



wwPDB EM Validation Summary Report ⓘ

Sep 24, 2026 – 04:50 PM JST

PDB ID : 27UR / pdb_000027ur
EMDB ID : EMD-81438
Title : In situ structure of the side-by-side PSII-LHCII dimer from *Oryza sativa* (composite)
Authors : Li, J.; Elias, E.; Zhang, K.; Croce, R.; Zhu, J.
Deposited on : 2026-06-12
Resolution : 3.50 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:

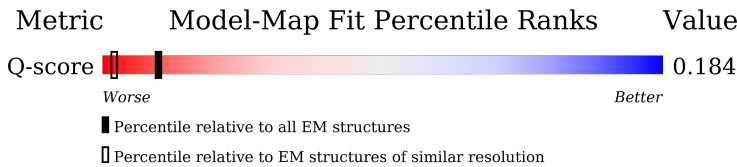
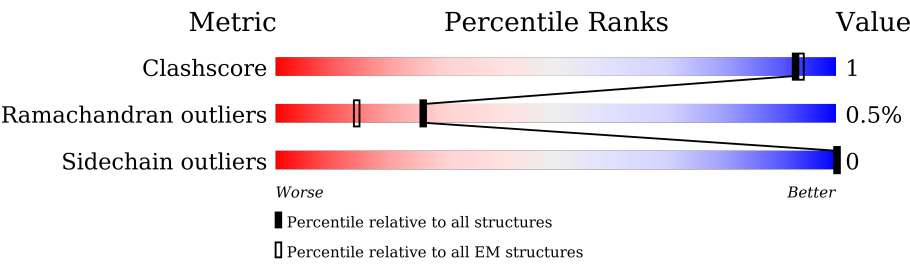
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



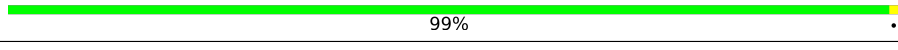
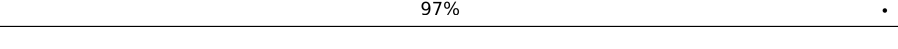
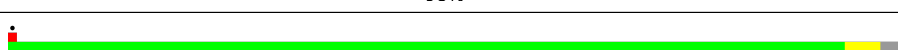
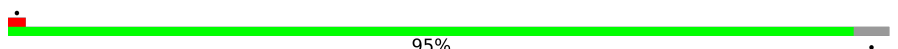
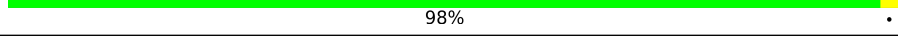
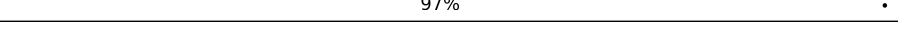
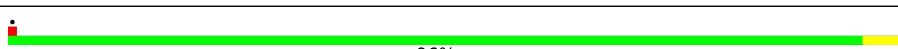
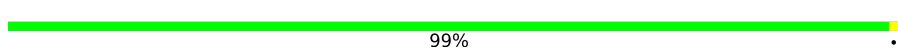
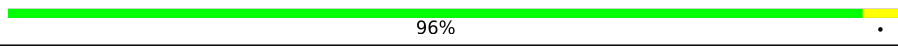
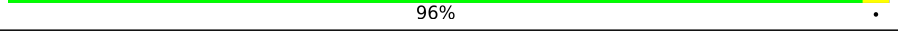
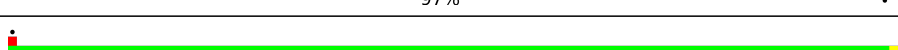
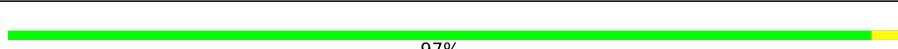
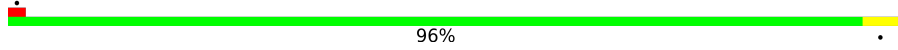
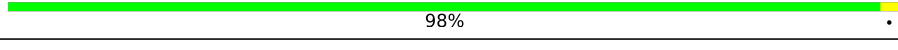
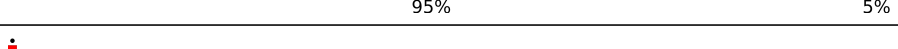
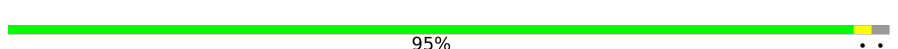
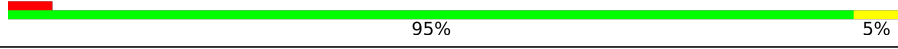
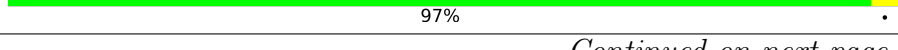
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	00	219	95%
1	01	219	98%
1	02	219	94%
1	05	219	95%

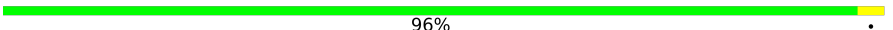
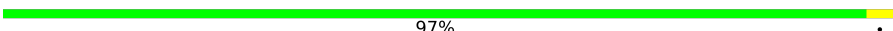
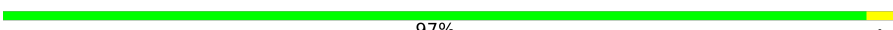
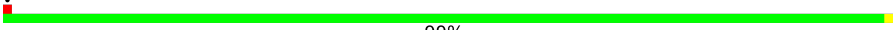
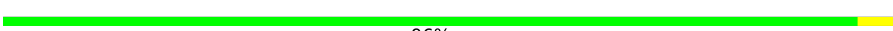
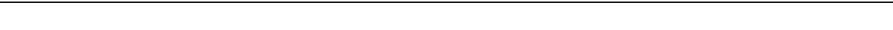
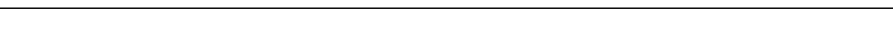
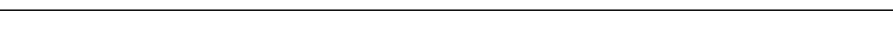
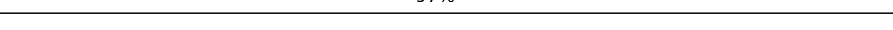
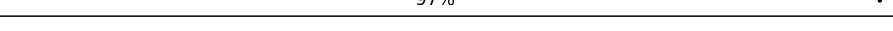
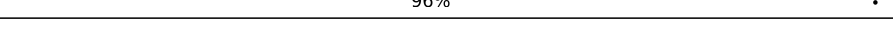
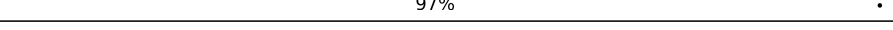
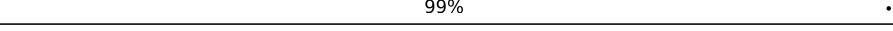
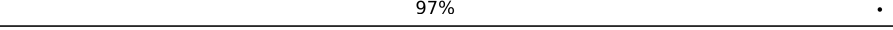
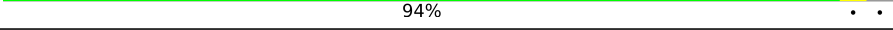
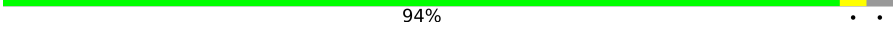
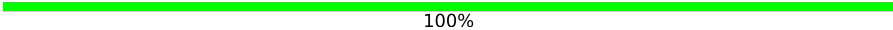
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Mol	Chain	Length	Quality of chain
1	06	219	 90% 5%
1	09	219	 99%
1	10	219	 97%
1	11	219	 98%
1	12	219	 94%
1	15	219	 95%
1	16	219	 89% 5% 5%
1	19	219	 98%
1	1G	219	 97%
1	1N	219	 96%
1	1g	219	 96%
1	1n	219	 99%
1	2G	219	 96%
1	2N	219	 96%
1	2g	219	 97%
1	2n	219	 99%
2	03	220	 97%
2	07	220	 96%
2	13	220	 98%
2	17	220	 95% 5%
3	04	205	 95%
3	08	205	 95% 5%
3	14	205	 95%
3	18	205	 5% 95% 5%
4	1A	334	97%

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Mol	Chain	Length	Quality of chain
4	1a	334	 96%
4	2A	334	 97%
4	2a	334	 97%
5	1B	503	 99%
5	1b	503	 96%
5	2B	503	 99%
5	2b	503	 96%
6	1C	450	 99%
6	1c	450	 97%
6	2C	450	 99%
6	2c	450	 98%
7	1D	341	 98%
7	1d	341	 98%
7	2D	341	 97%
7	2d	341	 97%
8	1E	75	 96%
8	1e	75	 97%
8	2E	75	 99%
8	2e	75	 97%
9	1F	36	 94%
9	1f	36	 81% 17%
9	2F	36	 94%
9	2f	36	 81% 17%
10	1H	60	 100%
10	1h	60	 100%

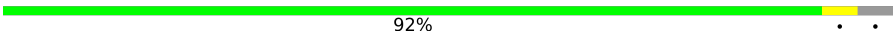
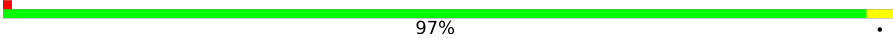
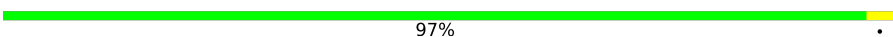
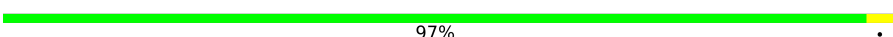
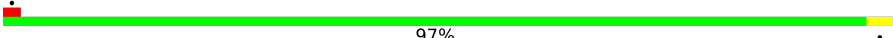
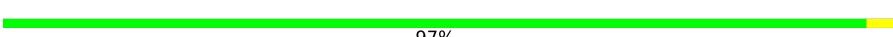
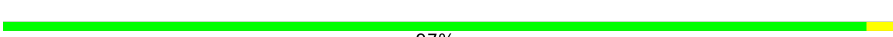
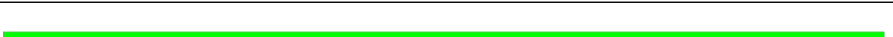
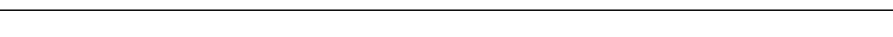
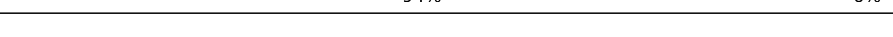
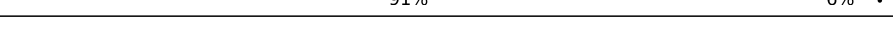
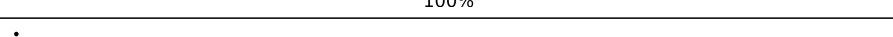
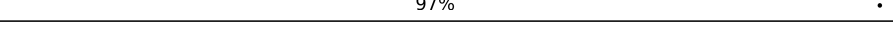
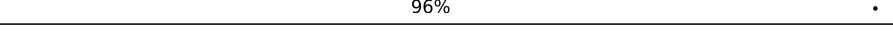
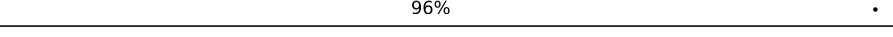
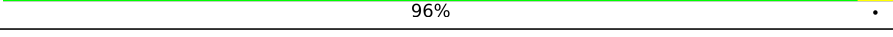
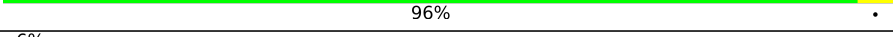
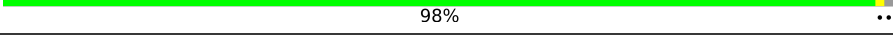
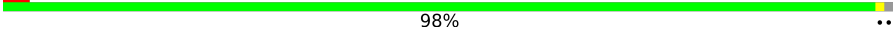
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Mol	Chain	Length	Quality of chain
10	2H	60	100%
10	2h	60	100%
11	1I	34	56% 26% 18%
11	1i	34	100%
11	2I	34	62% 32% 6%
11	2i	34	100%
12	1J	35	100%
12	1j	35	97% .
12	2J	35	100%
12	2j	35	97% .
13	1K	37	100%
13	1k	37	86% 14%
13	2K	37	100%
13	2k	37	86% 14%
14	1L	37	97% .
14	1l	37	95% 5%
14	2L	37	97% .
14	2l	37	95% 5%
15	1M	33	6% 88% 9% .
15	1m	33	6% 100%
15	2M	33	94% . .
15	2m	33	9% 100%
16	1O	248	94% 5%
16	1o	248	93% . .
16	2O	248	95% .

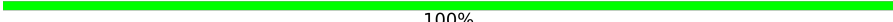
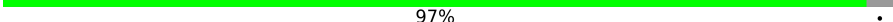
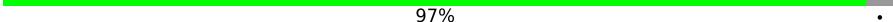
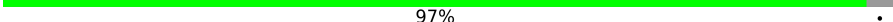
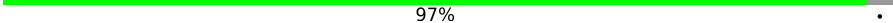
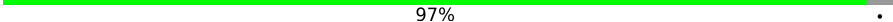
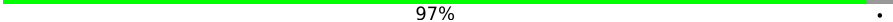
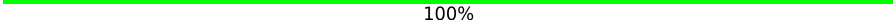
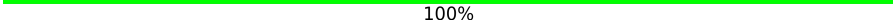
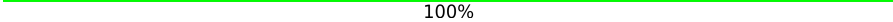
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Mol	Chain	Length	Quality of chain
16	2o	248	 92%
17	1P	186	 97%
17	1p	186	 97%
17	2P	186	 97%
17	2p	186	 97%
18	1R	234	 97%
18	1r	234	 97%
18	2R	234	 97%
18	2r	234	 98%
19	1S	218	 97%
19	1s	218	 99%
19	2S	218	 97%
19	2s	218	 99%
20	1T	32	 94%6%
20	1t	32	 91%6%
20	2T	32	 100%
20	2t	32	 97%
21	1U	27	 96%
21	1u	27	 96%
21	2U	27	 96%
21	2u	27	 96%
22	1V	99	 6%98%..
22	1v	99	 89%11%
22	2V	99	 98%..
22	2v	99	 89%11%

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Mol	Chain	Length	Quality of chain
23	1W	54	 100%
23	1w	54	 81% 19%
23	2W	54	 100%
23	2w	54	 81% 19%
24	1X	39	 100%
24	1x	39	 97% .
24	2X	39	 100%
24	2x	39	 97% .
25	1Y	35	 97% .
25	1y	35	 97% .
25	2Y	35	 97% .
25	2y	35	 97% .
26	1Z	62	 100%
26	1z	62	 100%
26	2Z	62	 100%
26	2z	62	 100%

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 93932 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 Chlorophyll a-b binding protein 2, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	00	219	Total	C	N	O	0	0
			1098	660	219	219		
1	01	219	Total	C	N	O	0	0
			1097	660	219	218		
1	02	214	Total	C	N	O	0	0
			1076	648	214	214		
1	05	210	Total	C	N	O	0	0
			1052	632	210	210		
1	06	207	Total	C	N	O	0	0
			1034	620	207	207		
1	09	219	Total	C	N	O	0	0
			1098	660	219	219		
1	10	219	Total	C	N	O	0	0
			1098	660	219	219		
1	11	219	Total	C	N	O	0	0
			1097	660	219	218		
1	12	214	Total	C	N	O	0	0
			1076	648	214	214		
1	15	210	Total	C	N	O	0	0
			1052	632	210	210		
1	16	207	Total	C	N	O	0	0
			1034	620	207	207		
1	19	219	Total	C	N	O	0	0
			1098	660	219	219		
1	1G	219	Total	C	N	O	0	0
			1098	660	219	219		
1	1N	219	Total	C	N	O	0	0
			1098	660	219	219		
1	1g	219	Total	C	N	O	0	0
			1098	660	219	219		
1	1n	219	Total	C	N	O	0	0
			1098	660	219	219		
1	2G	219	Total	C	N	O	0	0
			1098	660	219	219		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	2N	219	Total	C	N	O	0	0
			1098	660	219	219		
1	2g	219	Total	C	N	O	0	0
			1098	660	219	219		
1	2n	219	Total	C	N	O	0	0
			1098	660	219	219		

- Molecule 2 is a protein called Chlorophyll a/b-binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	03	220	Total	C	N	O	0	0
			1100	660	220	220		
2	07	220	Total	C	N	O	0	0
			1101	661	220	220		
2	13	220	Total	C	N	O	0	0
			1100	660	220	220		
2	17	220	Total	C	N	O	0	0
			1101	661	220	220		

- Molecule 3 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	04	200	Total	C	N	O	0	0
			1006	606	200	200		
3	08	205	Total	C	N	O	0	0
			1030	620	205	205		
3	14	200	Total	C	N	O	0	0
			1006	606	200	200		
3	18	205	Total	C	N	O	0	0
			1030	620	205	205		

- Molecule 4 is a protein called Photosystem II protein D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	1A	334	Total	C	N	O	0	0
			1666	998	334	334		
4	1a	333	Total	C	N	O	0	0
			1661	995	333	333		
4	2A	334	Total	C	N	O	0	0
			1666	998	334	334		
4	2a	333	Total	C	N	O	0	0
			1661	995	333	333		

- Molecule 5 is a protein called Photosystem II CP47 reaction center protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	1B	503	Total	C	N	O	0	0
			2510	1504	503	503		
5	1b	503	Total	C	N	O	0	0
			2510	1504	503	503		
5	2B	503	Total	C	N	O	0	0
			2510	1504	503	503		
5	2b	503	Total	C	N	O	0	0
			2510	1504	503	503		

- Molecule 6 is a protein called Photosystem II CP43 reaction center protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	1C	450	Total	C	N	O	0	0
			2238	1338	450	450		
6	1c	450	Total	C	N	O	0	0
			2237	1337	450	450		
6	2C	450	Total	C	N	O	0	0
			2238	1338	450	450		
6	2c	450	Total	C	N	O	0	0
			2237	1337	450	450		

- Molecule 7 is a protein called Photosystem II D2 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	1D	340	Total	C	N	O	0	0
			1698	1018	340	340		
7	1d	341	Total	C	N	O	0	0
			1703	1021	341	341		
7	2D	340	Total	C	N	O	0	0
			1698	1018	340	340		
7	2d	341	Total	C	N	O	0	0
			1703	1021	341	341		

- Molecule 8 is a protein called Cytochrome b559 subunit alpha.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	1E	75	Total	C	N	O	0	0
			379	229	75	75		
8	1e	75	Total	C	N	O	0	0
			379	229	75	75		
8	2E	75	Total	C	N	O	0	0
			379	229	75	75		

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Mol	Chain	Residues	Atoms				AltConf	Trace
8	2e	75	Total	C	N	O	0	0
			379	229	75	75		

- Molecule 9 is a protein called Cytochrome b559 subunit beta.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	1F	35	Total	C	N	O	0	0
			177	107	35	35		
9	1f	30	Total	C	N	O	0	0
			150	90	30	30		
9	2F	35	Total	C	N	O	0	0
			177	107	35	35		
9	2f	30	Total	C	N	O	0	0
			150	90	30	30		

- Molecule 10 is a protein called Photosystem II reaction center protein H.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	1H	60	Total	C	N	O	0	0
			301	181	60	60		
10	1h	60	Total	C	N	O	0	0
			301	181	60	60		
10	2H	60	Total	C	N	O	0	0
			301	181	60	60		
10	2h	60	Total	C	N	O	0	0
			301	181	60	60		

- Molecule 11 is a protein called Photosystem II reaction center protein I.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	1I	34	Total	C	N	O	0	0
			171	103	34	34		
11	1i	34	Total	C	N	O	0	0
			171	103	34	34		
11	2I	34	Total	C	N	O	0	0
			171	103	34	34		
11	2i	34	Total	C	N	O	0	0
			171	103	34	34		

- Molecule 12 is a protein called Photosystem II reaction center protein J.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	1J	35	Total	C	N	O	0	0
			169	99	35	35		
12	1j	35	Total	C	N	O	0	0
			169	99	35	35		
12	2J	35	Total	C	N	O	0	0
			169	99	35	35		
12	2j	35	Total	C	N	O	0	0
			169	99	35	35		

- Molecule 13 is a protein called Photosystem II reaction center protein K.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	1K	37	Total	C	N	O	0	0
			193	119	37	37		
13	1k	37	Total	C	N	O	0	0
			193	119	37	37		
13	2K	37	Total	C	N	O	0	0
			193	119	37	37		
13	2k	37	Total	C	N	O	0	0
			193	119	37	37		

- Molecule 14 is a protein called Photosystem II reaction center protein L.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	1L	36	Total	C	N	O	0	0
			181	109	36	36		
14	1l	35	Total	C	N	O	0	0
			176	106	35	35		
14	2L	36	Total	C	N	O	0	0
			181	109	36	36		
14	2l	35	Total	C	N	O	0	0
			176	106	35	35		

- Molecule 15 is a protein called Photosystem II reaction center protein M.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	1M	32	Total	C	N	O	0	0
			162	98	32	32		
15	1m	33	Total	C	N	O	0	0
			167	101	33	33		
15	2M	32	Total	C	N	O	0	0
			162	98	32	32		

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Mol	Chain	Residues	Atoms				AltConf	Trace
15	2m	33	Total	C	N	O	0	0
			167	101	33	33		

- Molecule 16 is a protein called 33 kDa subunit of oxygen evolving system of photosystem II.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	1O	247	Total	C	N	O	0	0
			1239	745	247	247		
16	1o	237	Total	C	N	O	0	0
			1186	712	237	237		
16	2O	247	Total	C	N	O	0	0
			1239	745	247	247		
16	2o	237	Total	C	N	O	0	0
			1186	712	237	237		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1O	248	SER	-	insertion	UNP Q943W1
1o	248	SER	-	insertion	UNP Q943W1
2O	248	SER	-	insertion	UNP Q943W1
2o	248	SER	-	insertion	UNP Q943W1

- Molecule 17 is a protein called 23 kDa subunit of oxygen evolving system of photosystem II.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	1P	186	Total	C	N	O	0	0
			926	554	186	186		
17	1p	186	Total	C	N	O	0	0
			926	554	186	186		
17	2P	186	Total	C	N	O	0	0
			926	554	186	186		
17	2p	186	Total	C	N	O	0	0
			926	554	186	186		

- Molecule 18 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	1R	234	Total	C	N	O	0	0
			1177	709	234	234		
18	1r	234	Total	C	N	O	0	0
			1177	709	234	234		

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Mol	Chain	Residues	Atoms				AltConf	Trace
18	2R	234	Total	C	N	O	0	0
			1177	709	234	234		
18	2r	234	Total	C	N	O	0	0
			1177	709	234	234		

- Molecule 19 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	1S	218	Total	C	N	O	0	0
			1094	658	218	218		
19	1s	217	Total	C	N	O	0	0
			1089	655	217	217		
19	2S	218	Total	C	N	O	0	0
			1094	658	218	218		
19	2s	217	Total	C	N	O	0	0
			1089	655	217	217		

- Molecule 20 is a protein called Photosystem II reaction center protein T.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	1T	32	Total	C	N	O	0	0
			165	101	32	32		
20	1t	31	Total	C	N	O	0	0
			160	98	31	31		
20	2T	32	Total	C	N	O	0	0
			165	101	32	32		
20	2t	31	Total	C	N	O	0	0
			160	98	31	31		

- Molecule 21 is a protein called Os02g0581100 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	1U	27	Total	C	N	O	0	0
			138	84	27	27		
21	1u	27	Total	C	N	O	0	0
			138	84	27	27		
21	2U	27	Total	C	N	O	0	0
			138	84	27	27		
21	2u	27	Total	C	N	O	0	0
			138	84	27	27		

- Molecule 22 is a protein called Photosystem II 10 kDa polypeptide, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	1V	98	Total	C	N	O	0	0
			482	286	98	98		
22	1v	99	Total	C	N	O	0	0
			487	289	99	99		
22	2V	98	Total	C	N	O	0	0
			482	286	98	98		
22	2v	99	Total	C	N	O	0	0
			487	289	99	99		

- Molecule 23 is a protein called Photosystem II reaction center W protein, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	1W	54	Total	C	N	O	0	0
			262	154	54	54		
23	1w	44	Total	C	N	O	0	0
			214	126	44	44		
23	2W	54	Total	C	N	O	0	0
			262	154	54	54		
23	2w	44	Total	C	N	O	0	0
			214	126	44	44		

- Molecule 24 is a protein called Os07g0673550 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	1X	39	Total	C	N	O	0	0
			195	117	39	39		
24	1x	38	Total	C	N	O	0	0
			191	115	38	38		
24	2X	39	Total	C	N	O	0	0
			195	117	39	39		
24	2x	38	Total	C	N	O	0	0
			191	115	38	38		

- Molecule 25 is a protein called cDNA clone:001-024-H10, full insert sequence.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	1Y	34	Total	C	N	O	0	0
			175	107	34	34		
25	1y	34	Total	C	N	O	0	0
			175	107	34	34		
25	2Y	34	Total	C	N	O	0	0
			175	107	34	34		

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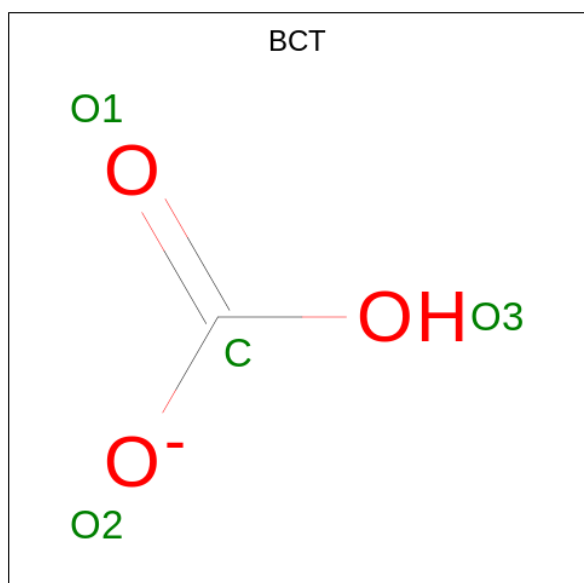
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Mol	Chain	Residues	Atoms				AltConf	Trace
25	2y	34	Total	C	N	O	0	0
			175	107	34	34		

- Molecule 26 is a protein called Photosystem II reaction center protein Z.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	1Z	62	Total	C	N	O	0	0
			311	187	62	62		
26	1z	62	Total	C	N	O	0	0
			311	187	62	62		
26	2Z	62	Total	C	N	O	0	0
			311	187	62	62		
26	2z	62	Total	C	N	O	0	0
			311	187	62	62		

- Molecule 27 is BICARBONATE ION (CCD ID: BCT) (formula: CHO_3) (labeled as "Ligand of Interest" by depositor).

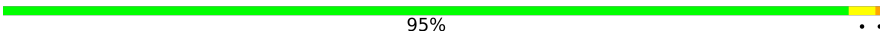


Mol	Chain	Residues	Atoms		AltConf
27	1A	1	Total	C	0
			1	1	
27	1d	1	Total	C	0
			1	1	
27	2A	1	Total	C	0
			1	1	
27	2d	1	Total	C	0
			1	1	

3 Residue-property plots [i](#)

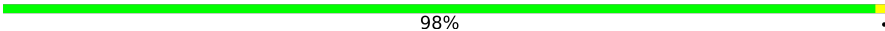
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

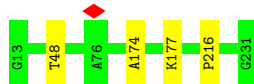
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 00:  95%

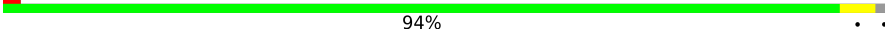


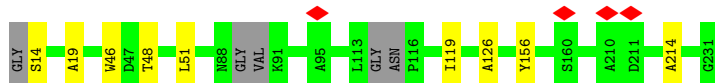
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 01:  98%

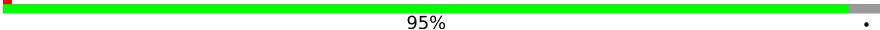


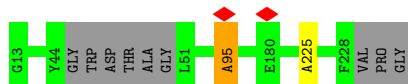
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 02:  94%



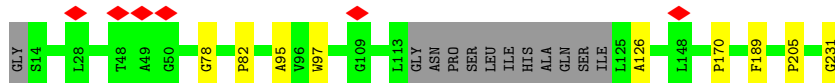
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 05:  95%

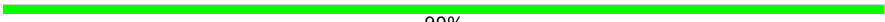


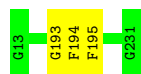
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 06:  90% 5%

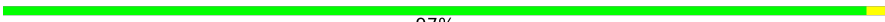


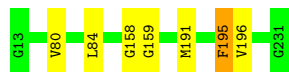
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 09:  99%

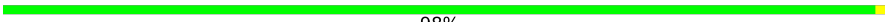


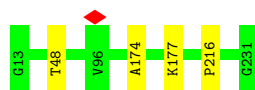
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 10:  97%



- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 11:  98%

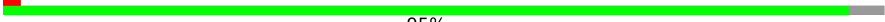


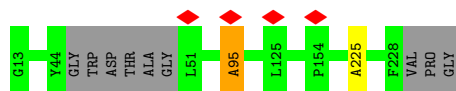
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 12:  94%



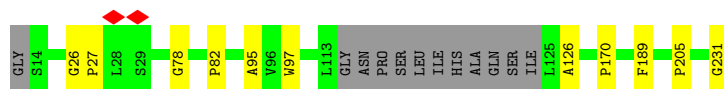
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 15:  95%

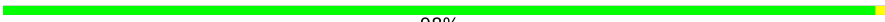


- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 16:  89%  5%  5%



- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 19:  98%



- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 1G: 97%



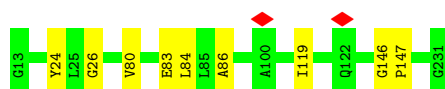
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 1N: 96%



- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 1g: 96%



- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 1n: 99%



- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 2G: 96%



- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 2N: 96%

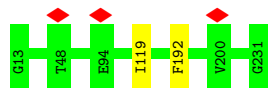


- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 2g: 97%



- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



- Molecule 2: Chlorophyll a/b-binding protein



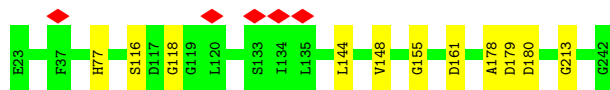
- Molecule 2: Chlorophyll a/b-binding protein



- Molecule 2: Chlorophyll a/b-binding protein



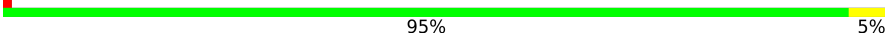
- Molecule 2: Chlorophyll a/b-binding protein

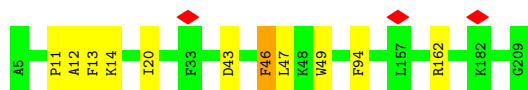


- Molecule 3: Chlorophyll a-b binding protein, chloroplastic

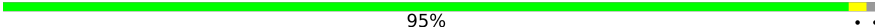


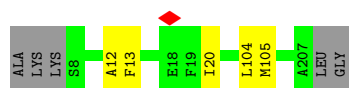
- Molecule 3: Chlorophyll a-b binding protein, chloroplastic

Chain 08:  95% 5%

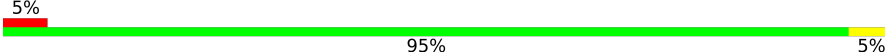


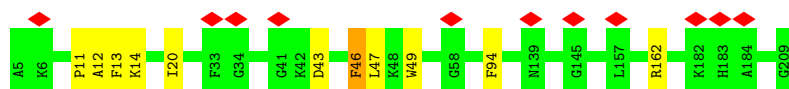
- Molecule 3: Chlorophyll a-b binding protein, chloroplastic

Chain 14:  95% ..

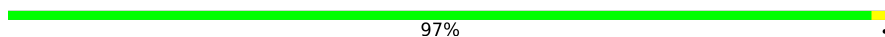


- Molecule 3: Chlorophyll a-b binding protein, chloroplastic

Chain 18:  5% 95% 5%

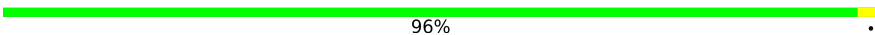


- Molecule 4: Photosystem II protein D1

Chain 1A:  97% .

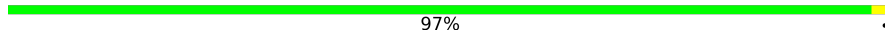


- Molecule 4: Photosystem II protein D1

Chain 1a:  96% .

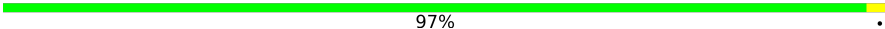


- Molecule 4: Photosystem II protein D1

Chain 2A:  97% .

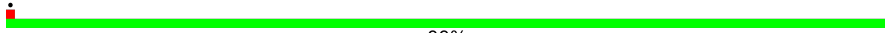


- Molecule 4: Photosystem II protein D1

Chain 2a:  97% .

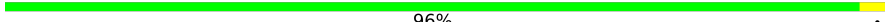


- Molecule 5: Photosystem II CP47 reaction center protein

Chain 1B:  99%

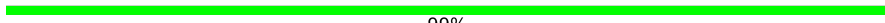


- Molecule 5: Photosystem II CP47 reaction center protein

Chain 1b:  96%

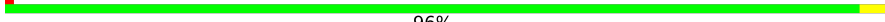


- Molecule 5: Photosystem II CP47 reaction center protein

Chain 2B:  99%



- Molecule 5: Photosystem II CP47 reaction center protein

Chain 2b:  96%

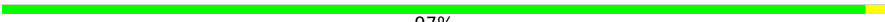


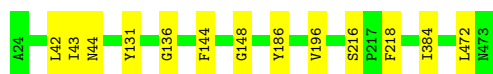
- Molecule 6: Photosystem II CP43 reaction center protein

Chain 1C:  99%

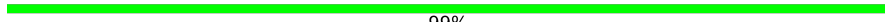


- Molecule 6: Photosystem II CP43 reaction center protein

Chain 1c:  97%

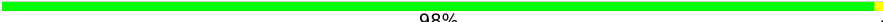


- Molecule 6: Photosystem II CP43 reaction center protein

Chain 2C:  99%

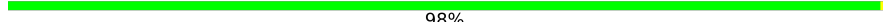


- Molecule 6: Photosystem II CP43 reaction center protein

Chain 2c:  98% .

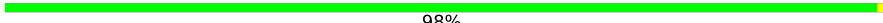


- Molecule 7: Photosystem II D2 protein

Chain 1D:  98% .

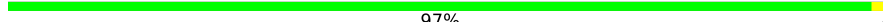


- Molecule 7: Photosystem II D2 protein

Chain 1d:  98% .

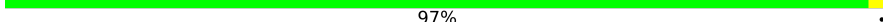


- Molecule 7: Photosystem II D2 protein

Chain 2D:  97% .

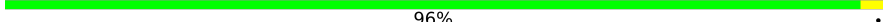


- Molecule 7: Photosystem II D2 protein

Chain 2d:  97% .

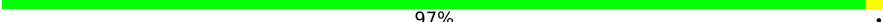


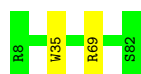
- Molecule 8: Cytochrome b559 subunit alpha

Chain 1E:  96% .

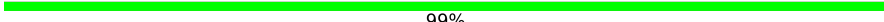


- Molecule 8: Cytochrome b559 subunit alpha

Chain 1e:  97% .

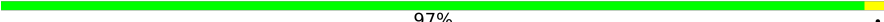


- Molecule 8: Cytochrome b559 subunit alpha

Chain 2E:  99%



- Molecule 8: Cytochrome b559 subunit alpha

Chain 2e:  97%



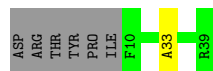
- Molecule 9: Cytochrome b559 subunit beta

Chain 1F:  94%

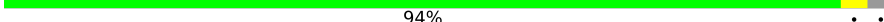


- Molecule 9: Cytochrome b559 subunit beta

Chain 1f:  81% 17%



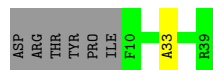
- Molecule 9: Cytochrome b559 subunit beta

Chain 2F:  94%



- Molecule 9: Cytochrome b559 subunit beta

Chain 2f:  81% 17%



- Molecule 10: Photosystem II reaction center protein H

Chain 1H:  100%

There are no outlier residues recorded for this chain.

- Molecule 10: Photosystem II reaction center protein H

Chain 1h:  100%

There are no outlier residues recorded for this chain.

- Molecule 10: Photosystem II reaction center protein H

Chain 2H:  100%

There are no outlier residues recorded for this chain.

- Molecule 10: Photosystem II reaction center protein H

Chain 2h:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: Photosystem II reaction center protein I

Chain 1I:  56% 26% 18%



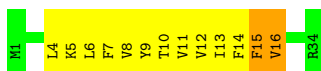
- Molecule 11: Photosystem II reaction center protein I

Chain 1i:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: Photosystem II reaction center protein I

Chain 2I:  62% 32% 6%



- Molecule 11: Photosystem II reaction center protein I

Chain 2i:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: Photosystem II reaction center protein J

Chain 1J:  100%

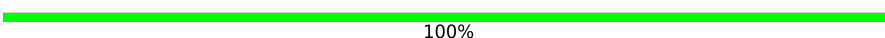
There are no outlier residues recorded for this chain.

- Molecule 12: Photosystem II reaction center protein J

Chain 1j:  97%

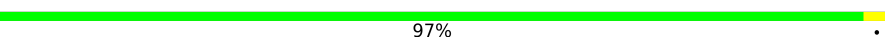


- Molecule 12: Photosystem II reaction center protein J

Chain 2J:  100%

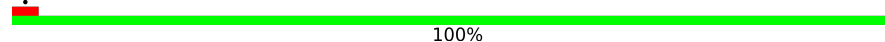
There are no outlier residues recorded for this chain.

- Molecule 12: Photosystem II reaction center protein J

Chain 2j:  97%



- Molecule 13: Photosystem II reaction center protein K

Chain 1K:  100%

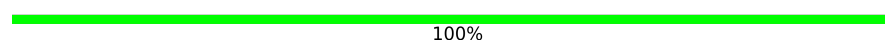


- Molecule 13: Photosystem II reaction center protein K

Chain 1k:  86%



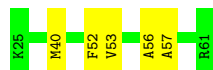
- Molecule 13: Photosystem II reaction center protein K

Chain 2K:  100%

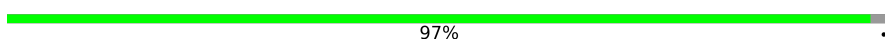
There are no outlier residues recorded for this chain.

- Molecule 13: Photosystem II reaction center protein K

Chain 2k:  86%

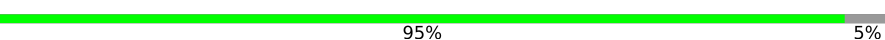


- Molecule 14: Photosystem II reaction center protein L

Chain 1L:  97%



- Molecule 14: Photosystem II reaction center protein L

Chain 1l:  95%



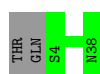
- Molecule 14: Photosystem II reaction center protein L

Chain 2L: 97%



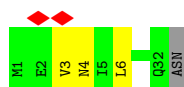
- Molecule 14: Photosystem II reaction center protein L

Chain 2l: 95%



- Molecule 15: Photosystem II reaction center protein M

Chain 1M: 6%



- Molecule 15: Photosystem II reaction center protein M

Chain 1m: 6%



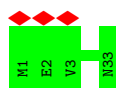
- Molecule 15: Photosystem II reaction center protein M

Chain 2M: 94%



- Molecule 15: Photosystem II reaction center protein M

Chain 2m: 9%



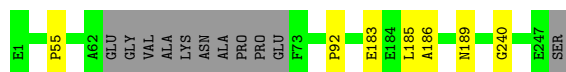
- Molecule 16: 33 kDa subunit of oxygen evolving system of photosystem II

Chain 10: 94%



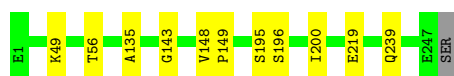
- Molecule 16: 33 kDa subunit of oxygen evolving system of photosystem II

Chain 1o: 93%



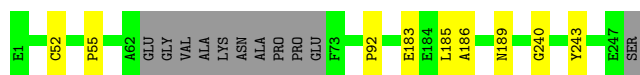
- Molecule 16: 33 kDa subunit of oxygen evolving system of photosystem II

Chain 20o: 95%



- Molecule 16: 33 kDa subunit of oxygen evolving system of photosystem II

Chain 2o: 92%



- Molecule 17: 23 kDa subunit of oxygen evolving system of photosystem II

Chain 1P: 97%



- Molecule 17: 23 kDa subunit of oxygen evolving system of photosystem II

Chain 1p: 97%



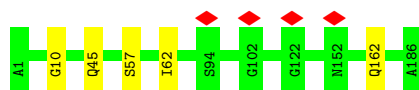
- Molecule 17: 23 kDa subunit of oxygen evolving system of photosystem II

Chain 2P: 97%



- Molecule 17: 23 kDa subunit of oxygen evolving system of photosystem II

Chain 2p: 97%



- Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain 1R: 97%



- Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain 1r: 97%



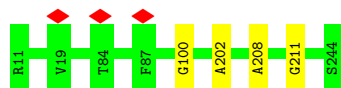
- Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain 2R: 97%



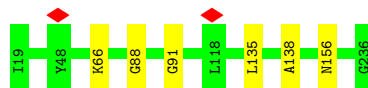
- Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain 2r: 98%



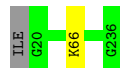
- Molecule 19: Chlorophyll a-b binding protein, chloroplastic

Chain 1S: 97%

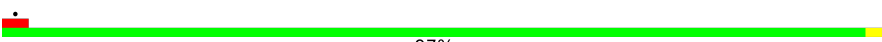


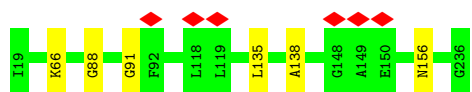
- Molecule 19: Chlorophyll a-b binding protein, chloroplastic

Chain 1s: 99%



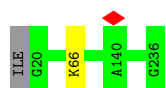
- Molecule 19: Chlorophyll a-b binding protein, chloroplastic

Chain 2S:  97%



- Molecule 19: Chlorophyll a-b binding protein, chloroplastic

Chain 2s:  99%



- Molecule 20: Photosystem II reaction center protein T

Chain 1T:  94% 6%



- Molecule 20: Photosystem II reaction center protein T

Chain 1t:  91% 6%



- Molecule 20: Photosystem II reaction center protein T

Chain 2T:  100%

There are no outlier residues recorded for this chain.

- Molecule 20: Photosystem II reaction center protein T

Chain 2t:  97%

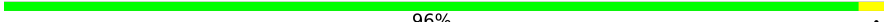


- Molecule 21: Os02g0581100 protein

Chain 1U:  96%

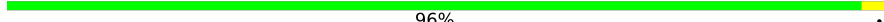


- Molecule 21: Os02g0581100 protein

Chain 1u:  96% .

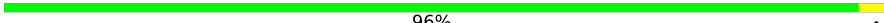


- Molecule 21: Os02g0581100 protein

Chain 2U:  96% .



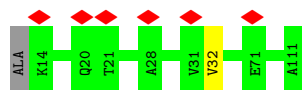
- Molecule 21: Os02g0581100 protein

Chain 2u:  96% .



- Molecule 22: Photosystem II 10 kDa polypeptide, chloroplastic

Chain 1V:  6% 98% ..

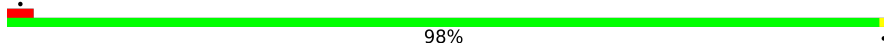


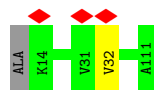
- Molecule 22: Photosystem II 10 kDa polypeptide, chloroplastic

Chain 1v:  89% 11%



- Molecule 22: Photosystem II 10 kDa polypeptide, chloroplastic

Chain 2V:  98% ..



- Molecule 22: Photosystem II 10 kDa polypeptide, chloroplastic

Chain 2v:  89% 11%



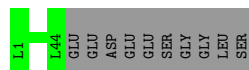
- Molecule 23: Photosystem II reaction center W protein, chloroplastic

Chain 1W:  100%

There are no outlier residues recorded for this chain.

- Molecule 23: Photosystem II reaction center W protein, chloroplastic

Chain 1w:  81% 19%



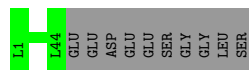
- Molecule 23: Photosystem II reaction center W protein, chloroplastic

Chain 2W:  100%

There are no outlier residues recorded for this chain.

- Molecule 23: Photosystem II reaction center W protein, chloroplastic

Chain 2w:  81% 19%



- Molecule 24: Os07g0673550 protein

Chain 1X:  100%

There are no outlier residues recorded for this chain.

- Molecule 24: Os07g0673550 protein

Chain 1x:  97% .



- Molecule 24: Os07g0673550 protein

Chain 2X:  100%

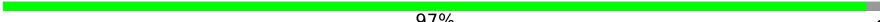
There are no outlier residues recorded for this chain.

- Molecule 24: Os07g0673550 protein

Chain 2x:  97% .

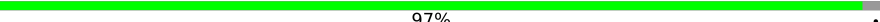


- Molecule 25: cDNA clone:001-024-H10, full insert sequence

Chain 1Y:  97% .

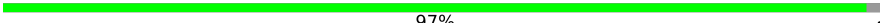


- Molecule 25: cDNA clone:001-024-H10, full insert sequence

Chain 1y:  97% .

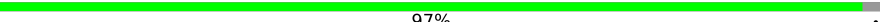


- Molecule 25: cDNA clone:001-024-H10, full insert sequence

Chain 2Y:  97% .



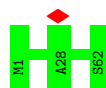
- Molecule 25: cDNA clone:001-024-H10, full insert sequence

Chain 2y:  97% .



- Molecule 26: Photosystem II reaction center protein Z

Chain 1Z:  100%

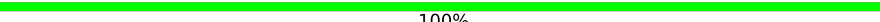


- Molecule 26: Photosystem II reaction center protein Z

Chain 1z:  100%

There are no outlier residues recorded for this chain.

- Molecule 26: Photosystem II reaction center protein Z

Chain 2Z:  100%

There are no outlier residues recorded for this chain.

- Molecule 26: Photosystem II reaction center protein Z

Chain 2z:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	60034	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.375	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.478	Depositor
Minimum map value	-0.074	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.0005	Depositor
Map size ($\text{\AA}$)	655.36, 655.36, 655.36	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.28, 1.28, 1.28	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	00	0.27	0/1113	0.62	3/1552 (0.2%)
1	01	0.28	1/1112 (0.1%)	0.69	2/1550 (0.1%)
1	02	0.27	0/1089	0.63	0/1516
1	05	0.26	0/1064	0.70	0/1482
1	06	0.58	3/1045 (0.3%)	1.12	10/1454 (0.7%)
1	09	0.25	0/1113	0.56	0/1552
1	10	0.25	0/1113	0.62	3/1552 (0.2%)
1	11	0.28	1/1112 (0.1%)	0.69	2/1550 (0.1%)
1	12	0.27	0/1089	0.63	0/1516
1	15	0.25	0/1064	0.70	0/1482
1	16	0.58	3/1045 (0.3%)	1.12	10/1454 (0.7%)
1	19	0.24	0/1113	0.55	0/1552
1	1G	0.27	0/1113	0.57	0/1552
1	1N	0.36	0/1113	0.75	3/1552 (0.2%)
1	1g	0.26	0/1113	0.59	0/1552
1	1n	0.24	0/1113	0.53	0/1552
1	2G	0.27	0/1113	0.57	0/1552
1	2N	0.36	0/1113	0.75	3/1552 (0.2%)
1	2g	0.26	0/1113	0.59	0/1552
1	2n	0.23	0/1113	0.53	0/1552
2	03	0.24	0/1113	0.67	0/1551
2	07	0.29	0/1115	0.73	1/1554 (0.1%)
2	13	0.24	0/1113	0.67	0/1551
2	17	0.29	0/1115	0.74	1/1554 (0.1%)
3	04	0.32	0/1020	0.82	4/1424 (0.3%)
3	08	0.31	0/1044	0.73	1/1457 (0.1%)
3	14	0.32	0/1020	0.82	4/1424 (0.3%)
3	18	0.32	0/1044	0.73	1/1457 (0.1%)
4	1A	0.28	0/1679	0.61	0/2341
4	1a	0.27	0/1674	0.61	1/2334 (0.0%)
4	2A	0.28	0/1679	0.61	0/2341
4	2a	0.27	0/1674	0.61	1/2334 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	1B	0.24	0/2537	0.54	0/3536
5	1b	0.24	0/2537	0.55	2/3536 (0.1%)
5	2B	0.24	0/2537	0.54	0/3536
5	2b	0.24	0/2537	0.55	2/3536 (0.1%)
6	1C	0.36	2/2261 (0.1%)	0.79	3/3147 (0.1%)
6	1c	0.22	0/2260	0.54	0/3145
6	2C	0.36	2/2261 (0.1%)	0.79	3/3147 (0.1%)
6	2c	0.22	0/2260	0.54	0/3145
7	1D	0.29	1/1711 (0.1%)	0.64	2/2387 (0.1%)
7	1d	0.45	2/1716 (0.1%)	0.89	6/2394 (0.3%)
7	2D	0.29	1/1711 (0.1%)	0.64	2/2387 (0.1%)
7	2d	0.45	2/1716 (0.1%)	0.89	6/2394 (0.3%)
8	1E	0.27	0/382	0.52	0/534
8	1e	0.25	0/382	0.55	0/534
8	2E	0.27	0/382	0.52	0/534
8	2e	0.25	0/382	0.55	0/534
9	1F	0.44	0/178	0.68	0/248
9	1f	0.24	0/150	0.53	0/208
9	2F	0.44	0/178	0.68	0/248
9	2f	0.24	0/150	0.54	0/208
10	1H	0.23	0/304	0.64	0/423
10	1h	0.23	0/304	0.64	0/423
10	2H	0.23	0/304	0.65	0/423
10	2h	0.23	0/304	0.64	0/423
11	1I	0.72	0/172	1.65	5/239 (2.1%)
11	1i	0.24	0/172	0.65	0/239
11	2I	0.56	0/172	0.80	0/239
11	2i	0.24	0/172	0.65	0/239
12	1J	0.22	0/169	0.64	0/231
12	1j	0.34	0/169	0.78	1/231 (0.4%)
12	2J	0.22	0/169	0.64	0/231
12	2j	0.34	0/169	0.78	1/231 (0.4%)
13	1K	0.31	0/196	0.66	0/276
13	1k	0.30	0/196	0.59	0/276
13	2K	0.31	0/196	0.65	0/276
13	2k	0.30	0/196	0.59	0/276
14	1L	0.21	0/181	0.54	0/252
14	1l	0.24	0/176	0.64	0/245
14	2L	0.21	0/181	0.54	0/252
14	2l	0.24	0/176	0.64	0/245
15	1M	0.34	0/162	0.90	0/226
15	1m	0.35	0/167	0.67	0/233
15	2M	0.34	0/162	0.90	0/226

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
15	2m	0.36	0/167	0.67	0/233
16	1O	0.23	0/1254	0.61	1/1750 (0.1%)
16	1o	0.21	0/1198	0.53	0/1669
16	2O	0.23	0/1254	0.61	1/1750 (0.1%)
16	2o	0.21	0/1198	0.53	0/1669
17	1P	0.19	0/932	0.53	0/1298
17	1p	0.17	0/932	0.45	0/1298
17	2P	0.19	0/932	0.53	0/1298
17	2p	0.17	0/932	0.45	0/1298
18	1R	0.24	0/1191	0.55	0/1664
18	1r	0.20	0/1191	0.52	0/1664
18	2R	0.24	0/1191	0.55	0/1664
18	2r	0.21	0/1191	0.52	0/1664
19	1S	0.24	0/1108	0.59	0/1546
19	1s	0.25	0/1103	0.62	0/1539
19	2S	0.24	0/1108	0.59	0/1546
19	2s	0.25	0/1103	0.62	0/1539
20	1T	0.18	0/167	0.40	0/234
20	1t	0.17	0/162	0.40	0/227
20	2T	0.19	0/167	0.40	0/234
20	2t	0.17	0/162	0.40	0/227
21	1U	0.14	0/139	0.37	0/194
21	1u	0.20	0/139	0.51	0/194
21	2U	0.14	0/139	0.37	0/194
21	2u	0.20	0/139	0.51	0/194
22	1V	0.21	0/485	0.52	0/671
22	1v	0.28	0/490	0.71	1/678 (0.1%)
22	2V	0.21	0/485	0.52	0/671
22	2v	0.28	0/490	0.70	1/678 (0.1%)
23	1W	0.27	0/261	0.56	0/359
23	1w	0.21	0/213	0.55	0/293
23	2W	0.27	0/261	0.56	0/359
23	2w	0.21	0/213	0.55	0/293
24	1X	0.20	0/196	0.40	0/272
24	1x	0.22	0/192	0.48	0/267
24	2X	0.20	0/196	0.40	0/272
24	2x	0.22	0/192	0.47	0/267
25	1Y	0.30	0/177	0.60	0/248
25	1y	0.27	0/177	0.54	0/248
25	2Y	0.30	0/177	0.61	0/248
25	2y	0.27	0/177	0.55	0/248
26	1Z	0.30	0/312	0.58	0/435
26	1z	0.24	0/312	0.47	0/435

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	2Z	0.29	0/312	0.58	0/435
26	2z	0.24	0/312	0.47	0/435
All	All	0.28	18/94892 (0.0%)	0.65	87/132242 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	02	0	1
1	05	0	1
1	06	0	1
1	12	0	1
1	15	0	1
1	16	0	1
1	1G	0	1
1	1N	0	2
1	1n	0	1
1	2G	0	1
1	2N	0	2
1	2n	0	1
3	04	0	1
3	14	0	1
4	1a	0	1
4	2a	0	1
16	1o	0	1
16	2o	0	1
All	All	0	20

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	1d	172	PRO	CB-CG	-11.40	0.92	1.49
7	2d	172	PRO	CB-CG	-11.39	0.92	1.49
1	06	82	PRO	CG-CD	-9.80	1.17	1.50
1	16	82	PRO	CG-CD	-9.79	1.17	1.50
6	1C	80	PRO	CG-CD	-9.57	1.18	1.50

The worst 5 of 87 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	1C	80	PRO	CB-CG-CD	23.09	179.98	106.10
6	2C	80	PRO	CB-CG-CD	23.07	179.91	106.10
1	16	82	PRO	N-CD-CG	-19.33	74.21	103.20
1	06	82	PRO	N-CD-CG	-19.32	74.23	103.20
1	16	82	PRO	CA-CB-CG	-18.66	69.04	104.50

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	02	156	TYR	Peptide
3	04	104	LEU	Peptide
1	05	95	ALA	Peptide
1	06	189	PHE	Peptide
1	12	156	TYR	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	00	1098	0	618	4	0
1	01	1097	0	618	1	0
1	02	1076	0	604	2	0
1	05	1052	0	582	0	0
1	06	1034	0	571	2	0
1	09	1098	0	618	2	0
1	10	1098	0	618	2	0
1	11	1097	0	618	1	0
1	12	1076	0	604	2	0
1	15	1052	0	582	0	0
1	16	1034	0	571	3	0
1	19	1098	0	618	2	0
1	1G	1098	0	618	2	0
1	1N	1098	0	618	4	0
1	1g	1098	0	618	4	0
1	1n	1098	0	618	0	0
1	2G	1098	0	618	3	0
1	2N	1098	0	618	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2g	1098	0	618	3	0
1	2n	1098	0	618	0	0
2	03	1100	0	596	2	0
2	07	1101	0	598	4	0
2	13	1100	0	596	1	0
2	17	1101	0	598	5	0
3	04	1006	0	564	1	0
3	08	1030	0	578	3	0
3	14	1006	0	564	0	0
3	18	1030	0	578	3	0
4	1A	1666	0	865	5	0
4	1a	1661	0	860	6	0
4	2A	1666	0	865	6	0
4	2a	1661	0	860	4	0
5	1B	2510	0	1326	3	0
5	1b	2510	0	1326	11	0
5	2B	2510	0	1326	3	0
5	2b	2510	0	1326	10	0
6	1C	2238	0	1199	1	0
6	1c	2237	0	1198	5	0
6	2C	2238	0	1199	1	0
6	2c	2237	0	1198	4	0
7	1D	1698	0	887	3	0
7	1d	1703	0	889	5	0
7	2D	1698	0	887	5	0
7	2d	1703	0	889	6	0
8	1E	379	0	182	2	0
8	1e	379	0	182	2	0
8	2E	379	0	182	1	0
8	2e	379	0	182	2	0
9	1F	177	0	90	1	0
9	1f	150	0	75	1	0
9	2F	177	0	90	1	0
9	2f	150	0	75	1	0
10	1H	301	0	158	0	0
10	1h	301	0	158	0	0
10	2H	301	0	158	0	0
10	2h	301	0	158	0	0
11	1I	171	0	83	12	0
11	1i	171	0	83	0	0
11	2I	171	0	83	6	0
11	2i	171	0	83	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	1J	169	0	85	0	0
12	1j	169	0	85	0	0
12	2J	169	0	85	0	0
12	2j	169	0	85	0	0
13	1K	193	0	108	0	0
13	1k	193	0	108	2	0
13	2K	193	0	108	0	0
13	2k	193	0	108	2	0
14	1L	181	0	80	0	0
14	1l	176	0	78	0	0
14	2L	181	0	80	0	0
14	2l	176	0	78	0	0
15	1M	162	0	83	1	0
15	1m	167	0	85	0	0
15	2M	162	0	83	0	0
15	2m	167	0	85	0	0
16	1O	1239	0	652	6	0
16	1o	1186	0	614	3	0
16	2O	1239	0	652	5	0
16	2o	1186	0	614	4	0
17	1P	926	0	484	2	0
17	1p	926	0	484	3	0
17	2P	926	0	484	2	0
17	2p	926	0	484	3	0
18	1R	1177	0	625	3	0
18	1r	1177	0	625	3	0
18	2R	1177	0	625	3	0
18	2r	1177	0	625	2	0
19	1S	1094	0	593	2	0
19	1s	1089	0	591	0	0
19	2S	1094	0	593	2	0
19	2s	1089	0	591	0	0
20	1T	165	0	88	1	0
20	1t	160	0	86	1	0
20	2T	165	0	88	0	0
20	2t	160	0	86	0	0
21	1U	138	0	73	1	0
21	1u	138	0	73	1	0
21	2U	138	0	73	1	0
21	2u	138	0	73	1	0
22	1V	482	0	264	0	0
22	1v	487	0	269	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	2V	482	0	264	0	0
22	2v	487	0	269	4	0
23	1W	262	0	118	0	0
23	1w	214	0	96	0	0
23	2W	262	0	118	0	0
23	2w	214	0	96	0	0
24	1X	195	0	100	0	0
24	1x	191	0	97	0	0
24	2X	195	0	100	0	0
24	2x	191	0	97	0	0
25	1Y	175	0	98	0	0
25	1y	175	0	98	0	0
25	2Y	175	0	98	0	0
25	2y	175	0	98	0	0
26	1Z	311	0	154	0	0
26	1z	311	0	154	0	0
26	2Z	311	0	154	0	0
26	2z	311	0	154	0	0
27	1A	1	0	0	0	0
27	1d	1	0	0	0	0
27	2A	1	0	0	0	0
27	2d	1	0	0	0	0
All	All	93932	0	50256	202	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

The worst 5 of 202 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:06:97:TRP:H	1:06:205:PRO:HG3	1.51	0.75
1:16:97:TRP:H	1:16:205:PRO:HG3	1.51	0.74
2:17:144:LEU:O	2:17:148:VAL:N	2.26	0.69
4:1A:85:THR:HA	4:1A:109:GLY:HA3	1.76	0.68
5:2b:205:ALA:O	5:2b:209:GLY:N	2.27	0.68

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	00	217/219 (99%)	197 (91%)	17 (8%)	3 (1%)	9	38
1	01	217/219 (99%)	191 (88%)	25 (12%)	1 (0%)	24	57
1	02	208/219 (95%)	173 (83%)	31 (15%)	4 (2%)	6	33
1	05	206/219 (94%)	176 (85%)	28 (14%)	2 (1%)	12	44
1	06	203/219 (93%)	174 (86%)	27 (13%)	2 (1%)	12	44
1	09	217/219 (99%)	196 (90%)	21 (10%)	0	100	100
1	10	217/219 (99%)	197 (91%)	18 (8%)	2 (1%)	14	47
1	11	217/219 (99%)	191 (88%)	25 (12%)	1 (0%)	24	57
1	12	208/219 (95%)	173 (83%)	31 (15%)	4 (2%)	6	33
1	15	206/219 (94%)	175 (85%)	29 (14%)	2 (1%)	12	44
1	16	203/219 (93%)	174 (86%)	27 (13%)	2 (1%)	12	44
1	19	217/219 (99%)	193 (89%)	22 (10%)	2 (1%)	14	47
1	1G	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	57
1	1N	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	57
1	1g	217/219 (99%)	197 (91%)	19 (9%)	1 (0%)	24	57
1	1n	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	57
1	2G	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	57
1	2N	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	57
1	2g	217/219 (99%)	197 (91%)	19 (9%)	1 (0%)	24	57
1	2n	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	57
2	03	218/220 (99%)	186 (85%)	30 (14%)	2 (1%)	14	47
2	07	218/220 (99%)	188 (86%)	29 (13%)	1 (0%)	24	57
2	13	218/220 (99%)	186 (85%)	30 (14%)	2 (1%)	14	47
2	17	218/220 (99%)	188 (86%)	29 (13%)	1 (0%)	24	57
3	04	198/205 (97%)	152 (77%)	44 (22%)	2 (1%)	12	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	08	203/205 (99%)	170 (84%)	28 (14%)	5 (2%)	4	28
3	14	198/205 (97%)	152 (77%)	44 (22%)	2 (1%)	12	44
3	18	203/205 (99%)	170 (84%)	28 (14%)	5 (2%)	4	28
4	1A	332/334 (99%)	314 (95%)	18 (5%)	0	100	100
4	1a	331/334 (99%)	313 (95%)	18 (5%)	0	100	100
4	2A	332/334 (99%)	314 (95%)	18 (5%)	0	100	100
4	2a	331/334 (99%)	313 (95%)	18 (5%)	0	100	100
5	1B	501/503 (100%)	476 (95%)	24 (5%)	1 (0%)	43	74
5	1b	501/503 (100%)	486 (97%)	15 (3%)	0	100	100
5	2B	501/503 (100%)	476 (95%)	24 (5%)	1 (0%)	43	74
5	2b	501/503 (100%)	486 (97%)	15 (3%)	0	100	100
6	1C	448/450 (100%)	429 (96%)	19 (4%)	0	100	100
6	1c	448/450 (100%)	428 (96%)	17 (4%)	3 (1%)	18	51
6	2C	448/450 (100%)	429 (96%)	19 (4%)	0	100	100
6	2c	448/450 (100%)	428 (96%)	17 (4%)	3 (1%)	18	51
7	1D	338/341 (99%)	319 (94%)	18 (5%)	1 (0%)	36	67
7	1d	339/341 (99%)	316 (93%)	23 (7%)	0	100	100
7	2D	338/341 (99%)	319 (94%)	18 (5%)	1 (0%)	36	67
7	2d	339/341 (99%)	316 (93%)	23 (7%)	0	100	100
8	1E	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
8	1e	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
8	2E	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
8	2e	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
9	1F	33/36 (92%)	33 (100%)	0	0	100	100
9	1f	28/36 (78%)	27 (96%)	1 (4%)	0	100	100
9	2F	33/36 (92%)	33 (100%)	0	0	100	100
9	2f	28/36 (78%)	27 (96%)	1 (4%)	0	100	100
10	1H	58/60 (97%)	53 (91%)	5 (9%)	0	100	100
10	1h	58/60 (97%)	57 (98%)	1 (2%)	0	100	100
10	2H	58/60 (97%)	53 (91%)	5 (9%)	0	100	100
10	2h	58/60 (97%)	57 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	1I	32/34 (94%)	23 (72%)	5 (16%)	4 (12%)	0	4
11	1i	32/34 (94%)	30 (94%)	2 (6%)	0	100	100
11	2I	32/34 (94%)	22 (69%)	7 (22%)	3 (9%)	0	6
11	2i	32/34 (94%)	30 (94%)	2 (6%)	0	100	100
12	1J	33/35 (94%)	33 (100%)	0	0	100	100
12	1j	33/35 (94%)	33 (100%)	0	0	100	100
12	2J	33/35 (94%)	33 (100%)	0	0	100	100
12	2j	33/35 (94%)	33 (100%)	0	0	100	100
13	1K	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
13	1k	35/37 (95%)	34 (97%)	0	1 (3%)	3	26
13	2K	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
13	2k	35/37 (95%)	34 (97%)	0	1 (3%)	3	26
14	1L	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
14	1l	33/37 (89%)	33 (100%)	0	0	100	100
14	2L	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
14	2l	33/37 (89%)	33 (100%)	0	0	100	100
15	1M	30/33 (91%)	24 (80%)	5 (17%)	1 (3%)	3	23
15	1m	31/33 (94%)	31 (100%)	0	0	100	100
15	2M	30/33 (91%)	24 (80%)	5 (17%)	1 (3%)	3	23
15	2m	31/33 (94%)	31 (100%)	0	0	100	100
16	1O	245/248 (99%)	210 (86%)	35 (14%)	0	100	100
16	1o	233/248 (94%)	209 (90%)	24 (10%)	0	100	100
16	2O	245/248 (99%)	211 (86%)	34 (14%)	0	100	100
16	2o	233/248 (94%)	209 (90%)	24 (10%)	0	100	100
17	1P	184/186 (99%)	164 (89%)	19 (10%)	1 (0%)	24	57
17	1p	184/186 (99%)	170 (92%)	14 (8%)	0	100	100
17	2P	184/186 (99%)	164 (89%)	19 (10%)	1 (0%)	24	57
17	2p	184/186 (99%)	170 (92%)	14 (8%)	0	100	100
18	1R	232/234 (99%)	209 (90%)	22 (10%)	1 (0%)	30	62
18	1r	232/234 (99%)	216 (93%)	16 (7%)	0	100	100
18	2R	232/234 (99%)	210 (90%)	21 (9%)	1 (0%)	30	62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	2r	232/234 (99%)	216 (93%)	16 (7%)	0	100	100
19	1S	216/218 (99%)	186 (86%)	28 (13%)	2 (1%)	14	47
19	1s	215/218 (99%)	188 (87%)	26 (12%)	1 (0%)	24	57
19	2S	216/218 (99%)	186 (86%)	28 (13%)	2 (1%)	14	47
19	2s	215/218 (99%)	188 (87%)	26 (12%)	1 (0%)	24	57
20	1T	30/32 (94%)	30 (100%)	0	0	100	100
20	1t	29/32 (91%)	29 (100%)	0	0	100	100
20	2T	30/32 (94%)	30 (100%)	0	0	100	100
20	2t	29/32 (91%)	29 (100%)	0	0	100	100
21	1U	25/27 (93%)	23 (92%)	2 (8%)	0	100	100
21	1u	25/27 (93%)	22 (88%)	3 (12%)	0	100	100
21	2U	25/27 (93%)	23 (92%)	2 (8%)	0	100	100
21	2u	25/27 (93%)	22 (88%)	3 (12%)	0	100	100
22	1V	96/99 (97%)	79 (82%)	16 (17%)	1 (1%)	12	44
22	1v	97/99 (98%)	81 (84%)	12 (12%)	4 (4%)	2	19
22	2V	96/99 (97%)	79 (82%)	16 (17%)	1 (1%)	12	44
22	2v	97/99 (98%)	81 (84%)	12 (12%)	4 (4%)	2	19
23	1W	52/54 (96%)	47 (90%)	5 (10%)	0	100	100
23	1w	42/54 (78%)	40 (95%)	2 (5%)	0	100	100
23	2W	52/54 (96%)	47 (90%)	5 (10%)	0	100	100
23	2w	42/54 (78%)	40 (95%)	2 (5%)	0	100	100
24	1X	37/39 (95%)	36 (97%)	1 (3%)	0	100	100
24	1x	36/39 (92%)	34 (94%)	2 (6%)	0	100	100
24	2X	37/39 (95%)	36 (97%)	1 (3%)	0	100	100
24	2x	36/39 (92%)	34 (94%)	2 (6%)	0	100	100
25	1Y	32/35 (91%)	31 (97%)	1 (3%)	0	100	100
25	1y	32/35 (91%)	32 (100%)	0	0	100	100
25	2Y	32/35 (91%)	31 (97%)	1 (3%)	0	100	100
25	2y	32/35 (91%)	32 (100%)	0	0	100	100
26	1Z	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
26	1z	60/62 (97%)	58 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	2Z	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
26	2z	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
All	All	18512/18916 (98%)	16881 (91%)	1537 (8%)	94 (0%)	26	57

5 of 94 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	08	13	PHE
3	18	13	PHE
5	1B	18	ARG
7	1D	268	LEU
6	1c	43	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	00	16/166 (10%)	16 (100%)	0	100	100
1	01	16/166 (10%)	16 (100%)	0	100	100
1	02	16/166 (10%)	16 (100%)	0	100	100
1	05	14/166 (8%)	14 (100%)	0	100	100
1	06	13/166 (8%)	13 (100%)	0	100	100
1	09	16/166 (10%)	16 (100%)	0	100	100
1	10	16/166 (10%)	16 (100%)	0	100	100
1	11	16/166 (10%)	16 (100%)	0	100	100
1	12	16/166 (10%)	16 (100%)	0	100	100
1	15	14/166 (8%)	14 (100%)	0	100	100
1	16	13/166 (8%)	13 (100%)	0	100	100
1	19	16/166 (10%)	16 (100%)	0	100	100
1	1G	16/166 (10%)	16 (100%)	0	100	100
1	1N	16/166 (10%)	16 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1g	16/166 (10%)	16 (100%)	0	100	100
1	1n	16/166 (10%)	16 (100%)	0	100	100
1	2G	16/166 (10%)	16 (100%)	0	100	100
1	2N	16/166 (10%)	16 (100%)	0	100	100
1	2g	16/166 (10%)	16 (100%)	0	100	100
1	2n	16/166 (10%)	16 (100%)	0	100	100
2	03	14/172 (8%)	14 (100%)	0	100	100
2	07	15/172 (9%)	15 (100%)	0	100	100
2	13	14/172 (8%)	14 (100%)	0	100	100
2	17	15/172 (9%)	15 (100%)	0	100	100
3	04	15/157 (10%)	15 (100%)	0	100	100
3	08	15/157 (10%)	15 (100%)	0	100	100
3	14	15/157 (10%)	15 (100%)	0	100	100
3	18	15/157 (10%)	15 (100%)	0	100	100
4	1A	14/270 (5%)	14 (100%)	0	100	100
4	1a	14/270 (5%)	14 (100%)	0	100	100
4	2A	14/270 (5%)	14 (100%)	0	100	100
4	2a	14/270 (5%)	14 (100%)	0	100	100
5	1B	28/402 (7%)	28 (100%)	0	100	100
5	1b	28/402 (7%)	28 (100%)	0	100	100
5	2B	28/402 (7%)	28 (100%)	0	100	100
5	2b	28/402 (7%)	28 (100%)	0	100	100
6	1C	24/350 (7%)	24 (100%)	0	100	100
6	1c	24/350 (7%)	24 (100%)	0	100	100
6	2C	24/350 (7%)	24 (100%)	0	100	100
6	2c	24/350 (7%)	24 (100%)	0	100	100
7	1D	14/275 (5%)	14 (100%)	0	100	100
7	1d	14/275 (5%)	14 (100%)	0	100	100
7	2D	14/275 (5%)	14 (100%)	0	100	100
7	2d	14/275 (5%)	14 (100%)	0	100	100
8	1E	4/68 (6%)	4 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	1e	4/68 (6%)	4 (100%)	0	100	100
8	2E	4/68 (6%)	4 (100%)	0	100	100
8	2e	4/68 (6%)	4 (100%)	0	100	100
9	1F	2/31 (6%)	2 (100%)	0	100	100
9	1f	1/31 (3%)	1 (100%)	0	100	100
9	2F	2/31 (6%)	2 (100%)	0	100	100
9	2f	1/31 (3%)	1 (100%)	0	100	100
10	1H	4/49 (8%)	4 (100%)	0	100	100
10	1h	4/49 (8%)	4 (100%)	0	100	100
10	2H	4/49 (8%)	4 (100%)	0	100	100
10	2h	4/49 (8%)	4 (100%)	0	100	100
11	1I	2/31 (6%)	2 (100%)	0	100	100
11	1i	2/31 (6%)	2 (100%)	0	100	100
11	2I	2/31 (6%)	2 (100%)	0	100	100
11	2i	2/31 (6%)	2 (100%)	0	100	100
12	1J	1/26 (4%)	1 (100%)	0	100	100
12	1j	1/26 (4%)	1 (100%)	0	100	100
12	2J	1/26 (4%)	1 (100%)	0	100	100
12	2j	1/26 (4%)	1 (100%)	0	100	100
13	1K	4/32 (12%)	4 (100%)	0	100	100
13	1k	4/32 (12%)	4 (100%)	0	100	100
13	2K	4/32 (12%)	4 (100%)	0	100	100
13	2k	4/32 (12%)	4 (100%)	0	100	100
14	1L	1/35 (3%)	1 (100%)	0	100	100
14	1l	1/35 (3%)	1 (100%)	0	100	100
14	2L	1/35 (3%)	1 (100%)	0	100	100
14	2l	1/35 (3%)	1 (100%)	0	100	100
15	1M	1/29 (3%)	1 (100%)	0	100	100
15	1m	1/29 (3%)	1 (100%)	0	100	100
15	2M	1/29 (3%)	1 (100%)	0	100	100
15	2m	1/29 (3%)	1 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	1O	16/204 (8%)	16 (100%)	0	100	100
16	1o	14/204 (7%)	14 (100%)	0	100	100
16	2O	16/204 (8%)	16 (100%)	0	100	100
16	2o	14/204 (7%)	14 (100%)	0	100	100
17	1P	7/149 (5%)	7 (100%)	0	100	100
17	1p	7/149 (5%)	7 (100%)	0	100	100
17	2P	7/149 (5%)	7 (100%)	0	100	100
17	2p	7/149 (5%)	7 (100%)	0	100	100
18	1R	15/191 (8%)	15 (100%)	0	100	100
18	1r	15/191 (8%)	15 (100%)	0	100	100
18	2R	15/191 (8%)	15 (100%)	0	100	100
18	2r	15/191 (8%)	15 (100%)	0	100	100
19	1S	15/173 (9%)	15 (100%)	0	100	100
19	1s	15/173 (9%)	15 (100%)	0	100	100
19	2S	15/173 (9%)	15 (100%)	0	100	100
19	2s	15/173 (9%)	15 (100%)	0	100	100
20	1T	3/29 (10%)	3 (100%)	0	100	100
20	1t	3/29 (10%)	3 (100%)	0	100	100
20	2T	3/29 (10%)	3 (100%)	0	100	100
20	2t	3/29 (10%)	3 (100%)	0	100	100
21	1U	2/23 (9%)	2 (100%)	0	100	100
21	1u	2/23 (9%)	2 (100%)	0	100	100
21	2U	2/23 (9%)	2 (100%)	0	100	100
21	2u	2/23 (9%)	2 (100%)	0	100	100
22	1V	4/71 (6%)	4 (100%)	0	100	100
22	1v	4/71 (6%)	4 (100%)	0	100	100
22	2V	4/71 (6%)	4 (100%)	0	100	100
22	2v	4/71 (6%)	4 (100%)	0	100	100
24	1X	2/32 (6%)	2 (100%)	0	100	100
24	1x	2/32 (6%)	2 (100%)	0	100	100
24	2X	2/32 (6%)	2 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	2x	2/32 (6%)	2 (100%)	0	100	100
25	1Y	3/29 (10%)	3 (100%)	0	100	100
25	1y	3/29 (10%)	3 (100%)	0	100	100
25	2Y	3/29 (10%)	3 (100%)	0	100	100
25	2y	3/29 (10%)	3 (100%)	0	100	100
26	1Z	2/54 (4%)	2 (100%)	0	100	100
26	1z	2/54 (4%)	2 (100%)	0	100	100
26	2Z	2/54 (4%)	2 (100%)	0	100	100
26	2z	2/54 (4%)	2 (100%)	0	100	100
All	All	1094/14848 (7%)	1094 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are modelled with single atom - 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](#)

There are no chain breaks in this entry.

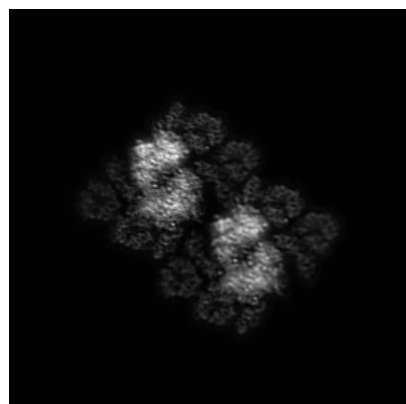
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-81438. These allow visual inspection of the internal detail of the map and identification of artifacts.

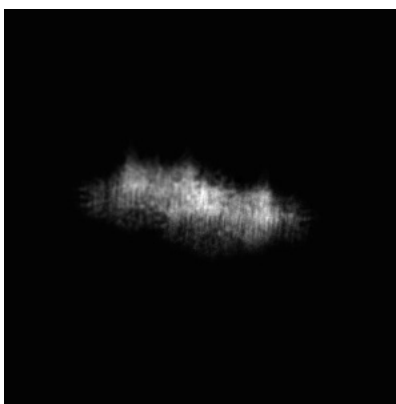
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

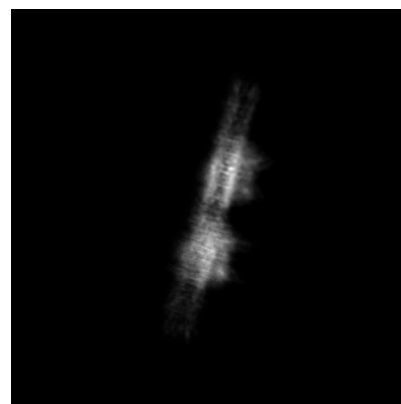
6.1.1 Primary map



X

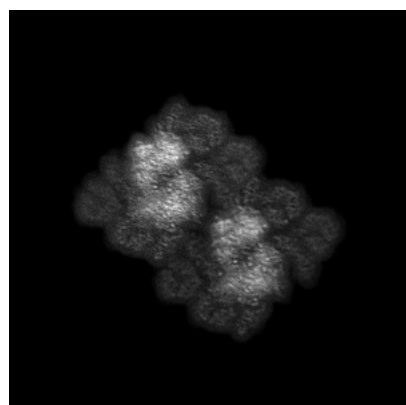


Y

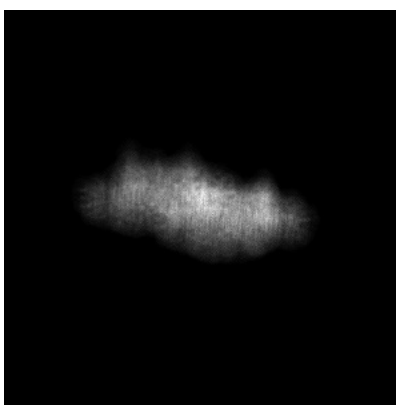


Z

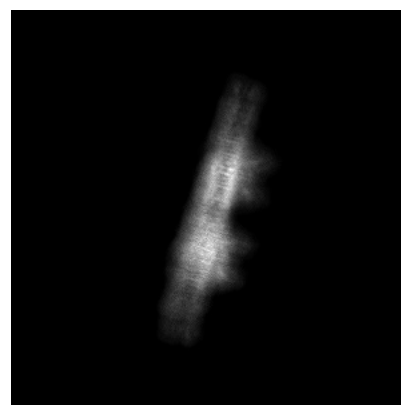
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

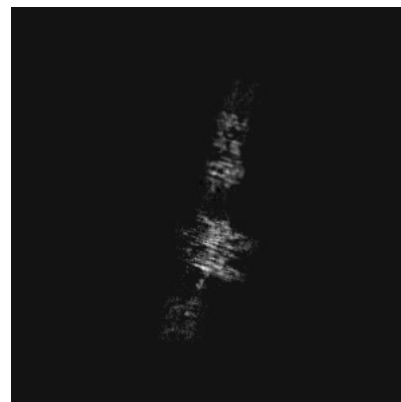
6.2.1 Primary map



X Index: 256

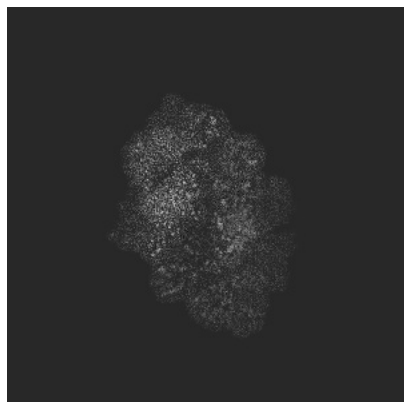


Y Index: 256

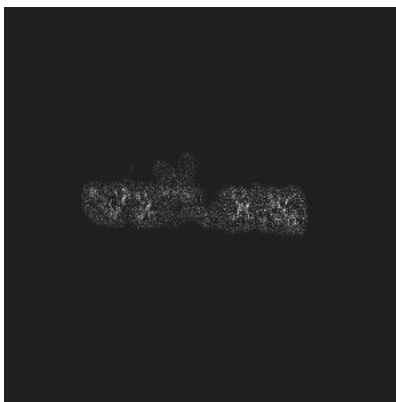


Z Index: 256

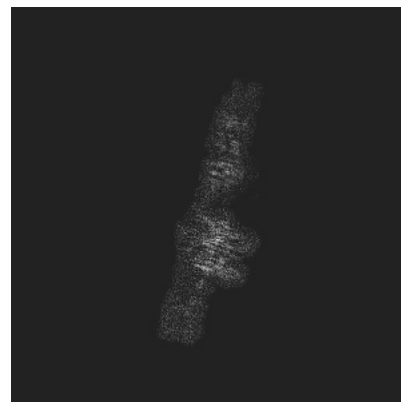
6.2.2 Raw map



X Index: 256



Y Index: 256

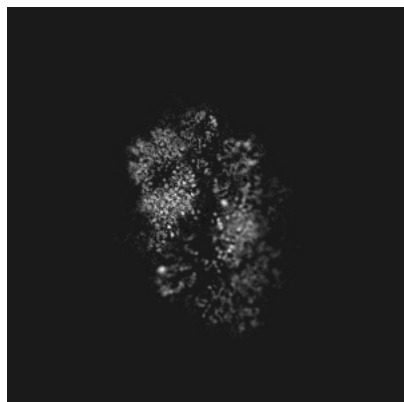


Z Index: 256

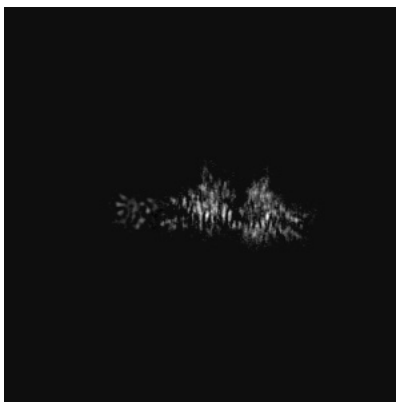
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

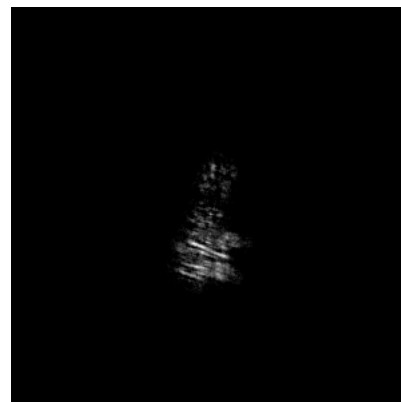
6.3.1 Primary map



X Index: 258

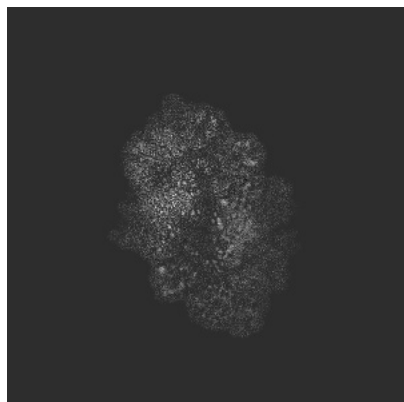


Y Index: 205

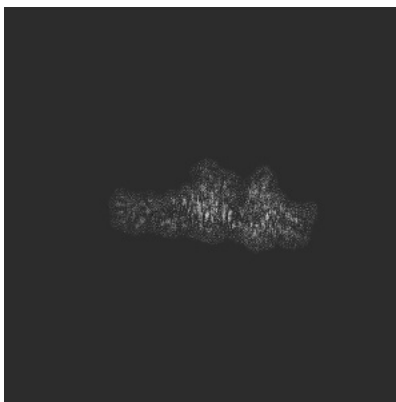


Z Index: 336

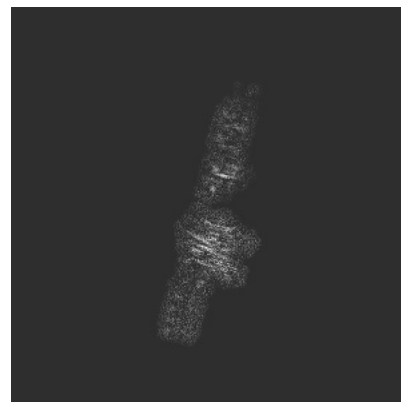
6.3.2 Raw map



X Index: 257



Y Index: 205

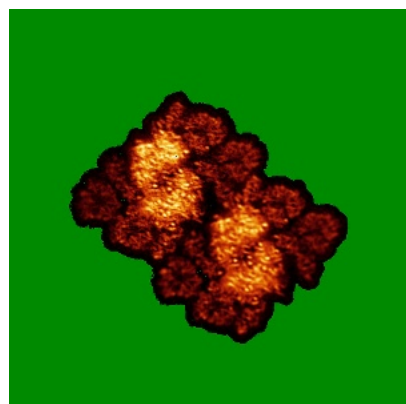


Z Index: 259

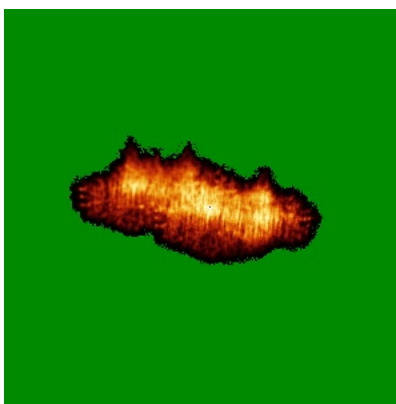
The images above show the largest variance slices of the map in three orthogonal directions.

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

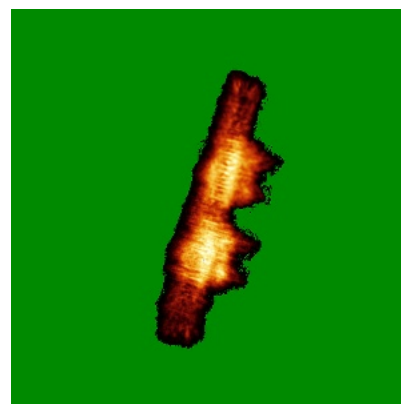
6.4.1 Primary map



X

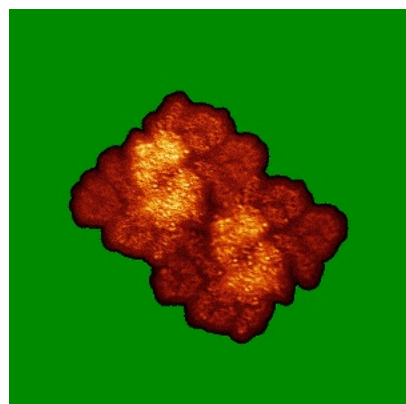


Y

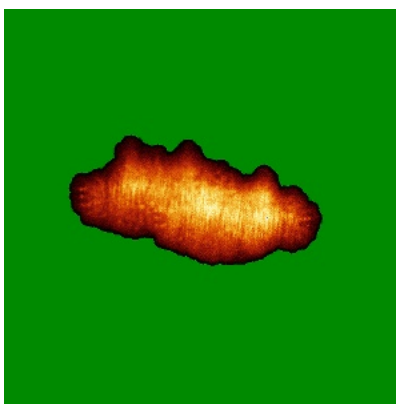


Z

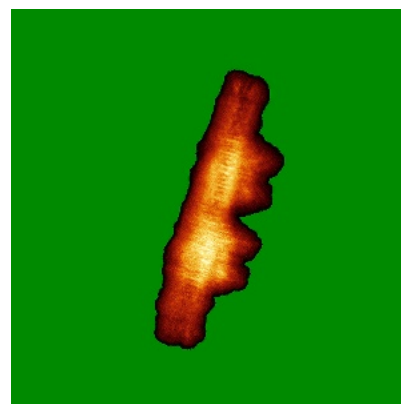
6.4.2 Raw map



X



Y

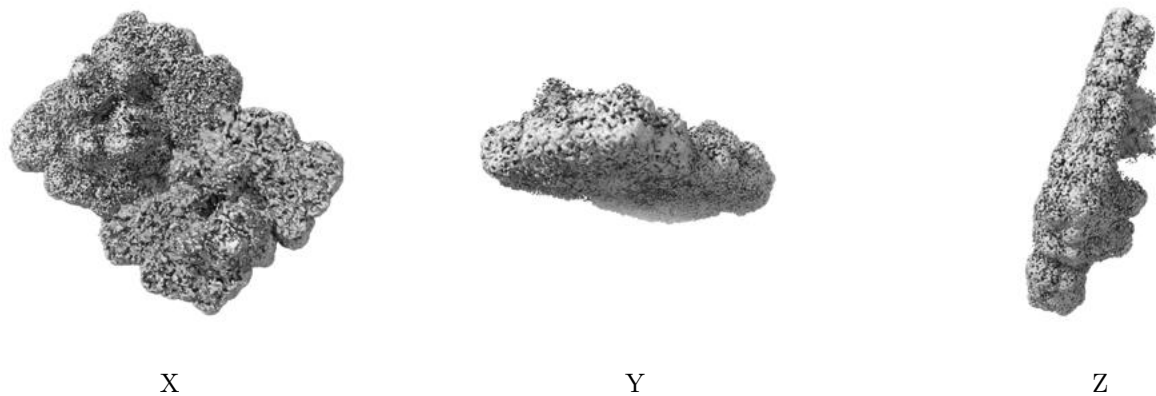


Z

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

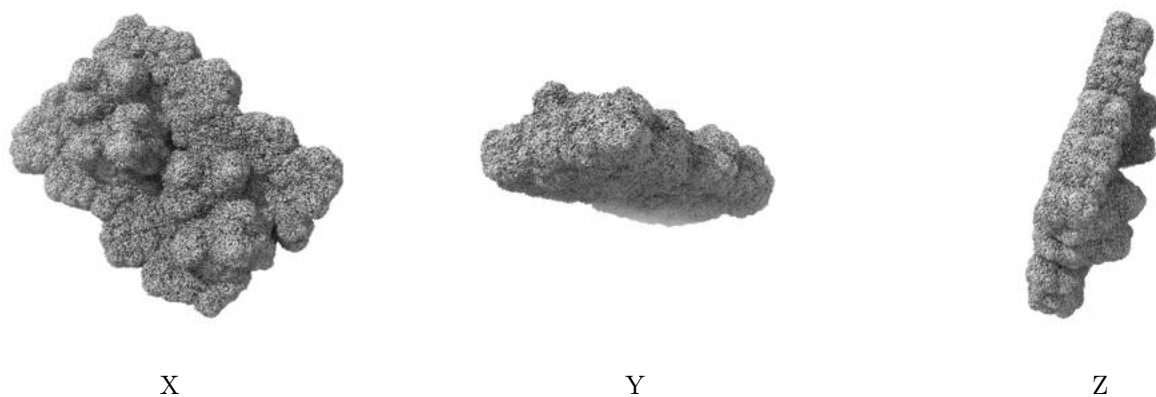
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

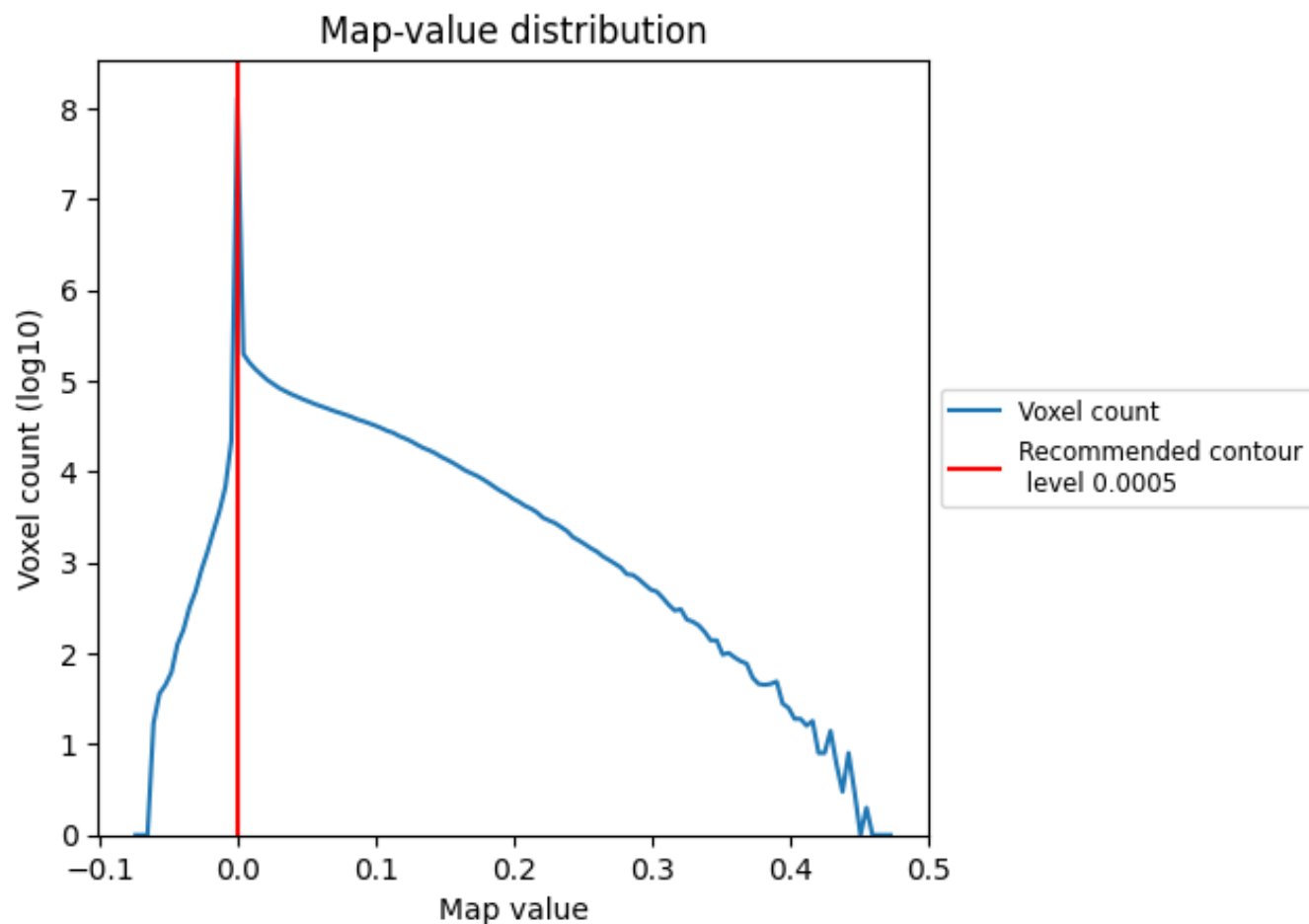
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

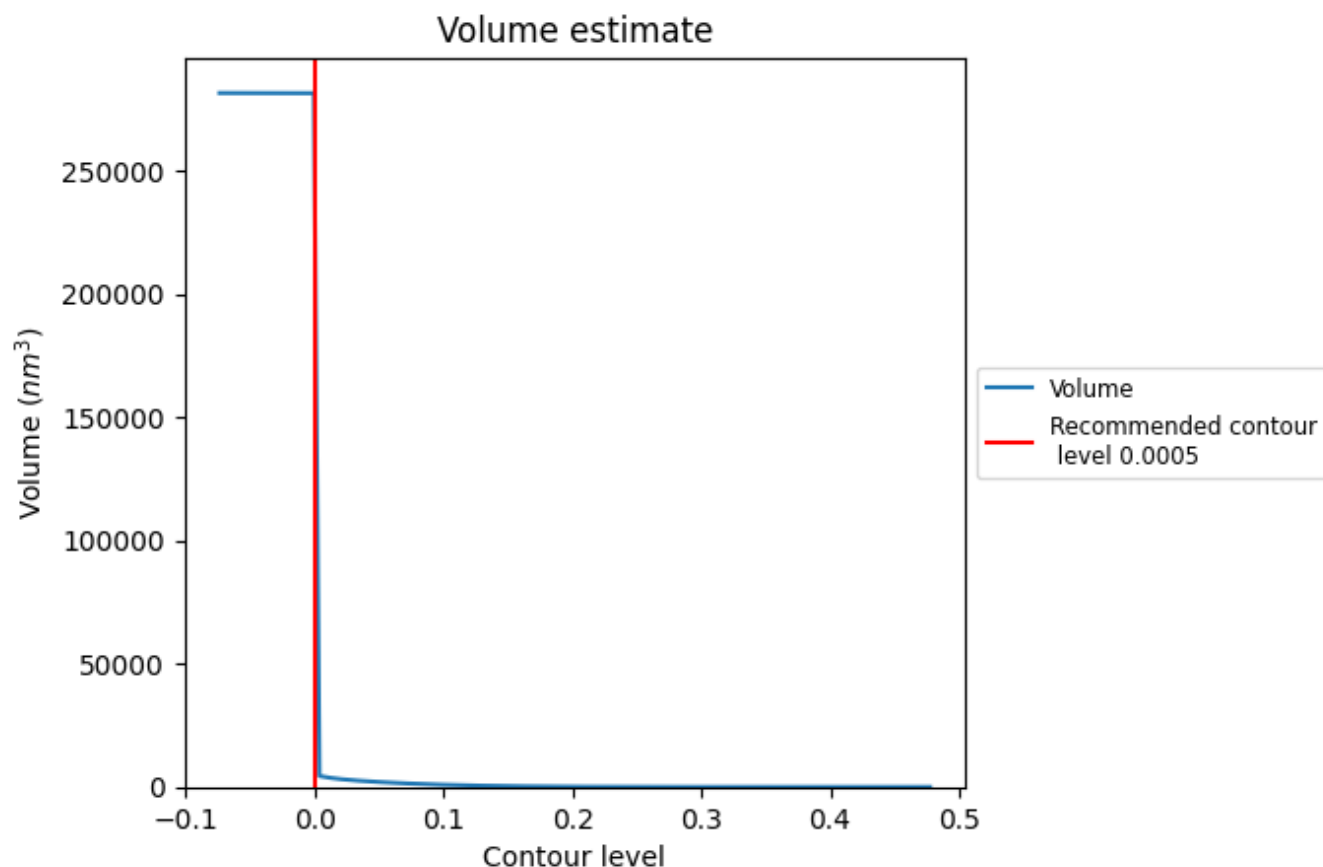
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

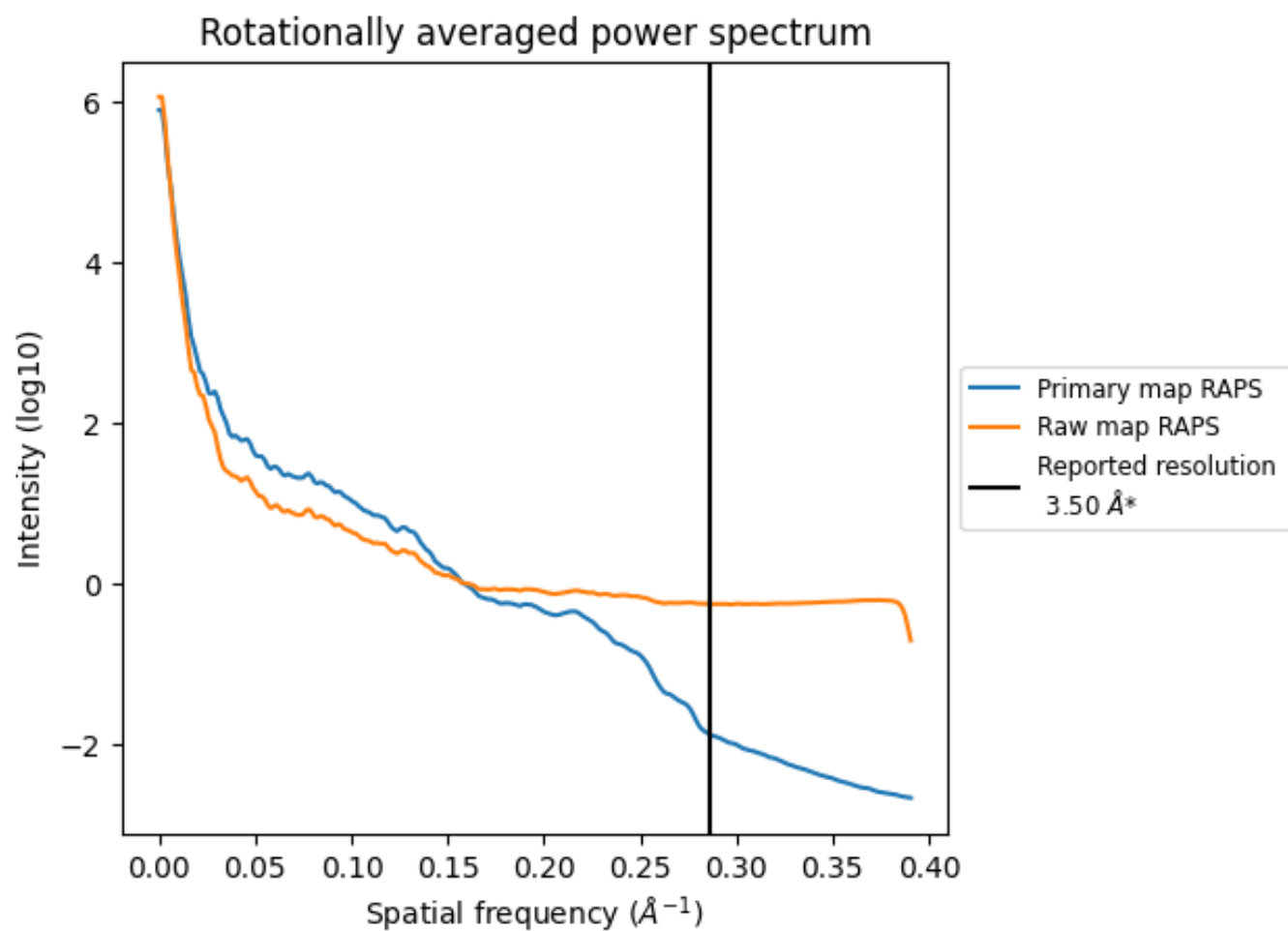
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 205420 nm^3 ; this corresponds to an approximate mass of 185561 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 ⓘ

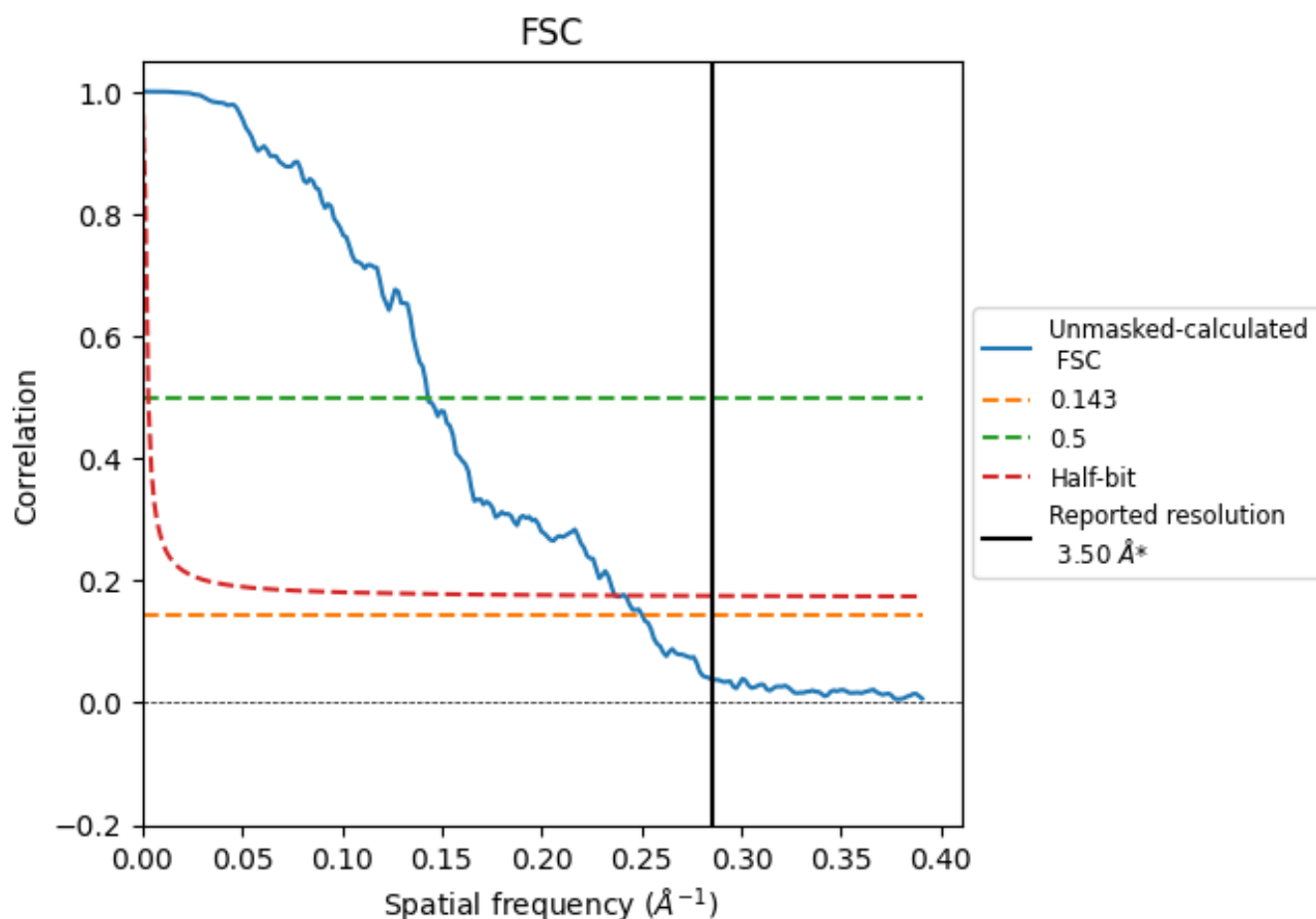


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

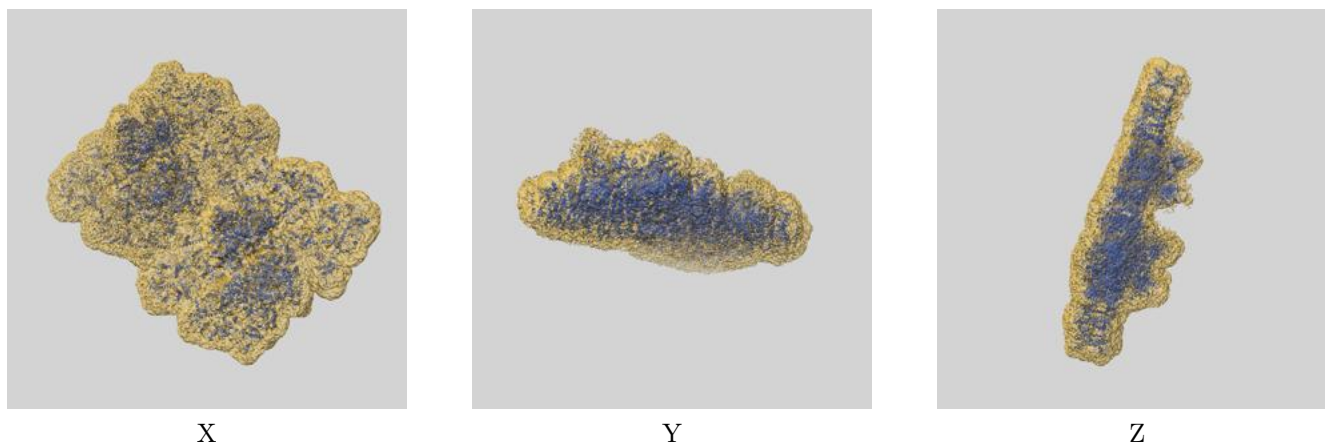
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.99	6.99	4.22

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.99 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

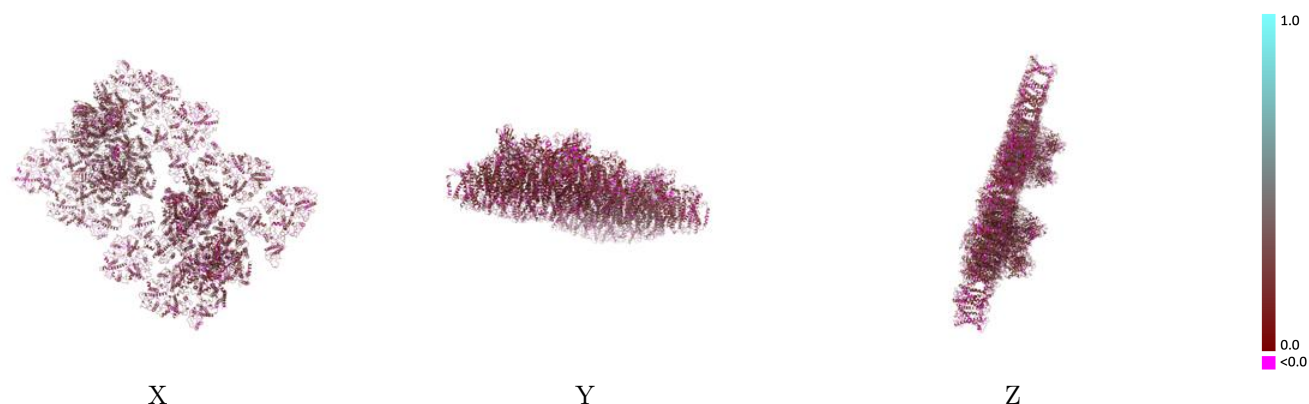
This section contains information regarding the fit between EMDB map EMD-81438 and PDB model 27UR. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



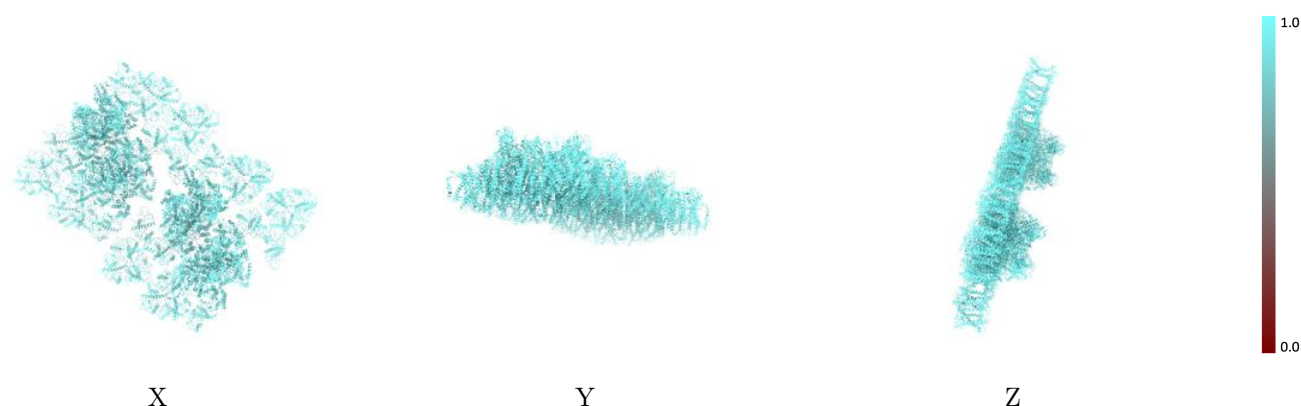
The images above show the 3D surface view of the map at the recommended contour level 0.0005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



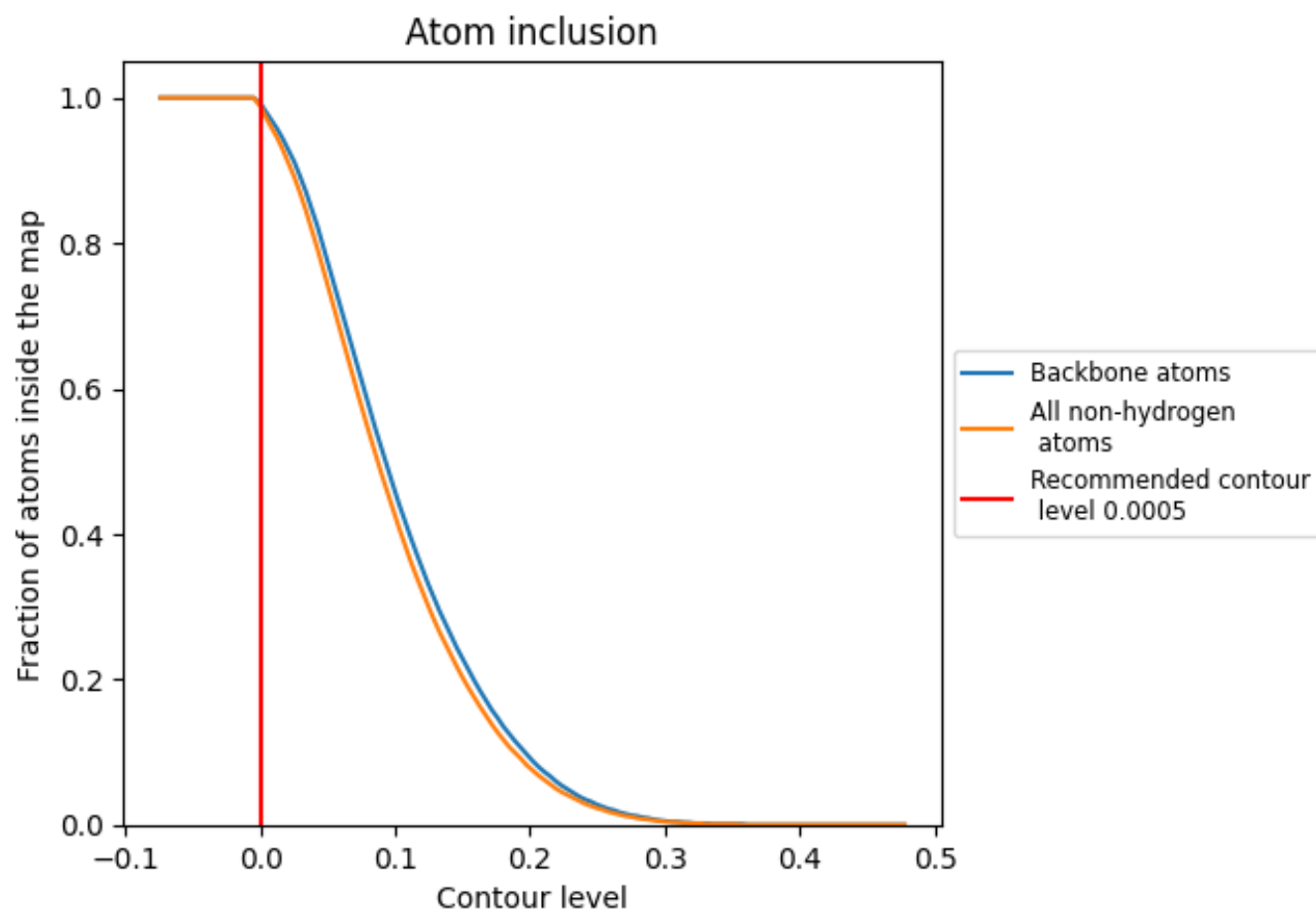
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.0005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9870	 0.1840
00	 0.9840	 0.2060
01	 0.9860	 0.1470
02	 0.9650	 0.1290
03	 0.9870	 0.1570
04	 0.9640	 0.1330
05	 0.9770	 0.1430
06	 0.9620	 0.1190
07	 0.9610	 0.1330
08	 0.9550	 0.1400
09	 0.9930	 0.2050
10	 0.9920	 0.1910
11	 0.9860	 0.1480
12	 0.9860	 0.1230
13	 0.9860	 0.1390
14	 0.9910	 0.1520
15	 0.9750	 0.1540
16	 0.9650	 0.1220
17	 0.9560	 0.1250
18	 0.9450	 0.1440
19	 0.9990	 0.2010
1A	 0.9940	 0.2270
1B	 0.9900	 0.2160
1C	 0.9950	 0.2430
1D	 0.9940	 0.2150
1E	 0.9970	 0.2310
1F	 1.0000	 0.2010
1G	 0.9820	 0.1880
1H	 0.9870	 0.2380
1I	 1.0000	 0.2690
1J	 1.0000	 0.2220
1K	 0.9790	 0.2120
1L	 1.0000	 0.2480
1M	 0.9630	 0.2150
1N	 0.9910	 0.1990



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Chain	Atom inclusion	Q-score
1O	 0.9920	 0.2140
1P	 0.9860	 0.2120
1R	 0.9710	 0.1820
1S	 0.9740	 0.1830
1T	 0.9940	 0.2460
1U	 1.0000	 0.2690
1V	 0.8980	 0.1470
1W	 0.9920	 0.2140
1X	 1.0000	 0.2450
1Y	 0.9770	 0.2180
1Z	 0.9780	 0.1950
1a	 0.9990	 0.2220
1b	 0.9990	 0.2220
1c	 0.9990	 0.2300
1d	 0.9990	 0.2270
1e	 0.9950	 0.2500
1f	 1.0000	 0.1970
1g	 0.9820	 0.1820
1h	 1.0000	 0.2540
1i	 1.0000	 0.2270
1j	 1.0000	 0.2270
1k	 1.0000	 0.2560
1l	 1.0000	 0.2520
1m	 0.9400	 0.2030
1n	 0.9830	 0.1720
1o	 0.9990	 0.2130
1p	 0.9990	 0.2160
1r	 0.9860	 0.2050
1s	 0.9740	 0.1790
1t	 0.9880	 0.2720
1u	 1.0000	 0.2150
1v	 0.9940	 0.1820
1w	 1.0000	 0.2490
1x	 1.0000	 0.2160
1y	 0.9940	 0.1610
1z	 0.9940	 0.1890
2A	 0.9990	 0.1790
2B	 0.9990	 0.1770
2C	 0.9980	 0.1790
2D	 1.0000	 0.1850
2E	 1.0000	 0.1980
2F	 1.0000	 0.1910

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Chain	Atom inclusion	Q-score
2G	 0.9800	 0.1660
2H	 1.0000	 0.1720
2I	 0.9940	 0.2040
2J	 1.0000	 0.2220
2K	 1.0000	 0.2020
2L	 1.0000	 0.2190
2M	 0.9940	 0.2040
2N	 0.9890	 0.1710
2O	 0.9960	 0.1560
2P	 0.9950	 0.1580
2R	 0.9980	 0.1650
2S	 0.9630	 0.1450
2T	 0.9940	 0.1970
2U	 1.0000	 0.1360
2V	 0.9540	 0.1120
2W	 1.0000	 0.1830
2X	 1.0000	 0.2300
2Y	 0.9940	 0.1920
2Z	 0.9810	 0.1840
2a	 0.9980	 0.1710
2b	 0.9920	 0.1750
2c	 1.0000	 0.1920
2d	 0.9990	 0.1770
2e	 0.9970	 0.1940
2f	 1.0000	 0.1930
2g	 0.9860	 0.1810
2h	 1.0000	 0.2000
2i	 1.0000	 0.1940
2j	 1.0000	 0.2260
2k	 1.0000	 0.1940
2l	 0.9940	 0.2010
2m	 0.9040	 0.2030
2n	 0.9780	 0.1570
2o	 0.9980	 0.1570
2p	 0.9690	 0.1560
2r	 0.9760	 0.1640
2s	 0.9840	 0.1780
2t	 0.9630	 0.2470
2u	 1.0000	 0.1940
2v	 0.9860	 0.1360
2w	 1.0000	 0.2150
2x	 1.0000	 0.2450

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Chain	Atom inclusion	Q-score
2y	 0.9710	 0.1910
2z	 0.9940	 0.1970