



wwPDB EM Validation Summary Report ⓘ

Sep 28, 2026 – 11:16 AM JST

PDB ID : 27UT / pdb_000027ut
EMDB ID : EMD-81447
Title : In situ structure of the trans-lumenal PSII-LHCII dimer from *Oryza sativa* (composite)
Authors : Li, J.; Elias, E.; Zhang, K.; Croce, R.; Zhu, J.
Deposited on : 2026-06-12
Resolution : 3.93 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:

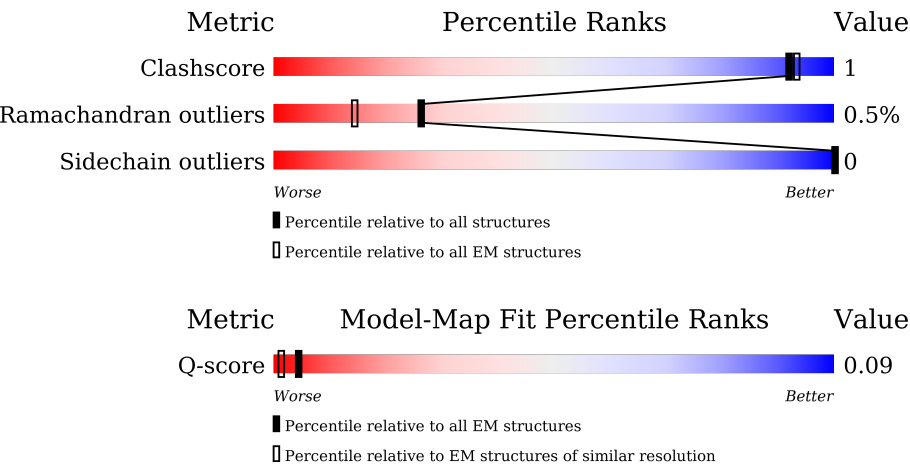
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

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 3.93 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	7811 (3.43 - 4.43)

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	9% 95% ..
1	01	219	6% 98% .
1	02	219	17% 94% ..
1	05	219	14% 95% .

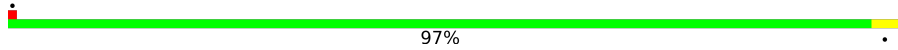
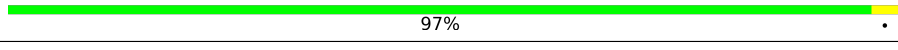
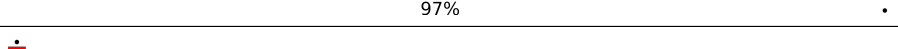
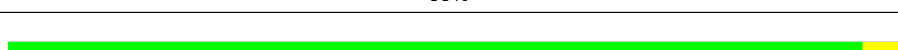
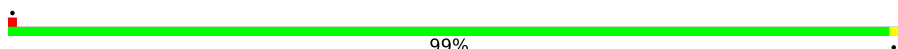
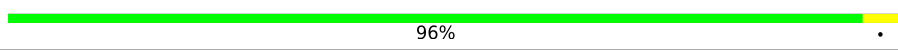
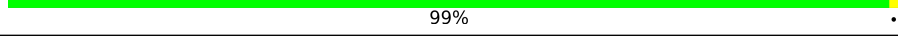
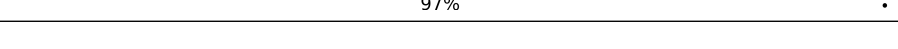
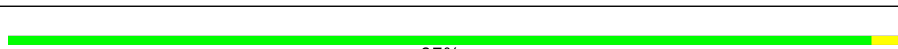
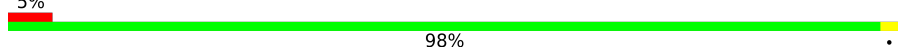
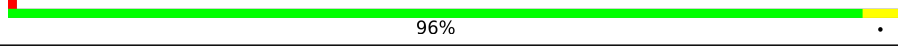
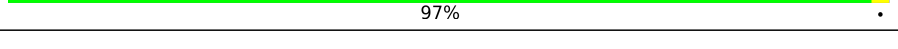
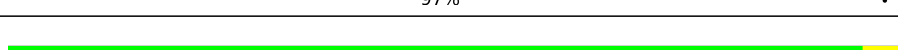
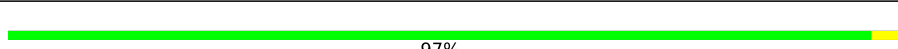
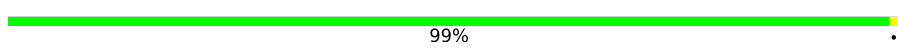
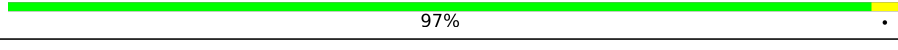
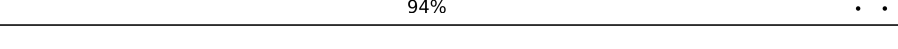
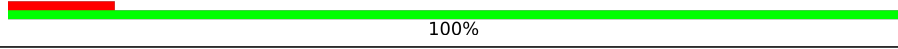
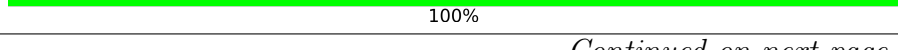
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Mol	Chain	Length	Quality of chain
1	06	219	12% 89% 5% 5%
1	09	219	10% 99% .
1	10	219	7% 97% .
1	11	219	7% 98% .
1	12	219	10% 94% ..
1	15	219	8% 95% .
1	16	219	11% 90% . 5%
1	19	219	. 97% .
1	1G	219	9% 96% .
1	1N	219	10% 96% .
1	1g	219	7% 97% .
1	1n	219	5% 99% .
1	2G	219	6% 97% .
1	2N	219	5% 96% .
1	2g	219	5% 97% .
1	2n	219	5% 99% .
2	03	220	15% 97% .
2	07	220	19% 95% 5%
2	13	220	10% 97% .
2	17	220	15% 95% 5%
3	04	205	16% 94% ..
3	08	205	13% 95% 5%
3	14	205	7% 95% ..
3	18	205	18% 95% 5%
4	1A	334	. 97% .

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Mol	Chain	Length	Quality of chain
4	1a	334	 97%
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	 97%
7	1D	341	 5% 98%
7	1d	341	 96%
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	 12% 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	5% 100%
13	1k	37	92% 8%
13	2K	37	95% 5%
13	2k	37	86% 14%
14	1L	37	8% 97% .
14	1l	37	95% 5%
14	2L	37	97% .
14	2l	37	95% 5%
15	1M	33	12% 88% 9% .
15	1m	33	12% 100%
15	2M	33	12% 88% 9% .
15	2m	33	9% 100%
16	1O	248	94% 5%
16	1o	248	92% . .
16	2O	248	95% .

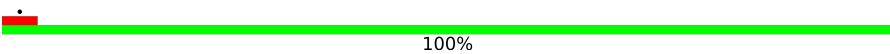
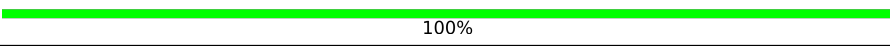
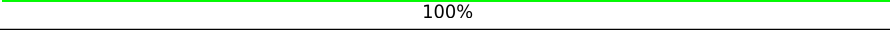
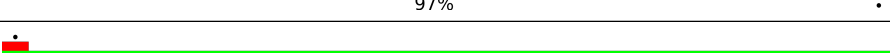
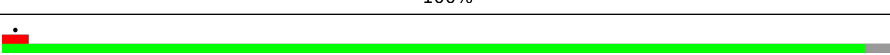
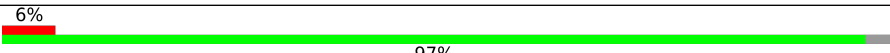
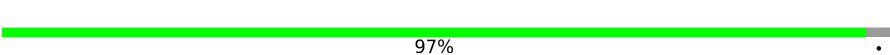
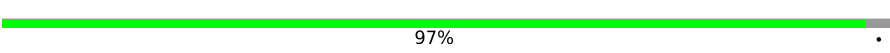
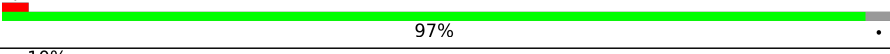
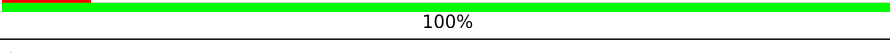
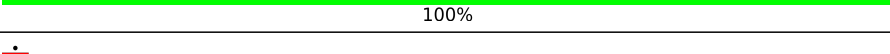
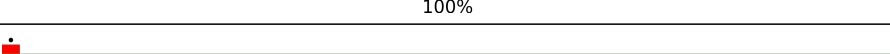
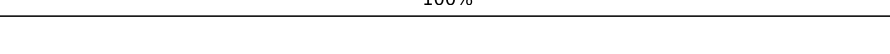
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Mol	Chain	Length	Quality of chain
16	2o	248	92%
17	1P	186	97%
17	1p	186	97%
17	2P	186	97%
17	2p	186	97%
18	1R	234	13%
18	1r	234	9%
18	2R	234	8%
18	2r	234	10%
19	1S	218	10%
19	1s	218	5%
19	2S	218	6%
19	2s	218	5%
20	1T	32	9%
20	1t	32	97%
20	2T	32	100%
20	2t	32	97%
21	1U	27	96%
21	1u	27	96%
21	2U	27	96%
21	2u	27	96%
22	1V	99	11%
22	1v	99	9%
22	2V	99	98%
22	2v	99	5%

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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	 6%97%.
25	1y	35	 97%.
25	2Y	35	 97%.
25	2y	35	 97%.
26	1Z	62	 10%100%
26	1z	62	 100%
26	2Z	62	 100%
26	2z	62	 100%

2 Entry composition [i](#)

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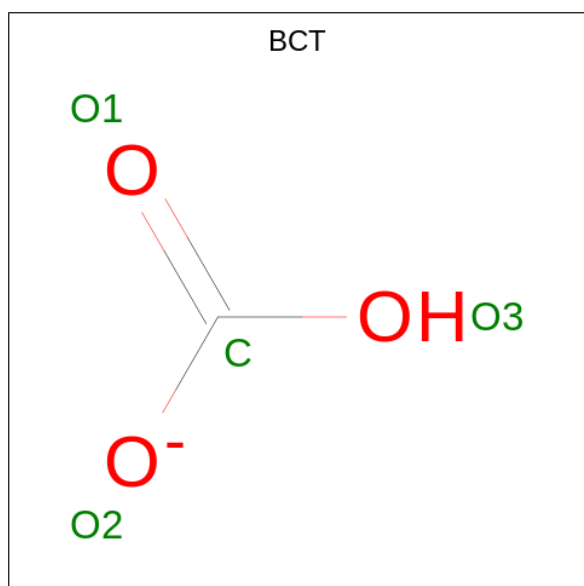
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Mol	Chain	Residues	Atoms				AltConf	Trace
25	2y	34	Total	C	N	O	0	0
			175	107	34	34		

- 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).

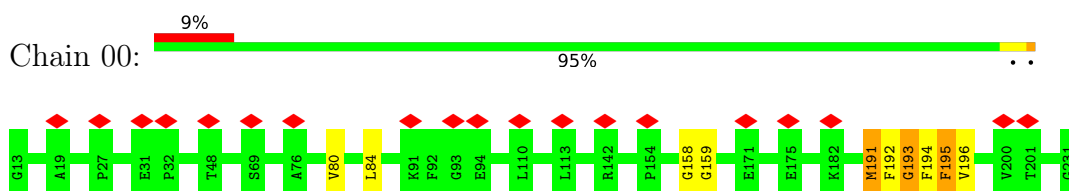


Mol	Chain	Residues	Atoms		AltConf
27	1A	1	Total	C	0
			1	1	
27	1d	1	Total	C	0
			1	1	
27	2A	1	Total	C	0
			1	1	
27	2d	1	Total	C	0
			1	1	

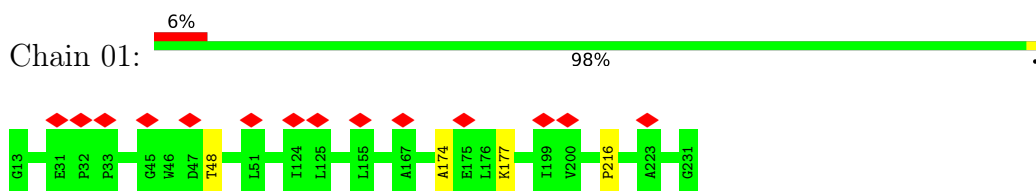
3 Residue-property plots [i](#)

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.

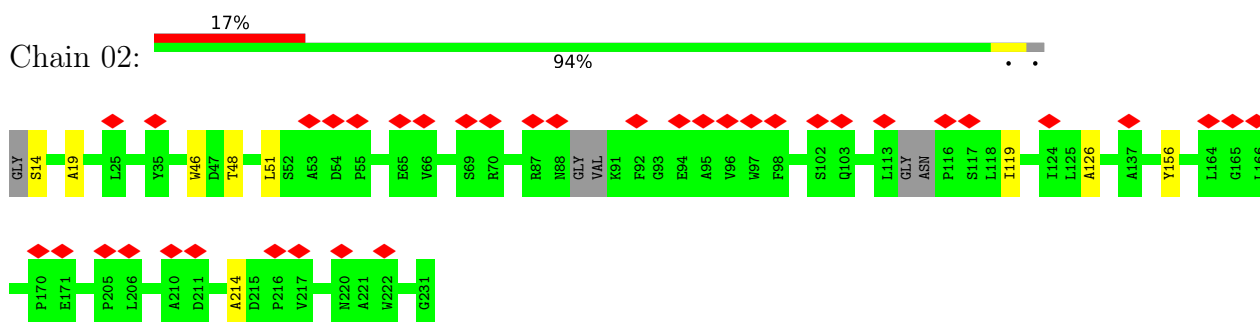
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



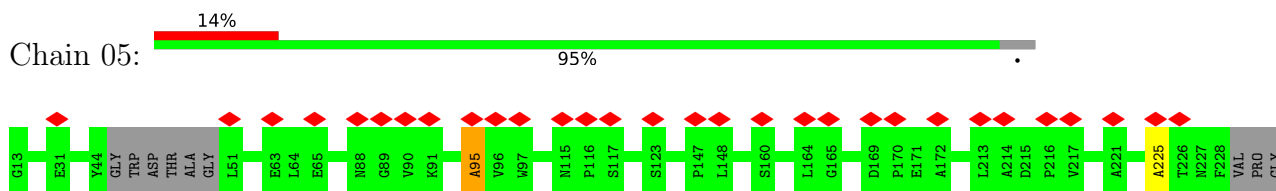
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



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

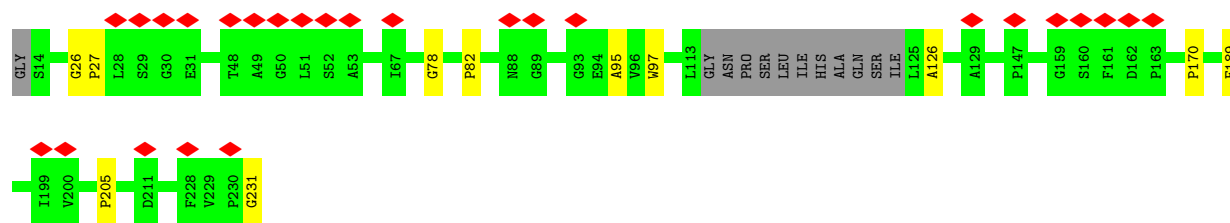


- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



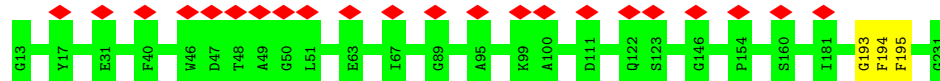
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic





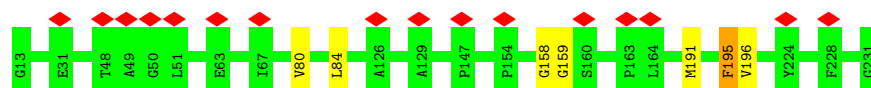
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 09: 10% 99%



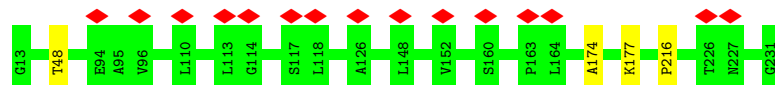
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 10: 7% 97%



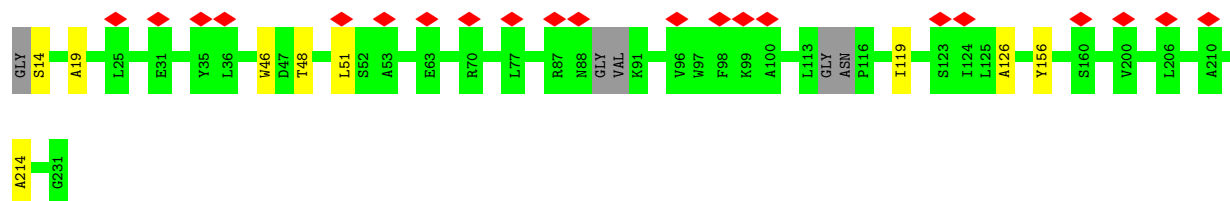
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 11: 7% 98%



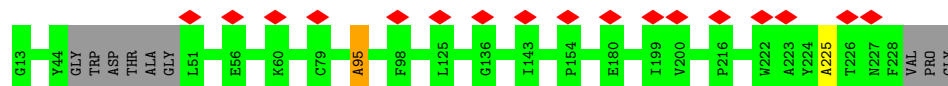
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

Chain 12: 10% 94%

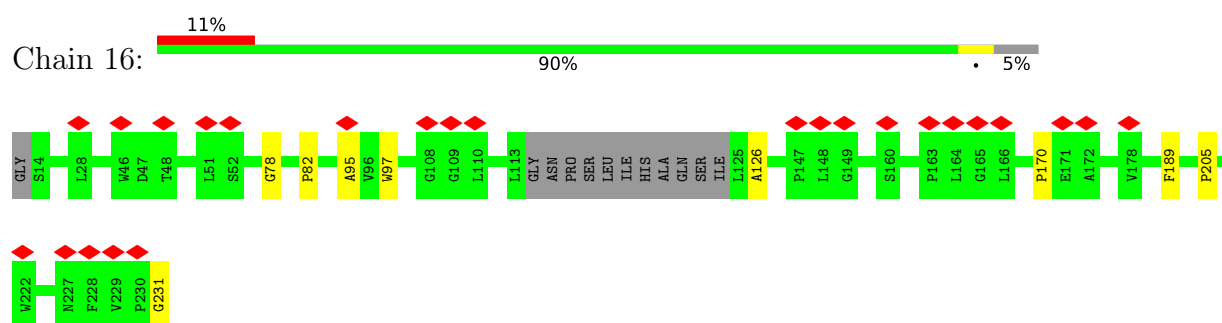


- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

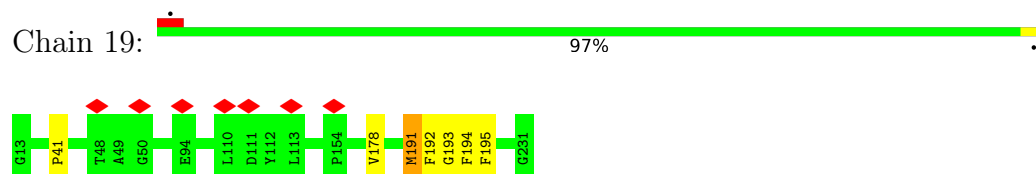
Chain 15: 8% 95%



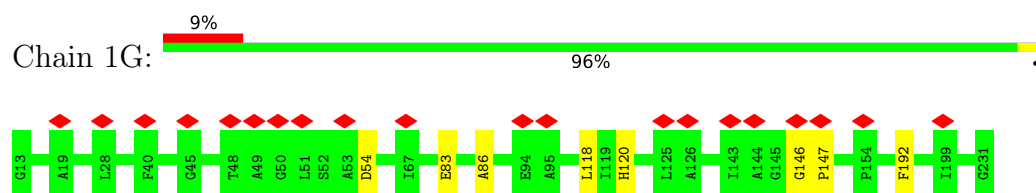
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



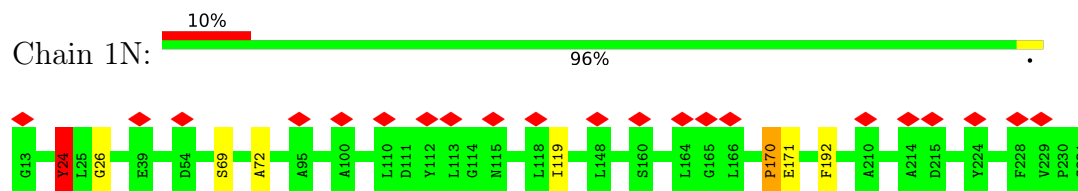
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



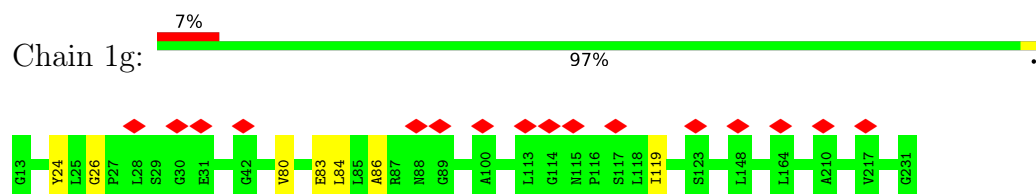
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



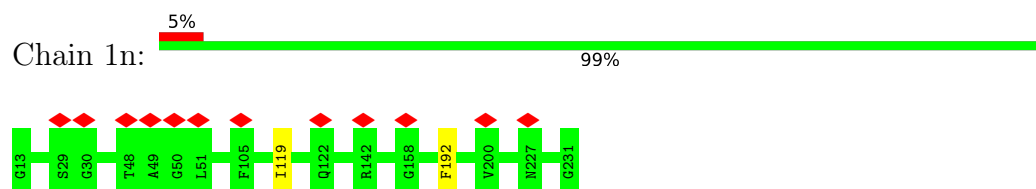
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



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

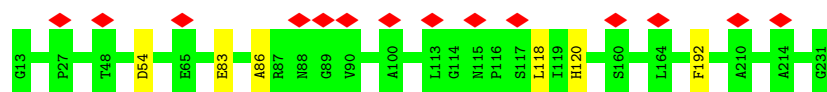


- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

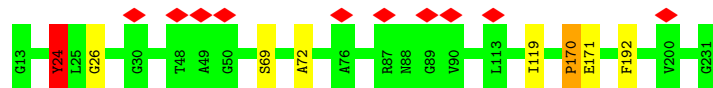


- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic

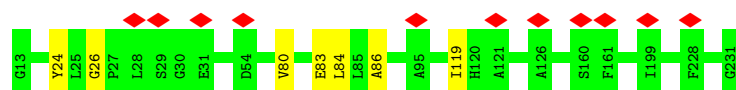




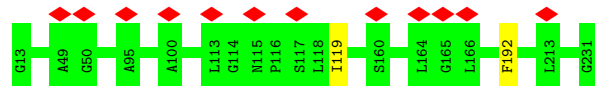
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



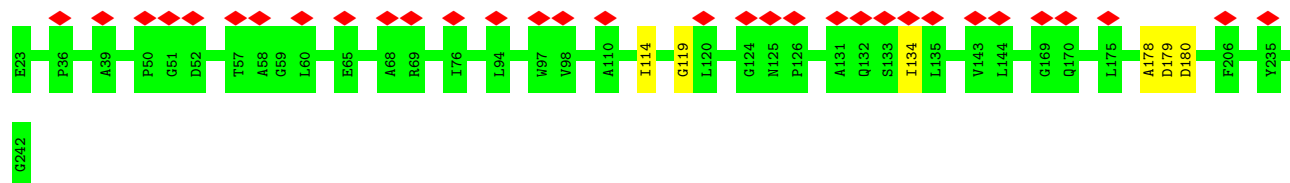
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



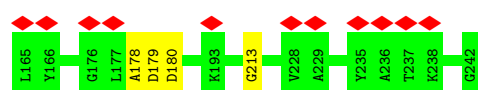
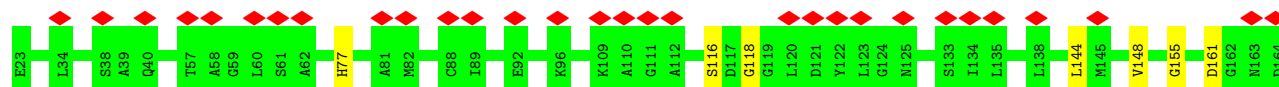
- Molecule 1: Chlorophyll a-b binding protein 2, chloroplastic



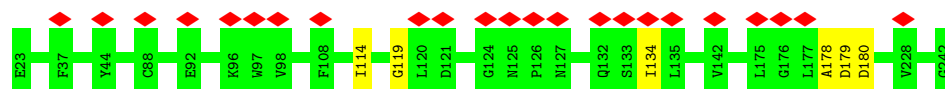
- Molecule 2: Chlorophyll a/b-binding protein



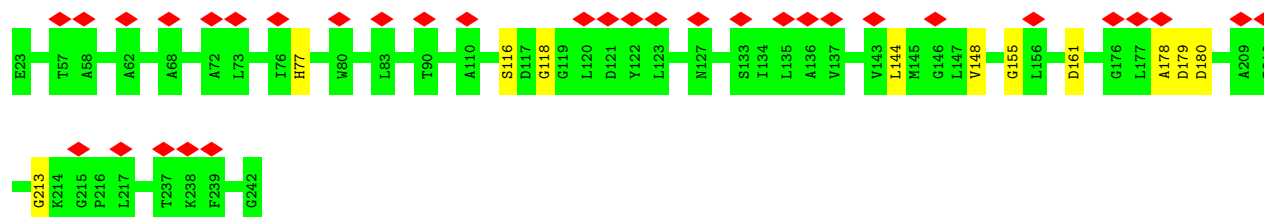
- Molecule 2: Chlorophyll a/b-binding protein



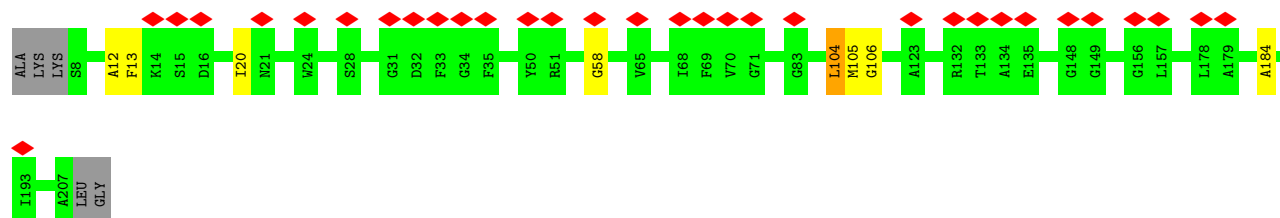
- Molecule 2: Chlorophyll a/b-binding protein



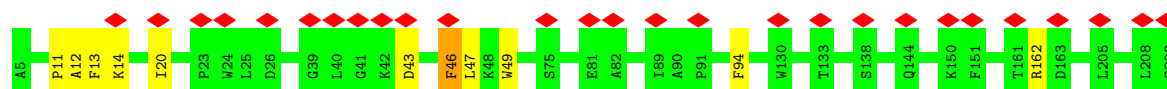
- Molecule 2: Chlorophyll a/b-binding protein



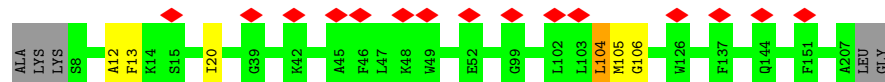
- Molecule 3: Chlorophyll a-b binding protein, chloroplastic



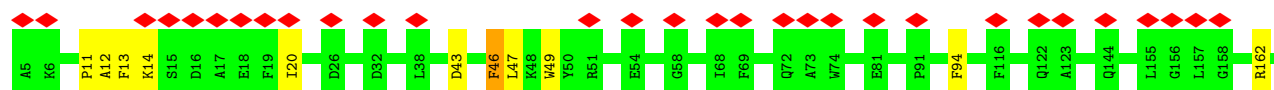
- Molecule 3: Chlorophyll a-b binding protein, chloroplastic

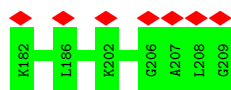


- Molecule 3: Chlorophyll a-b binding protein, chloroplastic

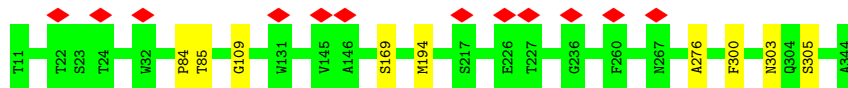


- Molecule 3: Chlorophyll a-b binding protein, chloroplastic

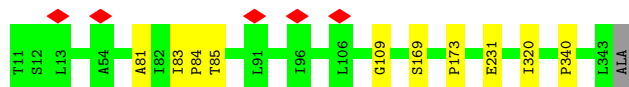




- Molecule 4: Photosystem II protein D1



- Molecule 4: Photosystem II protein D1



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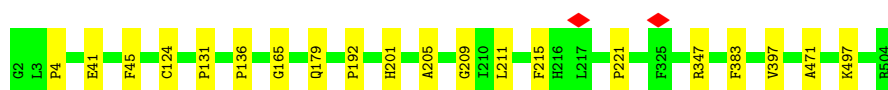
- Molecule 4: Photosystem II protein D1



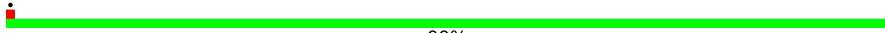
- Molecule 5: Photosystem II CP47 reaction center protein

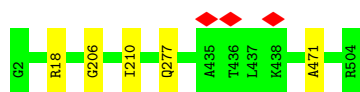


- Molecule 5: Photosystem II CP47 reaction center protein

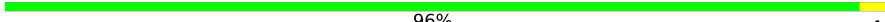


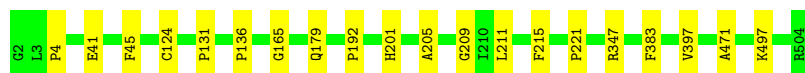
- Molecule 5: Photosystem II CP47 reaction center protein

Chain 2B:  99%



- Molecule 5: Photosystem II CP47 reaction center protein

Chain 2b:  96%

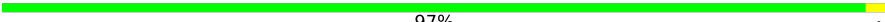


- Molecule 6: Photosystem II CP43 reaction center protein

Chain 1C:  99%



- Molecule 6: Photosystem II CP43 reaction center protein

Chain 1c:  97%

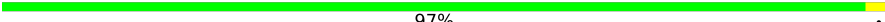


- Molecule 6: Photosystem II CP43 reaction center protein

Chain 2C:  99%



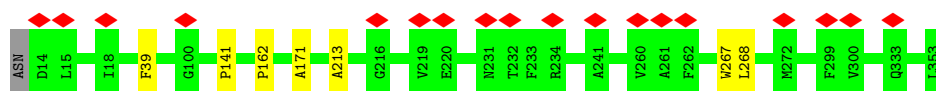
- Molecule 6: Photosystem II CP43 reaction center protein

Chain 2c:  97%

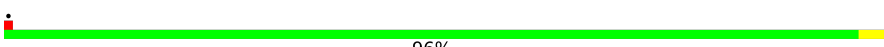


- Molecule 7: Photosystem II D2 protein

Chain 1D:  98%

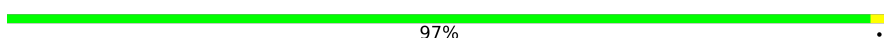


- Molecule 7: Photosystem II D2 protein

Chain 1d:  96%

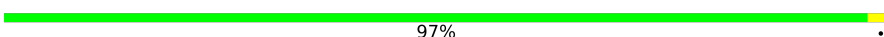


- Molecule 7: Photosystem II D2 protein

Chain 2D:  97%

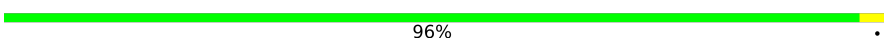


- Molecule 7: Photosystem II D2 protein

Chain 2d:  97%

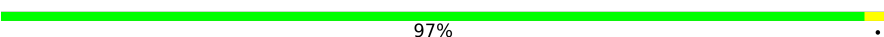


- Molecule 8: Cytochrome b559 subunit alpha

Chain 1E:  96%

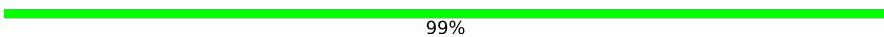


- Molecule 8: Cytochrome b559 subunit alpha

Chain 1e:  97%

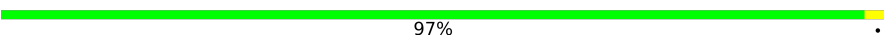


- Molecule 8: Cytochrome b559 subunit alpha

Chain 2E:  99%

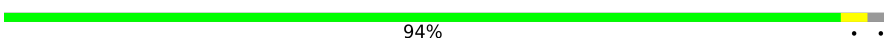


- Molecule 8: Cytochrome b559 subunit alpha

Chain 2e:  97%



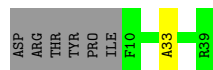
- Molecule 9: Cytochrome b559 subunit beta

Chain 1F:  94%

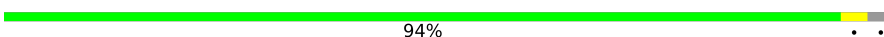


- Molecule 9: Cytochrome b559 subunit beta

Chain 1f:  81%



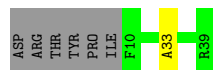
- Molecule 9: Cytochrome b559 subunit beta

Chain 2F:  94%



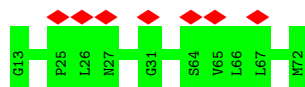
- Molecule 9: Cytochrome b559 subunit beta

Chain 2f:  81%



- Molecule 10: Photosystem II reaction center protein H

Chain 1H:  12%
100%

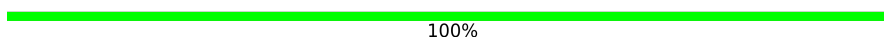


- Molecule 10: Photosystem II reaction center protein H

Chain 1h:  100%

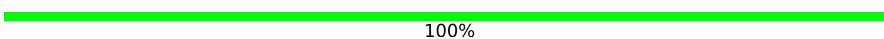
There are no outlier residues recorded for this chain.

- Molecule 10: Photosystem II reaction center protein H

Chain 2H:  100%

There are no outlier residues recorded for this chain.

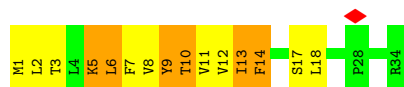
- Molecule 10: Photosystem II reaction center protein H

Chain 2h:  100%

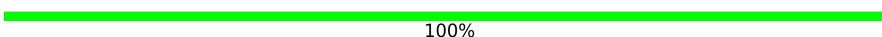
There are no outlier residues recorded for this chain.

- Molecule 11: Photosystem II reaction center protein I

Chain 1I: 



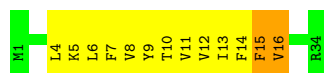
- Molecule 11: Photosystem II reaction center protein I

Chain 1i: 

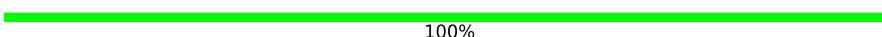
There are no outlier residues recorded for this chain.

- Molecule 11: Photosystem II reaction center protein I

Chain 2I: 

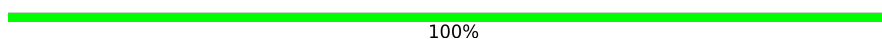


- Molecule 11: Photosystem II reaction center protein I

Chain 2i: 

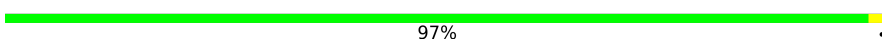
There are no outlier residues recorded for this chain.

- Molecule 12: Photosystem II reaction center protein J

Chain 1J: 

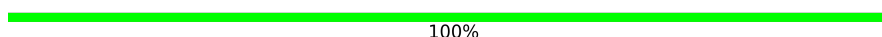
There are no outlier residues recorded for this chain.

- Molecule 12: Photosystem II reaction center protein J

Chain 1j: 

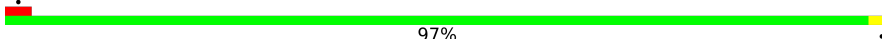


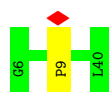
- Molecule 12: Photosystem II reaction center protein J

Chain 2J: 

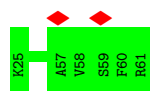
There are no outlier residues recorded for this chain.

- Molecule 12: Photosystem II reaction center protein J

Chain 2j: 



- Molecule 13: Photosystem II reaction center protein K



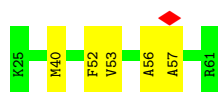
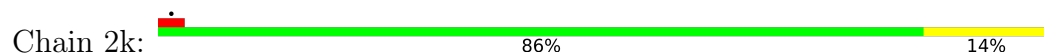
- Molecule 13: Photosystem II reaction center protein K



- Molecule 13: Photosystem II reaction center protein K



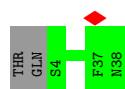
- Molecule 13: Photosystem II reaction center protein K



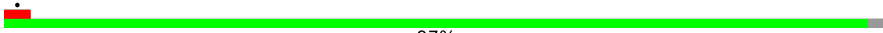
- Molecule 14: Photosystem II reaction center protein L

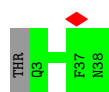


- Molecule 14: Photosystem II reaction center protein L



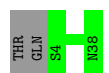
- Molecule 14: Photosystem II reaction center protein L

Chain 2L:  97%



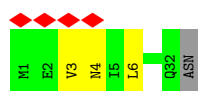
- Molecule 14: Photosystem II reaction center protein L

Chain 2l:  95%



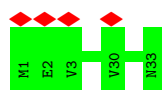
- Molecule 15: Photosystem II reaction center protein M

Chain 1M:  12% 88% 9%



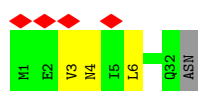
- Molecule 15: Photosystem II reaction center protein M

Chain 1m:  12% 100%



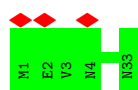
- Molecule 15: Photosystem II reaction center protein M

Chain 2M:  12% 88% 9%

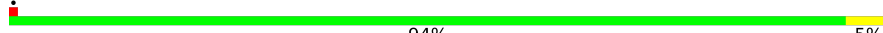


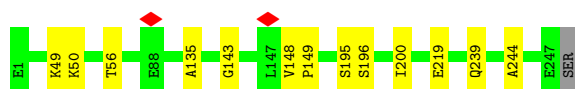
- Molecule 15: Photosystem II reaction center protein M

Chain 2m:  9% 100%

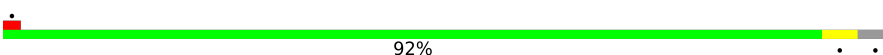


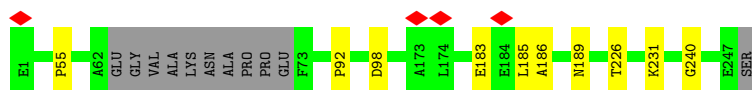
- Molecule 16: 33 kDa subunit of oxygen evolving system of photosystem II

Chain 10:  94% 5%

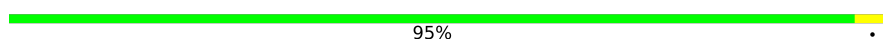


- Molecule 16: 33 kDa subunit of oxygen evolving system of photosystem II

Chain 1o:  92%

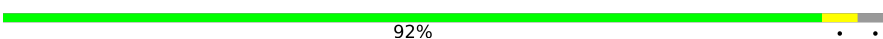


- Molecule 16: 33 kDa subunit of oxygen evolving system of photosystem II

Chain 2O:  95%

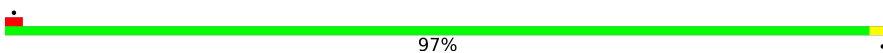


- Molecule 16: 33 kDa subunit of oxygen evolving system of photosystem II

Chain 2o:  92%

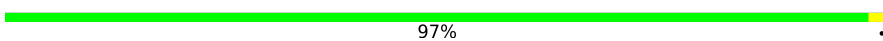


- Molecule 17: 23 kDa subunit of oxygen evolving system of photosystem II

Chain 1P:  97%

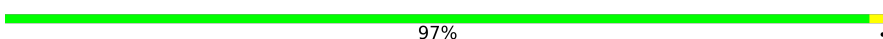


- Molecule 17: 23 kDa subunit of oxygen evolving system of photosystem II

Chain 1p:  97%

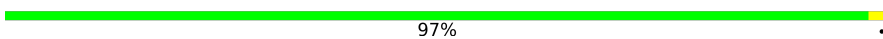


- Molecule 17: 23 kDa subunit of oxygen evolving system of photosystem II

Chain 2P:  97%

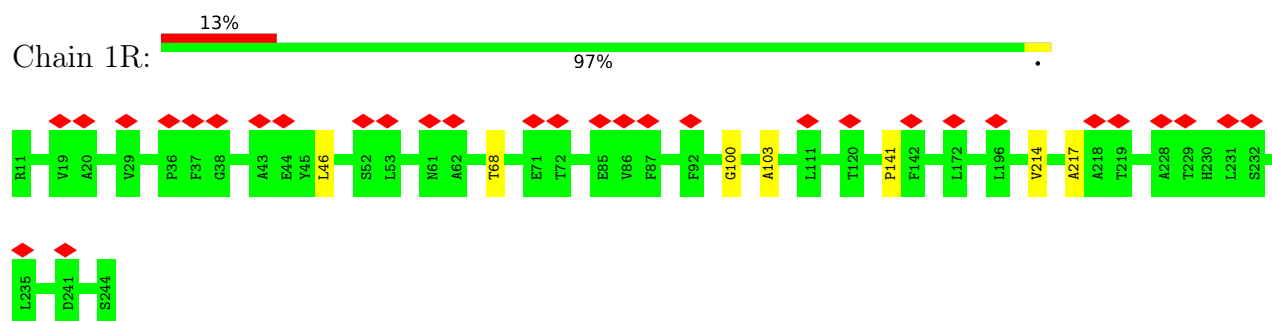


- Molecule 17: 23 kDa subunit of oxygen evolving system of photosystem II

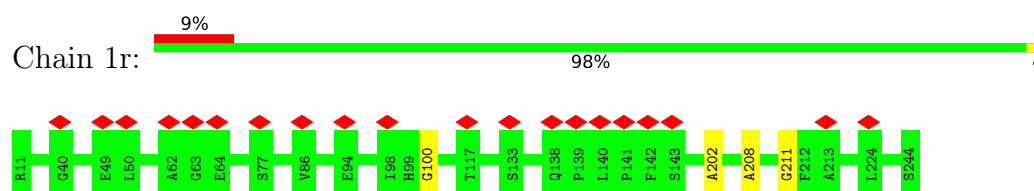
Chain 2p:  97%



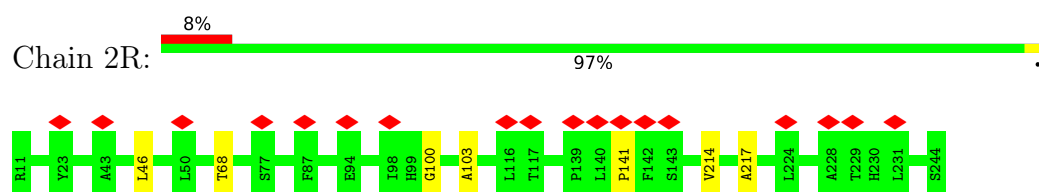
- Molecule 18: Chlorophyll a-b binding protein, chloroplastic



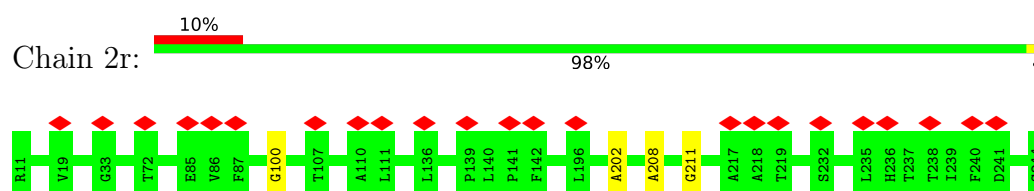
- Molecule 18: Chlorophyll a-b binding protein, chloroplastic



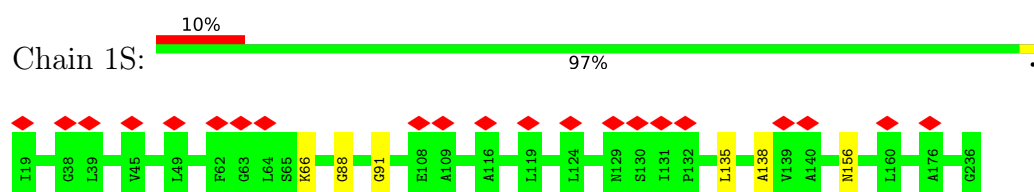
- Molecule 18: Chlorophyll a-b binding protein, chloroplastic



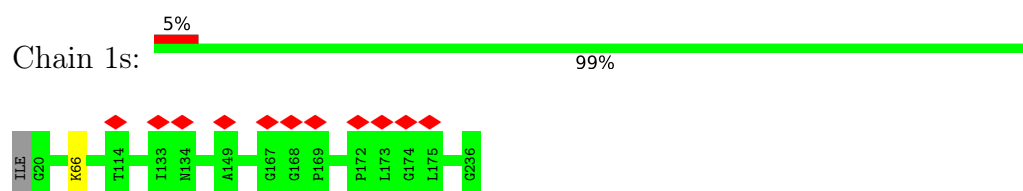
- Molecule 18: Chlorophyll a-b binding protein, chloroplastic



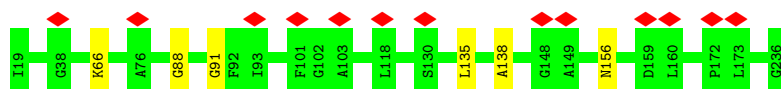
- Molecule 19: Chlorophyll a-b binding protein, chloroplastic



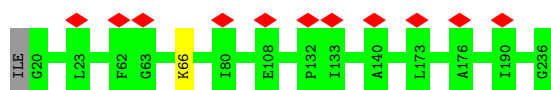
- Molecule 19: Chlorophyll a-b binding protein, chloroplastic



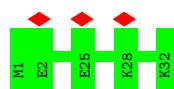
- Molecule 19: Chlorophyll a-b binding protein, chloroplastic



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



- Molecule 20: Photosystem II reaction center protein T



- Molecule 20: Photosystem II reaction center protein T



- Molecule 20: Photosystem II reaction center protein T



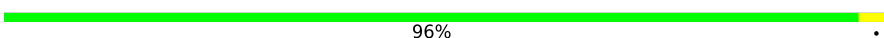
- Molecule 20: Photosystem II reaction center protein T



- Molecule 21: Os02g0581100 protein

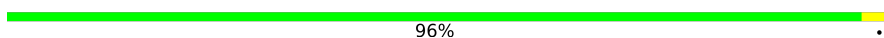


- Molecule 21: Os02g0581100 protein

Chain 1u:  96%

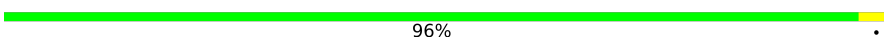


- Molecule 21: Os02g0581100 protein

Chain 2U:  96%

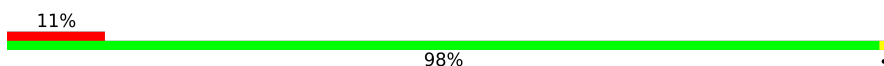


- Molecule 21: Os02g0581100 protein

Chain 2u:  96%

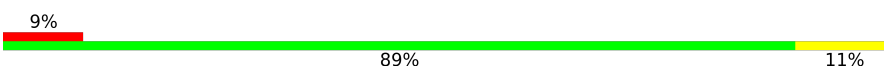


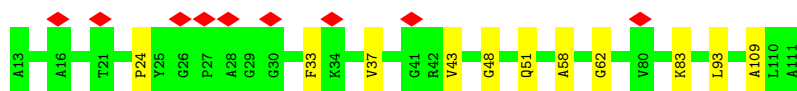
- Molecule 22: Photosystem II 10 kDa polypeptide, chloroplastic

Chain 1V:  11% 98%

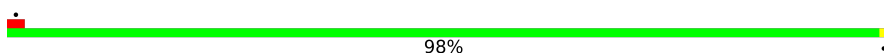


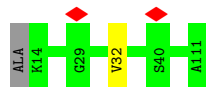
- Molecule 22: Photosystem II 10 kDa polypeptide, chloroplastic

Chain 1v:  9% 89% 11%



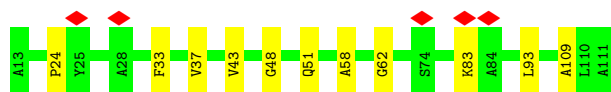
- Molecule 22: Photosystem II 10 kDa polypeptide, chloroplastic

Chain 2V:  98%

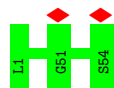


- Molecule 22: Photosystem II 10 kDa polypeptide, chloroplastic

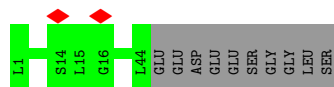
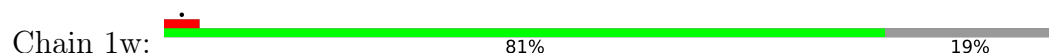
Chain 2v:  5% 89% 11%



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



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

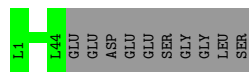
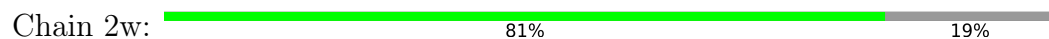


- Molecule 23: Photosystem II reaction center W protein, chloroplastic

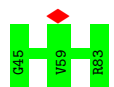


There are no outlier residues recorded for this chain.

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



- Molecule 24: Os07g0673550 protein

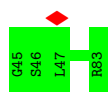


- Molecule 24: Os07g0673550 protein



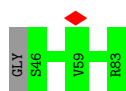
- Molecule 24: Os07g0673550 protein





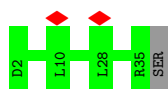
- Molecule 24: Os07g0673550 protein

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%



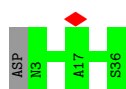
- Molecule 25: cDNA clone:001-024-H10, full insert sequence

Chain 2Y: 97%



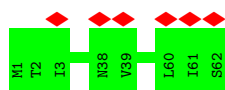
- Molecule 25: cDNA clone:001-024-H10, full insert sequence

Chain 2y: 97%



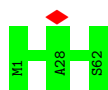
- Molecule 26: Photosystem II reaction center protein Z

Chain 1Z: 100%



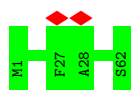
- Molecule 26: Photosystem II reaction center protein Z

Chain 1z:  100%



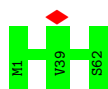
- Molecule 26: Photosystem II reaction center protein Z

Chain 2Z:  100%



- Molecule 26: Photosystem II reaction center protein Z

Chain 2z:  100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38275	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	0.602	Depositor
Minimum map value	-0.133	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.0008	Depositor
Map size (Å)	572.16003, 572.16003, 572.16003	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4900001, 1.4900001, 1.4900001	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	0.64	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	0.59	0/1552
1	10	0.25	0/1113	0.62	3/1552 (0.2%)
1	11	0.29	1/1112 (0.1%)	0.70	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	1/1113 (0.1%)	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	0.72	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	0.32	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	0.54	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	0.65	0/276
13	1k	0.29	0/196	0.60	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	0.22	0/1198	0.53	0/1669
16	2O	0.23	0/1254	0.61	1/1750 (0.1%)
16	2o	0.22	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	0.21	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	0.22	0/213	0.55	0/293
23	2W	0.27	0/261	0.56	0/359
23	2w	0.22	0/213	0.55	0/293
24	1X	0.20	0/196	0.39	0/272
24	1x	0.22	0/192	0.48	0/267
24	2X	0.20	0/196	0.40	0/272
24	2x	0.23	0/192	0.48	0/267
25	1Y	0.30	0/177	0.60	0/248
25	1y	0.27	0/177	0.54	0/248
25	2Y	0.31	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	0.29	19/94892 (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 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	2d	172	PRO	CB-CG	-11.39	0.92	1.49
7	1d	172	PRO	CB-CG	-11.38	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	-9.58	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	179.99	106.10
6	2C	80	PRO	CB-CG-CD	23.08	179.97	106.10
1	06	82	PRO	N-CD-CG	-19.34	74.20	103.20
1	16	82	PRO	N-CD-CG	-19.32	74.22	103.20
1	16	82	PRO	CA-CB-CG	-18.68	69.01	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	3	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	2	0
1	19	1098	0	618	3	0
1	1G	1098	0	618	3	0
1	1N	1098	0	618	4	0
1	1g	1098	0	618	3	0
1	1n	1098	0	618	0	0
1	2G	1098	0	618	2	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	5	0
2	13	1100	0	596	2	0
2	17	1101	0	598	5	0
3	04	1006	0	564	2	0
3	08	1030	0	578	3	0
3	14	1006	0	564	1	0
3	18	1030	0	578	3	0
4	1A	1666	0	865	5	0
4	1a	1661	0	860	5	0
4	2A	1666	0	865	6	0
4	2a	1661	0	860	5	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	11	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	5	0
7	1D	1698	0	887	3	0
7	1d	1703	0	889	7	0
7	2D	1698	0	887	4	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	1	0
13	2K	193	0	108	1	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	1	0
15	2m	167	0	85	0	0
16	1O	1239	0	652	6	0
16	1o	1186	0	614	9	0
16	2O	1239	0	652	5	0
16	2o	1186	0	614	8	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	2	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	0	0
20	1t	160	0	86	0	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	212	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 212 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)
1:16:97:TRP:H	1:16:205:PRO:HG3	1.51	0.76
1:06:97:TRP:H	1:06:205:PRO:HG3	1.51	0.74
16:1o:98:ASP:O	16:2o:98:ASP:CB	2.39	0.70
5:2b:205:ALA:O	5:2b:209:GLY:N	2.27	0.68
2:07:144:LEU:O	2:07:148:VAL:N	2.26	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	39
1	01	217/219 (99%)	191 (88%)	25 (12%)	1 (0%)	24	60
1	02	208/219 (95%)	173 (83%)	31 (15%)	4 (2%)	6	34
1	05	206/219 (94%)	176 (85%)	28 (14%)	2 (1%)	12	45
1	06	203/219 (93%)	174 (86%)	27 (13%)	2 (1%)	12	45
1	09	217/219 (99%)	196 (90%)	21 (10%)	0	100	100
1	10	217/219 (99%)	197 (91%)	18 (8%)	2 (1%)	14	48
1	11	217/219 (99%)	191 (88%)	25 (12%)	1 (0%)	24	60
1	12	208/219 (95%)	173 (83%)	31 (15%)	4 (2%)	6	34
1	15	206/219 (94%)	175 (85%)	29 (14%)	2 (1%)	12	45
1	16	203/219 (93%)	174 (86%)	27 (13%)	2 (1%)	12	45
1	19	217/219 (99%)	193 (89%)	22 (10%)	2 (1%)	14	48
1	1G	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	60
1	1N	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	60
1	1g	217/219 (99%)	197 (91%)	19 (9%)	1 (0%)	24	60
1	1n	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	60
1	2G	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	60
1	2N	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	60
1	2g	217/219 (99%)	197 (91%)	19 (9%)	1 (0%)	24	60
1	2n	217/219 (99%)	199 (92%)	17 (8%)	1 (0%)	24	60
2	03	218/220 (99%)	186 (85%)	30 (14%)	2 (1%)	14	48
2	07	218/220 (99%)	188 (86%)	29 (13%)	1 (0%)	24	60
2	13	218/220 (99%)	186 (85%)	30 (14%)	2 (1%)	14	48
2	17	218/220 (99%)	188 (86%)	29 (13%)	1 (0%)	24	60
3	04	198/205 (97%)	152 (77%)	44 (22%)	2 (1%)	12	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	08	203/205 (99%)	170 (84%)	28 (14%)	5 (2%)	4	29
3	14	198/205 (97%)	152 (77%)	44 (22%)	2 (1%)	12	45
3	18	203/205 (99%)	170 (84%)	28 (14%)	5 (2%)	4	29
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	75
5	1b	501/503 (100%)	486 (97%)	15 (3%)	0	100	100
5	2B	501/503 (100%)	476 (95%)	24 (5%)	1 (0%)	43	75
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	53
6	2C	448/450 (100%)	429 (96%)	19 (4%)	0	100	100
6	2c	448/450 (100%)	427 (95%)	18 (4%)	3 (1%)	18	53
7	1D	338/341 (99%)	319 (94%)	18 (5%)	1 (0%)	36	70
7	1d	339/341 (99%)	316 (93%)	23 (7%)	0	100	100
7	2D	338/341 (99%)	319 (94%)	18 (5%)	1 (0%)	36	70
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%)	23 (72%)	6 (19%)	3 (9%)	0	10
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	24
15	1m	31/33 (94%)	31 (100%)	0	0	100	100
15	2M	30/33 (91%)	24 (80%)	5 (17%)	1 (3%)	3	24
15	2m	31/33 (94%)	31 (100%)	0	0	100	100
16	1O	245/248 (99%)	211 (86%)	34 (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	60
17	1p	184/186 (99%)	170 (92%)	14 (8%)	0	100	100
17	2P	184/186 (99%)	164 (89%)	19 (10%)	1 (0%)	24	60
17	2p	184/186 (99%)	170 (92%)	14 (8%)	0	100	100
18	1R	232/234 (99%)	209 (90%)	22 (10%)	1 (0%)	30	65
18	1r	232/234 (99%)	216 (93%)	16 (7%)	0	100	100
18	2R	232/234 (99%)	210 (90%)	21 (9%)	1 (0%)	30	65

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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	48
19	1s	215/218 (99%)	188 (87%)	26 (12%)	1 (0%)	24	60
19	2S	216/218 (99%)	185 (86%)	29 (13%)	2 (1%)	14	48
19	2s	215/218 (99%)	188 (87%)	26 (12%)	1 (0%)	24	60
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	45
22	1v	97/99 (98%)	81 (84%)	12 (12%)	4 (4%)	2	21
22	2V	96/99 (97%)	79 (82%)	16 (17%)	1 (1%)	12	45
22	2v	97/99 (98%)	81 (84%)	12 (12%)	4 (4%)	2	21
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	60

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

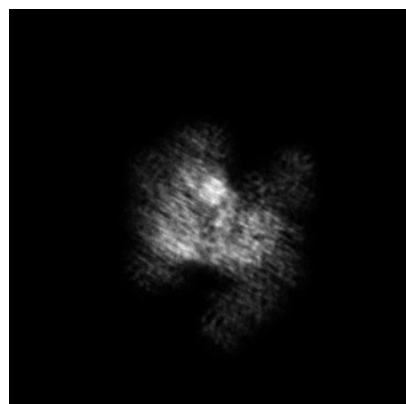
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-81447. These allow visual inspection of the internal detail of the map and identification of artifacts.

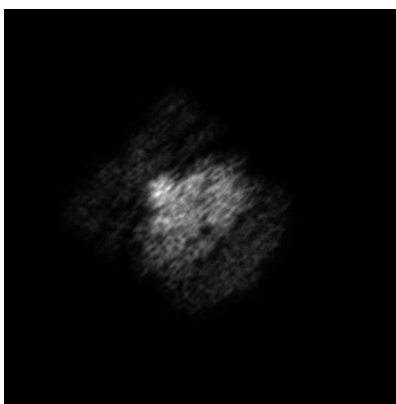
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

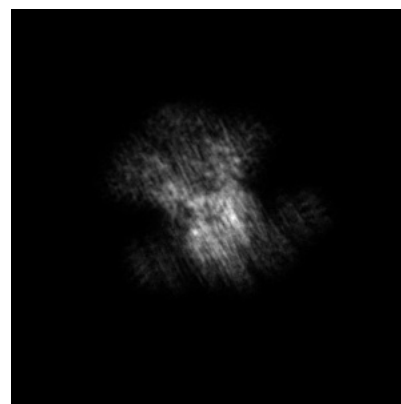
6.1.1 Primary map



X

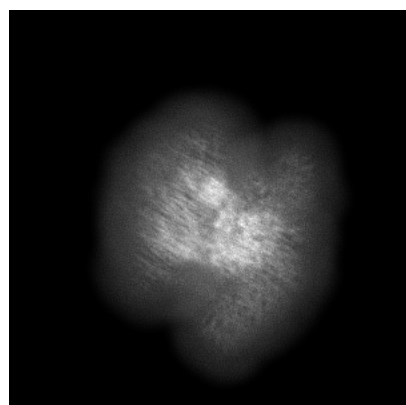


Y

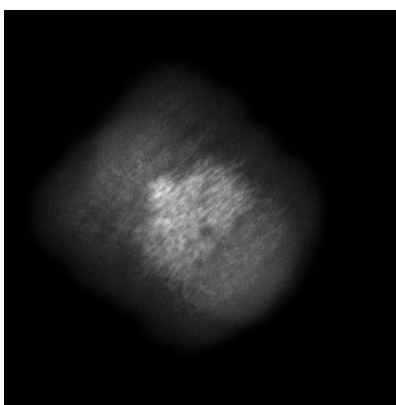


Z

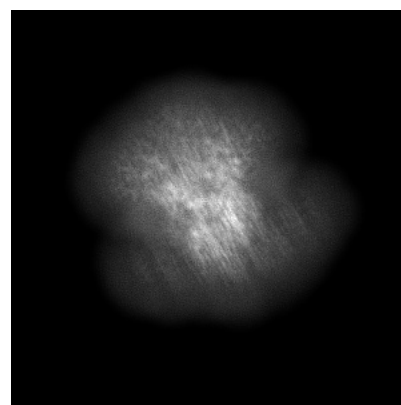
6.1.2 Raw map



X



Y

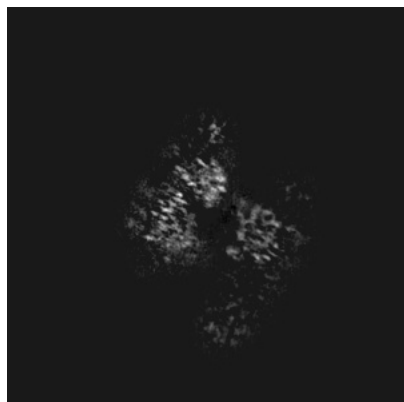


Z

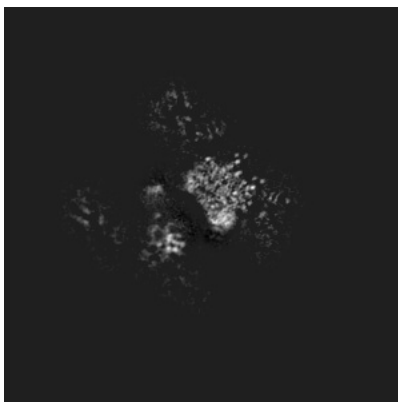
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

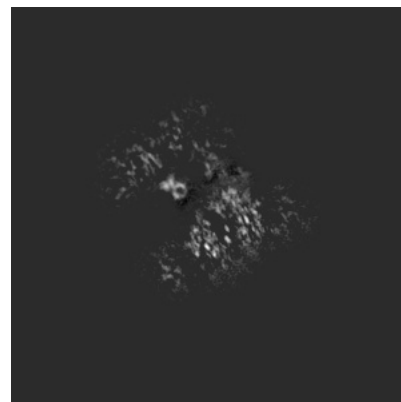
6.2.1 Primary map



X Index: 192

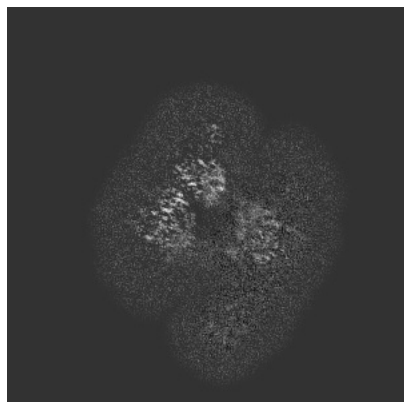


Y Index: 192

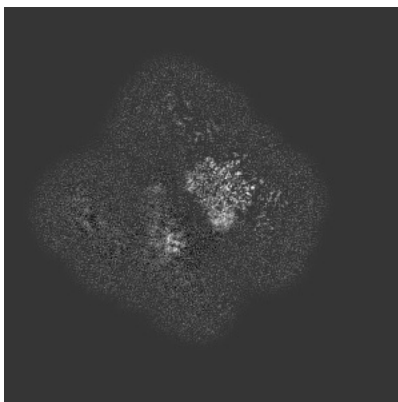


Z Index: 192

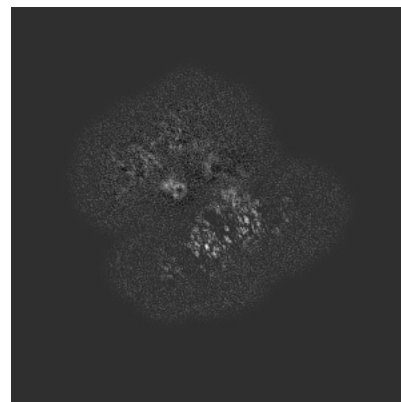
6.2.2 Raw map



X Index: 192



Y Index: 192

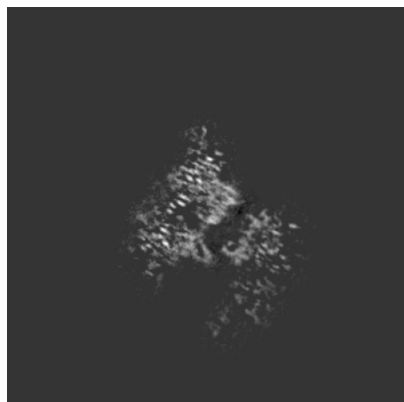


Z Index: 192

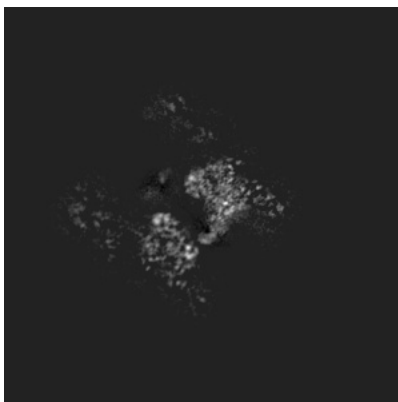
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

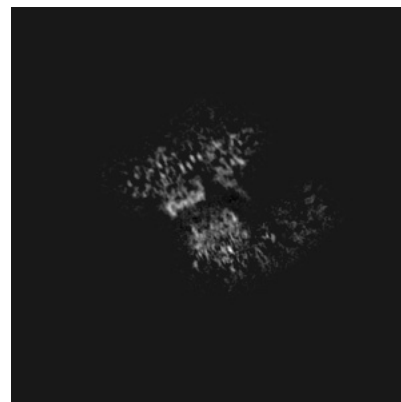
6.3.1 Primary map



X Index: 209

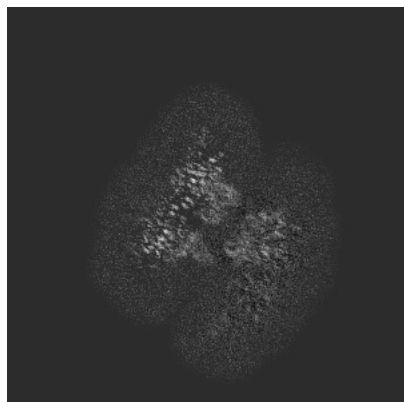


Y Index: 201

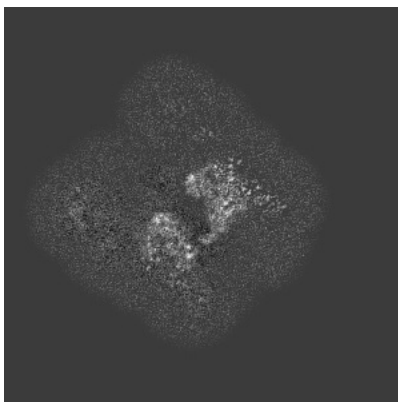


Z Index: 157

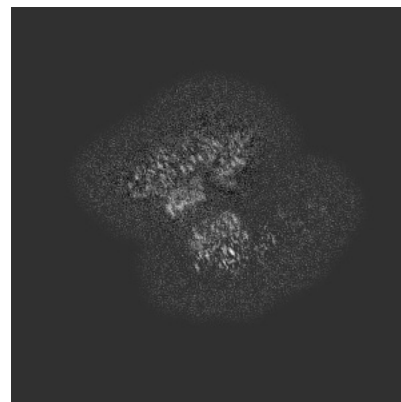
6.3.2 Raw map



X Index: 207



Y Index: 200

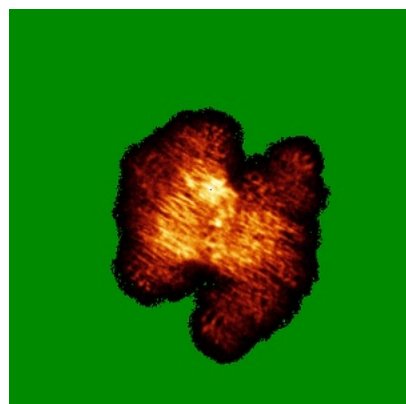


Z Index: 158

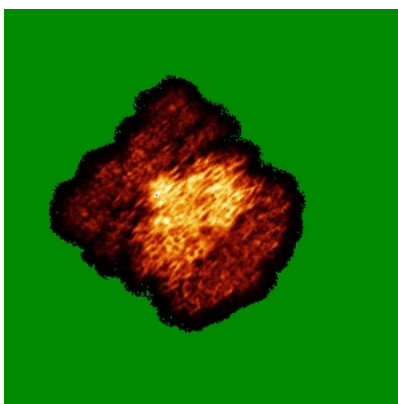
The images above show the largest variance slices of the map in three orthogonal directions.

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

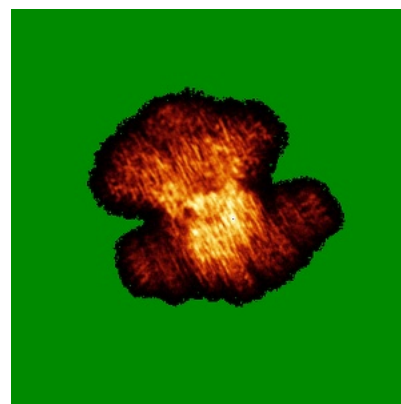
6.4.1 Primary map



X

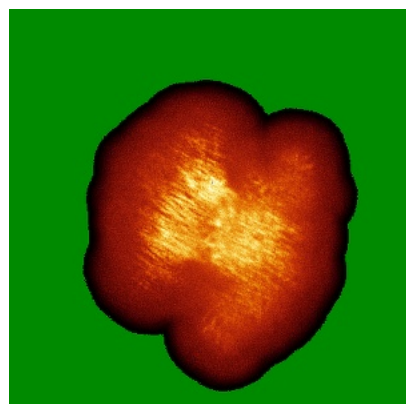


Y

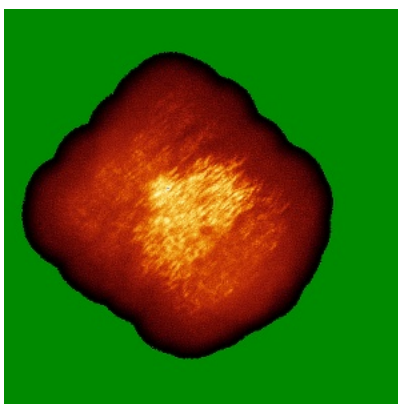


Z

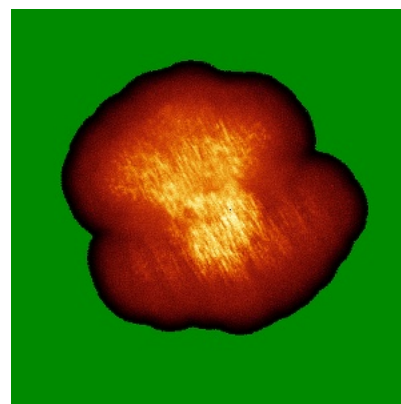
6.4.2 Raw map



X



Y

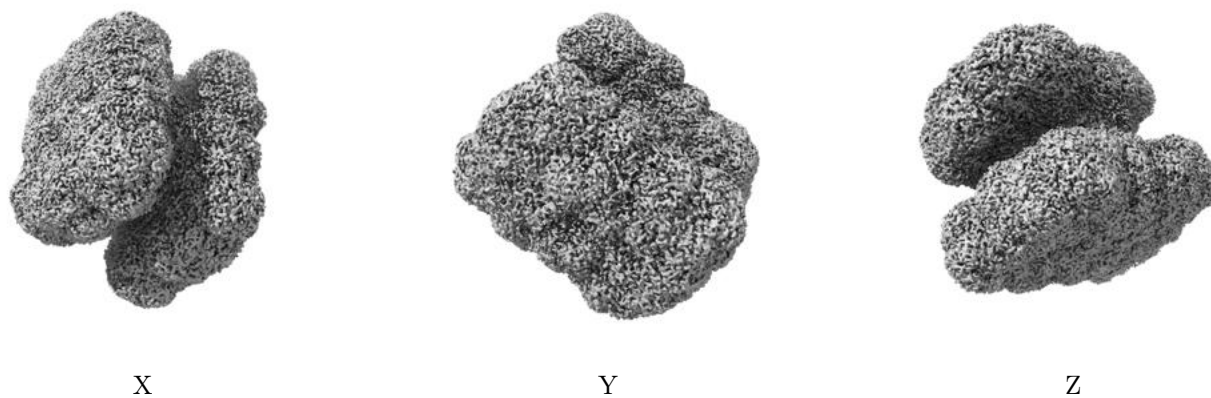


Z

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.

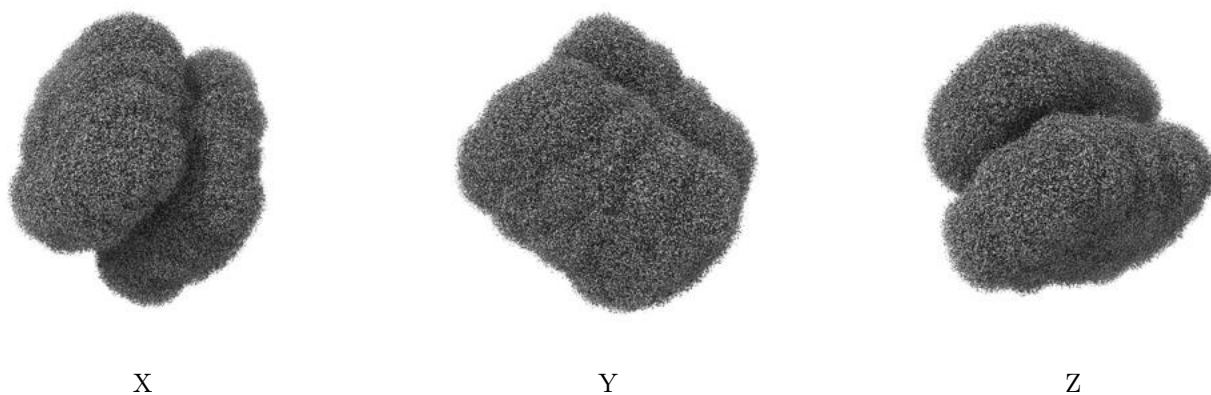
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0008. 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.

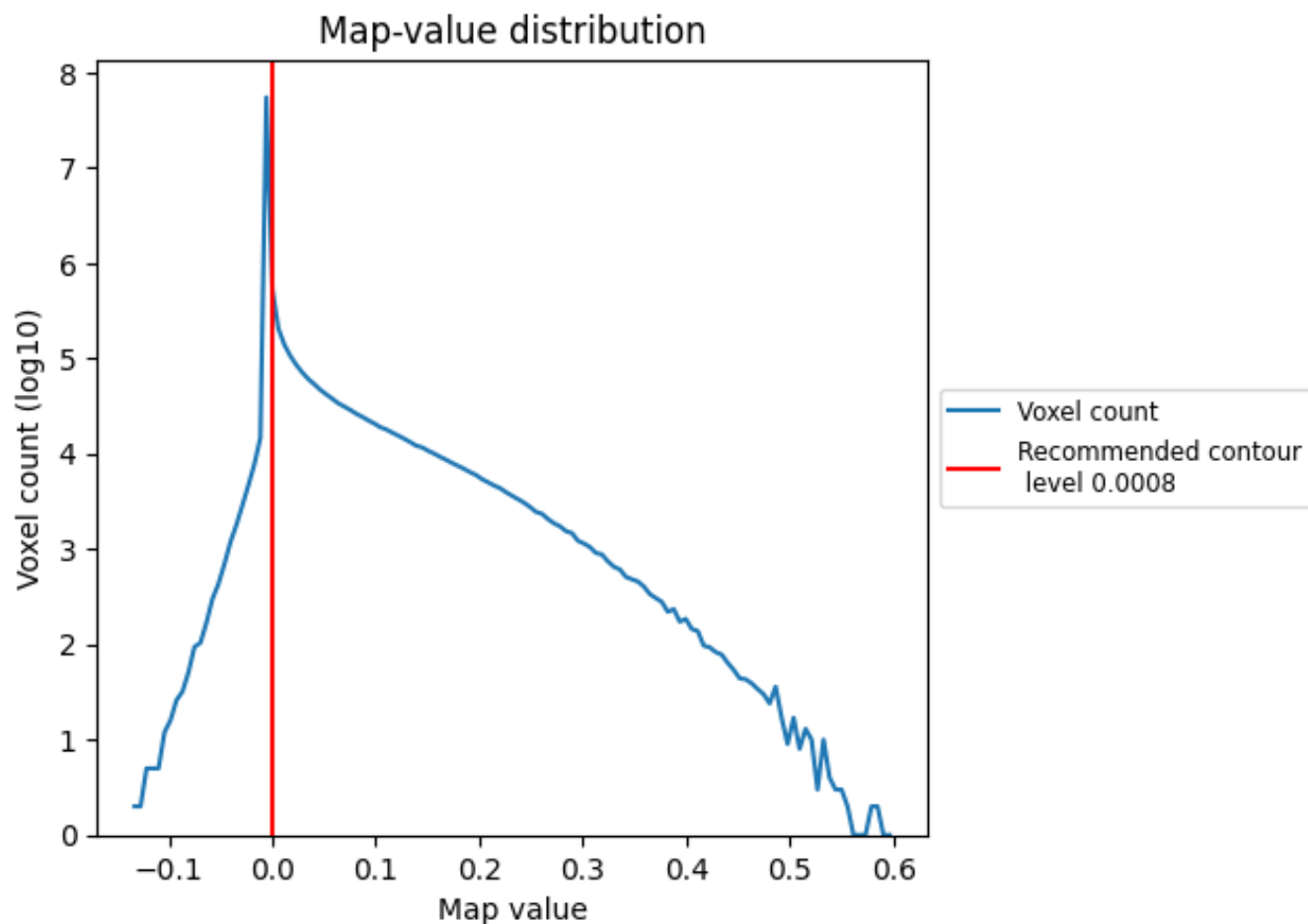
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

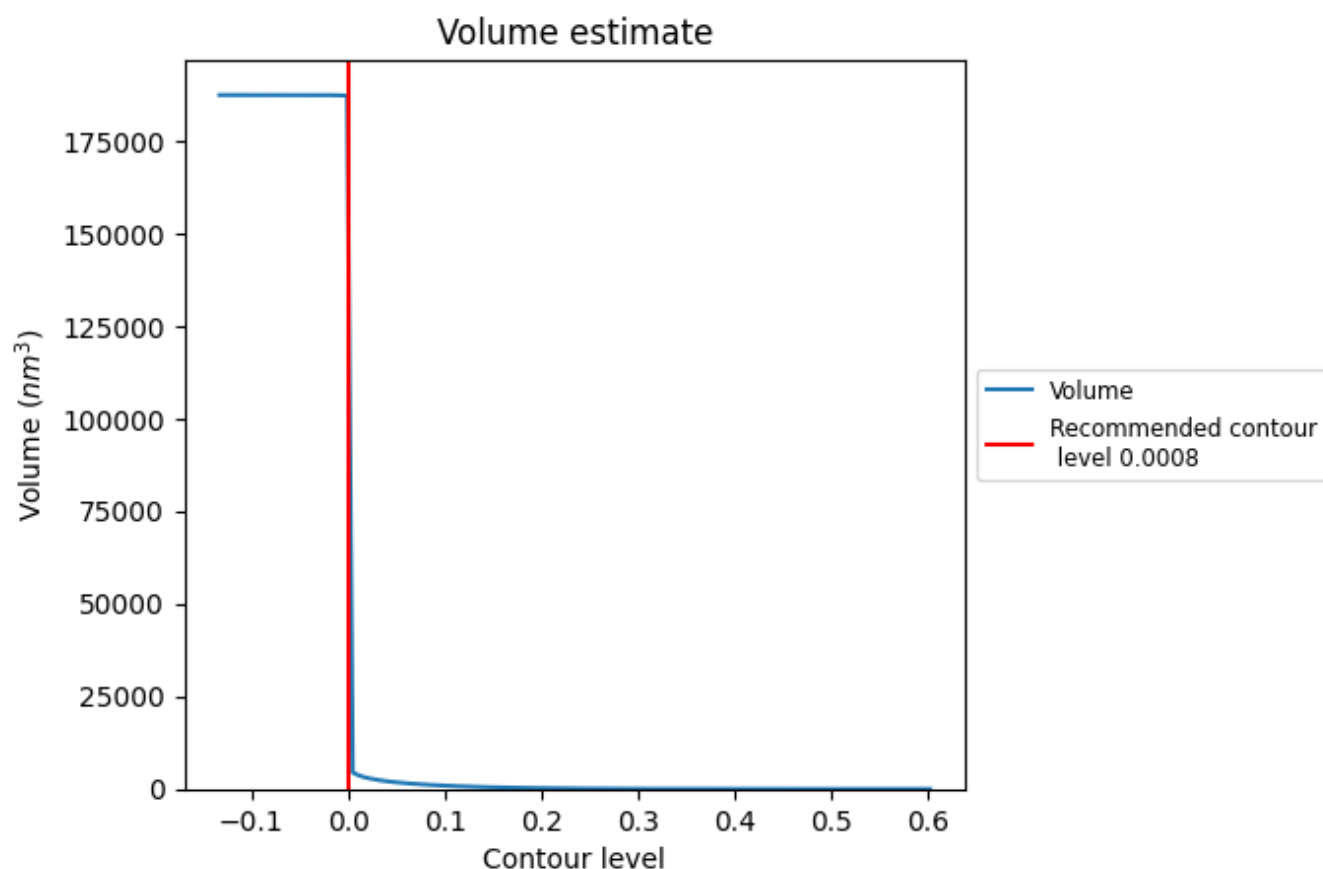
This section contains the results of statistical analysis of the map.

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.

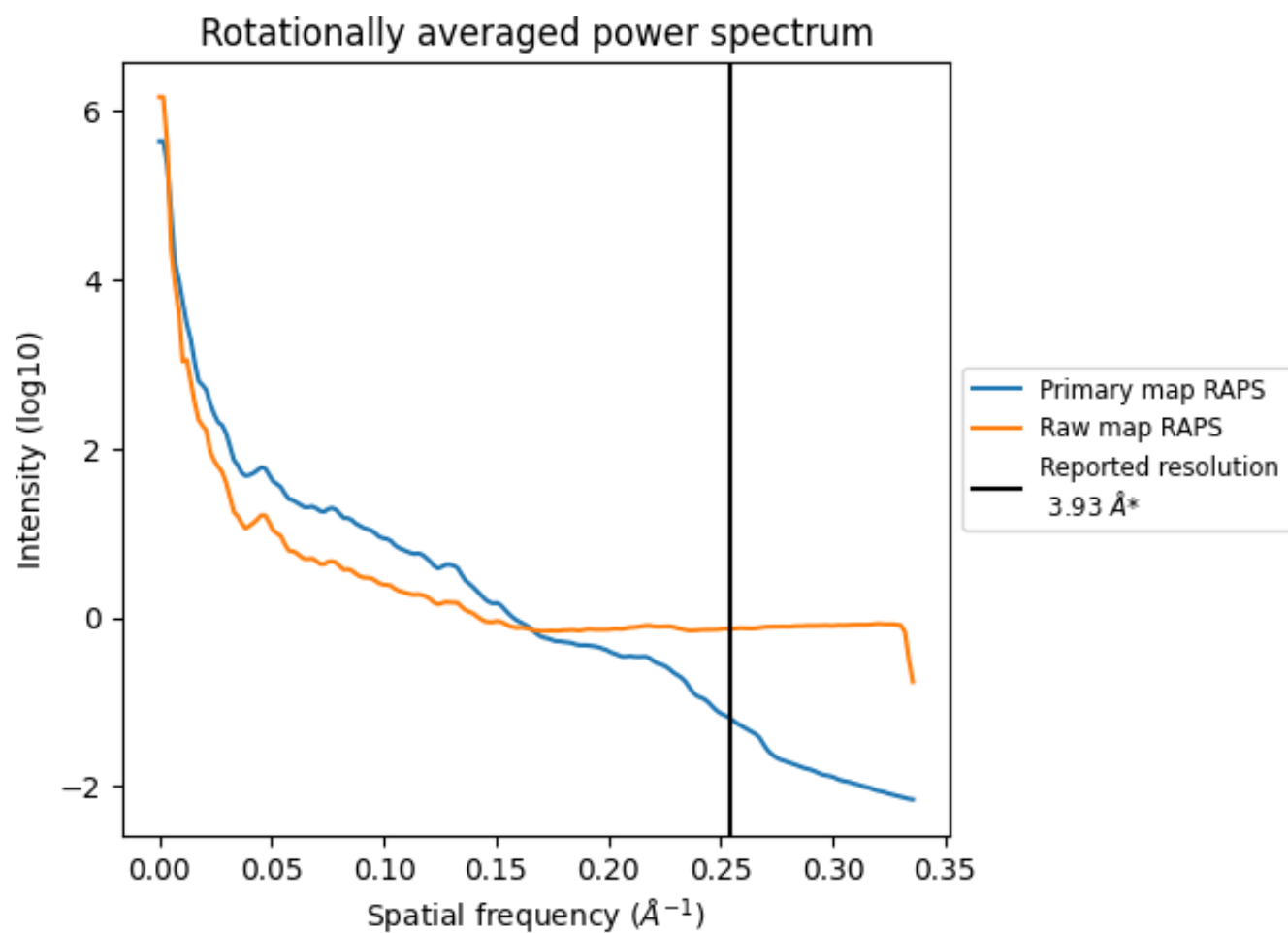
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 130785 nm^3 ; this corresponds to an approximate mass of 118142 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 ⓘ

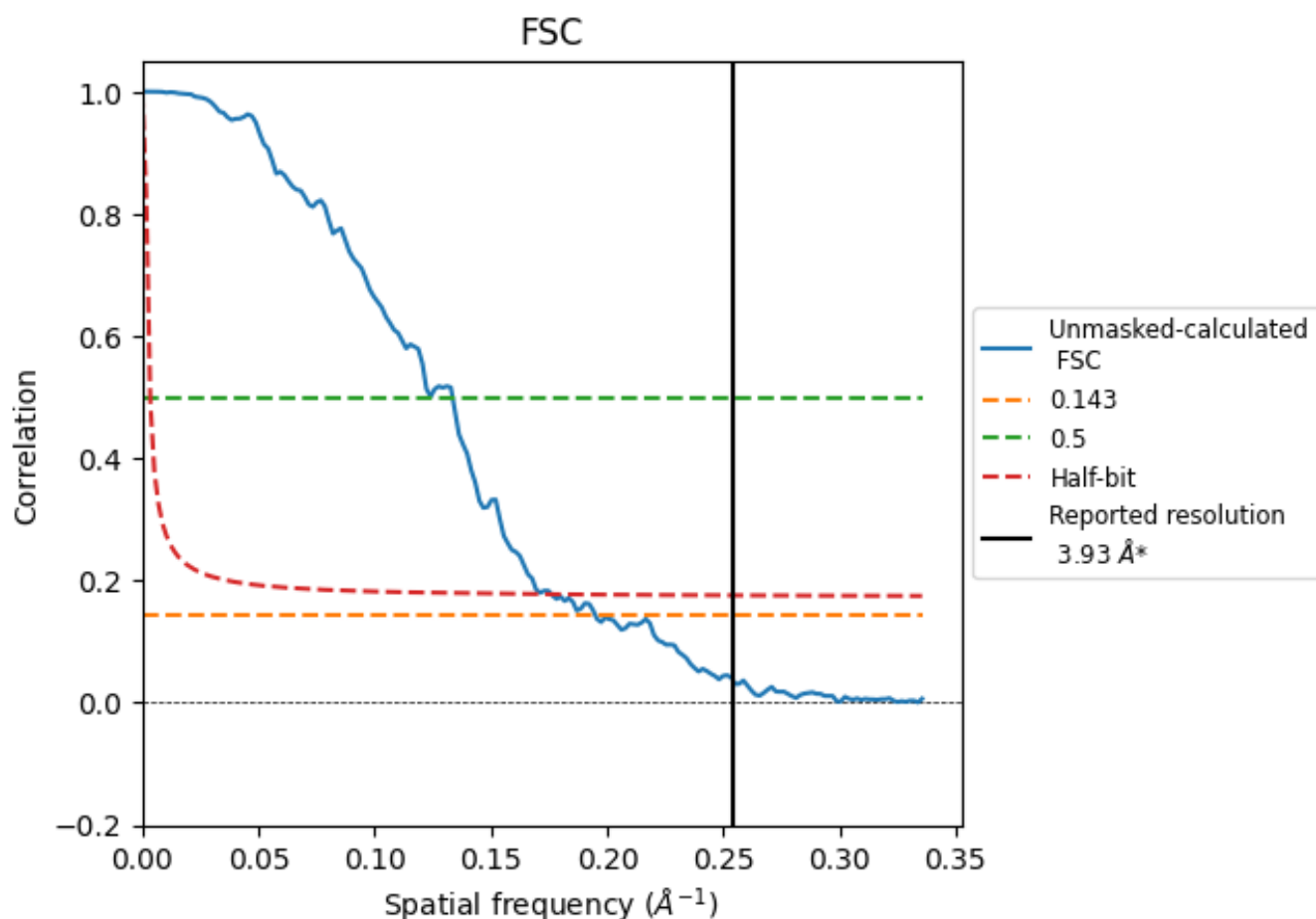


*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

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 0.254 Å⁻¹

8.2 Resolution estimates [i](#)

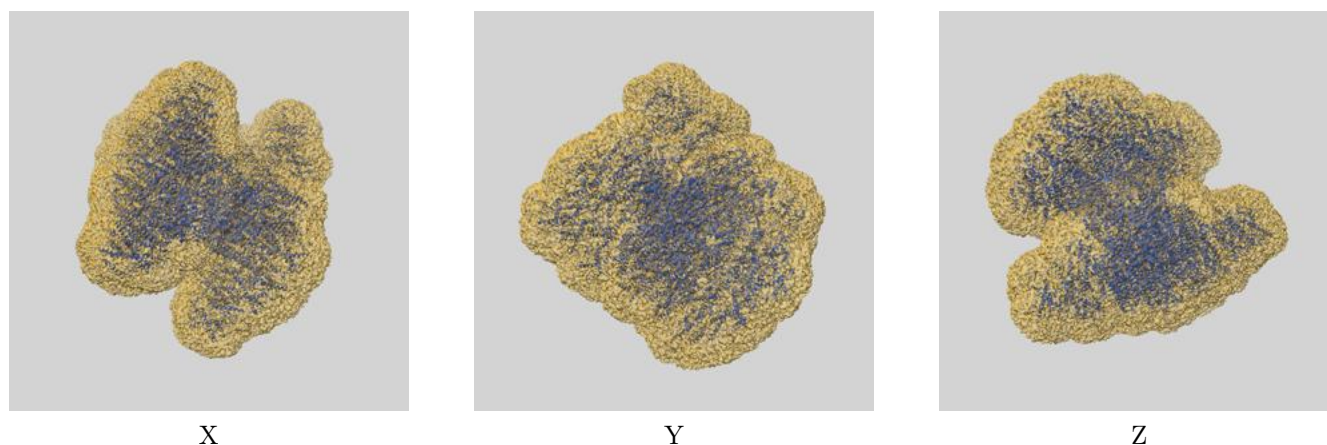
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.93	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.13	7.49	5.68

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.13 differs from the reported value 3.93 by more than 10 %

9 Map-model fit [i](#)

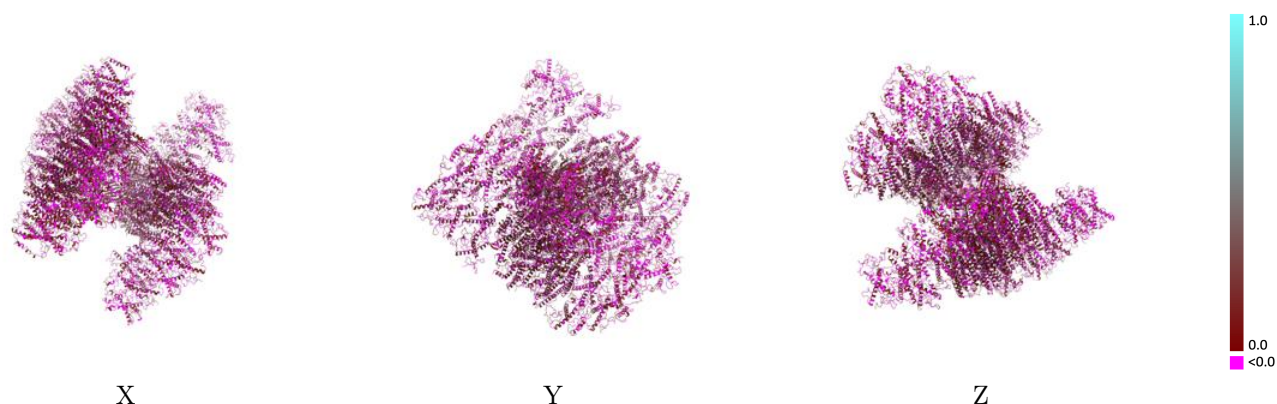
This section contains information regarding the fit between EMDB map EMD-81447 and PDB model 27UT. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



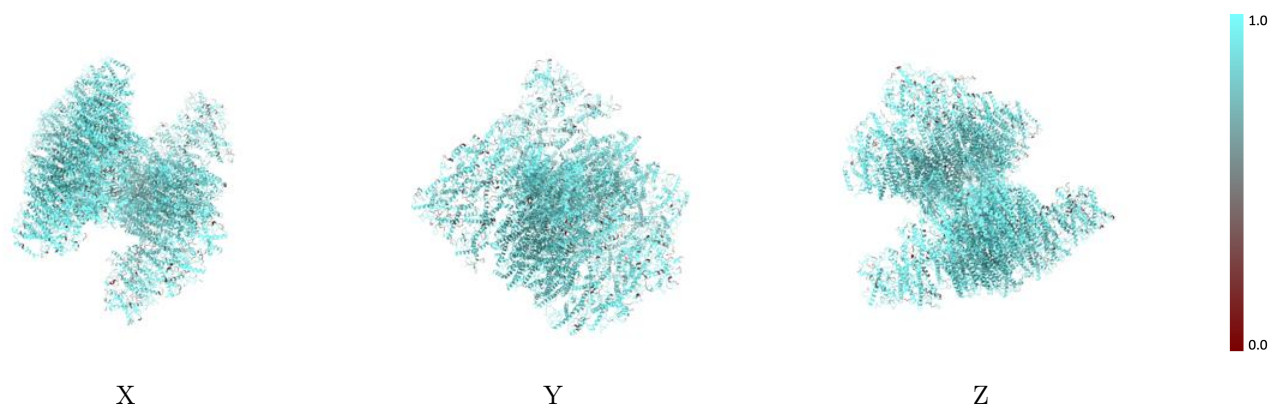
The images above show the 3D surface view of the map at the recommended contour level 0.0008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



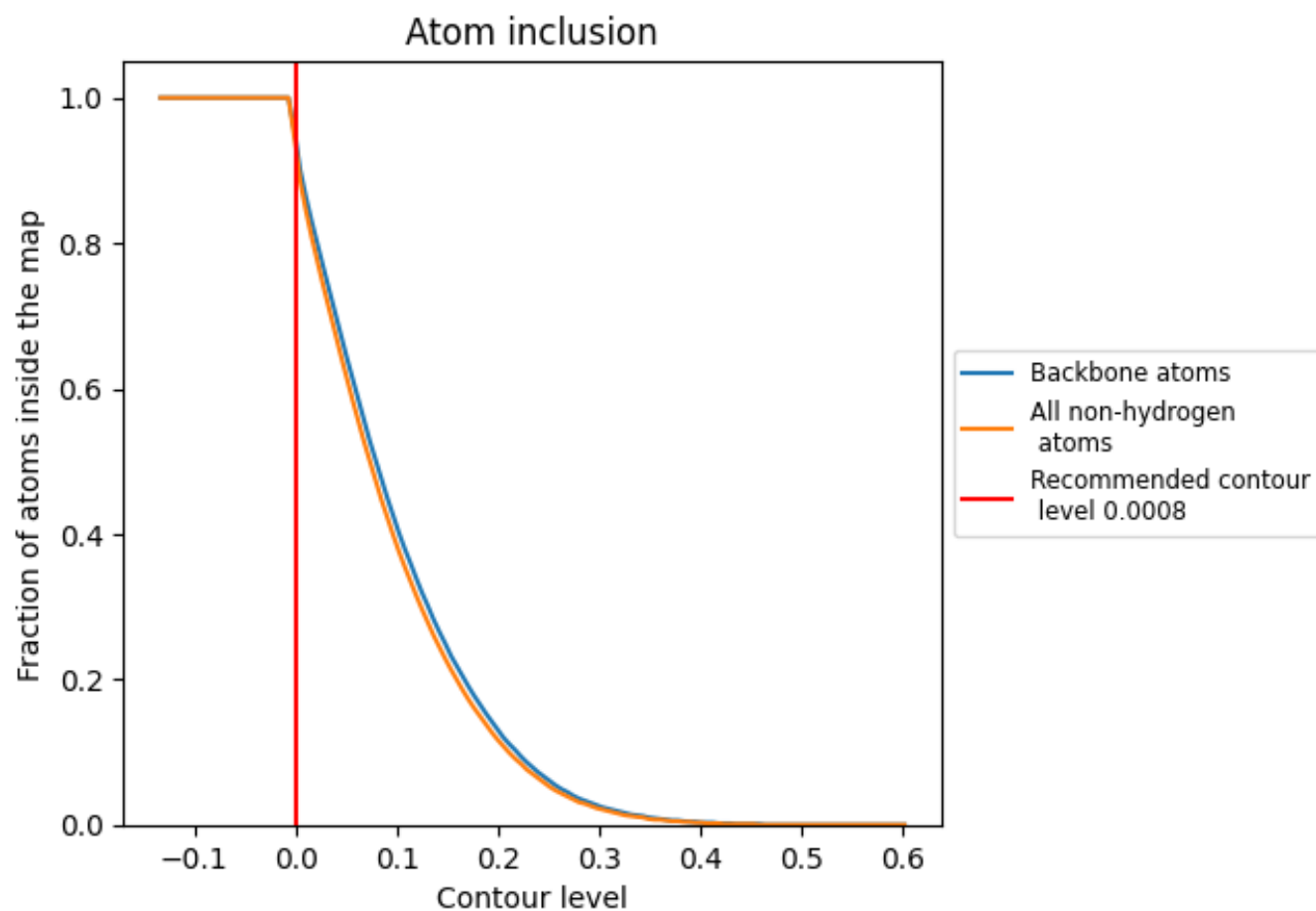
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0008).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.0008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9300	 0.0900
00	 0.8770	 0.0450
01	 0.8970	 0.0360
02	 0.8130	 -0.0060
03	 0.8310	 0.0410
04	 0.8180	 0.0340
05	 0.8330	 0.0410
06	 0.8560	 0.0360
07	 0.7850	 0.0190
08	 0.8300	 0.0480
09	 0.8770	 0.0680
10	 0.8950	 0.0750
11	 0.8970	 0.0430
12	 0.8690	 0.0430
13	 0.8550	 0.0480
14	 0.8790	 0.0510
15	 0.8700	 0.0220
16	 0.8440	 0.0060
17	 0.8370	 0.0160
18	 0.8040	 0.0100
19	 0.9220	 0.0470
1A	 0.9500	 0.0960
1B	 0.9570	 0.1030
1C	 0.9520	 0.0900
1D	 0.9210	 0.0720
1E	 0.9740	 0.1370
1F	 0.9890	 0.1150
1G	 0.8750	 0.0530
1H	 0.8310	 0.0540
1I	 0.9650	 0.1570
1J	 0.9470	 0.1420
1K	 0.9270	 0.1250
1L	 0.8670	 0.0950
1M	 0.8700	 0.1280
1N	 0.8640	 0.0350



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Chain	Atom inclusion	Q-score
1O	 0.9840	 0.1010
1P	 0.9730	 0.1190
1R	 0.8470	 0.0470
1S	 0.8690	 0.0410
1T	 0.8970	 0.1130
1U	 1.0000	 0.1330
1V	 0.8690	 0.0450
1W	 0.9390	 0.1340
1X	 0.9440	 0.1080
1Y	 0.8510	 0.0670
1Z	 0.8940	 0.1090
1a	 0.9680	 0.0970
1b	 0.9840	 0.1360
1c	 0.9790	 0.1410
1d	 0.9820	 0.1230
1e	 1.0000	 0.1760
1f	 0.9800	 0.1030
1g	 0.9010	 0.0570
1h	 0.9900	 0.1280
1i	 0.9830	 0.1680
1j	 1.0000	 0.1740
1k	 0.9740	 0.1370
1l	 0.9380	 0.1250
1m	 0.8620	 0.0960
1n	 0.9200	 0.0770
1o	 0.9800	 0.1270
1p	 0.9980	 0.1560
1r	 0.8780	 0.0690
1s	 0.9380	 0.1000
1t	 0.9500	 0.1510
1u	 1.0000	 0.1640
1v	 0.9050	 0.0710
1w	 0.9440	 0.1410
1x	 0.9900	 0.1970
1y	 0.9430	 0.1290
1z	 0.9450	 0.1630
2A	 0.9870	 0.1090
2B	 0.9890	 0.1330
2C	 0.9910	 0.1530
2D	 0.9870	 0.1210
2E	 0.9970	 0.1640
2F	 1.0000	 0.1530

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Chain	Atom inclusion	Q-score
2G	 0.9030	 0.0810
2H	 0.9730	 0.1160
2I	 1.0000	 0.1750
2J	 0.9880	 0.1630
2K	 0.9790	 0.1510
2L	 0.9340	 0.1140
2M	 0.8760	 0.1100
2N	 0.9110	 0.0760
2O	 0.9960	 0.1340
2P	 0.9980	 0.1560
2R	 0.8950	 0.0520
2S	 0.9010	 0.0960
2T	 0.9330	 0.1480
2U	 1.0000	 0.1940
2V	 0.9650	 0.1040
2W	 0.9890	 0.1480
2X	 0.9590	 0.1790
2Y	 0.9660	 0.1660
2Z	 0.9390	 0.1270
2a	 0.9990	 0.1290
2b	 0.9890	 0.1130
2c	 0.9910	 0.1200
2d	 0.9960	 0.0990
2e	 0.9760	 0.1130
2f	 1.0000	 0.1180
2g	 0.9030	 0.0660
2h	 0.9640	 0.0760
2i	 1.0000	 0.1680
2j	 0.9590	 0.0890
2k	 0.9480	 0.1230
2l	 0.9770	 0.1210
2m	 0.8860	 0.1400
2n	 0.9030	 0.0620
2o	 0.9980	 0.1080
2p	 0.9960	 0.0900
2r	 0.8680	 0.0490
2s	 0.9120	 0.0720
2t	 0.9880	 0.1490
2u	 1.0000	 0.1430
2v	 0.9260	 0.0800
2w	 0.9950	 0.1580
2x	 0.9420	 0.1120

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Chain	Atom inclusion	Q-score
2y	 0.9370	 0.0940
2z	 0.9320	 0.1020