wwPDB EM Validation Summary Report

Nov 3, 2022 – 09:38 AM EDT

PDB ID	:	5V7V
EMDB ID	:	EMD-8642
Title	:	Cryo-EM structure of ERAD-associated E3 ubiquitin-protein ligase component HRD3
Authors	:	Mi, W.; Schoebel, S.; Stein, A.; Rapoport, T.A.; Liao, M.
Deposited on	:	2017-03-20
Resolution	:	3.90 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

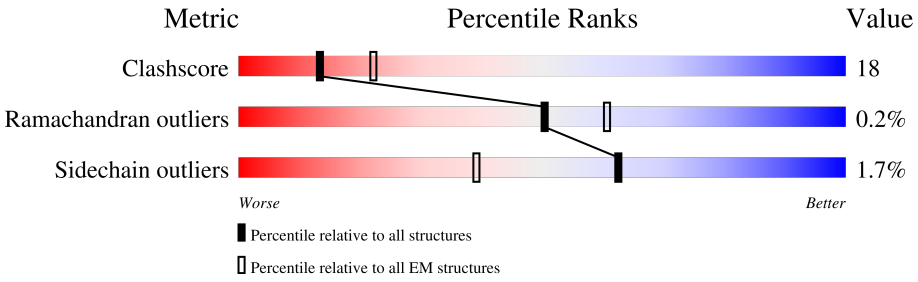
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (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 3.90 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)
Clashscore	158937	4297
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	818	20% 56% 18% · 25%
2	B	3	67% 33% 67%
2	C	3	67% 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	B	2	-	-	X	-
3	NAG	A	901	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10035 atoms, of which 4927 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 ERAD-associated E3 ubiquitin-protein ligase component HRD3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	613	9799	3192	4811	845	931	20	0	0

There are 51 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	768	GLY	-	expression tag	UNP Q05787
A	769	GLY	-	expression tag	UNP Q05787
A	770	GLY	-	expression tag	UNP Q05787
A	771	GLU	-	expression tag	UNP Q05787
A	772	ASN	-	expression tag	UNP Q05787
A	773	LEU	-	expression tag	UNP Q05787
A	774	TYR	-	expression tag	UNP Q05787
A	775	PHE	-	expression tag	UNP Q05787
A	776	GLN	-	expression tag	UNP Q05787
A	777	SER	-	expression tag	UNP Q05787
A	778	GLY	-	expression tag	UNP Q05787
A	779	GLY	-	expression tag	UNP Q05787
A	780	GLY	-	expression tag	UNP Q05787
A	781	MET	-	expression tag	UNP Q05787
A	782	ASP	-	expression tag	UNP Q05787
A	783	GLU	-	expression tag	UNP Q05787
A	784	LYS	-	expression tag	UNP Q05787
A	785	THR	-	expression tag	UNP Q05787
A	786	THR	-	expression tag	UNP Q05787
A	787	GLY	-	expression tag	UNP Q05787
A	788	TRP	-	expression tag	UNP Q05787
A	789	ARG	-	expression tag	UNP Q05787
A	790	GLY	-	expression tag	UNP Q05787
A	791	GLY	-	expression tag	UNP Q05787
A	792	HIS	-	expression tag	UNP Q05787
A	793	VAL	-	expression tag	UNP Q05787
A	794	VAL	-	expression tag	UNP Q05787
A	795	GLU	-	expression tag	UNP Q05787

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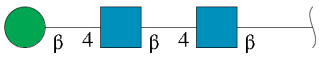
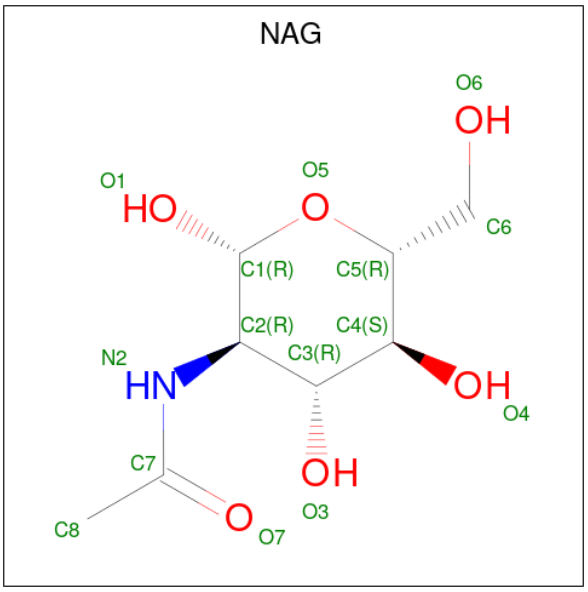
Chain	Residue	Modelled	Actual	Comment	Reference
A	796	GLY	-	expression tag	UNP Q05787
A	797	LEU	-	expression tag	UNP Q05787
A	798	ALA	-	expression tag	UNP Q05787
A	799	GLY	-	expression tag	UNP Q05787
A	800	GLU	-	expression tag	UNP Q05787
A	801	LEU	-	expression tag	UNP Q05787
A	802	GLU	-	expression tag	UNP Q05787
A	803	GLN	-	expression tag	UNP Q05787
A	804	LEU	-	expression tag	UNP Q05787
A	805	ARG	-	expression tag	UNP Q05787
A	806	ALA	-	expression tag	UNP Q05787
A	807	ARG	-	expression tag	UNP Q05787
A	808	LEU	-	expression tag	UNP Q05787
A	809	GLU	-	expression tag	UNP Q05787
A	810	HIS	-	expression tag	UNP Q05787
A	811	HIS	-	expression tag	UNP Q05787
A	812	PRO	-	expression tag	UNP Q05787
A	813	GLN	-	expression tag	UNP Q05787
A	814	GLY	-	expression tag	UNP Q05787
A	815	GLN	-	expression tag	UNP Q05787
A	816	ARG	-	expression tag	UNP Q05787
A	817	GLU	-	expression tag	UNP Q05787
A	818	PRO	-	expression tag	UNP Q05787

- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	3	Total	C	H	N	O	0	0
			76	22	37	2	15		
2	C	3	Total	C	H	N	O	0	0
			76	22	37	2	15		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



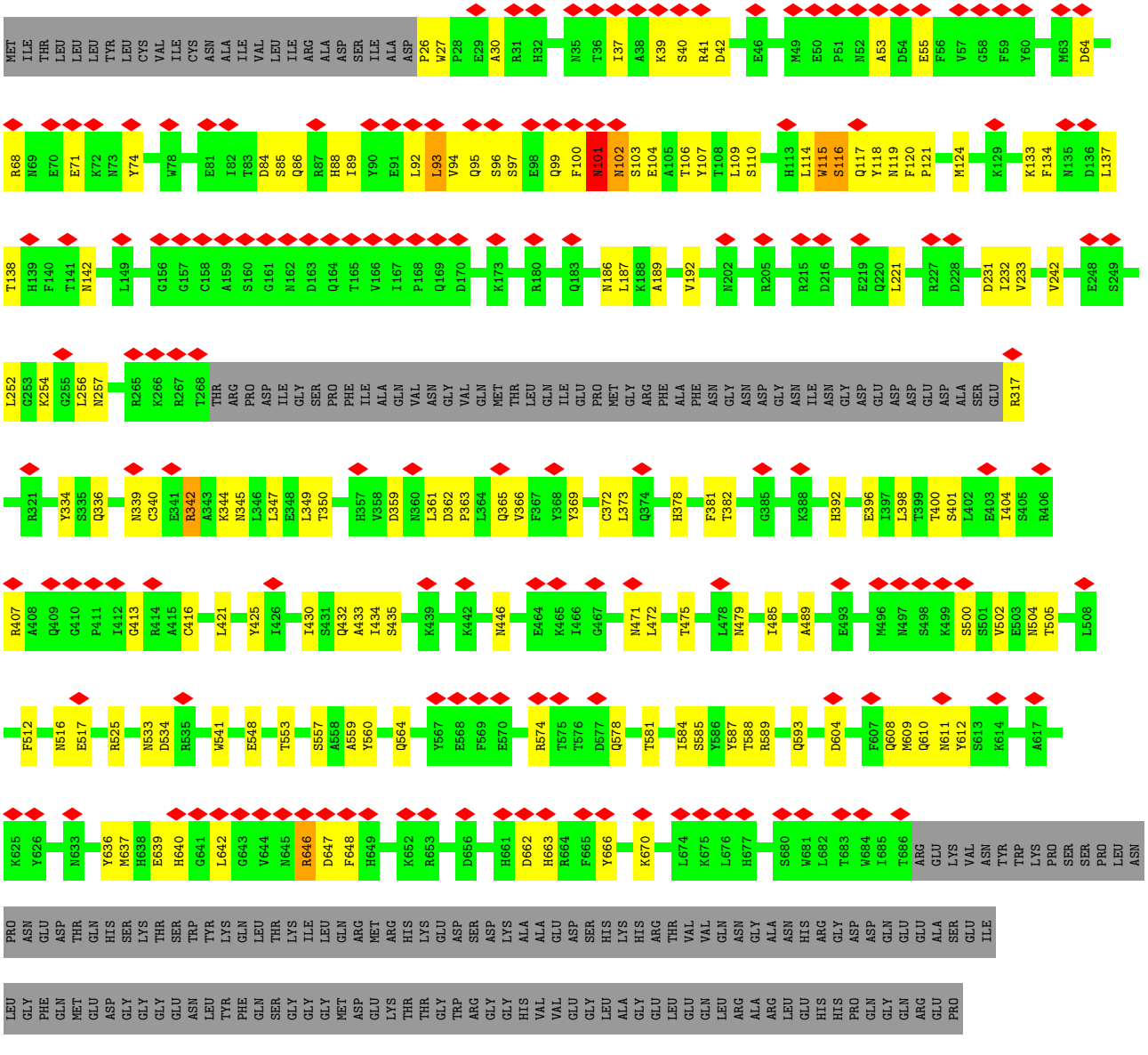
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	H	N	O	0
			84	24	42	3	15	
3	A	1	Total	C	H	N	O	0
			84	24	42	3	15	
3	A	1	Total	C	H	N	O	0
			84	24	42	3	15	

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: ERAD-associated E3 ubiquitin-protein ligase component HRD3

Chain A:

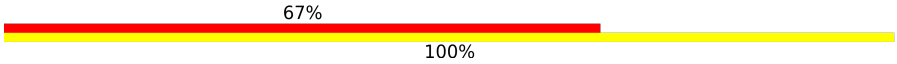


• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	204578	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	82	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.282	Depositor
Minimum map value	-0.162	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.074	Depositor
Map size (Å)	259.2, 259.2, 259.2	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG

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	0.56	2/5116 (0.0%)	0.67	5/6934 (0.1%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	646	ARG	CZ-NH2	7.21	1.42	1.33
1	A	646	ARG	CZ-NH1	6.95	1.42	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	102	ASN	N-CA-CB	8.83	126.49	110.60
1	A	116	SER	N-CA-CB	8.53	123.29	110.50
1	A	115	TRP	N-CA-C	5.70	126.40	111.00
1	A	116	SER	N-CA-C	-5.61	95.84	111.00
1	A	101	ASN	N-CA-C	5.18	124.98	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	93	LEU	Mainchain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4988	4811	4828	175	0
2	B	39	37	34	7	0
2	C	39	37	34	6	0
3	A	42	42	39	9	0
All	All	5108	4927	4935	182	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

The worst 5 of 182 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:SER:HB2	1:A:117:GLN:NE2	1.23	1.44
1:A:27:TRP:CG	1:A:104:GLU:OE2	1.71	1.38
1:A:40:SER:CB	1:A:117:GLN:HE22	1.37	1.37
1:A:37:ILE:HD11	1:A:118:TYR:CE1	1.59	1.35
1:A:37:ILE:HD11	1:A:118:TYR:CD1	1.69	1.28

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	609/818 (74%)	540 (89%)	68 (11%)	1 (0%)	47 79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	ASN

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	529/703 (75%)	520 (98%)	9 (2%)	60 78

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	471	ASN
1	A	609	MET
1	A	317	ARG
1	A	342	ARG
1	A	372	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	424	GLN
1	A	479	ASN
1	A	645	ASN
1	A	593	GLN
1	A	355	GLN

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)

6 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	NAG	B	1	1,2	14,14,15	0.53	0	17,19,21	0.49	0
2	NAG	B	2	2	14,14,15	0.42	0	17,19,21	1.16	2 (11%)
2	BMA	B	3	2	11,11,12	0.41	0	15,15,17	1.14	1 (6%)
2	NAG	C	1	1,2	14,14,15	0.47	0	17,19,21	0.47	0
2	NAG	C	2	2	14,14,15	0.71	0	17,19,21	1.30	2 (11%)
2	BMA	C	3	2	11,11,12	0.33	0	15,15,17	0.86	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	0/1/1/1
2	NAG	C	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	2	NAG	C8-C7-N2	3.45	121.94	116.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	3	BMA	C1-O5-C5	-3.41	107.58	112.19
2	B	2	NAG	C8-C7-N2	2.30	119.99	116.10
2	C	2	NAG	O7-C7-N2	-2.28	117.77	121.95
2	C	3	BMA	C1-O5-C5	2.27	115.27	112.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1	NAG	C4-C5-C6-O6
2	B	1	NAG	O5-C5-C6-O6
2	C	1	NAG	C1-C2-N2-C7

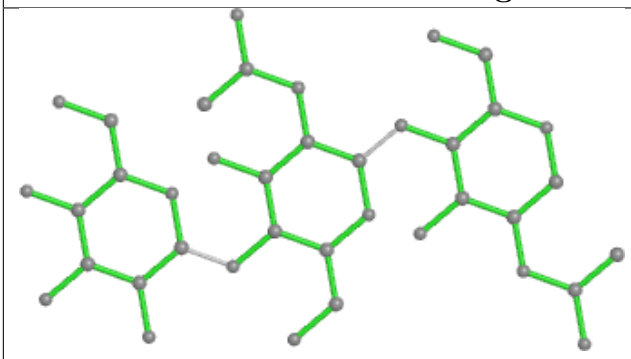
There are no ring outliers.

4 monomers are involved in 13 short contacts:

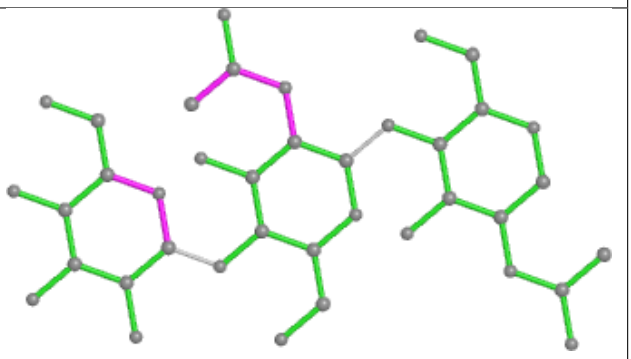
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	NAG	6	0
2	B	2	NAG	7	0
2	B	1	NAG	3	0
2	B	3	BMA	3	0

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

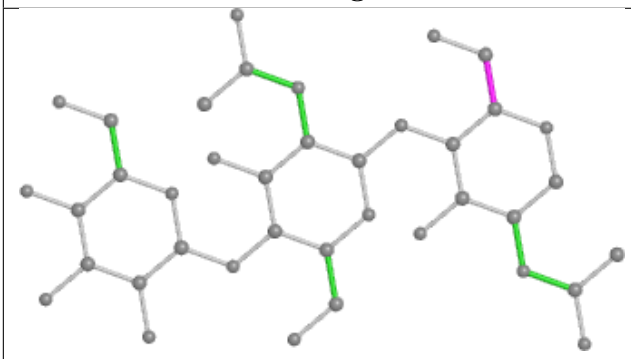
Oligosaccharide Chain B



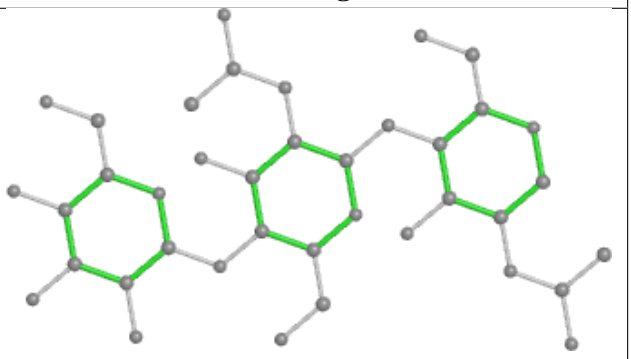
Bond lengths



Bond angles

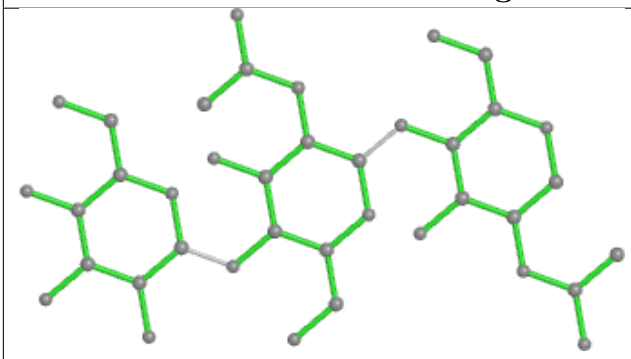


Torsions

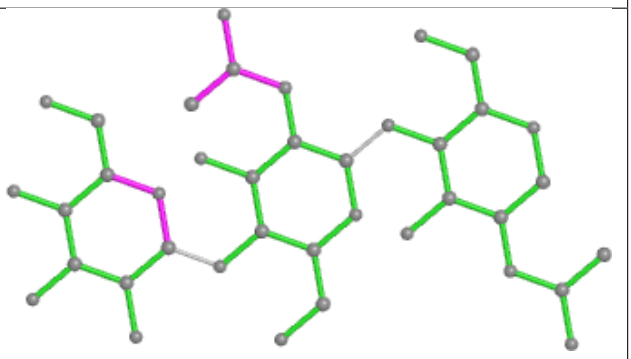


Rings

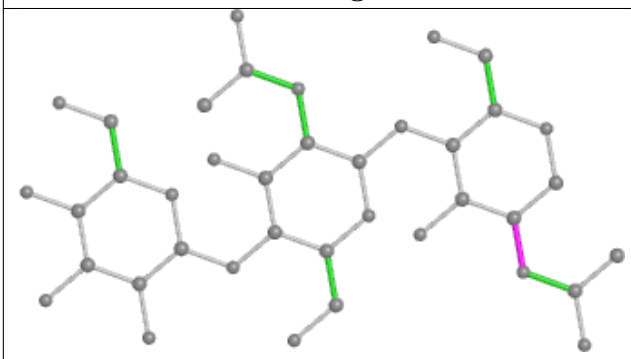
Oligosaccharide Chain C



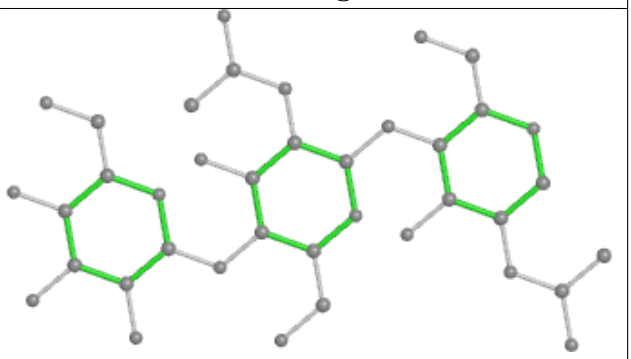
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	NAG	A	909	1	14,14,15	0.40	0	17,19,21	0.83	1 (5%)
3	NAG	A	901	-	14,14,15	0.60	0	17,19,21	1.41	2 (11%)
3	NAG	A	908	1	14,14,15	0.29	0	17,19,21	0.61	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	909	1	-	2/6/23/26	0/1/1/1
3	NAG	A	901	-	-	2/6/23/26	0/1/1/1
3	NAG	A	908	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	901	NAG	C8-C7-N2	3.36	121.79	116.10
3	A	909	NAG	C1-O5-C5	2.94	116.17	112.19
3	A	901	NAG	C1-C2-N2	2.62	114.96	110.49

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	908	NAG	O5-C5-C6-O6
3	A	908	NAG	C4-C5-C6-O6
3	A	909	NAG	C4-C5-C6-O6

Continued on next page...

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Mol	Chain	Res	Type	Atoms
3	A	901	NAG	C1-C2-N2-C7
3	A	909	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	901	NAG	8	0
3	A	908	NAG	1	0

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.

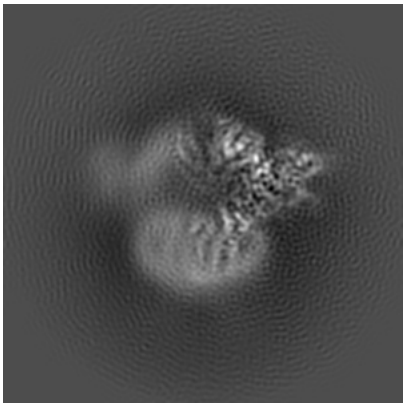
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-8642. These allow visual inspection of the internal detail of the map and identification of artifacts.

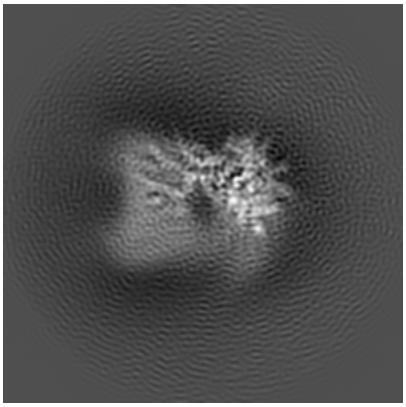
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

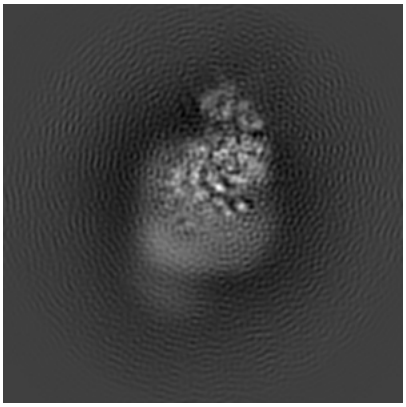
6.1.1 Primary map



X



Y

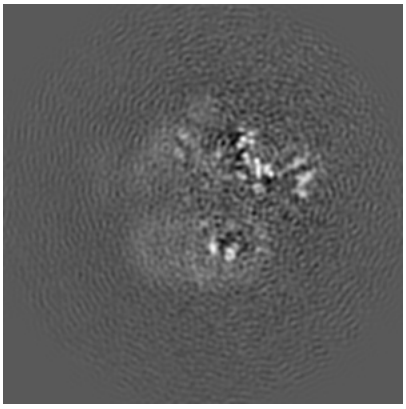


Z

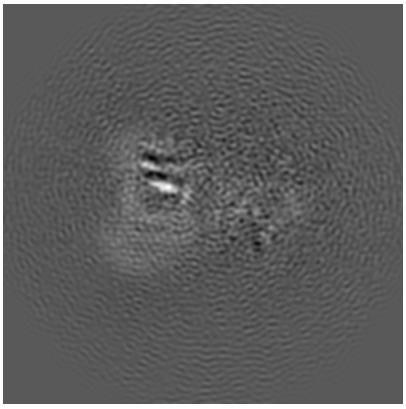
The images above show the map projected in three orthogonal directions.

6.2 Central slices

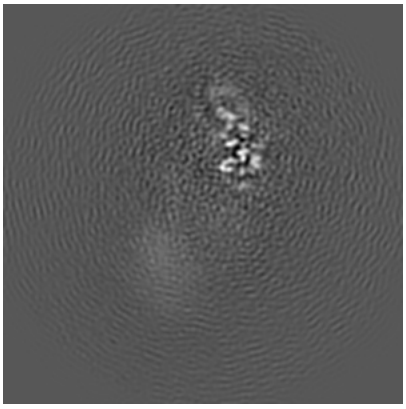
6.2.1 Primary map



X Index: 96



Y Index: 96

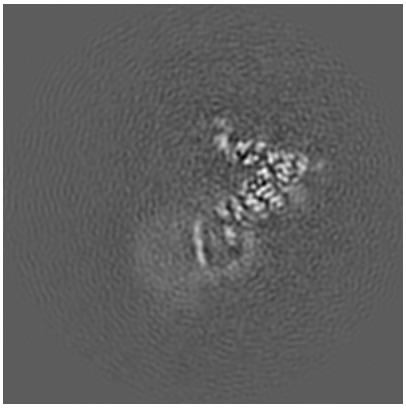


Z Index: 96

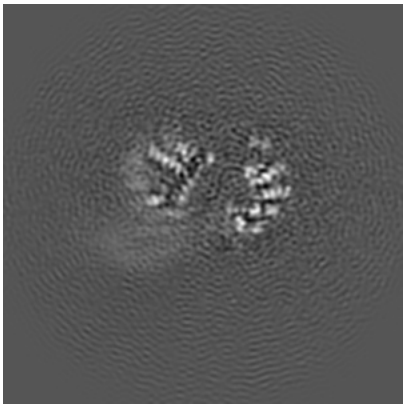
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

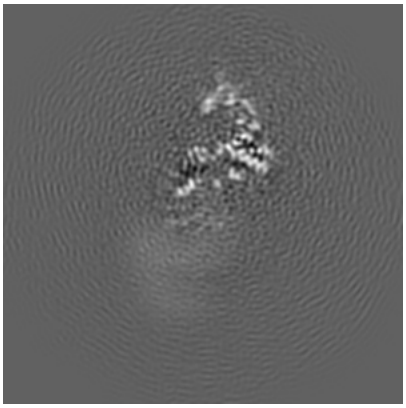
6.3.1 Primary map



X Index: 115



Y Index: 109

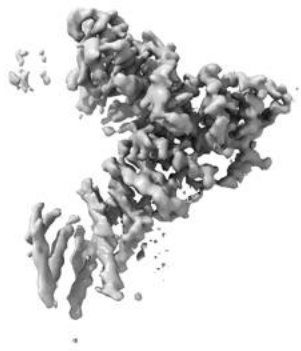


Z Index: 117

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

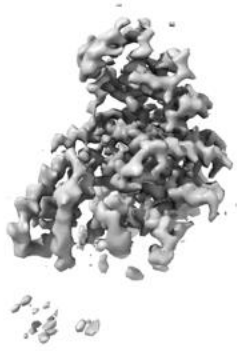
6.4 Orthogonal surface views (i)

6.4.1 Primary map



X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.074. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

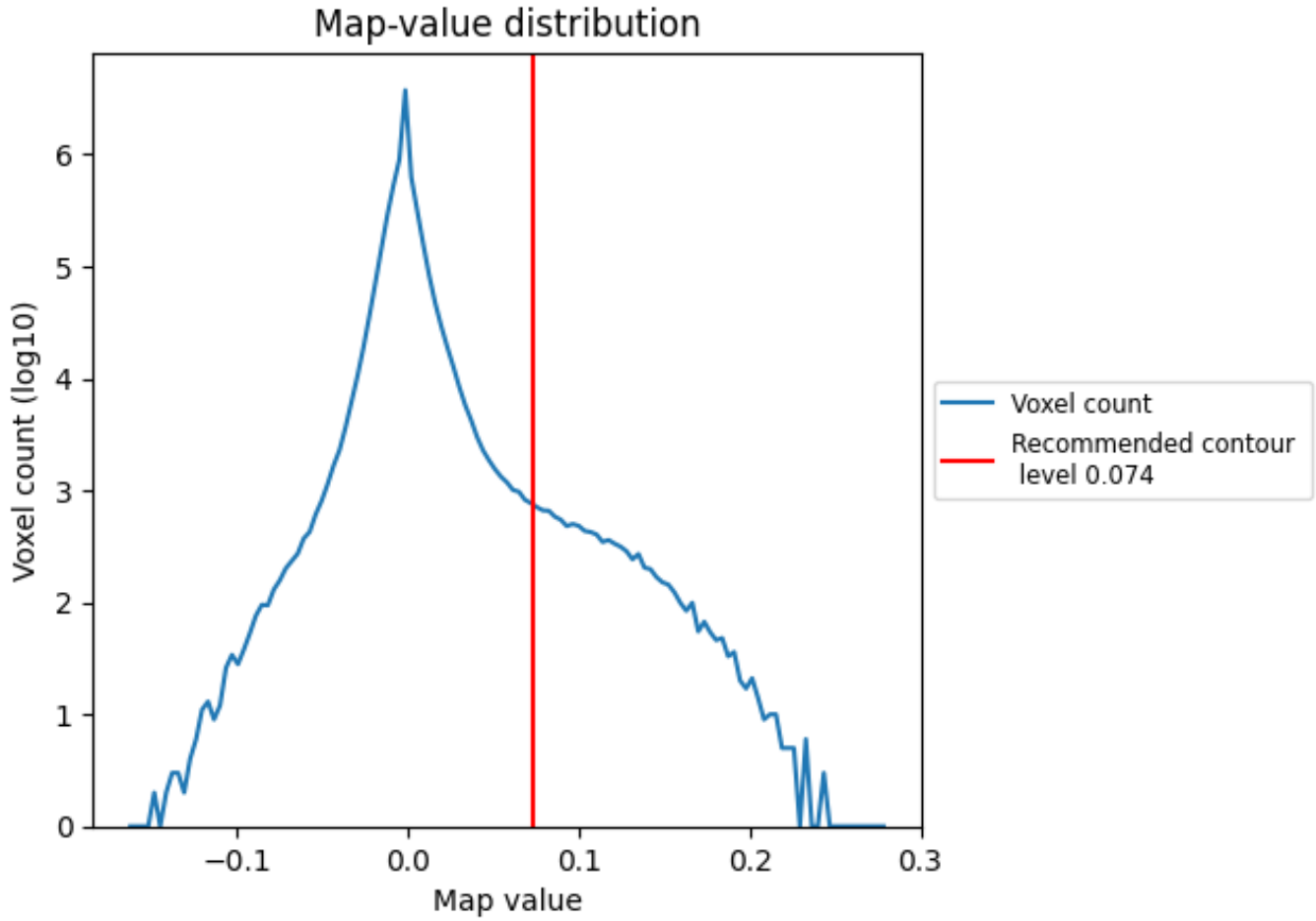
6.5 Mask visualisation (i)

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

7 Map analysis

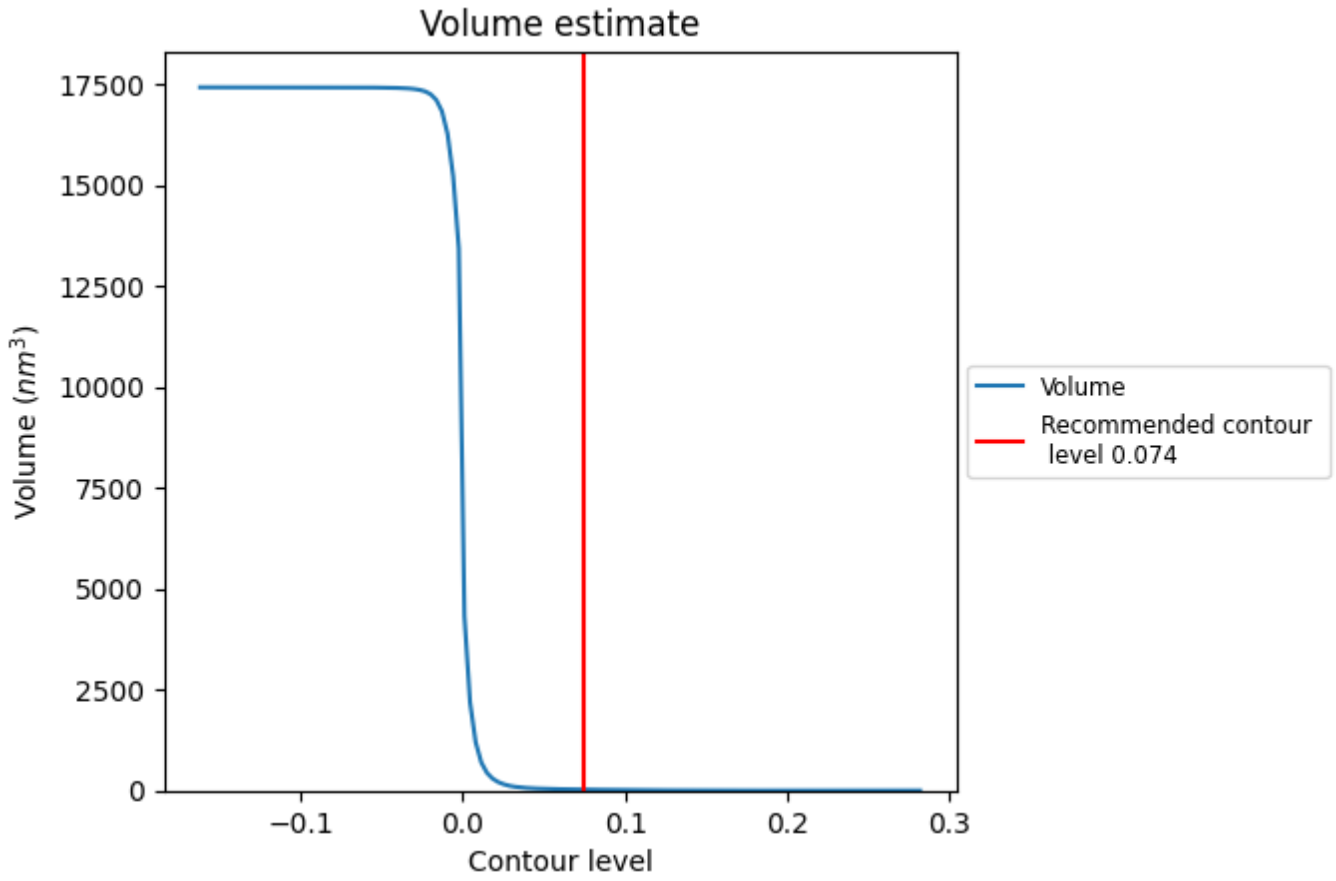
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

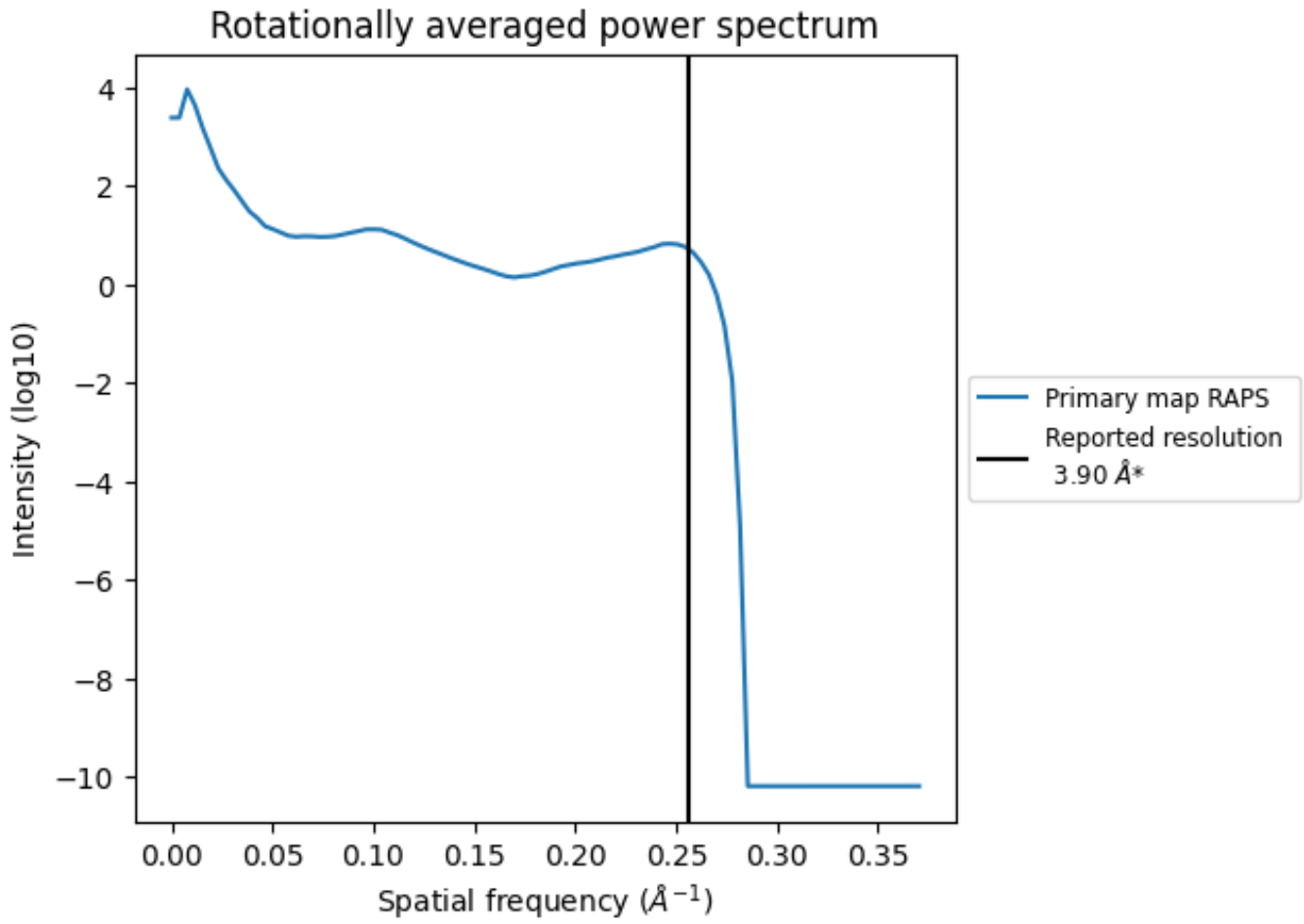
7.2 Volume estimate (i)



The volume at the recommended contour level is 25 nm^3; this corresponds to an approximate mass of 23 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)

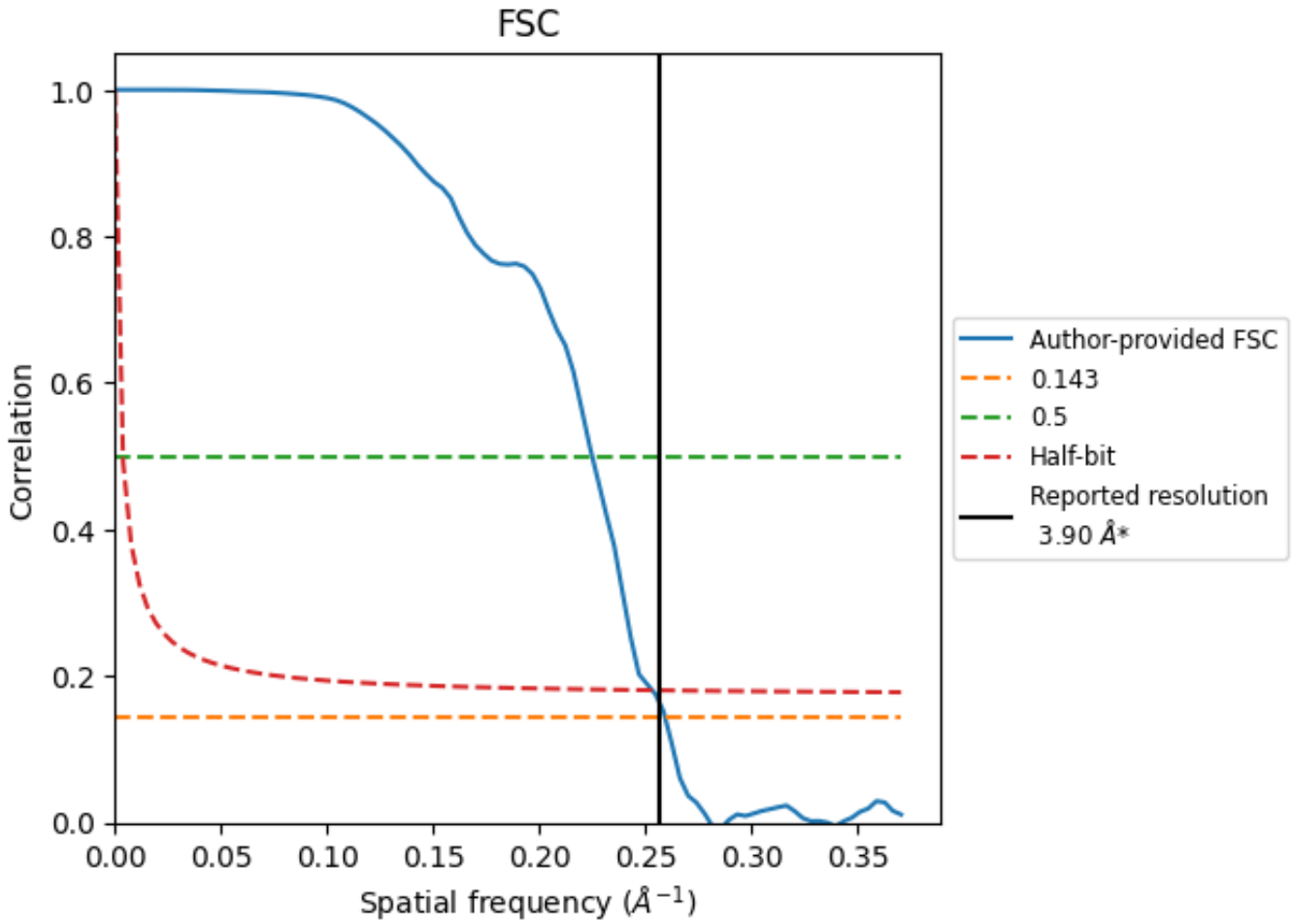


*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

8.2 Resolution estimates (i)

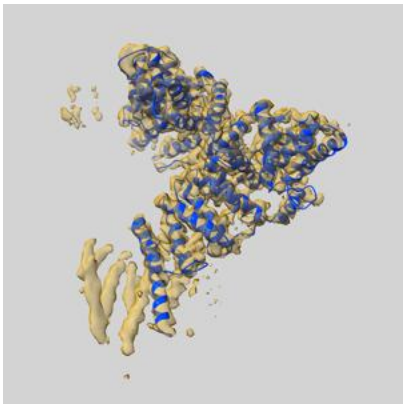
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.86	4.45	3.95
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

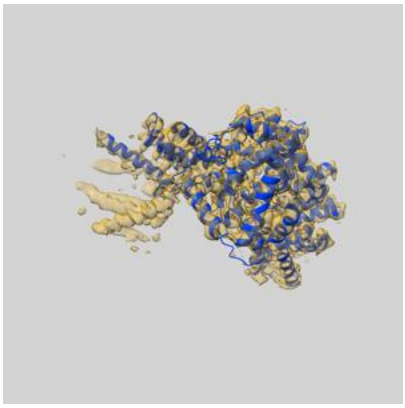
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-8642 and PDB model 5V7V. Per-residue inclusion information can be found in section 3 on page 6.

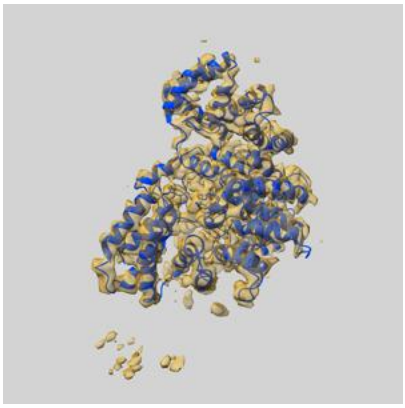
9.1 Map-model overlay



X



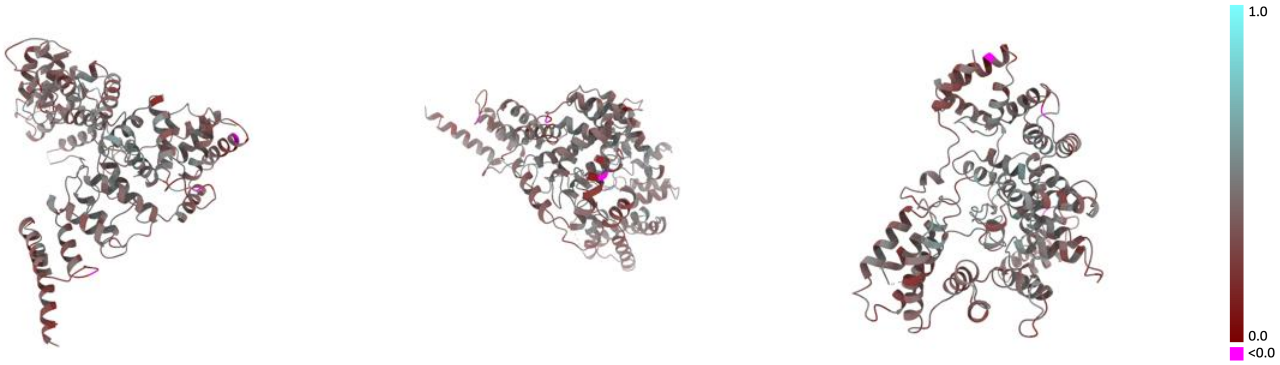
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.074 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.

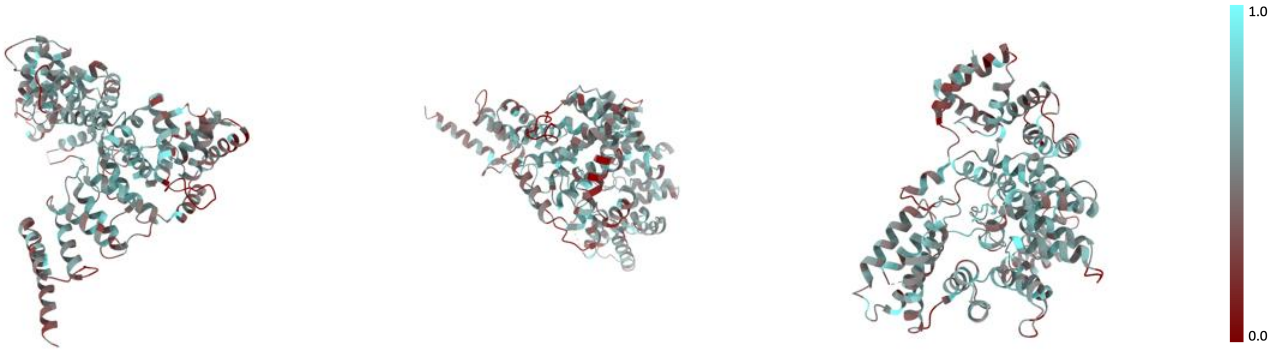
9.2 Q-score mapped to coordinate model



X Y Z

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.

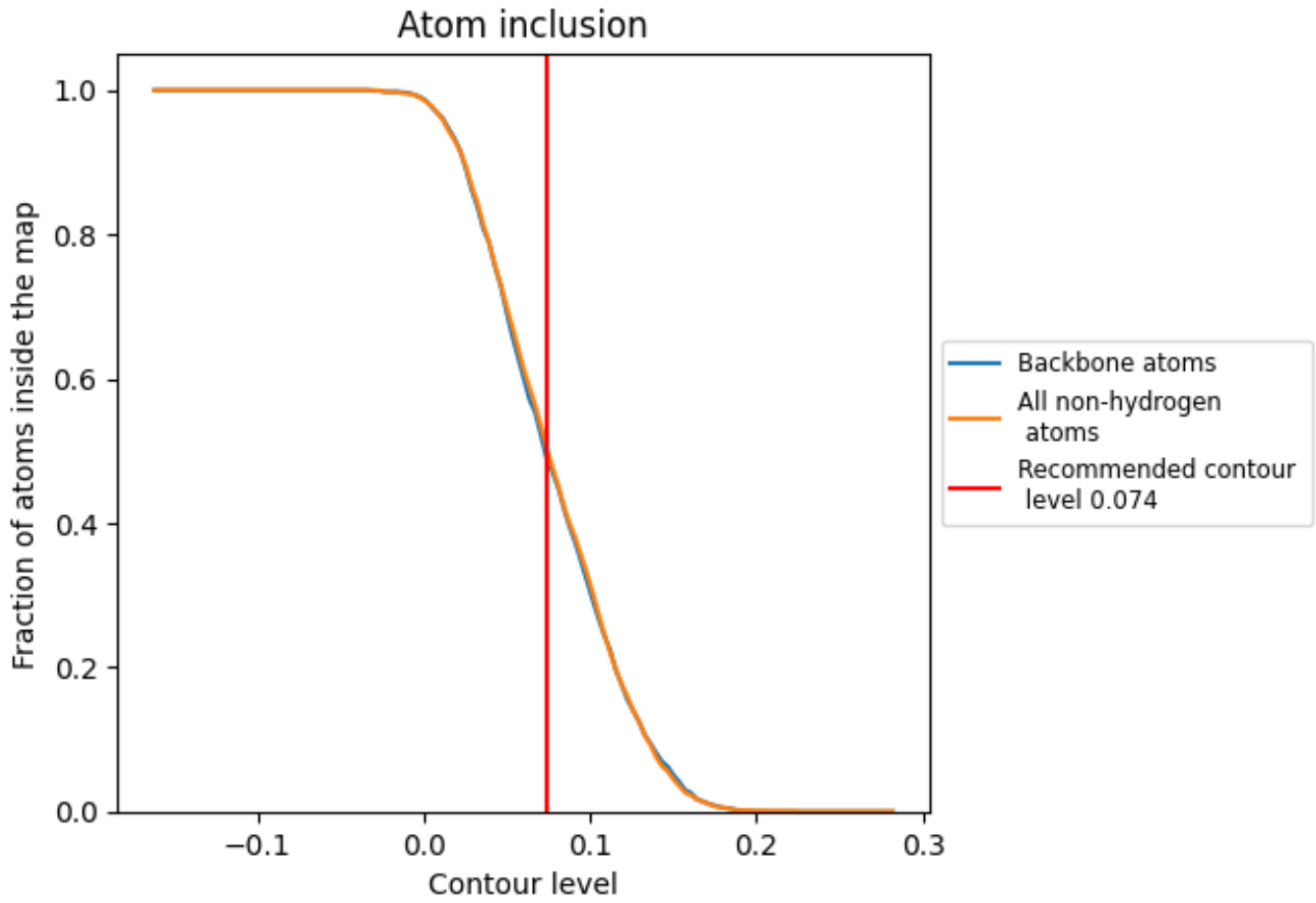
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.074).

9.4 Atom inclusion (i)



At the recommended contour level, 49% of all backbone atoms, 50% 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 (0.074) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5020	0.3960
A	0.5168	0.3970
B	0.3333	0.2950
C	0.2821	0.3330