



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 06:40 AM UTC

PDB ID : 9FLW / pdb_00009flw
EMDB ID : EMD-50541
Title : CryoEM structure of the fragment-6 (3571-4078) in the grappling hook protein A (GhpA) in the bacterium Aureispira sp. CCB-QB1
Authors : Lien, Y.-W.; Amendola, D.; Lee, K.S.; Bartlau, N.; Xu, J.; Furusawa, G.; Polz, M.F.; Stocker, R.; Weiss, G.L.; Pilhofer, M.
Deposited on : 2024-06-05
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

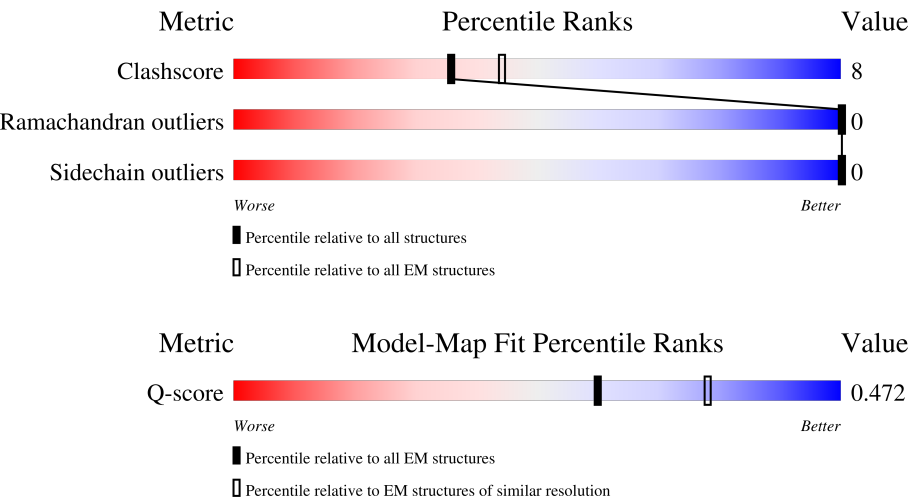
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.70 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.



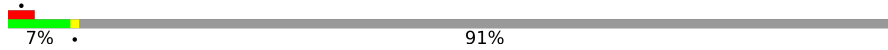
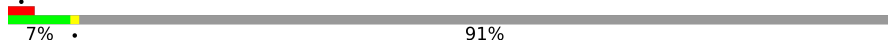
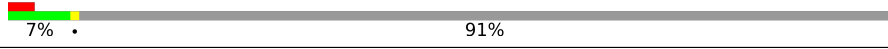
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11569 (3.20 - 4.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	5898	7% . 91%
1	B	5898	7% . 91%
1	C	5898	7% . 91%
1	D	5898	7% . 91%

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Mol	Chain	Length	Quality of chain
1	E	5898	 7% 91%
1	F	5898	 7% 91%
1	G	5898	 7% 91%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 26180 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 The grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	508	Total	C	N	O	S	0	0
			3740	2354	592	776	18		
1	B	508	Total	C	N	O	S	0	0
			3740	2354	592	776	18		
1	C	508	Total	C	N	O	S	0	0
			3740	2354	592	776	18		
1	D	508	Total	C	N	O	S	0	0
			3740	2354	592	776	18		
1	E	508	Total	C	N	O	S	0	0
			3740	2354	592	776	18		
1	F	508	Total	C	N	O	S	0	0
			3740	2354	592	776	18		
1	G	508	Total	C	N	O	S	0	0
			3740	2354	592	776	18		

















[illegible]

- Molecule 1: The grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1

Chain C: 7% 91%

[illegible]



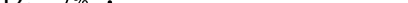






[illegible]

- Molecule 1: The grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1

Chain D:  7% 91%

VAL	ASP	GLY	THR	ASP	HIS	THR	HIS	THR	THR	ASP	ILE	THR	ASP	SER	ILE	ALA	GLY	THR	GLY	THR	VAL	TYR	MET
ASP	ILE	PRO	ILE	VAL	ASP	PRO	VAL	ILE	PRO	ILE	ASP	PRO	THR	THR	ASP	GLY	THR	THR	THR	THR	ARG	GLN	
SER	ILE	ASP	THR	SER	ALA	VAL	ASP	GLY	ASP	THR	VAL	GLY	LEU	ILE	THR	ASN	GLY	THR	THR	THR	ILE	ARG	
ASN	THR	THR	VAL	THR	LEU	ILE	ALA	ASN	ASN	THR	THR	THR	THR	GLY	THR	THR	CYS	GLY	THR	THR	VAL	HIS	
ALA	VAL	VAL	ASP	ALA	THR	ASP	THR	ASP	THR	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	PRO	SER	
PRO	ILE	PRO	ILE	ALA	VAL	ASP	ALA	ILE	ILE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	PHE	
ALA	PRO	PRO	PHE	THR	THR	PHE	THR	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
PHE	ASP	ALA	ASP	PHE	THR	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
GLY	GLY	ASN	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
PHE	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
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VAL	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR							



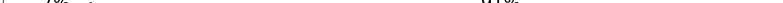






[illegible]

- Molecule 1: The grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1

Chain E:  7% 91%

[illegible]









[illegible]

- Molecule 1: The grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1

Chain F: 7% 91%

[illegible]









[illegible]

- Molecule 1: The grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1

[illegible]









[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C7	Depositor
Number of particles used	18696	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.214	Depositor
Minimum map value	-2.748	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.115	Depositor
Recommended contour level	1	Depositor
Map size (Å)	319.50003, 319.50003, 319.50003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.98	0/3835	1.34	59/5308 (1.1%)
1	B	0.98	0/3835	1.34	60/5308 (1.1%)
1	C	0.98	0/3835	1.34	62/5308 (1.2%)
1	D	0.98	0/3835	1.34	60/5308 (1.1%)
1	E	0.98	0/3835	1.34	59/5308 (1.1%)
1	F	0.98	0/3835	1.34	60/5308 (1.1%)
1	G	0.98	0/3835	1.34	60/5308 (1.1%)
All	All	0.98	0/26845	1.34	420/37156 (1.1%)

There are no bond length outliers.

All (420) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	3946	GLY	CA-C-N	8.49	129.32	119.47
1	F	3946	GLY	C-N-CA	8.49	129.32	119.47
1	B	3946	GLY	CA-C-N	8.47	129.30	119.47
1	B	3946	GLY	C-N-CA	8.47	129.30	119.47
1	E	3946	GLY	CA-C-N	8.47	129.29	119.47
1	E	3946	GLY	C-N-CA	8.47	129.29	119.47
1	A	3946	GLY	CA-C-N	8.46	129.28	119.47
1	A	3946	GLY	C-N-CA	8.46	129.28	119.47
1	G	3946	GLY	CA-C-N	8.46	129.28	119.47
1	G	3946	GLY	C-N-CA	8.46	129.28	119.47
1	C	3946	GLY	CA-C-N	8.45	129.27	119.47
1	C	3946	GLY	C-N-CA	8.45	129.27	119.47
1	D	3946	GLY	CA-C-N	8.41	129.23	119.47
1	D	3946	GLY	C-N-CA	8.41	129.23	119.47
1	D	3685	GLY	CA-C-N	8.39	128.42	119.78
1	D	3685	GLY	C-N-CA	8.39	128.42	119.78
1	B	3685	GLY	CA-C-N	8.38	128.41	119.78
1	B	3685	GLY	C-N-CA	8.38	128.41	119.78
1	G	3685	GLY	CA-C-N	8.37	128.41	119.78
1	G	3685	GLY	C-N-CA	8.37	128.41	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3685	GLY	CA-C-N	8.35	128.38	119.78
1	A	3685	GLY	C-N-CA	8.35	128.38	119.78
1	C	3685	GLY	CA-C-N	8.34	128.37	119.78
1	C	3685	GLY	C-N-CA	8.34	128.37	119.78
1	E	3685	GLY	CA-C-N	8.33	128.36	119.78
1	E	3685	GLY	C-N-CA	8.33	128.36	119.78
1	F	3685	GLY	CA-C-N	8.30	128.33	119.78
1	F	3685	GLY	C-N-CA	8.30	128.33	119.78
1	C	3767	GLY	CA-C-N	7.77	127.48	119.56
1	C	3767	GLY	C-N-CA	7.77	127.48	119.56
1	G	3767	GLY	CA-C-N	7.76	127.47	119.56
1	G	3767	GLY	C-N-CA	7.76	127.47	119.56
1	A	3767	GLY	CA-C-N	7.74	127.45	119.56
1	A	3767	GLY	C-N-CA	7.74	127.45	119.56
1	F	3767	GLY	CA-C-N	7.73	127.45	119.56
1	F	3767	GLY	C-N-CA	7.73	127.45	119.56
1	D	3767	GLY	CA-C-N	7.72	127.44	119.56
1	D	3767	GLY	C-N-CA	7.72	127.44	119.56
1	B	3767	GLY	CA-C-N	7.72	127.43	119.56
1	B	3767	GLY	C-N-CA	7.72	127.43	119.56
1	E	3767	GLY	CA-C-N	7.71	127.42	119.56
1	E	3767	GLY	C-N-CA	7.71	127.42	119.56
1	G	4045	LEU	CA-C-N	7.26	127.26	119.78
1	G	4045	LEU	C-N-CA	7.26	127.26	119.78
1	E	4045	LEU	CA-C-N	7.26	127.26	119.78
1	E	4045	LEU	C-N-CA	7.26	127.26	119.78
1	D	4045	LEU	CA-C-N	7.25	127.24	119.78
1	D	4045	LEU	C-N-CA	7.25	127.24	119.78
1	A	4045	LEU	CA-C-N	7.24	127.24	119.78
1	A	4045	LEU	C-N-CA	7.24	127.24	119.78
1	B	4045	LEU	CA-C-N	7.24	127.24	119.78
1	B	4045	LEU	C-N-CA	7.24	127.24	119.78
1	C	4045	LEU	CA-C-N	7.24	127.24	119.78
1	C	4045	LEU	C-N-CA	7.24	127.24	119.78
1	F	4045	LEU	CA-C-N	7.22	127.22	119.78
1	F	4045	LEU	C-N-CA	7.22	127.22	119.78
1	G	3662	PHE	CA-CB-CG	7.07	120.87	113.80
1	C	3662	PHE	CA-CB-CG	7.06	120.86	113.80
1	A	3662	PHE	CA-CB-CG	7.05	120.85	113.80
1	B	3662	PHE	CA-CB-CG	7.05	120.85	113.80
1	F	3662	PHE	CA-CB-CG	7.04	120.84	113.80
1	E	3662	PHE	CA-CB-CG	7.04	120.84	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	3662	PHE	CA-CB-CG	7.04	120.84	113.80
1	F	3655	THR	CA-C-N	7.00	126.98	119.78
1	F	3655	THR	C-N-CA	7.00	126.98	119.78
1	C	3661	ASN	CA-C-N	-6.99	110.19	123.32
1	C	3661	ASN	C-N-CA	-6.99	110.19	123.32
1	B	3661	ASN	CA-C-N	-6.98	110.20	123.32
1	B	3661	ASN	C-N-CA	-6.98	110.20	123.32
1	G	3661	ASN	CA-C-N	-6.98	110.20	123.32
1	G	3661	ASN	C-N-CA	-6.98	110.20	123.32
1	A	3661	ASN	CA-C-N	-6.97	110.21	123.32
1	A	3661	ASN	C-N-CA	-6.97	110.21	123.32
1	D	3661	ASN	CA-C-N	-6.97	110.21	123.32
1	D	3661	ASN	C-N-CA	-6.97	110.21	123.32
1	F	3661	ASN	CA-C-N	-6.97	110.22	123.32
1	F	3661	ASN	C-N-CA	-6.97	110.22	123.32
1	G	3655	THR	CA-C-N	6.96	126.95	119.78
1	G	3655	THR	C-N-CA	6.96	126.95	119.78
1	E	3661	ASN	CA-C-N	-6.96	110.24	123.32
1	E	3661	ASN	C-N-CA	-6.96	110.24	123.32
1	A	3655	THR	CA-C-N	6.95	126.94	119.78
1	A	3655	THR	C-N-CA	6.95	126.94	119.78
1	B	3655	THR	CA-C-N	6.95	126.94	119.78
1	B	3655	THR	C-N-CA	6.95	126.94	119.78
1	D	3655	THR	CA-C-N	6.95	126.93	119.78
1	D	3655	THR	C-N-CA	6.95	126.93	119.78
1	D	3695	ASN	CA-C-N	6.94	127.34	119.92
1	D	3695	ASN	C-N-CA	6.94	127.34	119.92
1	E	3655	THR	CA-C-N	6.93	126.92	119.78
1	E	3655	THR	C-N-CA	6.93	126.92	119.78
1	F	3695	ASN	CA-C-N	6.93	127.33	119.92
1	F	3695	ASN	C-N-CA	6.93	127.33	119.92
1	C	3695	ASN	CA-C-N	6.90	127.31	119.92
1	C	3695	ASN	C-N-CA	6.90	127.31	119.92
1	A	3695	ASN	CA-C-N	6.90	127.30	119.92
1	A	3695	ASN	C-N-CA	6.90	127.30	119.92
1	C	3655	THR	CA-C-N	6.89	126.88	119.78
1	C	3655	THR	C-N-CA	6.89	126.88	119.78
1	B	3695	ASN	CA-C-N	6.88	127.28	119.92
1	B	3695	ASN	C-N-CA	6.88	127.28	119.92
1	E	3695	ASN	CA-C-N	6.88	127.28	119.92
1	E	3695	ASN	C-N-CA	6.88	127.28	119.92
1	G	3695	ASN	CA-C-N	6.87	127.27	119.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	3695	ASN	C-N-CA	6.87	127.27	119.92
1	G	3807	TYR	CA-CB-CG	6.84	126.22	113.90
1	E	3807	TYR	CA-CB-CG	6.83	126.19	113.90
1	C	3807	TYR	CA-CB-CG	6.82	126.18	113.90
1	A	3807	TYR	CA-CB-CG	6.82	126.17	113.90
1	D	3807	TYR	CA-CB-CG	6.81	126.15	113.90
1	B	3807	TYR	CA-CB-CG	6.79	126.13	113.90
1	F	3807	TYR	CA-CB-CG	6.79	126.12	113.90
1	D	3778	THR	CA-C-N	6.56	126.47	119.85
1	D	3778	THR	C-N-CA	6.56	126.47	119.85
1	F	3778	THR	CA-C-N	6.56	126.47	119.85
1	F	3778	THR	C-N-CA	6.56	126.47	119.85
1	A	3778	THR	CA-C-N	6.55	126.47	119.85
1	A	3778	THR	C-N-CA	6.55	126.47	119.85
1	E	3778	THR	CA-C-N	6.55	126.47	119.85
1	E	3778	THR	C-N-CA	6.55	126.47	119.85
1	G	3778	THR	CA-C-N	6.55	126.47	119.85
1	G	3778	THR	C-N-CA	6.55	126.47	119.85
1	B	3778	THR	CA-C-N	6.55	126.46	119.85
1	B	3778	THR	C-N-CA	6.55	126.46	119.85
1	C	3778	THR	CA-C-N	6.55	126.46	119.85
1	C	3778	THR	C-N-CA	6.55	126.46	119.85
1	D	3966	ASN	N-CA-C	-6.37	105.37	113.02
1	C	3966	ASN	N-CA-C	-6.36	105.39	113.02
1	E	3966	ASN	N-CA-C	-6.35	105.40	113.02
1	A	3966	ASN	N-CA-C	-6.34	105.41	113.02
1	G	3966	ASN	N-CA-C	-6.34	105.42	113.02
1	B	3966	ASN	N-CA-C	-6.33	105.43	113.02
1	F	3966	ASN	N-CA-C	-6.32	105.44	113.02
1	A	3580	GLY	CA-C-N	6.29	126.25	119.78
1	A	3580	GLY	C-N-CA	6.29	126.25	119.78
1	G	3580	GLY	CA-C-N	6.28	126.25	119.78
1	G	3580	GLY	C-N-CA	6.28	126.25	119.78
1	C	3580	GLY	CA-C-N	6.28	126.25	119.78
1	C	3580	GLY	C-N-CA	6.28	126.25	119.78
1	D	3580	GLY	CA-C-N	6.27	126.24	119.78
1	D	3580	GLY	C-N-CA	6.27	126.24	119.78
1	B	3580	GLY	CA-C-N	6.26	126.23	119.78
1	B	3580	GLY	C-N-CA	6.26	126.23	119.78
1	E	3651	PRO	CB-CA-C	-6.26	103.22	111.23
1	E	3580	GLY	CA-C-N	6.26	126.23	119.78
1	E	3580	GLY	C-N-CA	6.26	126.23	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	3651	PRO	CB-CA-C	-6.25	103.22	111.23
1	F	3580	GLY	CA-C-N	6.25	126.22	119.78
1	F	3580	GLY	C-N-CA	6.25	126.22	119.78
1	F	3651	PRO	CB-CA-C	-6.24	103.24	111.23
1	A	3651	PRO	CB-CA-C	-6.24	103.24	111.23
1	C	3651	PRO	CB-CA-C	-6.24	103.24	111.23
1	G	3651	PRO	CB-CA-C	-6.24	103.24	111.23
1	D	3651	PRO	CB-CA-C	-6.23	103.26	111.23
1	B	3735	PRO	CA-C-N	6.21	126.18	120.03
1	B	3735	PRO	C-N-CA	6.21	126.18	120.03
1	G	3735	PRO	CA-C-N	6.20	126.17	120.03
1	G	3735	PRO	C-N-CA	6.20	126.17	120.03
1	F	3735	PRO	CA-C-N	6.19	126.16	120.03
1	F	3735	PRO	C-N-CA	6.19	126.16	120.03
1	D	3735	PRO	CA-C-N	6.17	126.14	120.03
1	D	3735	PRO	C-N-CA	6.17	126.14	120.03
1	A	3735	PRO	CA-C-N	6.17	126.13	120.03
1	A	3735	PRO	C-N-CA	6.17	126.13	120.03
1	C	3735	PRO	CA-C-N	6.15	126.12	120.03
1	C	3735	PRO	C-N-CA	6.15	126.12	120.03
1	E	3735	PRO	CA-C-N	6.14	126.11	120.03
1	E	3735	PRO	C-N-CA	6.14	126.11	120.03
1	F	3794	ILE	CA-C-N	6.13	126.09	119.78
1	F	3794	ILE	C-N-CA	6.13	126.09	119.78
1	E	3794	ILE	CA-C-N	6.12	126.08	119.78
1	E	3794	ILE	C-N-CA	6.12	126.08	119.78
1	B	3794	ILE	CA-C-N	6.11	126.08	119.78
1	B	3794	ILE	C-N-CA	6.11	126.08	119.78
1	G	3794	ILE	CA-C-N	6.11	126.08	119.78
1	G	3794	ILE	C-N-CA	6.11	126.08	119.78
1	A	3794	ILE	CA-C-N	6.11	126.08	119.78
1	A	3794	ILE	C-N-CA	6.11	126.08	119.78
1	D	3794	ILE	CA-C-N	6.11	126.07	119.78
1	D	3794	ILE	C-N-CA	6.11	126.07	119.78
1	C	3794	ILE	CA-C-N	6.10	126.07	119.78
1	C	3794	ILE	C-N-CA	6.10	126.07	119.78
1	G	4068	LEU	N-CA-C	-5.94	102.57	109.93
1	C	4068	LEU	N-CA-C	-5.92	102.59	109.93
1	E	4068	LEU	N-CA-C	-5.91	102.60	109.93
1	F	4068	LEU	N-CA-C	-5.91	102.61	109.93
1	A	4068	LEU	N-CA-C	-5.90	102.61	109.93
1	D	4068	LEU	N-CA-C	-5.88	102.64	109.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	3915	ILE	CA-C-N	5.88	125.83	119.78
1	G	3915	ILE	C-N-CA	5.88	125.83	119.78
1	D	3652	THR	CA-C-N	5.87	125.83	119.78
1	D	3652	THR	C-N-CA	5.87	125.83	119.78
1	B	4068	LEU	N-CA-C	-5.87	102.65	109.93
1	G	3652	THR	CA-C-N	5.87	125.82	119.78
1	G	3652	THR	C-N-CA	5.87	125.82	119.78
1	A	3652	THR	CA-C-N	5.85	125.81	119.78
1	A	3652	THR	C-N-CA	5.85	125.81	119.78
1	G	3917	ASN	CA-C-N	5.85	125.80	119.78
1	G	3917	ASN	C-N-CA	5.85	125.80	119.78
1	E	3652	THR	CA-C-N	5.84	125.79	119.78
1	E	3652	THR	C-N-CA	5.84	125.79	119.78
1	F	3652	THR	CA-C-N	5.84	125.79	119.78
1	F	3652	THR	C-N-CA	5.84	125.79	119.78
1	C	3652	THR	CA-C-N	5.83	125.79	119.78
1	C	3652	THR	C-N-CA	5.83	125.79	119.78
1	D	3915	ILE	CA-C-N	5.83	125.78	119.78
1	D	3915	ILE	C-N-CA	5.83	125.78	119.78
1	A	3915	ILE	CA-C-N	5.83	125.78	119.78
1	A	3915	ILE	C-N-CA	5.83	125.78	119.78
1	B	3917	ASN	CA-C-N	5.82	125.78	119.78
1	B	3917	ASN	C-N-CA	5.82	125.78	119.78
1	F	3917	ASN	CA-C-N	5.82	125.78	119.78
1	F	3917	ASN	C-N-CA	5.82	125.78	119.78
1	B	3915	ILE	CA-C-N	5.82	125.77	119.78
1	B	3915	ILE	C-N-CA	5.82	125.77	119.78
1	B	3652	THR	CA-C-N	5.81	125.77	119.78
1	B	3652	THR	C-N-CA	5.81	125.77	119.78
1	F	3915	ILE	CA-C-N	5.81	125.77	119.78
1	F	3915	ILE	C-N-CA	5.81	125.77	119.78
1	C	3915	ILE	CA-C-N	5.81	125.76	119.78
1	C	3915	ILE	C-N-CA	5.81	125.76	119.78
1	A	3917	ASN	CA-C-N	5.81	125.76	119.78
1	A	3917	ASN	C-N-CA	5.81	125.76	119.78
1	C	3917	ASN	CA-C-N	5.81	125.76	119.78
1	C	3917	ASN	C-N-CA	5.81	125.76	119.78
1	B	3877	THR	CA-C-N	5.80	125.78	120.03
1	B	3877	THR	C-N-CA	5.80	125.78	120.03
1	D	3877	THR	CA-C-N	5.80	125.77	120.03
1	D	3877	THR	C-N-CA	5.80	125.77	120.03
1	E	3915	ILE	CA-C-N	5.80	125.75	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	3915	ILE	C-N-CA	5.80	125.75	119.78
1	E	3917	ASN	CA-C-N	5.79	125.75	119.78
1	E	3917	ASN	C-N-CA	5.79	125.75	119.78
1	C	3631	LEU	N-CA-C	5.79	118.33	108.90
1	G	3877	THR	CA-C-N	5.79	125.76	120.03
1	G	3877	THR	C-N-CA	5.79	125.76	120.03
1	A	3877	THR	CA-C-N	5.79	125.76	120.03
1	A	3877	THR	C-N-CA	5.79	125.76	120.03
1	C	3877	THR	CA-C-N	5.78	125.75	120.03
1	C	3877	THR	C-N-CA	5.78	125.75	120.03
1	E	3877	THR	CA-C-N	5.78	125.75	120.03
1	E	3877	THR	C-N-CA	5.78	125.75	120.03
1	F	3631	LEU	N-CA-C	5.78	118.32	108.90
1	D	3631	LEU	N-CA-C	5.77	118.30	108.90
1	G	3631	LEU	N-CA-C	5.77	118.30	108.90
1	D	3917	ASN	CA-C-N	5.76	125.72	119.78
1	D	3917	ASN	C-N-CA	5.76	125.72	119.78
1	E	3631	LEU	N-CA-C	5.76	118.30	108.90
1	F	3877	THR	CA-C-N	5.76	125.74	120.03
1	F	3877	THR	C-N-CA	5.76	125.74	120.03
1	A	3631	LEU	N-CA-C	5.76	118.29	108.90
1	B	3631	LEU	N-CA-C	5.75	118.28	108.90
1	C	3829	ASN	CA-C-N	5.75	125.72	120.03
1	C	3829	ASN	C-N-CA	5.75	125.72	120.03
1	D	3829	ASN	CA-C-N	5.75	125.72	120.03
1	D	3829	ASN	C-N-CA	5.75	125.72	120.03
1	B	3829	ASN	CA-C-N	5.71	125.69	120.03
1	B	3829	ASN	C-N-CA	5.71	125.69	120.03
1	A	3829	ASN	CA-C-N	5.70	125.68	120.03
1	A	3829	ASN	C-N-CA	5.70	125.68	120.03
1	E	3829	ASN	CA-C-N	5.70	125.67	120.03
1	E	3829	ASN	C-N-CA	5.70	125.67	120.03
1	D	4068	LEU	CA-C-N	5.69	125.60	119.85
1	D	4068	LEU	C-N-CA	5.69	125.60	119.85
1	G	3829	ASN	CA-C-N	5.69	125.67	120.03
1	G	3829	ASN	C-N-CA	5.69	125.67	120.03
1	F	3829	ASN	CA-C-N	5.69	125.66	120.03
1	F	3829	ASN	C-N-CA	5.69	125.66	120.03
1	A	4068	LEU	CA-C-N	5.67	125.58	119.85
1	A	4068	LEU	C-N-CA	5.67	125.58	119.85
1	E	3996	THR	CA-C-N	5.67	125.57	119.85
1	E	3996	THR	C-N-CA	5.67	125.57	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3996	THR	CA-C-N	5.67	125.57	119.85
1	A	3996	THR	C-N-CA	5.67	125.57	119.85
1	B	3996	THR	CA-C-N	5.66	125.57	119.85
1	B	3996	THR	C-N-CA	5.66	125.57	119.85
1	F	4068	LEU	CA-C-N	5.65	125.56	119.85
1	F	4068	LEU	C-N-CA	5.65	125.56	119.85
1	E	4068	LEU	CA-C-N	5.65	125.55	119.85
1	E	4068	LEU	C-N-CA	5.65	125.55	119.85
1	G	4068	LEU	CA-C-N	5.64	125.55	119.85
1	G	4068	LEU	C-N-CA	5.64	125.55	119.85
1	B	4068	LEU	CA-C-N	5.64	125.55	119.85
1	B	4068	LEU	C-N-CA	5.64	125.55	119.85
1	D	3996	THR	CA-C-N	5.64	125.55	119.85
1	D	3996	THR	C-N-CA	5.64	125.55	119.85
1	G	3996	THR	CA-C-N	5.63	125.54	119.85
1	G	3996	THR	C-N-CA	5.63	125.54	119.85
1	C	4068	LEU	CA-C-N	5.63	125.54	119.85
1	C	4068	LEU	C-N-CA	5.63	125.54	119.85
1	C	3996	THR	CA-C-N	5.63	125.53	119.85
1	C	3996	THR	C-N-CA	5.63	125.53	119.85
1	F	3996	THR	CA-C-N	5.62	125.52	119.85
1	F	3996	THR	C-N-CA	5.62	125.52	119.85
1	C	3735	PRO	N-CA-C	-5.53	103.95	110.70
1	C	3658	VAL	CA-C-N	5.53	125.50	120.03
1	C	3658	VAL	C-N-CA	5.53	125.50	120.03
1	F	3658	VAL	CA-C-N	5.53	125.50	120.03
1	F	3658	VAL	C-N-CA	5.53	125.50	120.03
1	E	3658	VAL	CA-C-N	5.52	125.50	120.03
1	E	3658	VAL	C-N-CA	5.52	125.50	120.03
1	D	3658	VAL	CA-C-N	5.51	125.48	120.03
1	D	3658	VAL	C-N-CA	5.51	125.48	120.03
1	A	3658	VAL	CA-C-N	5.50	125.48	120.03
1	A	3658	VAL	C-N-CA	5.50	125.48	120.03
1	E	3735	PRO	N-CA-C	-5.50	103.99	110.70
1	C	3912	THR	CA-C-N	5.50	125.80	119.92
1	C	3912	THR	C-N-CA	5.50	125.80	119.92
1	B	3658	VAL	CA-C-N	5.50	125.47	120.03
1	B	3658	VAL	C-N-CA	5.50	125.47	120.03
1	F	3872	ILE	CB-CA-C	-5.49	105.32	111.80
1	A	3735	PRO	N-CA-C	-5.49	104.00	110.70
1	B	3735	PRO	N-CA-C	-5.49	104.00	110.70
1	F	3735	PRO	N-CA-C	-5.49	104.00	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	3872	ILE	CB-CA-C	-5.49	105.33	111.80
1	F	3912	THR	CA-C-N	5.49	125.79	119.92
1	F	3912	THR	C-N-CA	5.49	125.79	119.92
1	D	3912	THR	CA-C-N	5.48	125.79	119.92
1	D	3912	THR	C-N-CA	5.48	125.79	119.92
1	D	3872	ILE	CB-CA-C	-5.48	105.33	111.80
1	G	3658	VAL	CA-C-N	5.48	125.45	120.03
1	G	3658	VAL	C-N-CA	5.48	125.45	120.03
1	G	3912	THR	CA-C-N	5.48	125.78	119.92
1	G	3912	THR	C-N-CA	5.48	125.78	119.92
1	D	3735	PRO	N-CA-C	-5.48	104.02	110.70
1	A	3872	ILE	CB-CA-C	-5.48	105.34	111.80
1	G	3991	TYR	CA-C-N	5.47	125.38	119.85
1	G	3991	TYR	C-N-CA	5.47	125.38	119.85
1	G	3735	PRO	N-CA-C	-5.47	104.03	110.70
1	C	3872	ILE	CB-CA-C	-5.46	105.35	111.80
1	G	3872	ILE	CB-CA-C	-5.46	105.36	111.80
1	A	3912	THR	CA-C-N	5.46	125.76	119.92
1	A	3912	THR	C-N-CA	5.46	125.76	119.92
1	C	3991	TYR	CA-C-N	5.45	125.36	119.85
1	C	3991	TYR	C-N-CA	5.45	125.36	119.85
1	B	3991	TYR	CA-C-N	5.45	125.35	119.85
1	B	3991	TYR	C-N-CA	5.45	125.35	119.85
1	B	3872	ILE	CB-CA-C	-5.45	105.37	111.80
1	B	3912	THR	CA-C-N	5.44	125.75	119.92
1	B	3912	THR	C-N-CA	5.44	125.75	119.92
1	E	3991	TYR	CA-C-N	5.44	125.35	119.85
1	E	3991	TYR	C-N-CA	5.44	125.35	119.85
1	A	3991	TYR	CA-C-N	5.44	125.34	119.85
1	A	3991	TYR	C-N-CA	5.44	125.34	119.85
1	B	3921	THR	CA-C-N	5.44	125.36	119.76
1	B	3921	THR	C-N-CA	5.44	125.36	119.76
1	D	3991	TYR	CA-C-N	5.43	125.34	119.85
1	D	3991	TYR	C-N-CA	5.43	125.34	119.85
1	E	3921	THR	CA-C-N	5.43	125.36	119.76
1	E	3921	THR	C-N-CA	5.43	125.36	119.76
1	F	3991	TYR	CA-C-N	5.43	125.33	119.85
1	F	3991	TYR	C-N-CA	5.43	125.33	119.85
1	E	3912	THR	CA-C-N	5.42	125.72	119.92
1	E	3912	THR	C-N-CA	5.42	125.72	119.92
1	C	3921	THR	CA-C-N	5.39	125.31	119.76
1	C	3921	THR	C-N-CA	5.39	125.31	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3921	THR	CA-C-N	5.38	125.30	119.76
1	A	3921	THR	C-N-CA	5.38	125.30	119.76
1	D	3921	THR	CA-C-N	5.37	125.30	119.76
1	D	3921	THR	C-N-CA	5.37	125.30	119.76
1	F	3921	THR	CA-C-N	5.37	125.29	119.76
1	F	3921	THR	C-N-CA	5.37	125.29	119.76
1	G	3921	THR	CA-C-N	5.37	125.29	119.76
1	G	3921	THR	C-N-CA	5.37	125.29	119.76
1	E	3910	ASN	CA-C-N	5.34	125.28	119.78
1	E	3910	ASN	C-N-CA	5.34	125.28	119.78
1	D	3812	ASP	CA-CB-CG	-5.33	107.27	112.60
1	F	3812	ASP	CA-CB-CG	-5.32	107.28	112.60
1	G	3812	ASP	CA-CB-CG	-5.32	107.28	112.60
1	A	3910	ASN	CA-C-N	5.31	125.25	119.78
1	A	3910	ASN	C-N-CA	5.31	125.25	119.78
1	C	3910	ASN	CA-C-N	5.31	125.25	119.78
1	C	3910	ASN	C-N-CA	5.31	125.25	119.78
1	G	3910	ASN	CA-C-N	5.31	125.25	119.78
1	G	3910	ASN	C-N-CA	5.31	125.25	119.78
1	B	3910	ASN	CA-C-N	5.30	125.24	119.78
1	B	3910	ASN	C-N-CA	5.30	125.24	119.78
1	A	3812	ASP	CA-CB-CG	-5.30	107.30	112.60
1	C	3812	ASP	CA-CB-CG	-5.30	107.30	112.60
1	B	3812	ASP	CA-CB-CG	-5.29	107.31	112.60
1	E	3812	ASP	CA-CB-CG	-5.29	107.31	112.60
1	E	3923	LEU	N-CA-C	5.29	117.85	109.50
1	F	3910	ASN	CA-C-N	5.29	125.22	119.78
1	F	3910	ASN	C-N-CA	5.29	125.22	119.78
1	B	3923	LEU	N-CA-C	5.28	117.84	109.50
1	A	3923	LEU	N-CA-C	5.27	117.83	109.50
1	C	3923	LEU	N-CA-C	5.27	117.83	109.50
1	D	3910	ASN	CA-C-N	5.27	125.21	119.78
1	D	3910	ASN	C-N-CA	5.27	125.21	119.78
1	F	3923	LEU	N-CA-C	5.27	117.82	109.50
1	D	3923	LEU	N-CA-C	5.27	117.82	109.50
1	G	3923	LEU	N-CA-C	5.26	117.82	109.50
1	B	3617	ASN	CA-C-N	5.09	124.99	119.85
1	B	3617	ASN	C-N-CA	5.09	124.99	119.85
1	E	3617	ASN	CA-C-N	5.07	124.97	119.85
1	E	3617	ASN	C-N-CA	5.07	124.97	119.85
1	A	3617	ASN	CA-C-N	5.06	124.96	119.85
1	A	3617	ASN	C-N-CA	5.06	124.96	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	3617	ASN	CA-C-N	5.06	124.96	119.85
1	G	3617	ASN	C-N-CA	5.06	124.96	119.85
1	B	4042	SER	N-CA-C	5.05	116.61	108.32
1	F	4042	SER	N-CA-C	5.04	116.59	108.32
1	E	4042	SER	N-CA-C	5.04	116.59	108.32
1	A	4042	SER	N-CA-C	5.04	116.59	108.32
1	D	3617	ASN	CA-C-N	5.04	124.94	119.85
1	D	3617	ASN	C-N-CA	5.04	124.94	119.85
1	C	3617	ASN	CA-C-N	5.04	124.94	119.85
1	C	3617	ASN	C-N-CA	5.04	124.94	119.85
1	F	3617	ASN	CA-C-N	5.04	124.94	119.85
1	F	3617	ASN	C-N-CA	5.04	124.94	119.85
1	C	4042	SER	N-CA-C	5.04	116.58	108.32
1	D	4042	SER	N-CA-C	5.03	116.58	108.32
1	G	4042	SER	N-CA-C	5.03	116.57	108.32
1	B	3891	VAL	N-CA-C	5.02	115.35	108.12
1	C	3959	ILE	CA-C-N	5.01	125.45	120.14
1	C	3959	ILE	C-N-CA	5.01	125.45	120.14
1	D	3891	VAL	N-CA-C	5.01	115.33	108.12
1	G	3891	VAL	N-CA-C	5.01	115.33	108.12
1	F	3891	VAL	N-CA-C	5.00	115.33	108.12
1	C	3891	VAL	N-CA-C	5.00	115.32	108.12

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	A	3740	0	3574	82	0
1	B	3740	0	3574	85	0
1	C	3740	0	3574	83	0
1	D	3740	0	3574	78	0
1	E	3740	0	3574	80	0
1	F	3740	0	3574	85	0
1	G	3740	0	3574	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	26180	0	25018	400	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 8.

All (400) 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:D:3853:THR:HG22	1:E:3874:THR:OG1	1.19	1.32
1:C:3853:THR:HG22	1:D:3874:THR:OG1	1.18	1.31
1:B:3853:THR:HG22	1:C:3874:THR:OG1	1.18	1.30
1:F:3853:THR:HG22	1:G:3874:THR:OG1	1.18	1.28
1:A:3874:THR:OG1	1:G:3853:THR:HG22	1.19	1.28
1:E:4030:LEU:HD11	1:E:4032:ASN:OD1	1.14	1.27
1:A:3853:THR:HG22	1:B:3874:THR:OG1	1.18	1.26
1:D:4030:LEU:HD11	1:D:4032:ASN:OD1	1.14	1.26
1:E:3853:THR:HG22	1:F:3874:THR:OG1	1.17	1.26
1:F:4030:LEU:HD11	1:F:4032:ASN:OD1	1.14	1.26
1:G:4030:LEU:HD11	1:G:4032:ASN:OD1	1.14	1.25
1:A:4030:LEU:HD11	1:A:4032:ASN:OD1	1.14	1.24
1:C:4030:LEU:HD11	1:C:4032:ASN:OD1	1.14	1.24
1:B:4030:LEU:HD11	1:B:4032:ASN:OD1	1.14	1.23
1:E:4030:LEU:HD11	1:E:4032:ASN:CG	1.69	1.18
1:G:4030:LEU:HD11	1:G:4032:ASN:CG	1.69	1.18
1:B:4030:LEU:HD11	1:B:4032:ASN:CG	1.69	1.17
1:D:4030:LEU:HD11	1:D:4032:ASN:CG	1.69	1.17
1:F:4030:LEU:HD11	1:F:4032:ASN:CG	1.69	1.17
1:C:4030:LEU:HD11	1:C:4032:ASN:CG	1.69	1.16
1:A:4030:LEU:HD11	1:A:4032:ASN:CG	1.69	1.16
1:E:3995:GLN:NE2	1:F:4020:PHE:CE1	2.14	1.16
1:F:3995:GLN:NE2	1:G:4020:PHE:CE1	2.15	1.14
1:A:3995:GLN:NE2	1:B:4020:PHE:CE1	2.15	1.14
1:B:3995:GLN:NE2	1:C:4020:PHE:CE1	2.15	1.13
1:D:3995:GLN:NE2	1:E:4020:PHE:CE1	2.18	1.11
1:C:3995:GLN:NE2	1:D:4020:PHE:CE1	2.17	1.11
1:A:4020:PHE:CE1	1:G:3995:GLN:NE2	2.16	1.11
1:A:3995:GLN:OE1	1:B:4020:PHE:CD1	2.05	1.09
1:B:3995:GLN:OE1	1:C:4020:PHE:CD1	2.05	1.09
1:E:3995:GLN:OE1	1:F:4020:PHE:CD1	2.05	1.09
1:E:4030:LEU:CD1	1:E:4032:ASN:OD1	2.01	1.09
1:F:4030:LEU:CD1	1:F:4032:ASN:OD1	2.01	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3995:GLN:OE1	1:G:4020:PHE:CD1	2.06	1.08
1:A:4030:LEU:CD1	1:A:4032:ASN:OD1	2.01	1.08
1:B:4030:LEU:CD1	1:B:4032:ASN:OD1	2.01	1.07
1:A:4020:PHE:CD1	1:G:3995:GLN:OE1	2.06	1.07
1:D:4030:LEU:CD1	1:D:4032:ASN:OD1	2.01	1.07
1:G:4030:LEU:CD1	1:G:4032:ASN:OD1	2.01	1.07
1:C:3995:GLN:OE1	1:D:4020:PHE:CD1	2.07	1.07
1:C:4030:LEU:CD1	1:C:4032:ASN:OD1	2.01	1.06
1:D:3995:GLN:OE1	1:E:4020:PHE:CD1	2.07	1.05
1:E:3995:GLN:NE2	1:F:4020:PHE:CD1	2.35	0.94
1:A:4030:LEU:CD1	1:A:4032:ASN:CG	2.41	0.94
1:C:4030:LEU:CD1	1:C:4032:ASN:CG	2.41	0.94
1:B:3995:GLN:NE2	1:C:4020:PHE:CD1	2.35	0.93
1:E:3853:THR:CG2	1:F:3874:THR:OG1	2.14	0.93
1:F:3995:GLN:NE2	1:G:4020:PHE:CD1	2.36	0.93
1:B:4030:LEU:CD1	1:B:4032:ASN:CG	2.41	0.92
1:D:4030:LEU:CD1	1:D:4032:ASN:CG	2.41	0.92
1:C:3995:GLN:NE2	1:D:4020:PHE:CD1	2.37	0.92
1:B:3853:THR:CG2	1:C:3874:THR:OG1	2.14	0.92
1:A:3853:THR:CG2	1:B:3874:THR:OG1	2.15	0.92
1:A:3995:GLN:NE2	1:B:4020:PHE:CD1	2.36	0.92
1:E:3995:GLN:CD	1:F:4020:PHE:CD1	2.48	0.92
1:F:3853:THR:CG2	1:G:3874:THR:OG1	2.14	0.91
1:F:4030:LEU:CD1	1:F:4032:ASN:CG	2.41	0.91
1:A:4020:PHE:CD1	1:G:3995:GLN:NE2	2.37	0.91
1:A:3995:GLN:CD	1:B:4020:PHE:CD1	2.49	0.91
1:B:3995:GLN:CD	1:C:4020:PHE:CD1	2.49	0.91
1:D:3995:GLN:NE2	1:E:4020:PHE:CD1	2.40	0.90
1:F:3995:GLN:CD	1:G:4020:PHE:CD1	2.50	0.90
1:C:3853:THR:CG2	1:D:3874:THR:OG1	2.15	0.90
1:E:4030:LEU:CD1	1:E:4032:ASN:CG	2.41	0.90
1:G:4030:LEU:CD1	1:G:4032:ASN:CG	2.41	0.89
1:A:4030:LEU:HD12	1:A:4032:ASN:H	1.38	0.89
1:C:4030:LEU:HD12	1:C:4032:ASN:H	1.38	0.88
1:A:4020:PHE:CD1	1:G:3995:GLN:CD	2.51	0.88
1:A:3874:THR:OG1	1:G:3853:THR:CG2	2.16	0.88
1:C:3995:GLN:CD	1:D:4020:PHE:CD1	2.51	0.87
1:F:4030:LEU:HD12	1:F:4032:ASN:H	1.38	0.87
1:D:3995:GLN:CD	1:E:4020:PHE:CD1	2.52	0.86
1:E:3853:THR:HG22	1:F:3874:THR:CB	2.05	0.86
1:B:4030:LEU:HD12	1:B:4032:ASN:H	1.38	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4030:LEU:HD12	1:E:4032:ASN:H	1.38	0.86
1:F:3853:THR:HG22	1:G:3874:THR:CB	2.06	0.86
1:G:4030:LEU:HD12	1:G:4032:ASN:H	1.38	0.85
1:A:3853:THR:HG22	1:B:3874:THR:CB	2.06	0.85
1:B:3853:THR:HG22	1:C:3874:THR:CB	2.06	0.84
1:D:3853:THR:CG2	1:E:3874:THR:OG1	2.16	0.84
1:D:4030:LEU:HD12	1:D:4032:ASN:H	1.38	0.84
1:B:3853:THR:HG22	1:C:3874:THR:HG1	1.43	0.84
1:A:3874:THR:CB	1:G:3853:THR:HG22	2.08	0.84
1:C:3853:THR:HG22	1:D:3874:THR:CB	2.07	0.83
1:D:3853:THR:HG22	1:E:3874:THR:CB	2.09	0.82
1:A:3853:THR:HG22	1:B:3874:THR:HG1	1.45	0.80
1:A:3772:SER:HB3	1:B:3757:SER:OG	1.84	0.78
1:E:3995:GLN:OE1	1:F:4020:PHE:CG	2.37	0.77
1:B:3995:GLN:OE1	1:C:4020:PHE:CG	2.37	0.77
1:E:3772:SER:HB3	1:F:3757:SER:OG	1.85	0.77
1:B:3772:SER:HB3	1:C:3757:SER:OG	1.85	0.77
1:F:3772:SER:HB3	1:G:3757:SER:OG	1.85	0.76
1:D:3772:SER:HB3	1:E:3757:SER:OG	1.86	0.76
1:C:3581:PRO:HB2	1:C:3650:TYR:CE2	2.21	0.76
1:A:3757:SER:OG	1:G:3772:SER:HB3	1.86	0.76
1:A:3995:GLN:OE1	1:B:4020:PHE:CG	2.38	0.76
1:F:3995:GLN:OE1	1:G:4020:PHE:CG	2.38	0.76
1:A:3581:PRO:HB2	1:A:3650:TYR:CE2	2.21	0.75
1:B:3581:PRO:HB2	1:B:3650:TYR:CE2	2.21	0.75
1:F:3581:PRO:HB2	1:F:3650:TYR:CE2	2.21	0.75
1:C:3772:SER:HB3	1:D:3757:SER:OG	1.86	0.75
1:D:3581:PRO:HB2	1:D:3650:TYR:CE2	2.21	0.75
1:C:3995:GLN:OE1	1:D:4020:PHE:CG	2.39	0.75
1:E:3581:PRO:HB2	1:E:3650:TYR:CE2	2.21	0.75
1:G:3581:PRO:HB2	1:G:3650:TYR:CE2	2.21	0.75
1:A:4020:PHE:CG	1:G:3995:GLN:OE1	2.39	0.74
1:D:3995:GLN:OE1	1:E:4020:PHE:CG	2.41	0.74
1:F:3960:PRO:HG2	1:G:3989:THR:OG1	1.90	0.72
1:E:3960:PRO:HG2	1:F:3989:THR:OG1	1.90	0.72
1:E:3772:SER:CB	1:F:3757:SER:OG	2.38	0.71
1:C:3960:PRO:HG2	1:D:3989:THR:OG1	1.90	0.71
1:B:3960:PRO:HG2	1:C:3989:THR:OG1	1.90	0.71
1:A:3960:PRO:HG2	1:B:3989:THR:OG1	1.91	0.71
1:A:3772:SER:CB	1:B:3757:SER:OG	2.39	0.71
1:A:3989:THR:OG1	1:G:3960:PRO:HG2	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3772:SER:CB	1:D:3757:SER:OG	2.40	0.70
1:D:3772:SER:CB	1:E:3757:SER:OG	2.40	0.70
1:E:3837:PHE:CE1	1:F:3873:SER:HA	2.27	0.70
1:B:3772:SER:CB	1:C:3757:SER:OG	2.40	0.70
1:F:3772:SER:CB	1:G:3757:SER:OG	2.39	0.70
1:D:3960:PRO:HG2	1:E:3989:THR:OG1	1.92	0.69
1:B:3837:PHE:CE1	1:C:3873:SER:HA	2.28	0.69
1:E:3772:SER:CB	1:F:3757:SER:HG	2.06	0.69
1:F:3837:PHE:CE1	1:G:3873:SER:HA	2.27	0.69
1:A:3757:SER:OG	1:G:3772:SER:CB	2.40	0.69
1:A:4030:LEU:HD12	1:A:4032:ASN:N	2.09	0.68
1:C:3772:SER:CB	1:D:3757:SER:HG	2.07	0.68
1:C:3837:PHE:CE1	1:D:3873:SER:HA	2.28	0.68
1:A:3837:PHE:CE1	1:B:3873:SER:HA	2.28	0.68
1:E:3853:THR:HG21	1:F:3874:THR:HG21	1.76	0.68
1:C:4030:LEU:HD12	1:C:4032:ASN:N	2.09	0.67
1:E:4030:LEU:CD1	1:E:4032:ASN:H	2.08	0.67
1:E:3995:GLN:OE1	1:F:4020:PHE:HB2	1.94	0.67
1:B:3995:GLN:OE1	1:C:4020:PHE:HB2	1.94	0.67
1:G:4030:LEU:HD12	1:G:4032:ASN:N	2.09	0.67
1:A:3873:SER:HA	1:G:3837:PHE:CE1	2.29	0.67
1:B:4030:LEU:HD12	1:B:4032:ASN:N	2.09	0.67
1:C:4030:LEU:CD1	1:C:4032:ASN:H	2.08	0.67
1:D:3837:PHE:CE1	1:E:3873:SER:HA	2.30	0.66
1:D:4030:LEU:CD1	1:D:4032:ASN:H	2.08	0.66
1:F:4030:LEU:CD1	1:F:4032:ASN:H	2.08	0.66
1:G:4030:LEU:CD1	1:G:4032:ASN:H	2.08	0.66
1:B:4030:LEU:CD1	1:B:4032:ASN:H	2.07	0.66
1:F:3853:THR:HG21	1:G:3874:THR:HG21	1.77	0.66
1:D:3772:SER:CB	1:E:3757:SER:HG	2.08	0.66
1:A:3853:THR:HG21	1:B:3874:THR:HG21	1.76	0.66
1:A:4030:LEU:CD1	1:A:4032:ASN:H	2.08	0.66
1:F:3995:GLN:OE1	1:G:4020:PHE:HB2	1.95	0.66
1:A:3995:GLN:OE1	1:B:4020:PHE:HB2	1.95	0.66
1:B:3853:THR:HG21	1:C:3874:THR:HG21	1.77	0.65
1:A:3772:SER:CB	1:B:3757:SER:HG	2.10	0.65
1:E:4030:LEU:HD12	1:E:4032:ASN:N	2.09	0.65
1:C:3853:THR:HG21	1:D:3874:THR:HG21	1.78	0.65
1:A:4020:PHE:HB2	1:G:3995:GLN:OE1	1.96	0.65
1:C:3995:GLN:OE1	1:D:4020:PHE:HB2	1.96	0.65
1:D:4030:LEU:HD12	1:D:4032:ASN:N	2.09	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:4030:LEU:HD12	1:F:4032:ASN:N	2.09	0.65
1:D:3853:THR:HG21	1:E:3874:THR:HG21	1.79	0.64
1:D:3762:GLN:HB3	1:D:3786:TRP:HE1	1.62	0.64
1:E:3995:GLN:OE1	1:F:4020:PHE:HD1	1.78	0.64
1:D:4011:ASP:O	1:D:4013:THR:HG23	1.98	0.64
1:A:4011:ASP:O	1:A:4013:THR:HG23	1.98	0.64
1:E:4011:ASP:O	1:E:4013:THR:HG23	1.98	0.64
1:F:4011:ASP:O	1:F:4013:THR:HG23	1.98	0.64
1:A:3874:THR:HG21	1:G:3853:THR:HG21	1.79	0.64
1:F:3772:SER:CB	1:G:3757:SER:HG	2.11	0.64
1:B:4011:ASP:O	1:B:4013:THR:HG23	1.98	0.63
1:C:3762:GLN:HB3	1:C:3786:TRP:HE1	1.62	0.63
1:G:4011:ASP:O	1:G:4013:THR:HG23	1.98	0.63
1:F:3762:GLN:HB3	1:F:3786:TRP:HE1	1.62	0.63
1:A:3762:GLN:HB3	1:A:3786:TRP:HE1	1.62	0.63
1:D:3995:GLN:OE1	1:E:4020:PHE:HB2	1.99	0.63
1:G:3762:GLN:HB3	1:G:3786:TRP:HE1	1.62	0.63
1:B:3762:GLN:HB3	1:B:3786:TRP:HE1	1.62	0.63
1:C:4011:ASP:O	1:C:4013:THR:HG23	1.98	0.62
1:E:3762:GLN:HB3	1:E:3786:TRP:HE1	1.62	0.62
1:A:4020:PHE:HD1	1:G:3995:GLN:OE1	1.80	0.60
1:A:3757:SER:HG	1:G:3772:SER:CB	2.15	0.60
1:B:3772:SER:CB	1:C:3757:SER:HG	2.14	0.59
1:A:3581:PRO:HB2	1:A:3650:TYR:CZ	2.38	0.59
1:D:3581:PRO:HB2	1:D:3650:TYR:CZ	2.38	0.59
1:F:3581:PRO:HB2	1:F:3650:TYR:CZ	2.38	0.59
1:B:3581:PRO:HB2	1:B:3650:TYR:CZ	2.38	0.58
1:E:3581:PRO:HB2	1:E:3650:TYR:CZ	2.38	0.58
1:C:3581:PRO:HB2	1:C:3650:TYR:CZ	2.38	0.58
1:F:3995:GLN:OE1	1:G:4020:PHE:HD1	1.80	0.58
1:G:3581:PRO:HB2	1:G:3650:TYR:CZ	2.38	0.58
1:D:4004:PRO:HB2	1:D:4078:PRO:HB3	1.86	0.58
1:E:4004:PRO:HB2	1:E:4078:PRO:HB3	1.86	0.58
1:C:4004:PRO:HB2	1:C:4078:PRO:HB3	1.86	0.58
1:F:4004:PRO:HB2	1:F:4078:PRO:HB3	1.86	0.57
1:E:3853:THR:CG2	1:F:3874:THR:HG21	2.35	0.57
1:A:3853:THR:CG2	1:B:3874:THR:HG21	2.35	0.57
1:F:3853:THR:CG2	1:G:3874:THR:HG21	2.35	0.57
1:A:4004:PRO:HB2	1:A:4078:PRO:HB3	1.86	0.57
1:B:4004:PRO:HB2	1:B:4078:PRO:HB3	1.86	0.56
1:B:3995:GLN:OE1	1:C:4020:PHE:CB	2.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3853:THR:CG2	1:C:3874:THR:HG21	2.35	0.56
1:G:4004:PRO:HB2	1:G:4078:PRO:HB3	1.86	0.56
1:E:3995:GLN:OE1	1:F:4020:PHE:CB	2.54	0.56
1:B:3995:GLN:OE1	1:C:4020:PHE:HD1	1.79	0.56
1:A:3874:THR:HG21	1:G:3853:THR:CG2	2.37	0.55
1:A:3995:GLN:OE1	1:B:4020:PHE:CB	2.55	0.54
1:C:3853:THR:CG2	1:D:3874:THR:HG21	2.37	0.54
1:C:3995:GLN:OE1	1:D:4020:PHE:CB	2.56	0.54
1:F:3995:GLN:OE1	1:G:4020:PHE:CB	2.55	0.54
1:D:3853:THR:CG2	1:E:3874:THR:HG21	2.37	0.54
1:F:3837:PHE:CZ	1:G:3873:SER:HA	2.43	0.54
1:A:3995:GLN:OE1	1:B:4020:PHE:HD1	1.78	0.53
1:B:3837:PHE:CZ	1:C:3873:SER:HA	2.43	0.53
1:A:4020:PHE:CB	1:G:3995:GLN:OE1	2.56	0.53
1:C:3995:GLN:OE1	1:D:4020:PHE:HD1	1.81	0.53
1:A:3837:PHE:CZ	1:B:3873:SER:HA	2.43	0.53
1:E:3837:PHE:CZ	1:F:3873:SER:HA	2.42	0.53
1:C:3837:PHE:CZ	1:D:3873:SER:HA	2.44	0.52
1:A:3873:SER:HA	1:G:3837:PHE:CZ	2.45	0.51
1:A:3962:ILE:HG13	1:A:3966:ASN:HB2	1.91	0.51
1:B:3962:ILE:HG13	1:B:3966:ASN:HB2	1.91	0.51
1:D:3837:PHE:CZ	1:E:3873:SER:HA	2.45	0.51
1:C:3962:ILE:HG13	1:C:3966:ASN:HB2	1.91	0.51
1:D:3995:GLN:OE1	1:E:4020:PHE:CB	2.58	0.51
1:G:3962:ILE:HG13	1:G:3966:ASN:HB2	1.91	0.51
1:F:3772:SER:HB3	1:G:3757:SER:HG	1.75	0.51
1:E:3962:ILE:HG13	1:E:3966:ASN:HB2	1.91	0.51
1:D:3766:ILE:HD12	1:D:3807:TYR:CE2	2.46	0.51
1:F:3962:ILE:HG13	1:F:3966:ASN:HB2	1.91	0.51
1:A:3766:ILE:HD12	1:A:3807:TYR:CE2	2.47	0.50
1:E:3766:ILE:HD12	1:E:3807:TYR:CE2	2.46	0.50
1:E:3853:THR:HG22	1:F:3874:THR:CG2	2.41	0.50
1:G:3766:ILE:HD12	1:G:3807:TYR:CE2	2.47	0.50
1:C:3766:ILE:HD12	1:C:3807:TYR:CE2	2.46	0.50
1:D:3962:ILE:HG13	1:D:3966:ASN:HB2	1.91	0.50
1:F:3766:ILE:HD12	1:F:3807:TYR:CE2	2.46	0.50
1:B:3766:ILE:HD12	1:B:3807:TYR:CE2	2.46	0.50
1:C:3926:LEU:HD11	1:D:4020:PHE:CE2	2.46	0.50
1:C:4030:LEU:HD12	1:C:4030:LEU:C	2.37	0.50
1:E:4030:LEU:HD12	1:E:4030:LEU:C	2.37	0.50
1:G:4006:CYS:O	1:G:4007:GLU:C	2.55	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4006:CYS:O	1:A:4007:GLU:C	2.55	0.50
1:B:4030:LEU:HD12	1:B:4030:LEU:C	2.37	0.50
1:D:3995:GLN:OE1	1:E:4020:PHE:HD1	1.80	0.50
1:A:4030:LEU:HD12	1:A:4030:LEU:C	2.37	0.49
1:D:3926:LEU:HD11	1:E:4020:PHE:CE2	2.46	0.49
1:F:3853:THR:HG22	1:G:3874:THR:CG2	2.42	0.49
1:E:3853:THR:CG2	1:F:3874:THR:CG2	2.90	0.49
1:F:4006:CYS:O	1:F:4007:GLU:C	2.55	0.49
1:D:4030:LEU:HD12	1:D:4030:LEU:C	2.37	0.49
1:A:3853:THR:HG22	1:B:3874:THR:CG2	2.41	0.49
1:A:3853:THR:CG2	1:B:3874:THR:CG2	2.91	0.49
1:D:3613:SER:OG	1:D:3614:THR:N	2.45	0.49
1:B:4006:CYS:O	1:B:4007:GLU:C	2.55	0.49
1:E:4006:CYS:O	1:E:4007:GLU:C	2.55	0.49
1:F:4030:LEU:HD12	1:F:4030:LEU:C	2.37	0.49
1:F:3613:SER:OG	1:F:3614:THR:N	2.45	0.49
1:G:4030:LEU:HD12	1:G:4030:LEU:C	2.37	0.49
1:A:3613:SER:OG	1:A:3614:THR:N	2.45	0.49
1:E:3613:SER:OG	1:E:3614:THR:N	2.45	0.49
1:A:3772:SER:HB3	1:B:3757:SER:HG	1.73	0.49
1:C:4004:PRO:O	1:C:4078:PRO:HG3	2.13	0.49
1:G:3613:SER:OG	1:G:3614:THR:N	2.45	0.49
1:C:3613:SER:OG	1:C:3614:THR:N	2.45	0.49
1:D:4004:PRO:O	1:D:4078:PRO:HG3	2.13	0.49
1:A:4020:PHE:CE2	1:G:3926:LEU:HD11	2.47	0.48
1:D:4006:CYS:O	1:D:4007:GLU:C	2.55	0.48
1:F:3926:LEU:HD11	1:G:4020:PHE:CE2	2.48	0.48
1:G:4004:PRO:O	1:G:4078:PRO:HG3	2.13	0.48
1:B:3853:THR:CG2	1:C:3874:THR:CG2	2.91	0.48
1:B:4004:PRO:O	1:B:4078:PRO:HG3	2.13	0.48
1:B:3613:SER:OG	1:B:3614:THR:N	2.45	0.48
1:F:3853:THR:CG2	1:G:3874:THR:CG2	2.91	0.48
1:F:4004:PRO:O	1:F:4078:PRO:HG3	2.13	0.48
1:B:3853:THR:HG22	1:C:3874:THR:CG2	2.42	0.48
1:E:4004:PRO:O	1:E:4078:PRO:HG3	2.13	0.48
1:A:3926:LEU:HD11	1:B:4020:PHE:CE2	2.49	0.47
1:A:4004:PRO:O	1:A:4078:PRO:HG3	2.13	0.47
1:E:3837:PHE:CE1	1:F:3872:ILE:O	2.67	0.47
1:A:3874:THR:CG2	1:G:3853:THR:HG22	2.43	0.47
1:B:3926:LEU:HD11	1:C:4020:PHE:CE2	2.48	0.47
1:C:4006:CYS:O	1:C:4007:GLU:C	2.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3837:PHE:CE1	1:B:3872:ILE:O	2.67	0.47
1:D:3853:THR:HG22	1:E:3874:THR:CG2	2.44	0.47
1:C:3853:THR:CG2	1:D:3874:THR:CG2	2.92	0.47
1:A:3962:ILE:CG1	1:A:3966:ASN:HB2	2.45	0.47
1:C:3650:TYR:CD2	1:C:3718:ASN:ND2	2.83	0.47
1:C:3962:ILE:CG1	1:C:3966:ASN:HB2	2.45	0.47
1:D:3962:ILE:CG1	1:D:3966:ASN:HB2	2.45	0.47
1:E:3962:ILE:CG1	1:E:3966:ASN:HB2	2.45	0.47
1:F:3771:ASN:OD1	1:F:3771:ASN:N	2.48	0.47
1:A:3874:THR:CG2	1:G:3853:THR:CG2	2.93	0.47
1:F:3962:ILE:CG1	1:F:3966:ASN:HB2	2.45	0.47
1:E:3926:LEU:HD11	1:F:4020:PHE:CE2	2.49	0.47
1:C:3853:THR:HG22	1:D:3874:THR:CG2	2.44	0.47
1:D:3853:THR:CG2	1:E:3874:THR:CG2	2.93	0.47
1:G:3962:ILE:CG1	1:G:3966:ASN:HB2	2.45	0.47
1:D:3650:TYR:CD2	1:D:3718:ASN:ND2	2.83	0.46
1:B:3962:ILE:CG1	1:B:3966:ASN:HB2	2.45	0.46
1:B:4038:THR:OG1	1:B:4039:PHE:N	2.49	0.46
1:C:3579:ASP:OD1	1:C:3579:ASP:N	2.45	0.46
1:D:4011:ASP:OD1	1:D:4011:ASP:N	2.49	0.46
1:F:3837:PHE:CE1	1:G:3872:ILE:O	2.68	0.46
1:B:3650:TYR:CD2	1:B:3718:ASN:ND2	2.83	0.46
1:A:4038:THR:OG1	1:A:4039:PHE:N	2.49	0.46
1:B:3837:PHE:CE1	1:C:3872:ILE:O	2.68	0.46
1:E:4007:GLU:HB2	1:E:4050:VAL:HG13	1.98	0.46
1:C:4038:THR:OG1	1:C:4039:PHE:N	2.49	0.46
1:A:4007:GLU:HB2	1:A:4050:VAL:HG13	1.98	0.46
1:B:4007:GLU:HB2	1:B:4050:VAL:HG13	1.98	0.46
1:F:3650:TYR:CD2	1:F:3718:ASN:ND2	2.83	0.45
1:C:3837:PHE:CE1	1:D:3872:ILE:O	2.69	0.45
1:A:3650:TYR:CD2	1:A:3718:ASN:ND2	2.83	0.45
1:D:4007:GLU:HB2	1:D:4050:VAL:HG13	1.98	0.45
1:F:4007:GLU:HB2	1:F:4050:VAL:HG13	1.98	0.45
1:E:3650:TYR:CD2	1:E:3718:ASN:ND2	2.83	0.45
1:F:4011:ASP:HB3	1:F:4046:PRO:HA	1.99	0.45
1:G:3650:TYR:CD2	1:G:3718:ASN:ND2	2.83	0.45
1:G:4038:THR:OG1	1:G:4039:PHE:N	2.49	0.45
1:E:4011:ASP:OD1	1:E:4011:ASP:N	2.49	0.45
1:G:4011:ASP:HB3	1:G:4046:PRO:HA	1.99	0.45
1:E:4011:ASP:HB3	1:E:4046:PRO:HA	1.99	0.45
1:G:4007:GLU:HB2	1:G:4050:VAL:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3872:ILE:O	1:G:3837:PHE:CE1	2.70	0.45
1:A:4011:ASP:HB3	1:A:4046:PRO:HA	1.99	0.45
1:B:4011:ASP:N	1:B:4011:ASP:OD1	2.49	0.45
1:A:4011:ASP:OD1	1:A:4011:ASP:N	2.49	0.45
1:C:4007:GLU:HB2	1:C:4050:VAL:HG13	1.97	0.45
1:C:4011:ASP:OD1	1:C:4011:ASP:N	2.49	0.45
1:D:4038:THR:OG1	1:D:4039:PHE:N	2.49	0.45
1:A:3772:SER:OG	1:B:3757:SER:OG	2.35	0.45
1:B:4011:ASP:HB3	1:B:4046:PRO:HA	1.99	0.45
1:D:4011:ASP:HB3	1:D:4046:PRO:HA	1.99	0.45
1:E:4038:THR:OG1	1:E:4039:PHE:N	2.49	0.45
1:C:3771:ASN:OD1	1:C:3771:ASN:N	2.48	0.44
1:F:4038:THR:OG1	1:F:4039:PHE:N	2.49	0.44
1:B:3762:GLN:HB3	1:B:3786:TRP:NE1	2.31	0.44
1:C:4011:ASP:HB3	1:C:4046:PRO:HA	1.99	0.44
1:F:4011:ASP:OD1	1:F:4011:ASP:N	2.49	0.44
1:D:3837:PHE:CE1	1:E:3872:ILE:O	2.70	0.44
1:G:4011:ASP:N	1:G:4011:ASP:OD1	2.49	0.44
1:D:4051:GLN:OE1	1:D:4051:GLN:N	2.48	0.44
1:D:3812:ASP:OD1	1:D:3812:ASP:C	2.61	0.43
1:C:3762:GLN:HB3	1:C:3786:TRP:NE1	2.31	0.43
1:G:3762:GLN:HB3	1:G:3786:TRP:NE1	2.31	0.43
1:B:3771:ASN:OD1	1:B:3771:ASN:N	2.48	0.43
1:E:3762:GLN:HB3	1:E:3786:TRP:NE1	2.31	0.43
1:E:3853:THR:CG2	1:F:3874:THR:CB	2.89	0.43
1:A:3762:GLN:HB3	1:A:3786:TRP:NE1	2.31	0.43
1:F:3762:GLN:HB3	1:F:3786:TRP:NE1	2.31	0.43
1:B:4051:GLN:OE1	1:B:4051:GLN:N	2.48	0.43
1:C:3812:ASP:C	1:C:3812:ASP:OD1	2.60	0.43
1:D:3762:GLN:HB3	1:D:3786:TRP:NE1	2.31	0.43
1:D:3681:TYR:CZ	1:D:3694:GLN:HB3	2.54	0.42
1:E:3772:SER:OG	1:F:3757:SER:OG	2.34	0.42
1:B:3681:TYR:CZ	1:B:3694:GLN:HB3	2.54	0.42
1:G:3579:ASP:N	1:G:3579:ASP:OD1	2.45	0.42
1:B:3579:ASP:N	1:B:3579:ASP:OD1	2.45	0.42
1:G:4051:GLN:OE1	1:G:4051:GLN:N	2.48	0.42
1:E:3681:TYR:CZ	1:E:3694:GLN:HB3	2.54	0.42
1:E:4030:LEU:HD11	1:E:4032:ASN:ND2	2.29	0.42
1:E:4068:LEU:CD1	1:F:4024:VAL:HG21	2.50	0.42
1:G:3681:TYR:CZ	1:G:3694:GLN:HB3	2.54	0.42
1:A:3681:TYR:CZ	1:A:3694:GLN:HB3	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3681:TYR:CZ	1:F:3694:GLN:HB3	2.54	0.41
1:B:3772:SER:OG	1:C:3757:SER:OG	2.36	0.41
1:C:3681:TYR:CZ	1:C:3694:GLN:HB3	2.55	0.41
1:A:3757:SER:HG	1:G:3772:SER:HB3	1.77	0.41
1:B:3812:ASP:OD1	1:B:3812:ASP:C	2.60	0.41
1:C:4007:GLU:H	1:C:4077:TYR:HD1	1.69	0.41
1:D:4007:GLU:H	1:D:4077:TYR:HD1	1.69	0.41
1:A:3579:ASP:N	1:A:3579:ASP:OD1	2.45	0.41
1:F:4068:LEU:CD1	1:G:4024:VAL:HG21	2.50	0.41
1:B:3962:ILE:HG23	1:B:3962:ILE:O	2.21	0.41
1:E:3925:GLN:HG3	1:E:3964:PRO:HD3	2.02	0.41
1:E:3962:ILE:HG23	1:E:3962:ILE:O	2.21	0.41
1:F:3925:GLN:HG3	1:F:3964:PRO:HD3	2.02	0.41
1:F:4030:LEU:HD11	1:F:4032:ASN:ND2	2.29	0.41
1:B:4068:LEU:CD1	1:C:4024:VAL:HG21	2.50	0.41
1:C:3782:ASN:OD1	1:C:3782:ASN:N	2.53	0.41
1:C:4068:LEU:CD1	1:D:4024:VAL:HG21	2.51	0.41
1:E:4007:GLU:H	1:E:4077:TYR:HD1	1.69	0.41
1:F:3782:ASN:OD1	1:F:3782:ASN:N	2.53	0.41
1:B:4007:GLU:H	1:B:4077:TYR:HD1	1.69	0.41
1:C:3925:GLN:HG3	1:C:3964:PRO:HD3	2.02	0.41
1:D:3925:GLN:HG3	1:D:3964:PRO:HD3	2.02	0.41
1:F:3962:ILE:HG23	1:F:3962:ILE:O	2.21	0.41
1:F:4007:GLU:H	1:F:4077:TYR:HD1	1.69	0.41
1:G:3925:GLN:HG3	1:G:3964:PRO:HD3	2.02	0.41
1:G:4030:LEU:HD11	1:G:4032:ASN:ND2	2.29	0.41
1:B:3925:GLN:HG3	1:B:3964:PRO:HD3	2.02	0.41
1:E:4051:GLN:OE1	1:E:4051:GLN:N	2.48	0.41
1:A:3962:ILE:HG23	1:A:3962:ILE:O	2.21	0.40
1:C:3962:ILE:HG23	1:C:3962:ILE:O	2.21	0.40
1:D:3962:ILE:HG23	1:D:3962:ILE:O	2.21	0.40
1:A:3925:GLN:HG3	1:A:3964:PRO:HD3	2.02	0.40
1:A:4007:GLU:H	1:A:4077:TYR:HD1	1.69	0.40
1:A:4030:LEU:HD11	1:A:4032:ASN:ND2	2.29	0.40
1:F:3722:SER:OG	1:F:3723:GLY:N	2.55	0.40
1:F:3853:THR:CG2	1:G:3874:THR:CB	2.90	0.40
1:G:3722:SER:OG	1:G:3723:GLY:N	2.55	0.40
1:A:3757:SER:OG	1:G:3772:SER:OG	2.37	0.40
1:G:4007:GLU:H	1:G:4077:TYR:HD1	1.69	0.40

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	A	506/5898 (9%)	496 (98%)	10 (2%)	0	100	100
1	B	506/5898 (9%)	496 (98%)	10 (2%)	0	100	100
1	C	506/5898 (9%)	496 (98%)	10 (2%)	0	100	100
1	D	506/5898 (9%)	496 (98%)	10 (2%)	0	100	100
1	E	506/5898 (9%)	496 (98%)	10 (2%)	0	100	100
1	F	506/5898 (9%)	496 (98%)	10 (2%)	0	100	100
1	G	506/5898 (9%)	496 (98%)	10 (2%)	0	100	100
All	All	3542/41286 (9%)	3472 (98%)	70 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	434/4919 (9%)	434 (100%)	0	100	100
1	B	434/4919 (9%)	434 (100%)	0	100	100
1	C	434/4919 (9%)	434 (100%)	0	100	100
1	D	434/4919 (9%)	434 (100%)	0	100	100
1	E	434/4919 (9%)	434 (100%)	0	100	100
1	F	434/4919 (9%)	434 (100%)	0	100	100
1	G	434/4919 (9%)	434 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	3038/34433 (9%)	3038 (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. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3687	ASN
1	A	3694	GLN
1	A	4001	HIS
1	B	3687	ASN
1	B	3694	GLN
1	B	3695	ASN
1	B	4001	HIS
1	C	3687	ASN
1	C	3694	GLN
1	C	4001	HIS
1	D	3687	ASN
1	D	3694	GLN
1	D	4001	HIS
1	E	3687	ASN
1	E	3694	GLN
1	E	4001	HIS
1	F	3687	ASN
1	F	3694	GLN
1	F	4001	HIS
1	G	3687	ASN
1	G	3694	GLN
1	G	4001	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

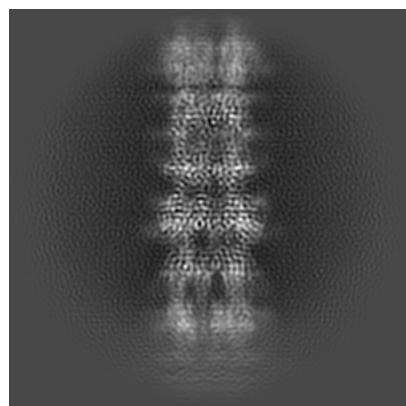
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50541. These allow visual inspection of the internal detail of the map and identification of artifacts.

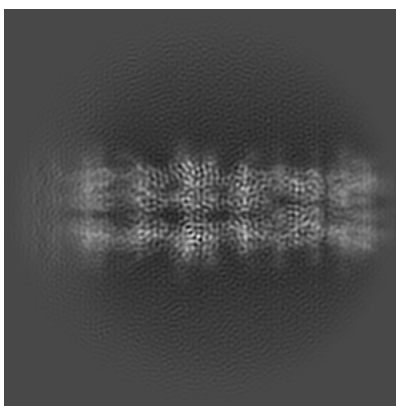
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

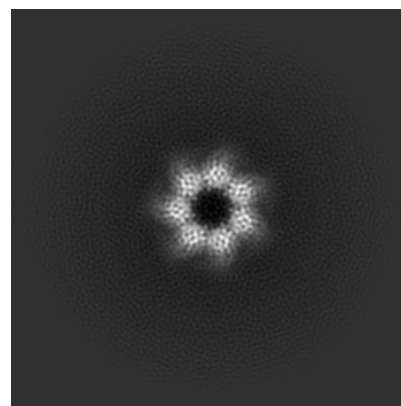
6.1.1 Primary map



X

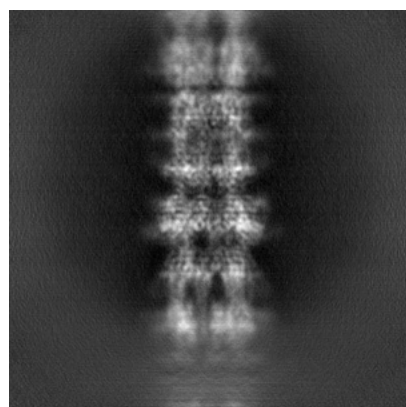


Y

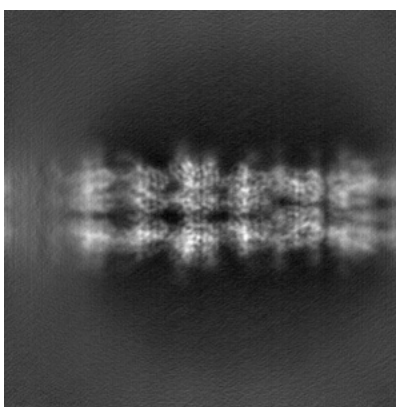


Z

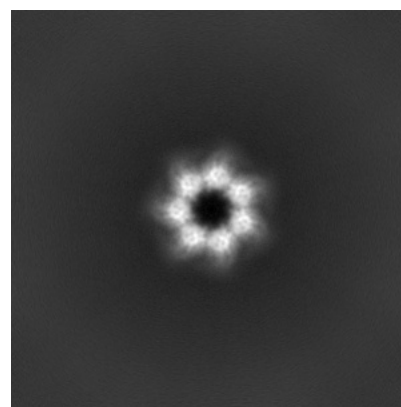
6.1.2 Raw map



X



Y

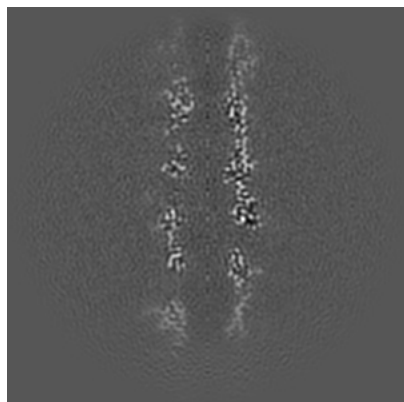


Z

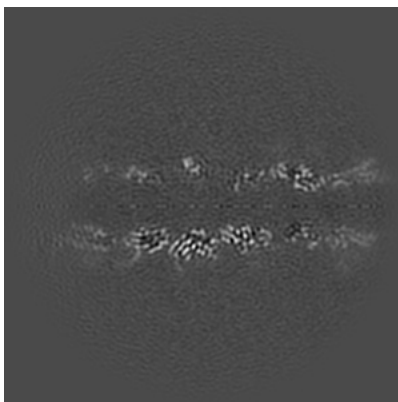
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

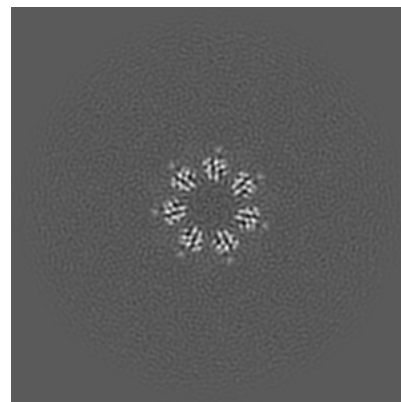
6.2.1 Primary map



X Index: 150

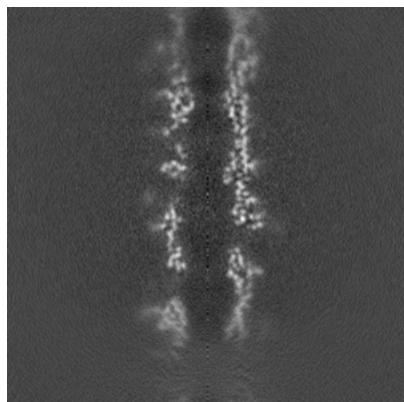


Y Index: 150

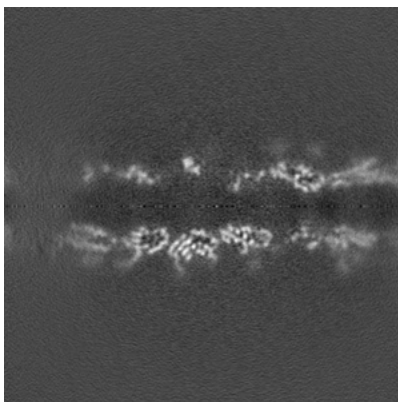


Z Index: 150

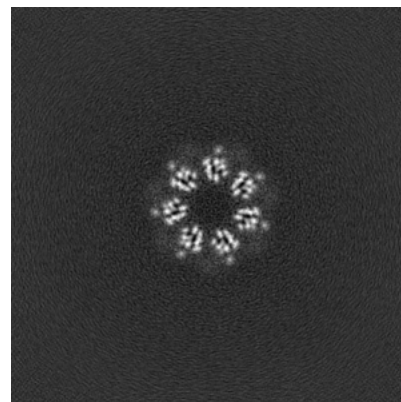
6.2.2 Raw map



X Index: 150



Y Index: 150

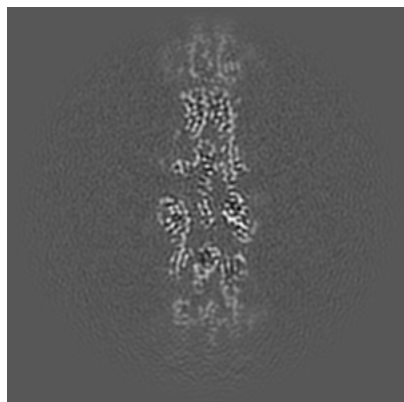


Z Index: 150

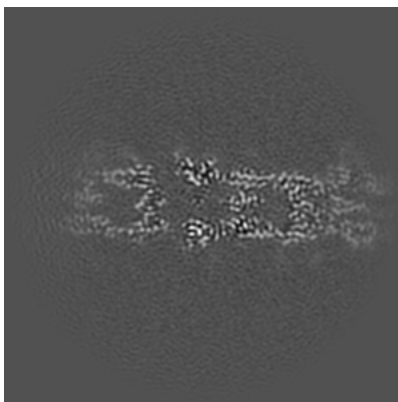
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

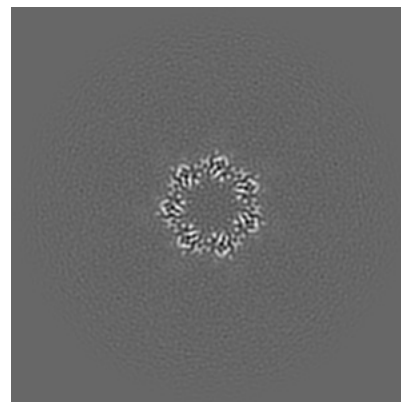
6.3.1 Primary map



X Index: 129

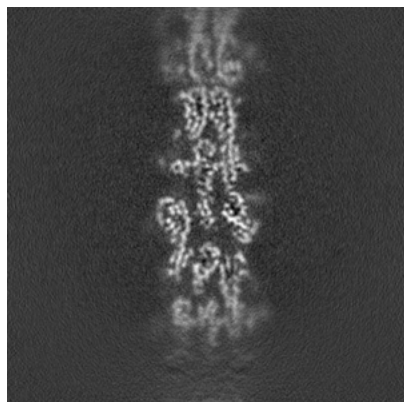


Y Index: 167

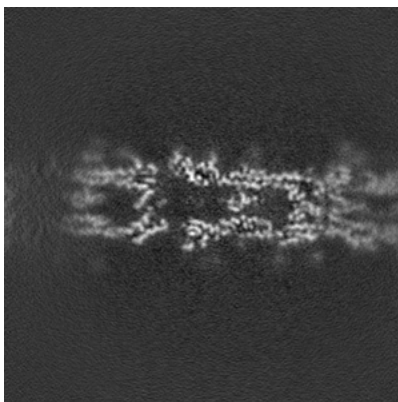


Z Index: 139

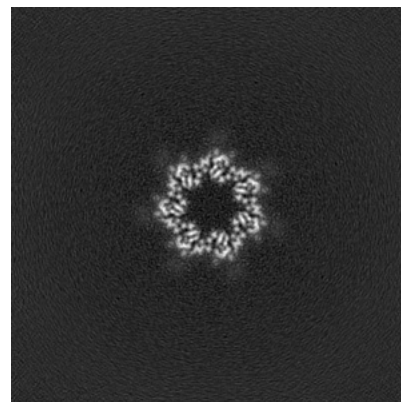
6.3.2 Raw map



X Index: 129



Y Index: 166

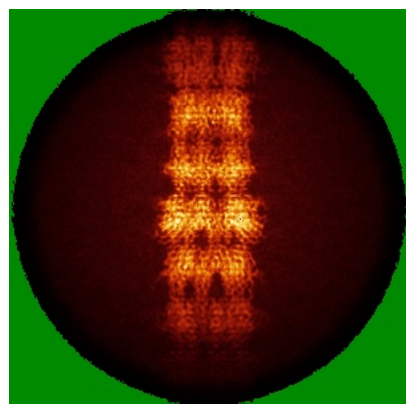


Z Index: 139

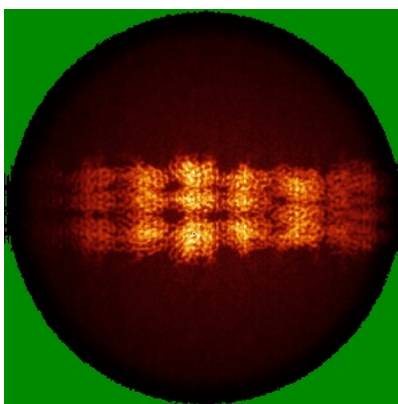
The images above show the largest variance slices of the map in three orthogonal directions.

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

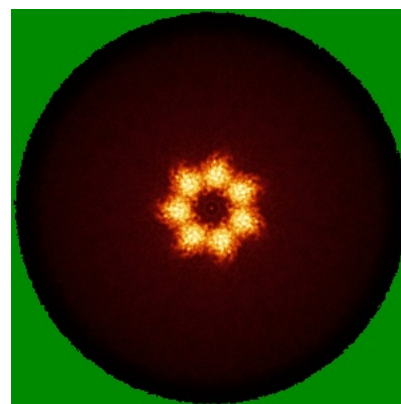
6.4.1 Primary map



X

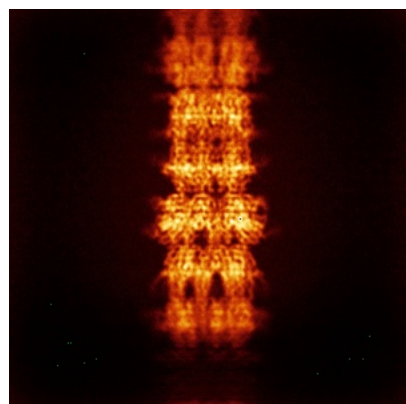


Y

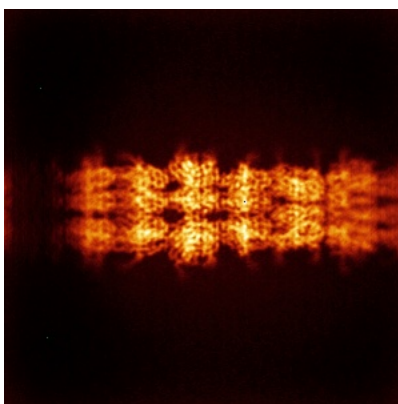


Z

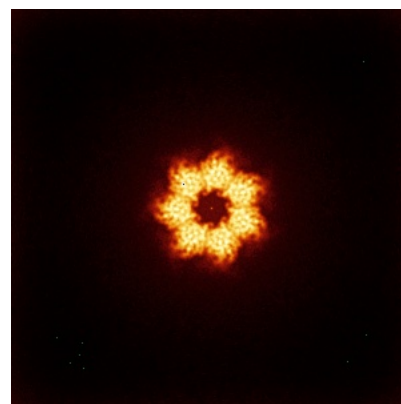
6.4.2 Raw map



X



Y

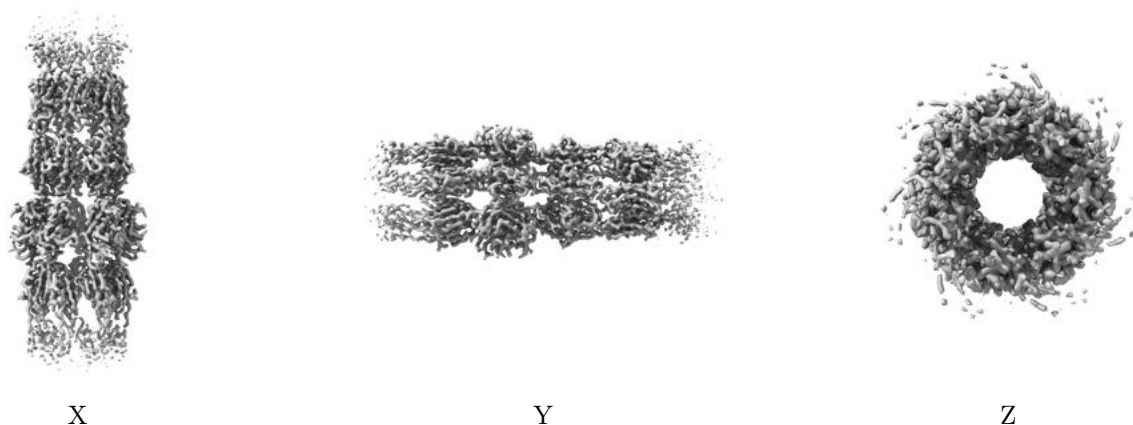


Z

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.

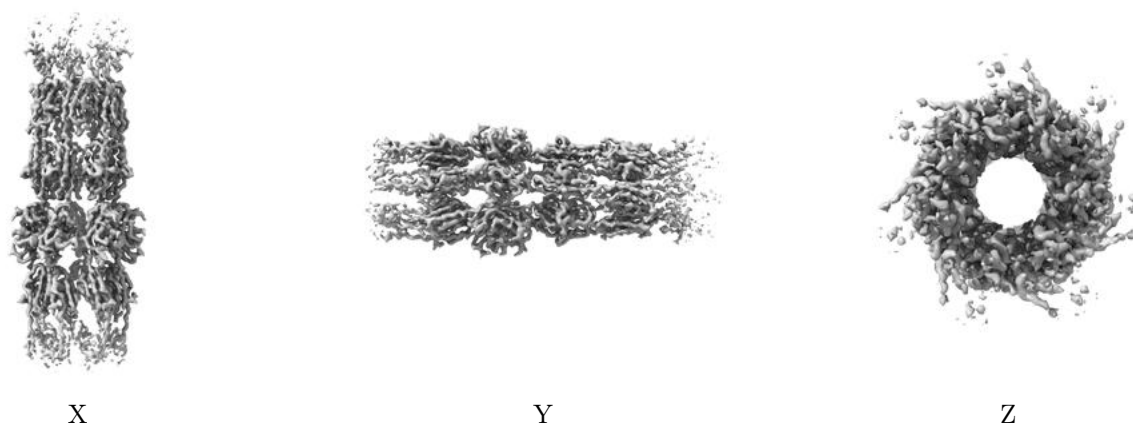
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. 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.

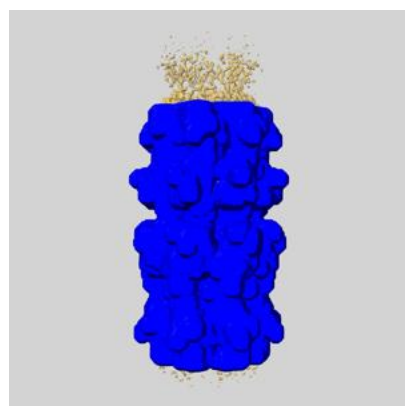
6.6 Mask visualisation [i](#)

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

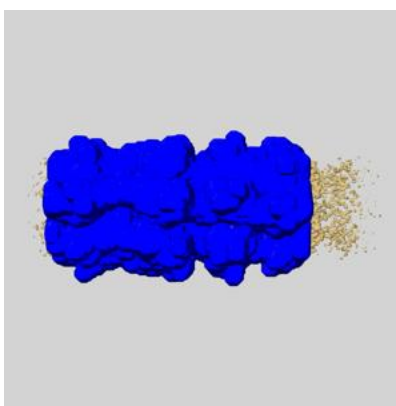
A mask typically either:

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

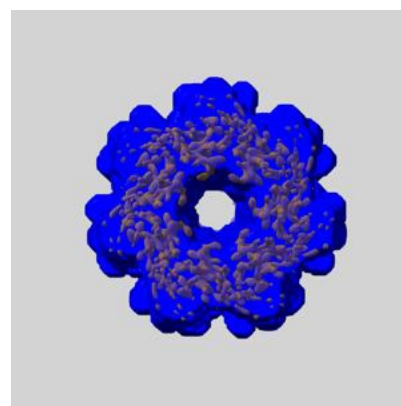
6.6.1 emd_50541_msk_1.map [i](#)



X



Y

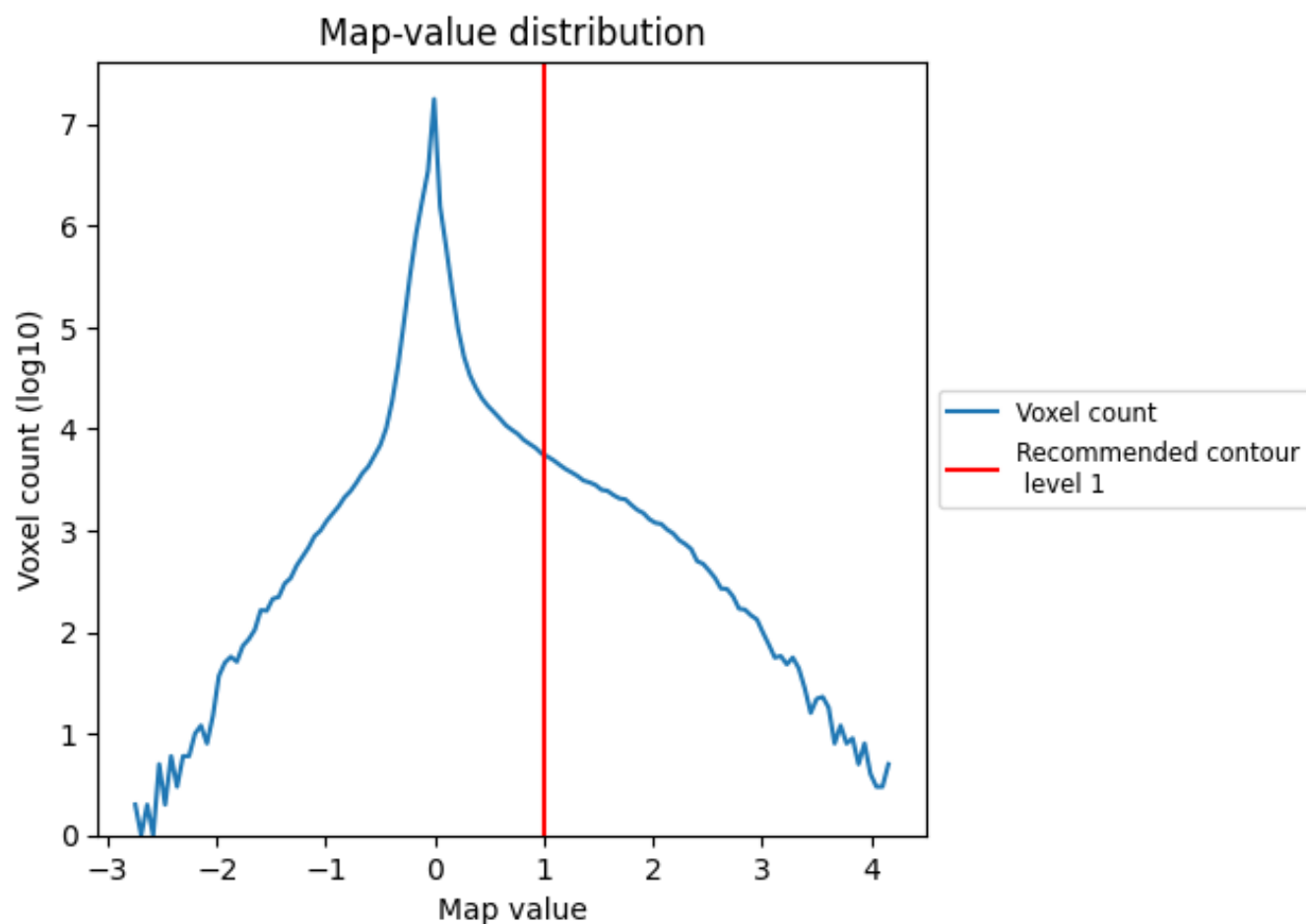


Z

7 Map analysis [i](#)

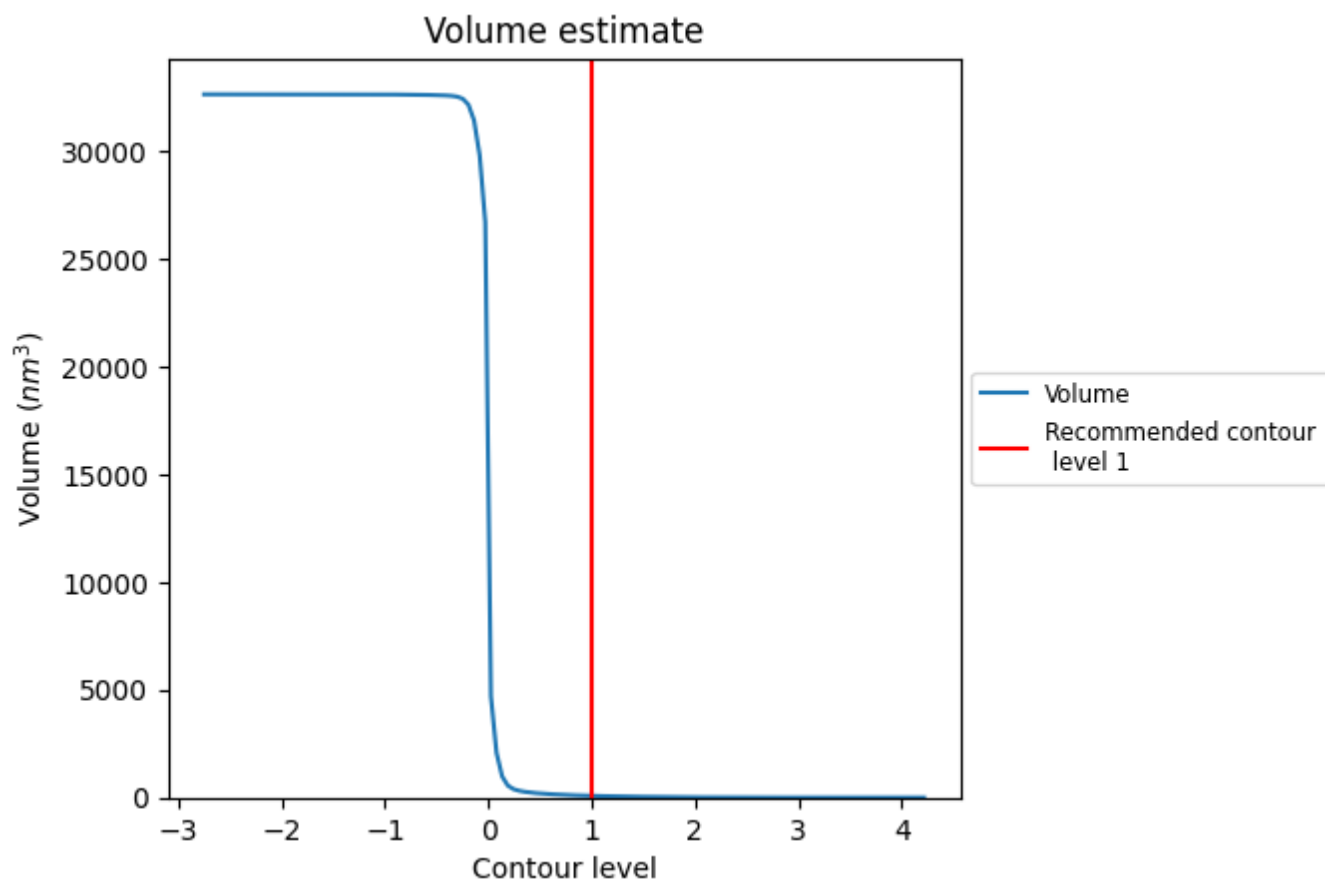
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

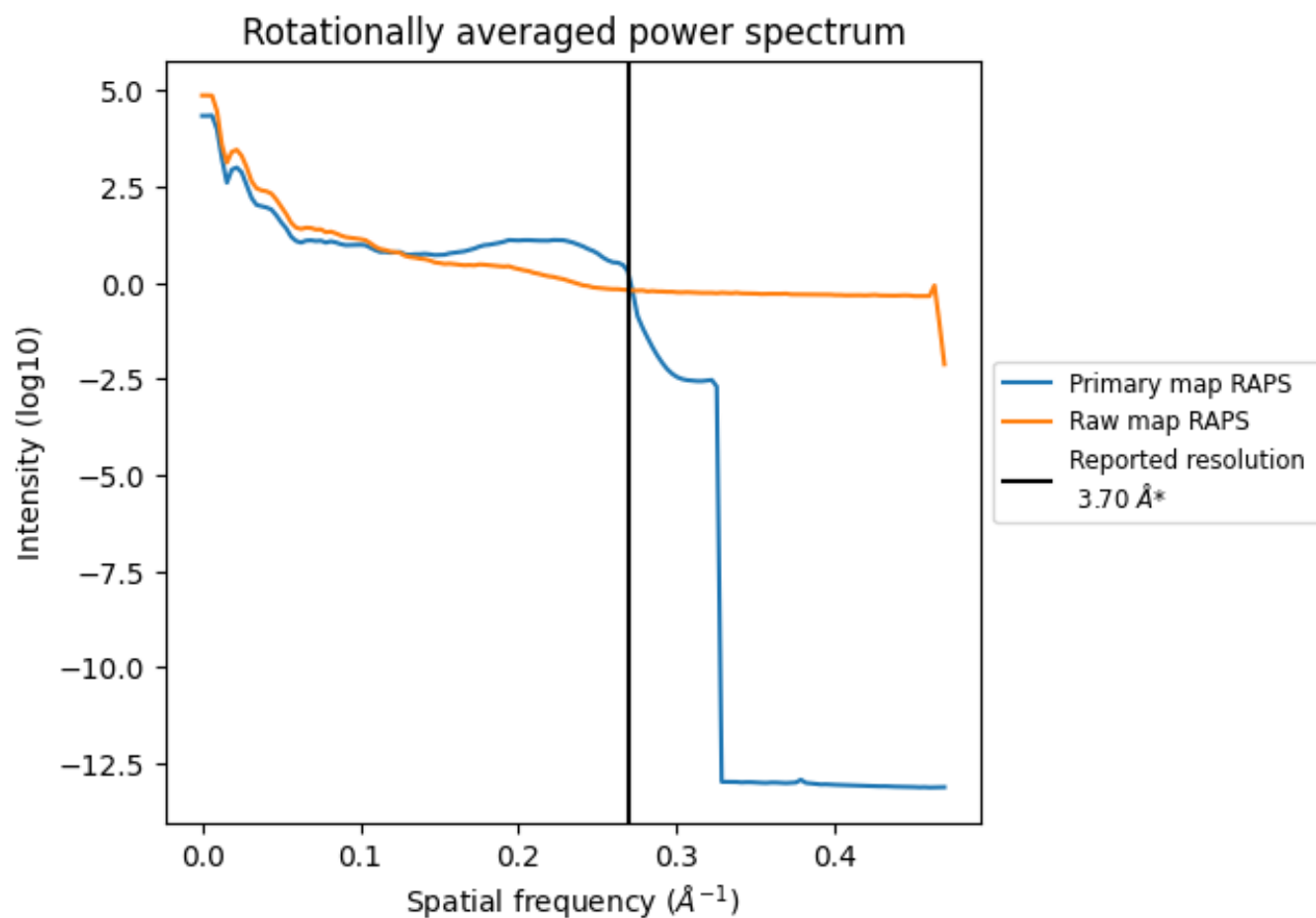
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 79 nm³; this corresponds to an approximate mass of 72 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 ⓘ

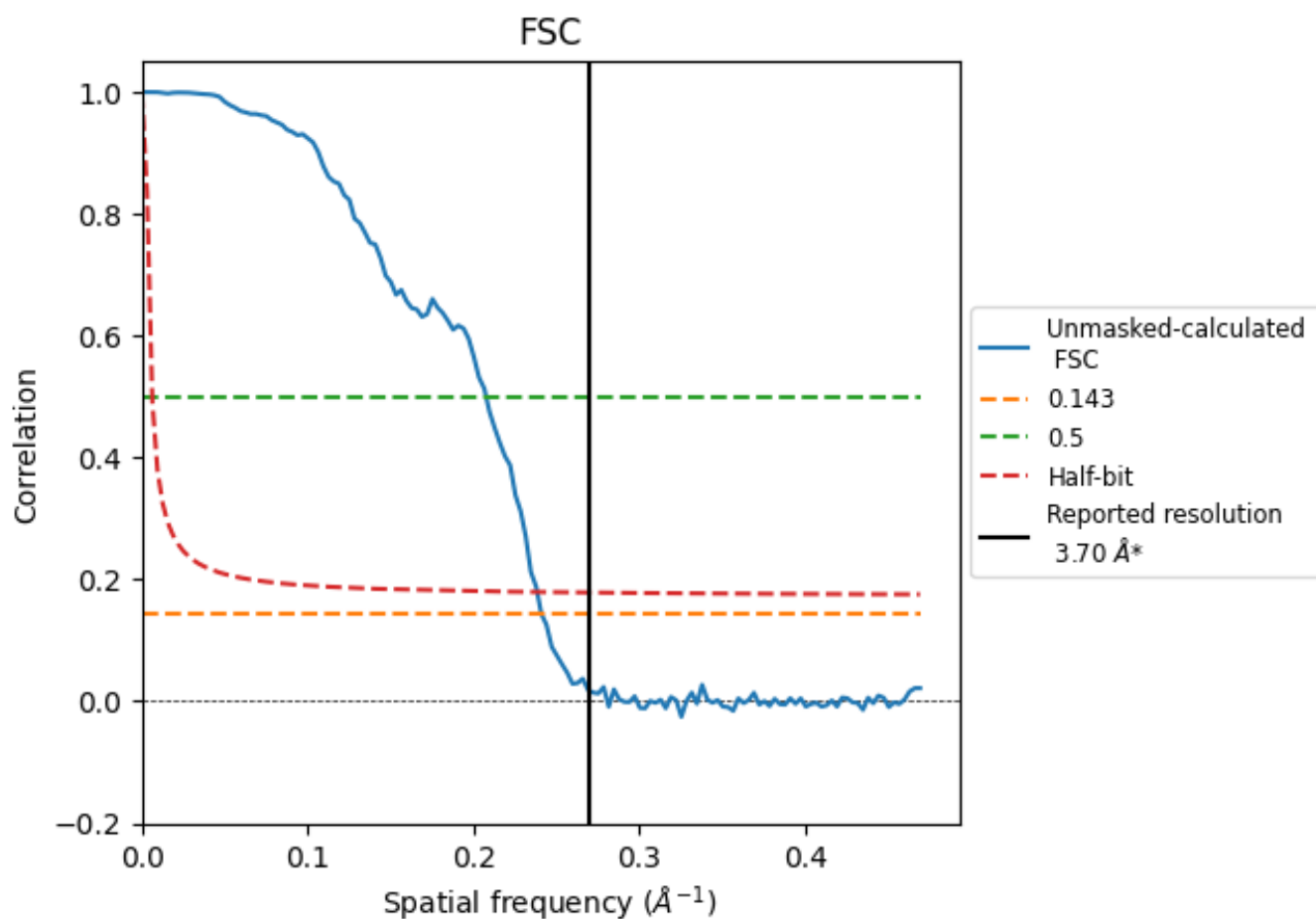


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

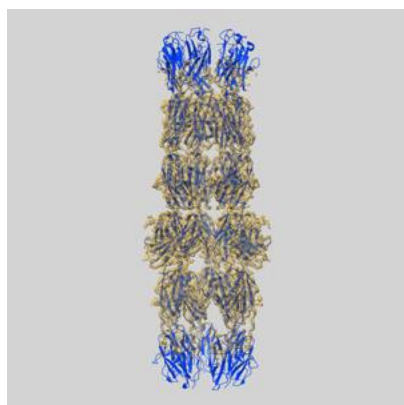
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.15	4.81	4.19

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.15 differs from the reported value 3.7 by more than 10 %

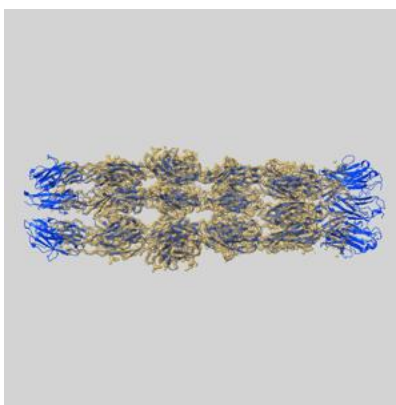
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-50541 and PDB model 9FLW. Per-residue inclusion information can be found in section [3](#) on page [5](#).

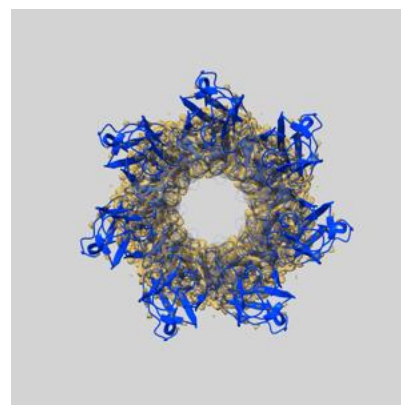
9.1 Map-model overlay [i](#)



X



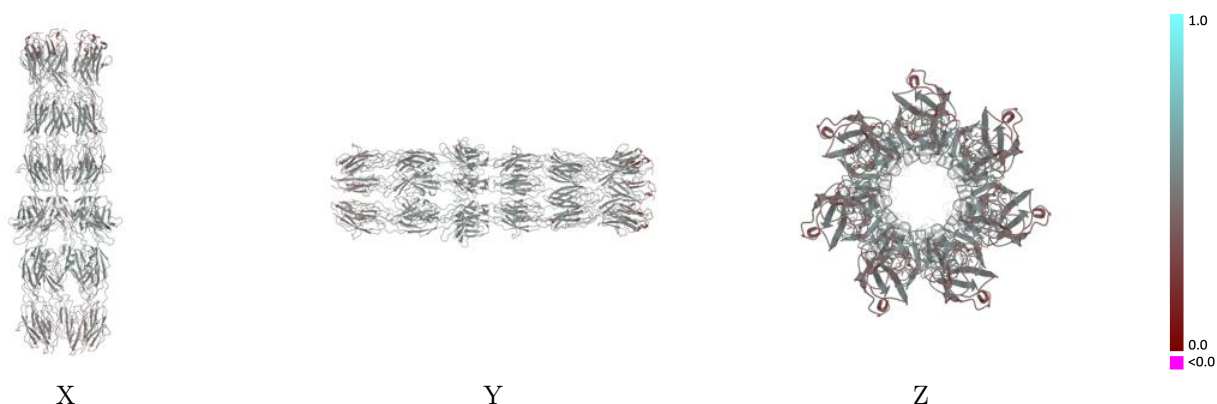
Y



Z

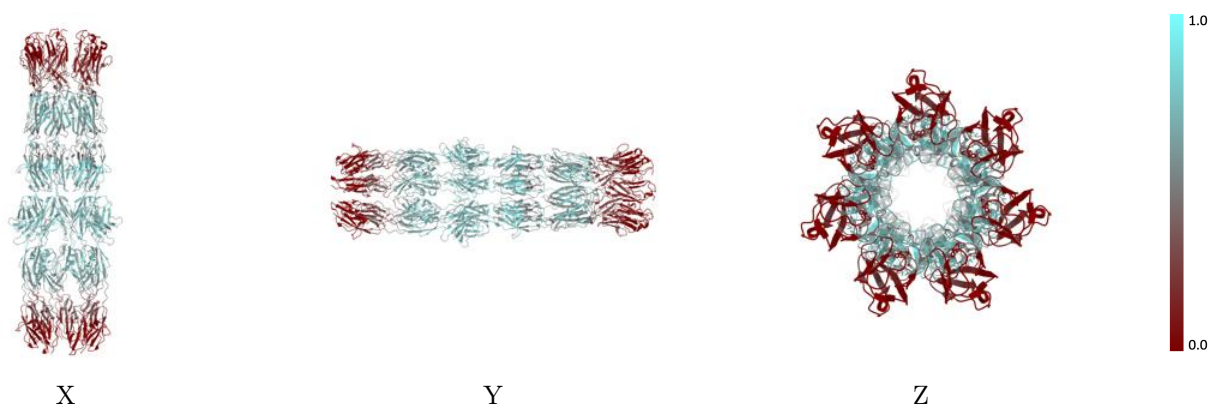
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



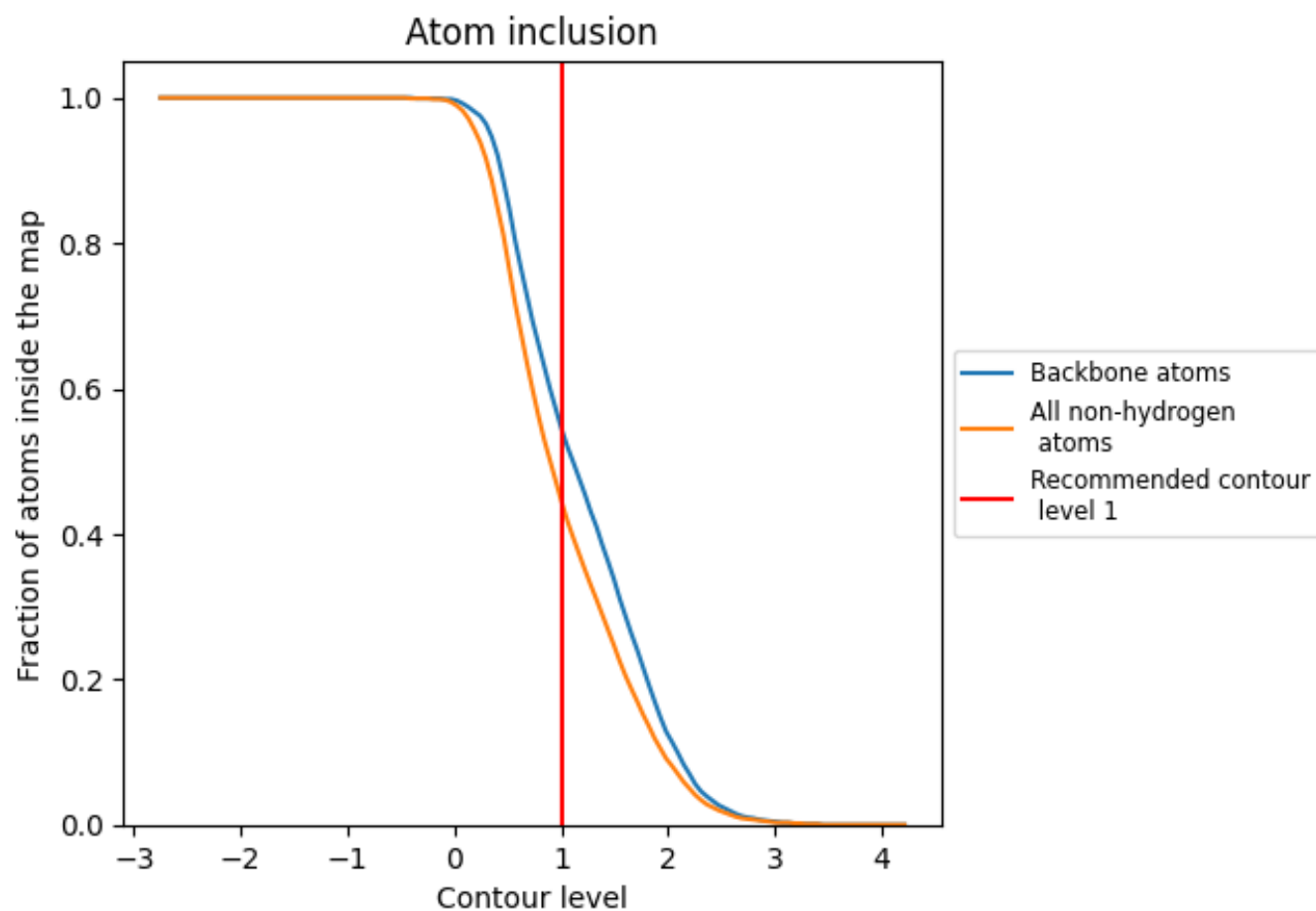
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 55% of all backbone atoms, 45% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4460	0.4720
A	0.4490	0.4720
B	0.4480	0.4720
C	0.4470	0.4720
D	0.4460	0.4720
E	0.4450	0.4730
F	0.4490	0.4710
G	0.4420	0.4720

1.0

0.0

<0.0