



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 05:48 AM UTC

PDB ID : 6E2Z / pdb_00006e2z
EMDB ID : EMD-8971
Title : Mechanism of cellular recognition by PCV2
Authors : Khayat, R.; Dhindwal, S.
Deposited on : 2018-07-12
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
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

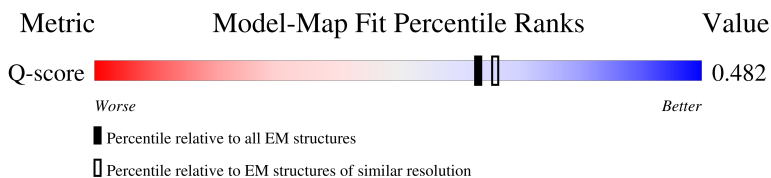
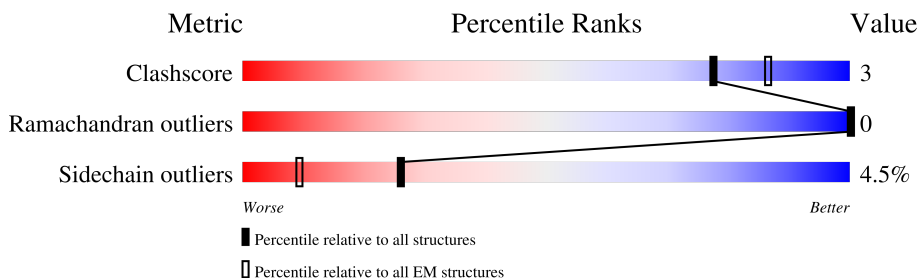
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

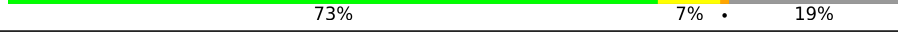
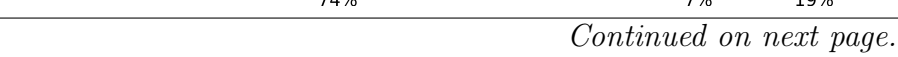
The reported resolution of this entry is 3.40 Å.

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	14717 (2.90 - 3.90)

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	A1	233	
1	A2	233	
1	A3	233	
1	A4	233	

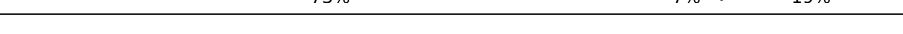
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Mol	Chain	Length	Quality of chain
1	A5	233	 73%8%19%
1	A6	233	 73%8%19%
1	A7	233	 73%7%19%
1	A8	233	 73%8%19%
1	A9	233	 73%7%19%
1	AA	233	 73%7%19%
1	AB	233	 74%7%19%
1	AC	233	 73%7%19%
1	AD	233	 72%8%19%
1	AE	233	 73%7%19%
1	AF	233	 74%6%19%
1	AG	233	 73%7%19%
1	AH	233	 73%8%19%
1	AI	233	 71%9%19%
1	AJ	233	 72%9%19%
1	AK	233	 72%9%19%
1	AL	233	 73%7%19%
1	AM	233	 73%7%19%
1	AN	233	 74%6%19%
1	AO	233	 76%5%19%
1	AP	233	 76%5%19%
1	AQ	233	 76%5%19%
1	AR	233	 75%6%19%
1	AS	233	 76%5%19%
1	AT	233	 76%5%19%

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Mol	Chain	Length	Quality of chain
1	AU	233	
1	AV	233	
1	AW	233	
1	AX	233	
1	AY	233	
1	AZ	233	
1	Aa	233	
1	Ab	233	
1	Ac	233	
1	Ad	233	
1	Ae	233	
1	Af	233	
1	Ag	233	
1	Ah	233	
1	Ai	233	
1	Aj	233	
1	Ak	233	
1	Al	233	
1	Am	233	
1	An	233	
1	Ao	233	
1	Ap	233	
1	Aq	233	
1	Ar	233	
1	As	233	

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Mol	Chain	Length	Quality of chain
1	At	233	 74%7%19%
1	Au	233	 74%7%19%
1	Av	233	 72%9%19%
1	Aw	233	 73%6%19%
1	Ax	233	 73%7%19%
1	Ay	233	 72%8%19%
2	A	3	 33%67%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 183216 atoms, of which 90169 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 Capsid protein of PCV2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A1	188	Total	C	H	N	O	S	0	0
			3034	989	1492	267	282	4		
1	A2	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	A3	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	A4	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	A5	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	A6	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	A7	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	A8	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	A9	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AA	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AB	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AC	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AD	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AE	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AF	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AG	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AH	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	AI	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AJ	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AK	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AL	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AM	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AN	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AO	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AP	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AQ	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AR	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AS	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AT	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AU	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AV	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AW	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AX	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AY	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	AZ	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Aa	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Ab	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Ac	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		

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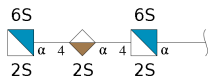
Mol	Chain	Residues	Atoms						AltConf	Trace
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			3053	995	1503	268	283	4		
1	Ae	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Af	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Ag	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Ah	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Ai	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Aj	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Ak	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Al	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Am	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	An	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Ao	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Ap	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Aq	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Ar	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	As	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	At	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Au	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Av	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Aw	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		
1	Ax	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		

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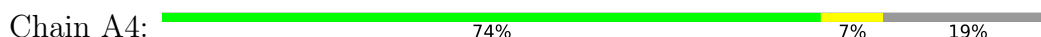
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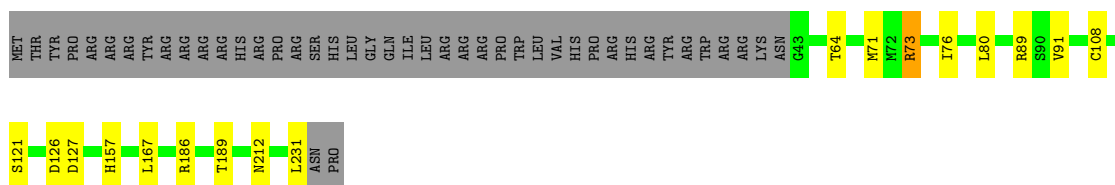
Mol	Chain	Residues	Atoms						AltConf	Trace
1	Ay	189	Total	C	H	N	O	S	0	0
			3053	995	1503	268	283	4		

- Molecule 2 is an oligosaccharide called 2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose.



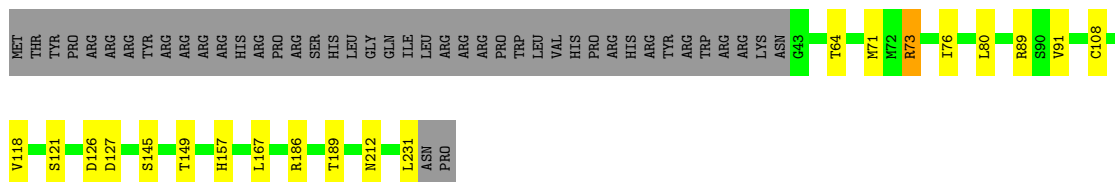
Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	3	Total	C	N	O	S	0	0
			55	18	2	30	5		





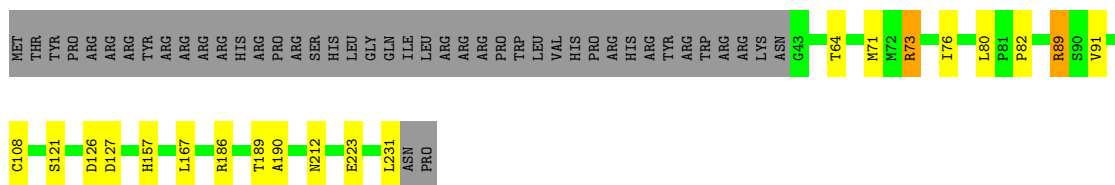
- Molecule 1: Capsid protein of PCV2

Chain A5: 73% 8% 19%



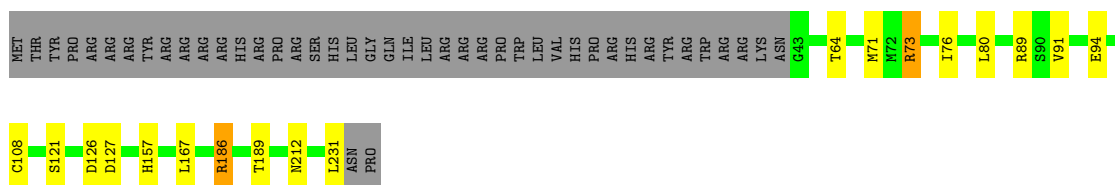
- Molecule 1: Capsid protein of PCV2

Chain A6: 73% 8% 19%



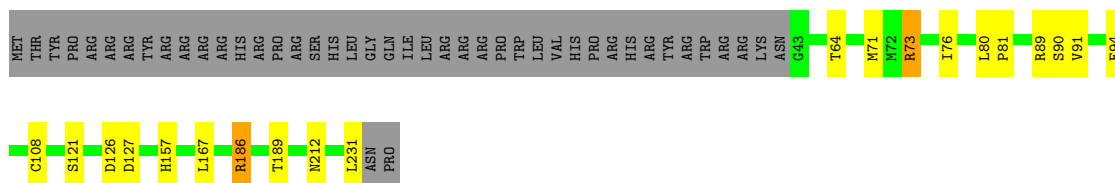
- Molecule 1: Capsid protein of PCV2

Chain A7: 73% 7% 19%



- Molecule 1: Capsid protein of PCV2

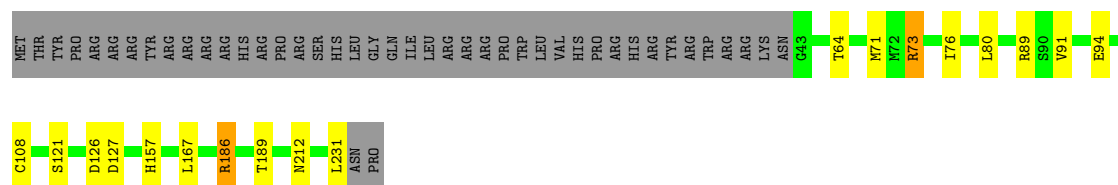
Chain A8: 73% 8% 19%



- Molecule 1: Capsid protein of PCV2

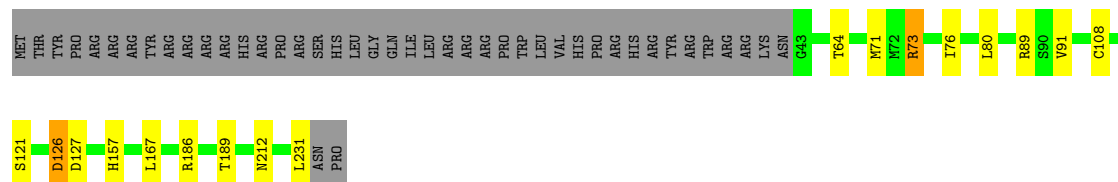
Chain A9: 73% 7% 19%





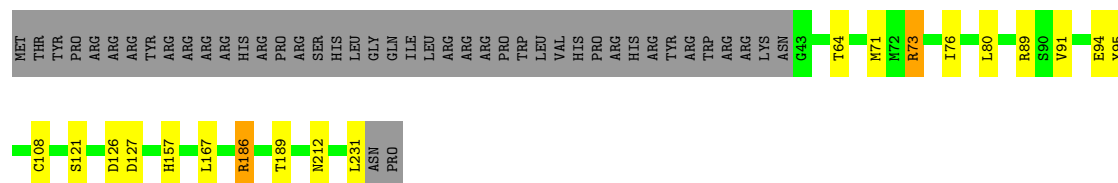
- Molecule 1: Capsid protein of PCV2

Chain AF: 74% 6% 19%



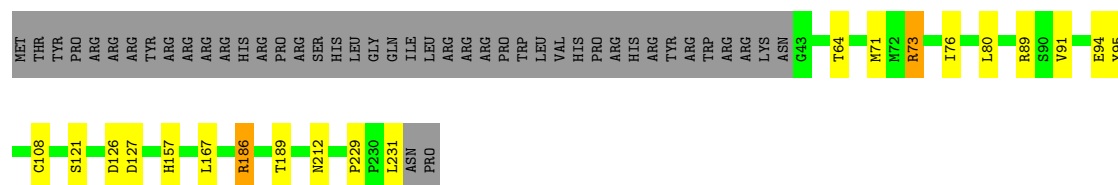
- Molecule 1: Capsid protein of PCV2

Chain AG: 73% 7% 19%



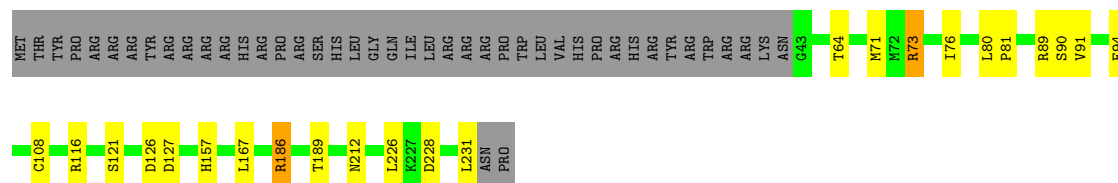
- Molecule 1: Capsid protein of PCV2

Chain AH: 73% 8% 19%



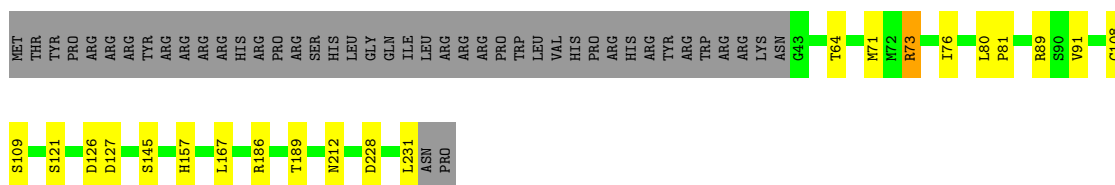
- Molecule 1: Capsid protein of PCV2

Chain AI: 71% 9% 19%



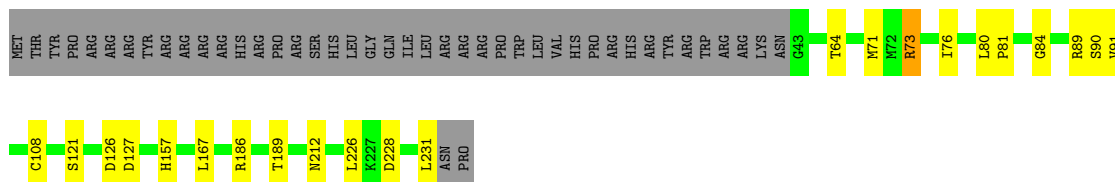
- Molecule 1: Capsid protein of PCV2

Chain AJ: 72% 9% 19%



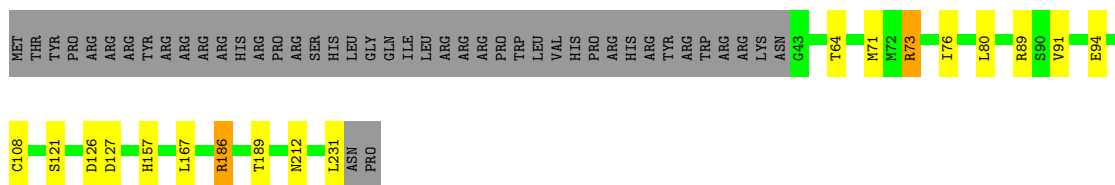
- Molecule 1: Capsid protein of PCV2

Chain AK: 72% 9% 19%



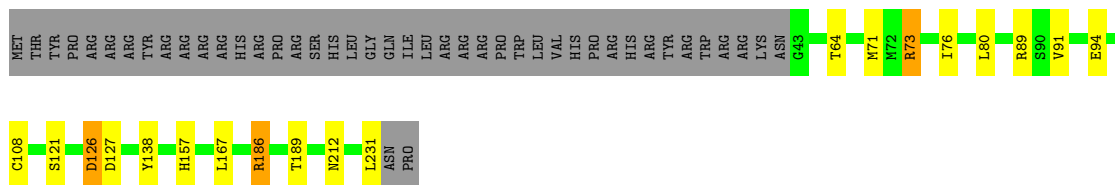
- Molecule 1: Capsid protein of PCV2

Chain AL: 73% 7% 19%



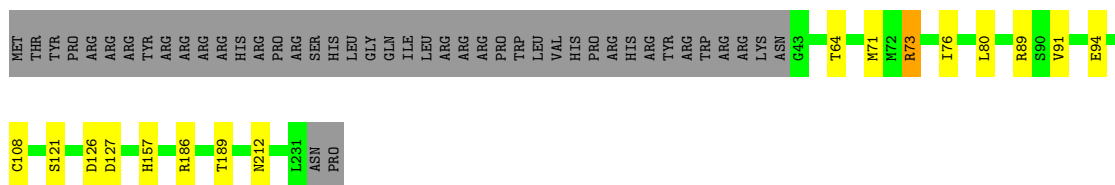
- Molecule 1: Capsid protein of PCV2

Chain AM: 73% 7% 19%



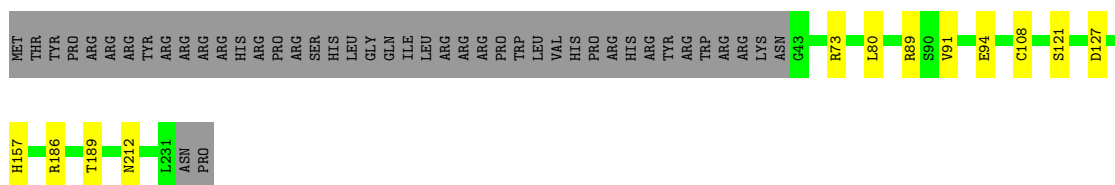
- Molecule 1: Capsid protein of PCV2

Chain AN: 74% 6% 19%



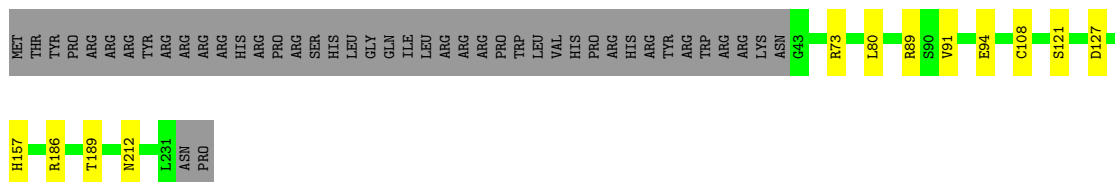
- Molecule 1: Capsid protein of PCV2

Chain AO: 76% 5% 19%



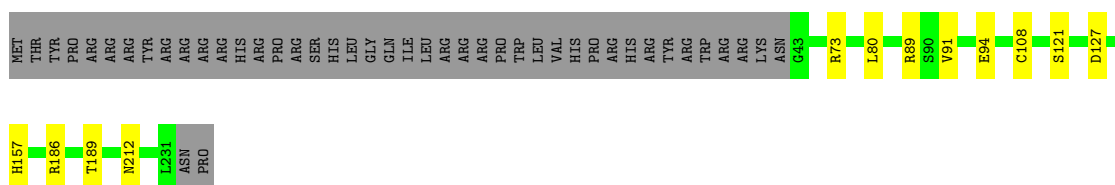
- Molecule 1: Capsid protein of PCV2

Chain AP: 76% 5% 19%



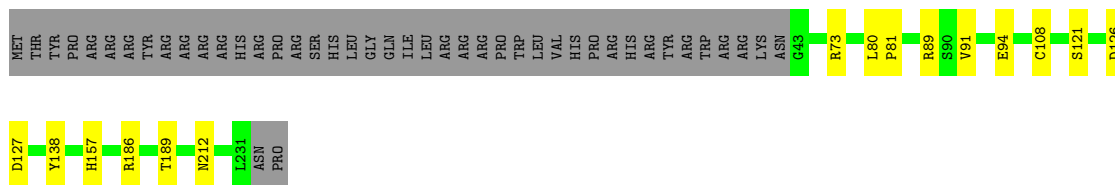
- Molecule 1: Capsid protein of PCV2

Chain AQ: 76% 5% 19%



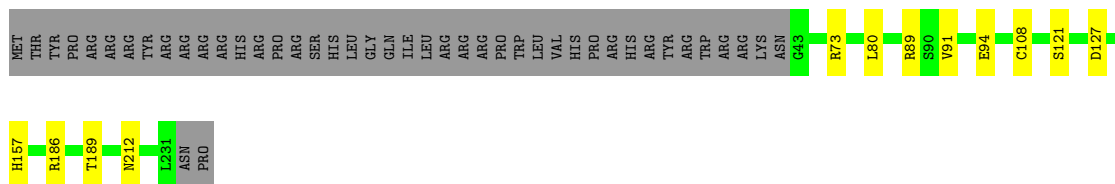
- Molecule 1: Capsid protein of PCV2

Chain AR: 75% 6% 19%



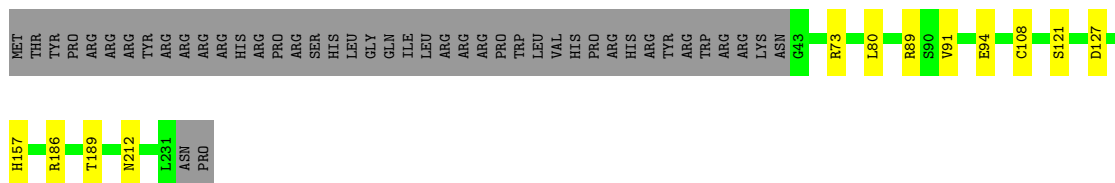
- Molecule 1: Capsid protein of PCV2

Chain AS: 76% 5% 19%

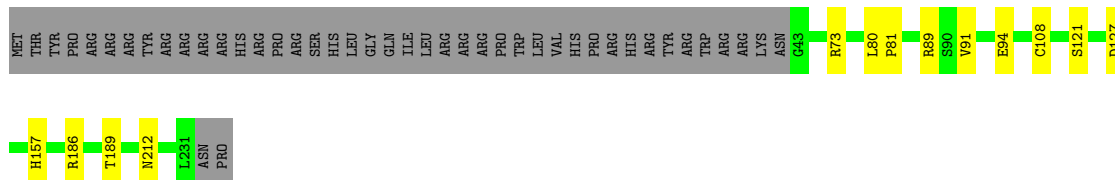
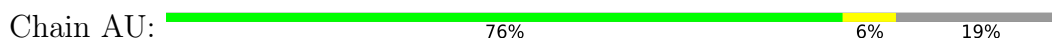


- Molecule 1: Capsid protein of PCV2

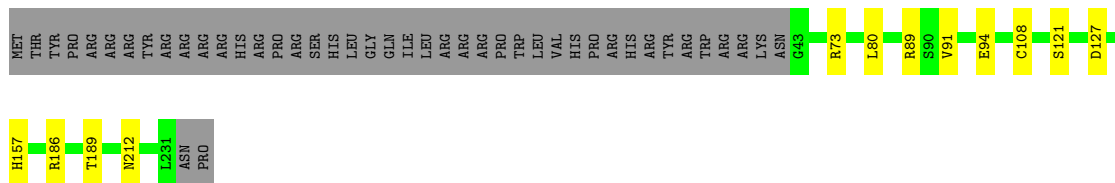
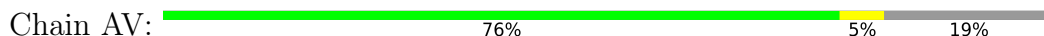
Chain AT: 76% 5% 19%



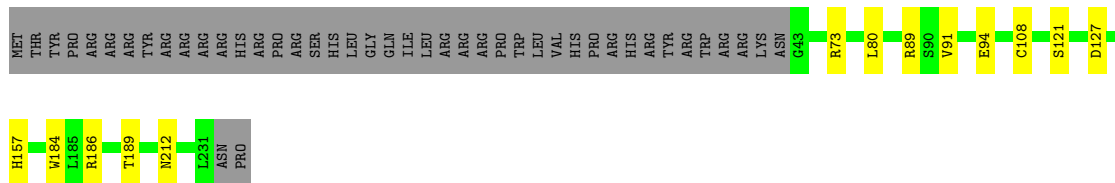
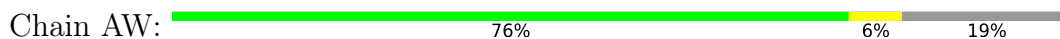
- Molecule 1: Capsid protein of PCV2



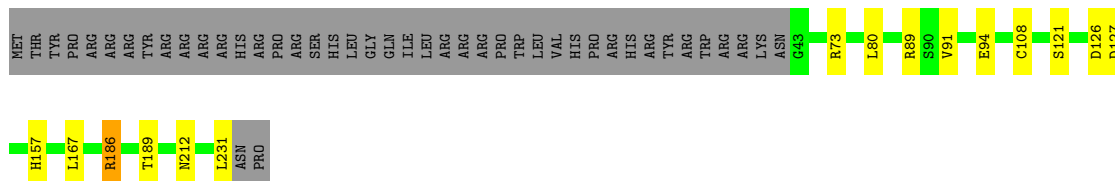
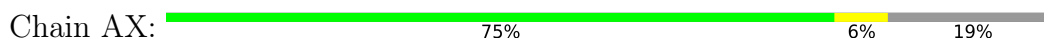
- Molecule 1: Capsid protein of PCV2



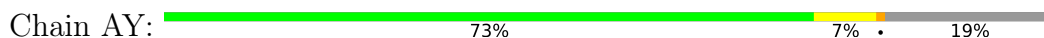
- Molecule 1: Capsid protein of PCV2

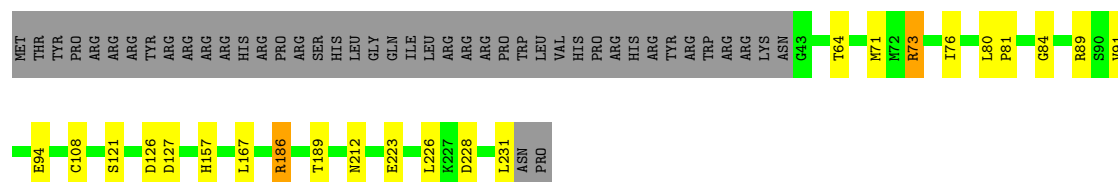


- Molecule 1: Capsid protein of PCV2



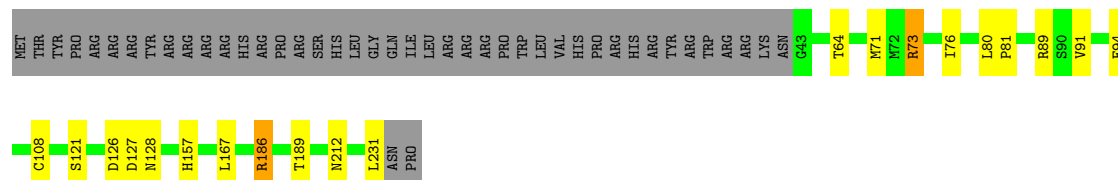
- Molecule 1: Capsid protein of PCV2





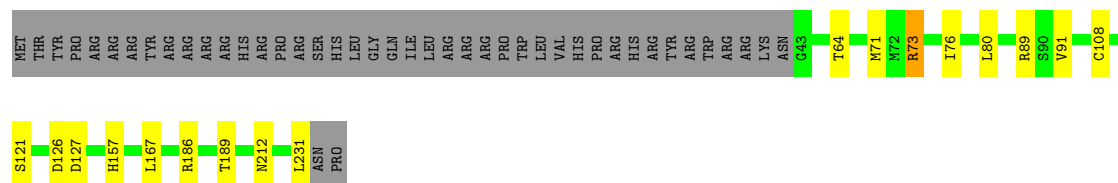
• Molecule 1: Capsid protein of PCV2

Chain Ae: 73% 8% 19%



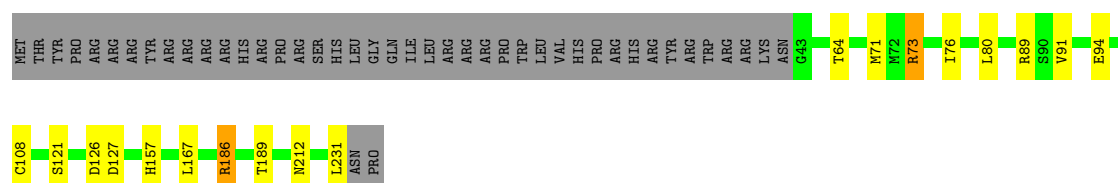
• Molecule 1: Capsid protein of PCV2

Chain Af: 74% 7% 19%



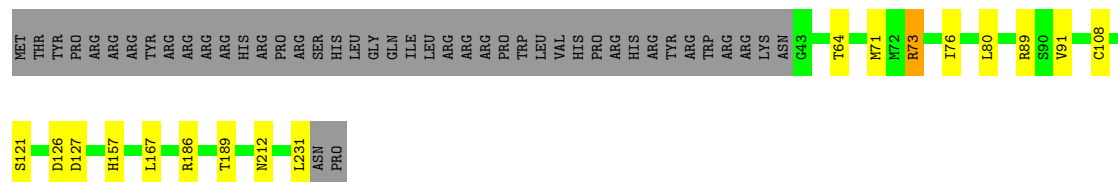
• Molecule 1: Capsid protein of PCV2

Chain Ag: 73% 7% 19%



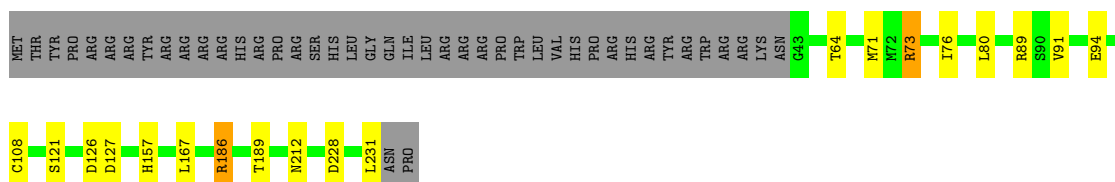
• Molecule 1: Capsid protein of PCV2

Chain Ah: 74% 7% 19%



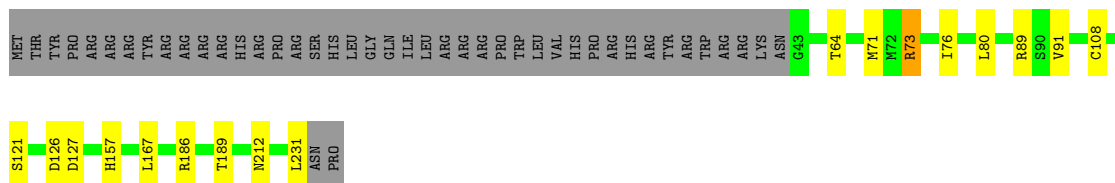
• Molecule 1: Capsid protein of PCV2

Chain Ai: 73% 7% 19%



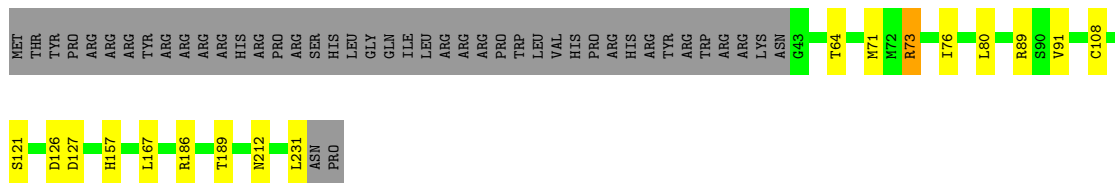
- Molecule 1: Capsid protein of PCV2

Chain Aj: 74% 7% 19%



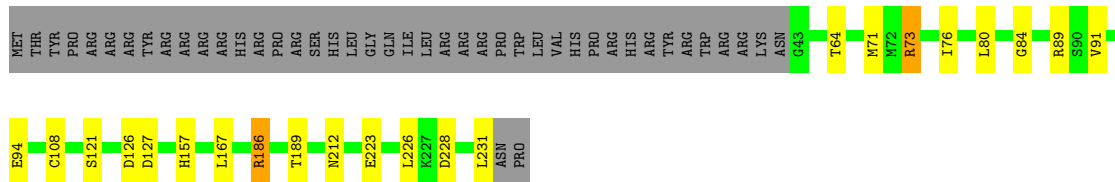
- Molecule 1: Capsid protein of PCV2

Chain Ak: 74% 7% 19%



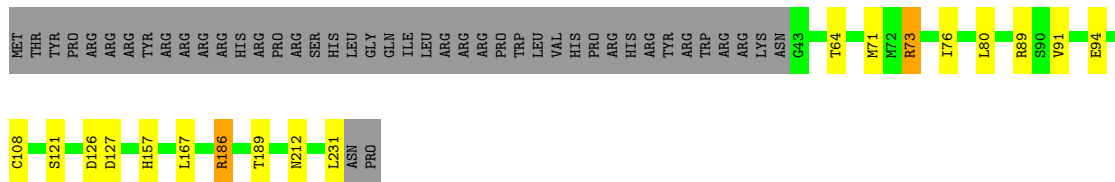
- Molecule 1: Capsid protein of PCV2

Chain Al: 72% 9% 19%



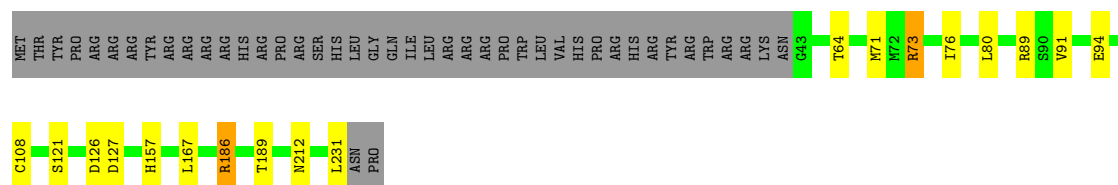
- Molecule 1: Capsid protein of PCV2

Chain Am: 73% 7% 19%



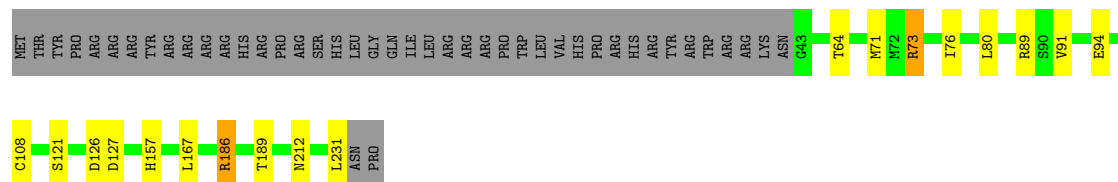
- Molecule 1: Capsid protein of PCV2

Chain An: 73% 7% 19%



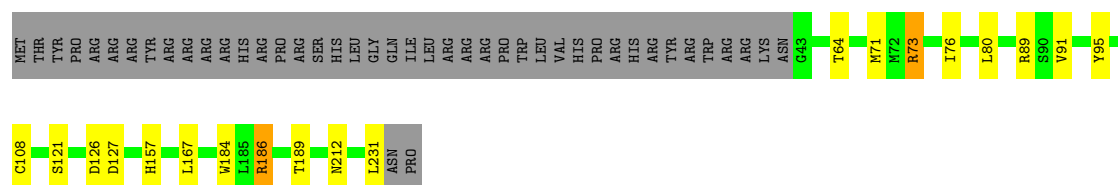
- Molecule 1: Capsid protein of PCV2

Chain Ao: 73% 7% 19%



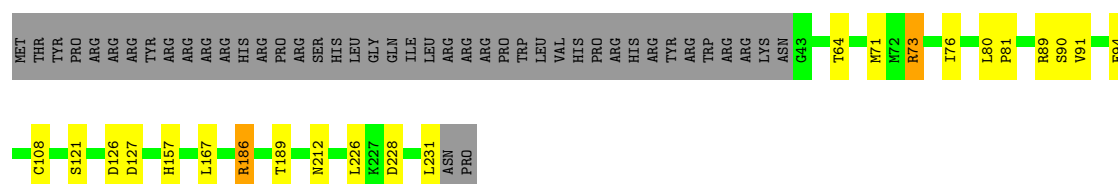
- Molecule 1: Capsid protein of PCV2

Chain Ap: 73% 7% 19%



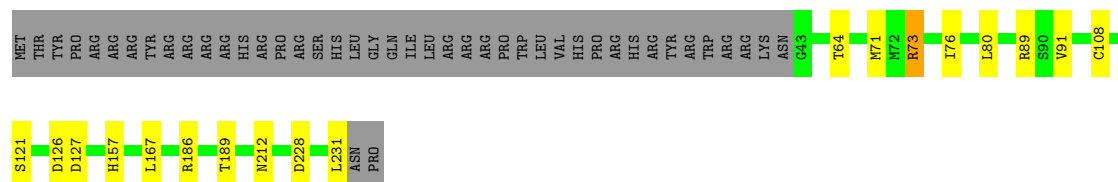
- Molecule 1: Capsid protein of PCV2

Chain Aq: 72% 9% 19%



- Molecule 1: Capsid protein of PCV2

Chain Ar: 73% 7% 19%



- Molecule 1: Capsid protein of PCV2

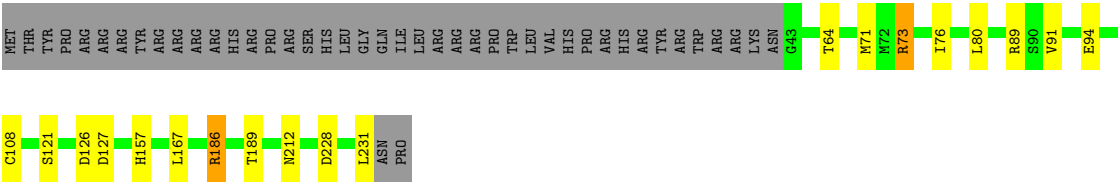
Chain Ax:

73%

7%

•

19%



- Molecule 1: Capsid protein of PCV2

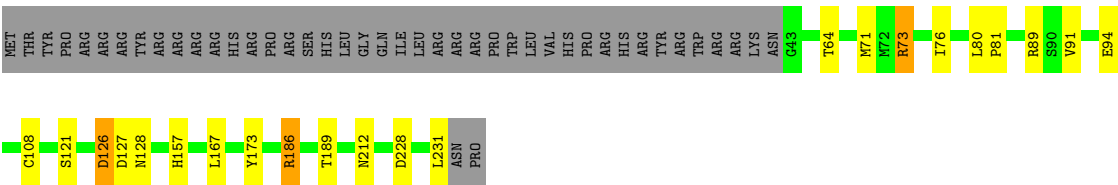
Chain Ay:

72%

8%

•

19%



- Molecule 2: 2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose

Chain A:

33%

67%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	90206	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Per particle estimation	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	32	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.082	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	327.0, 327.0, 327.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	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: SGN, IDS

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	A1	0.43	2/1589 (0.1%)	0.48	0/2164
1	A2	0.61	0/1597	0.51	0/2175
1	A3	0.61	0/1597	0.51	0/2175
1	A4	0.61	0/1597	0.50	0/2175
1	A5	0.61	0/1597	0.51	0/2175
1	A6	0.61	0/1597	0.51	0/2175
1	A7	0.61	0/1597	0.51	0/2175
1	A8	0.61	0/1597	0.50	0/2175
1	A9	0.61	0/1597	0.50	0/2175
1	AA	0.61	0/1597	0.51	0/2175
1	AB	0.61	0/1597	0.51	0/2175
1	AC	0.61	0/1597	0.51	0/2175
1	AD	0.61	0/1597	0.51	0/2175
1	AE	0.61	0/1597	0.51	0/2175
1	AF	0.60	0/1597	0.51	0/2175
1	AG	0.61	0/1597	0.50	0/2175
1	AH	0.61	0/1597	0.50	0/2175
1	AI	0.61	0/1597	0.51	0/2175
1	AJ	0.61	0/1597	0.51	0/2175
1	AK	0.61	0/1597	0.51	0/2175
1	AL	0.61	0/1597	0.51	0/2175
1	AM	0.61	0/1597	0.51	0/2175
1	AN	0.61	0/1597	0.51	0/2175
1	AO	0.61	0/1597	0.51	0/2175
1	AP	0.60	0/1597	0.50	0/2175
1	AQ	0.61	0/1597	0.51	0/2175
1	AR	0.61	0/1597	0.51	0/2175
1	AS	0.61	0/1597	0.51	0/2175
1	AT	0.61	0/1597	0.51	0/2175
1	AU	0.61	0/1597	0.51	0/2175
1	AV	0.61	0/1597	0.51	0/2175
1	AW	0.61	0/1597	0.50	0/2175

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AX	0.61	0/1597	0.51	0/2175
1	AY	0.61	0/1597	0.51	0/2175
1	AZ	0.61	0/1597	0.51	0/2175
1	Aa	0.61	0/1597	0.51	0/2175
1	Ab	0.61	0/1597	0.51	0/2175
1	Ac	0.61	0/1597	0.51	0/2175
1	Ad	0.61	0/1597	0.51	0/2175
1	Ae	0.61	0/1597	0.51	0/2175
1	Af	0.61	0/1597	0.51	0/2175
1	Ag	0.61	0/1597	0.51	0/2175
1	Ah	0.61	0/1597	0.50	0/2175
1	Ai	0.60	0/1597	0.51	0/2175
1	Aj	0.61	0/1597	0.51	0/2175
1	Ak	0.61	0/1597	0.51	0/2175
1	Al	0.61	0/1597	0.51	0/2175
1	Am	0.61	0/1597	0.51	0/2175
1	An	0.61	0/1597	0.50	0/2175
1	Ao	0.61	0/1597	0.51	0/2175
1	Ap	0.61	0/1597	0.51	0/2175
1	Aq	0.61	0/1597	0.51	0/2175
1	Ar	0.61	0/1597	0.50	0/2175
1	As	0.61	0/1597	0.50	0/2175
1	At	0.61	0/1597	0.50	0/2175
1	Au	0.61	0/1597	0.51	0/2175
1	Av	0.61	0/1597	0.50	0/2175
1	Aw	0.61	0/1597	0.51	0/2175
1	Ax	0.61	0/1597	0.51	0/2175
1	Ay	0.60	0/1597	0.51	0/2175
All	All	0.60	2/95812 (0.0%)	0.51	0/130489

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A1	0	1
1	A6	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A1	188	GLN	C-N	8.00	1.44	1.33
1	A1	189	THR	C-N	-5.22	1.25	1.34

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A1	116	ARG	Sidechain
1	A6	89	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	1542	1492	1492	16	0
1	A2	1550	1503	1503	12	0
1	A3	1550	1503	1503	9	0
1	A4	1550	1503	1503	7	0
1	A5	1550	1503	1503	10	0
1	A6	1550	1503	1503	11	0
1	A7	1550	1503	1503	9	0
1	A8	1550	1503	1503	13	0
1	A9	1550	1503	1503	8	0
1	AA	1550	1503	1503	9	0
1	AB	1550	1503	1503	7	0
1	AC	1550	1503	1503	10	0
1	AD	1550	1503	1503	13	0
1	AE	1550	1503	1503	8	0
1	AF	1550	1503	1503	9	0
1	AG	1550	1503	1503	10	0
1	AH	1550	1503	1503	11	0
1	AI	1550	1503	1503	13	0
1	AJ	1550	1503	1503	11	0
1	AK	1550	1503	1503	14	0
1	AL	1550	1503	1503	8	0
1	AM	1550	1503	1503	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AN	1550	1503	1503	8	0
1	AO	1550	1503	1503	9	0
1	AP	1550	1503	1503	8	0
1	AQ	1550	1503	1503	8	0
1	AR	1550	1503	1503	12	0
1	AS	1550	1503	1503	8	0
1	AT	1550	1503	1503	8	0
1	AU	1550	1503	1503	9	0
1	AV	1550	1503	1503	9	0
1	AW	1550	1503	1503	10	0
1	AX	1550	1503	1503	8	0
1	AY	1550	1503	1503	8	0
1	AZ	1550	1503	1503	8	0
1	Aa	1550	1503	1503	8	0
1	Ab	1550	1503	1503	8	0
1	Ac	1550	1503	1503	8	0
1	Ad	1550	1503	1503	16	0
1	Ae	1550	1503	1503	11	0
1	Af	1550	1503	1503	7	0
1	Ag	1550	1503	1503	9	0
1	Ah	1550	1503	1503	7	0
1	Ai	1550	1503	1503	9	0
1	Aj	1550	1503	1503	7	0
1	Ak	1550	1503	1503	7	0
1	Al	1550	1503	1503	14	0
1	Am	1550	1503	1503	8	0
1	An	1550	1503	1503	8	0
1	Ao	1550	1503	1503	8	0
1	Ap	1550	1503	1503	11	0
1	Aq	1550	1503	1503	12	0
1	Ar	1550	1503	1503	8	0
1	As	1550	1503	1503	8	0
1	At	1550	1503	1503	7	0
1	Au	1550	1503	1503	7	0
1	Av	1550	1503	1503	15	0
1	Aw	1550	1503	1503	9	0
1	Ax	1550	1503	1503	9	0
1	Ay	1550	1503	1503	14	0
2	A	55	0	20	3	0
All	All	93047	90169	90189	526	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 3.

The worst 5 of 526 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:A6:89:ARG:NH2	1:A6:189:THR:O	2.00	0.94
1:A1:98:ILE:HD12	1:A1:195:HIS:CD2	2.06	0.90
1:Aj:80:LEU:O	1:Aj:89:ARG:NH1	2.22	0.73
1:An:80:LEU:O	1:An:89:ARG:NH1	2.22	0.73
1:At:80:LEU:O	1:At:89:ARG:NH1	2.22	0.73

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	A1	186/233 (80%)	176 (95%)	10 (5%)	0	100	100
1	A2	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	A3	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	A4	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	A5	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	A6	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	A7	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	A8	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	A9	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AA	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AB	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	AC	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AD	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AE	187/233 (80%)	181 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AF	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AG	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AH	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AI	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AJ	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AK	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AL	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	AM	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	AN	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AO	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AP	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	AQ	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AR	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	AS	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	AT	187/233 (80%)	179 (96%)	8 (4%)	0	100	100
1	AU	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AV	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AW	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AX	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AY	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AZ	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Aa	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Ab	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Ac	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Ad	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Ae	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	Af	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	Ag	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	Ah	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Ai	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	Aj	187/233 (80%)	180 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Ak	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	Al	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	Am	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	An	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Ao	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Ap	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	Aq	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Ar	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	As	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	At	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Au	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Av	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Aw	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Ax	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	Ay	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
All	All	11219/13980 (80%)	10837 (97%)	382 (3%)	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	A1	171/215 (80%)	171 (100%)	0	100	100
1	A2	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	A3	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	A4	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	A5	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	A6	172/215 (80%)	164 (95%)	8 (5%)	23	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A7	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	A8	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	A9	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AA	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AB	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AC	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AD	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AE	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AF	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AG	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AH	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AI	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AJ	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AK	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AL	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AM	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AN	109/215 (51%)	104 (95%)	5 (5%)	24	50
1	AX	113/215 (53%)	109 (96%)	4 (4%)	32	56
1	AY	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	AZ	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Aa	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ab	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ac	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ad	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ae	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Af	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ag	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ah	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ai	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Aj	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ak	172/215 (80%)	164 (95%)	8 (5%)	23	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Al	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Am	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	An	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ao	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ap	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Aq	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ar	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	As	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	At	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Au	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Av	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Aw	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ax	172/215 (80%)	164 (95%)	8 (5%)	23	50
1	Ay	172/215 (80%)	164 (95%)	8 (5%)	23	50
All	All	8649/10965 (79%)	8256 (96%)	393 (4%)	26	51

5 of 393 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Ae	186	ARG
1	Al	167	LEU
1	Af	167	LEU
1	Ai	76	ILE
1	An	76	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 174 such sidechains are listed below:

Mol	Chain	Res	Type
1	Ai	77	ASN
1	Ap	212	ASN
1	Aj	128	ASN
1	Am	128	ASN
1	As	77	ASN

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 ⓘ

3 monosaccharides 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	SGN	A	1	2	20,20,20	4.06	6 (30%)	25,31,31	2.00	6 (24%)
2	IDS	A	2	2	16,16,17	1.26	1 (6%)	16,24,26	0.88	0
2	SGN	A	3	2	19,19,20	3.84	5 (26%)	23,29,31	1.82	6 (26%)

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	SGN	A	1	2	-	3/11/31/31	0/1/1/1
2	IDS	A	2	2	-	0/9/26/29	0/1/1/1
2	SGN	A	3	2	-	3/11/28/31	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	3	SGN	S1-N2	15.50	1.79	1.59
2	A	1	SGN	S1-N2	15.48	1.79	1.59
2	A	1	SGN	O1-C1	7.28	1.62	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	SGN	O1S-S1	3.10	1.45	1.42
2	A	3	SGN	O1S-S1	2.93	1.45	1.42

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	SGN	O1-C1-C2	-5.22	98.36	109.22
2	A	1	SGN	O1-C1-O5	-4.48	97.11	110.41
2	A	3	SGN	O1S-S1-O2S	-3.91	111.66	120.36
2	A	3	SGN	O1S-S1-N2	-3.69	102.72	108.88
2	A	1	SGN	O2S-S1-N2	-3.36	103.27	108.88

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

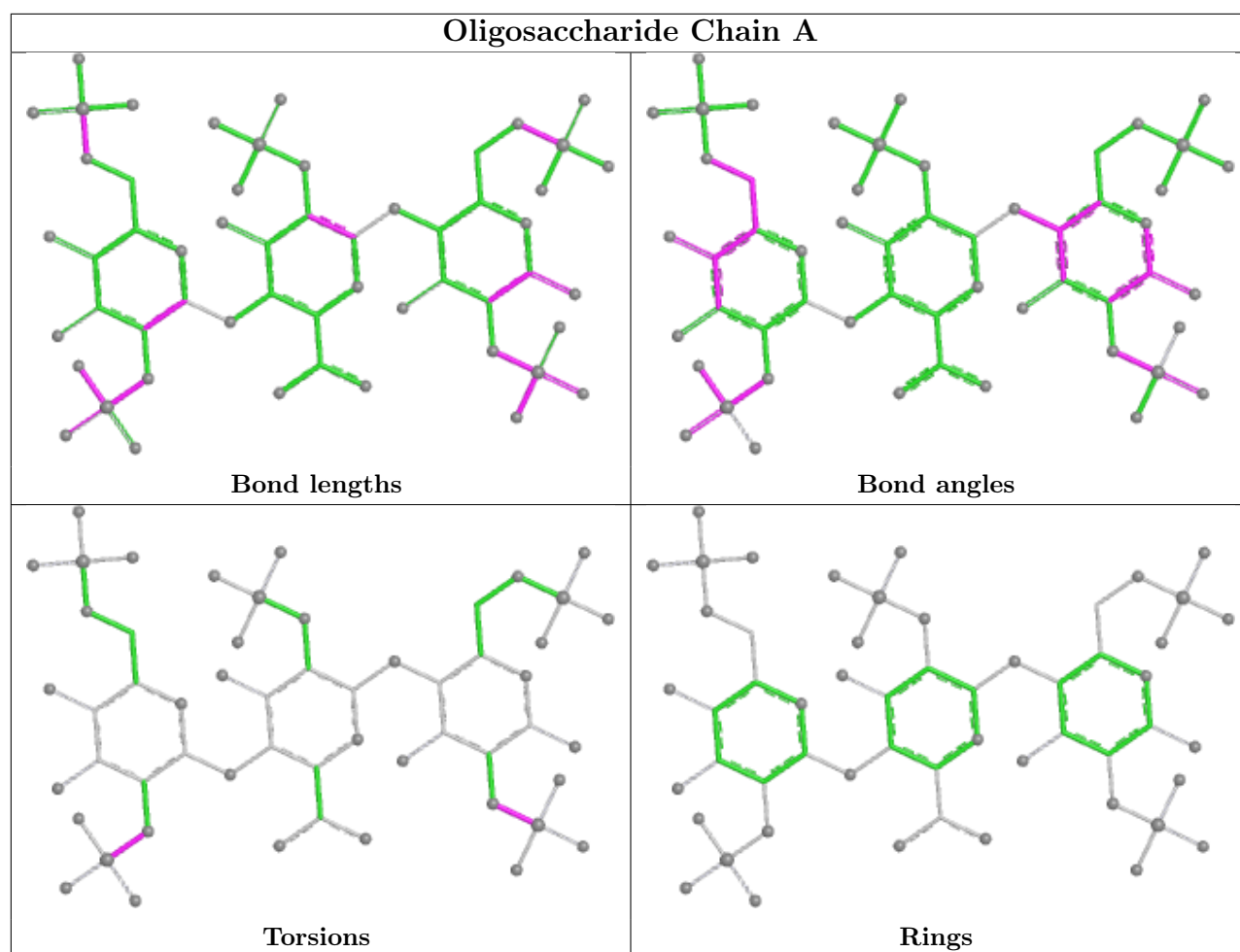
Mol	Chain	Res	Type	Atoms
2	A	1	SGN	C2-N2-S1-O2S
2	A	1	SGN	C2-N2-S1-O3S
2	A	3	SGN	C2-N2-S1-O1S
2	A	3	SGN	C2-N2-S1-O2S
2	A	3	SGN	C2-N2-S1-O3S

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2	IDS	2	0
2	A	3	SGN	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



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.

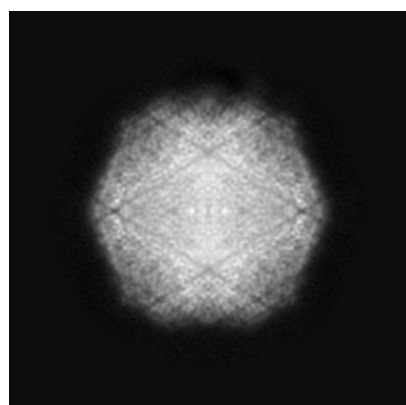
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8971. These allow visual inspection of the internal detail of the map and identification of artifacts.

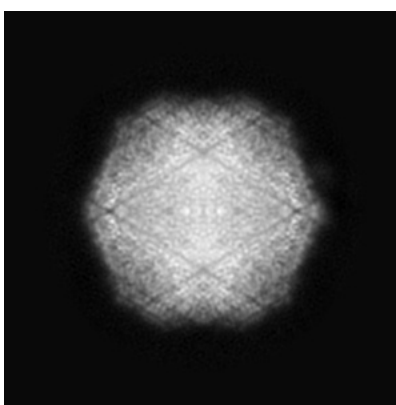
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

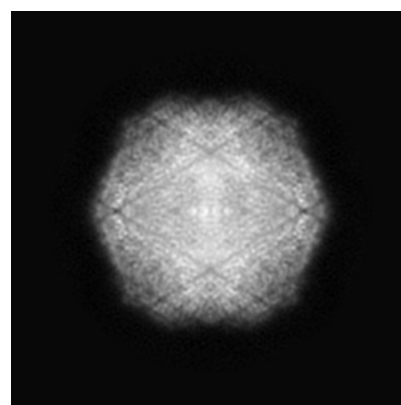
6.1.1 Primary map



X



Y

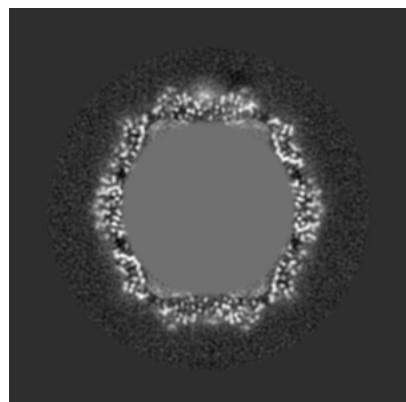


Z

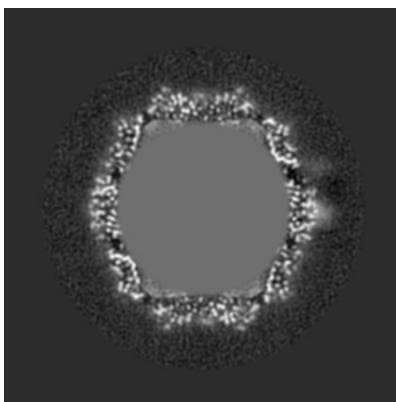
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

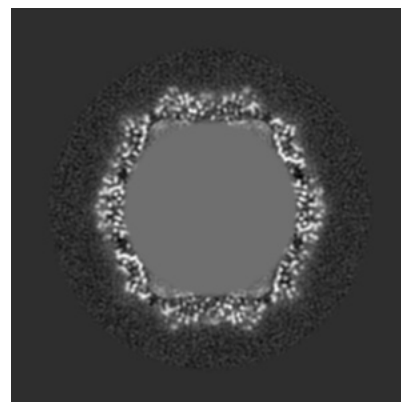
6.2.1 Primary map



X Index: 150



Y Index: 150

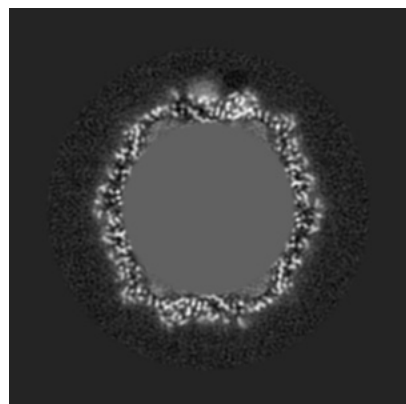


Z Index: 150

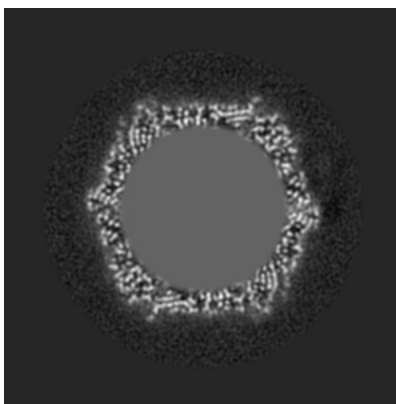
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

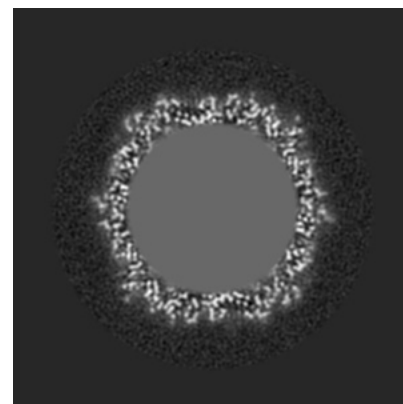
6.3.1 Primary map



X Index: 145



Y Index: 168

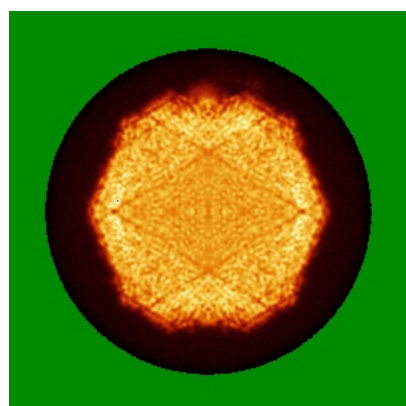


Z Index: 137

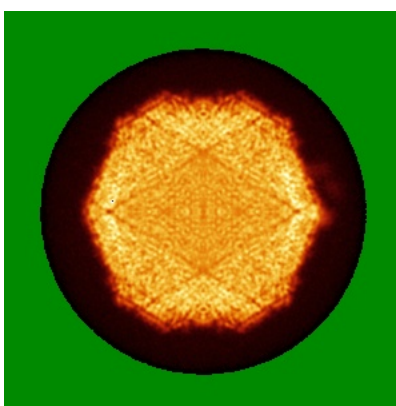
The images above show the largest variance slices of the map in three orthogonal directions.

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

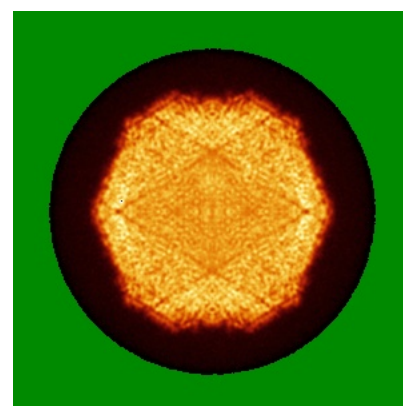
6.4.1 Primary map



X



Y

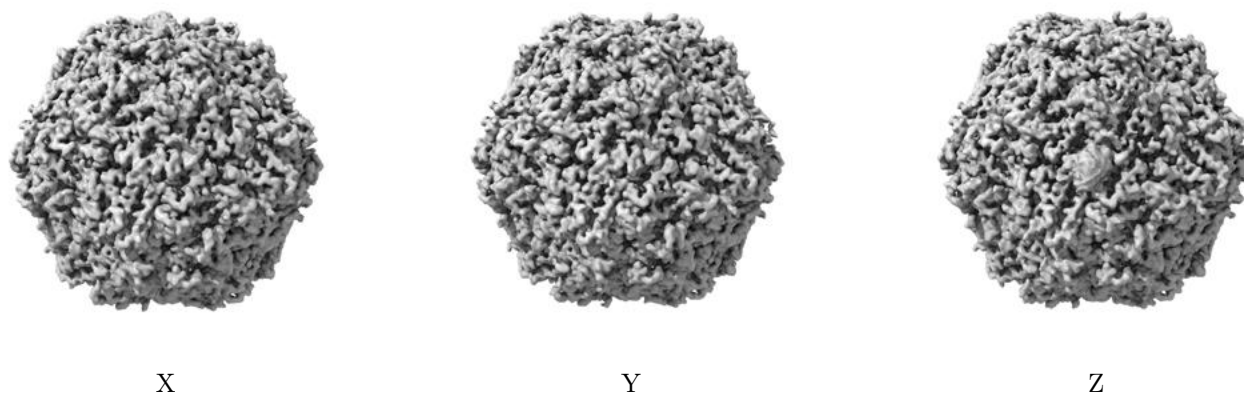


Z

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 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

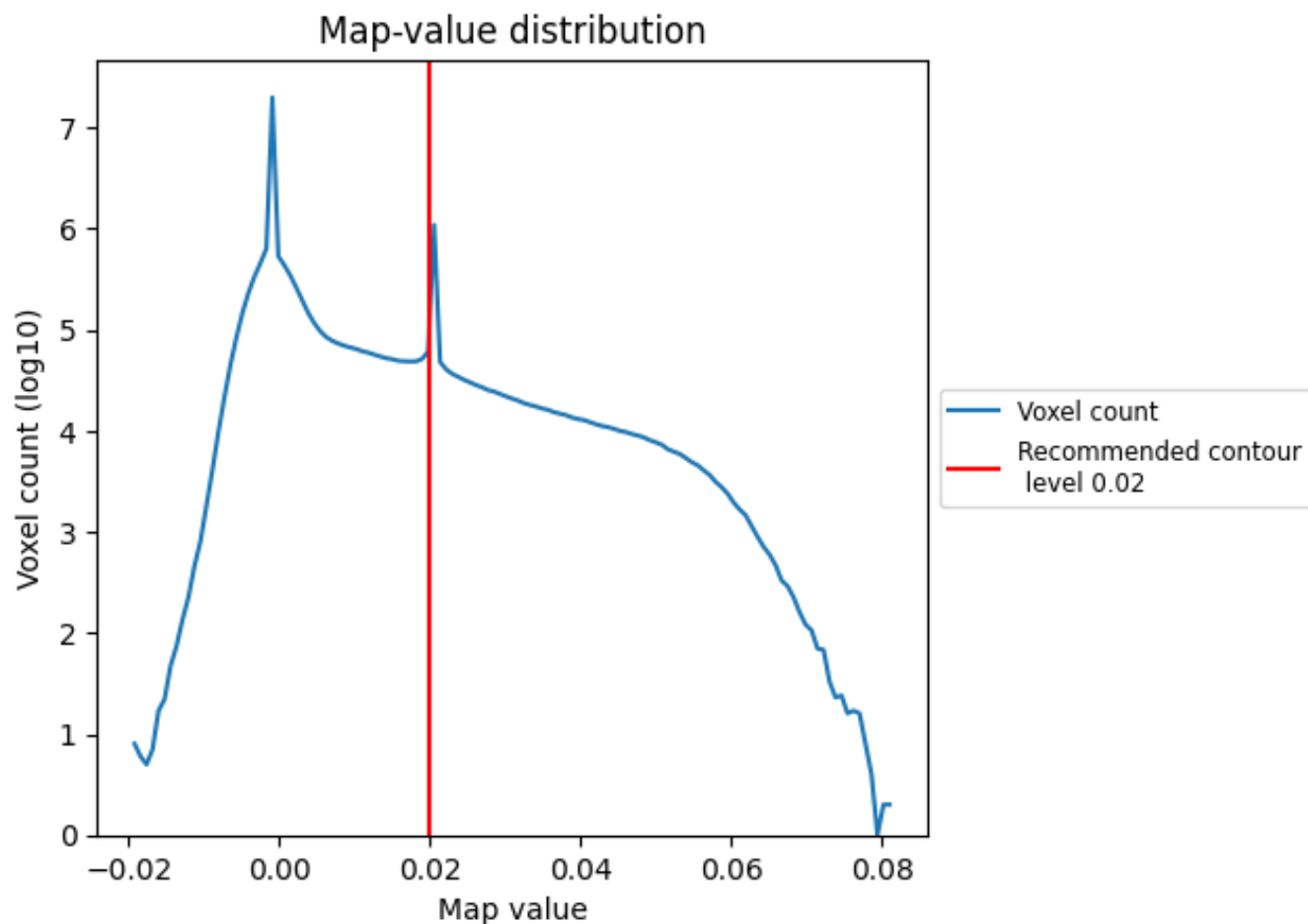
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

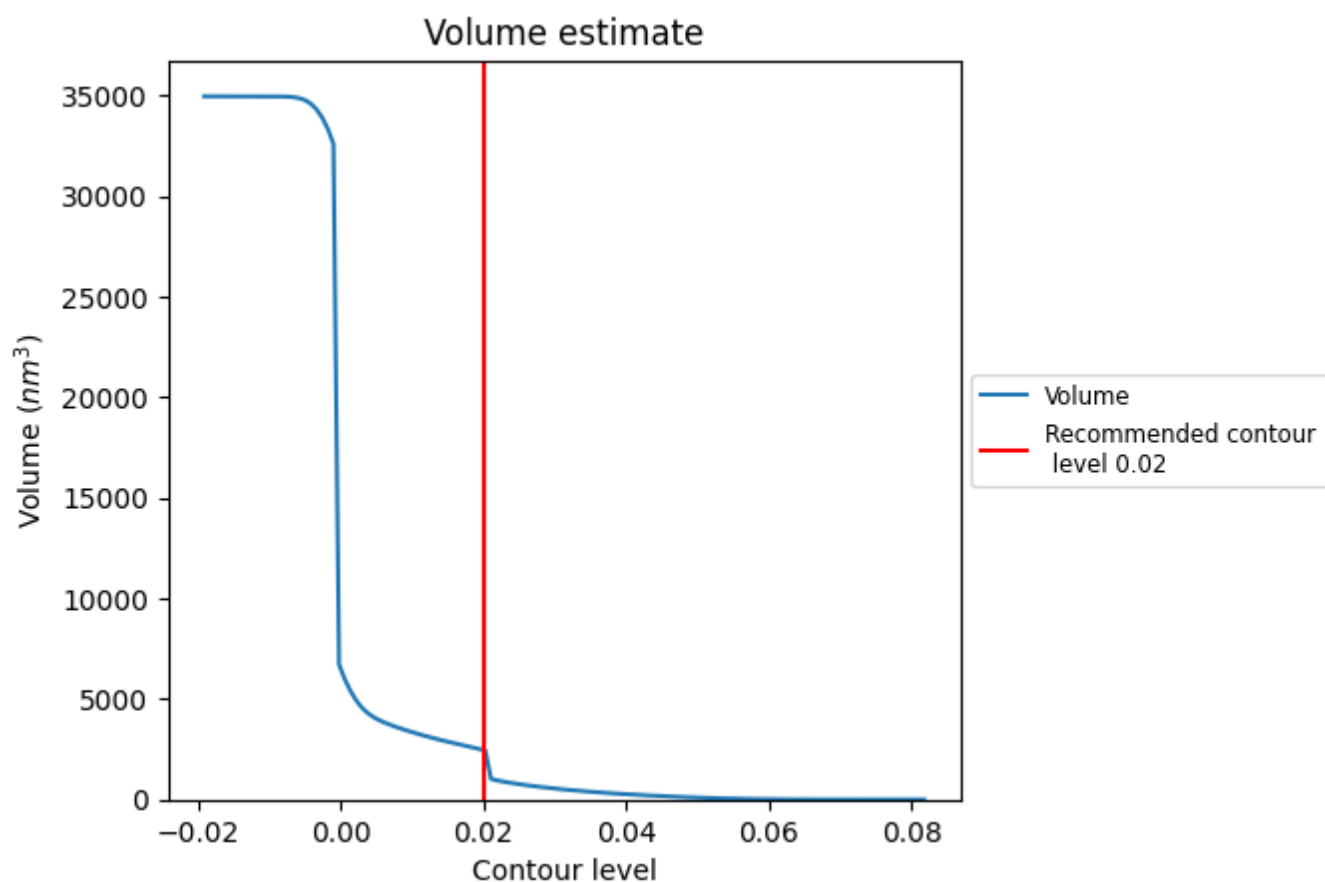
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

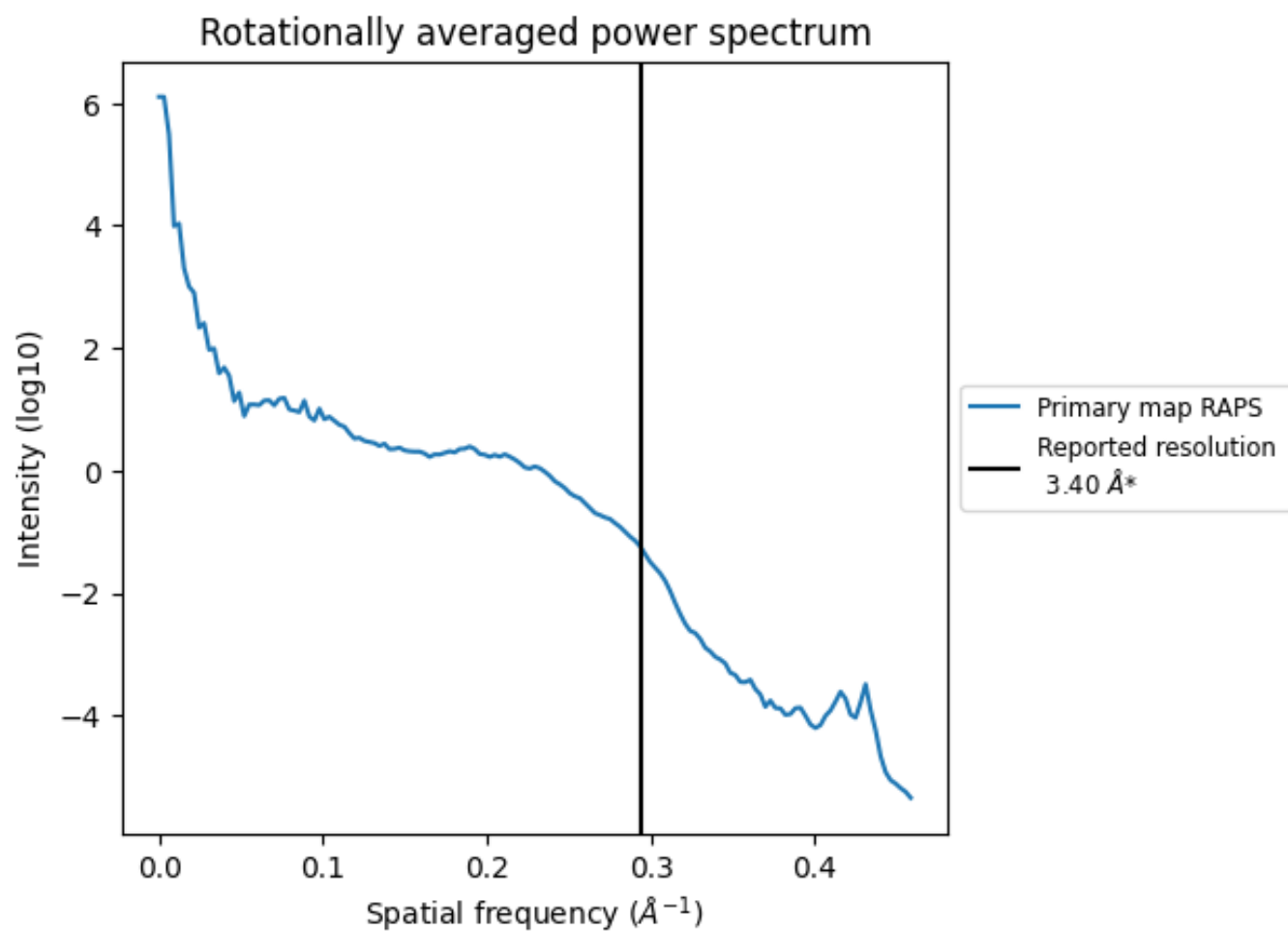
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2468 nm³; this corresponds to an approximate mass of 2229 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 0.294 Å⁻¹

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

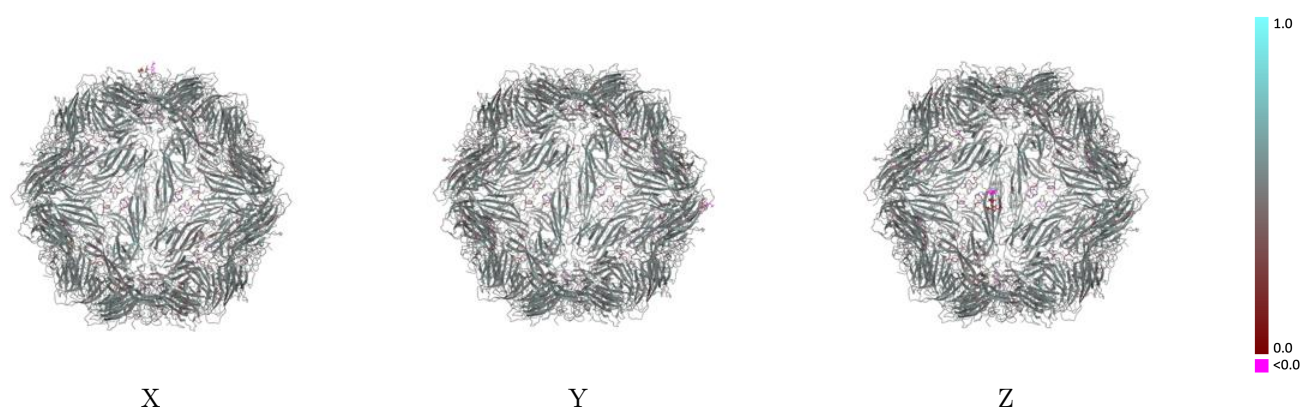
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8971 and PDB model 6E2Z. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

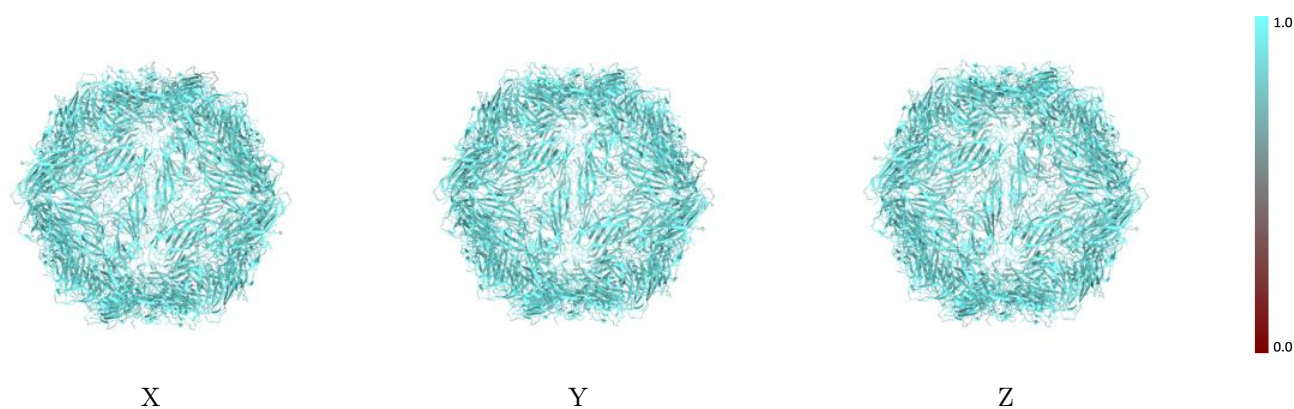
This section was not generated.

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



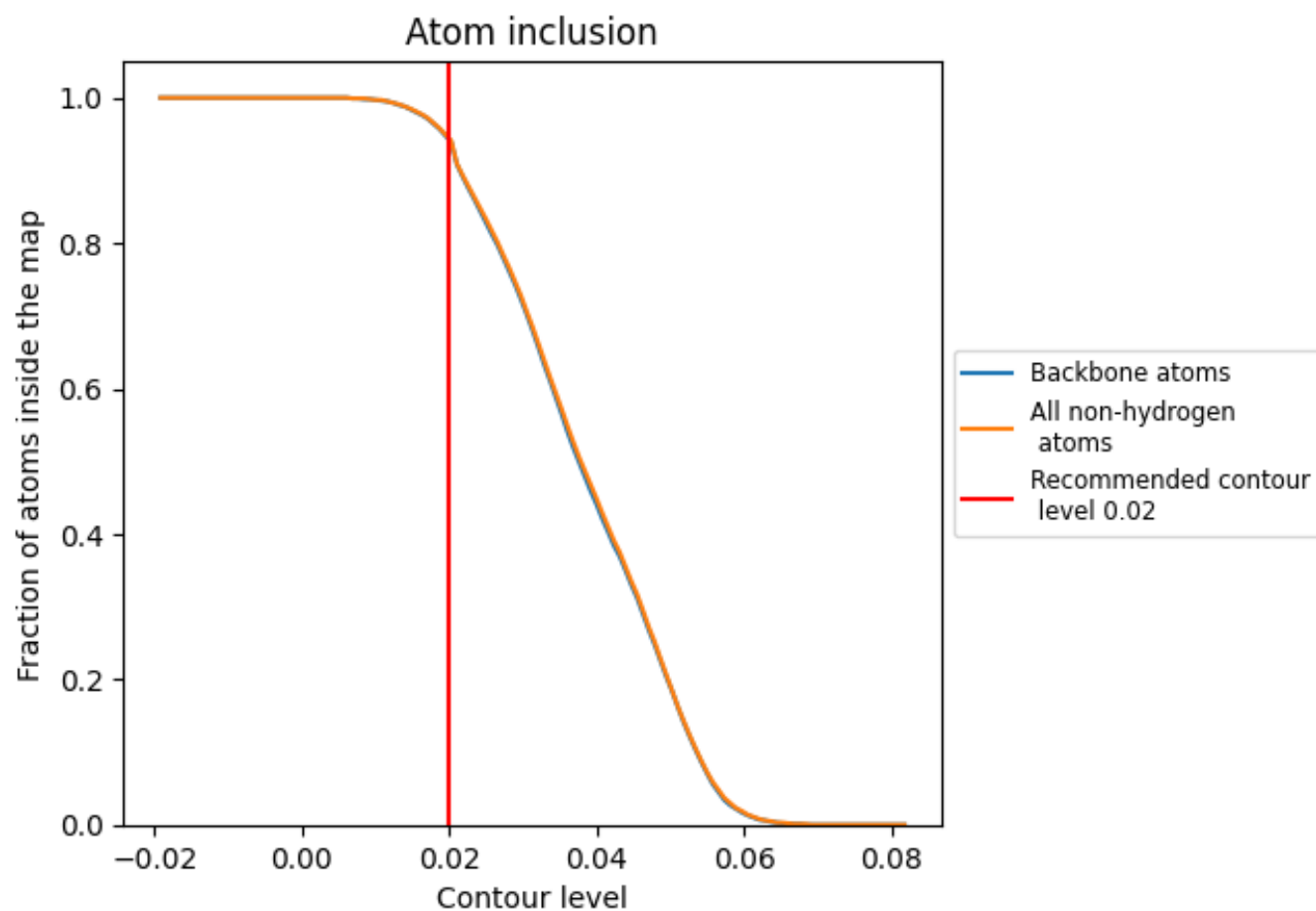
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.4820
A	 0.8730	 0.0220
A1	 0.9070	 0.4850
A2	 0.9480	 0.4660
A3	 0.9540	 0.4850
A4	 0.9480	 0.4860
A5	 0.9480	 0.4870
A6	 0.9210	 0.4690
A7	 0.9410	 0.4730
A8	 0.9540	 0.4830
A9	 0.9610	 0.4940
AA	 0.9500	 0.4900
AB	 0.9550	 0.4900
AC	 0.9400	 0.4700
AD	 0.9540	 0.4850
AE	 0.9490	 0.4820
AF	 0.9340	 0.4580
AG	 0.9540	 0.4960
AH	 0.9490	 0.4830
AI	 0.9540	 0.4720
AJ	 0.9480	 0.4770
AK	 0.9470	 0.4890
AL	 0.9540	 0.4890
AM	 0.9490	 0.4810
AN	 0.9500	 0.4860
AO	 0.9550	 0.4900
AP	 0.9540	 0.4870
AQ	 0.9500	 0.4940
AR	 0.9470	 0.4700
AS	 0.9480	 0.4880
AT	 0.9400	 0.4670
AU	 0.9450	 0.4610
AV	 0.9560	 0.4950
AW	 0.9460	 0.4800
AX	 0.9550	 0.4910



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Chain	Atom inclusion	Q-score
AY	 0.9470	 0.4740
AZ	 0.9560	 0.4890
Aa	 0.9540	 0.4910
Ab	 0.9480	 0.4800
Ac	 0.9490	 0.4870
Ad	 0.9520	 0.4680
Ae	 0.9460	 0.4700
Af	 0.9520	 0.4960
Ag	 0.9450	 0.4650
Ah	 0.9490	 0.4840
Ai	 0.9540	 0.4880
Aj	 0.9540	 0.4870
Ak	 0.9500	 0.4910
Al	 0.9560	 0.4890
Am	 0.9550	 0.4880
An	 0.9380	 0.4690
Ao	 0.9540	 0.4920
Ap	 0.9490	 0.4930
Aq	 0.9520	 0.4920
Ar	 0.9510	 0.4890
As	 0.9450	 0.4740
At	 0.9510	 0.4890
Au	 0.9530	 0.4900
Av	 0.9470	 0.4780
Aw	 0.9530	 0.4870
Ax	 0.9540	 0.4940
Ay	 0.9320	 0.4370