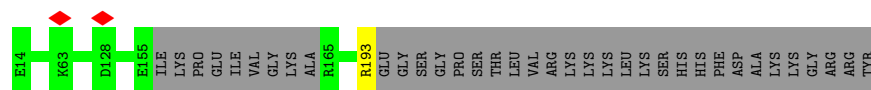
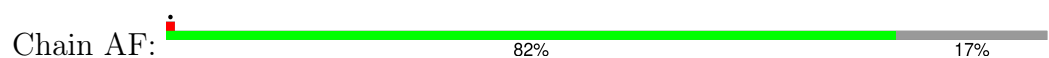
- Molecule 4: 50S ribosomal protein L3, chloroplastic



- Molecule 5: 50S ribosomal protein L4, chloroplastic

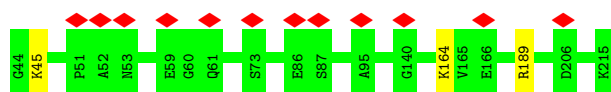


- Molecule 6: 50S ribosomal protein L5, chloroplastic



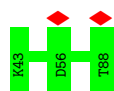
- Molecule 7: 50S ribosomal protein L6, chloroplastic





- Molecule 8: 50S ribosomal protein L9, chloroplastic

Chain AH: 100%



- Molecule 9: 50S ribosomal protein L13, chloroplastic

Chain AJ: 100%

There are no outlier residues recorded for this chain.

- Molecule 10: 50S ribosomal protein L14, chloroplastic

Chain AK: 98%



- Molecule 11: 50S ribosomal protein L15, chloroplastic

Chain AL: 99%



- Molecule 12: 50S ribosomal protein L16, chloroplastic

Chain AM: 99%



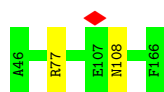
- Molecule 13: 50S ribosomal protein L17, chloroplastic

Chain AN: 98%



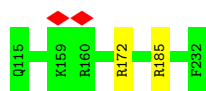
- Molecule 14: 50S ribosomal protein L18, chloroplastic

Chain AO: 98%



- Molecule 15: 50S ribosomal protein L19, chloroplastic

Chain AP: 98%



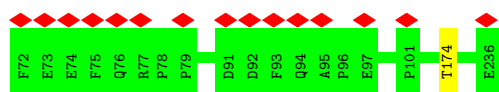
- Molecule 16: 50S ribosomal protein L20, chloroplastic

Chain AQ: 99%



- Molecule 17: 50S ribosomal protein L21, chloroplastic

Chain AR: 9% 99%



- Molecule 18: 50S ribosomal protein L22, chloroplastic

Chain AS: 100%



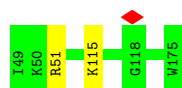
- Molecule 19: 50S ribosomal protein L23, chloroplastic

Chain AT: 100%

There are no outlier residues recorded for this chain.

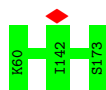
- Molecule 20: 50S ribosomal protein L24, chloroplastic

Chain AU: 98%



- Molecule 21: 50S ribosomal protein L27, chloroplastic

Chain AW: 100%



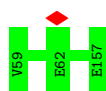
- Molecule 22: 50S ribosomal protein L28, chloroplastic

Chain AX: 99%



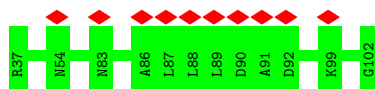
- Molecule 23: 50S ribosomal protein L29, chloroplastic

Chain AY: 100%



- Molecule 24: 50S ribosomal protein L31, chloroplastic

Chain AZ: 15% 100%



- Molecule 25: 50S ribosomal protein L32, chloroplastic

Chain Aa: 100%

There are no outlier residues recorded for this chain.

- Molecule 26: 50S ribosomal protein L33, chloroplastic

Chain Ab: 100%

There are no outlier residues recorded for this chain.

- Molecule 27: 50S ribosomal protein L34, chloroplastic

Chain Ac: 100%

There are no outlier residues recorded for this chain.

- Molecule 28: 50S ribosomal protein L35, chloroplastic

Chain Ad: 99%



- Molecule 29: 50S ribosomal protein L36, chloroplastic

Chain Ae:  100%

There are no outlier residues recorded for this chain.

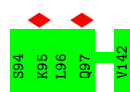
- Molecule 30: 50S ribosomal protein 6, chloroplastic

Chain Af:  98%



- Molecule 31: 50S ribosomal protein 5 alpha, chloroplastic

Chain Aw:  100%



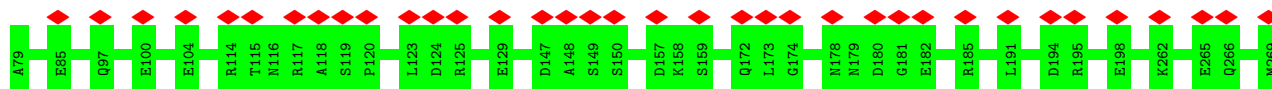
- Molecule 32: 5S ribosomal RNA

Chain Ax:  93% 7%



- Molecule 33: Ribosome-recycling factor, chloroplastic

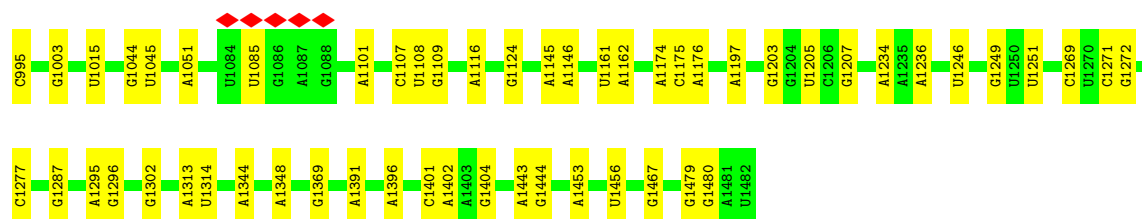
Chain Az:  19% 100%



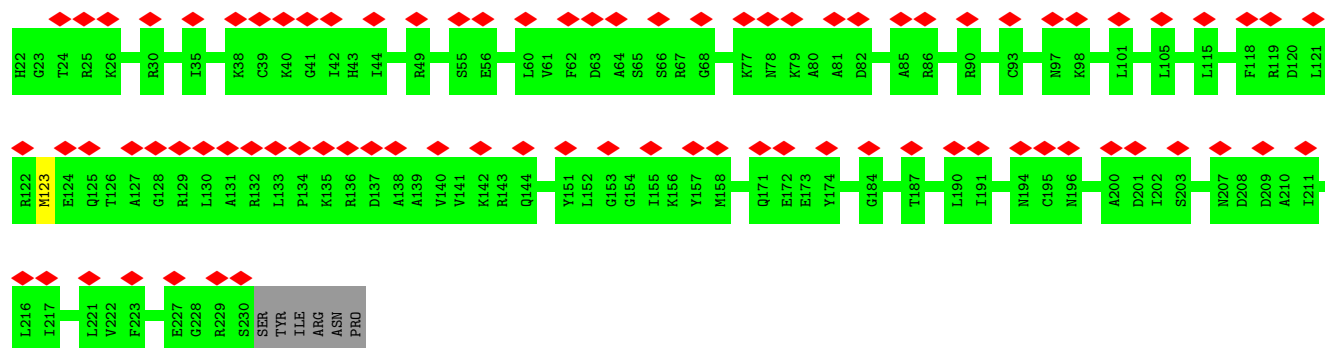
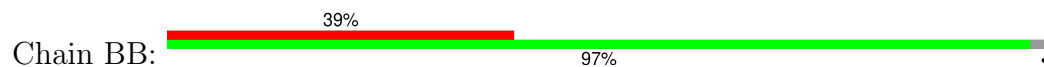
- Molecule 34: 16S ribosomal RNA

Chain BA:  90% 10%

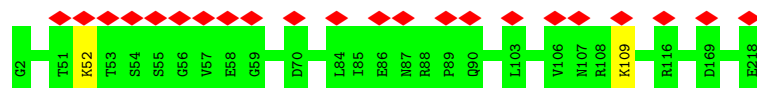




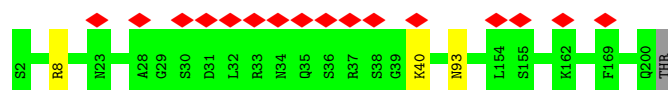
- Molecule 35: 30S ribosomal protein S2, chloroplastic



- Molecule 36: 30S ribosomal protein S3, chloroplastic



- Molecule 37: 30S ribosomal protein S4, chloroplastic

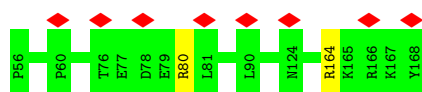


- Molecule 38: 30S ribosomal protein S5, chloroplastic

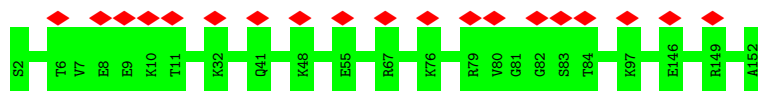


- Molecule 39: 30S ribosomal protein S6 alpha, chloroplastic

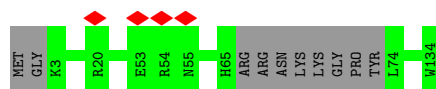




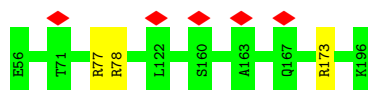
- Molecule 40: 30S ribosomal protein S7, chloroplastic



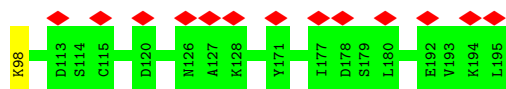
- Molecule 41: 30S ribosomal protein S8, chloroplastic



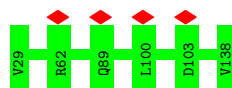
- Molecule 42: 30S ribosomal protein S9, chloroplastic



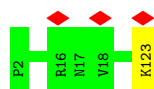
- Molecule 43: 30S ribosomal protein S10 alpha, chloroplastic



- Molecule 44: 30S ribosomal protein S11, chloroplastic



- Molecule 45: 30S ribosomal protein S12, chloroplastic



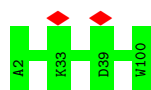
- Molecule 46: 30S ribosomal protein S13, chloroplastic

Chain BM:  99%



- Molecule 47: 30S ribosomal protein S14, chloroplastic

Chain BN:  100%



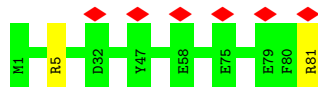
- Molecule 48: 30S ribosomal protein S15, chloroplastic

Chain BO:  97%



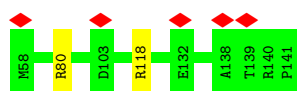
- Molecule 49: 30S ribosomal protein S16, chloroplastic

Chain BP:  98%



- Molecule 50: 30S ribosomal protein S17, chloroplastic

Chain BQ:  98%



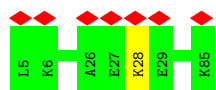
- Molecule 51: 30S ribosomal protein S18, chloroplastic

Chain BR:  94%

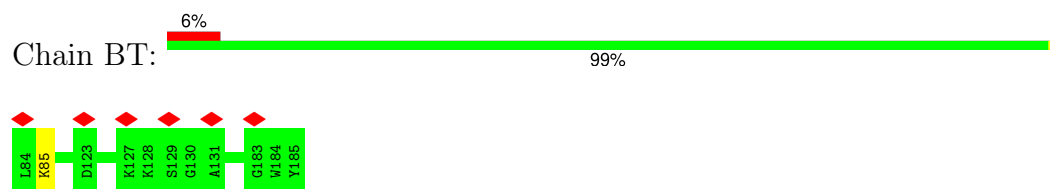


- Molecule 52: 30S ribosomal protein S19, chloroplastic

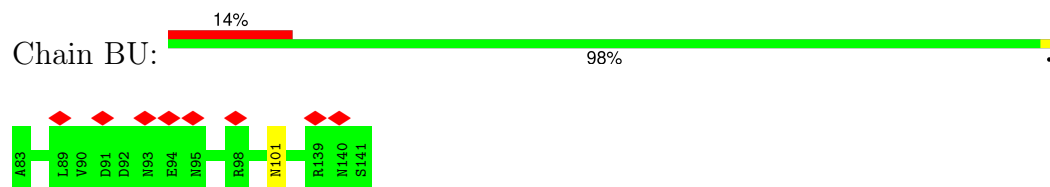
Chain BS:  99%



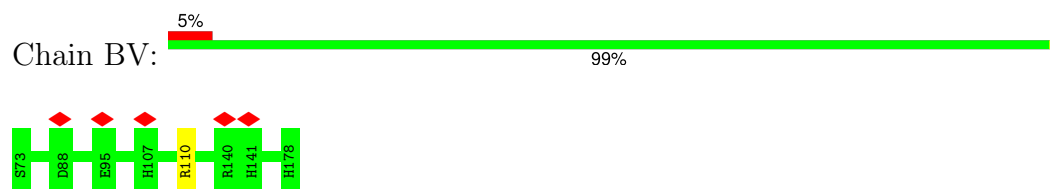
- Molecule 53: 30S ribosomal protein S20, chloroplastic



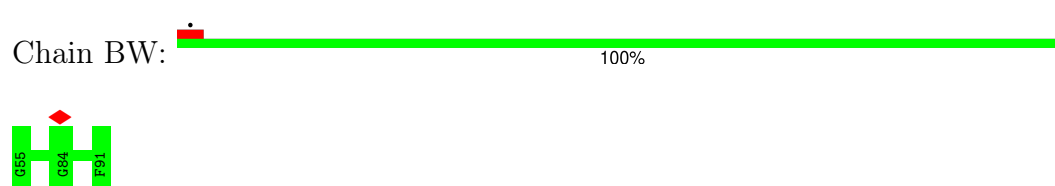
- Molecule 54: 30S ribosomal protein S21, chloroplastic



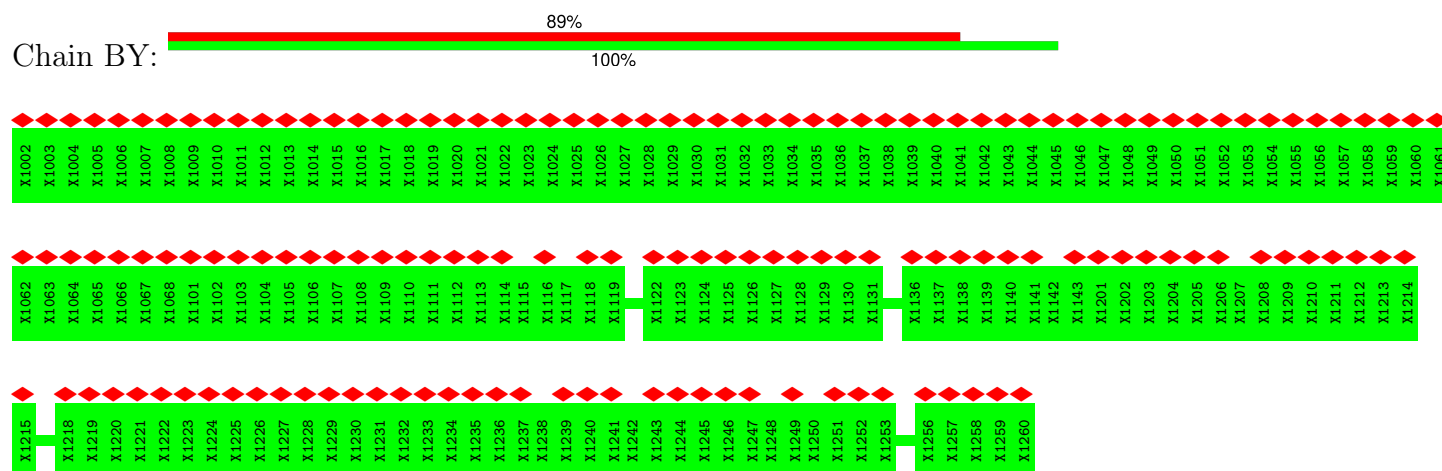
- Molecule 55: Ribosome-binding factor PSRP1, chloroplastic



- Molecule 56: 30S ribosomal protein S31, chloroplastic



- Molecule 57: bS1c



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	130300	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 ($e^-/\text{\AA}^2$)	4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.449	Depositor
Minimum map value	-0.272	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	445.19998, 445.19998, 445.19998	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.25	0/64858	0.70	2/101177 (0.0%)
2	AB	0.24	0/2551	0.72	0/3977
3	AC	0.27	0/1929	0.58	0/2588
4	AD	0.27	0/1713	0.53	0/2291
5	AE	0.27	0/1707	0.56	0/2298
6	AF	0.27	0/1347	0.53	0/1813
7	AG	0.28	0/1364	0.58	0/1835
8	AH	0.25	0/370	0.60	0/490
9	AJ	0.27	0/1659	0.51	0/2242
10	AK	0.26	0/943	0.59	0/1271
11	AL	0.28	0/1425	0.58	0/1889
12	AM	0.28	0/1093	0.60	0/1466
13	AN	0.26	0/959	0.56	0/1280
14	AO	0.27	0/968	0.51	0/1300
15	AP	0.27	0/967	0.57	0/1300
16	AQ	0.27	0/1011	0.60	0/1350
17	AR	0.28	0/1359	0.55	0/1850
18	AS	0.27	0/1412	0.57	0/1889
19	AT	0.26	0/753	0.53	0/1011
20	AU	0.25	0/1030	0.53	0/1375
21	AW	0.28	0/930	0.56	0/1235
22	AX	0.26	0/635	0.54	0/844
23	AY	0.26	0/840	0.53	0/1113
24	AZ	0.27	0/548	0.59	0/737
25	Aa	0.28	0/405	0.53	0/537
26	Ab	0.26	0/497	0.57	0/664
27	Ac	0.25	0/474	0.63	0/624
28	Ad	0.27	0/594	0.58	0/784
29	Ae	0.27	0/307	0.66	0/403
30	Af	0.27	0/389	0.51	0/528
31	Aw	0.25	0/426	0.68	0/552
32	Ax	0.21	0/2821	0.70	0/4396

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Az	0.25	0/1525	0.50	0/2048
34	BA	0.19	0/35618	0.69	1/55573 (0.0%)
35	BB	0.26	0/1666	0.55	0/2251
36	BC	0.26	0/1772	0.55	0/2382
37	BD	0.26	0/1661	0.57	0/2230
38	BE	0.26	0/1203	0.57	0/1620
39	BF	0.28	0/929	0.58	0/1255
40	BG	0.26	0/1192	0.55	0/1596
41	BH	0.26	0/1016	0.59	0/1363
42	BI	0.26	0/1110	0.54	0/1490
43	BJ	0.27	0/813	0.54	0/1099
44	BK	0.25	0/841	0.58	0/1135
45	BL	0.27	0/975	0.61	0/1312
46	BM	0.25	0/921	0.61	0/1230
47	BN	0.24	0/841	0.59	0/1123
48	BO	0.26	0/613	0.58	0/814
49	BP	0.27	0/685	0.58	0/916
50	BQ	0.26	0/690	0.57	0/926
51	BR	0.26	0/443	0.57	0/591
52	BS	0.26	0/668	0.49	0/899
53	BT	0.25	0/826	0.54	0/1100
54	BU	0.27	0/518	0.58	0/685
55	BV	0.25	0/843	0.55	0/1126
56	BW	0.27	0/296	0.62	0/390
All	All	0.24	0/155949	0.66	3/232263 (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
17	AR	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1334	U	C2-N1-C1'	6.57	125.58	117.70
34	BA	1107	C	C2-N1-C1'	6.41	125.85	118.80
1	AA	1621	C	C6-N1-C2	-5.10	118.26	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	AR	174	THR	Peptide

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	
3	AC	244/246 (99%)	232 (95%)	12 (5%)	0	100	100
4	AD	219/221 (99%)	206 (94%)	13 (6%)	0	100	100
5	AE	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
6	AF	167/207 (81%)	162 (97%)	5 (3%)	0	100	100
7	AG	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
8	AH	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
9	AJ	198/200 (99%)	191 (96%)	7 (4%)	0	100	100
10	AK	118/121 (98%)	115 (98%)	3 (2%)	0	100	100
11	AL	182/184 (99%)	174 (96%)	8 (4%)	0	100	100
12	AM	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
13	AN	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
14	AO	119/121 (98%)	117 (98%)	2 (2%)	0	100	100
15	AP	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
16	AQ	113/115 (98%)	109 (96%)	4 (4%)	0	100	100
17	AR	163/165 (99%)	150 (92%)	13 (8%)	0	100	100
18	AS	169/171 (99%)	163 (96%)	6 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	AT	90/92 (98%)	89 (99%)	1 (1%)	0	100	100
20	AU	125/127 (98%)	121 (97%)	4 (3%)	0	100	100
21	AW	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
22	AX	74/76 (97%)	72 (97%)	2 (3%)	0	100	100
23	AY	97/99 (98%)	97 (100%)	0	0	100	100
24	AZ	64/66 (97%)	55 (86%)	9 (14%)	0	100	100
25	Aa	46/48 (96%)	46 (100%)	0	0	100	100
26	Ab	58/60 (97%)	55 (95%)	3 (5%)	0	100	100
27	Ac	59/61 (97%)	59 (100%)	0	0	100	100
28	Ad	70/72 (97%)	66 (94%)	4 (6%)	0	100	100
29	Ae	35/37 (95%)	35 (100%)	0	0	100	100
30	Af	45/47 (96%)	40 (89%)	5 (11%)	0	100	100
31	Aw	47/49 (96%)	45 (96%)	2 (4%)	0	100	100
33	Az	189/191 (99%)	187 (99%)	2 (1%)	0	100	100
35	BB	207/215 (96%)	187 (90%)	20 (10%)	0	100	100
36	BC	215/217 (99%)	205 (95%)	10 (5%)	0	100	100
37	BD	197/200 (98%)	185 (94%)	12 (6%)	0	100	100
38	BE	156/158 (99%)	152 (97%)	4 (3%)	0	100	100
39	BF	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
40	BG	149/151 (99%)	143 (96%)	6 (4%)	0	100	100
41	BH	120/134 (90%)	117 (98%)	3 (2%)	0	100	100
42	BI	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
43	BJ	96/98 (98%)	91 (95%)	5 (5%)	0	100	100
44	BK	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
45	BL	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
46	BM	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
47	BN	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
48	BO	70/72 (97%)	69 (99%)	1 (1%)	0	100	100
49	BP	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
50	BQ	82/84 (98%)	73 (89%)	9 (11%)	0	100	100
51	BR	51/53 (96%)	51 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	BS	79/81 (98%)	69 (87%)	10 (13%)	0	100	100
53	BT	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
54	BU	57/59 (97%)	56 (98%)	1 (2%)	0	100	100
55	BV	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
56	BW	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
All	All	6070/6232 (97%)	5809 (96%)	261 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
3	AC	194/194 (100%)	192 (99%)	2 (1%)	73	88
4	AD	182/182 (100%)	180 (99%)	2 (1%)	70	87
5	AE	179/179 (100%)	177 (99%)	2 (1%)	70	87
6	AF	146/176 (83%)	145 (99%)	1 (1%)	81	91
7	AG	146/146 (100%)	143 (98%)	3 (2%)	48	77
8	AH	40/40 (100%)	40 (100%)	0	100	100
9	AJ	173/173 (100%)	173 (100%)	0	100	100
10	AK	100/101 (99%)	98 (98%)	2 (2%)	50	78
11	AL	141/141 (100%)	139 (99%)	2 (1%)	62	83
12	AM	108/108 (100%)	106 (98%)	2 (2%)	52	79
13	AN	96/96 (100%)	94 (98%)	2 (2%)	48	77
14	AO	99/99 (100%)	97 (98%)	2 (2%)	50	78
15	AP	104/104 (100%)	102 (98%)	2 (2%)	52	79
16	AQ	102/102 (100%)	101 (99%)	1 (1%)	73	88
17	AR	147/147 (100%)	147 (100%)	0	100	100
18	AS	151/151 (100%)	151 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	AT	81/81 (100%)	81 (100%)	0	100	100
20	AU	114/114 (100%)	112 (98%)	2 (2%)	54	80
21	AW	94/94 (100%)	94 (100%)	0	100	100
22	AX	66/66 (100%)	65 (98%)	1 (2%)	60	83
23	AY	92/92 (100%)	92 (100%)	0	100	100
24	AZ	57/57 (100%)	57 (100%)	0	100	100
25	Aa	41/41 (100%)	41 (100%)	0	100	100
26	Ab	56/56 (100%)	56 (100%)	0	100	100
27	Ac	50/50 (100%)	50 (100%)	0	100	100
28	Ad	62/62 (100%)	61 (98%)	1 (2%)	58	82
29	Ae	34/34 (100%)	34 (100%)	0	100	100
30	Af	41/41 (100%)	40 (98%)	1 (2%)	44	74
31	Aw	46/46 (100%)	46 (100%)	0	100	100
33	Az	175/175 (100%)	175 (100%)	0	100	100
35	BB	177/183 (97%)	176 (99%)	1 (1%)	84	93
36	BC	187/187 (100%)	185 (99%)	2 (1%)	70	87
37	BD	178/179 (99%)	175 (98%)	3 (2%)	56	81
38	BE	121/121 (100%)	120 (99%)	1 (1%)	79	90
39	BF	100/100 (100%)	98 (98%)	2 (2%)	50	78
40	BG	122/122 (100%)	122 (100%)	0	100	100
41	BH	109/117 (93%)	109 (100%)	0	100	100
42	BI	111/111 (100%)	108 (97%)	3 (3%)	40	71
43	BJ	90/90 (100%)	89 (99%)	1 (1%)	70	87
44	BK	86/86 (100%)	86 (100%)	0	100	100
45	BL	105/105 (100%)	104 (99%)	1 (1%)	73	88
46	BM	100/100 (100%)	99 (99%)	1 (1%)	73	88
47	BN	89/89 (100%)	89 (100%)	0	100	100
48	BO	67/67 (100%)	65 (97%)	2 (3%)	36	69
49	BP	72/72 (100%)	70 (97%)	2 (3%)	38	70
50	BQ	75/75 (100%)	73 (97%)	2 (3%)	40	71
51	BR	50/50 (100%)	47 (94%)	3 (6%)	16	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	BS	70/70 (100%)	69 (99%)	1 (1%)	62	83
53	BT	84/84 (100%)	83 (99%)	1 (1%)	67	86
54	BU	54/54 (100%)	53 (98%)	1 (2%)	52	79
55	BV	96/96 (100%)	95 (99%)	1 (1%)	73	88
56	BW	28/28 (100%)	28 (100%)	0	100	100
All	All	5288/5334 (99%)	5232 (99%)	56 (1%)	69	87

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	BB	123	MET
55	BV	110	ARG
39	BF	80	ARG
54	BU	101	ASN
51	BR	27	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
16	AQ	104	ASN
50	BQ	135	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	2691/2810 (95%)	284 (10%)	5 (0%)
2	AB	105/106 (99%)	11 (10%)	0
32	Ax	117/118 (99%)	8 (6%)	0
34	BA	1480/1481 (99%)	146 (9%)	3 (0%)
All	All	4393/4515 (97%)	449 (10%)	8 (0%)

5 of 449 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	33	A
1	AA	45	A
1	AA	62	A
1	AA	70	A

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Mol	Chain	Res	Type
1	AA	73	U

5 of 8 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	BA	1174	A
34	BA	707	G
1	AA	1927	A
1	AA	1500	U
34	BA	700	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 345 ligands modelled in this entry, 345 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
57	BY	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BY	1068:UNK	C	1101:UNK	N	65.42
1	BY	1143:UNK	C	1201:UNK	N	12.57

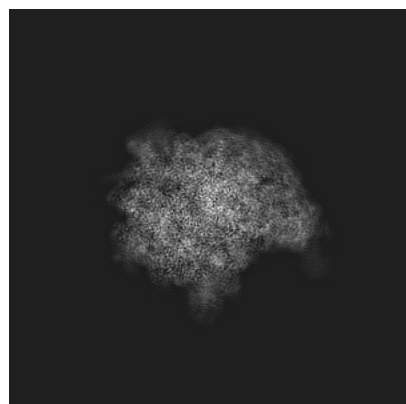
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3941. These allow visual inspection of the internal detail of the map and identification of artifacts.

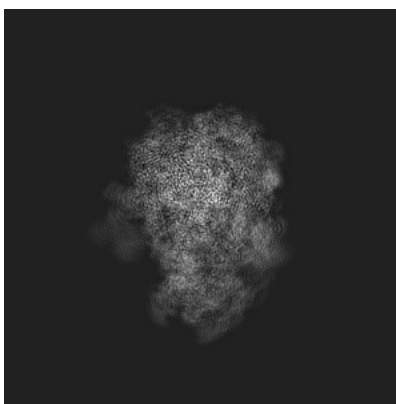
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

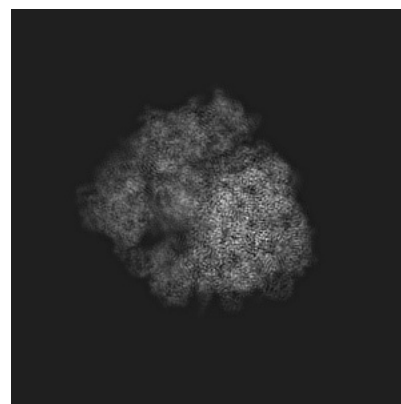
6.1.1 Primary map



X

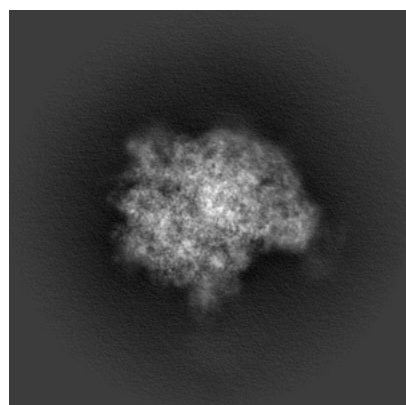


Y

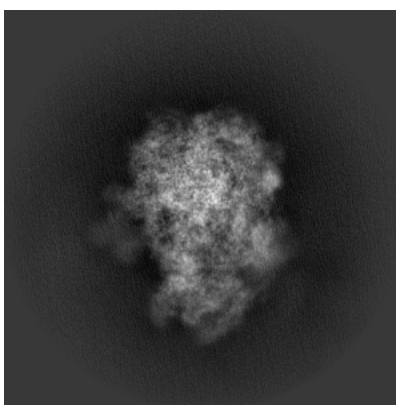


Z

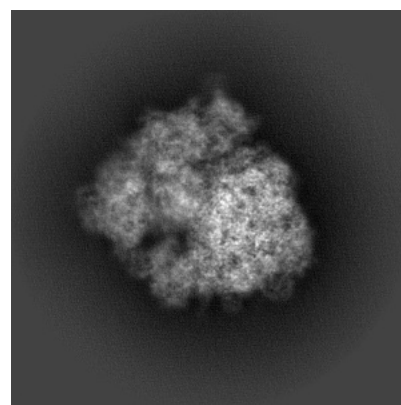
6.1.2 Raw map



X



Y

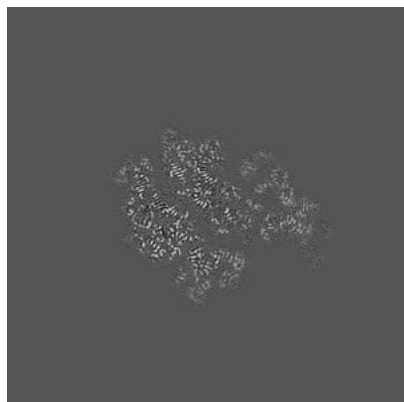


Z

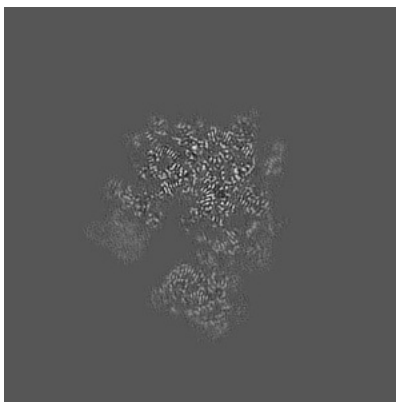
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

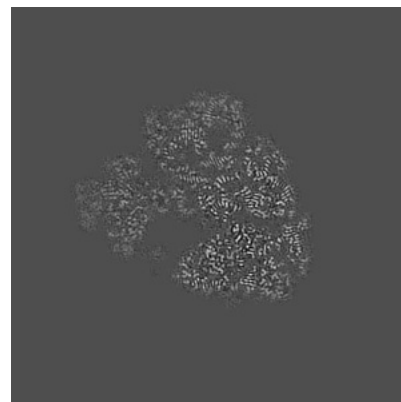
6.2.1 Primary map



X Index: 210

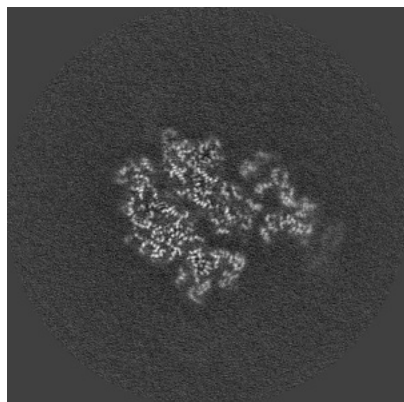


Y Index: 210

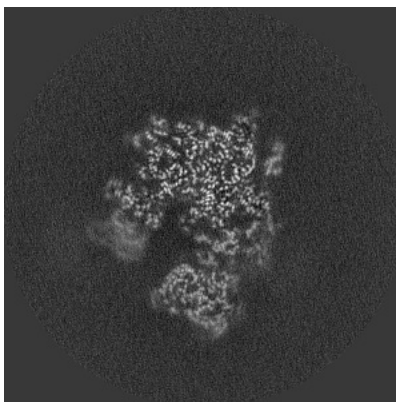


Z Index: 210

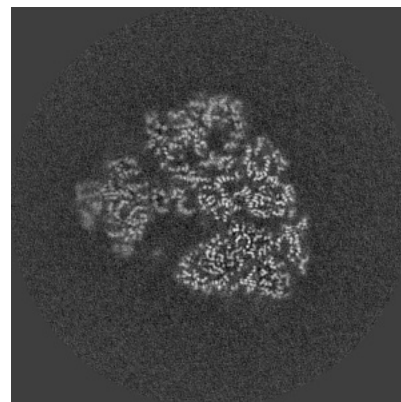
6.2.2 Raw map



X Index: 210



Y Index: 210

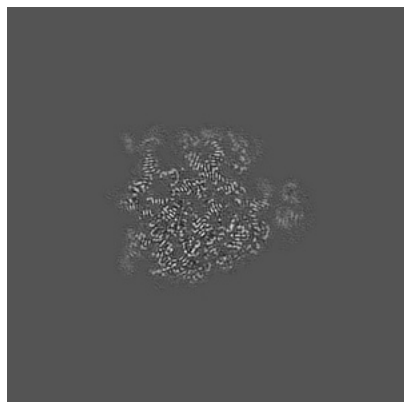


Z Index: 210

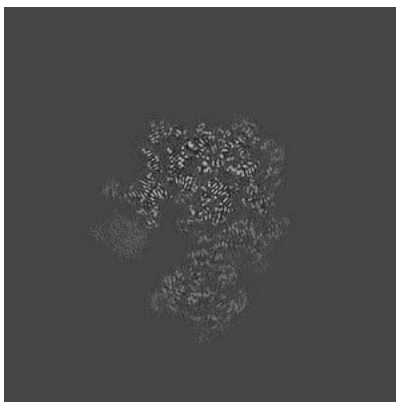
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

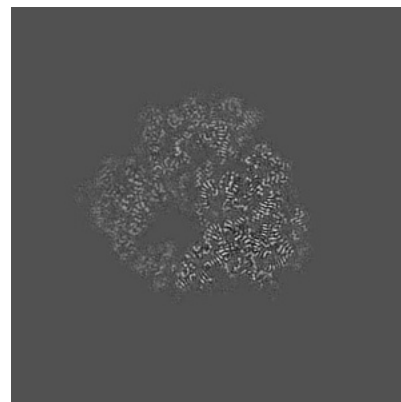
6.3.1 Primary map



X Index: 247

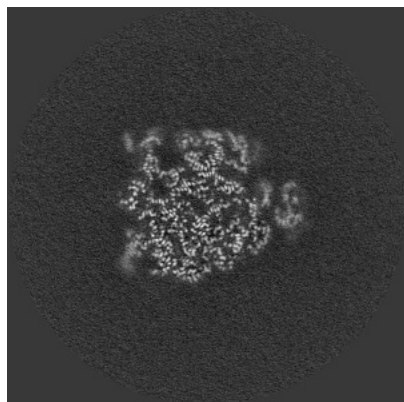


Y Index: 216

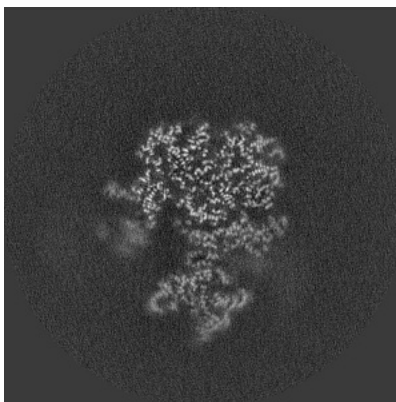


Z Index: 200

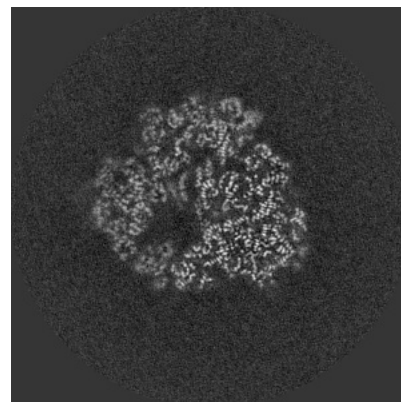
6.3.2 Raw map



X Index: 246



Y Index: 220

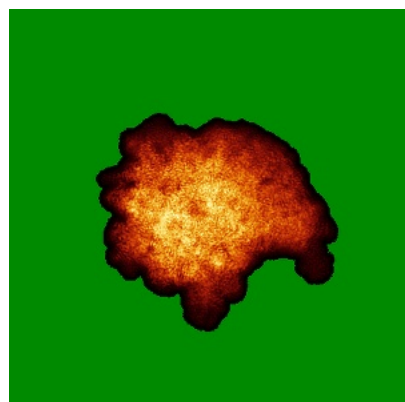


Z Index: 200

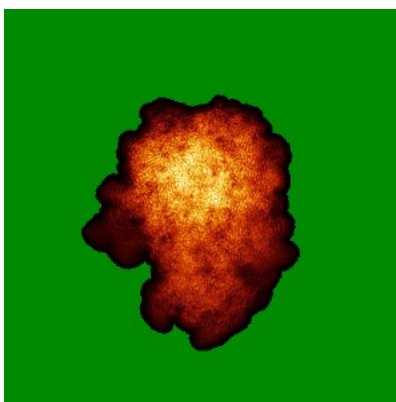
The images above show the largest variance slices of the map in three orthogonal directions.

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

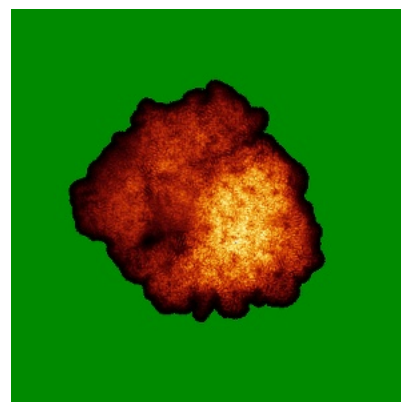
6.4.1 Primary map



X

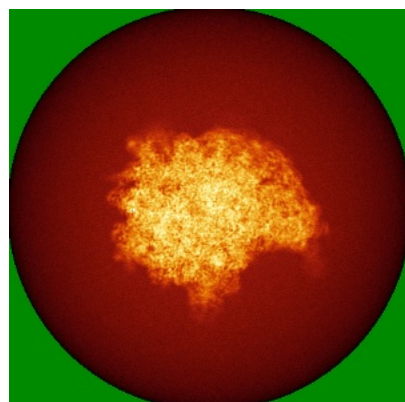


Y

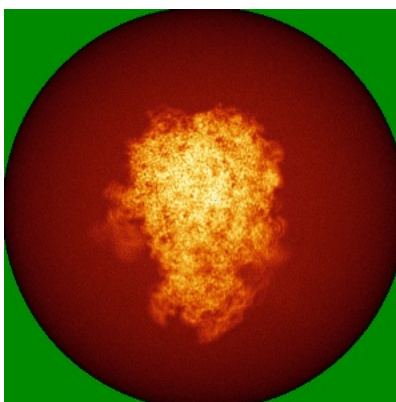


Z

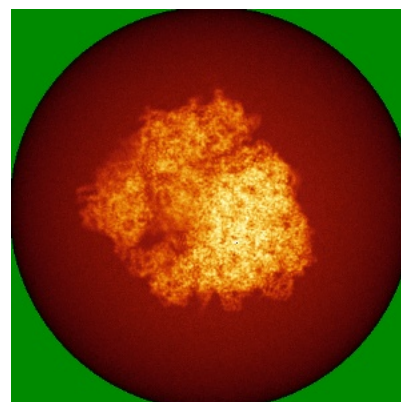
6.4.2 Raw map



X



Y



Z

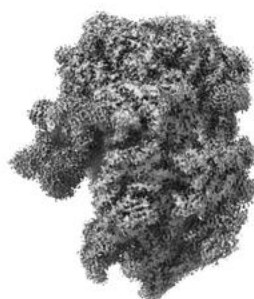
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

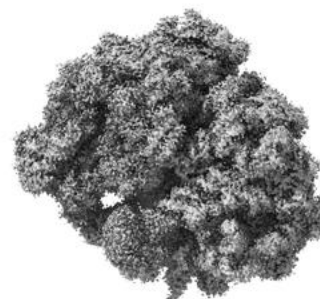
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. 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.

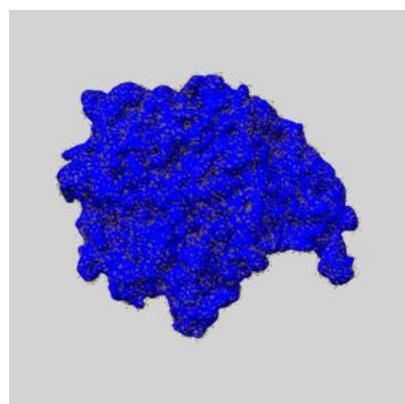
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

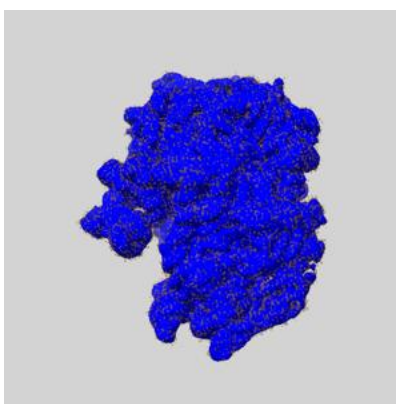
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

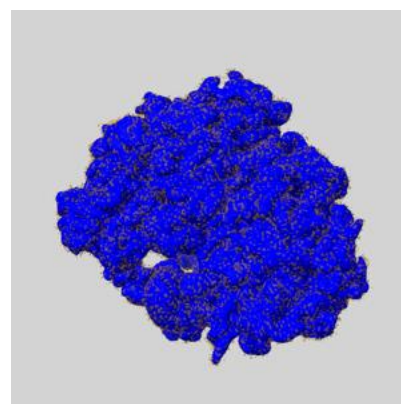
6.6.1 emd_3941_msk_1.map [i](#)



X



Y

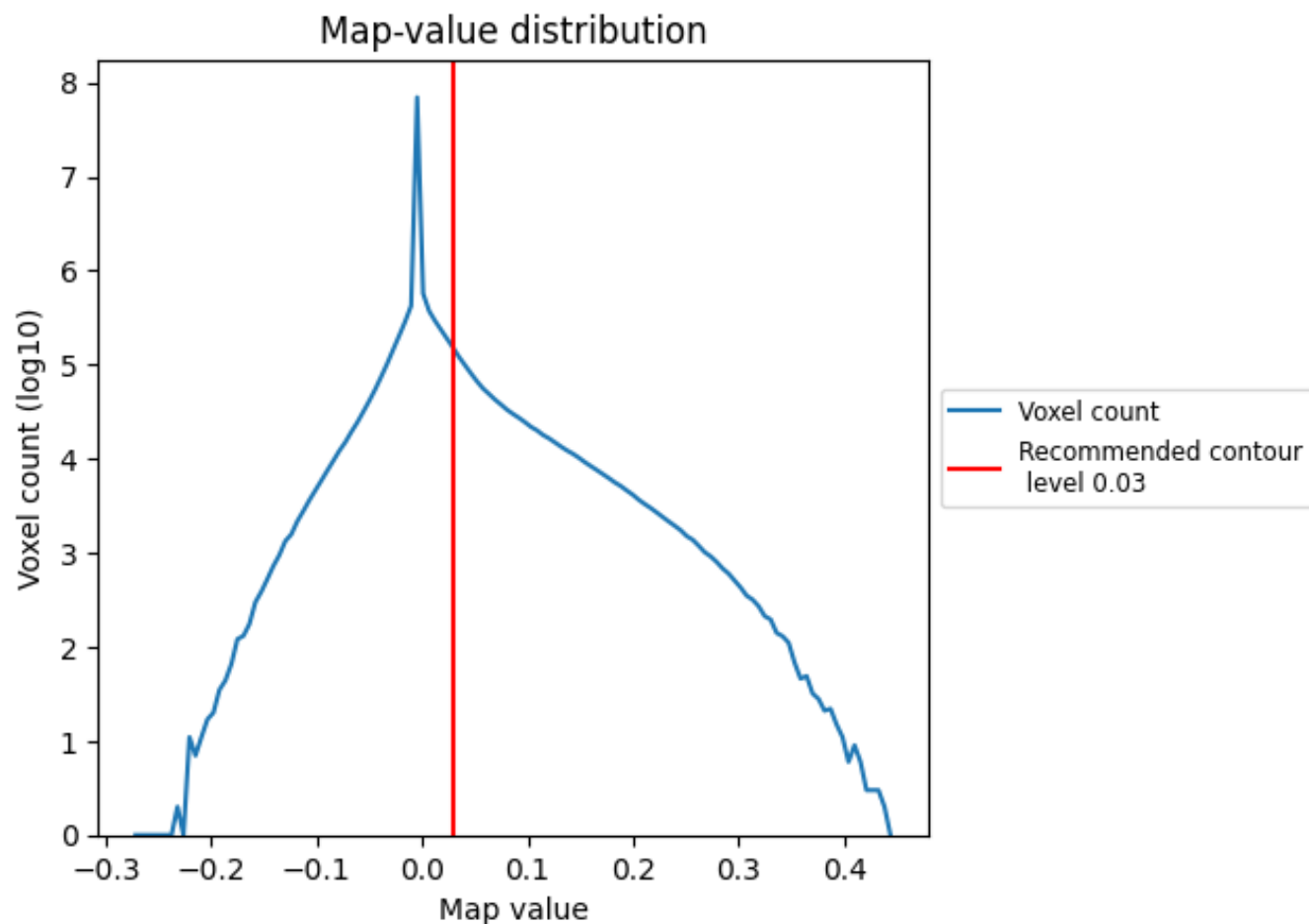


Z

7 Map analysis [i](#)

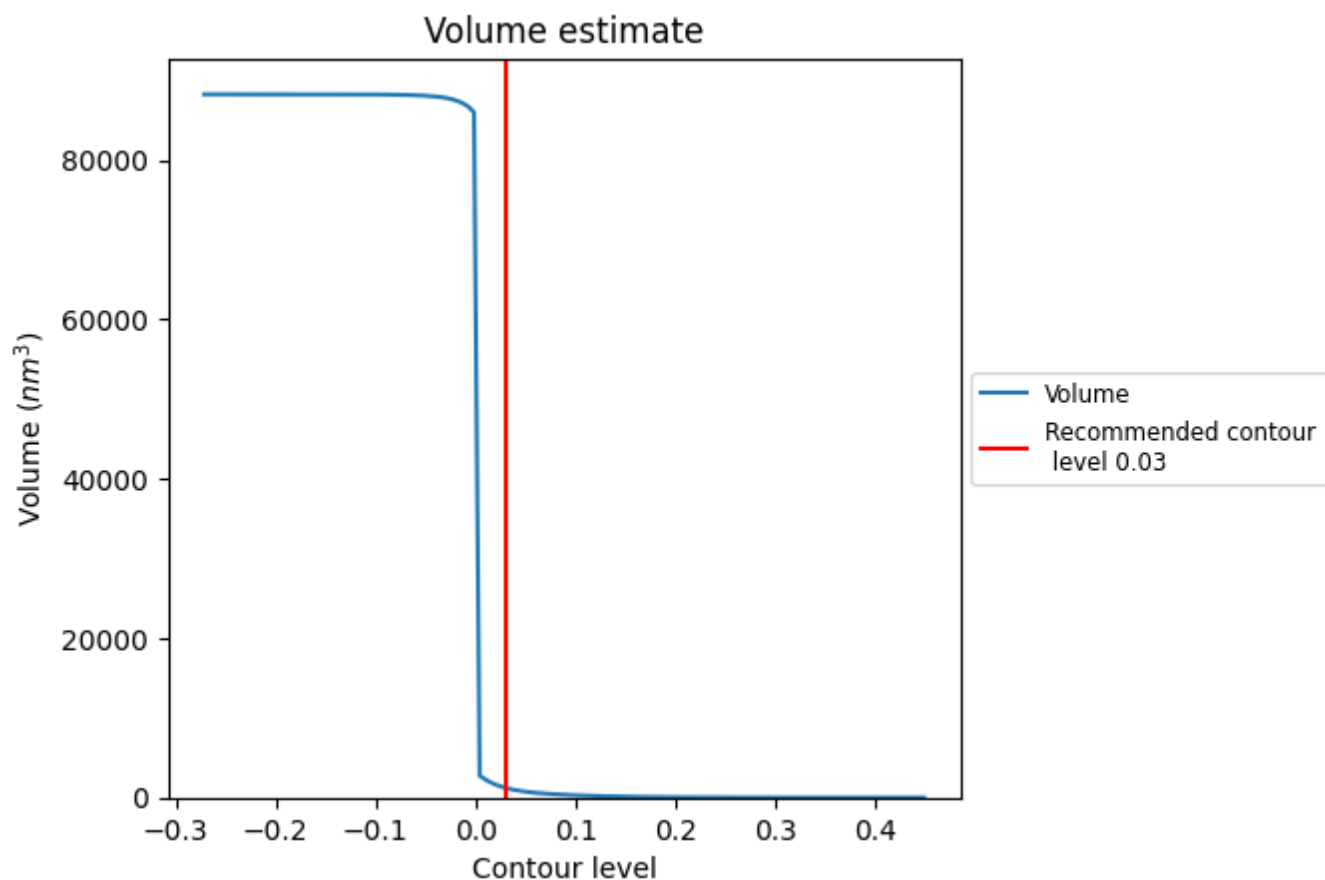
This section contains the results of statistical analysis of the map.

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.

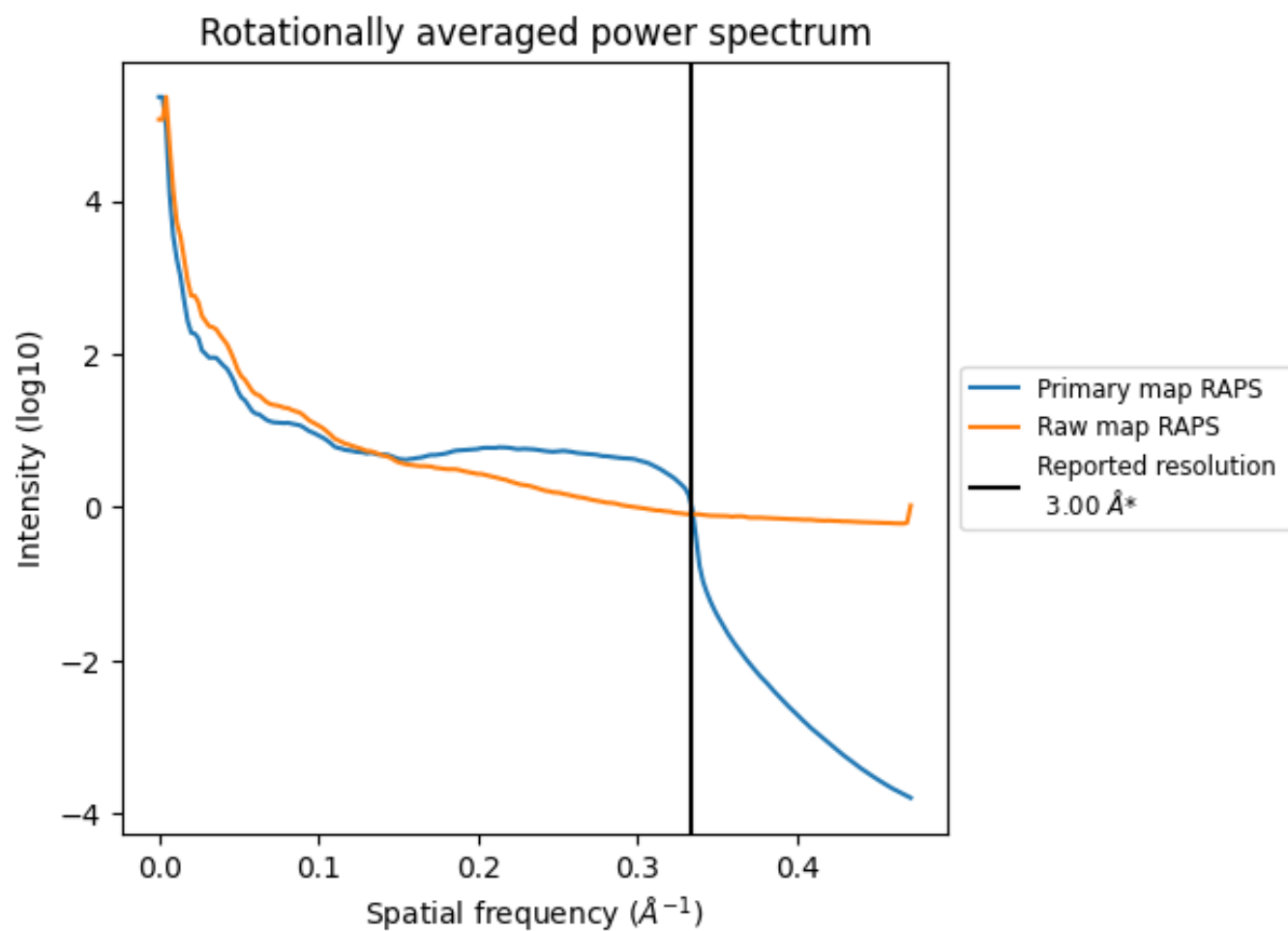
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1225 nm³; this corresponds to an approximate mass of 1106 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 ⓘ

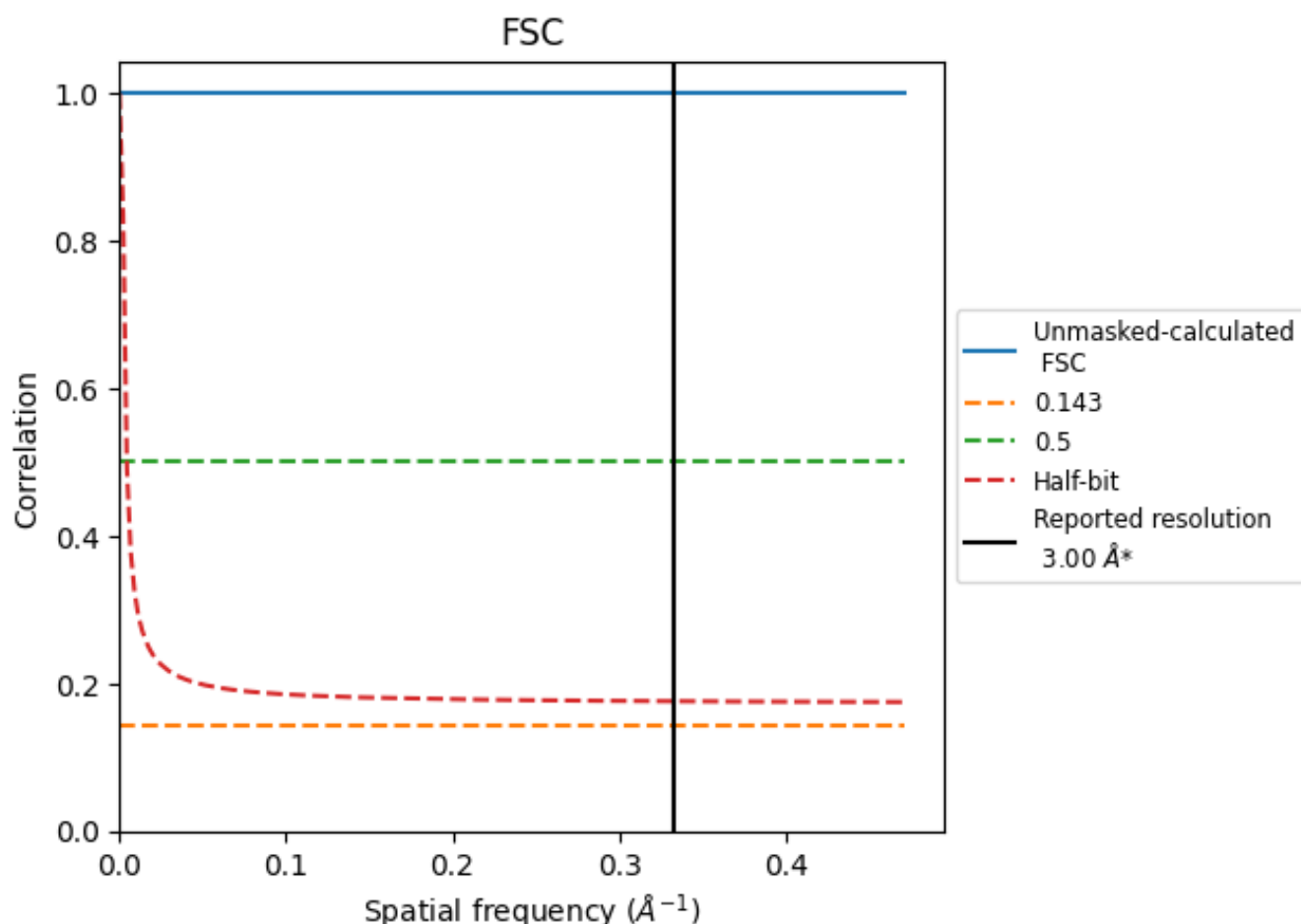


*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

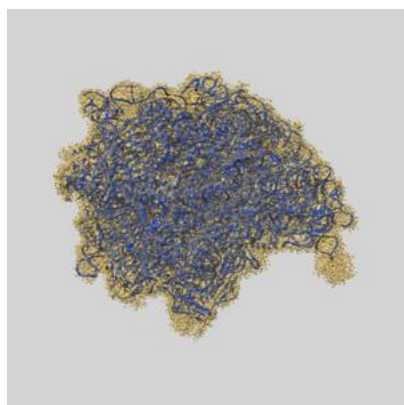
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

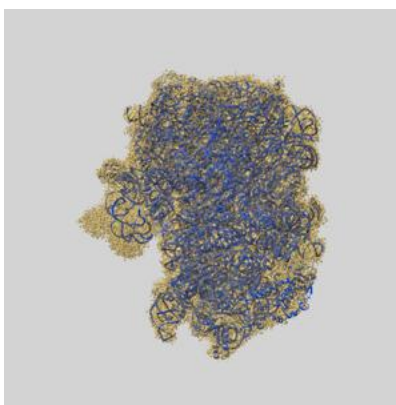
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3941 and PDB model 6ERI. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

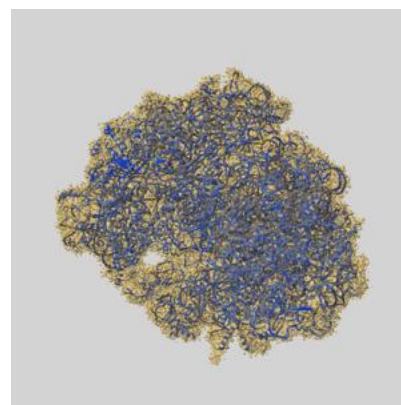
9.1 Map-model overlay [i](#)



X



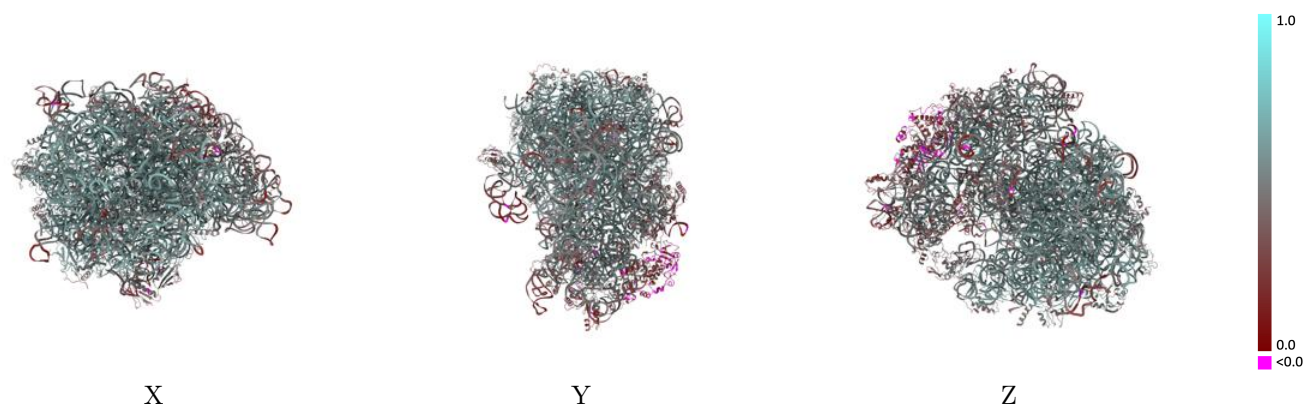
Y



Z

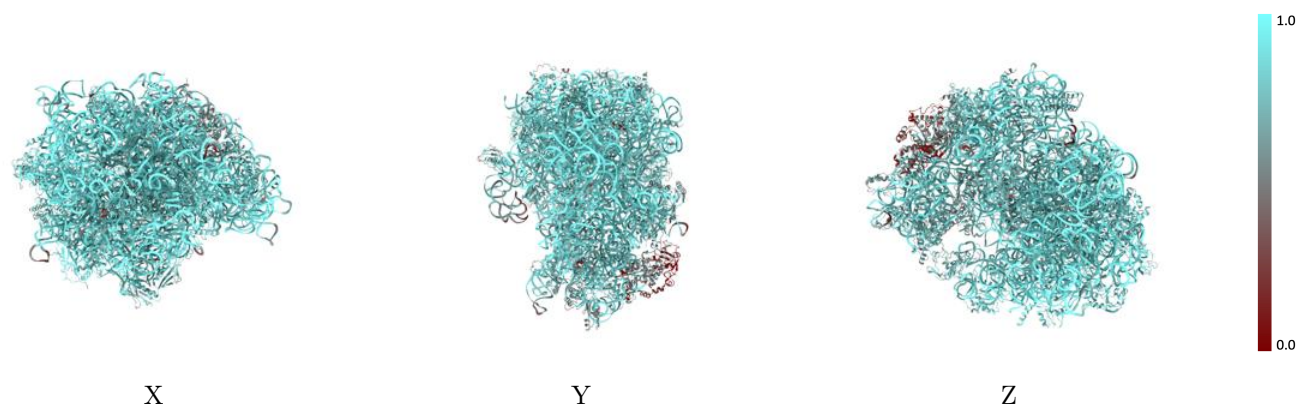
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



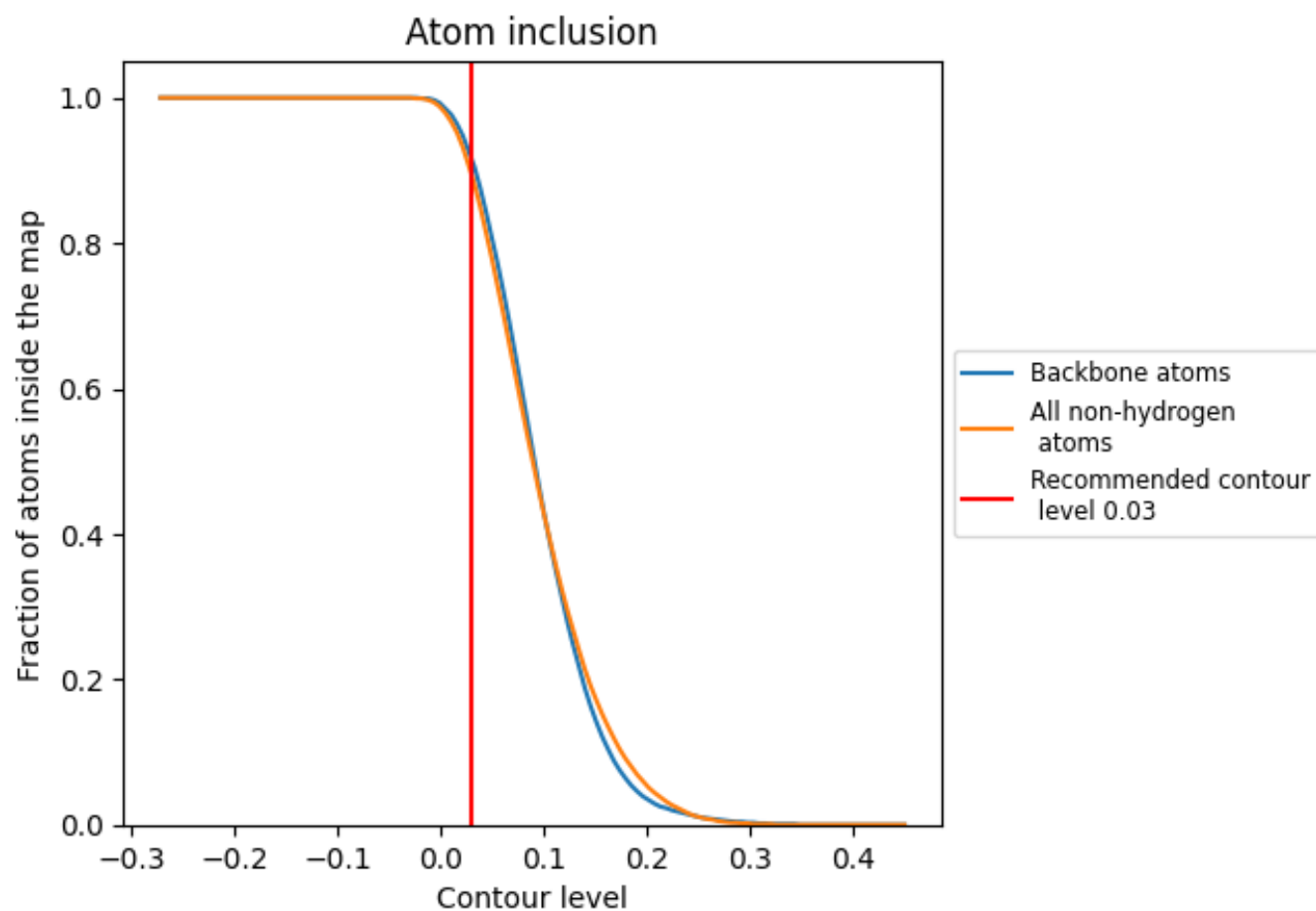
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 89% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8930	 0.5140
AA	 0.9580	 0.5680
AB	 0.9620	 0.5770
AC	 0.9000	 0.5370
AD	 0.9060	 0.5500
AE	 0.8680	 0.5260
AF	 0.8000	 0.4390
AG	 0.7430	 0.3820
AH	 0.6900	 0.4120
AJ	 0.9020	 0.5440
AK	 0.8660	 0.5190
AL	 0.8710	 0.5150
AM	 0.8840	 0.5200
AN	 0.8870	 0.5330
AO	 0.8440	 0.4830
AP	 0.8790	 0.5270
AQ	 0.9000	 0.5430
AR	 0.8050	 0.4650
AS	 0.8370	 0.4920
AT	 0.8160	 0.4840
AU	 0.8480	 0.4910
AW	 0.8770	 0.5230
AX	 0.8930	 0.5250
AY	 0.8190	 0.4750
AZ	 0.6860	 0.3260
Aa	 0.8670	 0.5340
Ab	 0.8480	 0.4950
Ac	 0.9220	 0.5630
Ad	 0.9190	 0.5690
Ae	 0.8760	 0.5180
Af	 0.8930	 0.5200
Aw	 0.7860	 0.4340
Ax	 0.9720	 0.5580
Az	 0.5810	 0.3980
BA	 0.9350	 0.5160



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Chain	Atom inclusion	Q-score
BB	 0.4880	 0.2620
BC	 0.7060	 0.3950
BD	 0.7290	 0.4000
BE	 0.8290	 0.4740
BF	 0.6790	 0.3510
BG	 0.6350	 0.3400
BH	 0.7810	 0.4170
BI	 0.7530	 0.3820
BJ	 0.6890	 0.3590
BK	 0.7520	 0.3840
BL	 0.8390	 0.4890
BM	 0.7760	 0.4090
BN	 0.7640	 0.4180
BO	 0.6970	 0.4020
BP	 0.7860	 0.4240
BQ	 0.7770	 0.4260
BR	 0.7660	 0.3890
BS	 0.7350	 0.3720
BT	 0.7730	 0.4110
BU	 0.6220	 0.3240
BV	 0.7380	 0.4230
BW	 0.8240	 0.4570
BY	 0.1550	 0.0480