



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 06:45 AM UTC

PDB ID : 7LGJ / pdb_00007lgj
EMDB ID : EMD-23325
Title : Cyanophycin synthetase 1 from *Synechocystis* sp. UTEX2470 with ADPCP and 8x(Asp-Arg)-NH₂
Authors : Sharon, I.; Grogg, M.; Hilvert, D.; Schmeing, T.M.
Deposited on : 2021-01-20
Resolution : 2.60 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

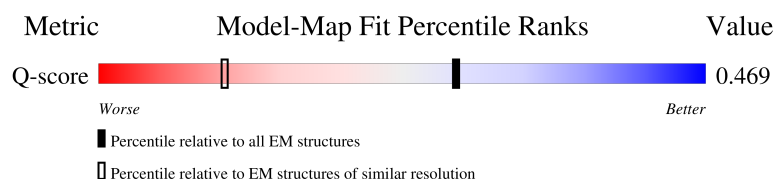
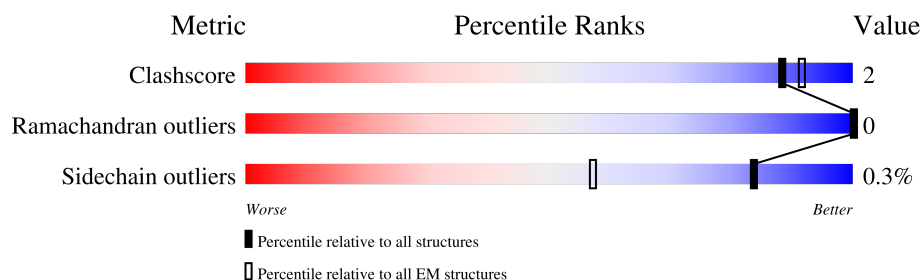
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

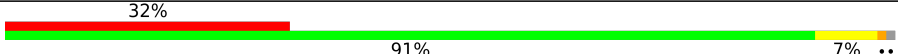
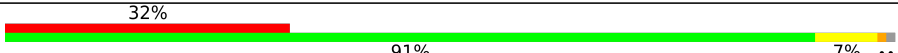
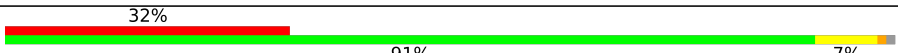
The reported resolution of this entry is 2.60 Å.

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	8728 (2.10 - 3.10)

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	879	
1	B	879	
1	C	879	
1	D	879	

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Mol	Chain	Length	Quality of chain
2	E	9	22%11%33%11%44%
2	F	9	22%11%33%11%44%
2	G	9	22%11%33%11%44%
2	H	9	22%11%33%11%44%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 27397 atoms, of which 305 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 Cyanophycin synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	869	Total	C	N	O	S	0	0
			6645	4182	1162	1277	24		
1	B	869	Total	C	N	O	S	0	0
			6645	4182	1162	1277	24		
1	C	869	Total	C	N	O	S	0	0
			6645	4182	1162	1277	24		
1	D	869	Total	C	N	O	S	0	0
			6645	4182	1162	1277	24		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	874	GLU	-	expression tag	UNP A0A068N621
A	875	ASN	-	expression tag	UNP A0A068N621
A	876	LEU	-	expression tag	UNP A0A068N621
A	877	TYR	-	expression tag	UNP A0A068N621
A	878	PHE	-	expression tag	UNP A0A068N621
A	879	GLN	-	expression tag	UNP A0A068N621
B	874	GLU	-	expression tag	UNP A0A068N621
B	875	ASN	-	expression tag	UNP A0A068N621
B	876	LEU	-	expression tag	UNP A0A068N621
B	877	TYR	-	expression tag	UNP A0A068N621
B	878	PHE	-	expression tag	UNP A0A068N621
B	879	GLN	-	expression tag	UNP A0A068N621
C	874	GLU	-	expression tag	UNP A0A068N621
C	875	ASN	-	expression tag	UNP A0A068N621
C	876	LEU	-	expression tag	UNP A0A068N621
C	877	TYR	-	expression tag	UNP A0A068N621
C	878	PHE	-	expression tag	UNP A0A068N621
C	879	GLN	-	expression tag	UNP A0A068N621
D	874	GLU	-	expression tag	UNP A0A068N621
D	875	ASN	-	expression tag	UNP A0A068N621
D	876	LEU	-	expression tag	UNP A0A068N621
D	877	TYR	-	expression tag	UNP A0A068N621

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Chain	Residue	Modelled	Actual	Comment	Reference
D	878	PHE	-	expression tag	UNP A0A068N621
D	879	GLN	-	expression tag	UNP A0A068N621

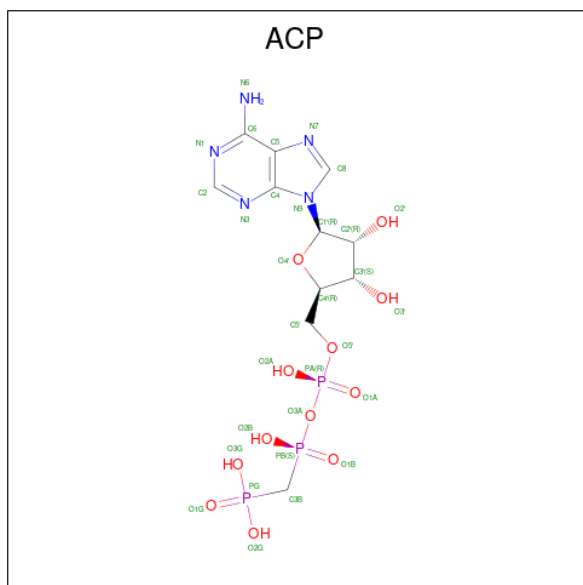
- Molecule 2 is a protein called 8x(Asp-Arg)-NH₂.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	E	5	Total	C	H	N	O	
			112	33	49	17	13	0
2	F	5	Total	C	H	N	O	
			111	33	48	17	13	0
2	G	5	Total	C	H	N	O	
			111	33	48	17	13	0
2	H	5	Total	C	H	N	O	
			111	33	48	17	13	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
3	A	3	Total	Mg	
			3	3	0
3	B	3	Total	Mg	
			3	3	0
3	C	3	Total	Mg	
			3	3	0
3	D	3	Total	Mg	
			3	3	0

- Molecule 4 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).

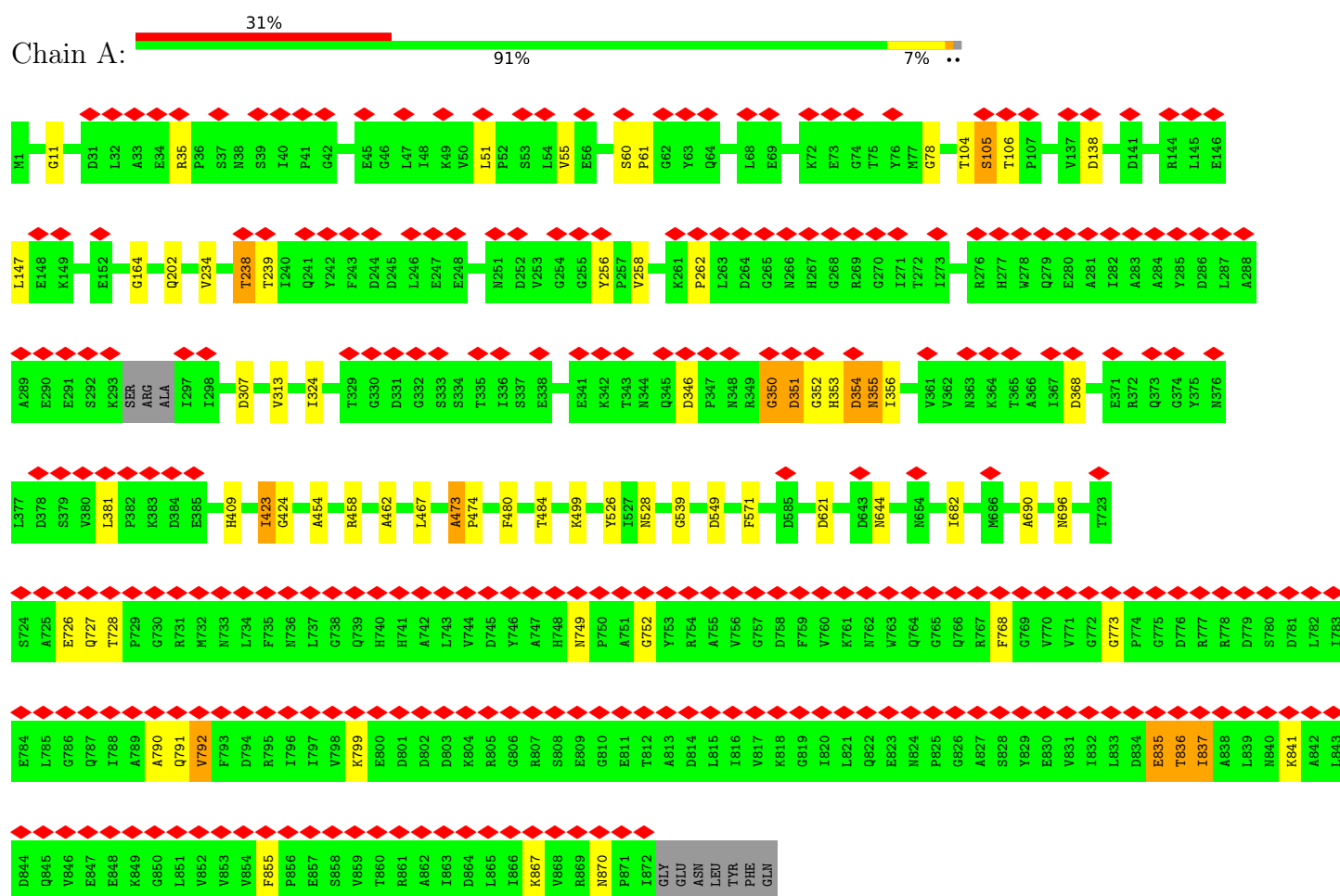


Mol	Chain	Residues	Atoms						AltConf
4	A	1	Total 45	C 11	H 14	N 5	O 12	P 3	0
4	A	1	Total 45	C 11	H 14	N 5	O 12	P 3	0
4	B	1	Total 45	C 11	H 14	N 5	O 12	P 3	0
4	B	1	Total 45	C 11	H 14	N 5	O 12	P 3	0
4	C	1	Total 45	C 11	H 14	N 5	O 12	P 3	0
4	C	1	Total 45	C 11	H 14	N 5	O 12	P 3	0
4	D	1	Total 45	C 11	H 14	N 5	O 12	P 3	0
4	D	1	Total 45	C 11	H 14	N 5	O 12	P 3	0

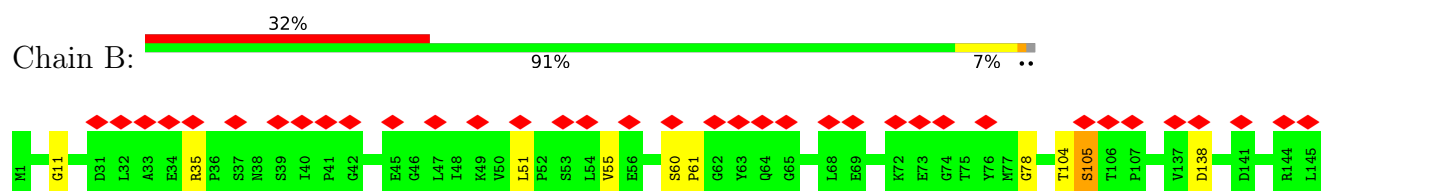
3 Residue-property plots

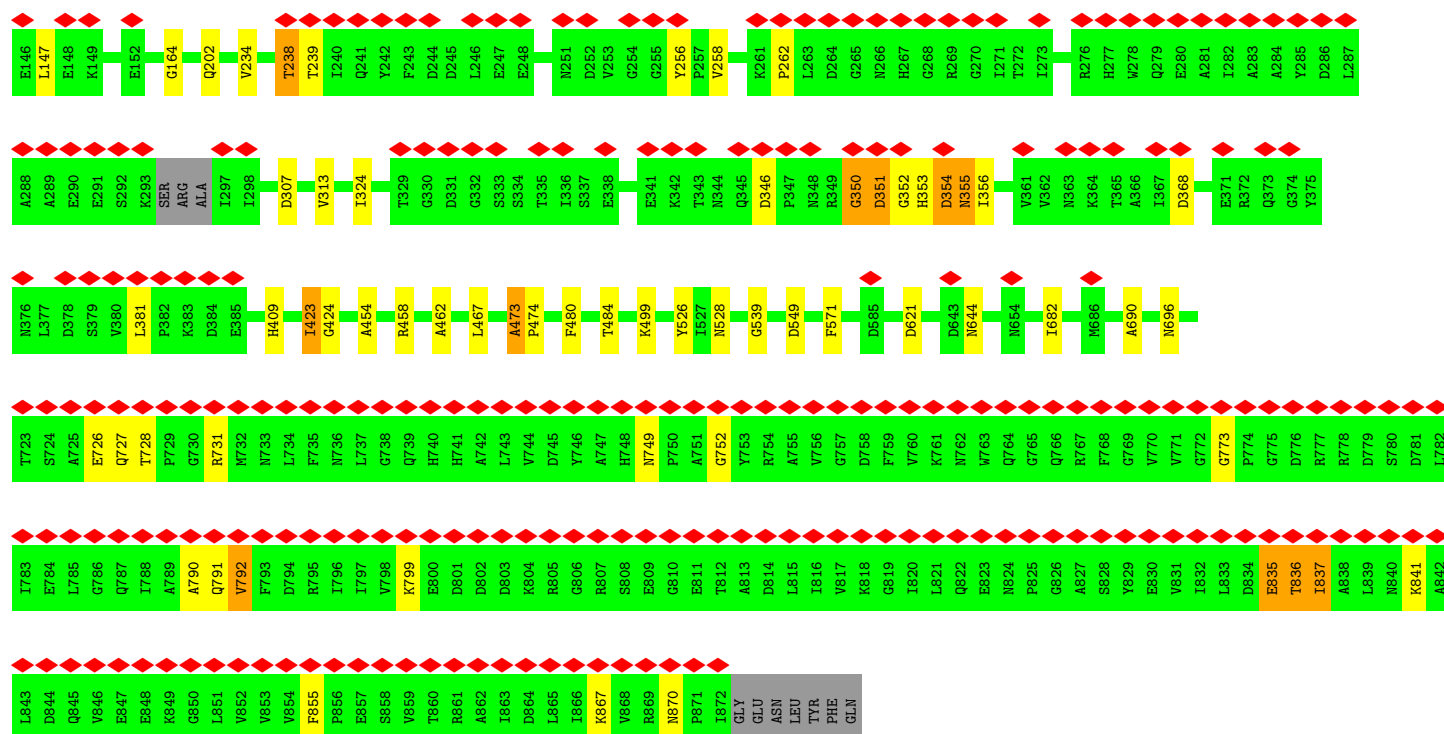
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Cyanophycin synthase

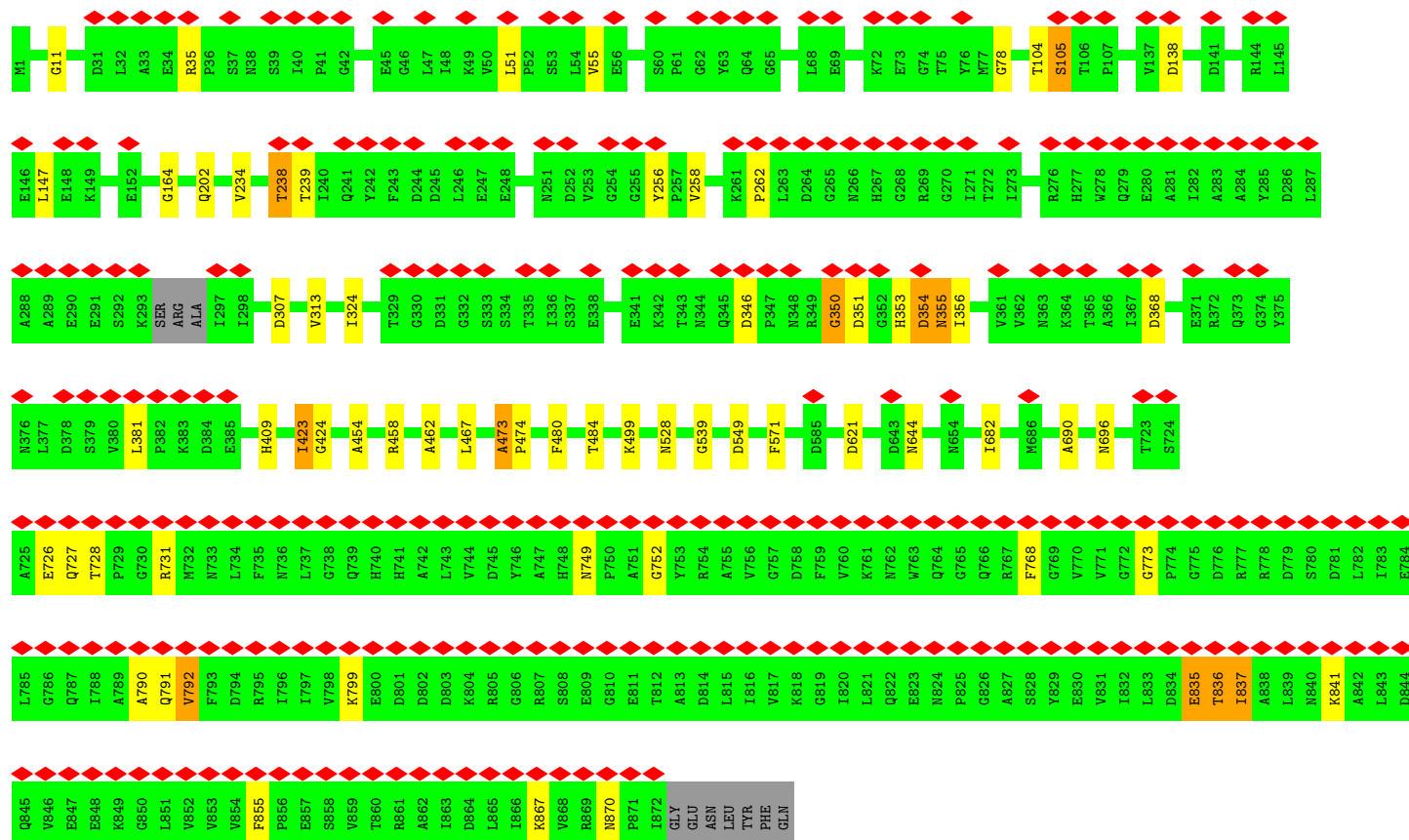
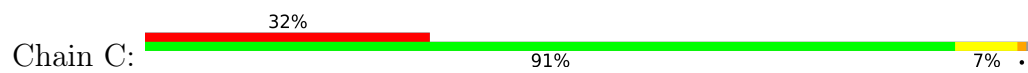


• Molecule 1: Cyanophycin synthase

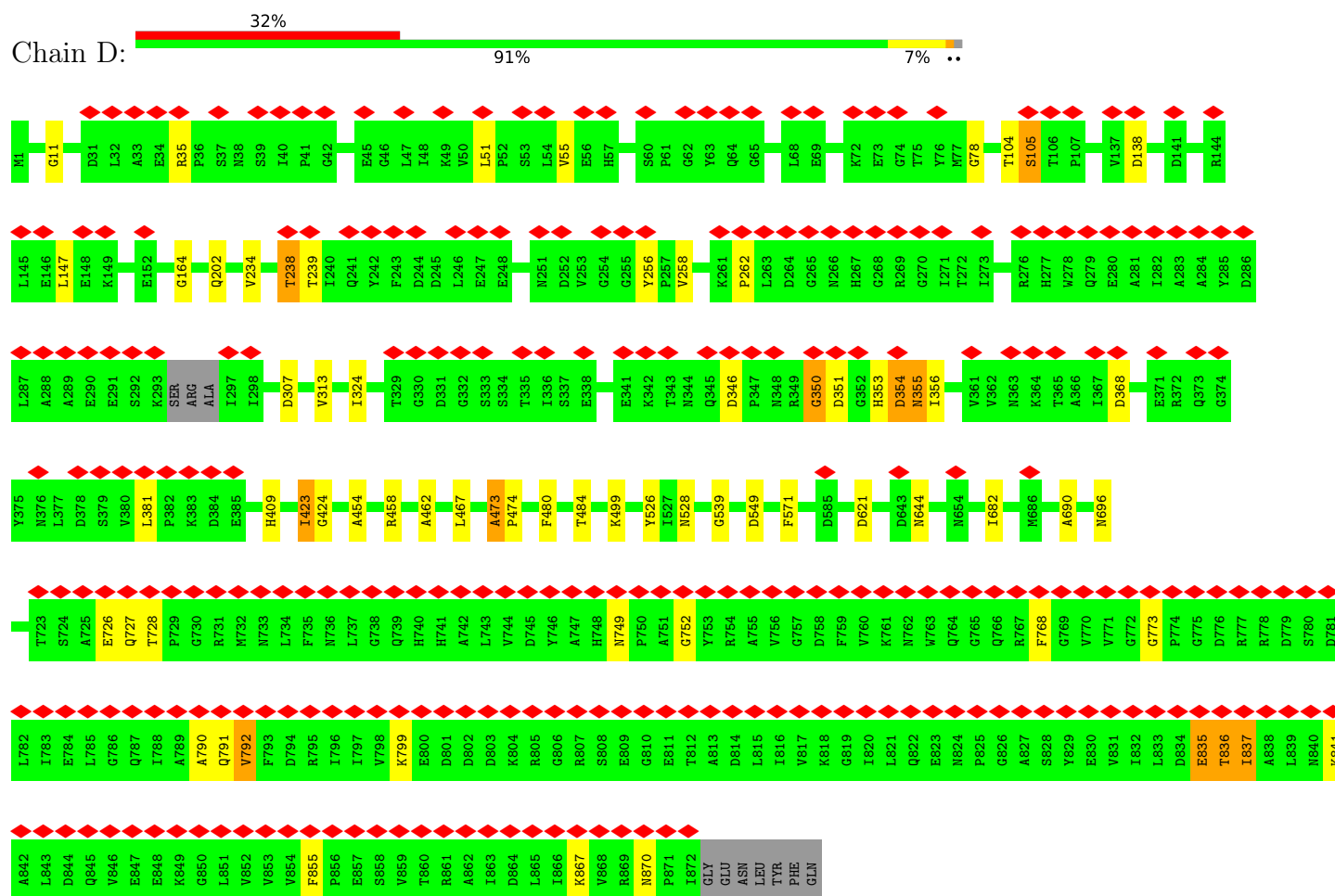




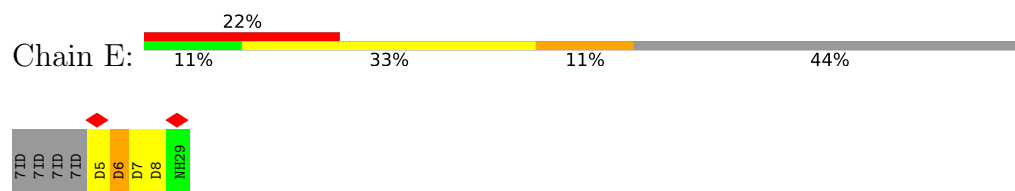
• Molecule 1: Cyanophycin synthase



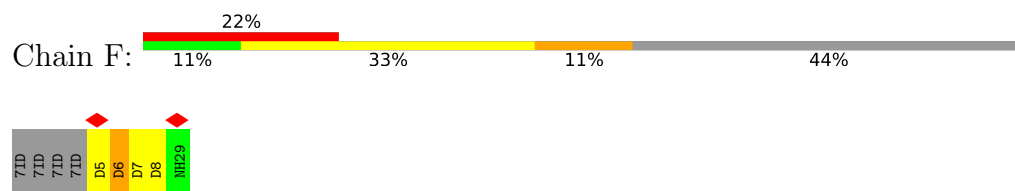
- Molecule 1: Cyanophycin synthase



- Molecule 2: 8x(Asp-Arg)-NH₂

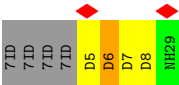


- Molecule 2: 8x(Asp-Arg)-NH₂

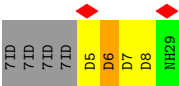


- Molecule 2: 8x(Asp-Arg)-NH₂





• Molecule 2: 8x(Asp-Arg)-NH2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	368761	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	6.421	Depositor
Minimum map value	-3.600	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.134	Depositor
Recommended contour level	0.68	Depositor
Map size (Å)	342.0, 342.0, 342.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.855, 0.855, 0.855	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ACP, NH2, 7ID

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	0.99	5/6758 (0.1%)	1.33	77/9182 (0.8%)
1	B	0.99	6/6758 (0.1%)	1.33	75/9182 (0.8%)
1	C	0.99	6/6758 (0.1%)	1.33	76/9182 (0.8%)
1	D	0.99	5/6758 (0.1%)	1.33	77/9182 (0.8%)
All	All	0.99	22/27032 (0.1%)	1.33	305/36728 (0.8%)

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	355	ASN	C-O	-6.33	1.15	1.23
1	A	355	ASN	C-O	-6.30	1.15	1.23
1	D	355	ASN	C-O	-6.30	1.15	1.23
1	B	355	ASN	C-O	-6.28	1.15	1.23
1	C	728	THR	C-N	6.04	1.41	1.33
1	D	728	THR	C-N	6.04	1.41	1.33
1	A	728	THR	C-N	6.01	1.41	1.33
1	B	728	THR	C-N	6.01	1.41	1.33
1	B	528	ASN	CB-CG	-5.46	1.38	1.52
1	C	528	ASN	CB-CG	-5.46	1.38	1.52
1	D	528	ASN	CB-CG	-5.46	1.38	1.52
1	A	528	ASN	CB-CG	-5.45	1.38	1.52
1	D	458	ARG	C-O	-5.45	1.17	1.24
1	A	458	ARG	C-O	-5.38	1.17	1.24
1	C	458	ARG	C-O	-5.34	1.17	1.24
1	B	458	ARG	C-O	-5.31	1.17	1.24
1	A	35	ARG	NE-CZ	5.21	1.38	1.33
1	B	35	ARG	NE-CZ	5.21	1.38	1.33
1	C	35	ARG	NE-CZ	5.21	1.38	1.33
1	D	35	ARG	NE-CZ	5.15	1.38	1.33
1	B	731	ARG	NE-CZ	5.05	1.38	1.33
1	C	731	ARG	NE-CZ	5.03	1.38	1.33

All (305) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	353	HIS	N-CA-CB	12.63	133.73	113.15
1	D	353	HIS	N-CA-CB	12.62	133.73	113.15
1	A	353	HIS	N-CA-CB	12.60	133.69	113.15
1	C	353	HIS	N-CA-CB	12.59	133.68	113.15
1	D	424	GLY	N-CA-C	10.61	128.98	113.48
1	A	424	GLY	N-CA-C	10.61	128.97	113.48
1	B	424	GLY	N-CA-C	10.61	128.96	113.48
1	C	424	GLY	N-CA-C	10.59	128.94	113.48
1	C	356	ILE	N-CA-C	10.36	120.37	110.42
1	A	356	ILE	N-CA-C	10.31	120.32	110.42
1	D	356	ILE	N-CA-C	10.30	120.31	110.42
1	B	356	ILE	N-CA-C	10.29	120.29	110.42
1	C	78	GLY	N-CA-C	-10.19	98.75	112.82
1	D	78	GLY	N-CA-C	-10.19	98.76	112.82
1	A	78	GLY	N-CA-C	-10.18	98.78	112.82
1	B	78	GLY	N-CA-C	-10.16	98.80	112.82
1	D	773	GLY	CA-C-N	9.82	130.43	119.92
1	D	773	GLY	C-N-CA	9.82	130.43	119.92
1	C	773	GLY	CA-C-N	9.81	130.42	119.92
1	C	773	GLY	C-N-CA	9.81	130.42	119.92
1	A	773	GLY	CA-C-N	9.80	130.41	119.92
1	A	773	GLY	C-N-CA	9.80	130.41	119.92
1	B	773	GLY	CA-C-N	9.76	130.37	119.92
1	B	773	GLY	C-N-CA	9.76	130.37	119.92
1	C	792	VAL	CB-CA-C	-9.73	102.50	111.06
1	A	792	VAL	CB-CA-C	-9.71	102.52	111.06
1	B	792	VAL	CB-CA-C	-9.71	102.52	111.06
1	D	792	VAL	CB-CA-C	-9.68	102.55	111.06
1	C	423	ILE	CB-CA-C	-8.77	96.90	111.29
1	A	423	ILE	CB-CA-C	-8.76	96.93	111.29
1	D	423	ILE	CB-CA-C	-8.76	96.92	111.29
1	B	423	ILE	CB-CA-C	-8.75	96.95	111.29
1	B	350	GLY	N-CA-C	8.54	133.41	113.18
1	C	350	GLY	N-CA-C	8.53	133.40	113.18
1	D	350	GLY	N-CA-C	8.53	133.40	113.18
1	A	350	GLY	N-CA-C	8.53	133.40	113.18
1	C	454	ALA	CA-C-N	8.10	128.04	120.03
1	C	454	ALA	C-N-CA	8.10	128.04	120.03
1	D	454	ALA	CA-C-N	8.08	128.03	120.03
1	D	454	ALA	C-N-CA	8.08	128.03	120.03
1	A	454	ALA	CA-C-N	8.07	128.02	120.03
1	A	454	ALA	C-N-CA	8.07	128.02	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	454	ALA	CA-C-N	8.04	127.99	120.03
1	B	454	ALA	C-N-CA	8.04	127.99	120.03
1	C	51	LEU	CA-C-N	8.04	127.76	119.56
1	C	51	LEU	C-N-CA	8.04	127.76	119.56
1	A	51	LEU	CA-C-N	8.04	127.76	119.56
1	A	51	LEU	C-N-CA	8.04	127.76	119.56
1	D	51	LEU	CA-C-N	8.02	127.74	119.56
1	D	51	LEU	C-N-CA	8.02	127.74	119.56
1	B	51	LEU	CA-C-N	8.02	127.74	119.56
1	B	51	LEU	C-N-CA	8.02	127.74	119.56
1	D	549	ASP	CA-C-N	7.97	127.64	119.82
1	D	549	ASP	C-N-CA	7.97	127.64	119.82
1	C	549	ASP	CA-C-N	7.95	127.61	119.82
1	C	549	ASP	C-N-CA	7.95	127.61	119.82
1	A	549	ASP	CA-C-N	7.94	127.60	119.82
1	A	549	ASP	C-N-CA	7.94	127.60	119.82
1	B	549	ASP	CA-C-N	7.92	127.58	119.82
1	B	549	ASP	C-N-CA	7.92	127.58	119.82
1	B	480	PHE	CA-C-N	7.88	125.41	119.66
1	B	480	PHE	C-N-CA	7.88	125.41	119.66
1	D	480	PHE	CA-C-N	7.86	125.40	119.66
1	D	480	PHE	C-N-CA	7.86	125.40	119.66
1	C	480	PHE	CA-C-N	7.85	125.39	119.66
1	C	480	PHE	C-N-CA	7.85	125.39	119.66
1	A	480	PHE	CA-C-N	7.83	125.38	119.66
1	A	480	PHE	C-N-CA	7.83	125.38	119.66
1	D	791	GLN	N-CA-CB	-7.79	98.96	110.49
1	A	791	GLN	N-CA-CB	-7.77	98.99	110.49
1	C	791	GLN	N-CA-CB	-7.77	99.00	110.49
1	B	791	GLN	N-CA-CB	-7.76	99.01	110.49
1	B	790	ALA	N-CA-C	7.70	121.61	111.75
1	A	790	ALA	N-CA-C	7.68	121.58	111.75
1	C	790	ALA	N-CA-C	7.68	121.58	111.75
1	D	790	ALA	N-CA-C	7.66	121.56	111.75
1	D	313	VAL	N-CA-C	7.50	118.01	111.56
1	C	313	VAL	N-CA-C	7.48	117.99	111.56
1	A	313	VAL	N-CA-C	7.46	117.97	111.56
1	B	351	ASP	N-CA-C	7.43	119.60	108.31
1	C	351	ASP	N-CA-C	7.43	119.60	108.31
1	D	351	ASP	N-CA-C	7.43	119.60	108.31
1	A	351	ASP	N-CA-C	7.42	119.60	108.31
1	B	313	VAL	N-CA-C	7.42	117.94	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	346	ASP	CA-C-N	7.39	127.06	119.82
1	D	346	ASP	C-N-CA	7.39	127.06	119.82
1	B	346	ASP	CA-C-N	7.37	127.04	119.82
1	B	346	ASP	C-N-CA	7.37	127.04	119.82
1	A	346	ASP	CA-C-N	7.37	127.04	119.82
1	A	346	ASP	C-N-CA	7.37	127.04	119.82
1	C	346	ASP	CA-C-N	7.37	127.04	119.82
1	C	346	ASP	C-N-CA	7.37	127.04	119.82
1	C	539	GLY	CA-C-N	7.31	127.02	119.56
1	C	539	GLY	C-N-CA	7.31	127.02	119.56
1	B	539	GLY	CA-C-N	7.28	126.98	119.56
1	B	539	GLY	C-N-CA	7.28	126.98	119.56
1	D	539	GLY	CA-C-N	7.28	126.98	119.56
1	D	539	GLY	C-N-CA	7.28	126.98	119.56
1	A	539	GLY	CA-C-N	7.27	126.98	119.56
1	A	539	GLY	C-N-CA	7.27	126.98	119.56
1	C	467	LEU	CA-C-N	7.24	127.22	119.76
1	C	467	LEU	C-N-CA	7.24	127.22	119.76
1	A	467	LEU	CA-C-N	7.24	127.22	119.76
1	A	467	LEU	C-N-CA	7.24	127.22	119.76
1	D	467	LEU	CA-C-N	7.22	127.20	119.76
1	D	467	LEU	C-N-CA	7.22	127.20	119.76
1	B	467	LEU	CA-C-N	7.20	127.18	119.76
1	B	467	LEU	C-N-CA	7.20	127.18	119.76
1	B	749	ASN	CA-C-N	7.20	127.82	119.47
1	B	749	ASN	C-N-CA	7.20	127.82	119.47
1	D	749	ASN	CA-C-N	7.15	127.77	119.47
1	D	749	ASN	C-N-CA	7.15	127.77	119.47
1	A	749	ASN	CA-C-N	7.15	127.76	119.47
1	A	749	ASN	C-N-CA	7.15	127.76	119.47
1	C	749	ASN	CA-C-N	7.15	127.76	119.47
1	C	749	ASN	C-N-CA	7.15	127.76	119.47
1	C	690	ALA	CA-C-N	7.04	127.63	119.47
1	C	690	ALA	C-N-CA	7.04	127.63	119.47
1	D	690	ALA	CA-C-N	7.04	127.63	119.47
1	D	690	ALA	C-N-CA	7.04	127.63	119.47
1	A	690	ALA	CA-C-N	7.02	127.61	119.47
1	A	690	ALA	C-N-CA	7.02	127.61	119.47
1	C	682	ILE	CA-C-N	7.00	127.60	119.47
1	C	682	ILE	C-N-CA	7.00	127.60	119.47
1	A	682	ILE	CA-C-N	7.00	127.59	119.47
1	A	682	ILE	C-N-CA	7.00	127.59	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	690	ALA	CA-C-N	7.00	127.59	119.47
1	B	690	ALA	C-N-CA	7.00	127.59	119.47
1	C	855	PHE	CA-C-N	6.98	127.15	120.31
1	C	855	PHE	C-N-CA	6.98	127.15	120.31
1	B	682	ILE	CA-C-N	6.97	127.56	119.47
1	B	682	ILE	C-N-CA	6.97	127.56	119.47
1	D	682	ILE	CA-C-N	6.97	127.55	119.47
1	D	682	ILE	C-N-CA	6.97	127.55	119.47
1	A	855	PHE	CA-C-N	6.96	127.14	120.31
1	A	855	PHE	C-N-CA	6.96	127.14	120.31
1	D	855	PHE	CA-C-N	6.94	127.11	120.31
1	D	855	PHE	C-N-CA	6.94	127.11	120.31
1	B	855	PHE	CA-C-N	6.93	127.10	120.31
1	B	855	PHE	C-N-CA	6.93	127.10	120.31
1	D	164	GLY	CA-C-N	6.93	126.63	119.56
1	D	164	GLY	C-N-CA	6.93	126.63	119.56
1	B	164	GLY	CA-C-N	6.90	126.60	119.56
1	B	164	GLY	C-N-CA	6.90	126.60	119.56
1	A	164	GLY	CA-C-N	6.87	126.57	119.56
1	A	164	GLY	C-N-CA	6.87	126.57	119.56
1	C	164	GLY	CA-C-N	6.86	126.56	119.56
1	C	164	GLY	C-N-CA	6.86	126.56	119.56
1	D	790	ALA	CB-CA-C	6.83	123.71	110.46
1	A	105	SER	CB-CA-C	-6.82	108.69	116.54
1	A	790	ALA	CB-CA-C	6.82	123.69	110.46
1	D	105	SER	CB-CA-C	-6.82	108.70	116.54
1	B	105	SER	CB-CA-C	-6.81	108.71	116.54
1	C	790	ALA	CB-CA-C	6.80	123.66	110.46
1	B	790	ALA	CB-CA-C	6.80	123.65	110.46
1	C	105	SER	CB-CA-C	-6.78	108.74	116.54
1	B	484	THR	CA-C-N	6.78	126.95	120.31
1	B	484	THR	C-N-CA	6.78	126.95	120.31
1	C	484	THR	CA-C-N	6.78	126.95	120.31
1	C	484	THR	C-N-CA	6.78	126.95	120.31
1	A	484	THR	CA-C-N	6.76	126.94	120.31
1	A	484	THR	C-N-CA	6.76	126.94	120.31
1	D	484	THR	CA-C-N	6.76	126.93	120.31
1	D	484	THR	C-N-CA	6.76	126.93	120.31
1	B	870	ASN	CA-C-N	6.66	126.62	120.03
1	B	870	ASN	C-N-CA	6.66	126.62	120.03
1	D	238	THR	N-CA-C	6.65	117.06	108.34
1	C	238	THR	N-CA-C	6.63	117.02	108.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	238	THR	N-CA-C	6.62	117.02	108.34
1	B	238	THR	N-CA-C	6.62	117.02	108.34
1	D	870	ASN	CA-C-N	6.61	126.57	120.03
1	D	870	ASN	C-N-CA	6.61	126.57	120.03
1	A	870	ASN	CA-C-N	6.60	126.56	120.03
1	A	870	ASN	C-N-CA	6.60	126.56	120.03
1	C	870	ASN	CA-C-N	6.59	126.56	120.03
1	C	870	ASN	C-N-CA	6.59	126.56	120.03
1	B	409	HIS	CA-C-N	6.50	127.01	119.47
1	B	409	HIS	C-N-CA	6.50	127.01	119.47
1	A	409	HIS	CA-C-N	6.45	126.96	119.47
1	A	409	HIS	C-N-CA	6.45	126.96	119.47
1	A	324	ILE	CA-C-N	6.45	126.42	120.03
1	A	324	ILE	C-N-CA	6.45	126.42	120.03
1	C	409	HIS	CA-C-N	6.45	126.95	119.47
1	C	409	HIS	C-N-CA	6.45	126.95	119.47
1	D	409	HIS	CA-C-N	6.45	126.95	119.47
1	D	409	HIS	C-N-CA	6.45	126.95	119.47
1	C	462	ALA	CA-C-N	6.45	126.41	120.03
1	C	462	ALA	C-N-CA	6.45	126.41	120.03
1	B	324	ILE	CA-C-N	6.43	126.40	120.03
1	B	324	ILE	C-N-CA	6.43	126.40	120.03
1	C	324	ILE	CA-C-N	6.43	126.40	120.03
1	C	324	ILE	C-N-CA	6.43	126.40	120.03
1	D	324	ILE	CA-C-N	6.43	126.40	120.03
1	D	324	ILE	C-N-CA	6.43	126.40	120.03
1	D	462	ALA	CA-C-N	6.42	126.39	120.03
1	D	462	ALA	C-N-CA	6.42	126.39	120.03
1	D	11	GLY	CA-C-N	6.41	126.44	119.90
1	D	11	GLY	C-N-CA	6.41	126.44	119.90
1	A	621	ASP	CA-C-N	6.40	126.32	119.28
1	A	621	ASP	C-N-CA	6.40	126.32	119.28
1	A	462	ALA	CA-C-N	6.40	126.37	120.03
1	A	462	ALA	C-N-CA	6.40	126.37	120.03
1	B	462	ALA	CA-C-N	6.39	126.36	120.03
1	B	462	ALA	C-N-CA	6.39	126.36	120.03
1	C	11	GLY	CA-C-N	6.39	126.42	119.90
1	C	11	GLY	C-N-CA	6.39	126.42	119.90
1	D	621	ASP	CA-C-N	6.39	126.31	119.28
1	D	621	ASP	C-N-CA	6.39	126.31	119.28
1	B	621	ASP	CA-C-N	6.38	126.30	119.28
1	B	621	ASP	C-N-CA	6.38	126.30	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	11	GLY	CA-C-N	6.38	126.41	119.90
1	B	11	GLY	C-N-CA	6.38	126.41	119.90
1	A	11	GLY	CA-C-N	6.38	126.41	119.90
1	A	11	GLY	C-N-CA	6.38	126.41	119.90
1	C	621	ASP	CA-C-N	6.36	126.28	119.28
1	C	621	ASP	C-N-CA	6.36	126.28	119.28
1	D	835	GLU	CB-CA-C	-6.22	100.65	111.35
1	A	835	GLU	CB-CA-C	-6.21	100.66	111.35
1	B	835	GLU	CB-CA-C	-6.21	100.67	111.35
1	C	835	GLU	CB-CA-C	-6.20	100.69	111.35
1	B	836	THR	N-CA-C	-6.00	101.90	111.02
1	B	262	PRO	N-CA-C	-5.98	101.70	111.21
1	D	381	LEU	CA-C-N	5.98	125.94	119.78
1	D	381	LEU	C-N-CA	5.98	125.94	119.78
1	B	381	LEU	CA-C-N	5.98	125.94	119.78
1	B	381	LEU	C-N-CA	5.98	125.94	119.78
1	D	262	PRO	N-CA-C	-5.98	101.71	111.21
1	A	262	PRO	N-CA-C	-5.98	101.71	111.21
1	B	473	ALA	CA-C-N	5.97	125.66	119.56
1	B	473	ALA	C-N-CA	5.97	125.66	119.56
1	C	473	ALA	CA-C-N	5.97	125.66	119.56
1	C	473	ALA	C-N-CA	5.97	125.66	119.56
1	C	836	THR	N-CA-C	-5.97	101.94	111.02
1	A	836	THR	N-CA-C	-5.97	101.94	111.02
1	A	381	LEU	CA-C-N	5.97	125.92	119.78
1	A	381	LEU	C-N-CA	5.97	125.92	119.78
1	D	836	THR	N-CA-C	-5.96	101.96	111.02
1	A	473	ALA	CA-C-N	5.96	125.64	119.56
1	A	473	ALA	C-N-CA	5.96	125.64	119.56
1	C	262	PRO	N-CA-C	-5.96	101.73	111.21
1	C	381	LEU	CA-C-N	5.95	125.91	119.78
1	C	381	LEU	C-N-CA	5.95	125.91	119.78
1	D	473	ALA	CA-C-N	5.95	125.62	119.56
1	D	473	ALA	C-N-CA	5.95	125.62	119.56
1	D	353	HIS	CA-CB-CG	5.90	119.70	113.80
1	C	353	HIS	CA-CB-CG	5.89	119.69	113.80
1	A	353	HIS	CA-CB-CG	5.88	119.68	113.80
1	B	55	VAL	N-CA-C	-5.87	107.54	113.47
1	C	55	VAL	N-CA-C	-5.87	107.54	113.47
1	B	353	HIS	CA-CB-CG	5.86	119.66	113.80
1	A	55	VAL	N-CA-C	-5.86	107.55	113.47
1	D	55	VAL	N-CA-C	-5.85	107.56	113.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	571	PHE	N-CA-C	5.65	120.87	113.30
1	B	571	PHE	N-CA-C	5.63	120.84	113.30
1	A	571	PHE	N-CA-C	5.62	120.84	113.30
1	D	571	PHE	N-CA-C	5.61	120.82	113.30
1	C	727	GLN	N-CA-C	-5.46	105.67	112.93
1	D	727	GLN	N-CA-C	-5.44	105.70	112.93
1	B	727	GLN	N-CA-C	-5.43	105.70	112.93
1	A	727	GLN	N-CA-C	-5.43	105.71	112.93
1	B	644	ASN	CA-C-N	5.40	125.74	119.47
1	B	644	ASN	C-N-CA	5.40	125.74	119.47
1	C	644	ASN	CA-C-N	5.40	125.73	119.47
1	C	644	ASN	C-N-CA	5.40	125.73	119.47
1	A	644	ASN	CA-C-N	5.37	125.70	119.47
1	A	644	ASN	C-N-CA	5.37	125.70	119.47
1	D	499	LYS	N-CA-C	5.37	116.81	111.07
1	A	499	LYS	N-CA-C	5.35	116.80	111.07
1	D	644	ASN	CA-C-N	5.35	125.68	119.47
1	D	644	ASN	C-N-CA	5.35	125.68	119.47
1	C	499	LYS	N-CA-C	5.34	116.79	111.07
1	B	499	LYS	N-CA-C	5.33	116.77	111.07
1	A	354	ASP	N-CA-C	5.19	118.07	111.69
1	B	147	LEU	N-CA-C	-5.18	106.64	113.12
1	A	138	ASP	N-CA-C	-5.18	105.18	112.12
1	B	354	ASP	N-CA-C	5.17	118.05	111.69
1	C	138	ASP	N-CA-C	-5.17	105.19	112.12
1	D	147	LEU	N-CA-C	-5.17	106.66	113.12
1	A	147	LEU	N-CA-C	-5.17	106.66	113.12
1	D	354	ASP	N-CA-C	5.16	118.04	111.69
1	A	234	VAL	CA-C-N	5.16	125.08	119.76
1	A	234	VAL	C-N-CA	5.16	125.08	119.76
1	D	138	ASP	N-CA-C	-5.16	105.20	112.12
1	B	234	VAL	CA-C-N	5.16	125.07	119.76
1	B	234	VAL	C-N-CA	5.16	125.07	119.76
1	C	234	VAL	CA-C-N	5.16	125.07	119.76
1	C	234	VAL	C-N-CA	5.16	125.07	119.76
1	D	234	VAL	CA-C-N	5.16	125.07	119.76
1	D	234	VAL	C-N-CA	5.16	125.07	119.76
1	C	354	ASP	N-CA-C	5.16	118.03	111.69
1	B	138	ASP	N-CA-C	-5.15	105.22	112.12
1	C	147	LEU	N-CA-C	-5.15	106.68	113.12
1	B	368	ASP	CA-CB-CG	5.10	117.70	112.60
1	A	368	ASP	CA-CB-CG	5.05	117.65	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	768	PHE	CA-C-N	-5.03	117.73	122.66
1	C	768	PHE	C-N-CA	-5.03	117.73	122.66
1	D	768	PHE	CA-C-N	-5.02	117.74	122.66
1	D	768	PHE	C-N-CA	-5.02	117.74	122.66
1	B	526	TYR	N-CA-C	5.01	117.75	109.72
1	D	526	TYR	N-CA-C	5.01	117.75	109.72
1	A	768	PHE	CA-C-N	-5.01	117.75	122.66
1	A	768	PHE	C-N-CA	-5.01	117.75	122.66
1	A	526	TYR	N-CA-C	5.01	117.73	109.72
1	C	368	ASP	CA-CB-CG	5.01	117.61	112.60
1	D	368	ASP	CA-CB-CG	5.01	117.61	112.60

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	6645	0	6683	27	0
1	B	6645	0	6683	26	0
1	C	6645	0	6683	24	0
1	D	6645	0	6683	24	0
2	E	63	49	0	1	0
2	F	63	48	0	1	0
2	G	63	48	0	1	0
2	H	63	48	0	1	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
4	A	62	28	28	4	0
4	B	62	28	28	4	0
4	C	62	28	28	4	0
4	D	62	28	28	4	0
All	All	27092	305	26844	101	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 2.

All (101) 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:A:423:ILE:HG22	1:A:423:ILE:O	1.49	1.13
1:B:423:ILE:O	1:B:423:ILE:HG22	1.49	1.13
1:C:423:ILE:HG22	1:C:423:ILE:O	1.49	1.09
1:D:423:ILE:HG22	1:D:423:ILE:O	1.49	1.09
1:B:696:ASN:HD21	4:B:904:ACP:H2	1.31	0.96
1:A:696:ASN:HD21	4:A:904:ACP:H2	1.31	0.95
1:C:696:ASN:HD21	4:C:904:ACP:H2	1.31	0.92
1:D:696:ASN:HD21	4:D:904:ACP:H2	1.31	0.91
1:B:423:ILE:O	1:B:423:ILE:CG2	2.20	0.89
1:A:423:ILE:O	1:A:423:ILE:CG2	2.20	0.89
1:C:423:ILE:O	1:C:423:ILE:CG2	2.20	0.88
1:D:423:ILE:O	1:D:423:ILE:CG2	2.20	0.87
1:A:350:GLY:HA3	1:A:355:ASN:OD1	1.79	0.83
1:B:350:GLY:HA3	1:B:355:ASN:OD1	1.79	0.82
1:C:350:GLY:HA3	1:C:355:ASN:OD1	1.79	0.82
1:D:350:GLY:HA3	1:D:355:ASN:OD1	1.79	0.82
1:C:696:ASN:HD21	4:C:904:ACP:C2	2.07	0.67
1:D:696:ASN:HD21	4:D:904:ACP:C2	2.07	0.67
1:B:799:LYS:HD2	1:B:835:GLU:HB3	1.78	0.66
1:A:799:LYS:HD2	1:A:835:GLU:HB3	1.78	0.66
1:C:799:LYS:HD2	1:C:835:GLU:HB3	1.78	0.66
1:D:799:LYS:HD2	1:D:835:GLU:HB3	1.78	0.66
1:A:350:GLY:O	1:A:354:ASP:HB2	1.97	0.65
1:B:350:GLY:O	1:B:354:ASP:HB2	1.97	0.65
1:A:799:LYS:HD2	1:A:835:GLU:CB	2.27	0.64
1:B:799:LYS:HD2	1:B:835:GLU:CB	2.27	0.64
1:C:799:LYS:HD2	1:C:835:GLU:CB	2.27	0.64
1:D:799:LYS:HD2	1:D:835:GLU:CB	2.27	0.64
1:D:350:GLY:O	1:D:354:ASP:HB2	1.97	0.64
1:C:350:GLY:O	1:C:354:ASP:HB2	1.97	0.64
1:A:696:ASN:HD21	4:A:904:ACP:C2	2.07	0.64
1:B:696:ASN:HD21	4:B:904:ACP:C2	2.07	0.64
1:C:350:GLY:H	1:C:355:ASN:HB2	1.65	0.62
1:D:350:GLY:H	1:D:355:ASN:HB2	1.65	0.62
1:A:350:GLY:N	1:A:355:ASN:HB2	2.15	0.62
1:B:350:GLY:N	1:B:355:ASN:HB2	2.15	0.61
1:D:752:GLY:HA2	4:D:904:ACP:H8	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:752:GLY:HA2	4:A:904:ACP:H8	1.82	0.61
1:C:752:GLY:HA2	4:C:904:ACP:H8	1.82	0.61
1:A:307:ASP:OD2	4:A:905:ACP:O3'	2.19	0.61
1:B:307:ASP:OD2	4:B:905:ACP:O3'	2.19	0.61
1:B:752:GLY:HA2	4:B:904:ACP:H8	1.82	0.61
1:C:350:GLY:N	1:C:355:ASN:HB2	2.15	0.61
1:D:307:ASP:OD2	4:D:905:ACP:O3'	2.19	0.61
1:D:350:GLY:N	1:D:355:ASN:HB2	2.15	0.61
1:B:350:GLY:H	1:B:355:ASN:HB2	1.65	0.60
1:A:350:GLY:H	1:A:355:ASN:HB2	1.64	0.60
1:C:307:ASP:OD2	4:C:905:ACP:O3'	2.19	0.57
1:A:350:GLY:HA3	1:A:355:ASN:CG	2.33	0.53
1:B:350:GLY:HA3	1:B:355:ASN:CG	2.33	0.52
1:C:792:VAL:O	1:C:792:VAL:HG12	2.11	0.51
1:D:792:VAL:HG12	1:D:792:VAL:O	2.11	0.51
1:C:350:GLY:HA3	1:C:355:ASN:CG	2.33	0.51
1:A:350:GLY:CA	1:A:355:ASN:HB2	2.41	0.51
1:D:350:GLY:HA3	1:D:355:ASN:CG	2.33	0.51
1:B:350:GLY:CA	1:B:355:ASN:HB2	2.41	0.51
1:D:350:GLY:CA	1:D:355:ASN:HB2	2.41	0.51
1:C:350:GLY:CA	1:C:355:ASN:HB2	2.41	0.51
1:C:837:ILE:O	1:C:841:LYS:HB3	2.12	0.51
1:B:837:ILE:O	1:B:841:LYS:HB3	2.11	0.50
1:D:837:ILE:O	1:D:841:LYS:HB3	2.12	0.50
1:A:837:ILE:O	1:A:841:LYS:HB3	2.12	0.50
1:B:792:VAL:HG12	1:B:792:VAL:O	2.11	0.49
1:A:792:VAL:HG12	1:A:792:VAL:O	2.10	0.49
1:C:104:THR:OG1	1:C:105:SER:N	2.47	0.48
1:D:104:THR:OG1	1:D:105:SER:N	2.47	0.48
1:A:104:THR:OG1	1:A:105:SER:N	2.47	0.46
1:B:104:THR:OG1	1:B:105:SER:N	2.47	0.46
1:C:238:THR:OG1	1:C:239:THR:N	2.48	0.46
1:D:238:THR:OG1	1:D:239:THR:N	2.48	0.46
1:A:238:THR:OG1	1:A:239:THR:N	2.48	0.46
1:B:238:THR:OG1	1:B:239:THR:N	2.48	0.46
1:D:726:GLU:OE2	1:D:867:LYS:NZ	2.32	0.44
1:B:473:ALA:HB3	1:B:474:PRO:HD3	2.00	0.44
1:A:473:ALA:HB3	1:A:474:PRO:HD3	2.00	0.44
1:C:350:GLY:N	1:C:355:ASN:CB	2.81	0.44
1:D:350:GLY:N	1:D:355:ASN:CB	2.81	0.43
1:A:726:GLU:OE2	1:A:867:LYS:NZ	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:256:TYR:O	1:C:258:VAL:N	2.51	0.43
1:D:256:TYR:O	1:D:258:VAL:N	2.52	0.43
1:B:256:TYR:O	1:B:258:VAL:N	2.51	0.43
1:C:202:GLN:HE21	2:G:6:7ID:CG2	2.32	0.43
1:D:202:GLN:HE21	2:H:6:7ID:CG2	2.32	0.43
1:A:256:TYR:O	1:A:258:VAL:N	2.52	0.43
1:B:726:GLU:OE2	1:B:867:LYS:NZ	2.32	0.43
1:A:202:GLN:HE21	2:E:6:7ID:CG2	2.32	0.42
1:B:202:GLN:HE21	2:F:6:7ID:CG2	2.32	0.42
1:B:350:GLY:N	1:B:355:ASN:CB	2.81	0.42
1:C:792:VAL:O	1:C:792:VAL:CG1	2.68	0.42
1:D:473:ALA:HB3	1:D:474:PRO:HD3	2.00	0.42
1:A:350:GLY:N	1:A:355:ASN:CB	2.81	0.42
1:D:792:VAL:O	1:D:792:VAL:CG1	2.68	0.42
1:C:473:ALA:HB3	1:C:474:PRO:HD3	2.00	0.42
1:B:351:ASP:HB3	1:B:352:GLY:H	1.75	0.41
1:A:351:ASP:HB3	1:A:352:GLY:H	1.75	0.41
1:A:60:SER:N	1:A:61:PRO:CD	2.84	0.41
1:B:60:SER:N	1:B:61:PRO:CD	2.84	0.41
1:C:726:GLU:OE2	1:C:867:LYS:NZ	2.32	0.41
1:A:105:SER:OG	1:A:106:THR:N	2.53	0.40
1:A:792:VAL:O	1:A:792:VAL:CG1	2.68	0.40
1:B:792:VAL:O	1:B:792:VAL:CG1	2.68	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	865/879 (98%)	821 (95%)	44 (5%)	0	100	100
1	B	865/879 (98%)	821 (95%)	44 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	865/879 (98%)	821 (95%)	44 (5%)	0	100	100
1	D	865/879 (98%)	821 (95%)	44 (5%)	0	100	100
All	All	3460/3516 (98%)	3284 (95%)	176 (5%)	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	711/719 (99%)	709 (100%)	2 (0%)	86	94
1	B	711/719 (99%)	709 (100%)	2 (0%)	86	94
1	C	711/719 (99%)	709 (100%)	2 (0%)	86	94
1	D	711/719 (99%)	709 (100%)	2 (0%)	86	94
All	All	2844/2876 (99%)	2836 (100%)	8 (0%)	84	94

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	836	THR
1	A	837	ILE
1	B	836	THR
1	B	837	ILE
1	C	836	THR
1	C	837	ILE
1	D	836	THR
1	D	837	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	241	GLN

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Mol	Chain	Res	Type
1	A	460	HIS
1	A	537	ASN
1	A	586	HIS
1	A	650	HIS
1	A	696	ASN
1	A	739	GLN
1	A	741	HIS
1	A	748	HIS
1	B	241	GLN
1	B	460	HIS
1	B	537	ASN
1	B	586	HIS
1	B	650	HIS
1	B	696	ASN
1	B	739	GLN
1	B	741	HIS
1	B	748	HIS
1	C	241	GLN
1	C	460	HIS
1	C	537	ASN
1	C	586	HIS
1	C	650	HIS
1	C	696	ASN
1	C	739	GLN
1	C	741	HIS
1	C	748	HIS
1	D	241	GLN
1	D	460	HIS
1	D	537	ASN
1	D	586	HIS
1	D	650	HIS
1	D	696	ASN
1	D	739	GLN
1	D	741	HIS
1	D	748	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

16 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	7ID	H	5	2	3,4,19	1.04	0	2,4,24	1.74	1 (50%)
2	7ID	F	5	2	3,4,19	1.04	0	2,4,24	1.72	1 (50%)
2	7ID	G	8	2	17,18,19	2.63	5 (29%)	16,22,24	2.08	5 (31%)
2	7ID	F	8	2	17,18,19	2.63	5 (29%)	16,22,24	2.09	5 (31%)
2	7ID	G	6	2	17,18,19	3.34	5 (29%)	16,22,24	2.25	8 (50%)
2	7ID	G	5	2	3,4,19	1.04	0	2,4,24	1.73	1 (50%)
2	7ID	G	7	2	17,18,19	2.65	5 (29%)	16,22,24	1.33	2 (12%)
2	7ID	E	8	2	17,18,19	2.64	5 (29%)	16,22,24	2.05	4 (25%)
2	7ID	F	6	2	17,18,19	3.36	5 (29%)	16,22,24	2.24	8 (50%)
2	7ID	H	8	2	17,18,19	2.63	5 (29%)	16,22,24	2.05	4 (25%)
2	7ID	F	7	2	17,18,19	2.65	5 (29%)	16,22,24	1.33	2 (12%)
2	7ID	H	7	2	17,18,19	2.63	5 (29%)	16,22,24	1.37	2 (12%)
2	7ID	E	5	2	3,4,19	1.05	0	2,4,24	1.73	1 (50%)
2	7ID	H	6	2	17,18,19	3.37	5 (29%)	16,22,24	2.19	7 (43%)
2	7ID	E	7	2	17,18,19	2.63	5 (29%)	16,22,24	1.37	2 (12%)
2	7ID	E	6	2	17,18,19	3.37	5 (29%)	16,22,24	2.18	7 (43%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	7ID	H	5	2	-	0/1/2/23	-
2	7ID	F	5	2	-	0/1/2/23	-
2	7ID	G	8	2	-	3/20/21/23	-
2	7ID	F	8	2	-	3/20/21/23	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	7ID	G	6	2	-	5/20/21/23	-
2	7ID	G	5	2	-	0/1/2/23	-
2	7ID	G	7	2	-	2/20/21/23	-
2	7ID	E	8	2	-	3/20/21/23	-
2	7ID	F	6	2	-	5/20/21/23	-
2	7ID	H	8	2	-	3/20/21/23	-
2	7ID	F	7	2	-	2/20/21/23	-
2	7ID	H	7	2	-	4/20/21/23	-
2	7ID	E	5	2	-	0/1/2/23	-
2	7ID	H	6	2	-	5/20/21/23	-
2	7ID	E	7	2	-	4/20/21/23	-
2	7ID	E	6	2	-	5/20/21/23	-

All (60) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	6	7ID	CZ2-NE2	8.65	1.49	1.33
2	E	6	7ID	CZ2-NE2	8.61	1.49	1.33
2	G	6	7ID	CZ2-NE2	8.59	1.49	1.33
2	H	6	7ID	CZ2-NE2	8.59	1.49	1.33
2	F	6	7ID	CG-N2	8.47	1.52	1.34
2	H	6	7ID	CG-N2	8.47	1.52	1.34
2	E	6	7ID	CG-N2	8.43	1.51	1.34
2	G	6	7ID	CG-N2	8.43	1.51	1.34
2	H	7	7ID	CZ2-NE2	7.06	1.46	1.33
2	E	7	7ID	CZ2-NE2	7.05	1.46	1.33
2	F	7	7ID	CZ2-NE2	7.05	1.46	1.33
2	G	7	7ID	CZ2-NE2	7.05	1.46	1.33
2	E	8	7ID	CZ2-NE2	6.55	1.45	1.33
2	F	8	7ID	CZ2-NE2	6.55	1.45	1.33
2	G	8	7ID	CZ2-NE2	6.55	1.45	1.33
2	H	8	7ID	CZ2-NE2	6.53	1.45	1.33
2	E	8	7ID	CG-N2	6.06	1.46	1.34
2	G	8	7ID	CG-N2	6.05	1.46	1.34
2	H	8	7ID	CG-N2	6.05	1.46	1.34
2	F	8	7ID	CG-N2	6.03	1.46	1.34
2	G	7	7ID	CG-N2	5.97	1.46	1.34
2	E	7	7ID	CG-N2	5.96	1.46	1.34
2	F	7	7ID	CG-N2	5.94	1.46	1.34
2	H	7	7ID	CG-N2	5.94	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	6	7ID	CZ2-NH1	4.02	1.46	1.32
2	H	6	7ID	CZ2-NH1	4.02	1.46	1.32
2	E	6	7ID	CZ2-NH1	4.00	1.46	1.32
2	F	6	7ID	CZ2-NH1	4.00	1.46	1.32
2	F	7	7ID	CZ2-NH1	3.72	1.45	1.32
2	H	7	7ID	CZ2-NH1	3.72	1.45	1.32
2	E	7	7ID	CZ2-NH1	3.71	1.45	1.32
2	G	7	7ID	CZ2-NH1	3.71	1.45	1.32
2	F	8	7ID	CZ2-NH1	3.53	1.44	1.32
2	H	8	7ID	CZ2-NH1	3.53	1.44	1.32
2	E	8	7ID	CZ2-NH1	3.53	1.44	1.32
2	G	8	7ID	CZ2-NH1	3.51	1.44	1.32
2	E	8	7ID	OD1-CG	-2.94	1.17	1.23
2	F	8	7ID	OD1-CG	-2.92	1.17	1.23
2	G	8	7ID	OD1-CG	-2.92	1.17	1.23
2	H	8	7ID	OD1-CG	-2.89	1.17	1.23
2	E	8	7ID	CZ2-NH2	-2.69	1.24	1.34
2	F	8	7ID	CZ2-NH2	-2.69	1.24	1.34
2	G	8	7ID	CZ2-NH2	-2.69	1.24	1.34
2	H	8	7ID	CZ2-NH2	-2.69	1.24	1.34
2	E	6	7ID	CB-CG	2.56	1.57	1.51
2	G	6	7ID	CB-CG	2.55	1.57	1.51
2	H	6	7ID	CB-CG	2.55	1.57	1.51
2	F	6	7ID	CB-CG	2.54	1.57	1.51
2	F	6	7ID	OD1-CG	-2.51	1.18	1.23
2	H	6	7ID	OD1-CG	-2.51	1.18	1.23
2	E	6	7ID	OD1-CG	-2.49	1.18	1.23
2	G	6	7ID	OD1-CG	-2.46	1.18	1.23
2	H	7	7ID	CZ2-NH2	-2.29	1.25	1.34
2	E	7	7ID	CZ2-NH2	-2.27	1.26	1.34
2	H	7	7ID	OD1-CG	-2.26	1.18	1.23
2	E	7	7ID	OD1-CG	-2.26	1.18	1.23
2	F	7	7ID	CZ2-NH2	-2.26	1.26	1.34
2	G	7	7ID	CZ2-NH2	-2.26	1.26	1.34
2	F	7	7ID	OD1-CG	-2.26	1.18	1.23
2	G	7	7ID	OD1-CG	-2.26	1.18	1.23

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	8	7ID	CB-CG-N2	5.07	123.17	116.25
2	H	8	7ID	CB-CG-N2	5.06	123.17	116.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	8	7ID	CB-CG-N2	5.05	123.15	116.25
2	G	8	7ID	CB-CG-N2	5.05	123.14	116.25
2	H	6	7ID	CB2-CA2-N2	3.58	118.00	110.91
2	F	6	7ID	CB2-CA2-N2	3.57	117.98	110.91
2	E	6	7ID	CB2-CA2-N2	3.56	117.96	110.91
2	G	6	7ID	CB2-CA2-N2	3.55	117.94	110.91
2	G	6	7ID	OD1-CG-CB	-3.45	116.49	121.54
2	E	6	7ID	OD1-CG-CB	-3.45	116.49	121.54
2	H	6	7ID	OD1-CG-CB	-3.44	116.50	121.54
2	F	6	7ID	OD1-CG-CB	-3.43	116.52	121.54
2	F	6	7ID	CB2-CG2-CD2	3.22	121.35	112.07
2	E	6	7ID	CB2-CG2-CD2	3.22	121.35	112.07
2	G	6	7ID	CB2-CG2-CD2	3.21	121.33	112.07
2	H	6	7ID	CB2-CG2-CD2	3.20	121.31	112.07
2	F	8	7ID	OD1-CG-CB	-3.08	117.04	121.54
2	H	8	7ID	OD1-CG-CB	-3.08	117.04	121.54
2	E	8	7ID	OD1-CG-CB	-3.06	117.06	121.54
2	G	8	7ID	OD1-CG-CB	-3.05	117.08	121.54
2	G	6	7ID	CB-CG-N2	3.04	120.40	116.25
2	H	6	7ID	CB-CG-N2	3.02	120.38	116.25
2	E	6	7ID	CB-CG-N2	3.01	120.37	116.25
2	F	6	7ID	CB-CG-N2	3.01	120.36	116.25
2	H	6	7ID	OX2-CO2-O2	-2.94	117.40	124.08
2	G	6	7ID	OX2-CO2-O2	-2.94	117.41	124.08
2	E	6	7ID	OX2-CO2-O2	-2.91	117.47	124.08
2	F	6	7ID	OX2-CO2-O2	-2.91	117.47	124.08
2	E	8	7ID	NH2-CZ2-NE2	2.87	125.78	119.27
2	H	8	7ID	NH2-CZ2-NE2	2.86	125.77	119.27
2	F	8	7ID	NH2-CZ2-NE2	2.85	125.75	119.27
2	G	8	7ID	NH2-CZ2-NE2	2.85	125.75	119.27
2	G	6	7ID	OX2-CO2-CA2	2.69	122.61	113.51
2	F	6	7ID	OX2-CO2-CA2	2.68	122.57	113.51
2	G	6	7ID	NH2-CZ2-NE2	2.62	125.22	119.27
2	H	6	7ID	NH2-CZ2-NE2	2.62	125.22	119.27
2	E	6	7ID	NH2-CZ2-NE2	2.61	125.21	119.27
2	F	6	7ID	NH2-CZ2-NE2	2.59	125.16	119.27
2	G	6	7ID	CA2-N2-CG	2.53	128.03	121.68
2	E	6	7ID	CA2-N2-CG	2.51	127.98	121.68
2	F	6	7ID	CA2-N2-CG	2.51	127.97	121.68
2	H	6	7ID	CA2-N2-CG	2.51	127.97	121.68
2	H	5	7ID	O-C-CA	-2.45	116.39	124.23
2	G	5	7ID	O-C-CA	-2.44	116.41	124.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	5	7ID	O-C-CA	-2.44	116.41	124.23
2	F	5	7ID	O-C-CA	-2.43	116.45	124.23
2	H	7	7ID	NH2-CZ2-NE2	2.29	124.48	119.27
2	E	7	7ID	NH2-CZ2-NE2	2.29	124.48	119.27
2	F	7	7ID	NH2-CZ2-NE2	2.28	124.46	119.27
2	G	7	7ID	NH2-CZ2-NE2	2.28	124.46	119.27
2	F	7	7ID	CB-CG-N2	2.27	119.35	116.25
2	G	7	7ID	CB-CG-N2	2.25	119.33	116.25
2	E	7	7ID	CB-CG-N2	2.25	119.33	116.25
2	H	7	7ID	CB-CG-N2	2.25	119.33	116.25
2	F	8	7ID	OX2-CO2-CA2	2.25	121.11	113.51
2	G	8	7ID	OX2-CO2-CA2	2.25	121.11	113.51
2	H	8	7ID	OX2-CO2-O2	-2.15	119.20	124.08
2	E	8	7ID	OX2-CO2-O2	-2.14	119.22	124.08
2	F	8	7ID	OX2-CO2-O2	-2.14	119.22	124.08
2	G	8	7ID	OX2-CO2-O2	-2.14	119.23	124.08

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	6	7ID	N-CA-CB-CG
2	E	6	7ID	CB2-CA2-N2-CG
2	F	6	7ID	N-CA-CB-CG
2	F	6	7ID	CB2-CA2-N2-CG
2	G	6	7ID	N-CA-CB-CG
2	G	6	7ID	CB2-CA2-N2-CG
2	H	6	7ID	N-CA-CB-CG
2	H	6	7ID	CB2-CA2-N2-CG
2	E	6	7ID	NE2-CD2-CG2-CB2
2	F	6	7ID	NE2-CD2-CG2-CB2
2	G	6	7ID	NE2-CD2-CG2-CB2
2	H	6	7ID	NE2-CD2-CG2-CB2
2	E	7	7ID	CA2-CB2-CG2-CD2
2	F	7	7ID	CA2-CB2-CG2-CD2
2	G	7	7ID	CA2-CB2-CG2-CD2
2	H	7	7ID	CA2-CB2-CG2-CD2
2	E	7	7ID	CO2-CA2-CB2-CG2
2	F	7	7ID	CO2-CA2-CB2-CG2
2	G	7	7ID	CO2-CA2-CB2-CG2
2	H	7	7ID	CO2-CA2-CB2-CG2
2	E	8	7ID	NE2-CD2-CG2-CB2

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Mol	Chain	Res	Type	Atoms
2	F	8	7ID	NE2-CD2-CG2-CB2
2	G	8	7ID	NE2-CD2-CG2-CB2
2	H	8	7ID	NE2-CD2-CG2-CB2
2	E	8	7ID	CB2-CA2-CO2-O2
2	F	8	7ID	CB2-CA2-CO2-OX2
2	G	8	7ID	CB2-CA2-CO2-OX2
2	H	8	7ID	CB2-CA2-CO2-O2
2	E	8	7ID	CB2-CA2-CO2-OX2
2	H	8	7ID	CB2-CA2-CO2-OX2
2	E	6	7ID	N2-CA2-CB2-CG2
2	F	6	7ID	N2-CA2-CB2-CG2
2	G	6	7ID	N2-CA2-CB2-CG2
2	H	6	7ID	N2-CA2-CB2-CG2
2	F	8	7ID	CB2-CA2-CO2-O2
2	G	8	7ID	CB2-CA2-CO2-O2
2	E	6	7ID	CO2-CA2-CB2-CG2
2	F	6	7ID	CO2-CA2-CB2-CG2
2	G	6	7ID	CO2-CA2-CB2-CG2
2	H	6	7ID	CO2-CA2-CB2-CG2
2	E	7	7ID	N2-CA2-CO2-OX2
2	H	7	7ID	N2-CA2-CO2-OX2
2	E	7	7ID	N2-CA2-CO2-O2
2	H	7	7ID	N2-CA2-CO2-O2

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	6	7ID	1	0
2	F	6	7ID	1	0
2	H	6	7ID	1	0
2	E	6	7ID	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 12 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	ACP	A	905	-	31,33,33	0.84	2 (6%)	47,52,52	0.69	0
4	ACP	C	905	-	31,33,33	0.83	2 (6%)	47,52,52	0.69	0
4	ACP	B	905	-	31,33,33	0.84	2 (6%)	47,52,52	0.69	0
4	ACP	A	904	3	31,33,33	1.16	3 (9%)	47,52,52	0.89	3 (6%)
4	ACP	B	904	3	31,33,33	1.16	3 (9%)	47,52,52	0.89	3 (6%)
4	ACP	D	905	-	31,33,33	0.84	2 (6%)	47,52,52	0.69	0
4	ACP	D	904	3	31,33,33	1.16	3 (9%)	47,52,52	0.89	3 (6%)
4	ACP	C	904	3	31,33,33	1.16	3 (9%)	47,52,52	0.89	3 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ACP	A	905	-	-	2/19/38/38	0/3/3/3
4	ACP	C	905	-	-	2/19/38/38	0/3/3/3
4	ACP	B	905	-	-	2/19/38/38	0/3/3/3
4	ACP	A	904	3	-	4/19/38/38	0/3/3/3
4	ACP	B	904	3	-	4/19/38/38	0/3/3/3
4	ACP	D	905	-	-	2/19/38/38	0/3/3/3
4	ACP	D	904	3	-	4/19/38/38	0/3/3/3
4	ACP	C	904	3	-	4/19/38/38	0/3/3/3

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	904	ACP	PB-O2B	-3.33	1.48	1.56
4	A	904	ACP	PB-O2B	-3.30	1.48	1.56
4	B	904	ACP	PB-O2B	-3.28	1.48	1.56
4	D	904	ACP	PB-O2B	-3.28	1.48	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	904	ACP	PG-O3G	-3.26	1.47	1.55
4	D	904	ACP	PG-O3G	-3.26	1.47	1.55
4	A	904	ACP	PG-O3G	-3.25	1.47	1.55
4	C	904	ACP	PG-O3G	-3.23	1.47	1.55
4	C	904	ACP	PG-O2G	-3.03	1.48	1.55
4	A	904	ACP	PG-O2G	-3.03	1.48	1.55
4	D	904	ACP	PG-O2G	-3.02	1.48	1.55
4	B	904	ACP	PG-O2G	-3.01	1.48	1.55
4	D	905	ACP	PB-O2B	-2.52	1.50	1.56
4	B	905	ACP	PB-O2B	-2.51	1.50	1.56
4	A	905	ACP	PB-O2B	-2.50	1.50	1.56
4	C	905	ACP	PB-O2B	-2.49	1.50	1.56
4	D	905	ACP	PG-O3G	-2.38	1.49	1.55
4	A	905	ACP	PG-O3G	-2.38	1.49	1.55
4	B	905	ACP	PG-O3G	-2.38	1.49	1.55
4	C	905	ACP	PG-O3G	-2.35	1.49	1.55

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	904	ACP	PB-O3A-PA	2.91	141.86	132.37
4	B	904	ACP	PB-O3A-PA	2.90	141.84	132.37
4	A	904	ACP	PB-O3A-PA	2.89	141.81	132.37
4	D	904	ACP	PB-O3A-PA	2.89	141.78	132.37
4	D	904	ACP	C2'-C1'-N9	2.24	118.87	113.30
4	B	904	ACP	C2'-C1'-N9	2.23	118.85	113.30
4	C	904	ACP	C2'-C1'-N9	2.23	118.85	113.30
4	A	904	ACP	C2'-C1'-N9	2.23	118.85	113.30
4	D	904	ACP	O2A-PA-O3A	2.23	113.29	107.27
4	C	904	ACP	O2A-PA-O3A	2.22	113.28	107.27
4	A	904	ACP	O2A-PA-O3A	2.22	113.26	107.27
4	B	904	ACP	O2A-PA-O3A	2.20	113.23	107.27

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	904	ACP	PB-C3B-PG-O1G
4	A	904	ACP	PB-C3B-PG-O2G
4	A	904	ACP	PB-C3B-PG-O3G
4	A	905	ACP	O4'-C4'-C5'-O5'
4	B	904	ACP	PB-C3B-PG-O1G

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Mol	Chain	Res	Type	Atoms
4	B	904	ACP	PB-C3B-PG-O2G
4	B	904	ACP	PB-C3B-PG-O3G
4	B	905	ACP	O4'-C4'-C5'-O5'
4	C	904	ACP	PB-C3B-PG-O1G
4	C	904	ACP	PB-C3B-PG-O2G
4	C	904	ACP	PB-C3B-PG-O3G
4	C	905	ACP	O4'-C4'-C5'-O5'
4	D	904	ACP	PB-C3B-PG-O1G
4	D	904	ACP	PB-C3B-PG-O2G
4	D	904	ACP	PB-C3B-PG-O3G
4	D	905	ACP	O4'-C4'-C5'-O5'
4	A	905	ACP	C3'-C4'-C5'-O5'
4	B	905	ACP	C3'-C4'-C5'-O5'
4	C	905	ACP	C3'-C4'-C5'-O5'
4	D	905	ACP	C3'-C4'-C5'-O5'
4	A	904	ACP	O4'-C1'-N9-C8
4	B	904	ACP	O4'-C1'-N9-C8
4	C	904	ACP	O4'-C1'-N9-C8
4	D	904	ACP	O4'-C1'-N9-C8

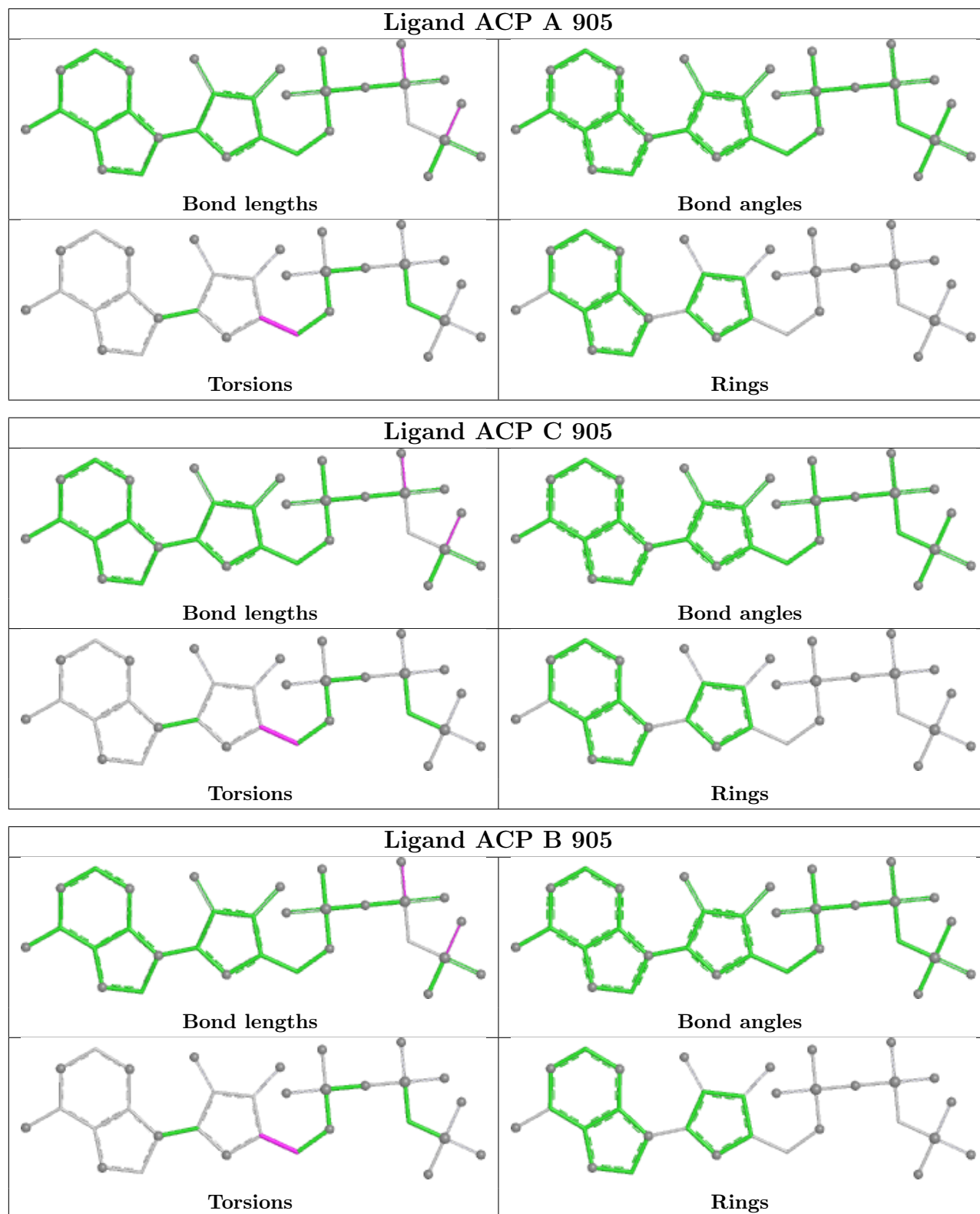
There are no ring outliers.

8 monomers are involved in 16 short contacts:

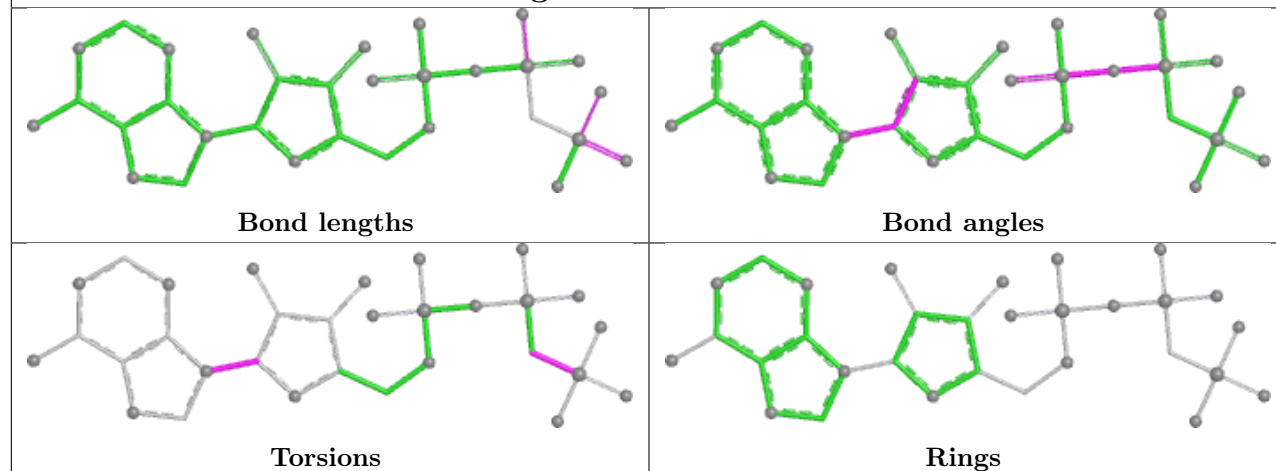
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	905	ACP	1	0
4	C	905	ACP	1	0
4	B	905	ACP	1	0
4	A	904	ACP	3	0
4	B	904	ACP	3	0
4	D	905	ACP	1	0
4	D	904	ACP	3	0
4	C	904	ACP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

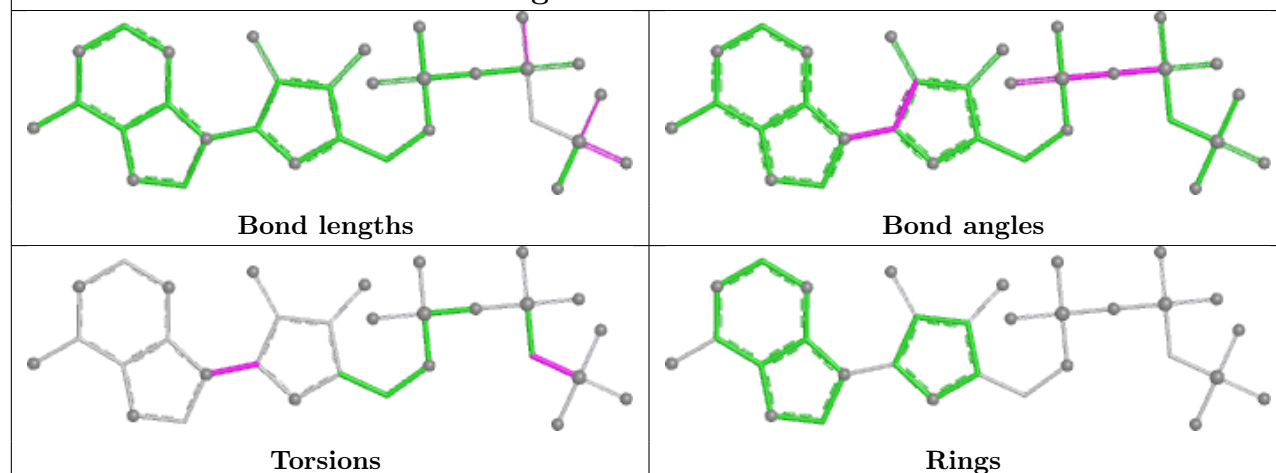
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



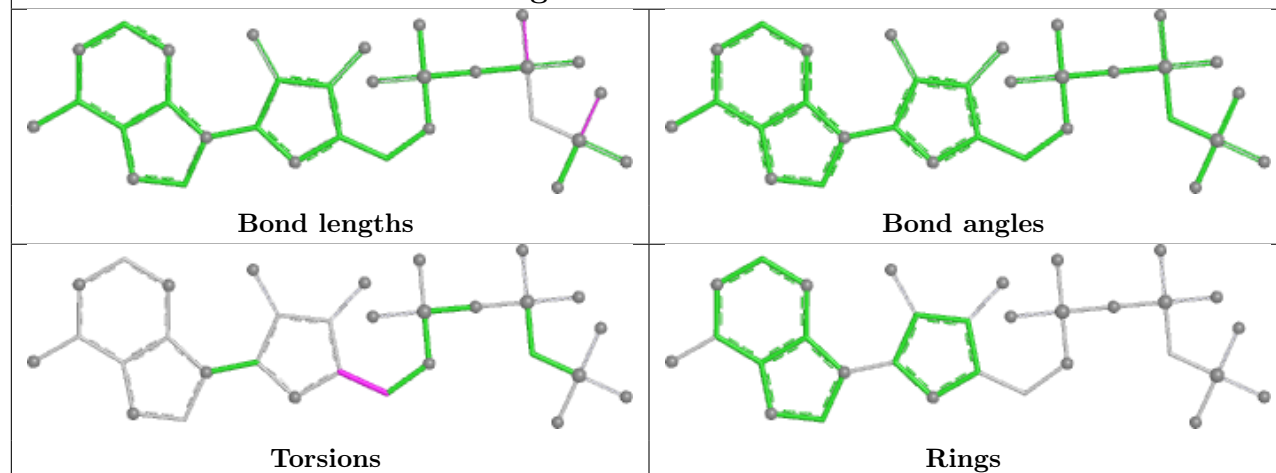
Ligand ACP A 904

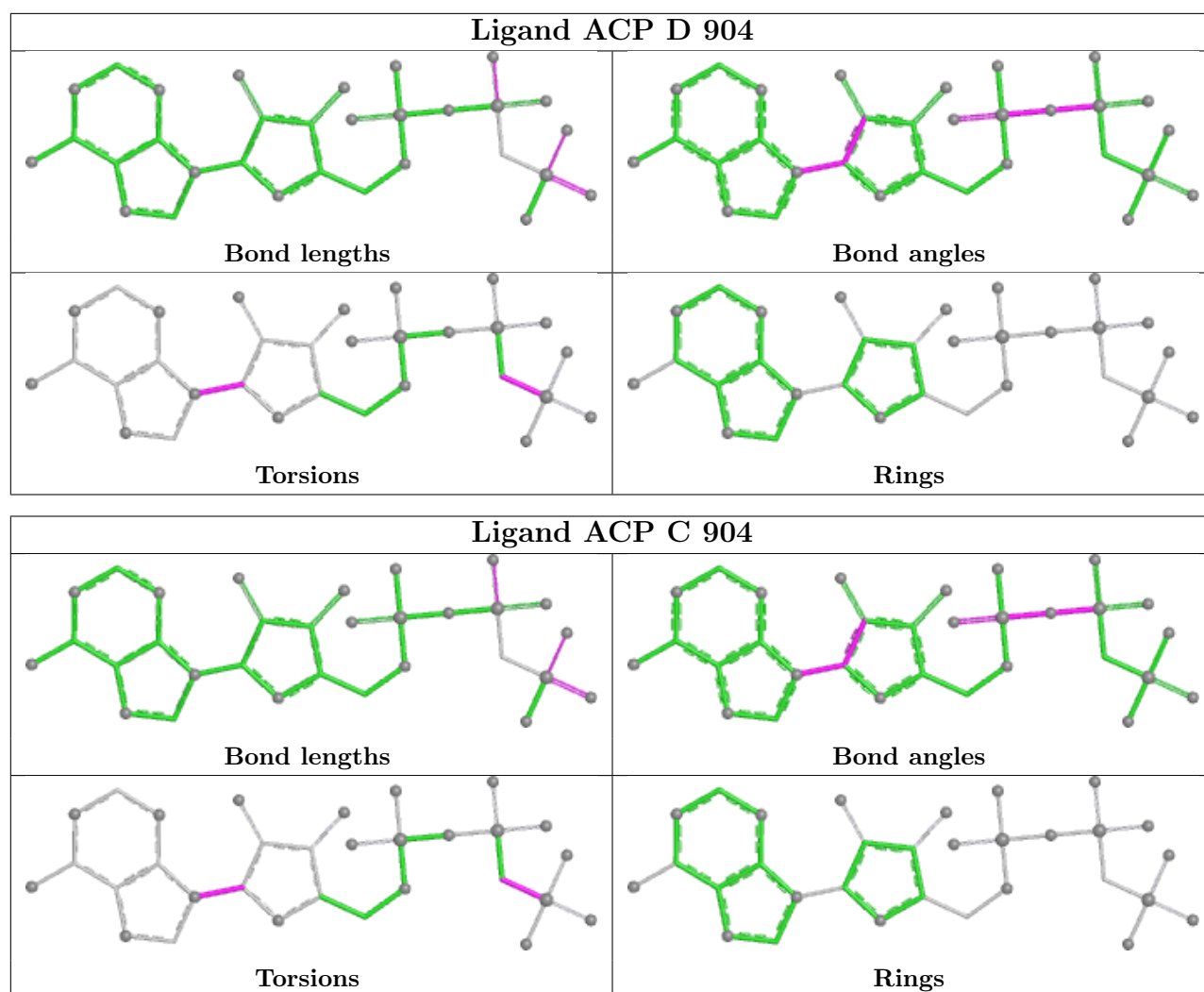


Ligand ACP B 904



Ligand ACP D 905





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.

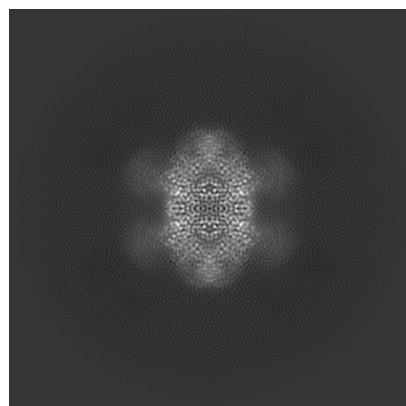
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23325. These allow visual inspection of the internal detail of the map and identification of artifacts.

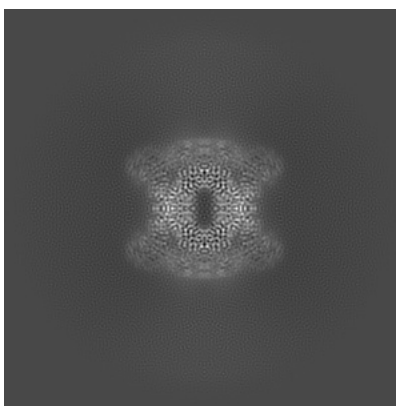
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

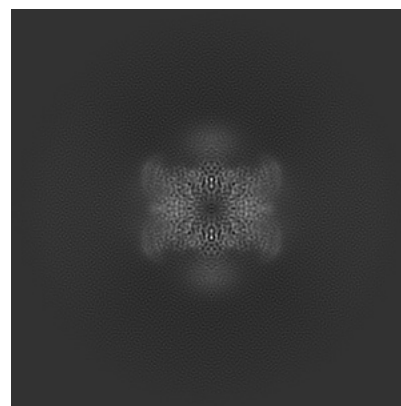
6.1.1 Primary map



X

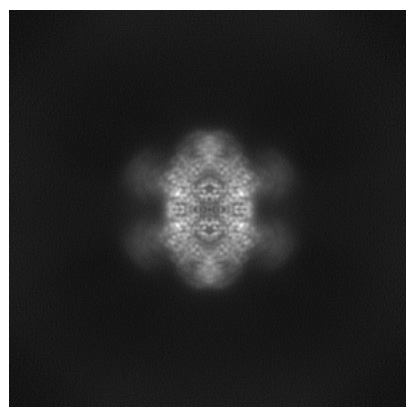


Y

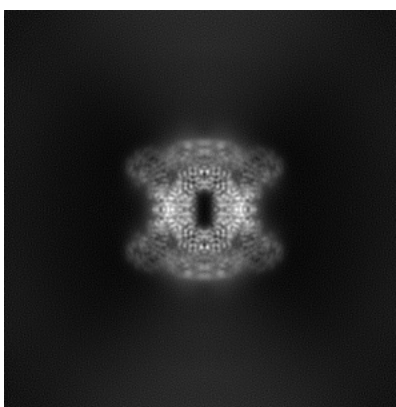


Z

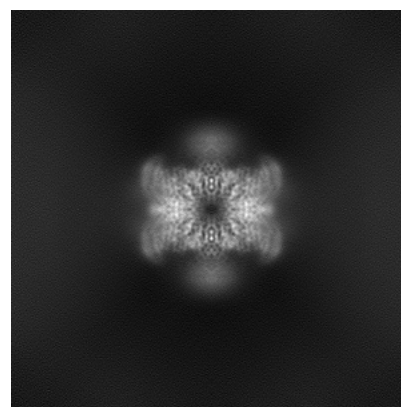
6.1.2 Raw map



X



Y

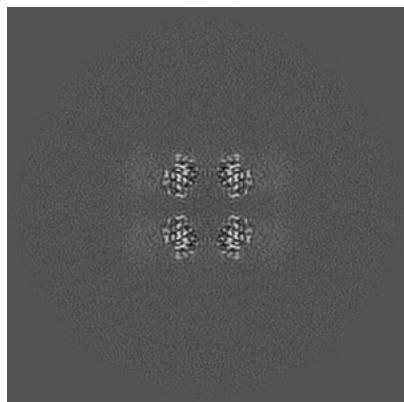


Z

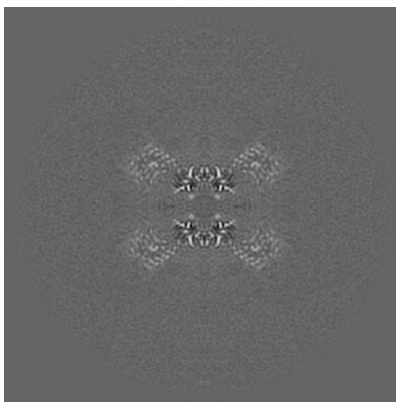
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

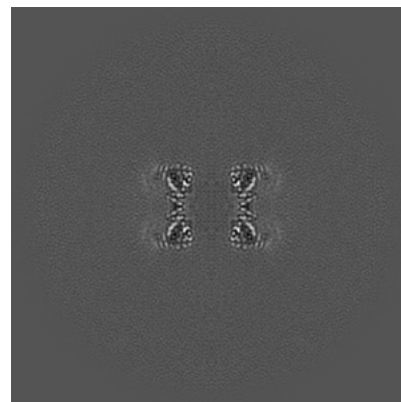
6.2.1 Primary map



X Index: 200

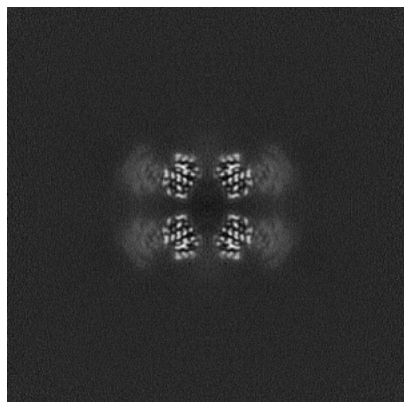


Y Index: 200

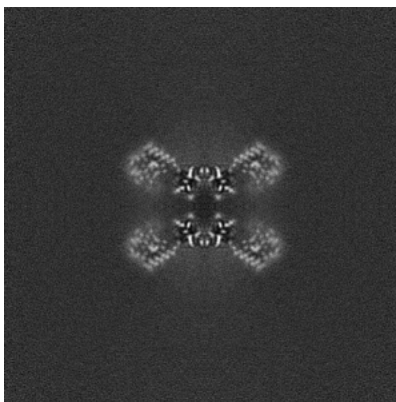


Z Index: 200

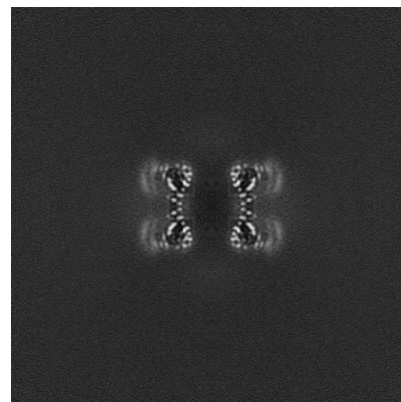
6.2.2 Raw map



X Index: 200



Y Index: 200

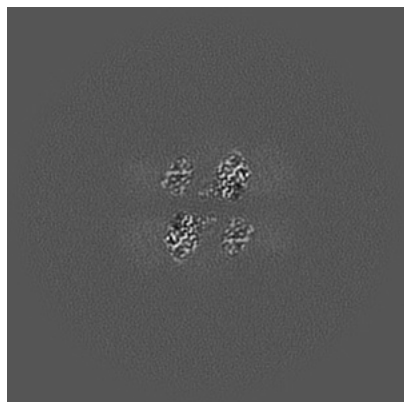


Z Index: 200

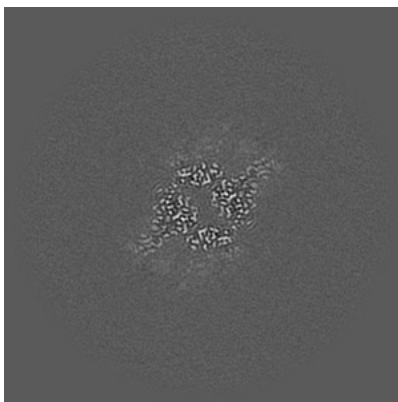
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

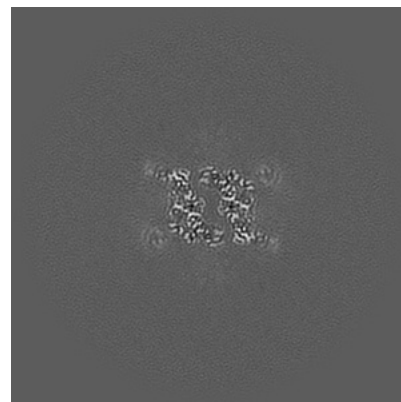
6.3.1 Primary map



X Index: 189

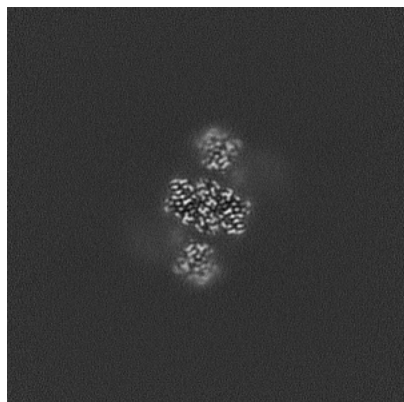


Y Index: 179

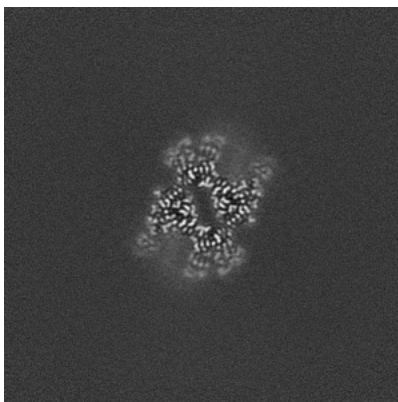


Z Index: 186

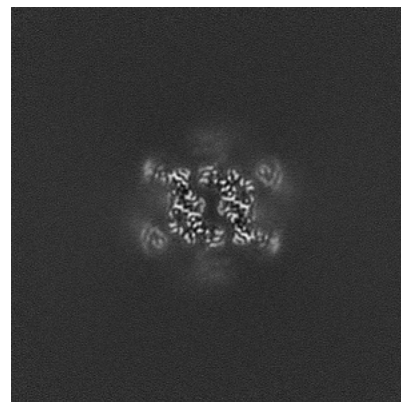
6.3.2 Raw map



X Index: 165



Y Index: 172

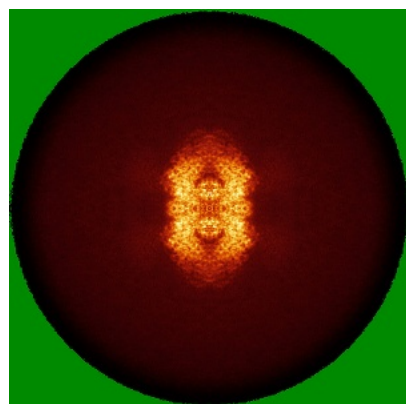


Z Index: 186

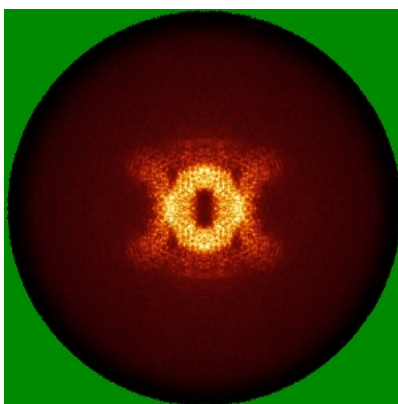
The images above show the largest variance slices of the map in three orthogonal directions.

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

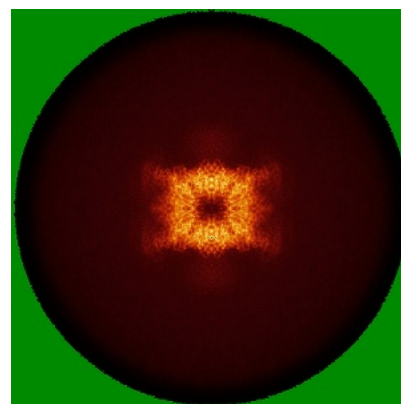
6.4.1 Primary map



X

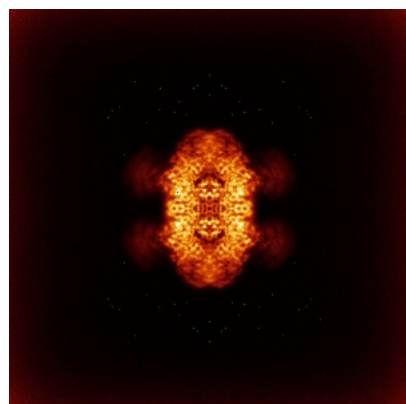


Y

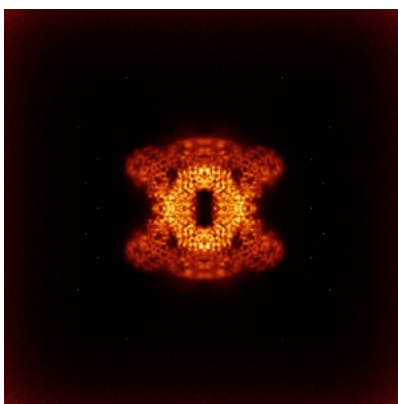


Z

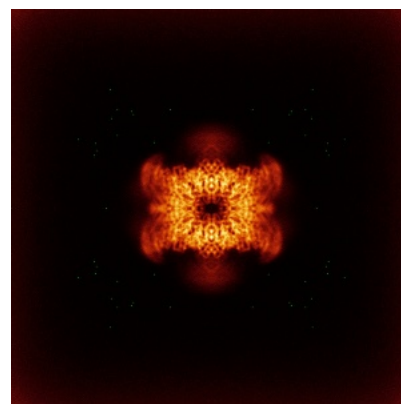
6.4.2 Raw map



X



Y

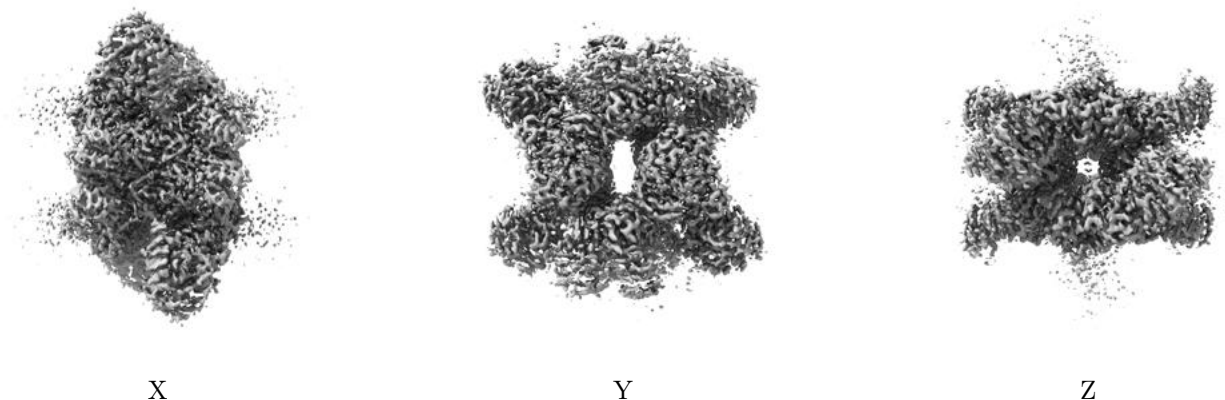


Z

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.

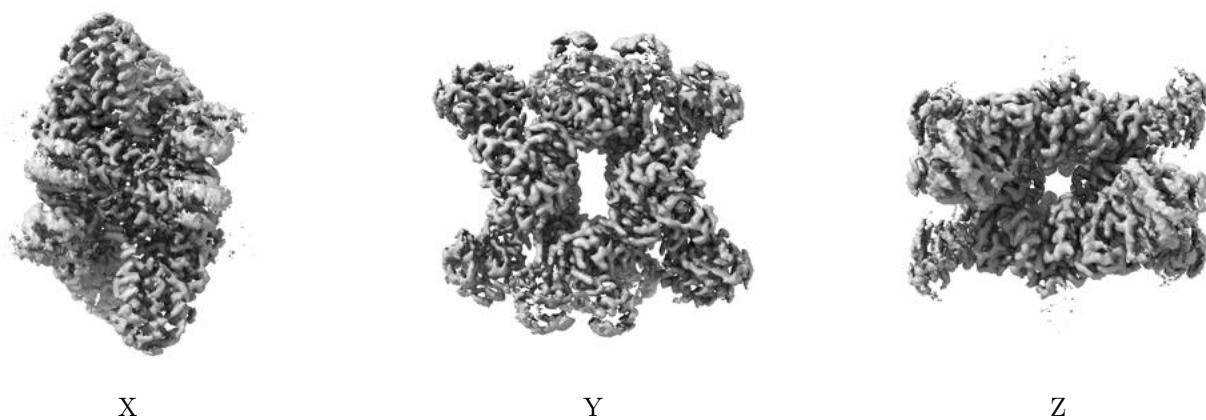
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.68. 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.

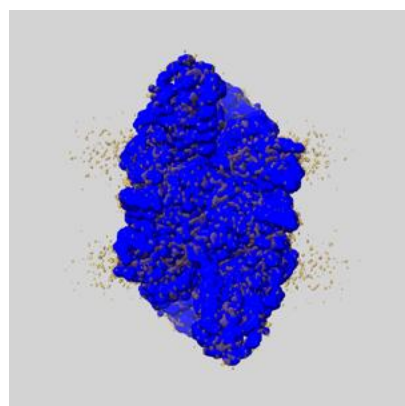
6.6 Mask visualisation [i](#)

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

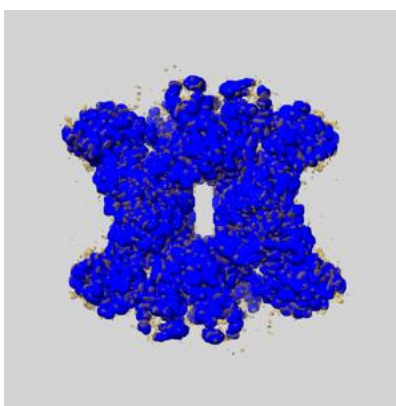
A mask typically either:

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

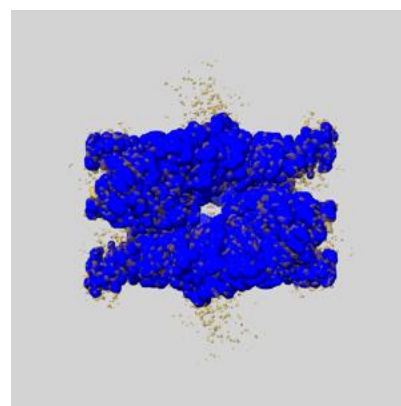
6.6.1 emd_23325_msk_1.map [i](#)



X



Y

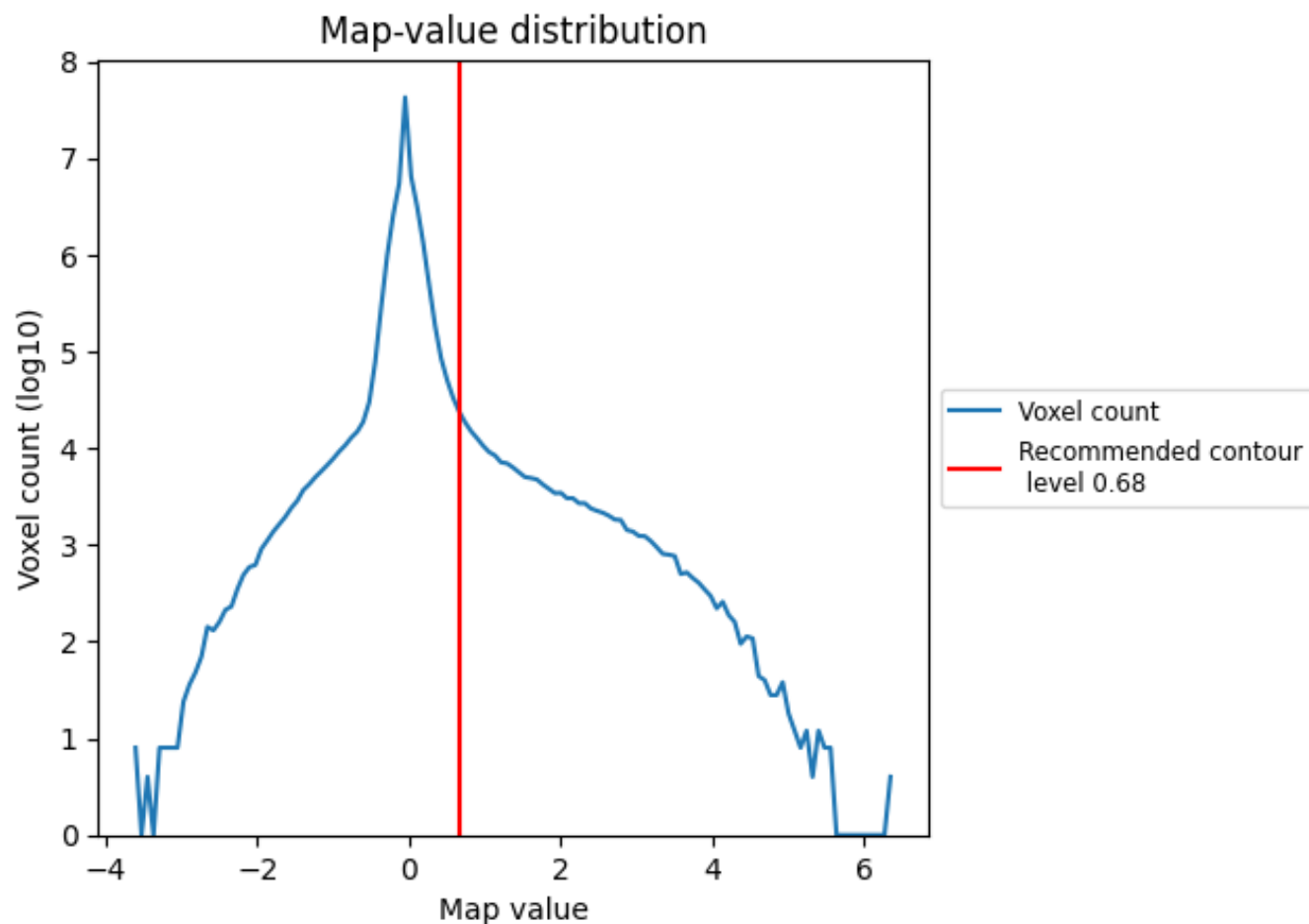


Z

7 Map analysis [i](#)

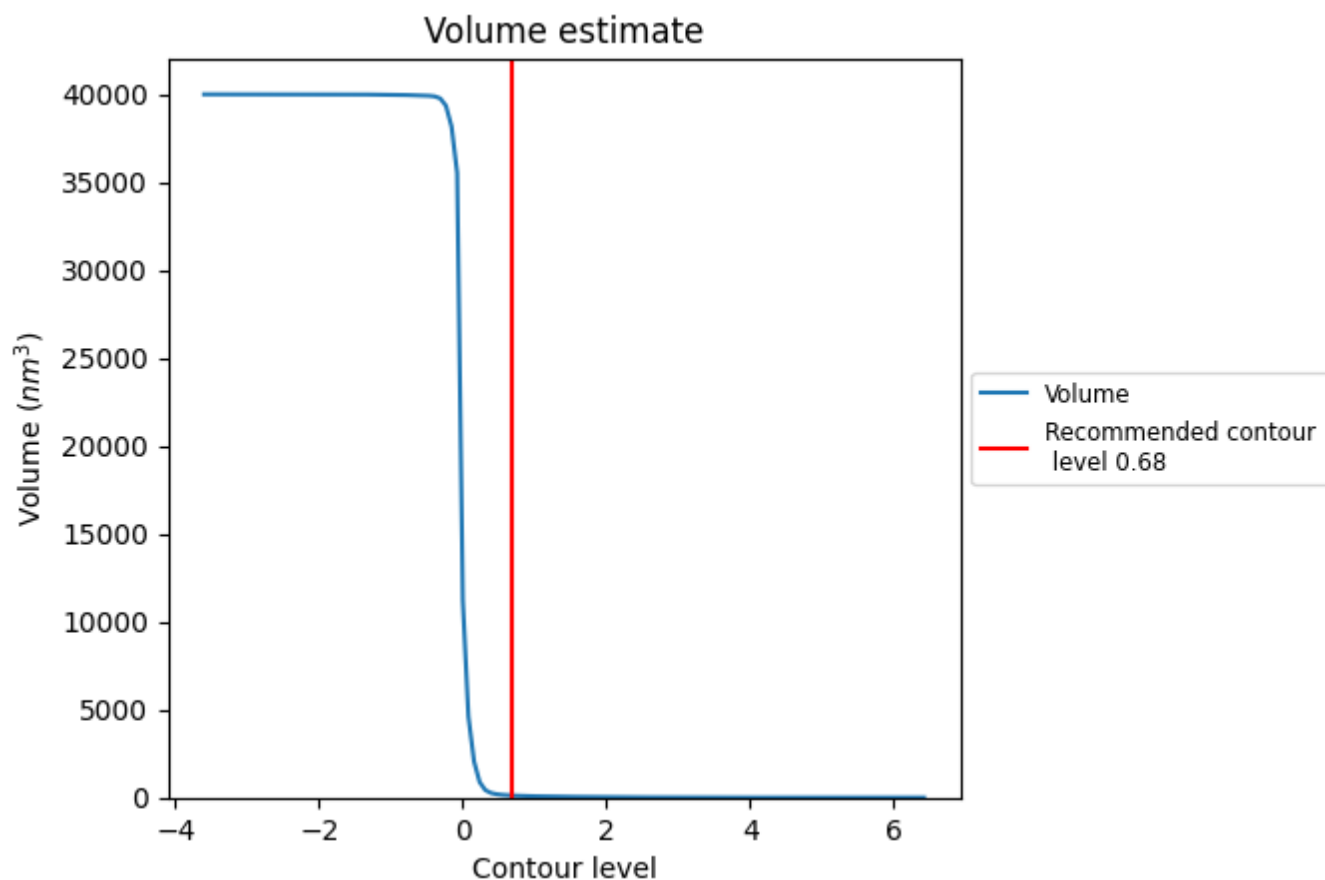
This section contains the results of statistical analysis of the map.

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.

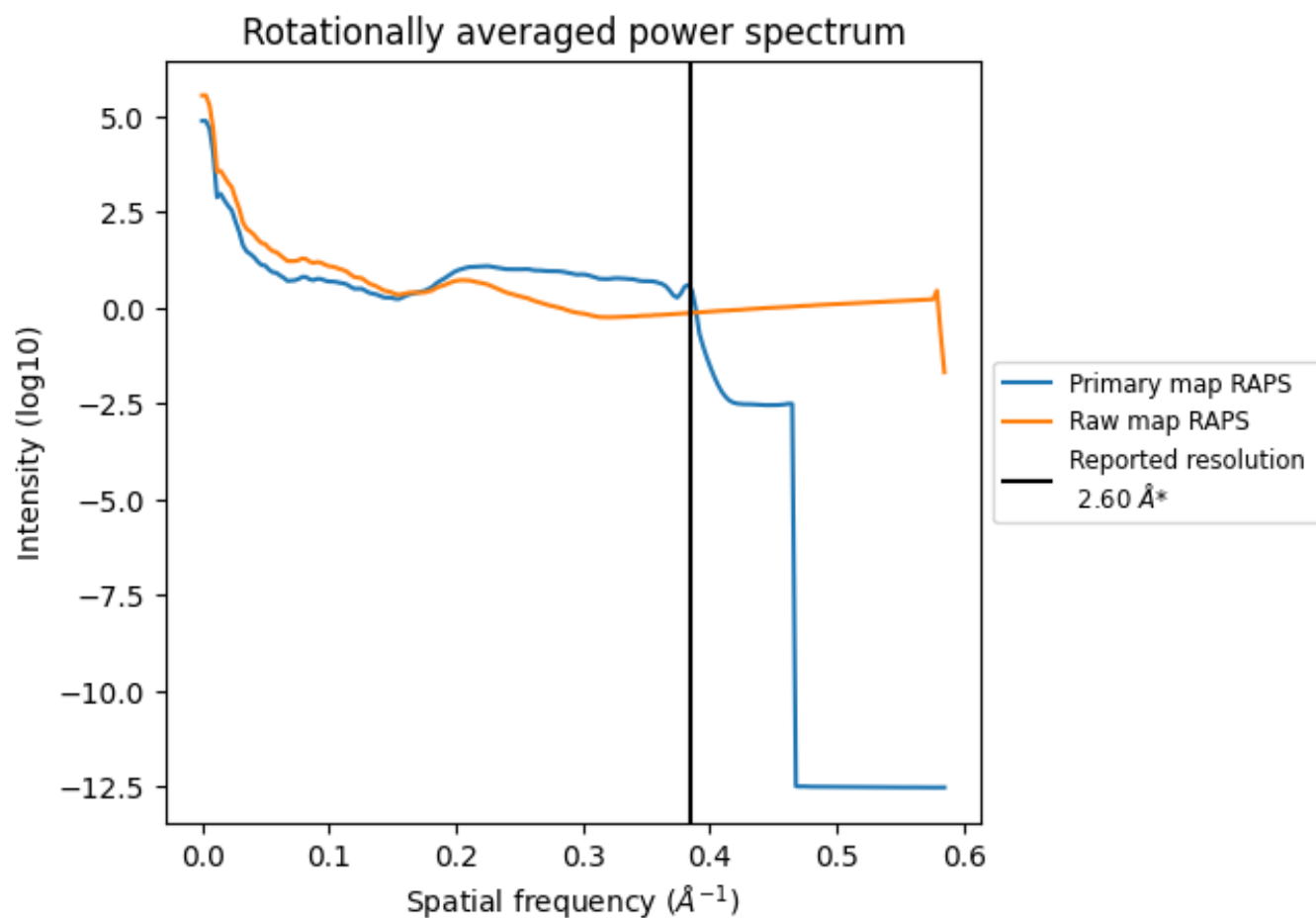
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 116 nm^3 ; this corresponds to an approximate mass of 105 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 ⓘ

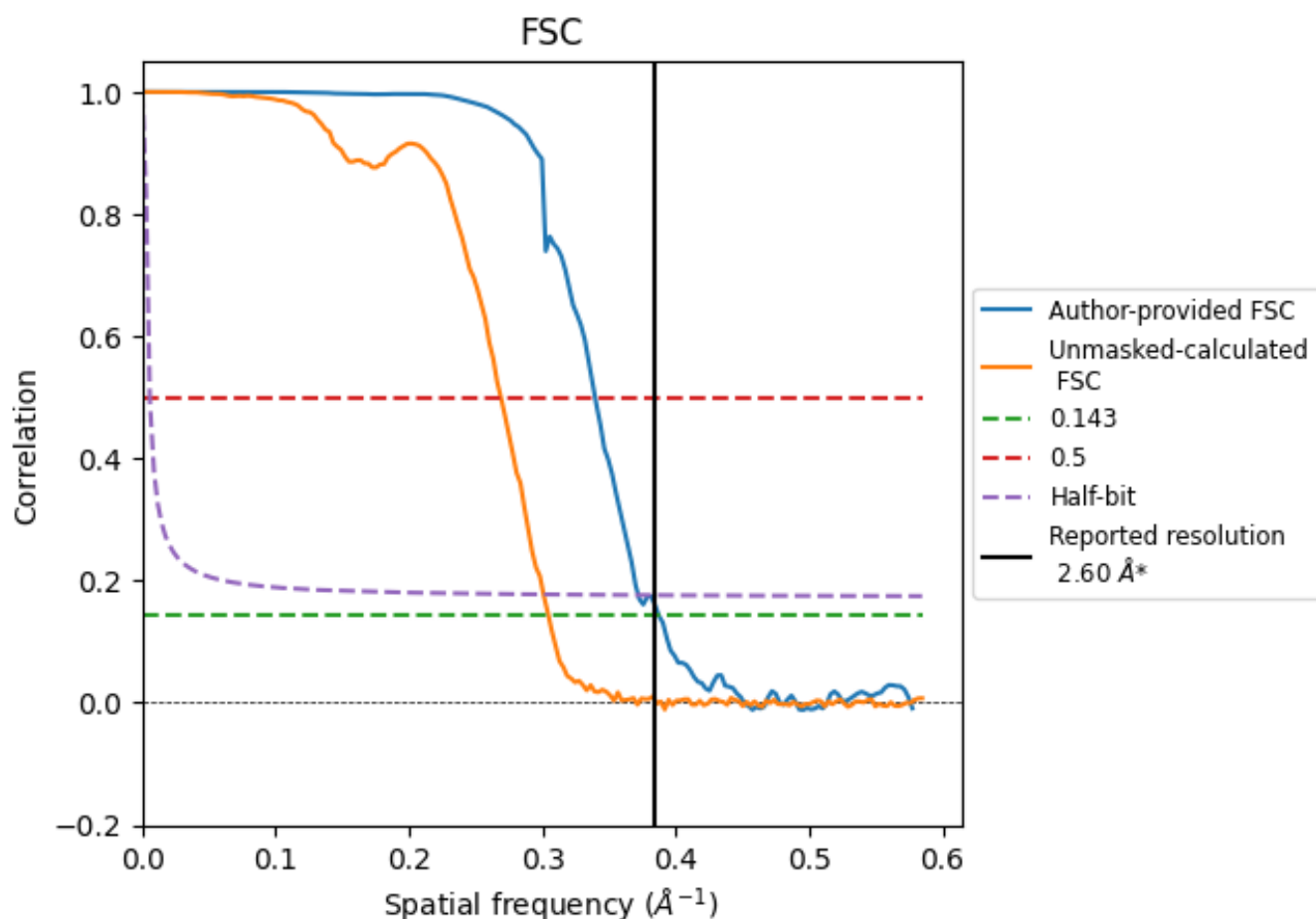


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 0.385 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

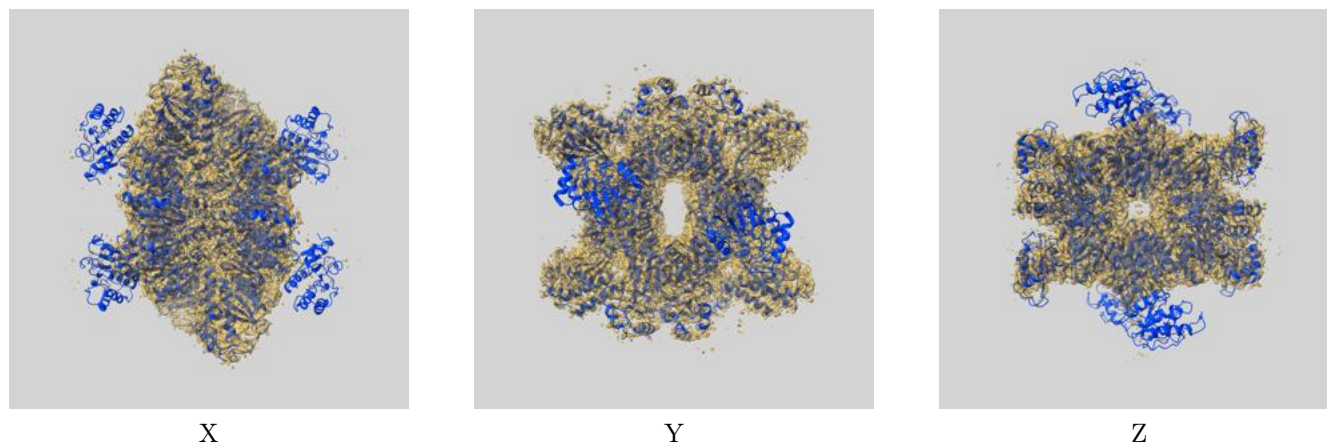
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.58	2.94	2.69
Unmasked-calculated*	3.28	3.72	3.32

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.28 differs from the reported value 2.6 by more than 10 %

9 Map-model fit [i](#)

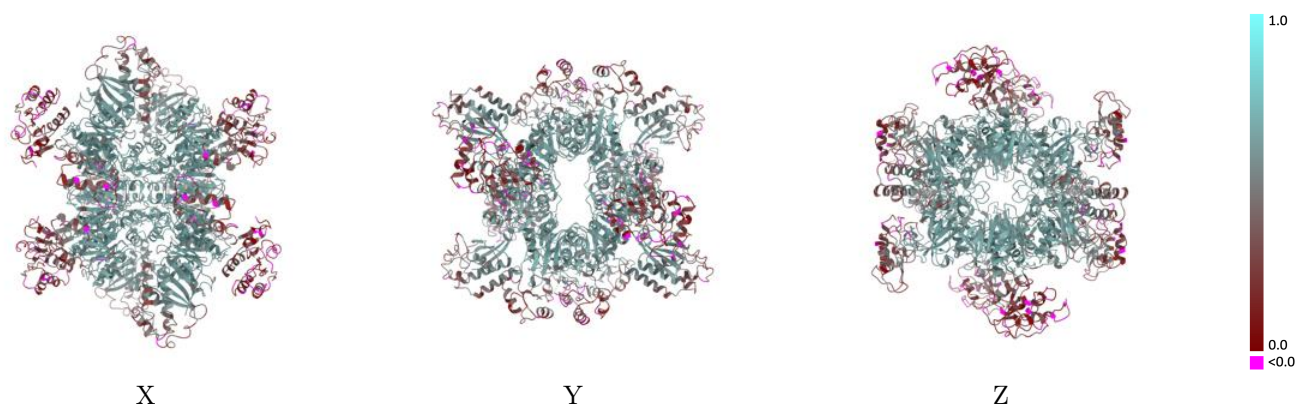
This section contains information regarding the fit between EMDB map EMD-23325 and PDB model 7LGJ. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



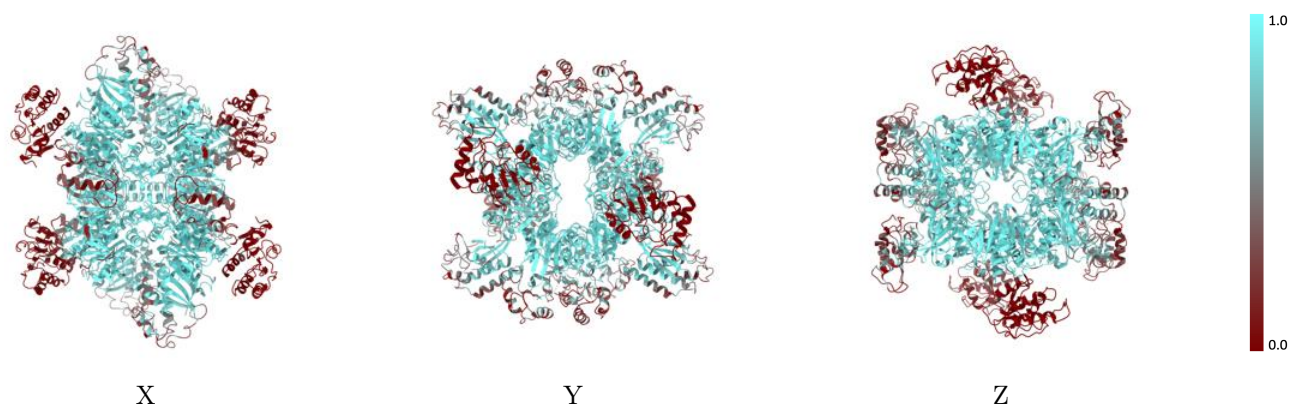
The images above show the 3D surface view of the map at the recommended contour level 0.68 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



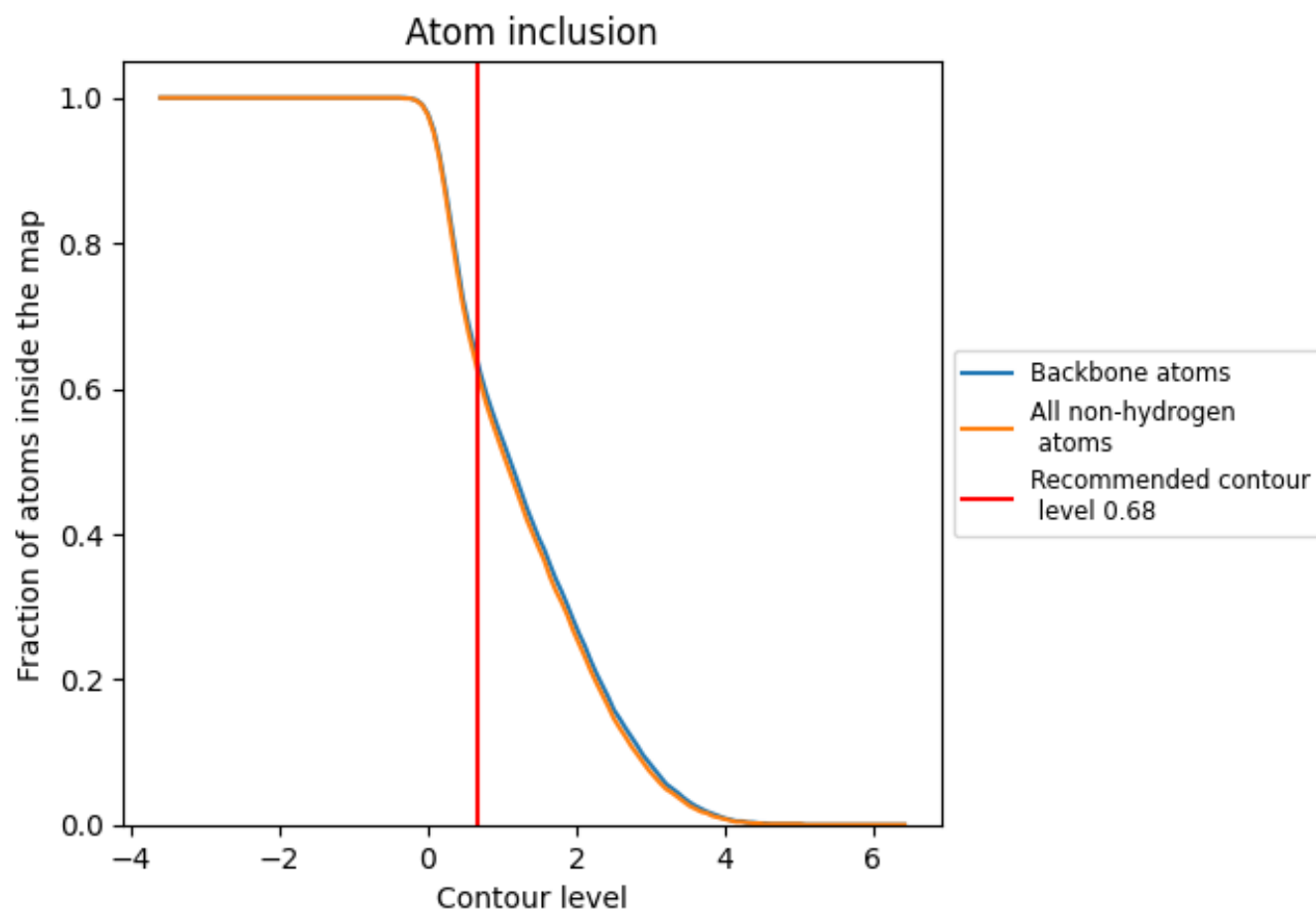
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.68).

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 62% 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 (0.68) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6200	0.4690
A	0.6250	0.4680
B	0.6250	0.4670
C	0.6250	0.4680
D	0.6250	0.4680
E	0.6490	0.5580
F	0.6490	0.5640
G	0.6490	0.5580
H	0.6490	0.5640

1.0

0.0

<0.0