



Full wwPDB EM Validation Report ⓘ

Mar 11, 2024 – 08:48 AM EDT

PDB ID : 6E2R
EMDB ID : EMD-8969
Title : Mechanism of cellular recognition by PCV2
Authors : Khayat, R.; Dhindwal, S.
Deposited on : 2018-07-12
Resolution : 2.80 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:

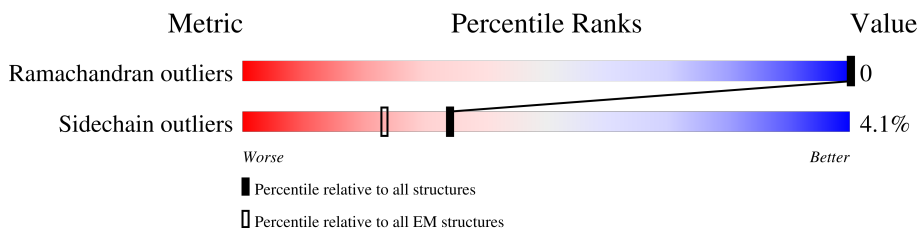
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.80 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.














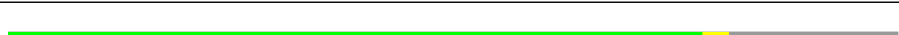

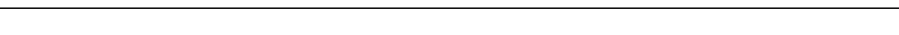
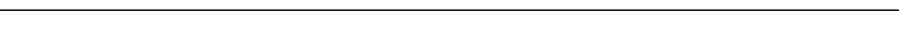
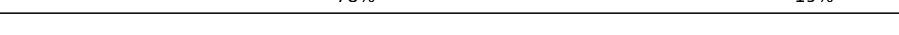

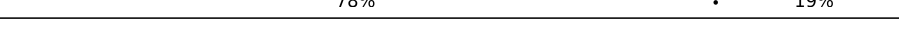







Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	78% 19%
1	A2	233	78% 19%
1	A3	233	78% 19%
1	A4	233	78% 19%
1	A5	233	78% 19%
1	A6	233	78% 19%
1	A7	233	78% 19%
1	A8	233	78% 19%
1	A9	233	78% 19%












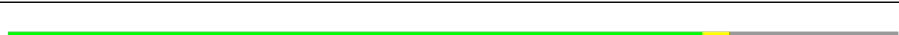

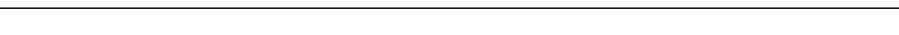
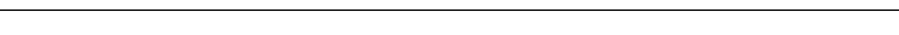
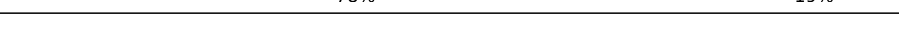

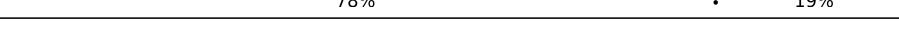







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Mol	Chain	Length	Quality of chain
1	AA	233	 78% 19%
1	AB	233	 78% 19%
1	AC	233	 78% 19%
1	AD	233	 78% 19%
1	AE	233	 78% 19%
1	AF	233	 78% 19%
1	AG	233	 78% 19%
1	AH	233	 78% 19%
1	AI	233	 78% 19%
1	AJ	233	 78% 19%
1	AK	233	 78% 19%
1	AL	233	 78% 19%
1	AM	233	 78% 19%
1	AN	233	 78% 19%
1	AO	233	 78% 19%
1	AP	233	 78% 19%
1	AQ	233	 78% 19%
1	AR	233	 78% 19%
1	AS	233	 78% 19%
1	AT	233	 78% 19%
1	AU	233	 78% 19%
1	AV	233	 78% 19%
1	AW	233	 78% 19%
1	AX	233	 78% 19%
1	AY	233	 78% 19%


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Mol	Chain	Length	Quality of chain
1	AZ	233	 78% 19%
1	Aa	233	 78% 19%
1	Ab	233	 78% 19%
1	Ac	233	 78% 19%
1	Ad	233	 78% 19%
1	Ae	233	 78% 19%
1	Af	233	 78% 19%
1	Ag	233	 78% 19%
1	Ah	233	 78% 19%
1	Ai	233	 78% 19%
1	Aj	233	 78% 19%
1	Ak	233	 78% 19%
1	Al	233	 78% 19%
1	Am	233	 78% 19%
1	An	233	 78% 19%
1	Ao	233	 78% 19%
1	Ap	233	 78% 19%
1	Aq	233	 78% 19%
1	Ar	233	 78% 19%
1	As	233	 78% 19%
1	At	233	 78% 19%
1	Au	233	 78% 19%
1	Av	233	 78% 19%
1	Aw	233	 78% 19%
1	Ax	233	 78% 19%

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Mol	Chain	Length	Quality of chain
1	Ay	233	 78% . 19%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 183180 atoms, of which 90180 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
			Total	C	H	N	O	S		
1	A1	189	3053	995	1503	268	283	4	0	0
1	A2	189	3053	995	1503	268	283	4	0	0
1	A3	189	3053	995	1503	268	283	4	0	0
1	A4	189	3053	995	1503	268	283	4	0	0
1	A5	189	3053	995	1503	268	283	4	0	0
1	A6	189	3053	995	1503	268	283	4	0	0
1	A7	189	3053	995	1503	268	283	4	0	0
1	A8	189	3053	995	1503	268	283	4	0	0
1	A9	189	3053	995	1503	268	283	4	0	0
1	AA	189	3053	995	1503	268	283	4	0	0
1	AB	189	3053	995	1503	268	283	4	0	0
1	AC	189	3053	995	1503	268	283	4	0	0
1	AD	189	3053	995	1503	268	283	4	0	0
1	AE	189	3053	995	1503	268	283	4	0	0
1	AF	189	3053	995	1503	268	283	4	0	0
1	AG	189	3053	995	1503	268	283	4	0	0
1	AH	189	3053	995	1503	268	283	4	0	0

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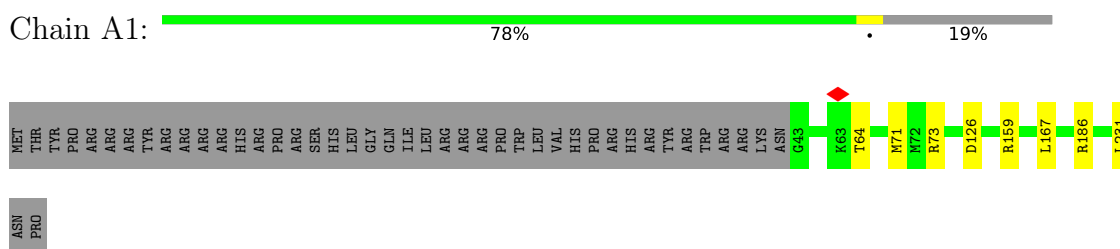
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Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	Ay	189	3053	995	1503	268	283	4	0	0

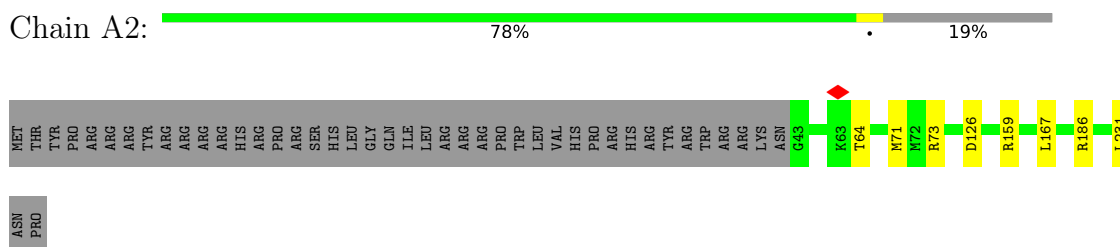
3 Residue-property plots [i](#)

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

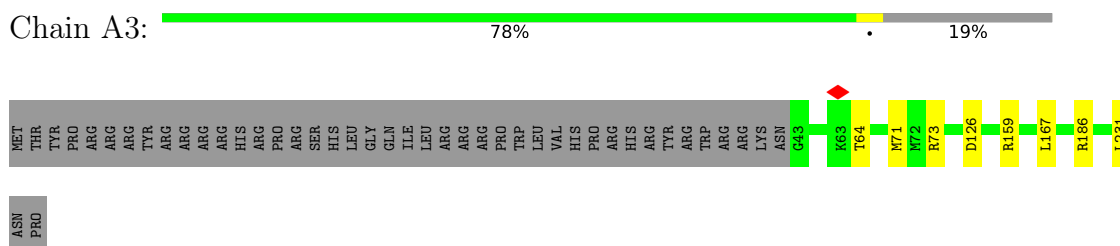
- Molecule 1: Capsid protein of PCV2



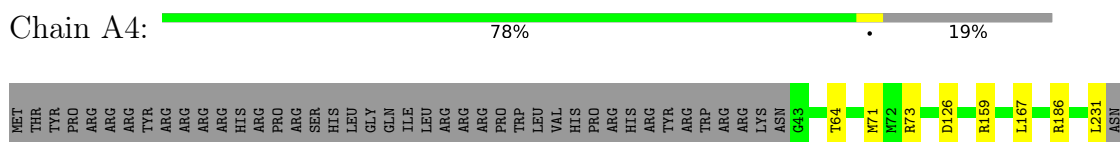
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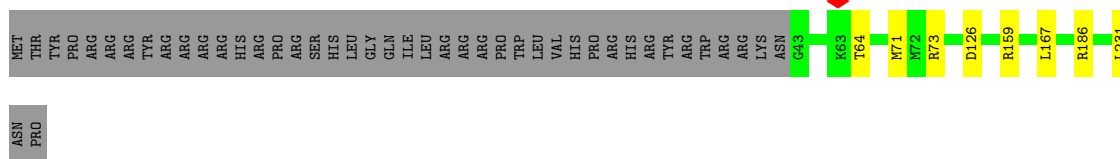
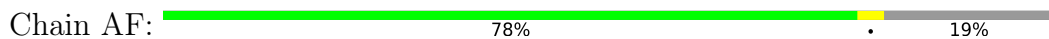
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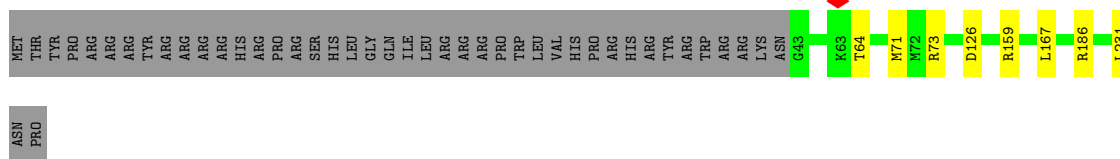
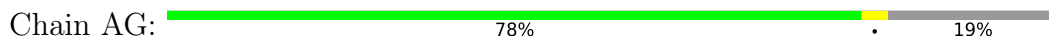
- Molecule 1: Capsid protein of PCV2



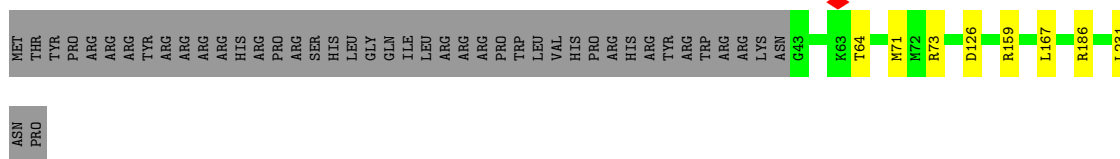
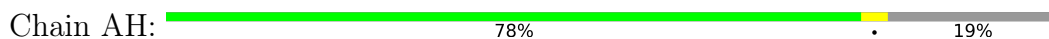
• Molecule 1: Capsid protein of PCV2



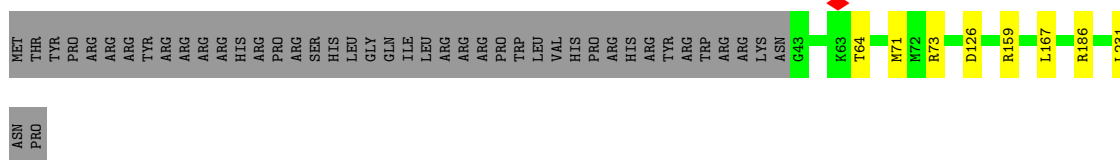
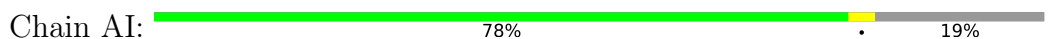
• Molecule 1: Capsid protein of PCV2



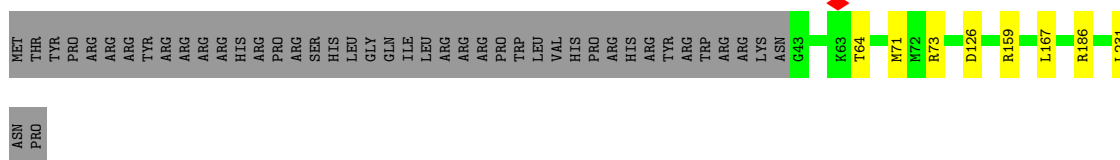
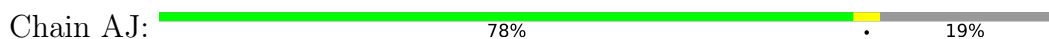
• Molecule 1: Capsid protein of PCV2



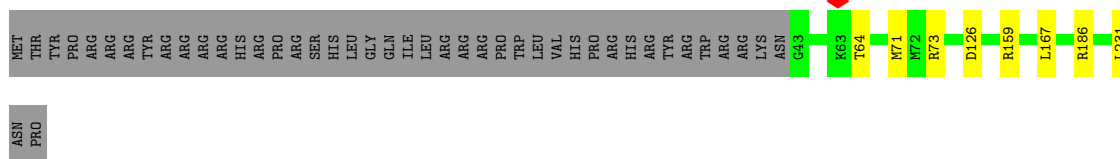
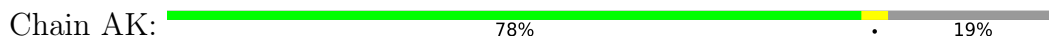
• Molecule 1: Capsid protein of PCV2



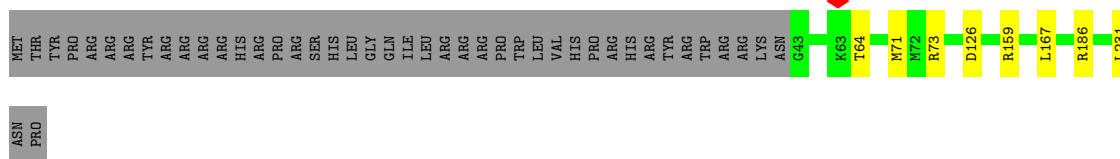
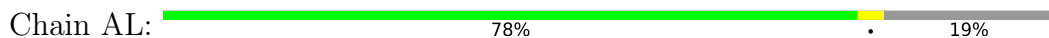
• Molecule 1: Capsid protein of PCV2



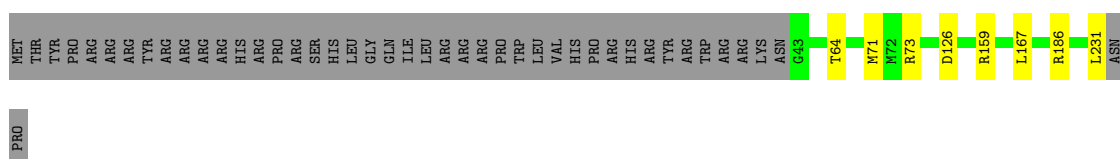
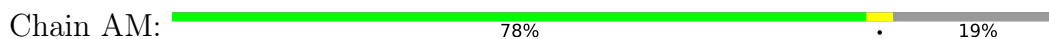
• Molecule 1: Capsid protein of PCV2



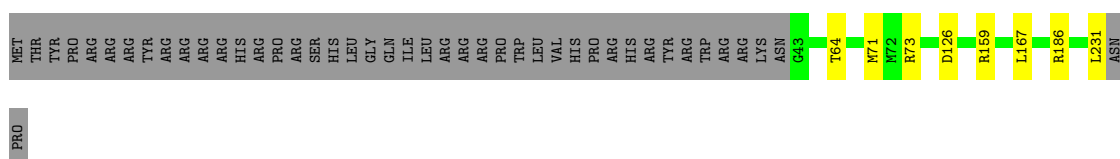
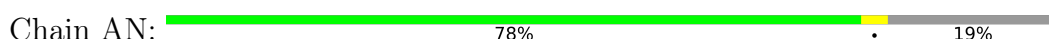
• Molecule 1: Capsid protein of PCV2



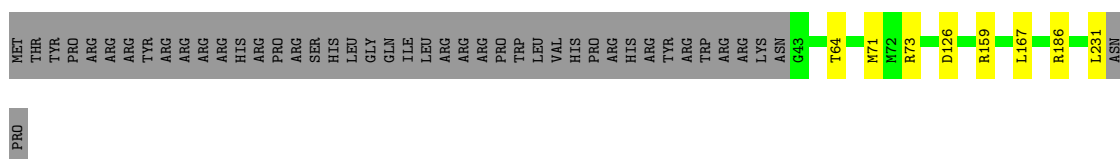
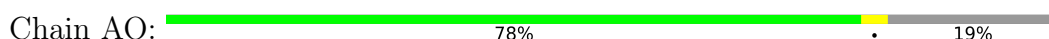
• Molecule 1: Capsid protein of PCV2




• Molecule 1: Capsid protein of PCV2

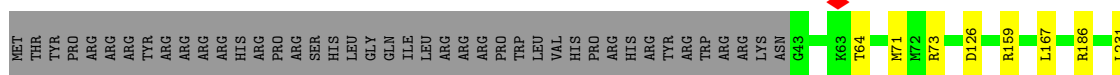


• Molecule 1: Capsid protein of PCV2




• Molecule 1: Capsid protein of PCV2

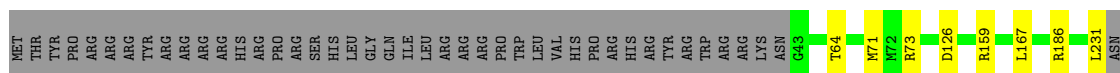
Chain AP:  78% 19%



ASN
PRO


• Molecule 1: Capsid protein of PCV2

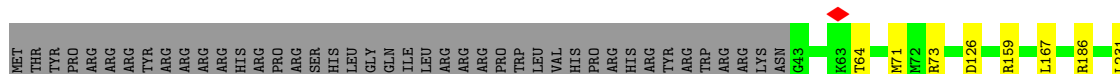
Chain AQ:  78% 19%



PRO


• Molecule 1: Capsid protein of PCV2

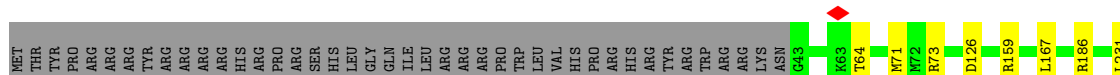
Chain AR:  78% 19%



ASN
PRO


• Molecule 1: Capsid protein of PCV2

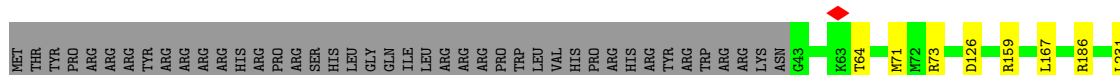
Chain AS:  78% 19%



ASN
PRO


• Molecule 1: Capsid protein of PCV2

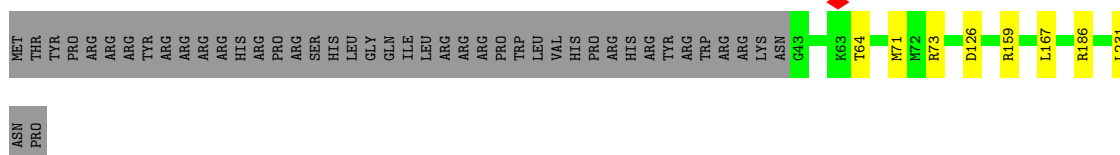
Chain AT:  78% 19%




ASN
PRO

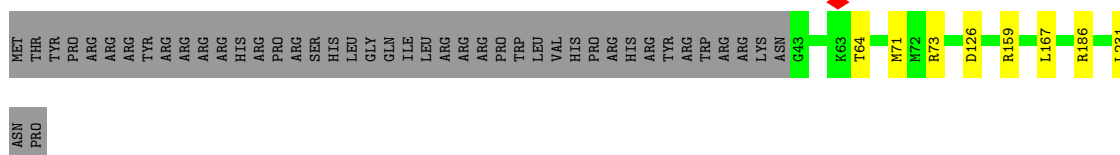
• Molecule 1: Capsid protein of PCV2

Chain AU:  78% 19%




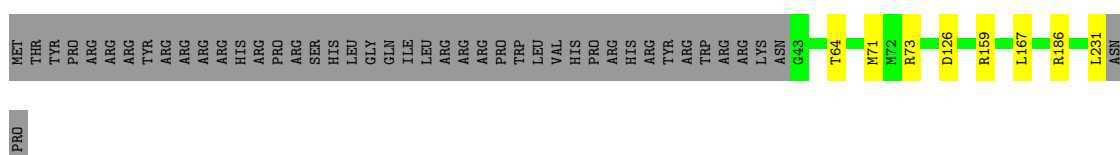
• Molecule 1: Capsid protein of PCV2

Chain AV:  78% 19%




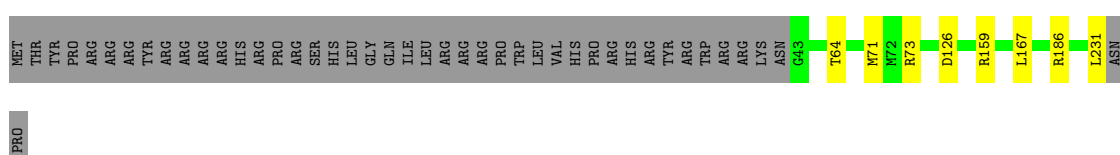
• Molecule 1: Capsid protein of PCV2

Chain AW:  78% 19%



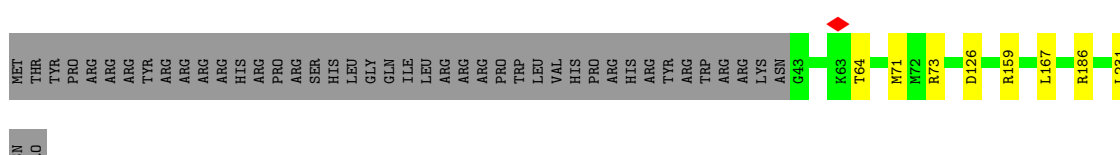
• Molecule 1: Capsid protein of PCV2

Chain AX:  78% 19%




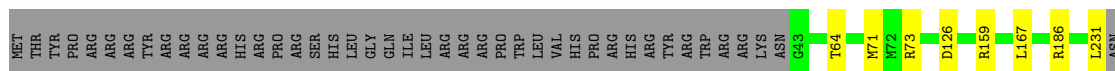
• Molecule 1: Capsid protein of PCV2

Chain AY:  78% 19%



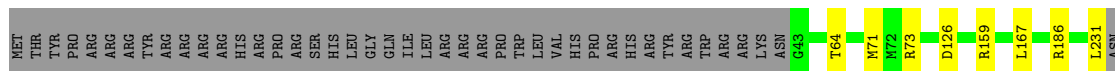
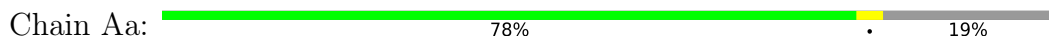
• Molecule 1: Capsid protein of PCV2

Chain AZ:  78% 19%



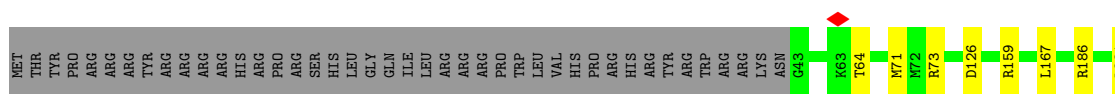
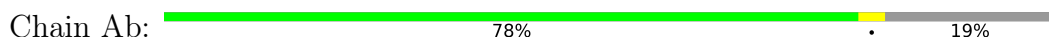
PRO

• Molecule 1: Capsid protein of PCV2



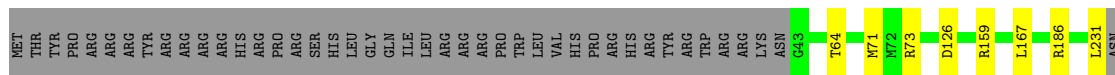
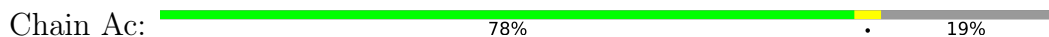
PRO

• Molecule 1: Capsid protein of PCV2



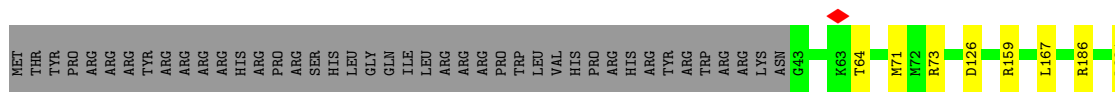
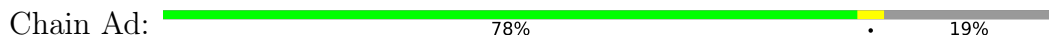
ASN
PRO

• Molecule 1: Capsid protein of PCV2



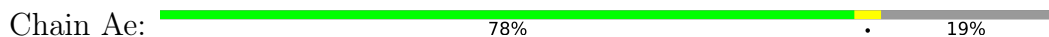
PRO

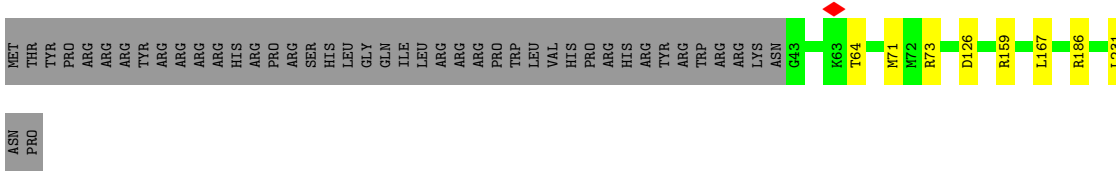
• Molecule 1: Capsid protein of PCV2



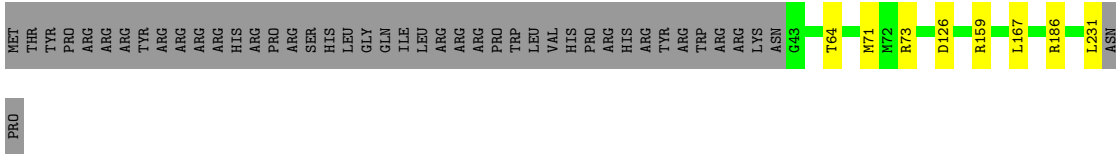
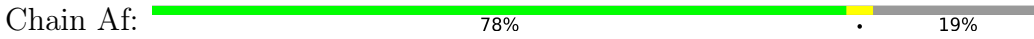
ASN
PRO

• Molecule 1: Capsid protein of PCV2

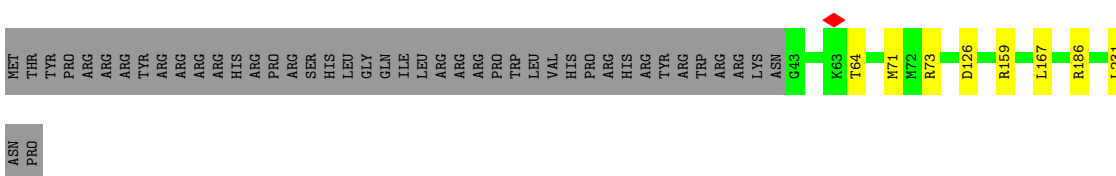
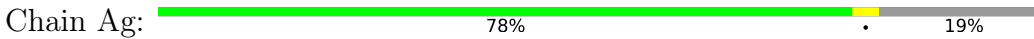




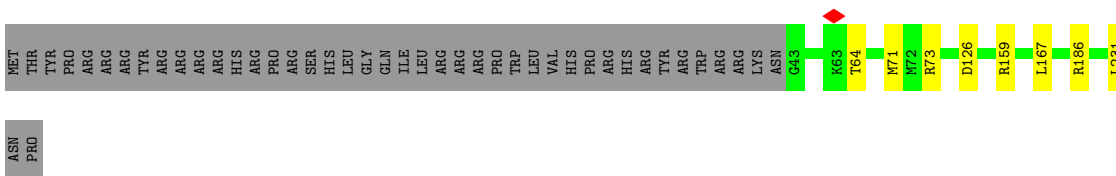
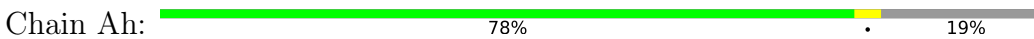
● Molecule 1: Capsid protein of PCV2



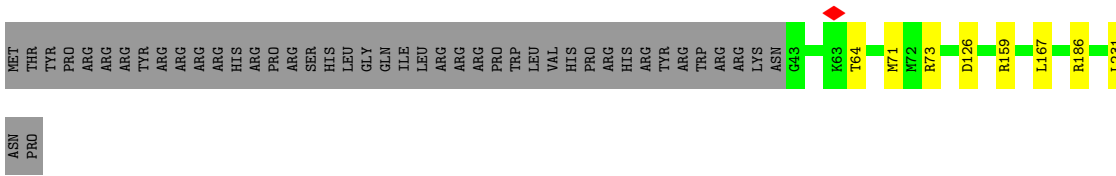
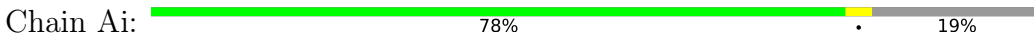
● Molecule 1: Capsid protein of PCV2



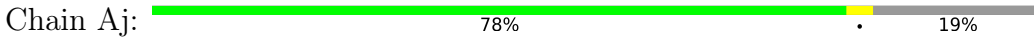
● Molecule 1: Capsid protein of PCV2

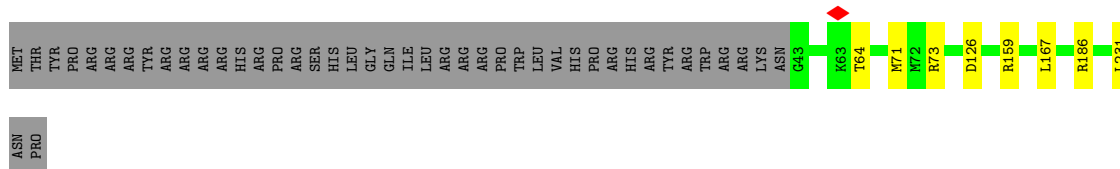


● Molecule 1: Capsid protein of PCV2

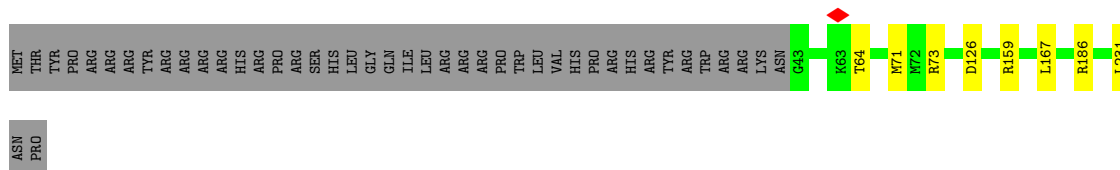
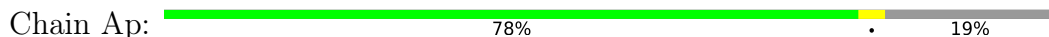


● Molecule 1: Capsid protein of PCV2

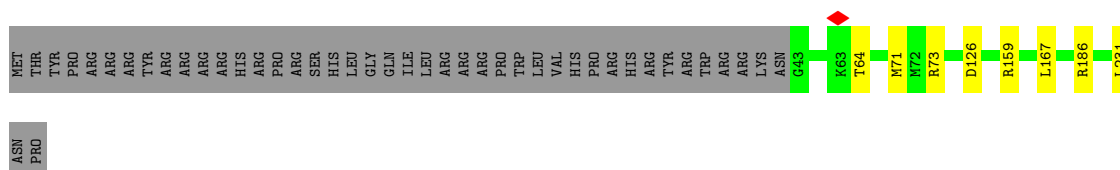
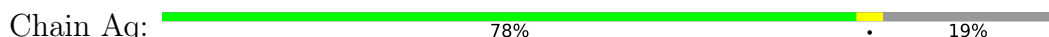




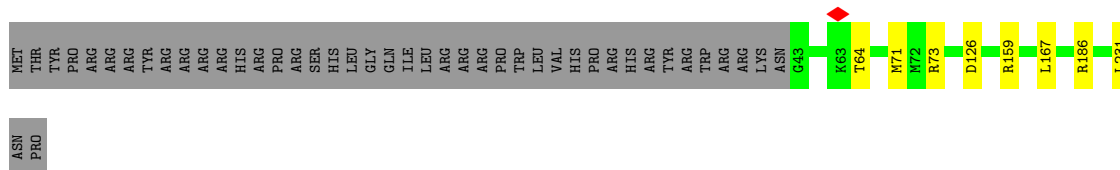
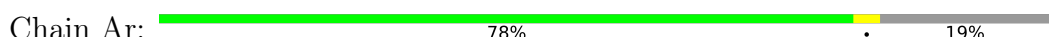
● Molecule 1: Capsid protein of PCV2



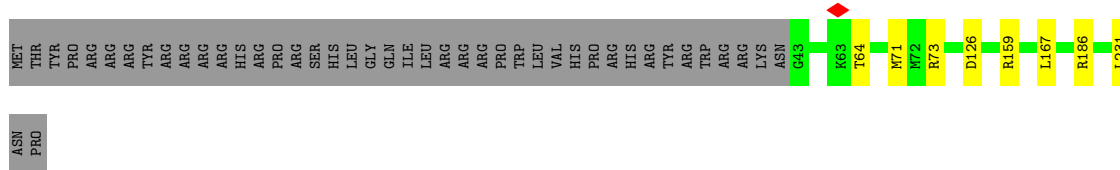
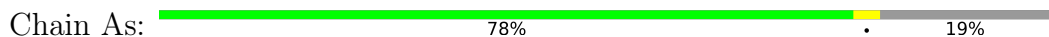
● Molecule 1: Capsid protein of PCV2



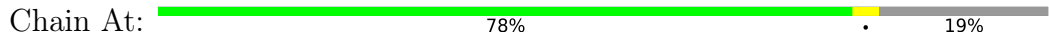
● Molecule 1: Capsid protein of PCV2

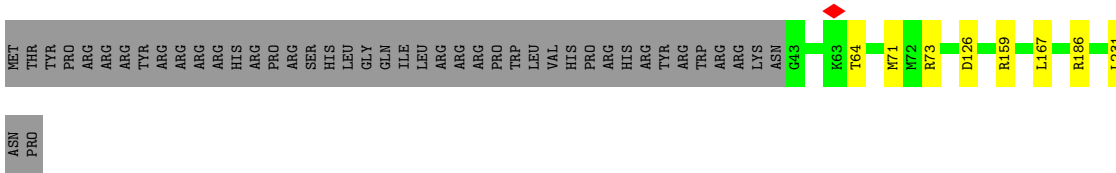


● Molecule 1: Capsid protein of PCV2

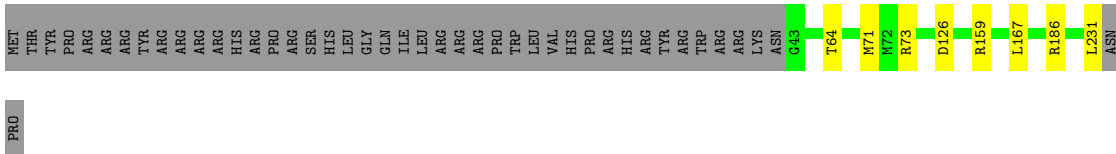
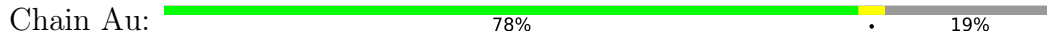


● Molecule 1: Capsid protein of PCV2

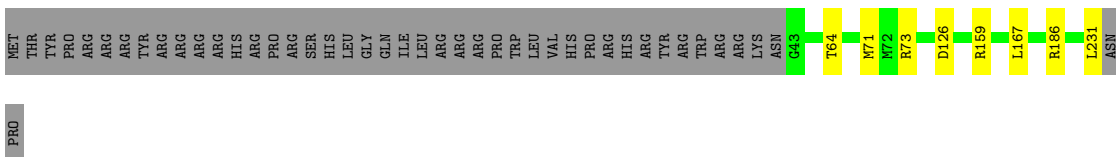
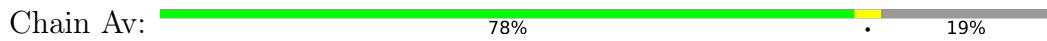




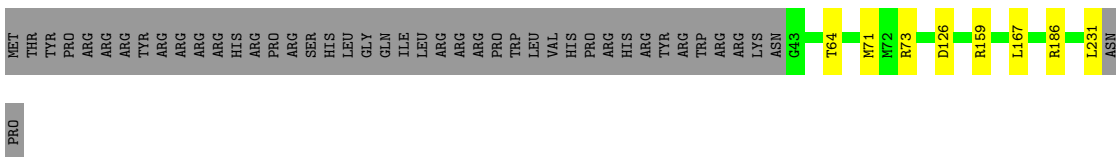
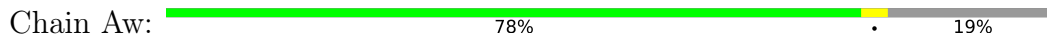
• Molecule 1: Capsid protein of PCV2



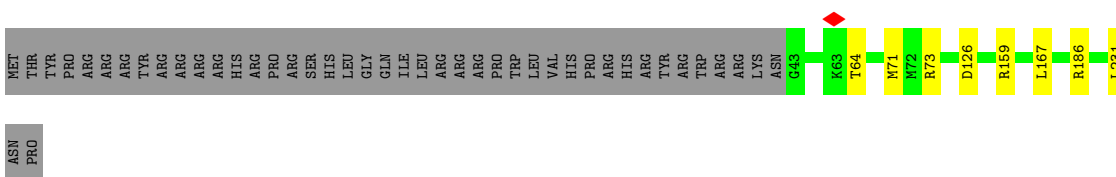
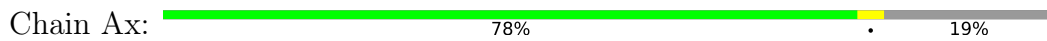
• Molecule 1: Capsid protein of PCV2



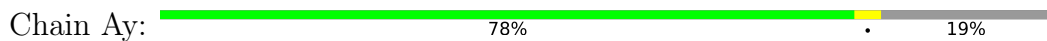
• Molecule 1: Capsid protein of PCV2



• Molecule 1: Capsid protein of PCV2



• Molecule 1: Capsid protein of PCV2



MET	THR	TYR	PRO	ARG	ARG	ARG	TYR	ARG	ARG	ARG	HIS	ARG	PRO	ARG	SER	HIS	HIS	LEU	GLY	GLN	ILE	LEU	LEU	ARG	ARG	ARG	PRO	TRP	TRP	LEU	VAL	VAL	HIS	PRO	ARG	HIS	HIS	ARG	TYR	ARG	TRP	TRP	ARG	ARG	LYS	ASN	ASN	C43	T64	M71	M72	R73	D126	R159	L167	R186	L231	ASN
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PRO

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	93725	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	280	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.338	Depositor
Minimum map value	-0.174	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.04	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](#)

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	0.76	0/1597	0.63	1/2175 (0.0%)
1	A2	0.76	0/1597	0.63	1/2175 (0.0%)
1	A3	0.76	0/1597	0.63	1/2175 (0.0%)
1	A4	0.76	0/1597	0.63	1/2175 (0.0%)
1	A5	0.76	0/1597	0.63	1/2175 (0.0%)
1	A6	0.76	0/1597	0.63	1/2175 (0.0%)
1	A7	0.76	0/1597	0.63	1/2175 (0.0%)
1	A8	0.76	0/1597	0.63	1/2175 (0.0%)
1	A9	0.76	0/1597	0.63	1/2175 (0.0%)
1	AA	0.76	0/1597	0.63	1/2175 (0.0%)
1	AB	0.76	0/1597	0.63	1/2175 (0.0%)
1	AC	0.76	0/1597	0.63	1/2175 (0.0%)
1	AD	0.76	0/1597	0.63	1/2175 (0.0%)
1	AE	0.76	0/1597	0.63	1/2175 (0.0%)
1	AF	0.76	0/1597	0.63	1/2175 (0.0%)
1	AG	0.76	0/1597	0.63	1/2175 (0.0%)
1	AH	0.76	0/1597	0.63	1/2175 (0.0%)
1	AI	0.76	0/1597	0.63	1/2175 (0.0%)
1	AJ	0.76	0/1597	0.63	1/2175 (0.0%)
1	AK	0.76	0/1597	0.63	1/2175 (0.0%)
1	AL	0.76	0/1597	0.63	1/2175 (0.0%)
1	AM	0.76	0/1597	0.63	1/2175 (0.0%)
1	AN	0.76	0/1597	0.63	1/2175 (0.0%)
1	AO	0.76	0/1597	0.63	1/2175 (0.0%)
1	AP	0.76	0/1597	0.63	1/2175 (0.0%)
1	AQ	0.76	0/1597	0.63	1/2175 (0.0%)
1	AR	0.76	0/1597	0.63	1/2175 (0.0%)
1	AS	0.76	0/1597	0.63	1/2175 (0.0%)
1	AT	0.76	0/1597	0.63	1/2175 (0.0%)
1	AU	0.76	0/1597	0.63	1/2175 (0.0%)
1	AV	0.76	0/1597	0.63	1/2175 (0.0%)
1	AW	0.76	0/1597	0.63	1/2175 (0.0%)
1	AX	0.76	0/1597	0.63	1/2175 (0.0%)
1	AY	0.76	0/1597	0.63	1/2175 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AZ	0.76	0/1597	0.63	1/2175 (0.0%)
1	Aa	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ab	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ac	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ad	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ae	0.76	0/1597	0.63	1/2175 (0.0%)
1	Af	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ag	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ah	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ai	0.76	0/1597	0.63	1/2175 (0.0%)
1	Aj	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ak	0.76	0/1597	0.63	1/2175 (0.0%)
1	Al	0.76	0/1597	0.63	1/2175 (0.0%)
1	Am	0.76	0/1597	0.63	1/2175 (0.0%)
1	An	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ao	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ap	0.76	0/1597	0.63	1/2175 (0.0%)
1	Aq	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ar	0.76	0/1597	0.63	1/2175 (0.0%)
1	As	0.76	0/1597	0.63	1/2175 (0.0%)
1	At	0.76	0/1597	0.63	1/2175 (0.0%)
1	Au	0.76	0/1597	0.63	1/2175 (0.0%)
1	Av	0.76	0/1597	0.63	1/2175 (0.0%)
1	Aw	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ax	0.76	0/1597	0.63	1/2175 (0.0%)
1	Ay	0.76	0/1597	0.63	1/2175 (0.0%)
All	All	0.76	0/95820	0.63	60/130500 (0.0%)

There are no bond length outliers.

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AV	159	ARG	NE-CZ-NH2	6.18	123.39	120.30
1	A3	159	ARG	NE-CZ-NH2	6.14	123.37	120.30
1	AD	159	ARG	NE-CZ-NH2	6.11	123.35	120.30
1	AI	159	ARG	NE-CZ-NH2	6.10	123.35	120.30
1	AU	159	ARG	NE-CZ-NH2	6.10	123.35	120.30
1	Ap	159	ARG	NE-CZ-NH2	6.09	123.35	120.30
1	Ak	159	ARG	NE-CZ-NH2	6.09	123.34	120.30
1	Af	159	ARG	NE-CZ-NH2	6.08	123.34	120.30
1	Ah	159	ARG	NE-CZ-NH2	6.07	123.33	120.30
1	AK	159	ARG	NE-CZ-NH2	6.07	123.33	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	159	ARG	NE-CZ-NH2	6.05	123.32	120.30
1	A7	159	ARG	NE-CZ-NH2	6.04	123.32	120.30
1	AF	159	ARG	NE-CZ-NH2	6.03	123.32	120.30
1	AX	159	ARG	NE-CZ-NH2	6.03	123.32	120.30
1	Aw	159	ARG	NE-CZ-NH2	6.03	123.32	120.30
1	A1	159	ARG	NE-CZ-NH2	6.03	123.31	120.30
1	AP	159	ARG	NE-CZ-NH2	6.03	123.31	120.30
1	Aa	159	ARG	NE-CZ-NH2	6.02	123.31	120.30
1	Ag	159	ARG	NE-CZ-NH2	6.02	123.31	120.30
1	AW	159	ARG	NE-CZ-NH2	6.02	123.31	120.30
1	AQ	159	ARG	NE-CZ-NH2	6.01	123.31	120.30
1	AS	159	ARG	NE-CZ-NH2	6.01	123.31	120.30
1	A5	159	ARG	NE-CZ-NH2	6.01	123.31	120.30
1	AO	159	ARG	NE-CZ-NH2	6.00	123.30	120.30
1	A9	159	ARG	NE-CZ-NH2	6.00	123.30	120.30
1	AT	159	ARG	NE-CZ-NH2	6.00	123.30	120.30
1	Aj	159	ARG	NE-CZ-NH2	6.00	123.30	120.30
1	At	159	ARG	NE-CZ-NH2	6.00	123.30	120.30
1	Ae	159	ARG	NE-CZ-NH2	5.99	123.30	120.30
1	Ac	159	ARG	NE-CZ-NH2	5.99	123.29	120.30
1	Aq	159	ARG	NE-CZ-NH2	5.99	123.29	120.30
1	AJ	159	ARG	NE-CZ-NH2	5.99	123.29	120.30
1	AN	159	ARG	NE-CZ-NH2	5.98	123.29	120.30
1	Ar	159	ARG	NE-CZ-NH2	5.98	123.29	120.30
1	AM	159	ARG	NE-CZ-NH2	5.97	123.29	120.30
1	Ao	159	ARG	NE-CZ-NH2	5.97	123.29	120.30
1	As	159	ARG	NE-CZ-NH2	5.97	123.28	120.30
1	AY	159	ARG	NE-CZ-NH2	5.97	123.28	120.30
1	Al	159	ARG	NE-CZ-NH2	5.96	123.28	120.30
1	Ai	159	ARG	NE-CZ-NH2	5.96	123.28	120.30
1	AL	159	ARG	NE-CZ-NH2	5.96	123.28	120.30
1	Ab	159	ARG	NE-CZ-NH2	5.95	123.28	120.30
1	A2	159	ARG	NE-CZ-NH2	5.95	123.27	120.30
1	A4	159	ARG	NE-CZ-NH2	5.94	123.27	120.30
1	Am	159	ARG	NE-CZ-NH2	5.94	123.27	120.30
1	AC	159	ARG	NE-CZ-NH2	5.93	123.26	120.30
1	AH	159	ARG	NE-CZ-NH2	5.93	123.26	120.30
1	An	159	ARG	NE-CZ-NH2	5.93	123.26	120.30
1	AB	159	ARG	NE-CZ-NH2	5.92	123.26	120.30
1	Av	159	ARG	NE-CZ-NH2	5.92	123.26	120.30
1	Ay	159	ARG	NE-CZ-NH2	5.91	123.25	120.30
1	AE	159	ARG	NE-CZ-NH2	5.90	123.25	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AG	159	ARG	NE-CZ-NH2	5.89	123.25	120.30
1	Ad	159	ARG	NE-CZ-NH2	5.89	123.25	120.30
1	Au	159	ARG	NE-CZ-NH2	5.89	123.25	120.30
1	AR	159	ARG	NE-CZ-NH2	5.89	123.24	120.30
1	AZ	159	ARG	NE-CZ-NH2	5.87	123.24	120.30
1	A8	159	ARG	NE-CZ-NH2	5.84	123.22	120.30
1	Ax	159	ARG	NE-CZ-NH2	5.83	123.22	120.30
1	A6	159	ARG	NE-CZ-NH2	5.81	123.21	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	187/233 (80%)	181 (97%)	6 (3%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	181 (97%)	6 (3%)	0	100	100
1	AF	187/233 (80%)	180 (96%)	7 (4%)	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%)	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%)	180 (96%)	7 (4%)	0	100	100
1	AS	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AT	187/233 (80%)	180 (96%)	7 (4%)	0	100	100
1	AU	187/233 (80%)	181 (97%)	6 (3%)	0	100	100
1	AV	187/233 (80%)	180 (96%)	7 (4%)	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

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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%)	181 (97%)	6 (3%)	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%)	181 (97%)	6 (3%)	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%)	181 (97%)	6 (3%)	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%)	180 (96%)	7 (4%)	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	11220/13980 (80%)	10851 (97%)	369 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	172/215 (80%)	165 (96%)	7 (4%)	30	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A2	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	A3	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	A4	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	A5	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	A6	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	A7	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	A8	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	A9	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AA	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AB	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AC	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AD	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AE	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AF	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AG	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AH	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AI	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AJ	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AK	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AL	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AM	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AN	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AO	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AP	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AQ	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AR	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AS	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AT	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AU	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AV	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AW	172/215 (80%)	165 (96%)	7 (4%)	30	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AX	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AY	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	AZ	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Aa	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ab	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ac	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ad	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ae	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Af	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ag	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ah	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ai	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Aj	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ak	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Al	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Am	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	An	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ao	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ap	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Aq	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ar	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	As	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	At	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Au	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Av	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Aw	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ax	172/215 (80%)	165 (96%)	7 (4%)	30	64
1	Ay	172/215 (80%)	165 (96%)	7 (4%)	30	64
All	All	10320/12900 (80%)	9900 (96%)	420 (4%)	34	64

All (420) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A1	64	THR
1	A1	71	MET
1	A1	73	ARG
1	A1	126	ASP
1	A1	167	LEU
1	A1	186	ARG
1	A1	231	LEU
1	A2	64	THR
1	A2	71	MET
1	A2	73	ARG
1	A2	126	ASP
1	A2	167	LEU
1	A2	186	ARG
1	A2	231	LEU
1	A3	64	THR
1	A3	71	MET
1	A3	73	ARG
1	A3	126	ASP
1	A3	167	LEU
1	A3	186	ARG
1	A3	231	LEU
1	A4	64	THR
1	A4	71	MET
1	A4	73	ARG
1	A4	126	ASP
1	A4	167	LEU
1	A4	186	ARG
1	A4	231	LEU
1	A5	64	THR
1	A5	71	MET
1	A5	73	ARG
1	A5	126	ASP
1	A5	167	LEU
1	A5	186	ARG
1	A5	231	LEU
1	A6	64	THR
1	A6	71	MET
1	A6	73	ARG
1	A6	126	ASP
1	A6	167	LEU
1	A6	186	ARG
1	A6	231	LEU
1	A7	64	THR

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Mol	Chain	Res	Type
1	A7	71	MET
1	A7	73	ARG
1	A7	126	ASP
1	A7	167	LEU
1	A7	186	ARG
1	A7	231	LEU
1	A8	64	THR
1	A8	71	MET
1	A8	73	ARG
1	A8	126	ASP
1	A8	167	LEU
1	A8	186	ARG
1	A8	231	LEU
1	A9	64	THR
1	A9	71	MET
1	A9	73	ARG
1	A9	126	ASP
1	A9	167	LEU
1	A9	186	ARG
1	A9	231	LEU
1	AA	64	THR
1	AA	71	MET
1	AA	73	ARG
1	AA	126	ASP
1	AA	167	LEU
1	AA	186	ARG
1	AA	231	LEU
1	AB	64	THR
1	AB	71	MET
1	AB	73	ARG
1	AB	126	ASP
1	AB	167	LEU
1	AB	186	ARG
1	AB	231	LEU
1	AC	64	THR
1	AC	71	MET
1	AC	73	ARG
1	AC	126	ASP
1	AC	167	LEU
1	AC	186	ARG
1	AC	231	LEU
1	AD	64	THR

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Mol	Chain	Res	Type
1	AD	71	MET
1	AD	73	ARG
1	AD	126	ASP
1	AD	167	LEU
1	AD	186	ARG
1	AD	231	LEU
1	AE	64	THR
1	AE	71	MET
1	AE	73	ARG
1	AE	126	ASP
1	AE	167	LEU
1	AE	186	ARG
1	AE	231	LEU
1	AF	64	THR
1	AF	71	MET
1	AF	73	ARG
1	AF	126	ASP
1	AF	167	LEU
1	AF	186	ARG
1	AF	231	LEU
1	AG	64	THR
1	AG	71	MET
1	AG	73	ARG
1	AG	126	ASP
1	AG	167	LEU
1	AG	186	ARG
1	AG	231	LEU
1	AH	64	THR
1	AH	71	MET
1	AH	73	ARG
1	AH	126	ASP
1	AH	167	LEU
1	AH	186	ARG
1	AH	231	LEU
1	AI	64	THR
1	AI	71	MET
1	AI	73	ARG
1	AI	126	ASP
1	AI	167	LEU
1	AI	186	ARG
1	AI	231	LEU
1	AJ	64	THR

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Mol	Chain	Res	Type
1	AJ	71	MET
1	AJ	73	ARG
1	AJ	126	ASP
1	AJ	167	LEU
1	AJ	186	ARG
1	AJ	231	LEU
1	AK	64	THR
1	AK	71	MET
1	AK	73	ARG
1	AK	126	ASP
1	AK	167	LEU
1	AK	186	ARG
1	AK	231	LEU
1	AL	64	THR
1	AL	71	MET
1	AL	73	ARG
1	AL	126	ASP
1	AL	167	LEU
1	AL	186	ARG
1	AL	231	LEU
1	AM	64	THR
1	AM	71	MET
1	AM	73	ARG
1	AM	126	ASP
1	AM	167	LEU
1	AM	186	ARG
1	AM	231	LEU
1	AN	64	THR
1	AN	71	MET
1	AN	73	ARG
1	AN	126	ASP
1	AN	167	LEU
1	AN	186	ARG
1	AN	231	LEU
1	AO	64	THR
1	AO	71	MET
1	AO	73	ARG
1	AO	126	ASP
1	AO	167	LEU
1	AO	186	ARG
1	AO	231	LEU
1	AP	64	THR

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Mol	Chain	Res	Type
1	AP	71	MET
1	AP	73	ARG
1	AP	126	ASP
1	AP	167	LEU
1	AP	186	ARG
1	AP	231	LEU
1	AQ	64	THR
1	AQ	71	MET
1	AQ	73	ARG
1	AQ	126	ASP
1	AQ	167	LEU
1	AQ	186	ARG
1	AQ	231	LEU
1	AR	64	THR
1	AR	71	MET
1	AR	73	ARG
1	AR	126	ASP
1	AR	167	LEU
1	AR	186	ARG
1	AR	231	LEU
1	AS	64	THR
1	AS	71	MET
1	AS	73	ARG
1	AS	126	ASP
1	AS	167	LEU
1	AS	186	ARG
1	AS	231	LEU
1	AT	64	THR
1	AT	71	MET
1	AT	73	ARG
1	AT	126	ASP
1	AT	167	LEU
1	AT	186	ARG
1	AT	231	LEU
1	AU	64	THR
1	AU	71	MET
1	AU	73	ARG
1	AU	126	ASP
1	AU	167	LEU
1	AU	186	ARG
1	AU	231	LEU
1	AV	64	THR

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Mol	Chain	Res	Type
1	AV	71	MET
1	AV	73	ARG
1	AV	126	ASP
1	AV	167	LEU
1	AV	186	ARG
1	AV	231	LEU
1	AW	64	THR
1	AW	71	MET
1	AW	73	ARG
1	AW	126	ASP
1	AW	167	LEU
1	AW	186	ARG
1	AW	231	LEU
1	AX	64	THR
1	AX	71	MET
1	AX	73	ARG
1	AX	126	ASP
1	AX	167	LEU
1	AX	186	ARG
1	AX	231	LEU
1	AY	64	THR
1	AY	71	MET
1	AY	73	ARG
1	AY	126	ASP
1	AY	167	LEU
1	AY	186	ARG
1	AY	231	LEU
1	AZ	64	THR
1	AZ	71	MET
1	AZ	73	ARG
1	AZ	126	ASP
1	AZ	167	LEU
1	AZ	186	ARG
1	AZ	231	LEU
1	Aa	64	THR
1	Aa	71	MET
1	Aa	73	ARG
1	Aa	126	ASP
1	Aa	167	LEU
1	Aa	186	ARG
1	Aa	231	LEU
1	Ab	64	THR

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Mol	Chain	Res	Type
1	Ab	71	MET
1	Ab	73	ARG
1	Ab	126	ASP
1	Ab	167	LEU
1	Ab	186	ARG
1	Ab	231	LEU
1	Ac	64	THR
1	Ac	71	MET
1	Ac	73	ARG
1	Ac	126	ASP
1	Ac	167	LEU
1	Ac	186	ARG
1	Ac	231	LEU
1	Ad	64	THR
1	Ad	71	MET
1	Ad	73	ARG
1	Ad	126	ASP
1	Ad	167	LEU
1	Ad	186	ARG
1	Ad	231	LEU
1	Ae	64	THR
1	Ae	71	MET
1	Ae	73	ARG
1	Ae	126	ASP
1	Ae	167	LEU
1	Ae	186	ARG
1	Ae	231	LEU
1	Af	64	THR
1	Af	71	MET
1	Af	73	ARG
1	Af	126	ASP
1	Af	167	LEU
1	Af	186	ARG
1	Af	231	LEU
1	Ag	64	THR
1	Ag	71	MET
1	Ag	73	ARG
1	Ag	126	ASP
1	Ag	167	LEU
1	Ag	186	ARG
1	Ag	231	LEU
1	Ah	64	THR

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Mol	Chain	Res	Type
1	Ah	71	MET
1	Ah	73	ARG
1	Ah	126	ASP
1	Ah	167	LEU
1	Ah	186	ARG
1	Ah	231	LEU
1	Ai	64	THR
1	Ai	71	MET
1	Ai	73	ARG
1	Ai	126	ASP
1	Ai	167	LEU
1	Ai	186	ARG
1	Ai	231	LEU
1	Aj	64	THR
1	Aj	71	MET
1	Aj	73	ARG
1	Aj	126	ASP
1	Aj	167	LEU
1	Aj	186	ARG
1	Aj	231	LEU
1	Ak	64	THR
1	Ak	71	MET
1	Ak	73	ARG
1	Ak	126	ASP
1	Ak	167	LEU
1	Ak	186	ARG
1	Ak	231	LEU
1	Al	64	THR
1	Al	71	MET
1	Al	73	ARG
1	Al	126	ASP
1	Al	167	LEU
1	Al	186	ARG
1	Al	231	LEU
1	Am	64	THR
1	Am	71	MET
1	Am	73	ARG
1	Am	126	ASP
1	Am	167	LEU
1	Am	186	ARG
1	Am	231	LEU
1	An	64	THR

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Mol	Chain	Res	Type
1	An	71	MET
1	An	73	ARG
1	An	126	ASP
1	An	167	LEU
1	An	186	ARG
1	An	231	LEU
1	Ao	64	THR
1	Ao	71	MET
1	Ao	73	ARG
1	Ao	126	ASP
1	Ao	167	LEU
1	Ao	186	ARG
1	Ao	231	LEU
1	Ap	64	THR
1	Ap	71	MET
1	Ap	73	ARG
1	Ap	126	ASP
1	Ap	167	LEU
1	Ap	186	ARG
1	Ap	231	LEU
1	Aq	64	THR
1	Aq	71	MET
1	Aq	73	ARG
1	Aq	126	ASP
1	Aq	167	LEU
1	Aq	186	ARG
1	Aq	231	LEU
1	Ar	64	THR
1	Ar	71	MET
1	Ar	73	ARG
1	Ar	126	ASP
1	Ar	167	LEU
1	Ar	186	ARG
1	Ar	231	LEU
1	As	64	THR
1	As	71	MET
1	As	73	ARG
1	As	126	ASP
1	As	167	LEU
1	As	186	ARG
1	As	231	LEU
1	At	64	THR

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Mol	Chain	Res	Type
1	At	71	MET
1	At	73	ARG
1	At	126	ASP
1	At	167	LEU
1	At	186	ARG
1	At	231	LEU
1	Au	64	THR
1	Au	71	MET
1	Au	73	ARG
1	Au	126	ASP
1	Au	167	LEU
1	Au	186	ARG
1	Au	231	LEU
1	Av	64	THR
1	Av	71	MET
1	Av	73	ARG
1	Av	126	ASP
1	Av	167	LEU
1	Av	186	ARG
1	Av	231	LEU
1	Aw	64	THR
1	Aw	71	MET
1	Aw	73	ARG
1	Aw	126	ASP
1	Aw	167	LEU
1	Aw	186	ARG
1	Aw	231	LEU
1	Ax	64	THR
1	Ax	71	MET
1	Ax	73	ARG
1	Ax	126	ASP
1	Ax	167	LEU
1	Ax	186	ARG
1	Ax	231	LEU
1	Ay	64	THR
1	Ay	71	MET
1	Ay	73	ARG
1	Ay	126	ASP
1	Ay	167	LEU
1	Ay	186	ARG
1	Ay	231	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (61)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A1	212	ASN
1	A2	212	ASN
1	A3	212	ASN
1	A4	212	ASN
1	A5	212	ASN
1	A6	212	ASN
1	A7	212	ASN
1	A8	212	ASN
1	A9	212	ASN
1	AA	212	ASN
1	AB	212	ASN
1	AC	212	ASN
1	AD	212	ASN
1	AE	212	ASN
1	AF	212	ASN
1	AG	212	ASN
1	AH	212	ASN
1	AI	212	ASN
1	AJ	212	ASN
1	AK	212	ASN
1	AL	212	ASN
1	AM	212	ASN
1	AN	212	ASN
1	AO	212	ASN
1	AP	212	ASN
1	AQ	212	ASN
1	AR	212	ASN
1	AS	212	ASN
1	AT	212	ASN
1	AU	212	ASN
1	AV	212	ASN
1	AW	212	ASN
1	AX	212	ASN
1	AY	212	ASN
1	AZ	212	ASN
1	Aa	212	ASN
1	Ab	212	ASN
1	Ac	212	ASN
1	Ad	212	ASN
1	Ae	212	ASN
1	Af	212	ASN
1	Ag	212	ASN

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Mol	Chain	Res	Type
1	Ah	178	ASN
1	Ah	212	ASN
1	Ai	212	ASN
1	Aj	212	ASN
1	Ak	212	ASN
1	Al	212	ASN
1	Am	212	ASN
1	An	212	ASN
1	Ao	212	ASN
1	Ap	212	ASN
1	Aq	212	ASN
1	Ar	212	ASN
1	As	212	ASN
1	At	212	ASN
1	Au	212	ASN
1	Av	212	ASN
1	Aw	212	ASN
1	Ax	212	ASN
1	Ay	212	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

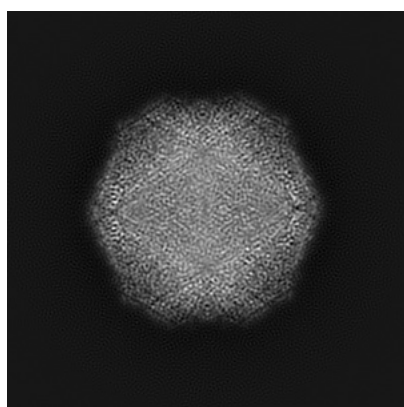
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8969. These allow visual inspection of the internal detail of the map and identification of artifacts.

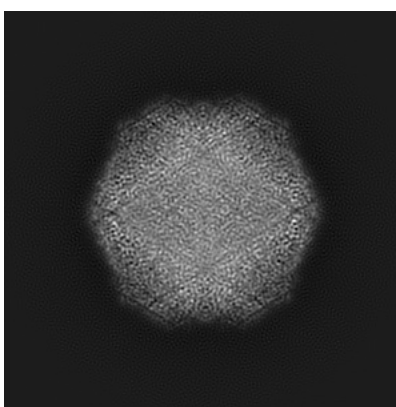
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

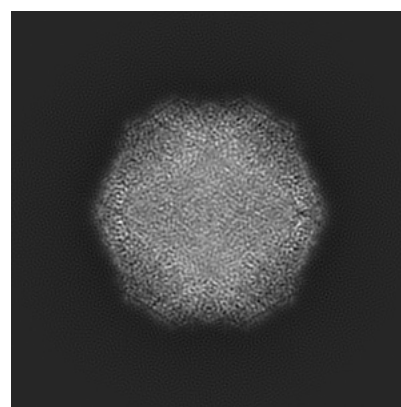
6.1.1 Primary map



X



Y

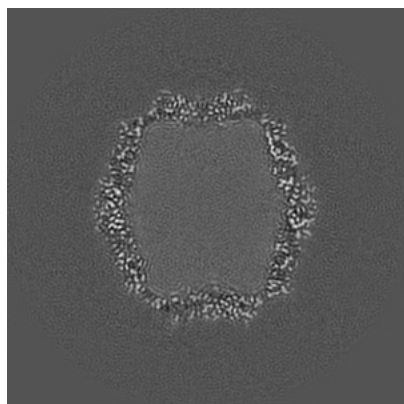


Z

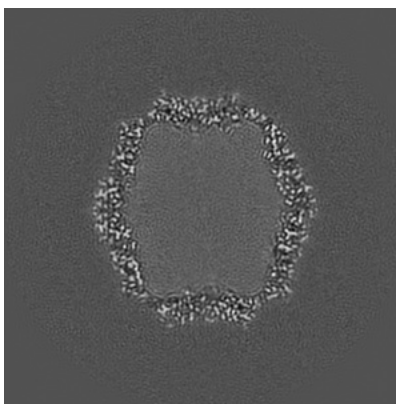
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

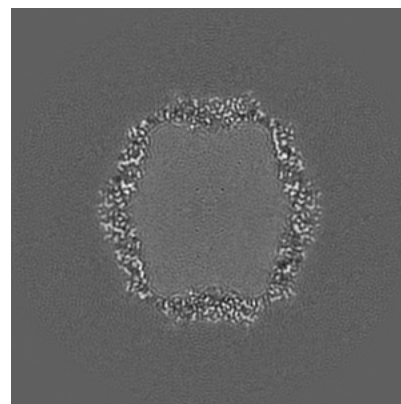
6.2.1 Primary map



X Index: 150



Y Index: 150

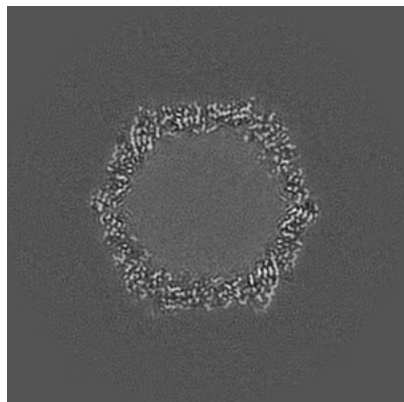


Z Index: 150

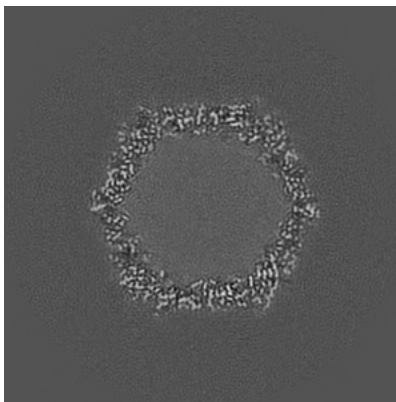
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

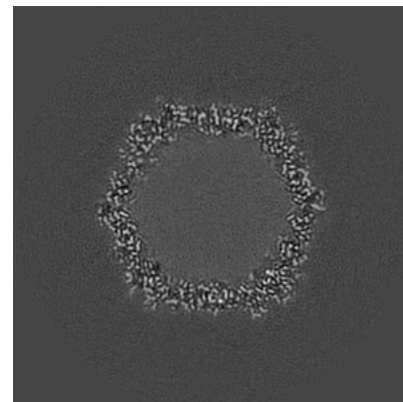
6.3.1 Primary map



X Index: 168



Y Index: 167

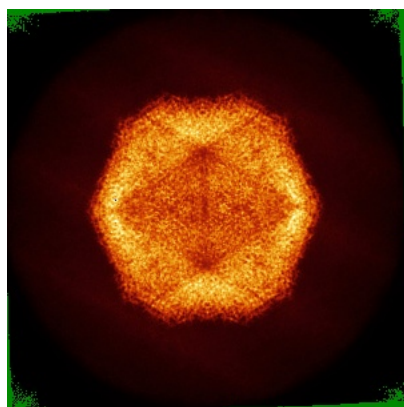


Z Index: 132

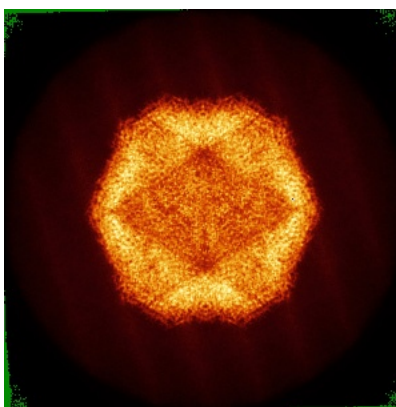
The images above show the largest variance slices of the map in three orthogonal directions.

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

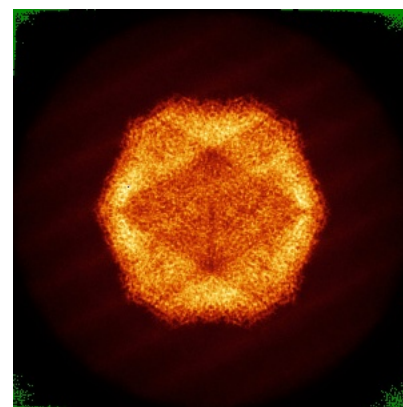
6.4.1 Primary map



X



Y

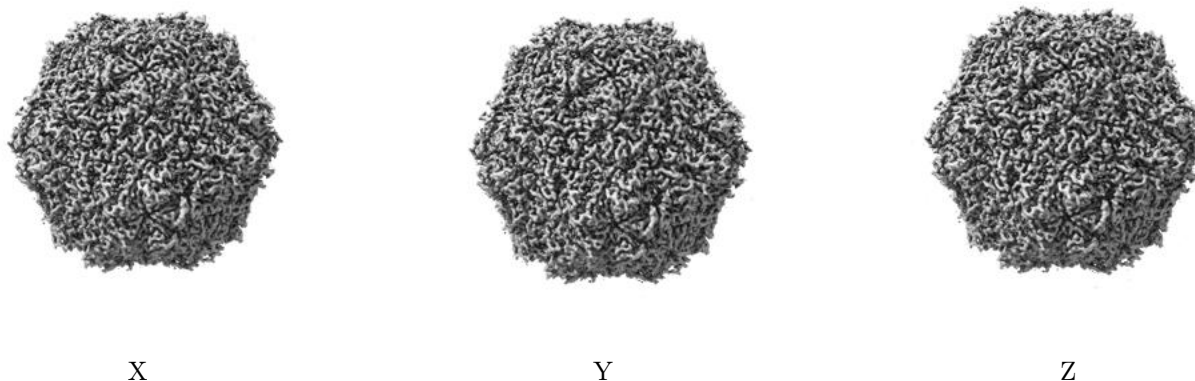


Z

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

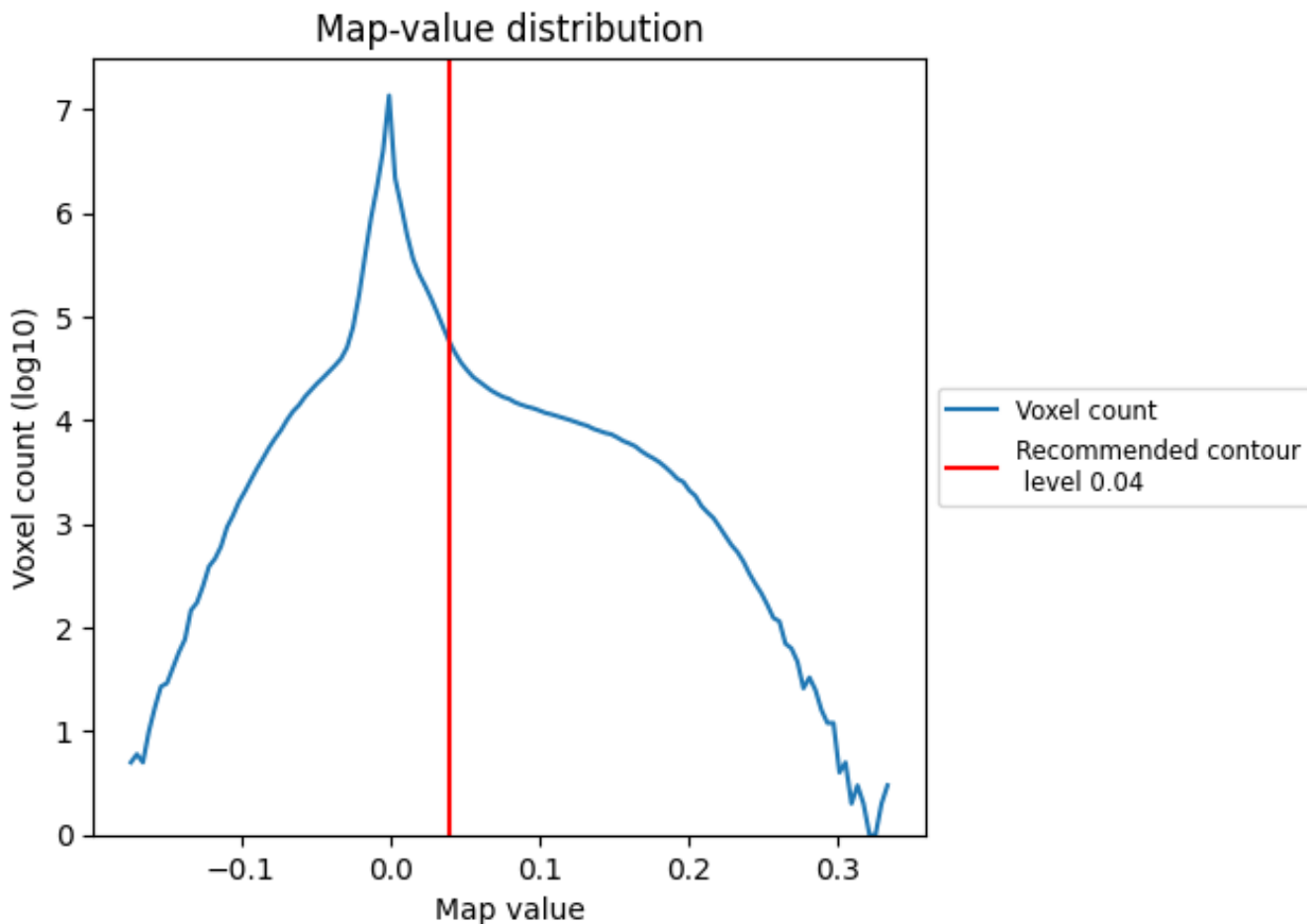
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

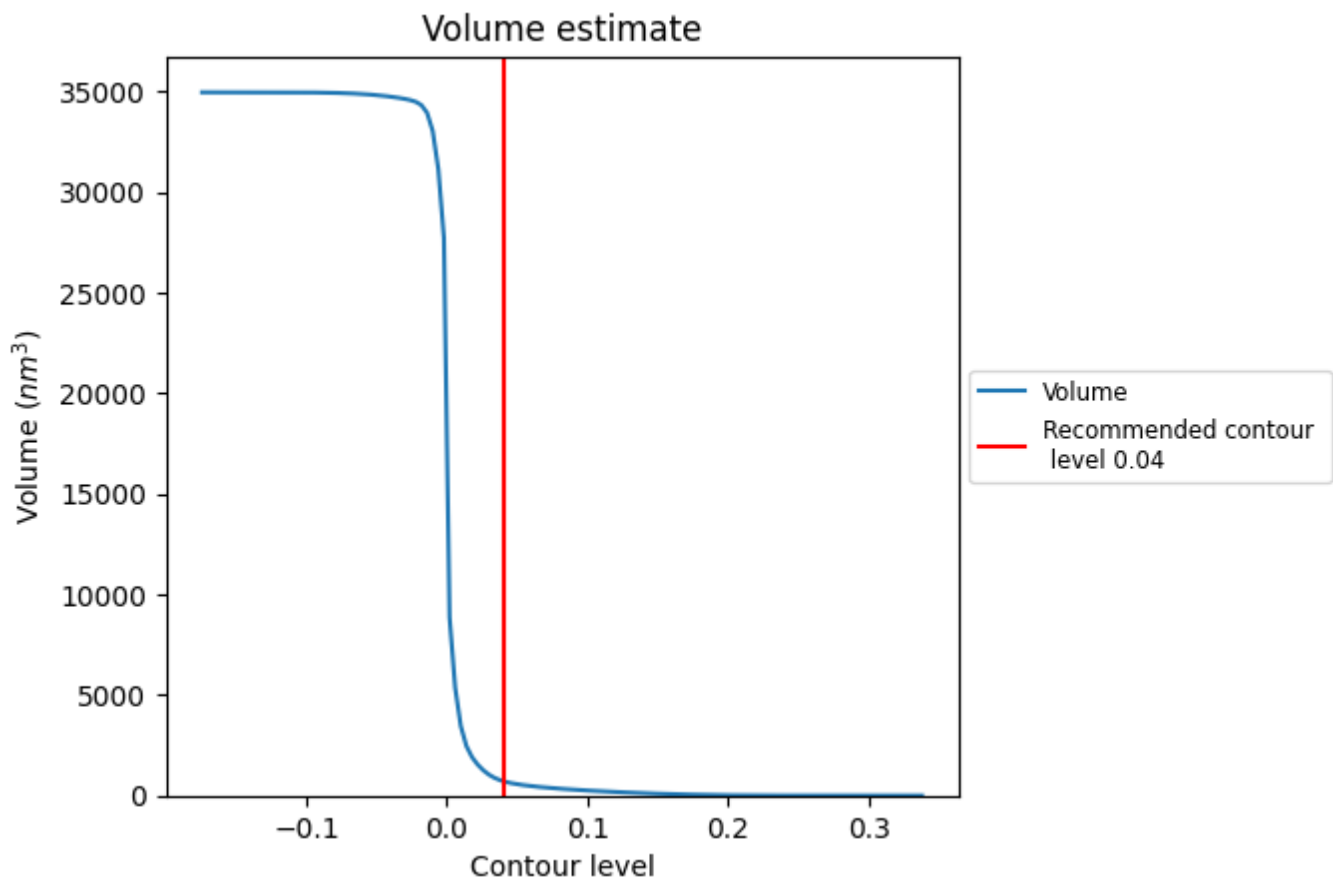
This section contains the results of statistical analysis of the map.

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.

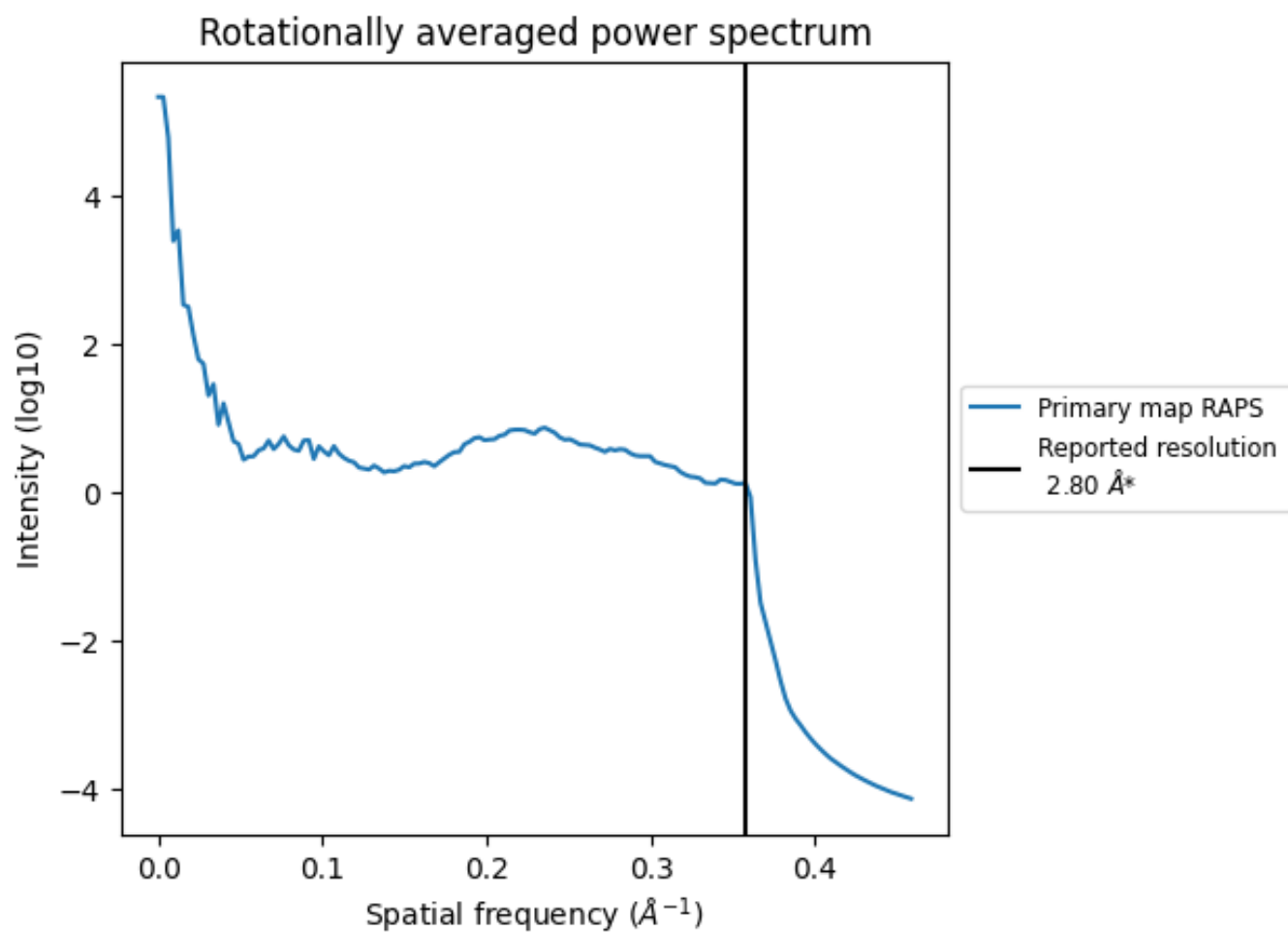
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 719 nm³; this corresponds to an approximate mass of 649 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.357\AA^{-1}

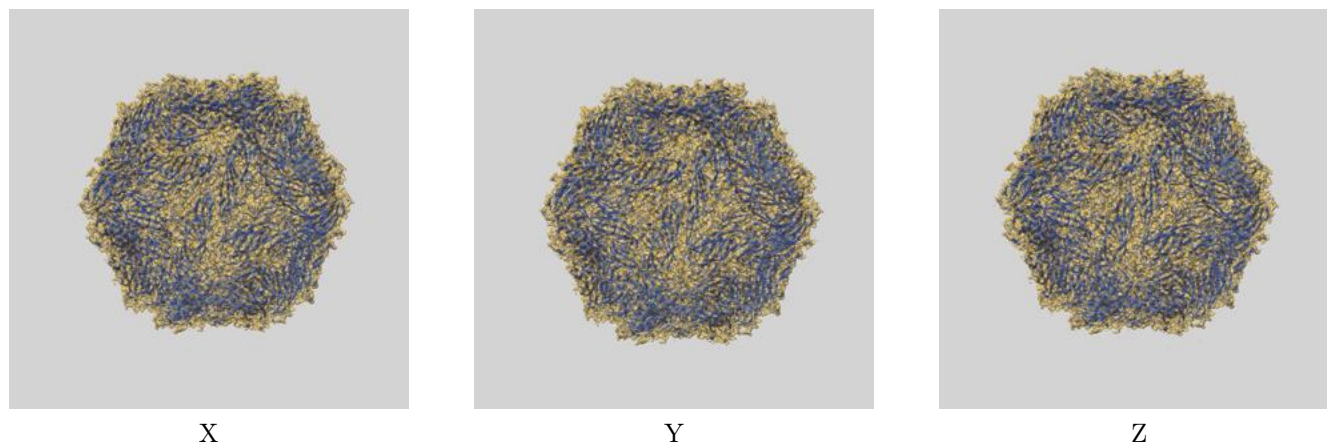
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

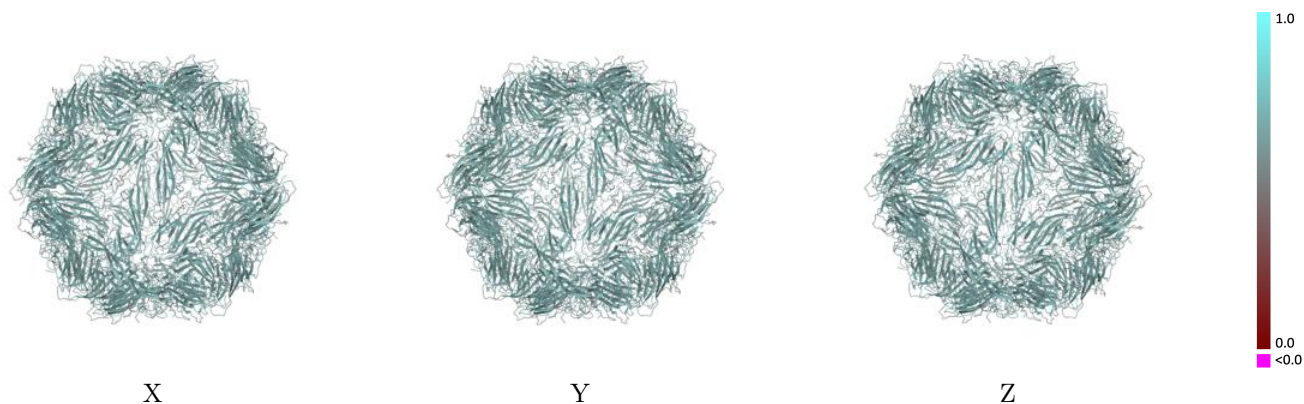
This section contains information regarding the fit between EMDB map EMD-8969 and PDB model 6E2R. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



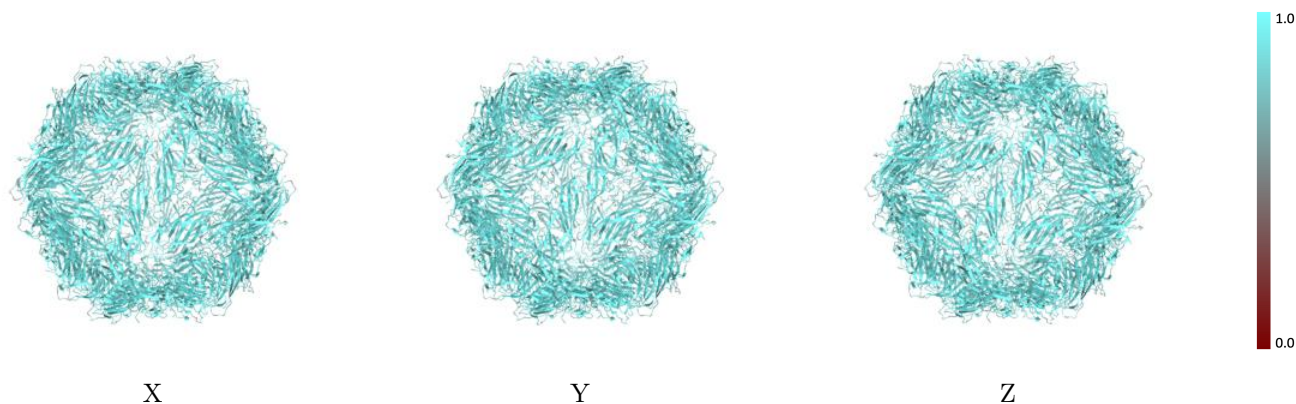
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



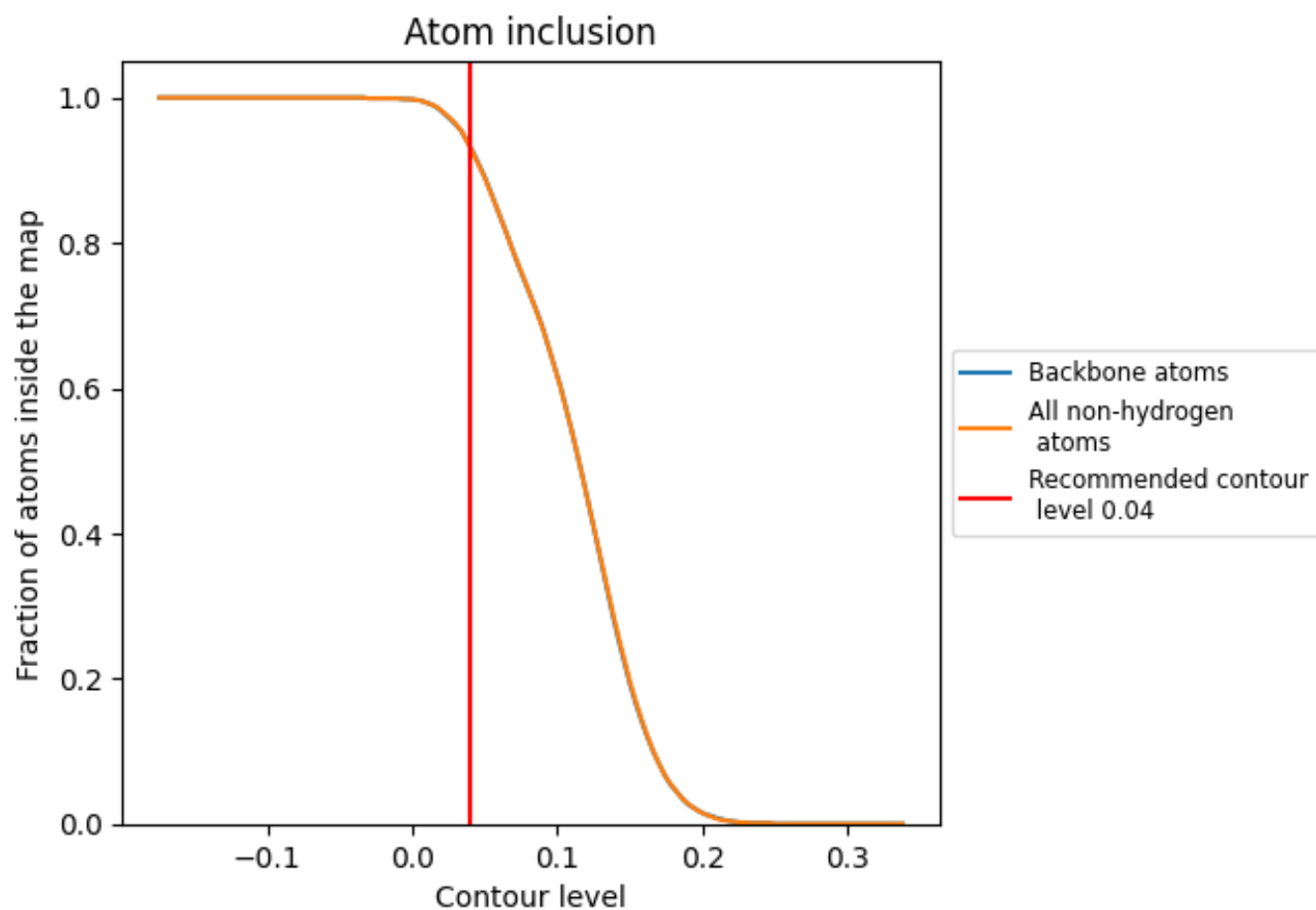
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9310	 0.6250
A1	 0.9370	 0.6310
A2	 0.9300	 0.6210
A3	 0.9340	 0.6250
A4	 0.9360	 0.6240
A5	 0.9350	 0.6270
A6	 0.9360	 0.6290
A7	 0.9340	 0.6250
A8	 0.9360	 0.6260
A9	 0.9360	 0.6250
AA	 0.9360	 0.6220
AB	 0.9350	 0.6230
AC	 0.9340	 0.6230
AD	 0.9360	 0.6270
AE	 0.9340	 0.6200
AF	 0.9320	 0.6230
AG	 0.9310	 0.6240
AH	 0.9340	 0.6180
AI	 0.9280	 0.6230
AJ	 0.9330	 0.6220
AK	 0.9380	 0.6280
AL	 0.9340	 0.6240
AM	 0.9350	 0.6160
AN	 0.9360	 0.6240
AO	 0.9390	 0.6260
AP	 0.9240	 0.6180
AQ	 0.9340	 0.6250
AR	 0.9360	 0.6280
AS	 0.9340	 0.6240
AT	 0.9330	 0.6220
AU	 0.9400	 0.6240
AV	 0.9320	 0.6270
AW	 0.9400	 0.6260
AX	 0.9290	 0.6200
AY	 0.9330	 0.6270



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Chain	Atom inclusion	Q-score
AZ	 0.9430	 0.6300
Aa	 0.9300	 0.6250
Ab	 0.9410	 0.6220
Ac	 0.9300	 0.6220
Ad	 0.9270	 0.6210
Ae	 0.9380	 0.6290
Af	 0.9360	 0.6260
Ag	 0.9340	 0.6250
Ah	 0.9330	 0.6250
Ai	 0.9300	 0.6250
Aj	 0.9400	 0.6260
Ak	 0.9380	 0.6310
Al	 0.9280	 0.6180
Am	 0.9330	 0.6260
An	 0.9300	 0.6270
Ao	 0.9310	 0.6250
Ap	 0.9320	 0.6260
Aq	 0.9360	 0.6260
Ar	 0.9340	 0.6250
As	 0.9330	 0.6220
At	 0.9300	 0.6250
Au	 0.9360	 0.6270
Av	 0.9360	 0.6260
Aw	 0.9310	 0.6250
Ax	 0.9420	 0.6280
Ay	 0.9320	 0.6260