Full wwPDB EM Validation Report (i)

Nov 8, 2022 – 09:21 AM EST

PDB ID	:	6OJ0
EMDB ID	:	EMD-20083
Title	:	Cryo-EM reconstruction of Sulfolobus polyhedral virus 1 (SPV1)
Authors	:	Wang, F.; Liu, Y.; Conway, J.F.; Krupovic, M.; Prangishvili, D.; Egelman, E.H.
Deposited on	:	2019-04-10
Resolution	:	3.70 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

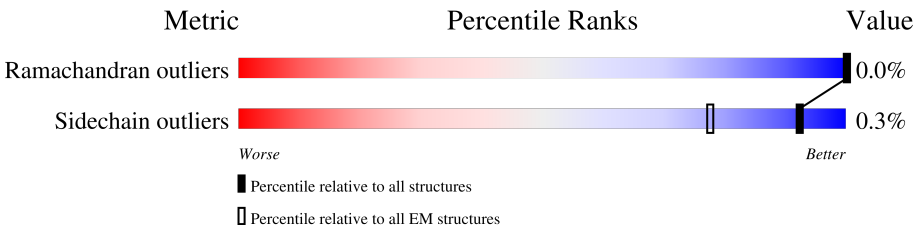
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	181	97%
1	B	181	97%
1	C	181	97%
1	D	181	97%
1	E	181	98%
1	F	181	97%
1	G	181	97%
1	H	181	5% 98%
1	I	181	5% 97%

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Mol	Chain	Length	Quality of chain
1	J	181	97%
1	K	181	97%
1	L	181	97%
1	M	181	97%
1	N	181	97%
1	O	181	97%
1	P	181	96%
1	Q	181	6% 97%
1	R	181	97%
1	S	181	98%
1	T	181	98%
1	U	181	98%
1	V	181	96%
1	W	181	97%
1	X	181	97%
1	a	181	97%
1	b	181	98%
1	c	181	97%
1	d	181	97%
1	e	181	96%
1	f	181	98%
1	g	181	98%
1	h	181	98%
1	i	181	98%
1	j	181	97%

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Mol	Chain	Length	Quality of chain
1	k	181	97%
1	l	181	97%
1	m	181	97%
1	n	181	98%
1	o	181	98%
1	p	181	98%
1	q	181	97%
1	r	181	98%
2	Z	187	96%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 57764 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Structural protein VP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	T	178	1342	860	212	266	4	0	0
1	U	178	1342	860	212	266	4	0	0
1	V	178	1342	860	212	266	4	0	0
1	W	178	1342	860	212	266	4	0	0
1	X	178	1342	860	212	266	4	0	0
1	G	178	1342	860	212	266	4	0	0
1	n	178	1342	860	212	266	4	0	0
1	o	178	1342	860	212	266	4	0	0
1	p	178	1342	860	212	266	4	0	0
1	q	178	1342	860	212	266	4	0	0
1	r	178	1342	860	212	266	4	0	0
1	g	178	1342	860	212	266	4	0	0
1	N	178	1342	860	212	266	4	0	0
1	O	178	1342	860	212	266	4	0	0
1	P	178	1342	860	212	266	4	0	0
1	Q	178	1342	860	212	266	4	0	0
1	R	178	1342	860	212	266	4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	S	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	h	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	i	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	j	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	k	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	l	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	m	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	H	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	I	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	J	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	K	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	L	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	M	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	a	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	b	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	c	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	d	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	e	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	f	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	A	178	1342	860	212	266	4	0	0
			Total	C	N	O	S		
1	B	178	1342	860	212	266	4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	C	178	1342	860	212	266	4	0	0
1	D	178	1342	860	212	266	4	0	0
1	E	178	1342	860	212	266	4	0	0
1	F	178	1342	860	212	266	4	0	0

- Molecule 2 is a protein called Uncharacterized protein.

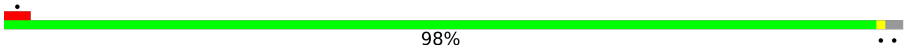
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	Z	180	1400	903	221	272	4	0	0

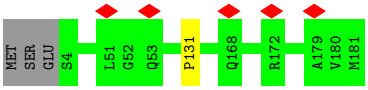
3 Residue-property plots (i)

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: Structural protein VP4

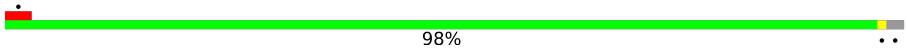
Chain T:

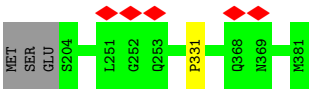




- Molecule 1: Structural protein VP4

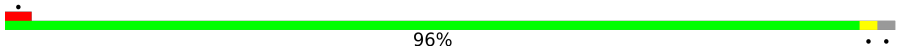
Chain U:

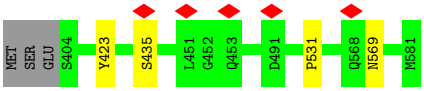




- Molecule 1: Structural protein VP4

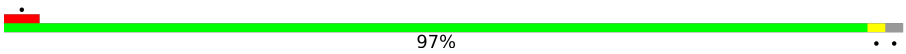
Chain V:

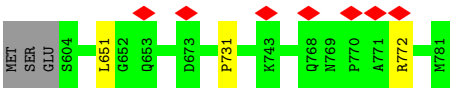




- Molecule 1: Structural protein VP4

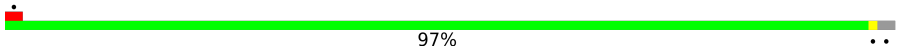
Chain W:

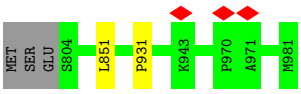




- Molecule 1: Structural protein VP4

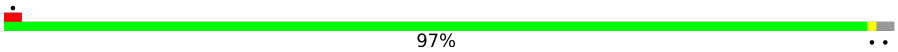
Chain X:

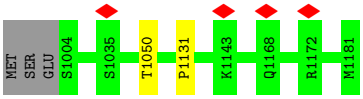




- Molecule 1: Structural protein VP4

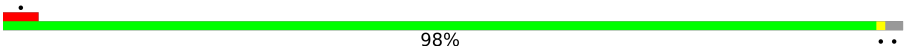
Chain G:

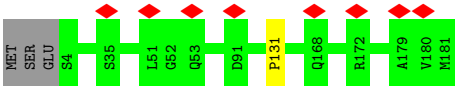




- Molecule 1: Structural protein VP4

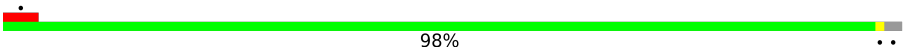
Chain n:

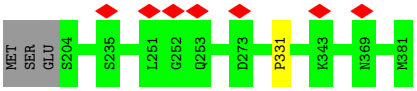




- Molecule 1: Structural protein VP4

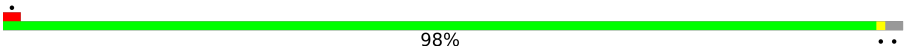
Chain o:

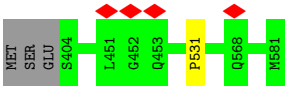




- Molecule 1: Structural protein VP4

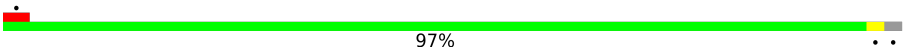
Chain p:

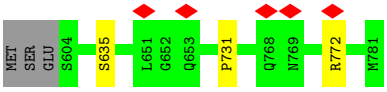




- Molecule 1: Structural protein VP4

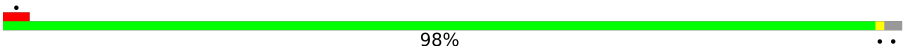
Chain q:

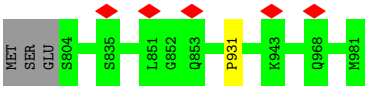




- Molecule 1: Structural protein VP4

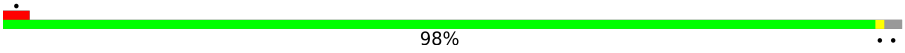
Chain r:

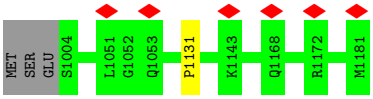




- Molecule 1: Structural protein VP4

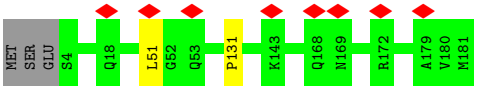
Chain g:





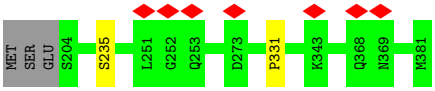
• Molecule 1: Structural protein VP4

Chain N: 97%



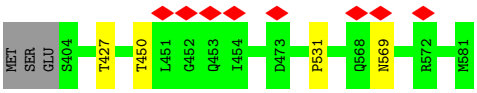
• Molecule 1: Structural protein VP4

Chain O: 97%



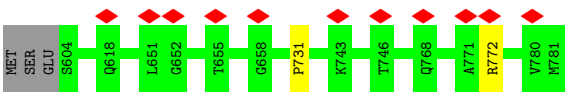
• Molecule 1: Structural protein VP4

Chain P: 96%



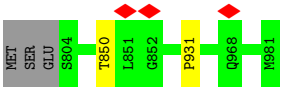
• Molecule 1: Structural protein VP4

Chain Q: 6% 97%



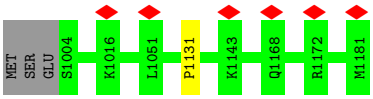
• Molecule 1: Structural protein VP4

Chain R: 97%



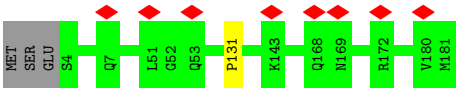
• Molecule 1: Structural protein VP4

Chain S: 98%



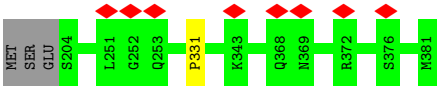
• Molecule 1: Structural protein VP4

Chain h: 98%



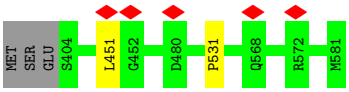
• Molecule 1: Structural protein VP4

Chain i: 98%



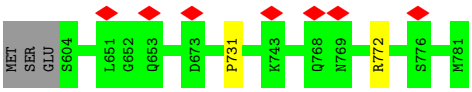
• Molecule 1: Structural protein VP4

Chain j: 97%



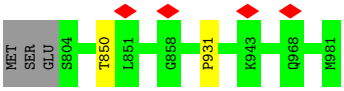
• Molecule 1: Structural protein VP4

Chain k: 97%



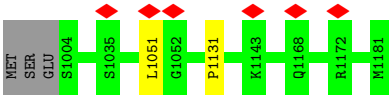
• Molecule 1: Structural protein VP4

Chain l: 97%



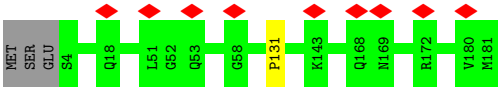
• Molecule 1: Structural protein VP4

Chain m: 97%



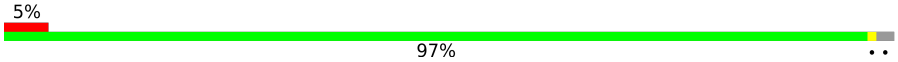
• Molecule 1: Structural protein VP4

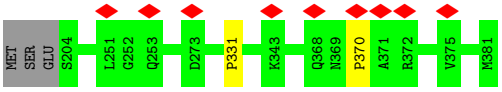
Chain H: 5% 98%



• Molecule 1: Structural protein VP4

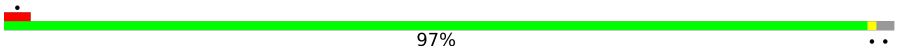
Chain I:

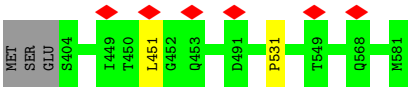




• Molecule 1: Structural protein VP4

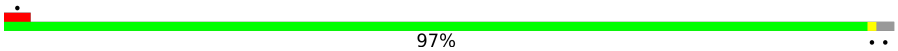
Chain J:

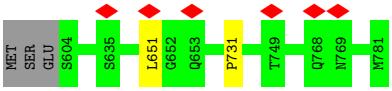




• Molecule 1: Structural protein VP4

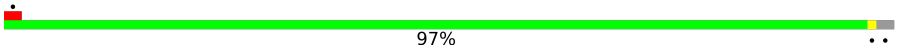
Chain K:

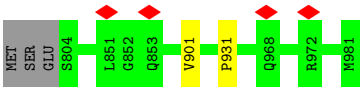




• Molecule 1: Structural protein VP4

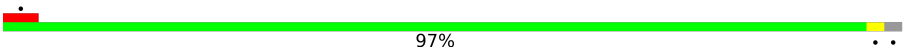
Chain L:

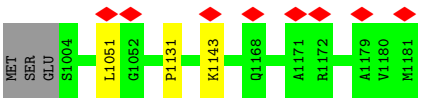




• Molecule 1: Structural protein VP4

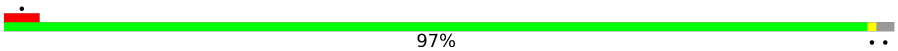
Chain M:

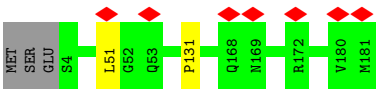




• Molecule 1: Structural protein VP4

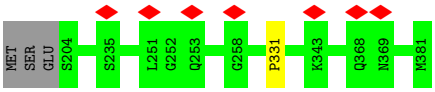
Chain a:





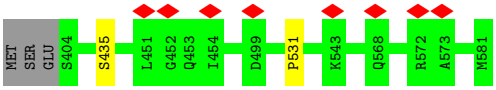
• Molecule 1: Structural protein VP4

Chain b: 98%



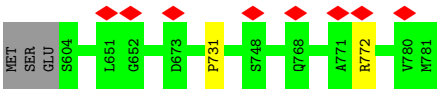
• Molecule 1: Structural protein VP4

Chain c: 97%



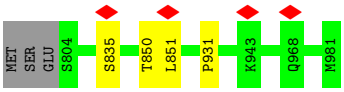
• Molecule 1: Structural protein VP4

Chain d: 97%



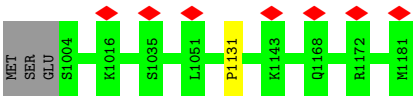
• Molecule 1: Structural protein VP4

Chain e: 96%



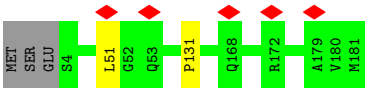
• Molecule 1: Structural protein VP4

Chain f: 98%



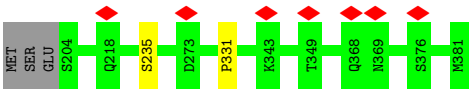
• Molecule 1: Structural protein VP4

Chain A: 97%



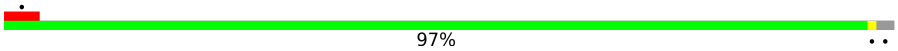
• Molecule 1: Structural protein VP4

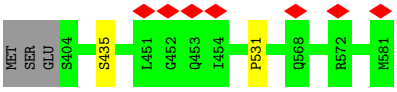
Chain B: 97%



• Molecule 1: Structural protein VP4

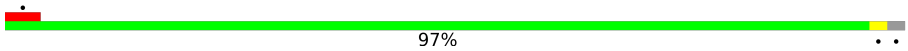
Chain C:

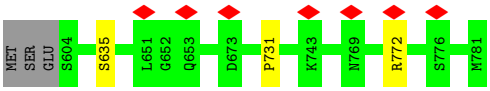




• Molecule 1: Structural protein VP4

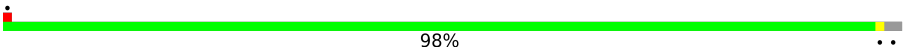
Chain D:

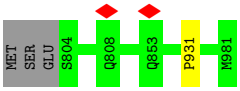




• Molecule 1: Structural protein VP4

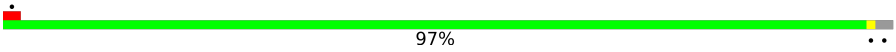
Chain E:

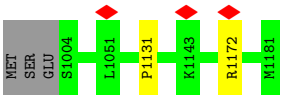




• Molecule 1: Structural protein VP4

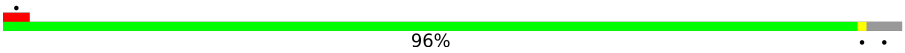
Chain F:

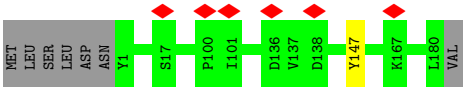




• Molecule 2: Uncharacterized protein

Chain Z:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19092	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.188	Depositor
Minimum map value	-0.084	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	1120.0, 1120.0, 1120.0	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4, 1.4, 1.4	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	A	0.37	0/1372	0.61	1/1886 (0.1%)
1	B	0.37	0/1372	0.61	0/1886
1	C	0.38	0/1372	0.57	0/1886
1	D	0.37	0/1372	0.58	0/1886
1	E	0.39	0/1372	0.59	0/1886
1	F	0.38	0/1372	0.58	0/1886
1	G	0.39	0/1372	0.57	0/1886
1	H	0.38	0/1372	0.59	0/1886
1	I	0.38	0/1372	0.60	0/1886
1	J	0.37	0/1372	0.60	1/1886 (0.1%)
1	K	0.37	0/1372	0.58	1/1886 (0.1%)
1	L	0.39	0/1372	0.59	0/1886
1	M	0.37	0/1372	0.58	1/1886 (0.1%)
1	N	0.39	0/1372	0.61	1/1886 (0.1%)
1	O	0.37	0/1372	0.59	0/1886
1	P	0.39	0/1372	0.58	0/1886
1	Q	0.37	0/1372	0.60	0/1886
1	R	0.40	0/1372	0.61	0/1886
1	S	0.39	0/1372	0.59	0/1886
1	T	0.39	0/1372	0.60	0/1886
1	U	0.39	0/1372	0.60	0/1886
1	V	0.40	0/1372	0.62	0/1886
1	W	0.37	0/1372	0.61	1/1886 (0.1%)
1	X	0.38	0/1372	0.61	1/1886 (0.1%)
1	a	0.38	0/1372	0.61	1/1886 (0.1%)
1	b	0.38	0/1372	0.61	0/1886
1	c	0.40	0/1372	0.60	0/1886
1	d	0.38	0/1372	0.60	0/1886
1	e	0.37	0/1372	0.61	1/1886 (0.1%)
1	f	0.38	0/1372	0.58	0/1886
1	g	0.39	0/1372	0.58	0/1886
1	h	0.38	0/1372	0.61	0/1886
1	i	0.37	0/1372	0.59	0/1886
1	j	0.37	0/1372	0.56	0/1886

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	k	0.37	0/1372	0.59	0/1886
1	l	0.38	0/1372	0.60	0/1886
1	m	0.37	0/1372	0.57	1/1886 (0.1%)
1	n	0.38	0/1372	0.58	0/1886
1	o	0.36	0/1372	0.61	0/1886
1	p	0.38	0/1372	0.59	0/1886
1	q	0.36	0/1372	0.56	0/1886
1	r	0.39	0/1372	0.58	0/1886
2	Z	0.36	0/1433	0.58	0/1958
All	All	0.38	0/59057	0.59	10/81170 (0.0%)

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	A	0	1
1	B	0	2
1	C	0	2
1	D	0	2
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
1	O	0	2
1	P	0	1
1	Q	0	1
1	R	0	1
1	S	0	1
1	T	0	1
1	U	0	1
1	V	0	2
1	W	0	1
1	X	0	1
1	a	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	b	0	1
1	c	0	2
1	d	0	1
1	e	0	2
1	f	0	1
1	g	0	1
1	h	0	1
1	i	0	1
1	j	0	1
1	k	0	1
1	l	0	1
1	m	0	1
1	n	0	1
1	o	0	1
1	p	0	1
1	q	0	2
1	r	0	1
All	All	0	50

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	W	651	LEU	CA-CB-CG	6.53	130.32	115.30
1	m	1051	LEU	CA-CB-CG	5.95	128.99	115.30
1	N	51	LEU	CA-CB-CG	5.72	128.45	115.30
1	X	851	LEU	CA-CB-CG	5.60	128.18	115.30
1	J	451	LEU	CA-CB-CG	5.54	128.04	115.30
1	M	1051	LEU	CA-CB-CG	5.41	127.75	115.30
1	e	851	LEU	CA-CB-CG	5.29	127.47	115.30
1	a	51	LEU	CA-CB-CG	5.27	127.42	115.30
1	K	651	LEU	CA-CB-CG	5.05	126.92	115.30
1	A	51	LEU	CA-CB-CG	5.04	126.90	115.30

There are no chirality outliers.

All (50) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	131	PRO	Peptide
1	B	235	SER	Peptide
1	B	331	PRO	Peptide

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Mol	Chain	Res	Type	Group
1	C	435	SER	Peptide
1	C	531	PRO	Peptide
1	D	635	SER	Peptide
1	D	731	PRO	Peptide
1	E	931	PRO	Peptide
1	F	1131	PRO	Peptide
1	G	1131	PRO	Peptide
1	H	131	PRO	Peptide
1	I	331	PRO	Peptide
1	J	531	PRO	Peptide
1	K	731	PRO	Peptide
1	L	931	PRO	Peptide
1	M	1131	PRO	Peptide
1	N	131	PRO	Peptide
1	O	235	SER	Peptide
1	O	331	PRO	Peptide
1	P	531	PRO	Peptide
1	Q	731	PRO	Peptide
1	R	931	PRO	Peptide
1	S	1131	PRO	Peptide
1	T	131	PRO	Peptide
1	U	331	PRO	Peptide
1	V	435	SER	Peptide
1	V	531	PRO	Peptide
1	W	731	PRO	Peptide
1	X	931	PRO	Peptide
1	a	131	PRO	Peptide
1	b	331	PRO	Peptide
1	c	435	SER	Peptide
1	c	531	PRO	Peptide
1	d	731	PRO	Peptide
1	e	835	SER	Peptide
1	e	931	PRO	Peptide
1	f	1131	PRO	Peptide
1	g	1131	PRO	Peptide
1	h	131	PRO	Peptide
1	i	331	PRO	Peptide
1	j	531	PRO	Peptide
1	k	731	PRO	Peptide
1	l	931	PRO	Peptide
1	m	1131	PRO	Peptide
1	n	131	PRO	Peptide

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Mol	Chain	Res	Type	Group
1	o	331	PRO	Peptide
1	p	531	PRO	Peptide
1	q	635	SER	Peptide
1	q	731	PRO	Peptide
1	r	931	PRO	Peptide

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	A	176/181 (97%)	156 (89%)	20 (11%)	0	100	100
1	B	176/181 (97%)	158 (90%)	18 (10%)	0	100	100
1	C	176/181 (97%)	160 (91%)	16 (9%)	0	100	100
1	D	176/181 (97%)	161 (92%)	15 (8%)	0	100	100
1	E	176/181 (97%)	161 (92%)	15 (8%)	0	100	100
1	F	176/181 (97%)	162 (92%)	14 (8%)	0	100	100
1	G	176/181 (97%)	160 (91%)	16 (9%)	0	100	100
1	H	176/181 (97%)	152 (86%)	24 (14%)	0	100	100
1	I	176/181 (97%)	157 (89%)	18 (10%)	1 (1%)	25	62
1	J	176/181 (97%)	160 (91%)	16 (9%)	0	100	100
1	K	176/181 (97%)	161 (92%)	15 (8%)	0	100	100
1	L	176/181 (97%)	157 (89%)	19 (11%)	0	100	100
1	M	176/181 (97%)	158 (90%)	18 (10%)	0	100	100
1	N	176/181 (97%)	158 (90%)	18 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	176/181 (97%)	159 (90%)	17 (10%)	0	100	100
1	P	176/181 (97%)	158 (90%)	18 (10%)	0	100	100
1	Q	176/181 (97%)	160 (91%)	16 (9%)	0	100	100
1	R	176/181 (97%)	157 (89%)	19 (11%)	0	100	100
1	S	176/181 (97%)	157 (89%)	19 (11%)	0	100	100
1	T	176/181 (97%)	157 (89%)	19 (11%)	0	100	100
1	U	176/181 (97%)	159 (90%)	17 (10%)	0	100	100
1	V	176/181 (97%)	160 (91%)	16 (9%)	0	100	100
1	W	176/181 (97%)	159 (90%)	17 (10%)	0	100	100
1	X	176/181 (97%)	159 (90%)	17 (10%)	0	100	100
1	a	176/181 (97%)	155 (88%)	21 (12%)	0	100	100
1	b	176/181 (97%)	159 (90%)	17 (10%)	0	100	100
1	c	176/181 (97%)	160 (91%)	16 (9%)	0	100	100
1	d	176/181 (97%)	157 (89%)	19 (11%)	0	100	100
1	e	176/181 (97%)	159 (90%)	17 (10%)	0	100	100
1	f	176/181 (97%)	157 (89%)	19 (11%)	0	100	100
1	g	176/181 (97%)	159 (90%)	17 (10%)	0	100	100
1	h	176/181 (97%)	153 (87%)	23 (13%)	0	100	100
1	i	176/181 (97%)	158 (90%)	18 (10%)	0	100	100
1	j	176/181 (97%)	160 (91%)	16 (9%)	0	100	100
1	k	176/181 (97%)	161 (92%)	15 (8%)	0	100	100
1	l	176/181 (97%)	161 (92%)	15 (8%)	0	100	100
1	m	176/181 (97%)	157 (89%)	19 (11%)	0	100	100
1	n	176/181 (97%)	152 (86%)	24 (14%)	0	100	100
1	o	176/181 (97%)	157 (89%)	19 (11%)	0	100	100
1	p	176/181 (97%)	162 (92%)	14 (8%)	0	100	100
1	q	176/181 (97%)	158 (90%)	18 (10%)	0	100	100
1	r	176/181 (97%)	155 (88%)	21 (12%)	0	100	100
2	Z	178/187 (95%)	163 (92%)	14 (8%)	1 (1%)	25	62
All	All	7570/7789 (97%)	6809 (90%)	759 (10%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Z	147	TYR
1	I	370	PRO

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	A	154/157 (98%)	154 (100%)	0	100	100
1	B	154/157 (98%)	154 (100%)	0	100	100
1	C	154/157 (98%)	154 (100%)	0	100	100
1	D	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	E	154/157 (98%)	154 (100%)	0	100	100
1	F	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	G	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	H	154/157 (98%)	154 (100%)	0	100	100
1	I	154/157 (98%)	154 (100%)	0	100	100
1	J	154/157 (98%)	154 (100%)	0	100	100
1	K	154/157 (98%)	154 (100%)	0	100	100
1	L	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	M	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	N	154/157 (98%)	154 (100%)	0	100	100
1	O	154/157 (98%)	154 (100%)	0	100	100
1	P	154/157 (98%)	151 (98%)	3 (2%)	57	76
1	Q	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	R	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	S	154/157 (98%)	154 (100%)	0	100	100
1	T	154/157 (98%)	154 (100%)	0	100	100
1	U	154/157 (98%)	154 (100%)	0	100	100
1	V	154/157 (98%)	152 (99%)	2 (1%)	69	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	W	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	X	154/157 (98%)	154 (100%)	0	100	100
1	a	154/157 (98%)	154 (100%)	0	100	100
1	b	154/157 (98%)	154 (100%)	0	100	100
1	c	154/157 (98%)	154 (100%)	0	100	100
1	d	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	e	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	f	154/157 (98%)	154 (100%)	0	100	100
1	g	154/157 (98%)	154 (100%)	0	100	100
1	h	154/157 (98%)	154 (100%)	0	100	100
1	i	154/157 (98%)	154 (100%)	0	100	100
1	j	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	k	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	l	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	m	154/157 (98%)	154 (100%)	0	100	100
1	n	154/157 (98%)	154 (100%)	0	100	100
1	o	154/157 (98%)	154 (100%)	0	100	100
1	p	154/157 (98%)	154 (100%)	0	100	100
1	q	154/157 (98%)	153 (99%)	1 (1%)	86	93
1	r	154/157 (98%)	154 (100%)	0	100	100
2	Z	161/168 (96%)	161 (100%)	0	100	100
All	All	6629/6762 (98%)	6610 (100%)	19 (0%)	92	96

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	V	423	TYR
1	V	569	ASN
1	W	772	ARG
1	G	1050	THR
1	q	772	ARG
1	P	427	THR
1	P	450	THR
1	P	569	ASN
1	Q	772	ARG

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Mol	Chain	Res	Type
1	R	850	THR
1	j	451	LEU
1	k	772	ARG
1	l	850	THR
1	L	901	VAL
1	M	1143	LYS
1	d	772	ARG
1	e	850	THR
1	D	772	ARG
1	F	1172	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (74) such sidechains are listed below:

Mol	Chain	Res	Type
1	T	46	ASN
1	T	125	GLN
1	U	246	ASN
1	U	325	GLN
1	V	441	GLN
1	V	446	ASN
1	V	483	ASN
1	G	1083	ASN
1	G	1125	GLN
1	n	46	ASN
1	n	53	GLN
1	n	122	HIS
1	n	125	GLN
1	o	246	ASN
1	p	446	ASN
1	r	846	ASN
1	r	886	ASN
1	r	932	GLN
1	g	1086	ASN
1	g	1125	GLN
1	g	1169	ASN
1	N	46	ASN
1	O	246	ASN
1	O	325	GLN
1	R	846	ASN
1	R	978	ASN
1	S	1046	ASN
1	S	1086	ASN

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Mol	Chain	Res	Type
1	h	46	ASN
1	h	125	GLN
1	i	246	ASN
1	i	325	GLN
1	l	846	ASN
1	l	886	ASN
1	m	1046	ASN
1	m	1125	GLN
1	H	46	ASN
1	H	125	GLN
1	I	241	GLN
1	I	246	ASN
1	I	283	ASN
1	I	325	GLN
1	J	446	ASN
1	K	769	ASN
1	L	846	ASN
1	M	1046	ASN
1	M	1083	ASN
1	M	1122	HIS
1	a	46	ASN
1	a	83	ASN
1	a	125	GLN
1	b	246	ASN
1	b	283	ASN
1	b	286	ASN
1	c	446	ASN
1	d	725	GLN
1	e	846	ASN
1	e	883	ASN
1	f	1011	ASN
1	f	1028	ASN
1	f	1083	ASN
1	f	1086	ASN
1	f	1125	GLN
1	A	46	ASN
1	A	125	GLN
1	B	246	ASN
1	B	325	GLN
1	C	446	ASN
1	C	532	GLN
1	D	778	ASN

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Mol	Chain	Res	Type
1	F	1011	ASN
1	F	1046	ASN
1	F	1083	ASN
2	Z	48	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 (i)

There are no chain breaks in this entry.

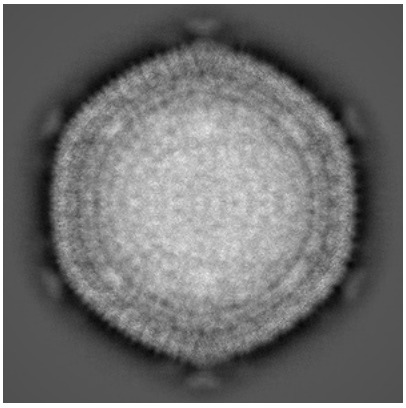
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-20083. These allow visual inspection of the internal detail of the map and identification of artifacts.

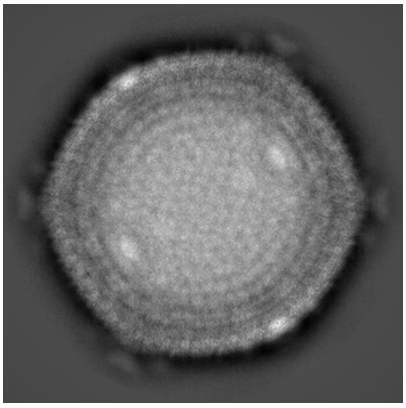
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

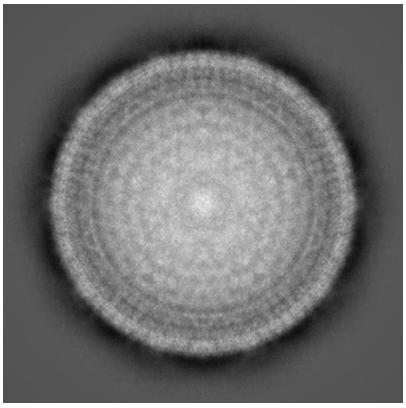
6.1.1 Primary map



X



Y

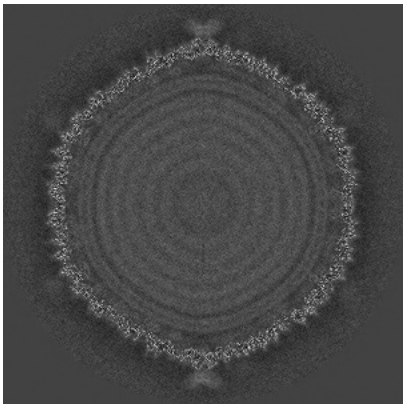


Z

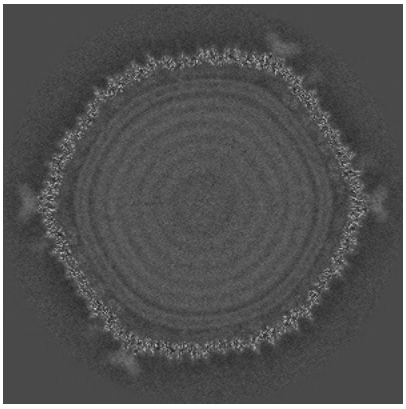
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

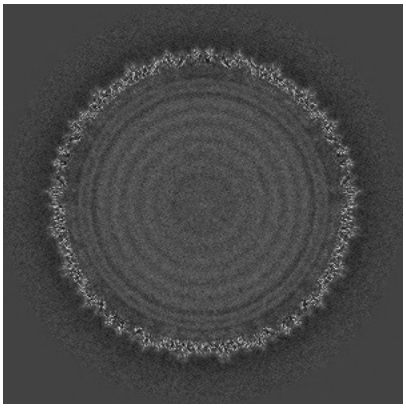
6.2.1 Primary map



X Index: 400



Y Index: 400

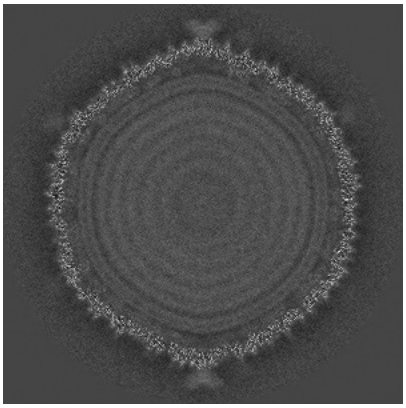


Z Index: 400

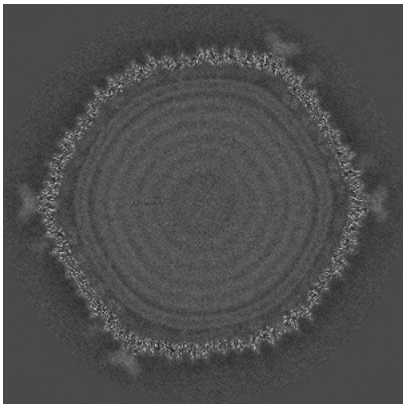
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

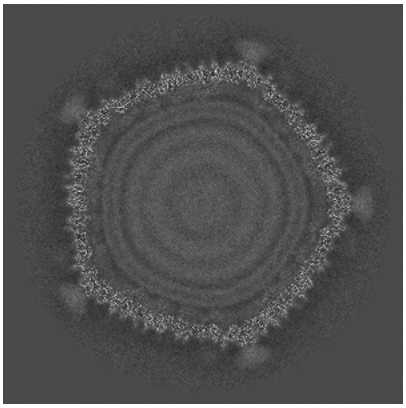
6.3.1 Primary map



X Index: 406



Y Index: 400

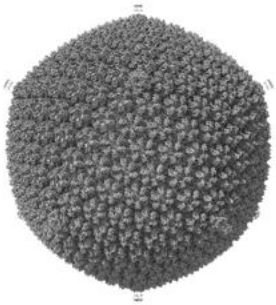


Z Index: 547

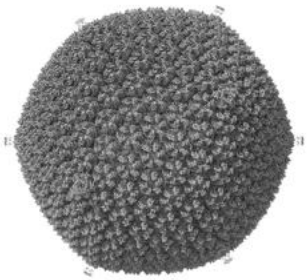
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

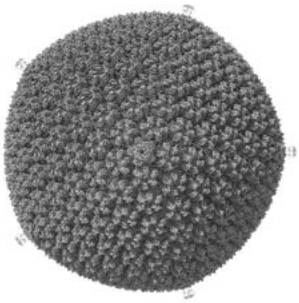
6.4.1 Primary map



X



Y



Z

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.

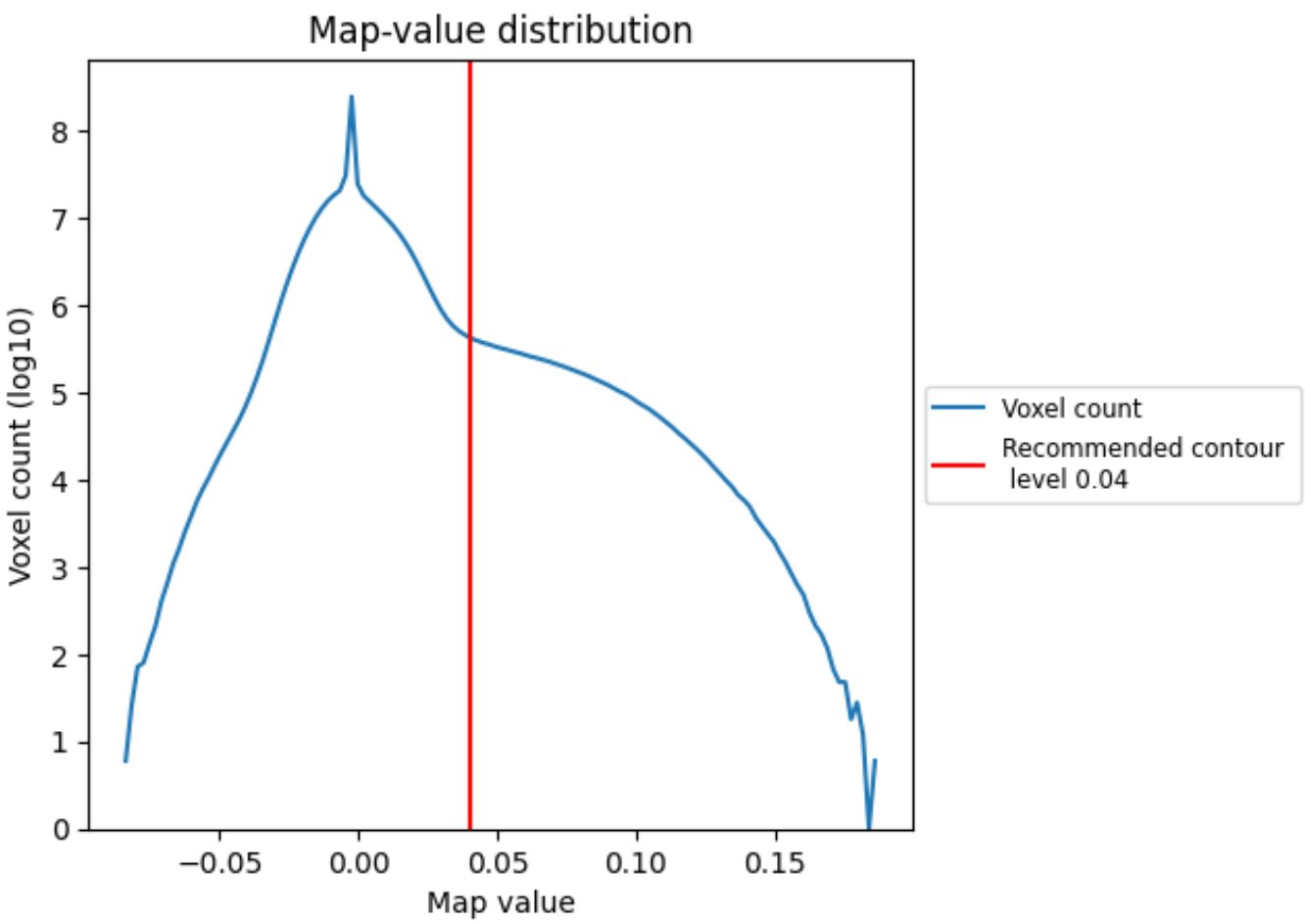
6.5 Mask visualisation (i)

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

7 Map analysis (i)

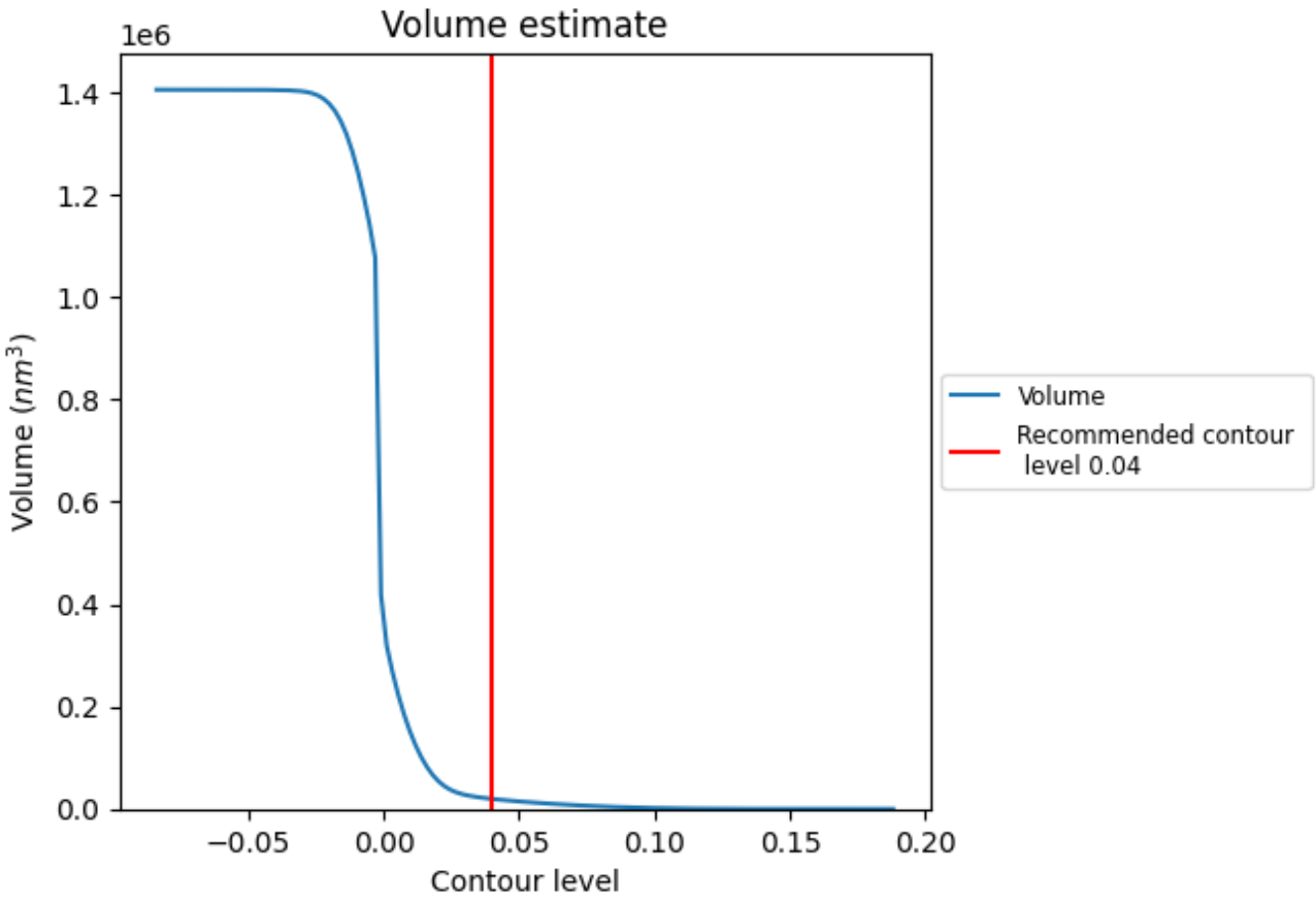
This section contains the results of statistical analysis of the map.

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.

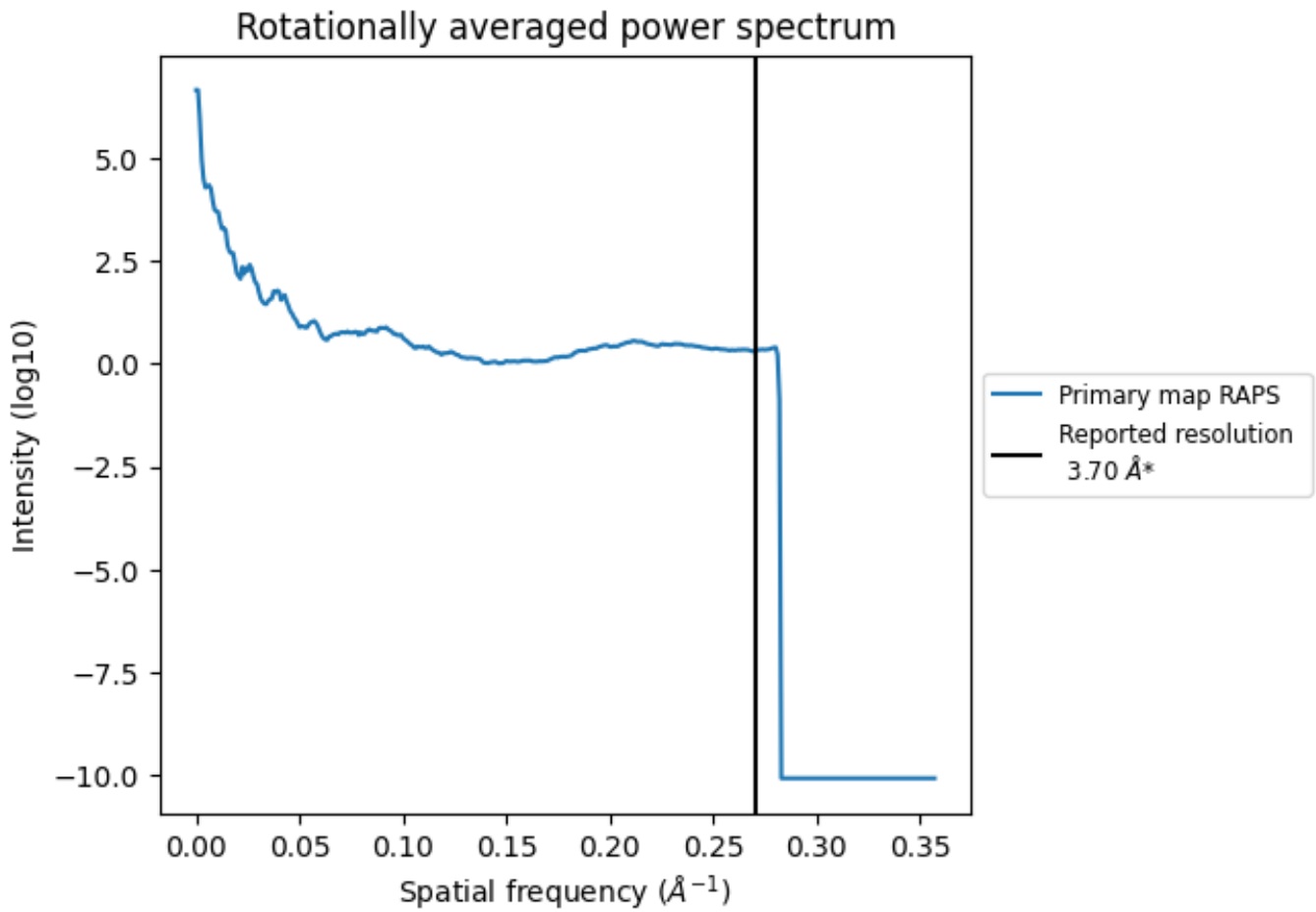
7.2 Volume estimate (i)



The volume at the recommended contour level is 19566 nm^3; this corresponds to an approximate mass of 17674 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 0.270 Å^{-1}

8 Fourier-Shell correlation (i)

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

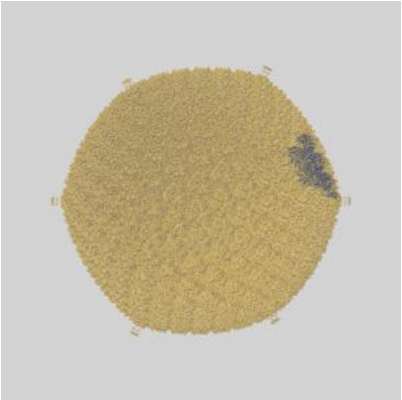
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-20083 and PDB model 6OJ0. Per-residue inclusion information can be found in section 3 on page 8.

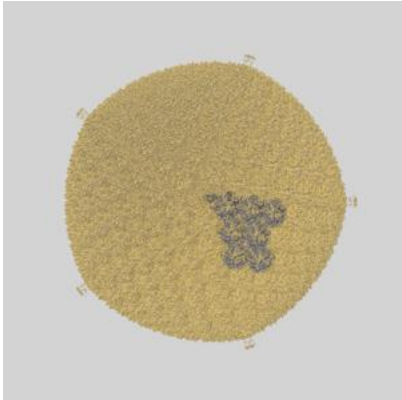
9.1 Map-model overlays

9.1.1 Map-model overlay (i)

X

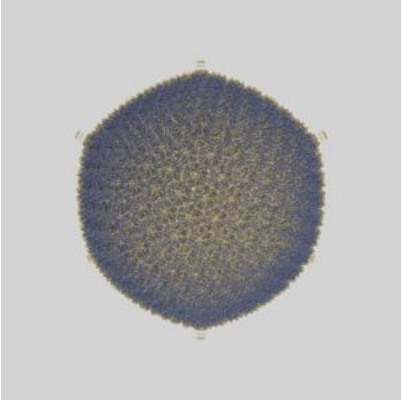


Y

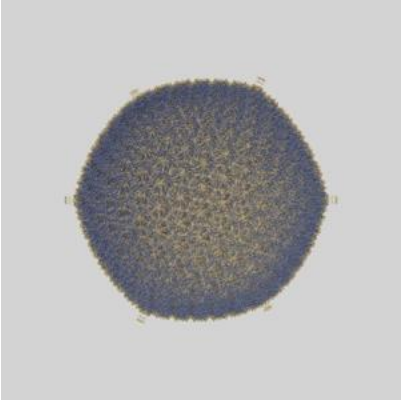


Z

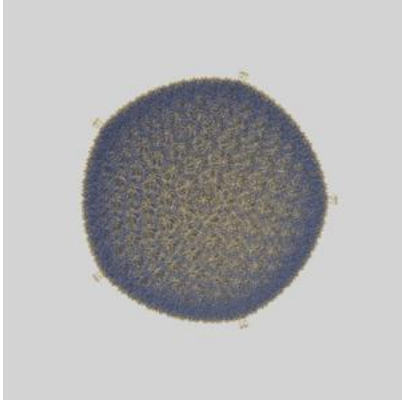
9.1.2 Map-model assembly overlay (i)



X



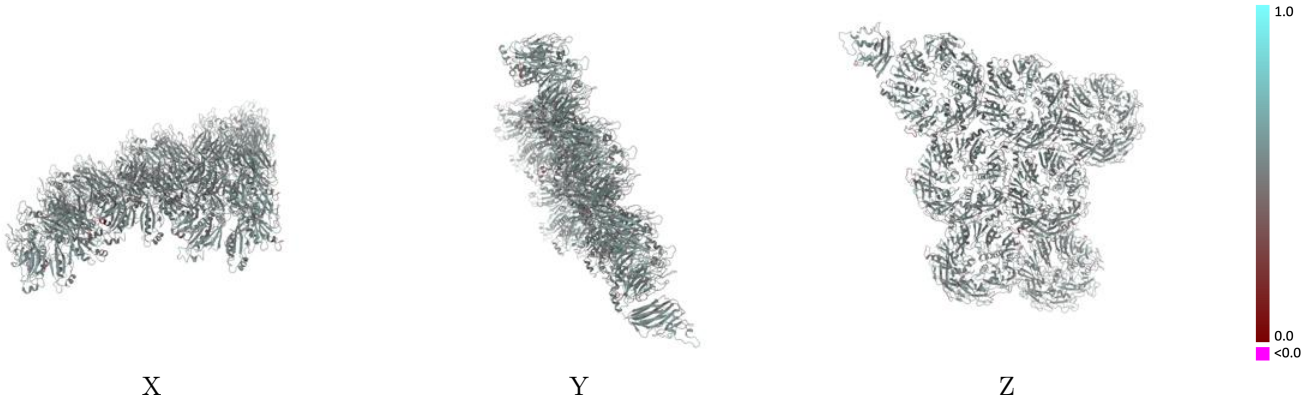
Y



Z

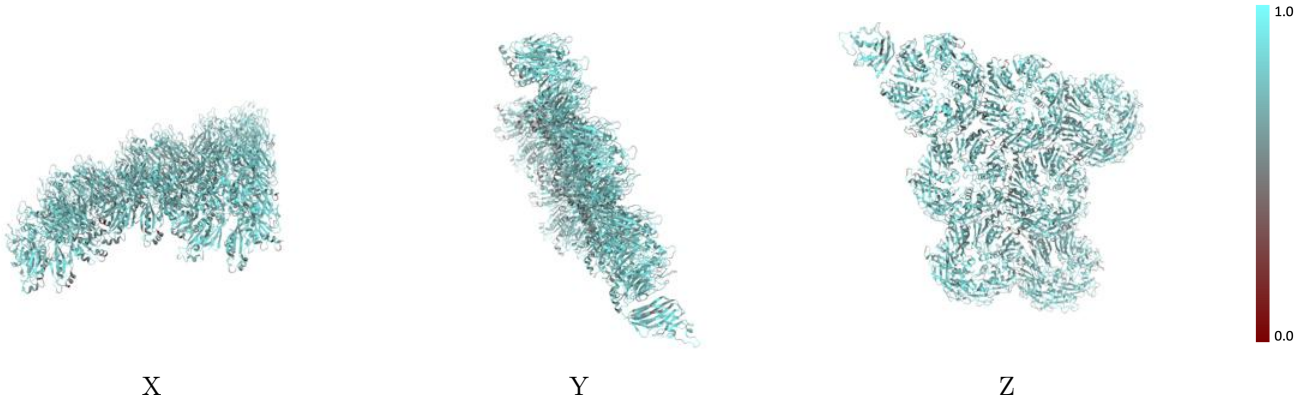
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



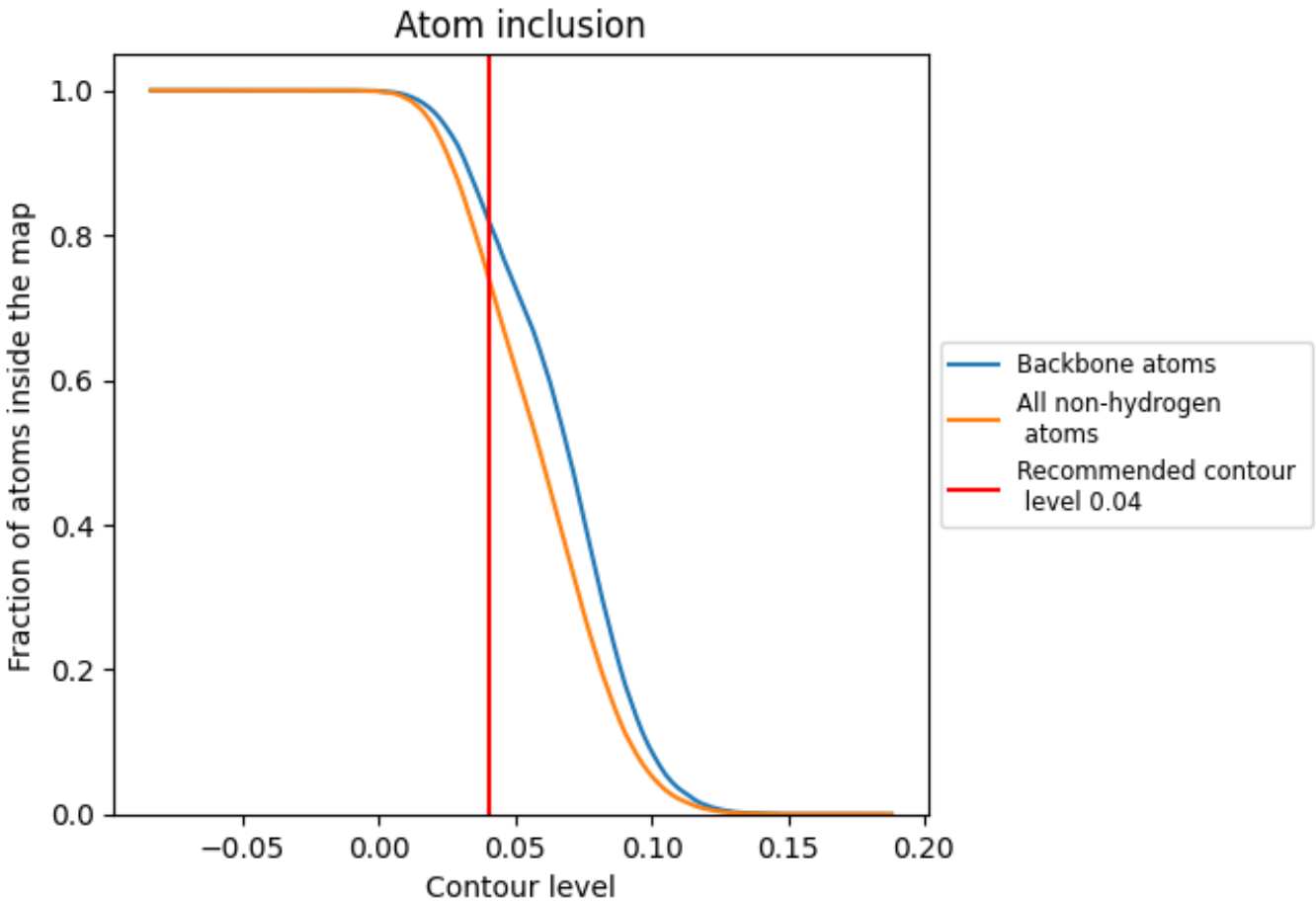
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 82% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

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	0.7432	0.5140
A	0.7428	0.5180
B	0.7677	0.5190
C	0.7330	0.5160
D	0.7391	0.5140
E	0.7564	0.5240
F	0.7406	0.5210
G	0.7549	0.5200
H	0.7210	0.5050
I	0.7353	0.5010
J	0.7308	0.5070
K	0.7519	0.5110
L	0.7338	0.5110
M	0.7308	0.5150
N	0.7376	0.5140
O	0.7504	0.5150
P	0.7293	0.5160
Q	0.7323	0.5080
R	0.7481	0.5150
S	0.7338	0.5200
T	0.7519	0.5190
U	0.7624	0.5190
V	0.7519	0.5170
W	0.7534	0.5060
X	0.7443	0.5130
Z	0.7429	0.5120
a	0.7232	0.5040
b	0.7549	0.5110
c	0.7353	0.5070
d	0.7368	0.5110
e	0.7572	0.5190
f	0.7323	0.5210
g	0.7436	0.5200
h	0.7157	0.5050
i	0.7398	0.5140

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Chain	Atom inclusion	Q-score
j	0.7519	0.5140
k	0.7685	0.5200
l	0.7511	0.5160
m	0.7428	0.5180
n	0.7179	0.5100
o	0.7443	0.5070
p	0.7617	0.5150
q	0.7587	0.5170
r	0.7436	0.5140