



# wwPDB EM Validation Summary Report ⓘ

Jun 26, 2024 – 09:33 AM JST

PDB ID : 7XJ3  
EMDB ID : EMD-33218  
Title : Structure of human TRPV3  
Authors : Fan, J.; Yue, Z.; Jiang, D.; Lei, X.  
Deposited on : 2022-04-14  
Resolution : 3.54 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev92  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
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) : 2.37.1

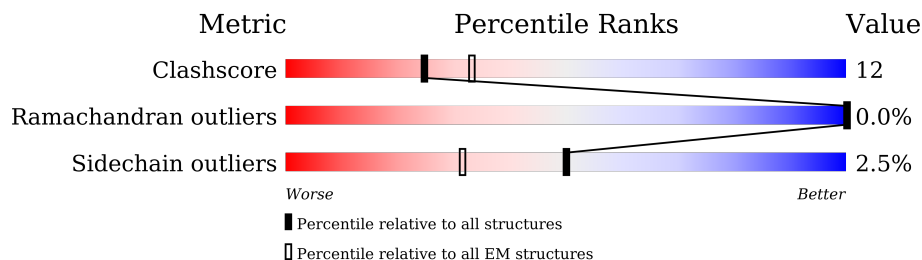
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.54 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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1061	 44% 13% 43%
1	B	1061	 44% 13% 43%
1	C	1061	 45% 12% 43%
1	D	1061	 45% 12% 43%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18493 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.

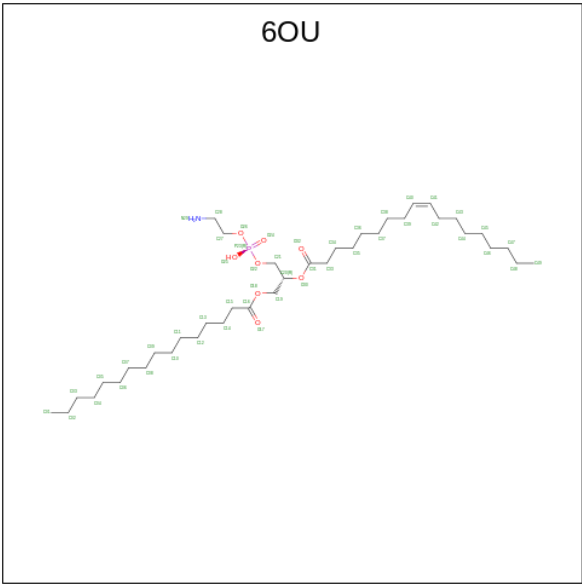
- Molecule 1 is a protein called fusion of transient receptor potential cation channel subfamily V member 3 and 3C-GFP.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	607	Total	C	N	O	S	0	0
			4590	3018	763	781	28		
1	C	607	Total	C	N	O	S	0	0
			4580	3014	762	776	28		
1	A	607	Total	C	N	O	S	0	0
			4576	3011	761	776	28		
1	D	607	Total	C	N	O	S	0	0
			4576	3011	761	776	28		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	25	ILE	VAL	conflict	UNP B2KYM6
B	117	ARG	GLY	conflict	UNP B2KYM6
B	246	LYS	ARG	conflict	UNP B2KYM6
B	247	GLY	GLU	conflict	UNP B2KYM6
B	772	ASN	ASP	conflict	UNP B2KYM6
C	25	ILE	VAL	conflict	UNP B2KYM6
C	117	ARG	GLY	conflict	UNP B2KYM6
C	246	LYS	ARG	conflict	UNP B2KYM6
C	247	GLY	GLU	conflict	UNP B2KYM6
C	772	ASN	ASP	conflict	UNP B2KYM6
A	25	ILE	VAL	conflict	UNP B2KYM6
A	117	ARG	GLY	conflict	UNP B2KYM6
A	246	LYS	ARG	conflict	UNP B2KYM6
A	247	GLY	GLU	conflict	UNP B2KYM6
A	772	ASN	ASP	conflict	UNP B2KYM6
D	25	ILE	VAL	conflict	UNP B2KYM6
D	117	ARG	GLY	conflict	UNP B2KYM6
D	246	LYS	ARG	conflict	UNP B2KYM6
D	247	GLY	GLU	conflict	UNP B2KYM6
D	772	ASN	ASP	conflict	UNP B2KYM6

- Molecule 2 is [(2 {R})-1-[2-azanylethoxy(oxidanyl)phosphoryl]oxy-3-hexadecanoyloxy-prop an-2-yl] ( {Z})-octadec-9-enoate (three-letter code: 6OU) (formula: C<sub>39</sub>H<sub>76</sub>NO<sub>8</sub>P).



Mol	Chain	Residues	Atoms		AltConf
2	B	1	Total	C	0
			14	14	
2	B	1	Total	C	0
			11	11	
2	B	1	Total	C	0
			14	14	
2	C	1	Total	C	0
			8	8	
2	C	1	Total	C	0
			12	12	
2	C	1	Total	C	0
			13	13	
2	C	1	Total	C	0
			14	14	
2	A	1	Total	C	0
			14	14	
2	A	1	Total	C	0
			14	14	
2	A	1	Total	C	0
			12	12	
2	A	1	Total	C	0
			8	8	
2	D	1	Total	C	0
			14	14	

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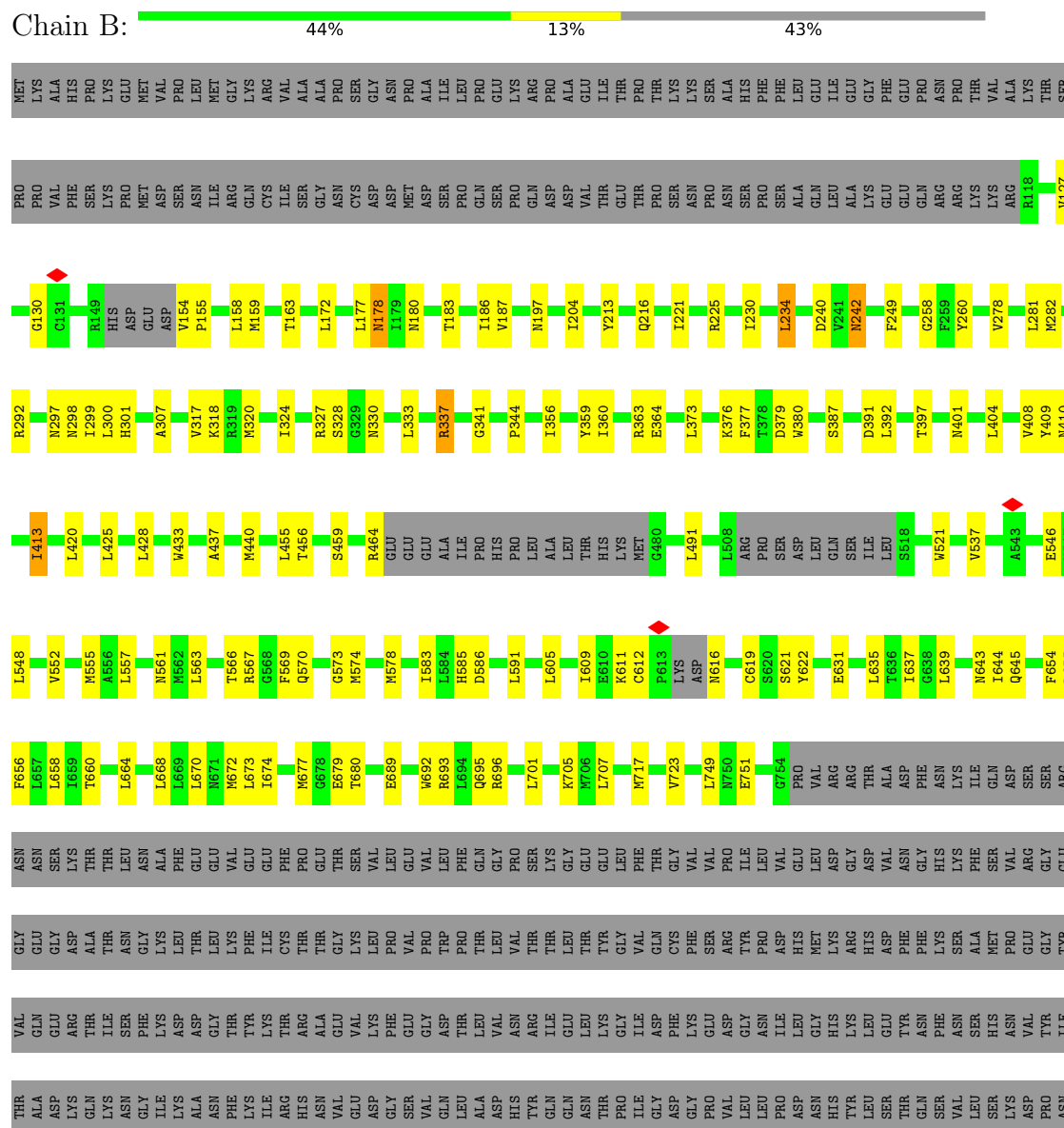
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Mol	Chain	Residues	Atoms		AltConf
2	D	1	Total	C	0
			9	9	
2	D	1	Total	C	0
			14	14	

### 3 Residue-property plots

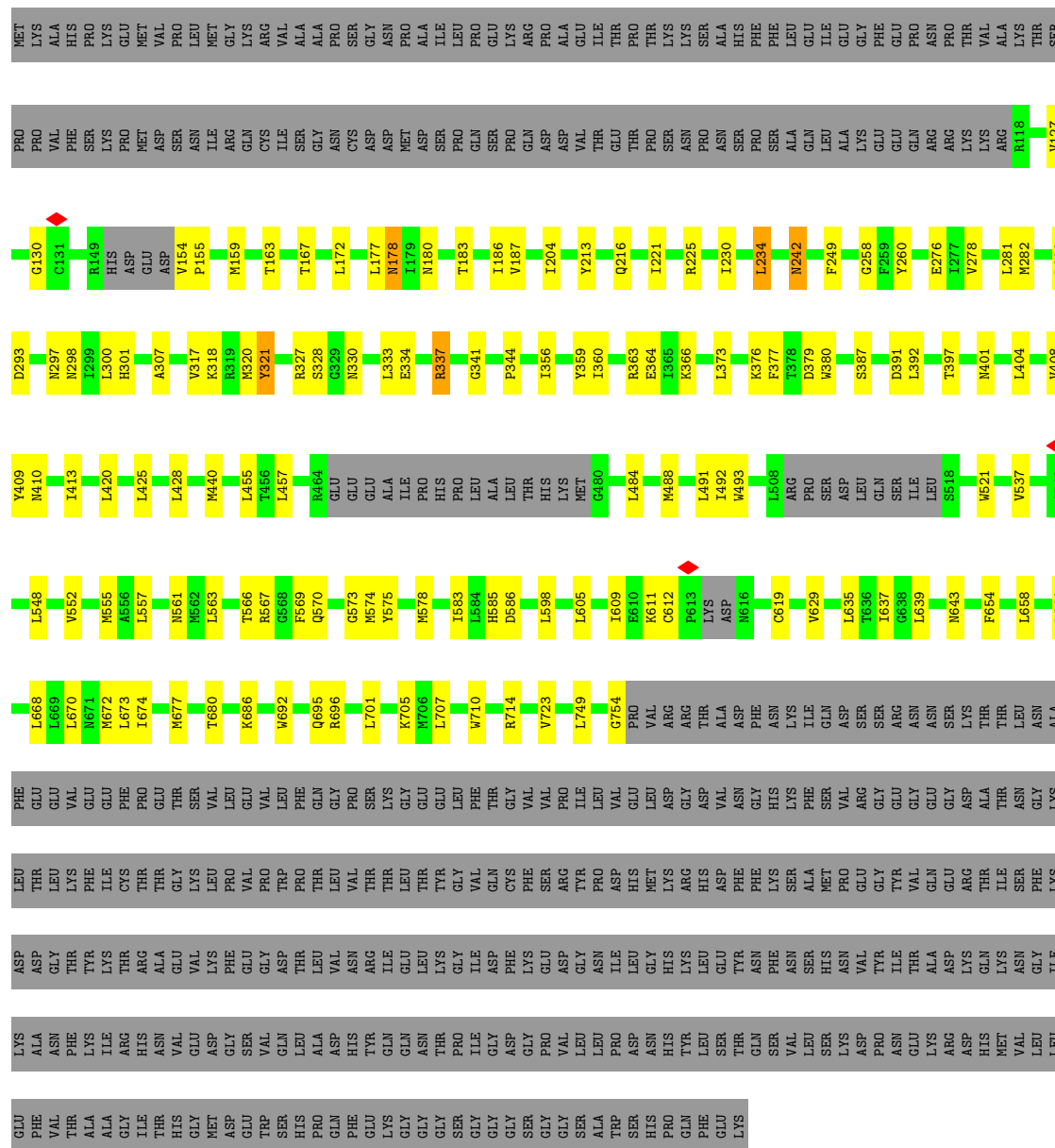
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: fusion of transient receptor potential cation channel subfamily V member 3 and 3C-GFP



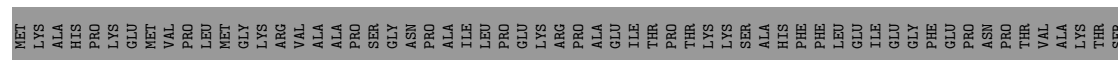
- Molecule 1: fusion of transient receptor potential cation channel subfamily V member 3 and 3C-GFP

Chain C:  45% 12% 43%



- Molecule 1: fusion of transient receptor potential cation channel subfamily V member 3 and 3C-GFP

Chain A:  44% 13% 43%







R292 D293	Y409 N410	L548	L655	ALA	LYS	ILE	LEU
N297	I413	V552	L658	PHE	LEU	LYS	THR
N298	L420	M555	L664	GLU	THR	ASP	VAL
I299	L425	A556	L668	VAL	LYS	THR	THR
L300	L428	L557	M672	GLU	ILE	TYR	ALA
H301	W433	M561	M677	PHE	CYS	THR	ALA
A307	A437	L563	E678	GLU	THR	ARG	GLY
V317	M440	T566	E679	THR	LYS	ILE	THR
K318	T456	G568	T680	GLY	LEU	VAL	GLU
K319	L457	F569	K686	VAL	PRO	GLY	VAL
M320	V458	Q570	W692	LEU	TRP	ASP	TRP
I324	R464	G573	Q695	PHE	THR	THR	SER
R327	R464	M574	L701	GLN	LEU	LEU	ALA
N330	GLU	M578	K705	GLY	VAL	VAL	ASP
L333	GLU	I583	L706	PRO	THR	ASN	HIS
R337	ALA	L584	L707	SER	VAL	ILE	TYR
G341	ILE	H585	W710	LYS	GLY	GLN	GLY
P344	HIS	D586	R714	THR	THR	LEU	ASN
I356	PRO	L605	V723	GLY	THR	LYS	THR
Y359	LEU	I609	L749	VAL	VAL	GLY	PRO
I360	THR	E610	G754	PRO	ARG	ASP	VAL
R363	HIS	P613	PRO	LEU	THR	GLY	LEU
E364	LYS	LYS	VAL	VAL	ASP	ILE	ASP
I365	MET	ASP	GLU	GLY	LEU	GLY	ASN
K366	G480	N616	LEU	LEU	MET	ASN	ASN
L373	Q483	C619	ARG	ARG	LYS	HIS	HIS
K376	L484	S620	THR	THR	ARG	ASP	LEU
F377	R487	S621	ALA	VAL	ASP	GLY	THR
I378	M488	Y622	ASP	ASP	PHE	THR	THR
D379	L508	E631	PHE	ASN	GLY	ASN	GLN
W380	ARG	L635	LYS	ASN	LYS	LYS	VAL
S387	PRO	T636	ILE	ILE	ALA	ALA	THR
D391	SER	I637	GLN	SER	PHE	MET	THR
L392	ASP	G638	VAL	VAL	GLY	GLY	GLY
T397	LEU	L639	SER	SER	THR	THR	THR
M401	ILE	N643	ASN	ASN	GLY	GLY	GLY
L404	S518	I644	LYS	LYS	GLY	GLY	GLY
V408	W521	Q645	THR	THR	ASP	ASP	ASP
	A543	N647	LEU	THR	THR	GLN	HIS
		I652	ASN	LEU	ASN	LYS	MET
				GLY	PHE	ASN	VAL
						LEU	LEU

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	347665	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.339	Depositor
Minimum map value	-2.597	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.113	Depositor
Recommended contour level	0.38	Depositor
Map size ( $\text{\AA}$ )	279.04, 279.04, 279.04	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.09, 1.09, 1.09	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 6OU

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	0.42	0/4674	0.49	0/6361
1	B	0.41	0/4688	0.49	0/6378
1	C	0.41	0/4678	0.49	0/6365
1	D	0.43	0/4674	0.49	0/6361
All	All	0.42	0/18714	0.49	0/25465

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	4576	0	4410	112	0
1	B	4590	0	4431	132	0
1	C	4580	0	4421	113	0
1	D	4576	0	4410	98	0
2	A	48	0	0	0	0
2	B	39	0	0	0	0
2	C	47	0	0	0	0
2	D	37	0	0	0	0
All	All	18493	0	17672	423	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 12.

The worst 5 of 423 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:B:456:THR:HA	1:B:555:MET:SD	1.90	1.11
1:D:456:THR:HA	1:D:555:MET:SD	1.94	1.07
1:B:635:LEU:CD1	1:A:639:LEU:HD11	1.93	0.98
1:C:639:LEU:HD11	1:D:635:LEU:CD1	1.94	0.97
1:A:635:LEU:CD1	1:D:639:LEU:HD11	1.94	0.96

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	597/1061 (56%)	544 (91%)	53 (9%)	0	100	100
1	B	597/1061 (56%)	543 (91%)	54 (9%)	0	100	100
1	C	597/1061 (56%)	544 (91%)	53 (9%)	0	100	100
1	D	597/1061 (56%)	546 (92%)	50 (8%)	1 (0%)	47	80
All	All	2388/4244 (56%)	2177 (91%)	210 (9%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	619	CYS

### 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	433/933 (46%)	421 (97%)	12 (3%)	43	73
1	B	437/933 (47%)	428 (98%)	9 (2%)	53	79
1	C	434/933 (46%)	426 (98%)	8 (2%)	59	81
1	D	433/933 (46%)	418 (96%)	15 (4%)	36	68
All	All	1737/3732 (46%)	1693 (98%)	44 (2%)	50	76

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	679	GLU
1	D	293	ASP
1	D	178	ASN
1	D	240	ASP
1	D	458	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	297	ASN
1	D	585	HIS
1	A	410	ASN
1	D	346	GLN
1	A	346	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

14 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	$\# Z  > 2$
2	6OU	A	1404	-	7,7,48	0.39	0	5,6,53	0.65	0
2	6OU	C	1702	-	11,11,48	0.34	0	9,10,53	0.75	0
2	6OU	C	1703	-	12,12,48	0.31	0	11,11,53	0.78	0
2	6OU	B	1501	-	13,13,48	0.29	0	12,12,53	0.81	0
2	6OU	D	1703	-	13,13,48	0.30	0	12,12,53	0.79	0
2	6OU	B	1502	-	10,10,48	0.38	0	9,9,53	0.89	0
2	6OU	C	1701	-	7,7,48	0.39	0	5,6,53	0.65	0
2	6OU	C	1704	-	13,13,48	0.31	0	12,12,53	0.81	0
2	6OU	B	1503	-	13,13,48	0.30	0	12,12,53	0.78	0
2	6OU	A	1402	-	13,13,48	0.29	0	12,12,53	0.73	0
2	6OU	D	1701	-	13,13,48	0.29	0	12,12,53	0.80	0
2	6OU	D	1702	-	8,8,48	0.26	0	7,7,53	0.80	0
2	6OU	A	1403	-	11,11,48	0.33	0	9,10,53	0.82	0
2	6OU	A	1401	-	13,13,48	0.30	0	12,12,53	0.75	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
2	6OU	A	1404	-	-	2/5/5/52	-
2	6OU	C	1702	-	-	3/9/9/52	-
2	6OU	C	1703	-	-	3/10/10/52	-
2	6OU	B	1501	-	-	4/11/11/52	-
2	6OU	D	1703	-	-	4/11/11/52	-
2	6OU	B	1502	-	-	4/8/8/52	-
2	6OU	C	1701	-	-	2/5/5/52	-
2	6OU	C	1704	-	-	4/11/11/52	-
2	6OU	B	1503	-	-	6/11/11/52	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	6OU	A	1402	-	-	4/11/11/52	-
2	6OU	D	1701	-	-	1/11/11/52	-
2	6OU	D	1702	-	-	0/6/6/52	-
2	6OU	A	1403	-	-	3/9/9/52	-
2	6OU	A	1401	-	-	7/11/11/52	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

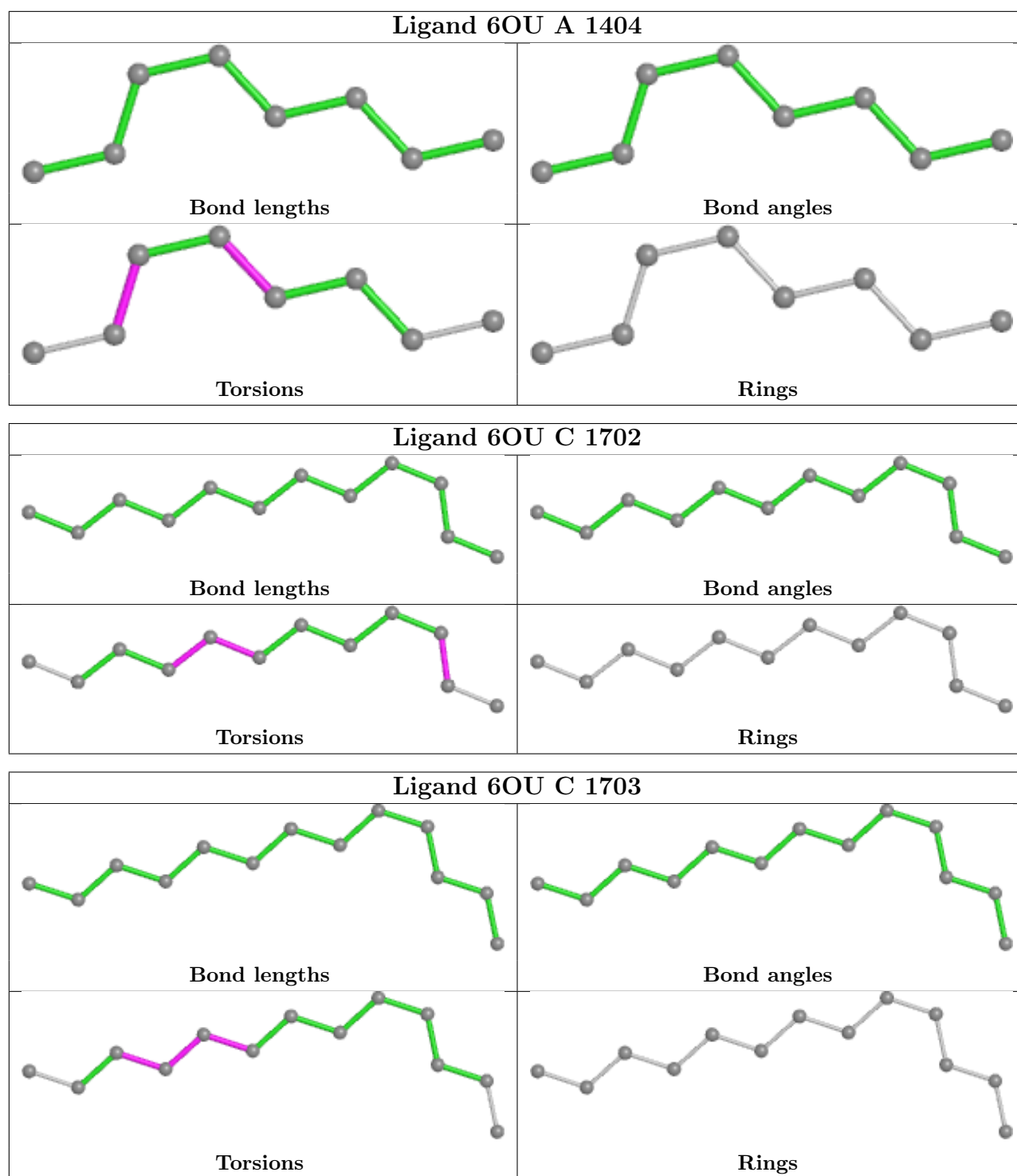
5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1702	6OU	C38-C39-C40-C41
2	A	1403	6OU	C44-C45-C46-C47
2	A	1401	6OU	C42-C43-C44-C45
2	B	1503	6OU	C44-C45-C46-C47
2	A	1401	6OU	C43-C44-C45-C46

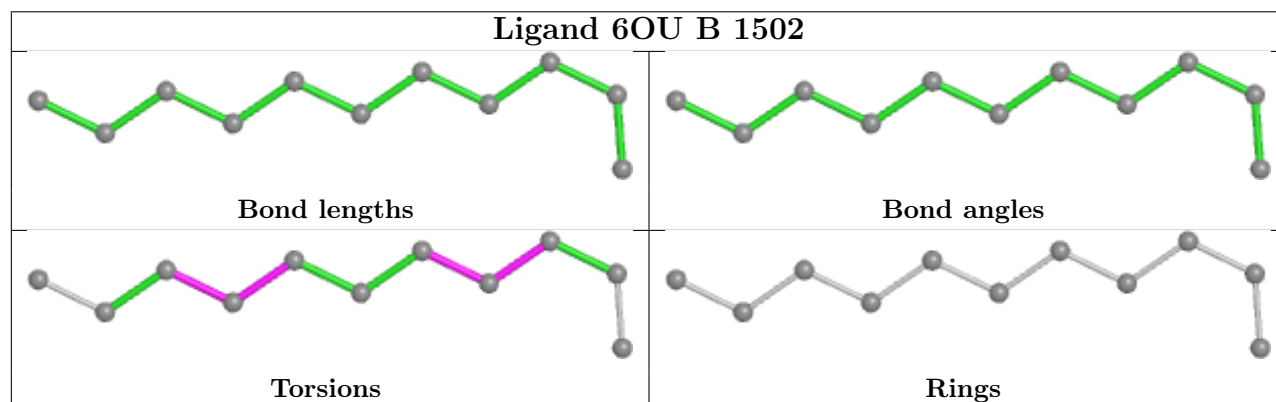
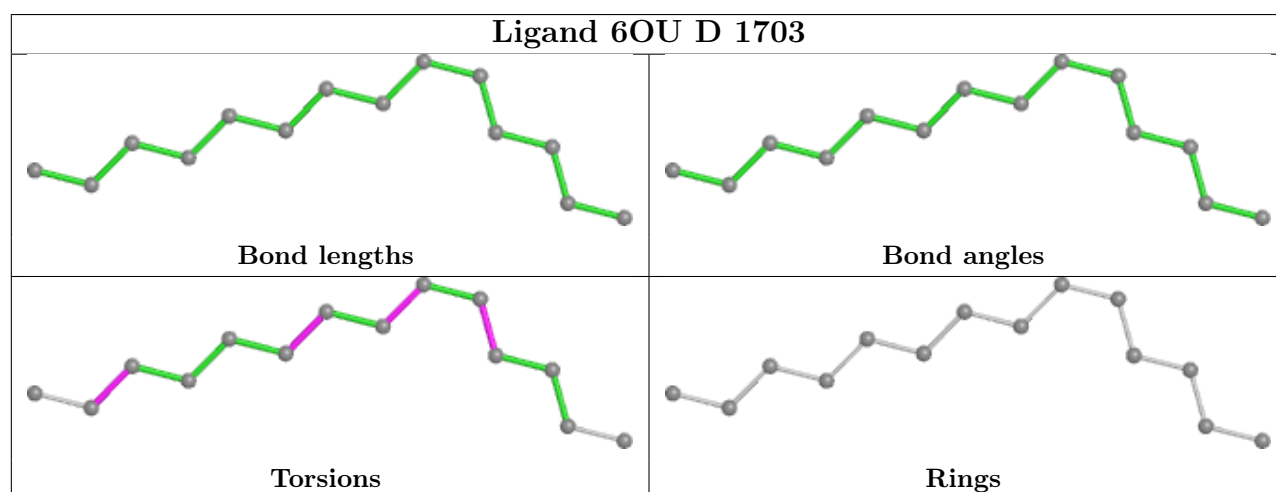
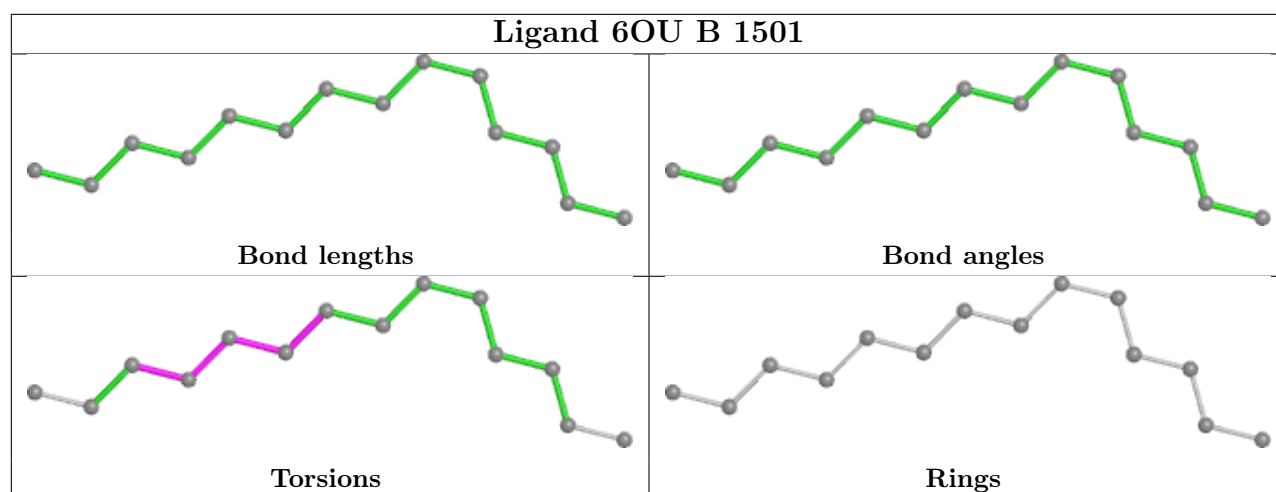
There are no ring outliers.

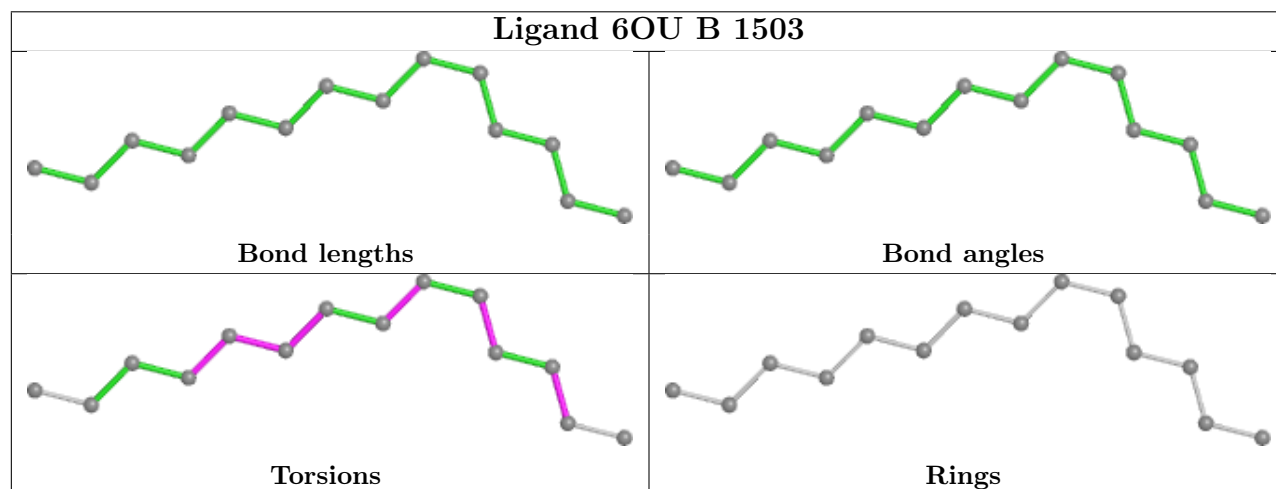
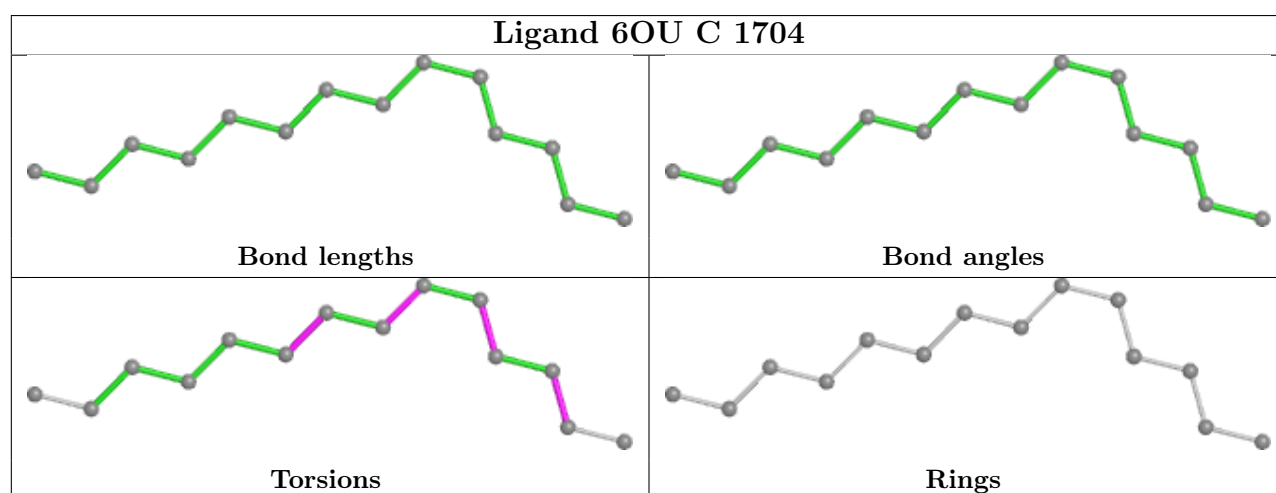
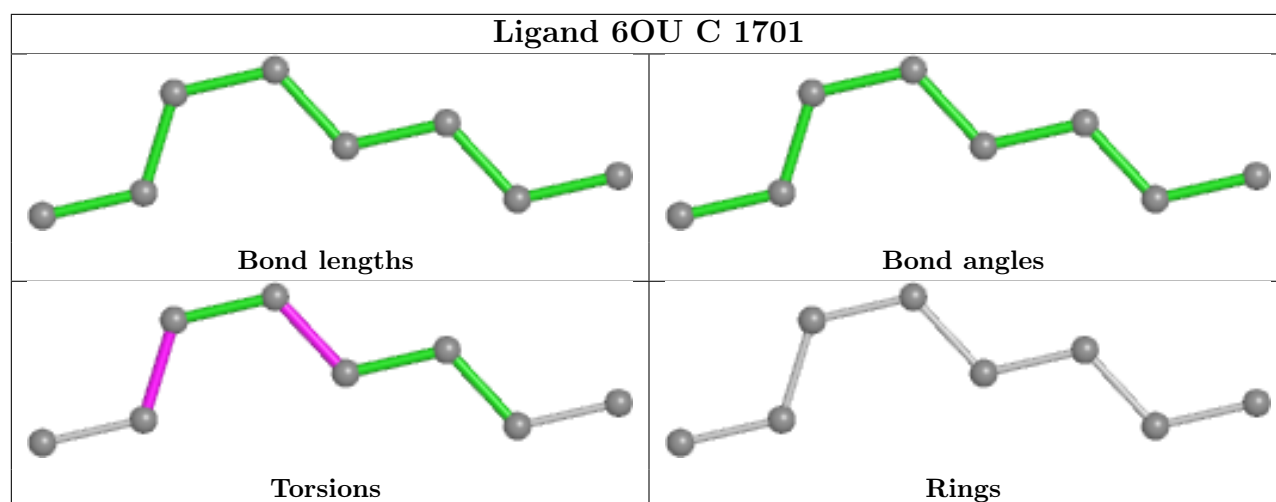
No monomer is involved in short contacts.

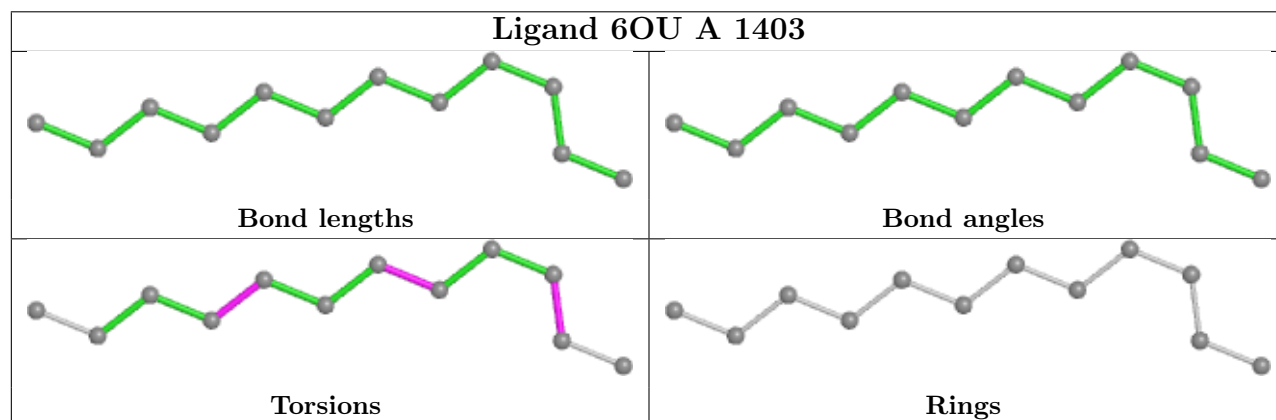
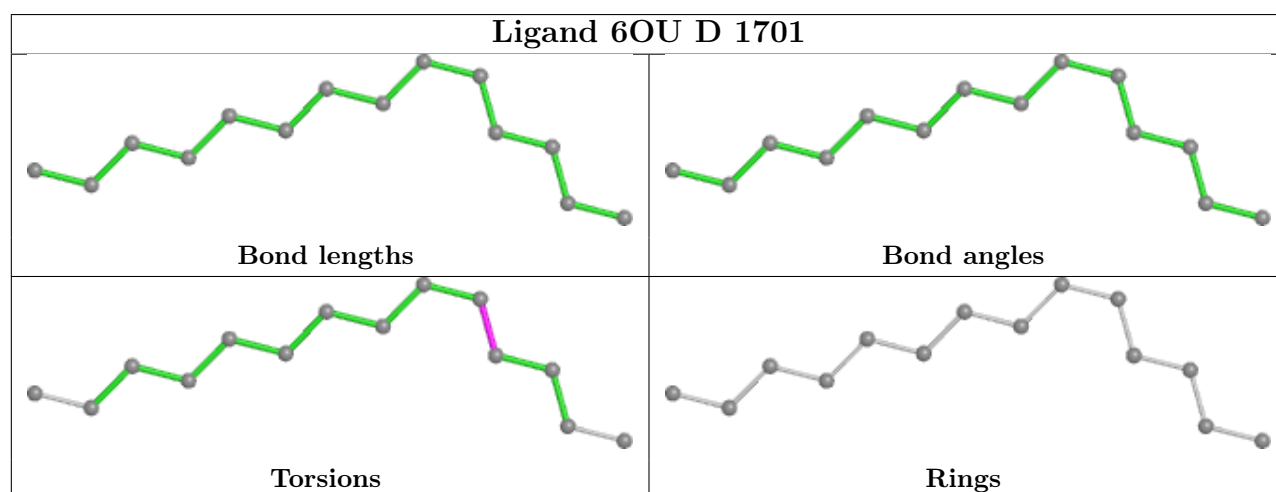
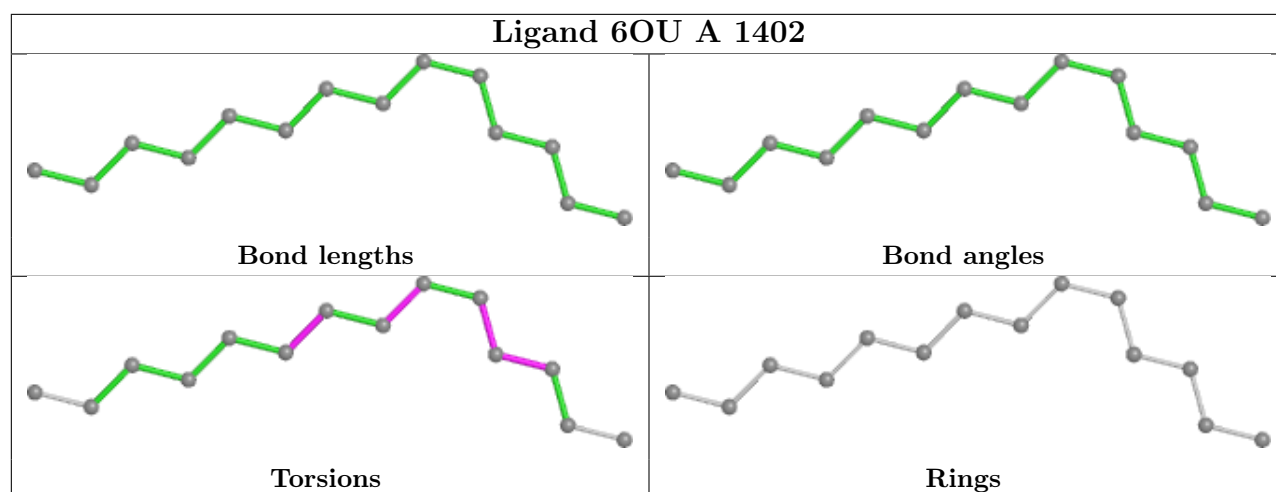
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

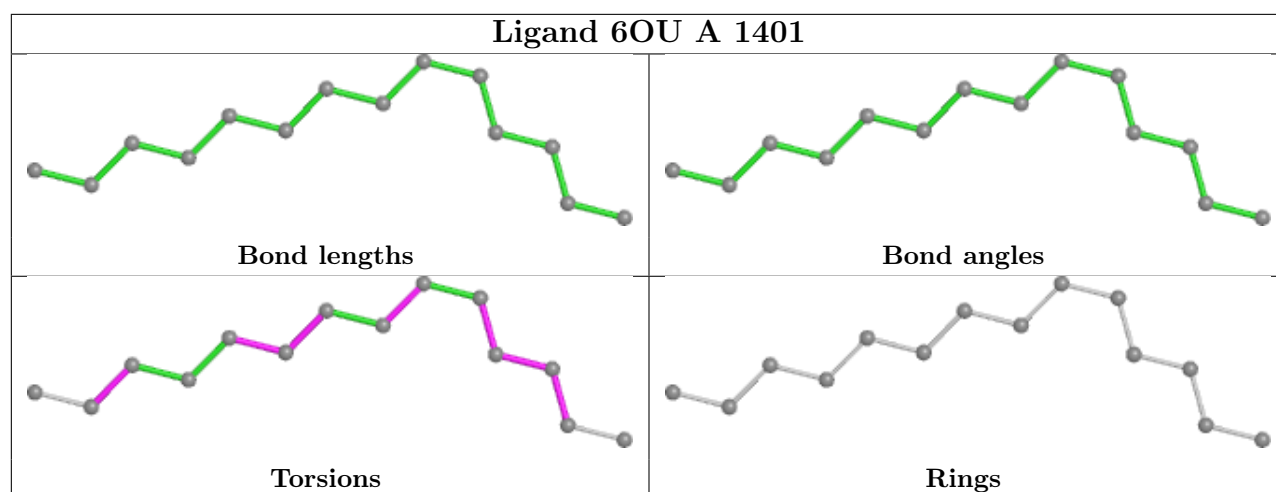












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

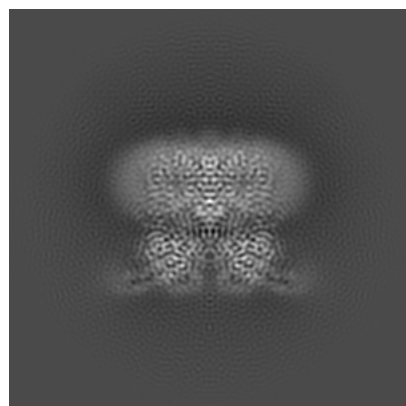
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33218. These allow visual inspection of the internal detail of the map and identification of artifacts.

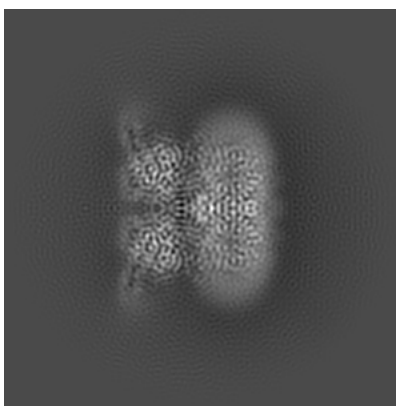
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

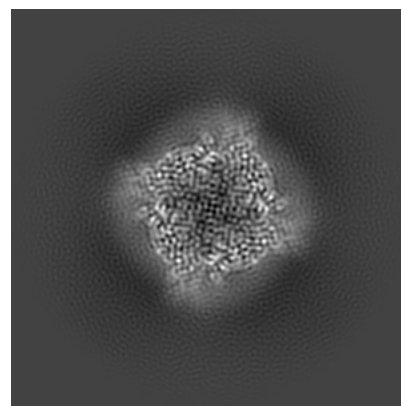
#### 6.1.1 Primary map



X

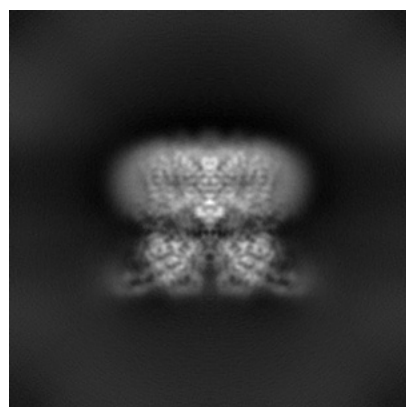


Y

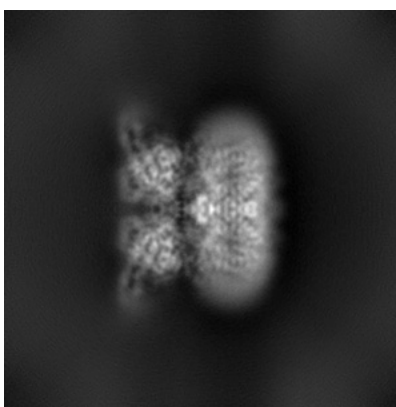


Z

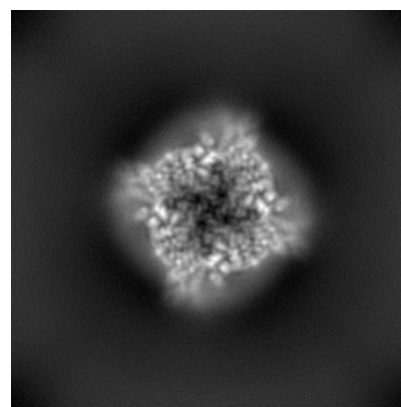
#### 6.1.2 Raw map



X



Y

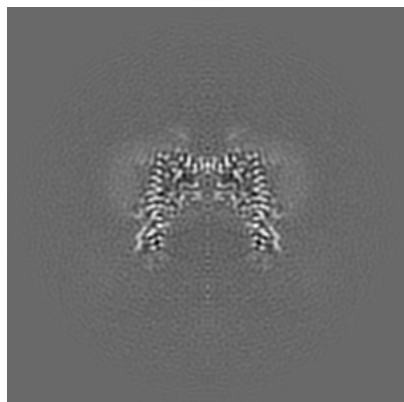


Z

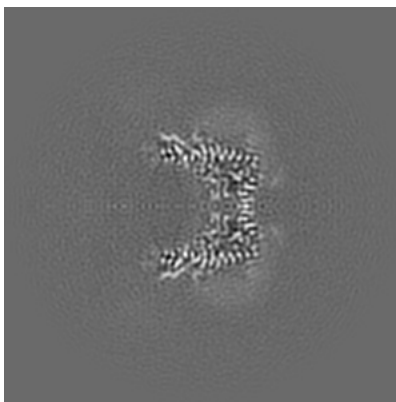
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

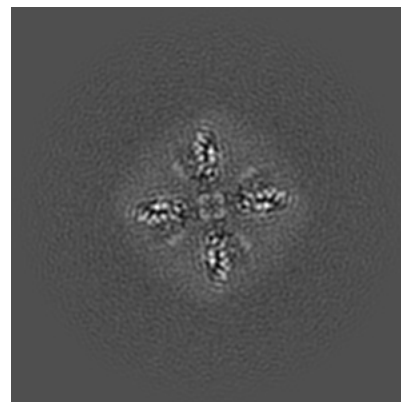
### 6.2.1 Primary map



X Index: 128

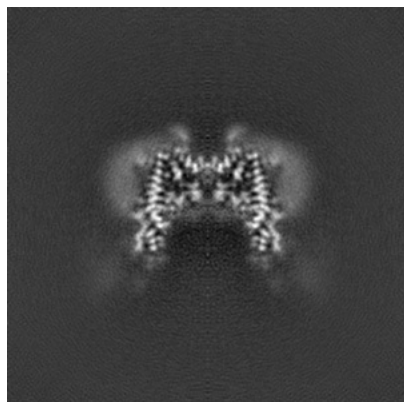


Y Index: 128

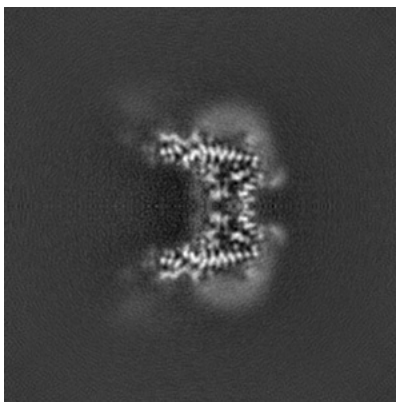


Z Index: 128

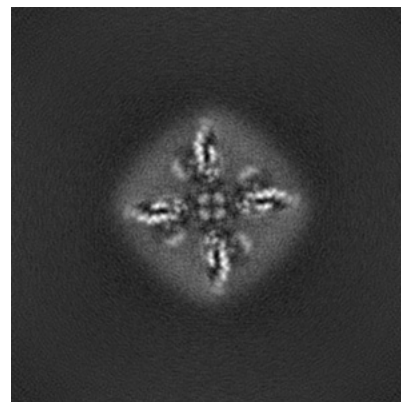
### 6.2.2 Raw map



X Index: 128



Y Index: 128

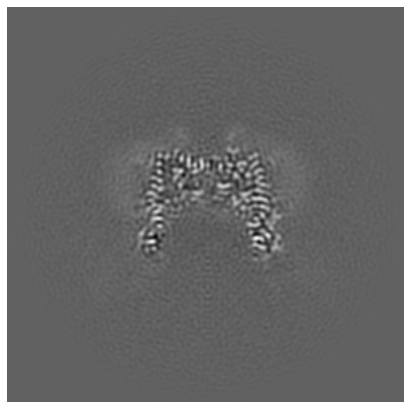


Z Index: 128

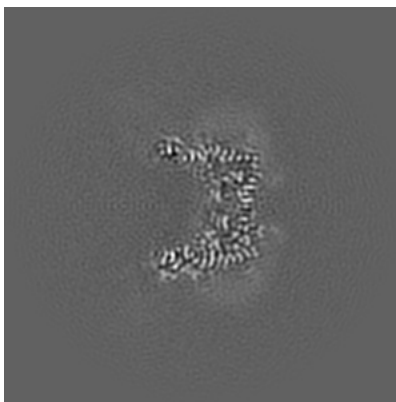
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

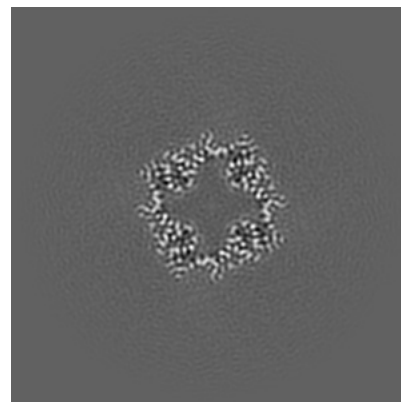
### 6.3.1 Primary map



X Index: 127

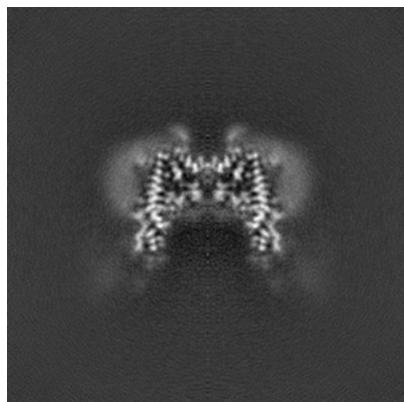


Y Index: 127

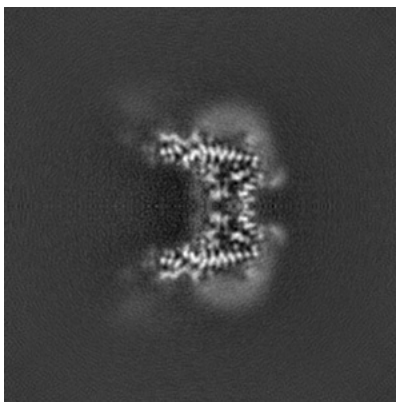


Z Index: 101

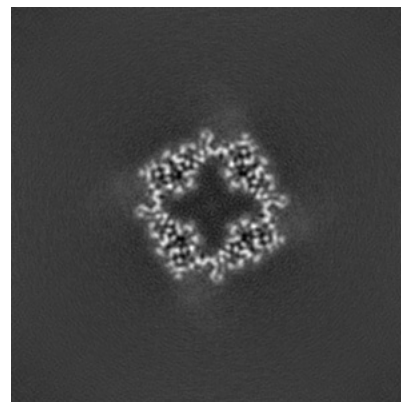
### 6.3.2 Raw map



X Index: 128



Y Index: 128

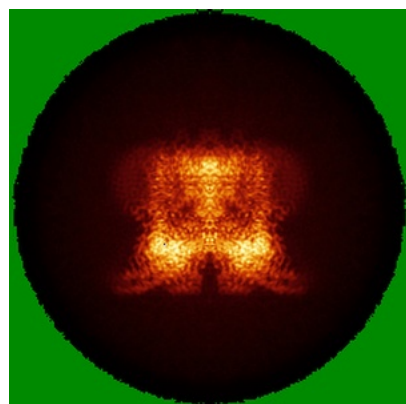


Z Index: 101

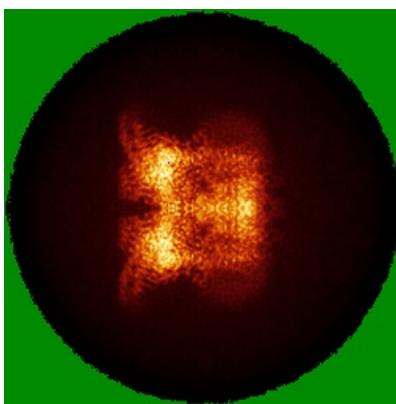
The images above show the largest variance slices of the map in three orthogonal directions.

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

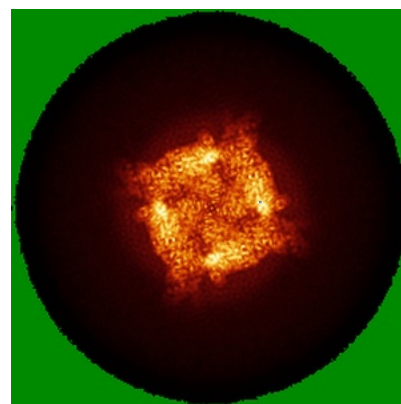
### 6.4.1 Primary map



X

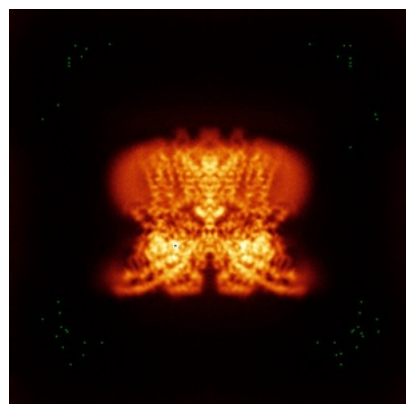


Y

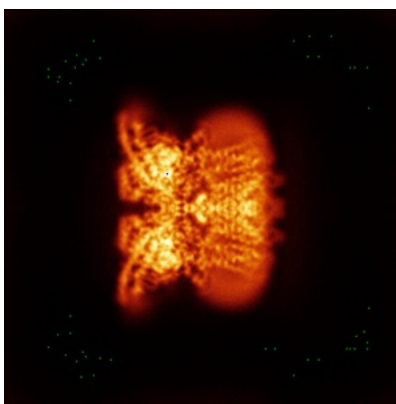


Z

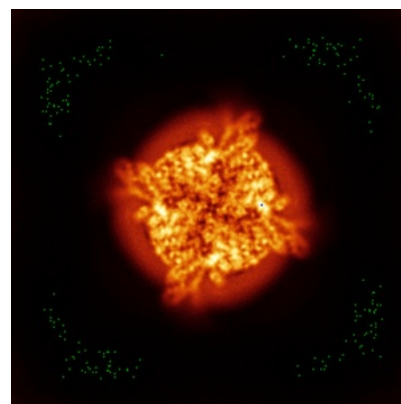
### 6.4.2 Raw map



X



Y



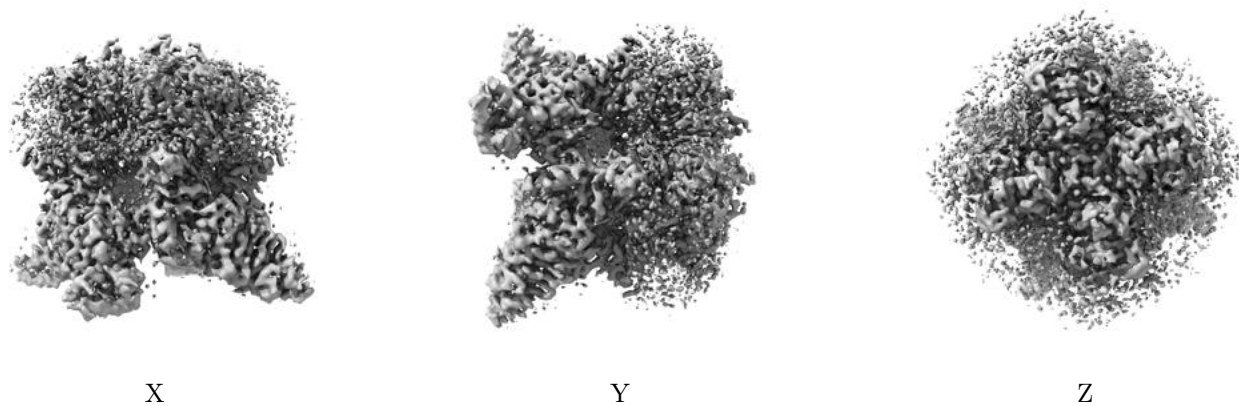
Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



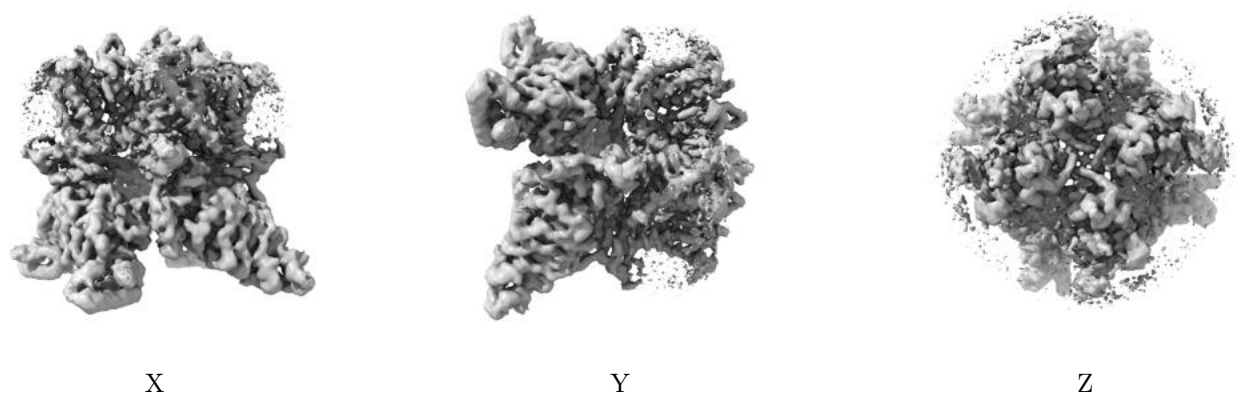
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.38. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

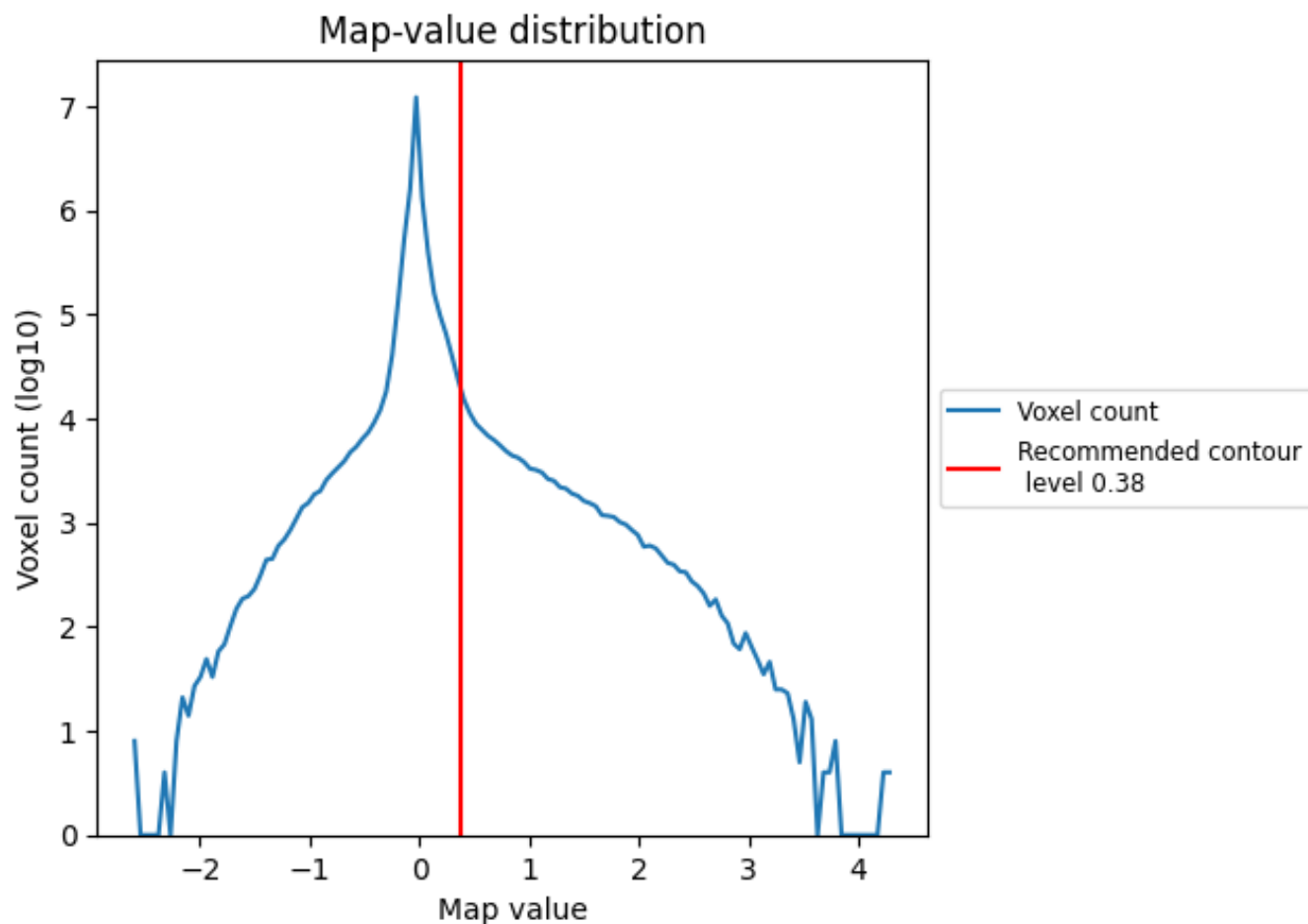
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

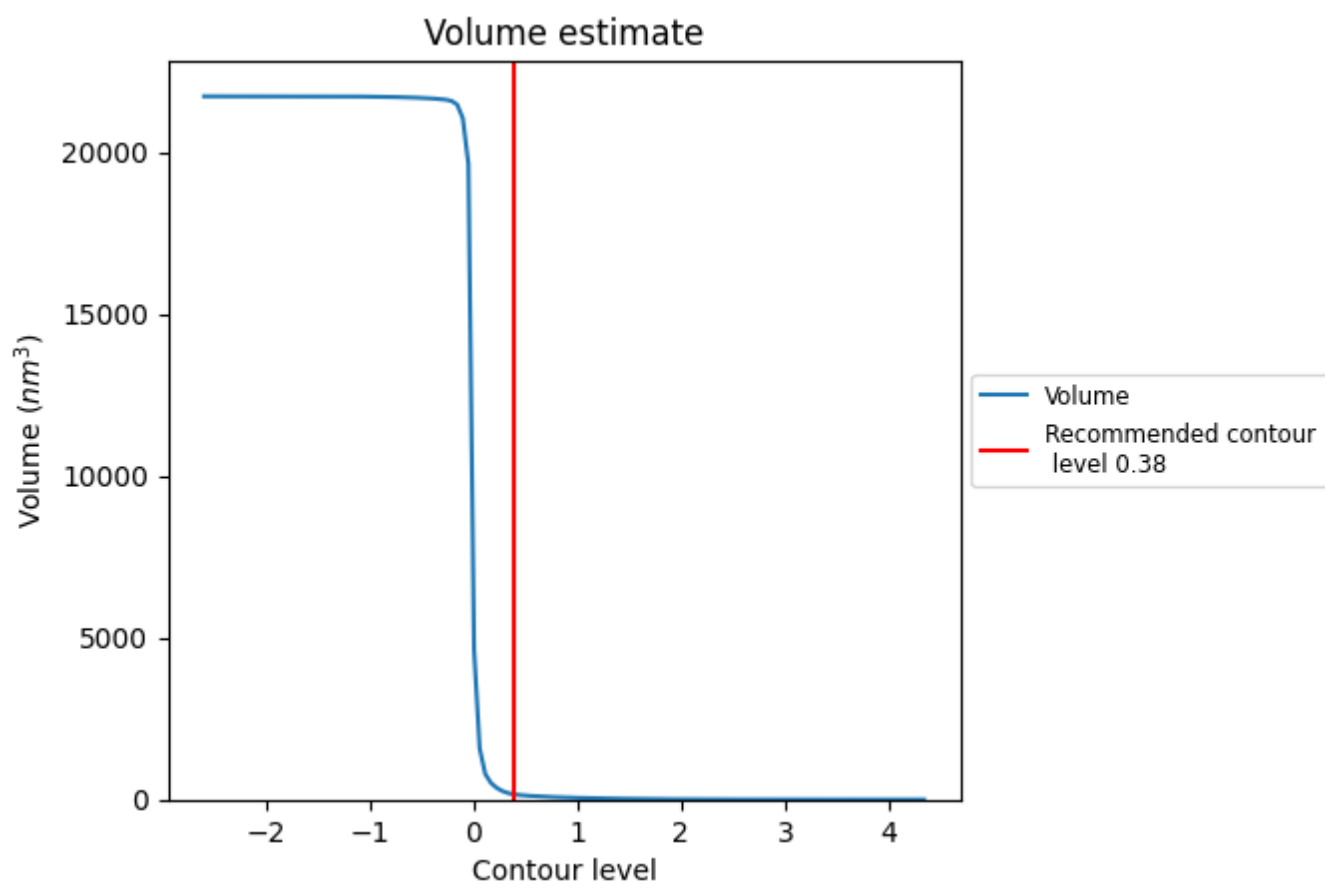
This section contains the results of statistical analysis of the map.

### 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.

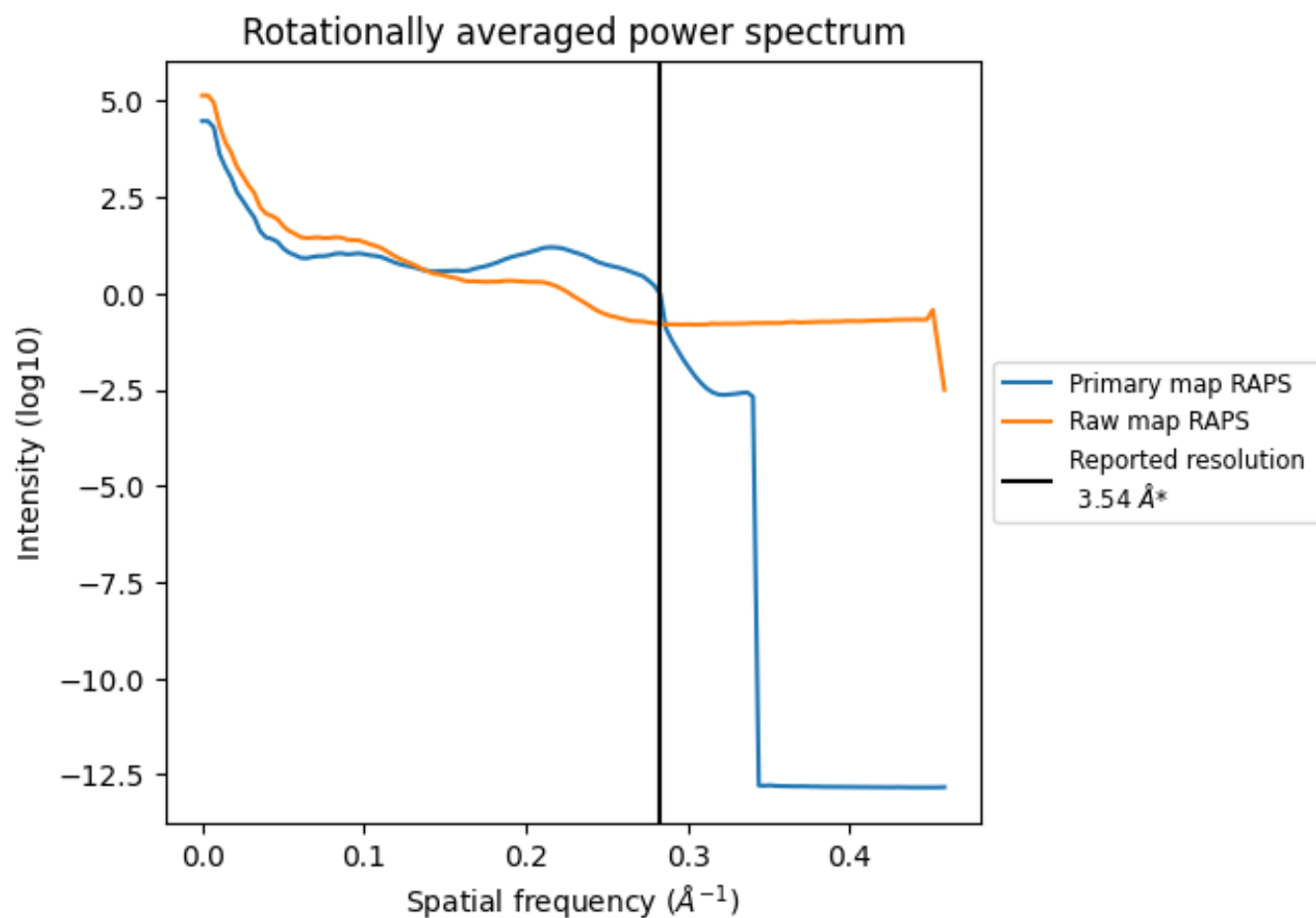
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 167 nm<sup>3</sup>; this corresponds to an approximate mass of 151 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ

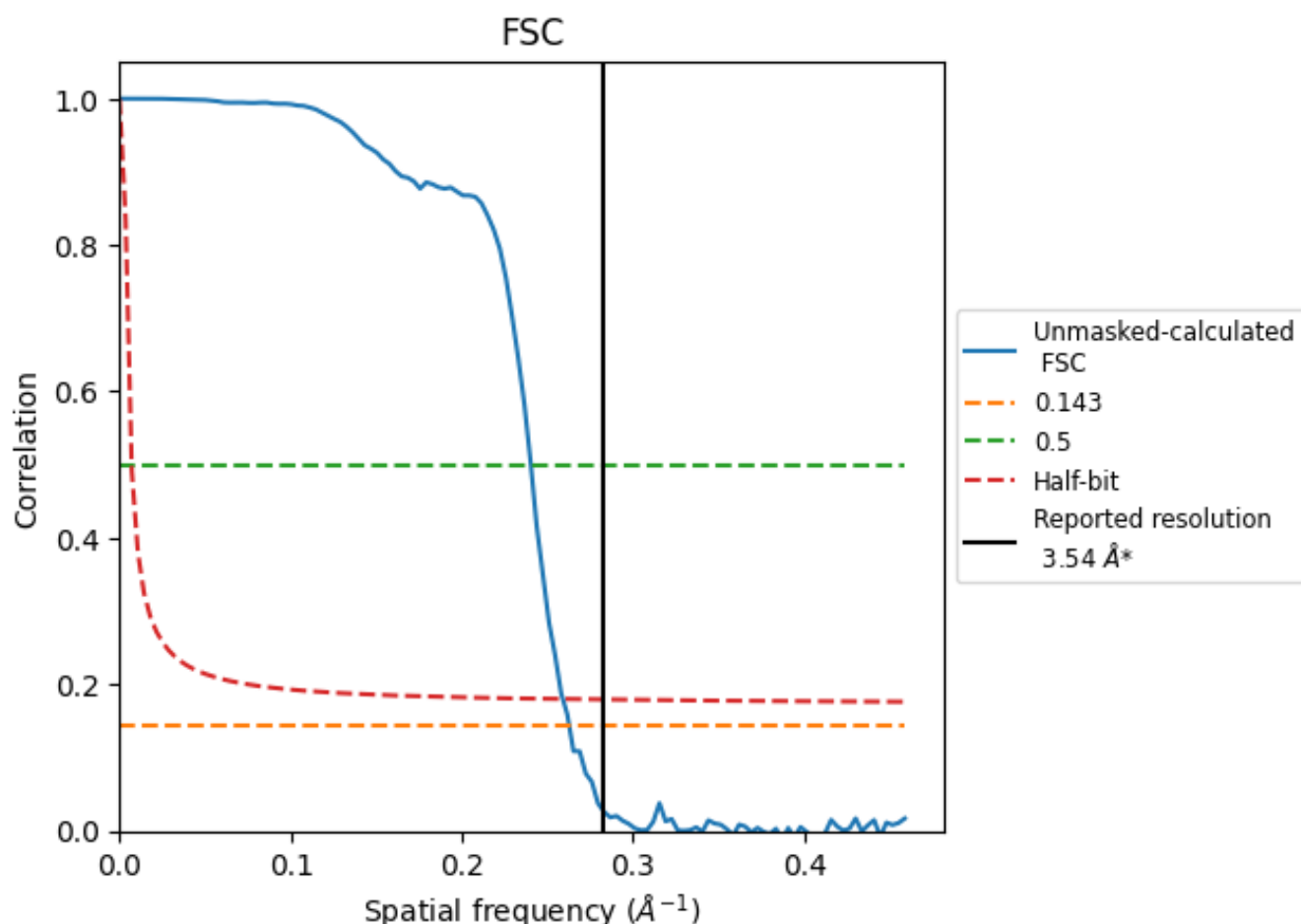


\*Reported resolution corresponds to spatial frequency of 0.282  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.282 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

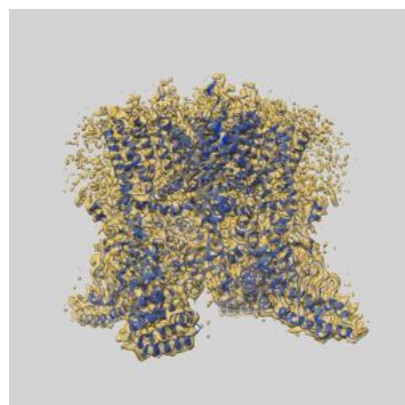
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.81	4.16	3.86

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

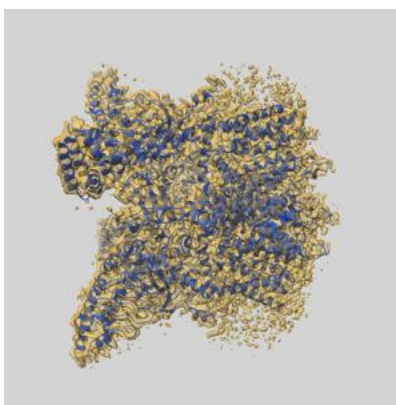
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33218 and PDB model 7XJ3. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

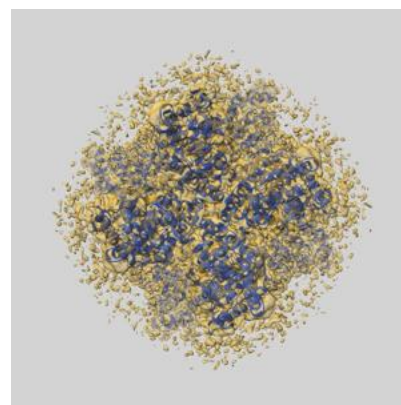
### 9.1 Map-model overlay [i](#)



X



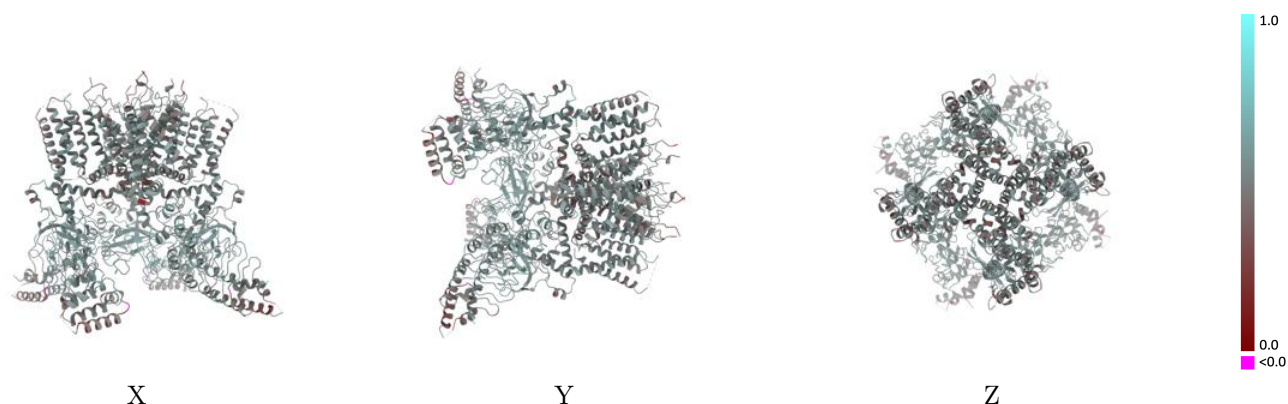
Y



Z

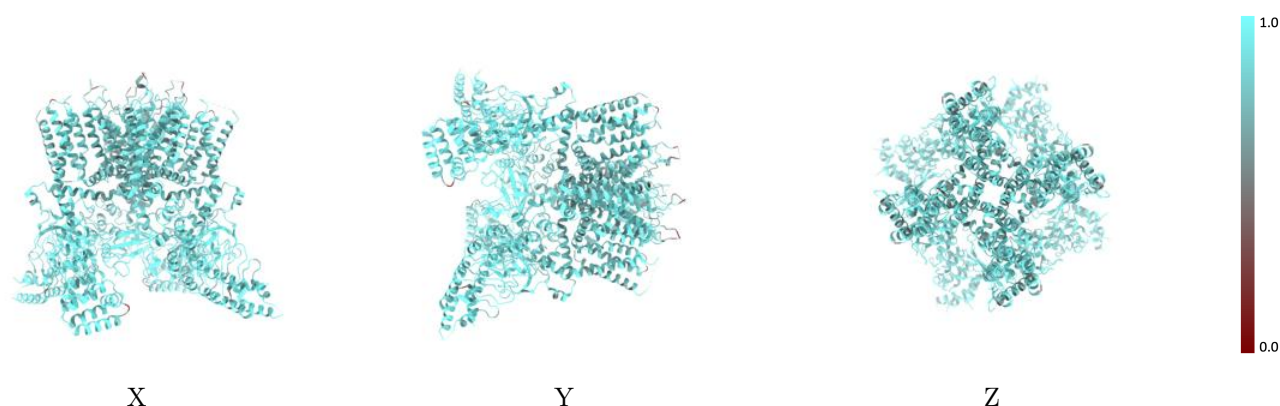
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

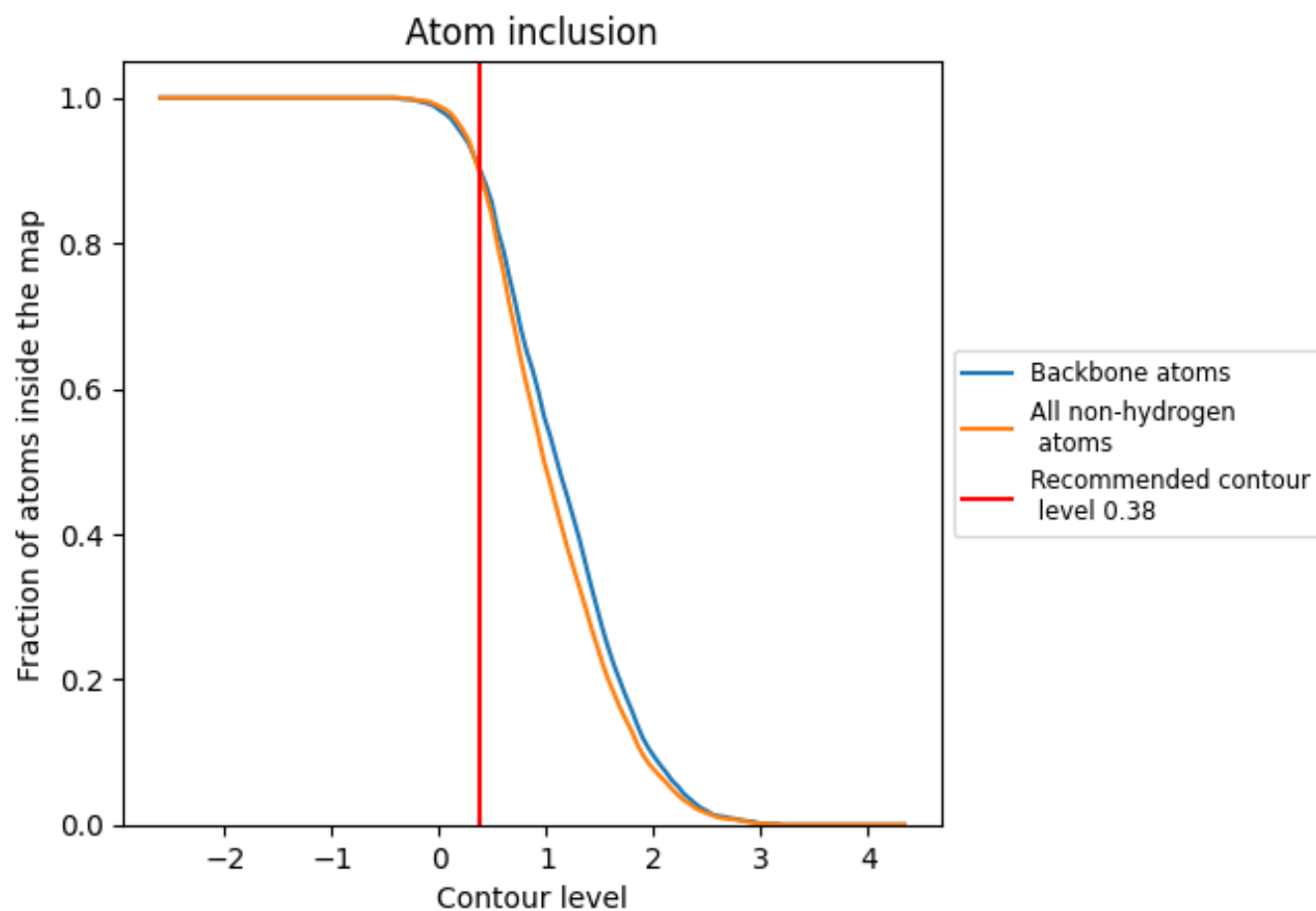
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.38).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 90% 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 (0.38) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8960	<div><div></div></div> 0.5210
A	<div><div></div></div> 0.8960	<div><div></div></div> 0.5220
B	<div><div></div></div> 0.8950	<div><div></div></div> 0.5200
C	<div><div></div></div> 0.8970	<div><div></div></div> 0.5200
D	<div><div></div></div> 0.8980	<div><div></div></div> 0.5220

