



## wwPDB EM Validation Summary Report ⓘ

Sep 16, 2025 – 02:11 PM JST

PDB ID : 8YRA / pdb\_00008yra  
EMDB ID : EMD-39539  
Title : The Cryo-EM Structure of human SLC26A3 with specific inhibitor DRAinh-A250  
Authors : Feng, J.R.; Dang, S.  
Deposited on : 2024-03-20  
Resolution : 3.78 Å(reported)  
Based on initial model : .

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.dev126  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

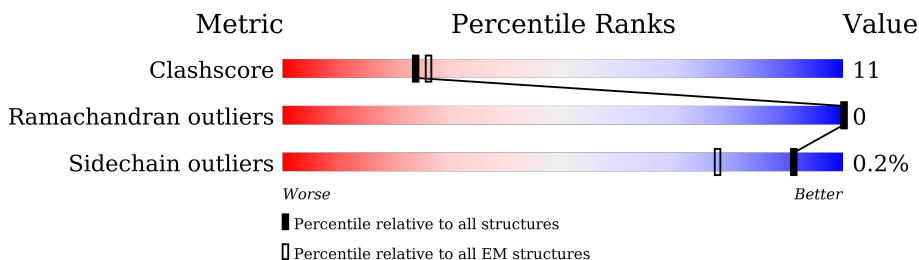
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.78 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	764	 68% 24% 8%
1	B	764	 70% 22% 8%

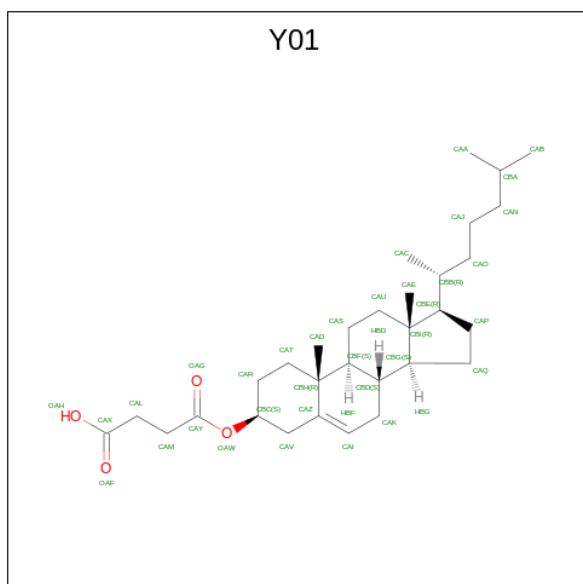


In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Chloride anion exchanger.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	703	Total 5486	C 3601	N 897	O 968	S 20	0	0
1	B	703	Total 5486	C 3601	N 897	O 968	S 20	0	0

- Molecule 2 is CHOLESTEROL HEMISUCCINATE (CCD ID: Y01) (formula:  $\text{C}_{31}\text{H}_{50}\text{O}_4$ ) (labeled as "Ligand of Interest" by depositor).



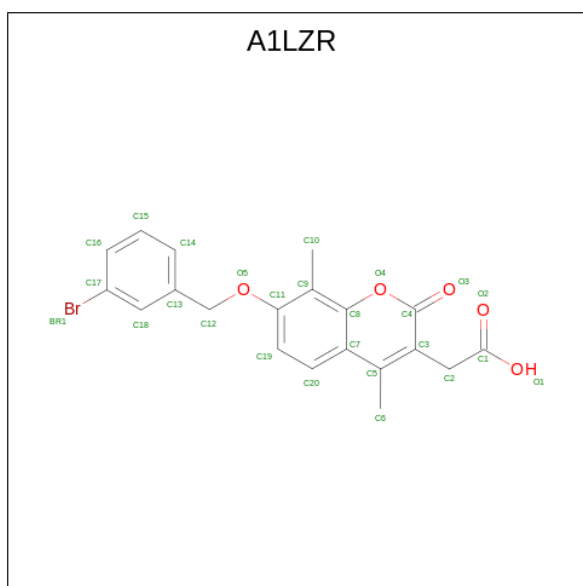
Mol	Chain	Residues	Atoms			AltConf
2	A	1	Total 35	C 31	O 4	0
2	A	1	Total 35	C 31	O 4	0
2	A	1	Total 35	C 31	O 4	0
2	A	1	Total 35	C 31	O 4	0

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Mol	Chain	Residues	Atoms			AltConf
2	B	1	Total	C	O	0
			35	31	4	
2	B	1	Total	C	O	0
			35	31	4	
2	B	1	Total	C	O	0
			35	31	4	
2	B	1	Total	C	O	0
			35	31	4	

- Molecule 3 is 2-[7-[(3-bromophenyl)methoxy]-4,8-dimethyl-2-oxidanylidene-chromen-3-yl]ethanoic acid (CCD ID: A1LZR) (formula: C<sub>20</sub>H<sub>17</sub>BrO<sub>5</sub>) (labeled as "Ligand of Interest" by depositor).

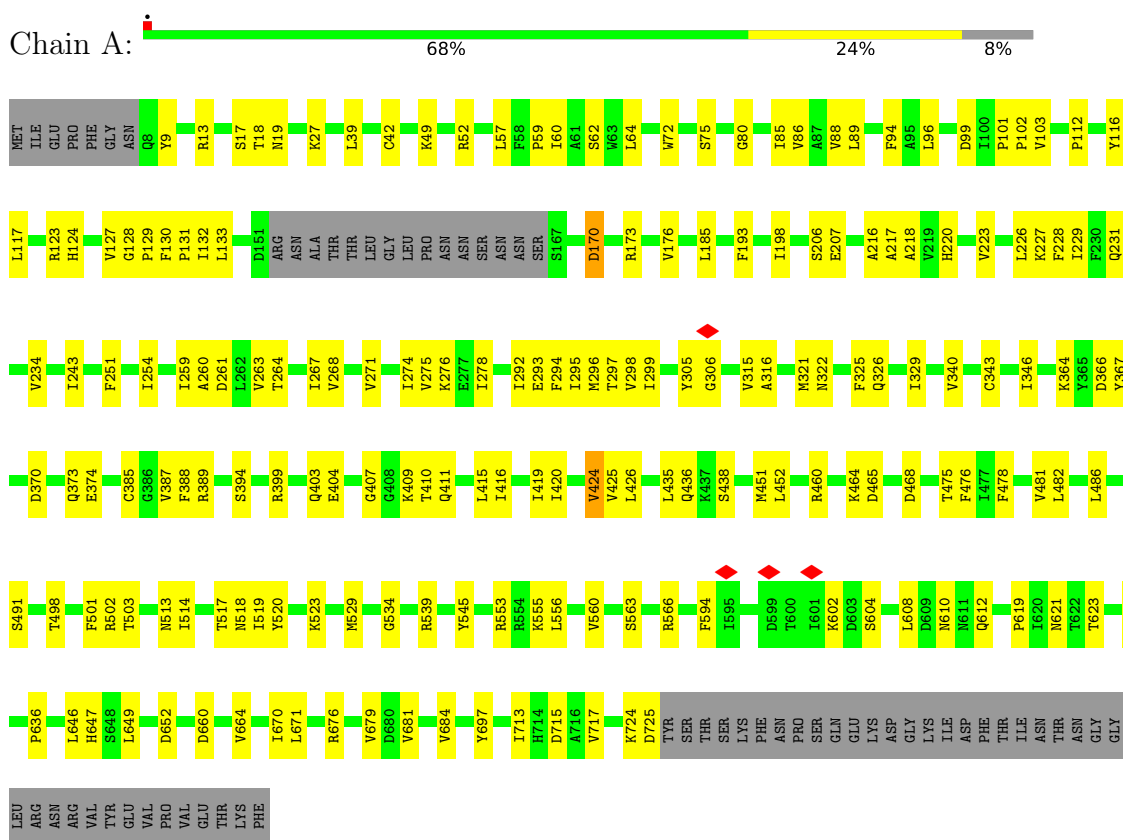


Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	Br	C	O	0
			26	1	20	5	
3	B	1	Total	Br	C	O	0
			26	1	20	5	

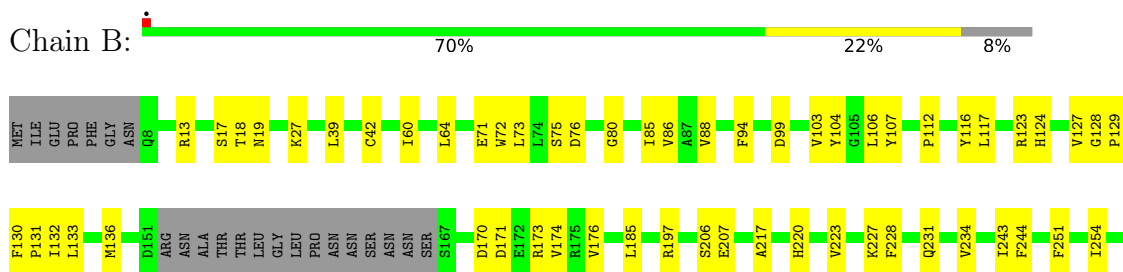
### 3 Residue-property plots

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: Chloride anion exchanger



- Molecule 1: Chloride anion exchanger



THR LYS PHE	D652	N518	E404	D261
	D660	I519	G407	T264
	V664	K523	A413	I267
	I670	M529	G414	V271
	L671	G534	I416	
	R676	G539	I420	I274
	V681	Y545	V425	V275
	V684	R553	I428	I278
	Y697	L556	L431	I292
	I713	S563	L432	E293
	H714	R566	A433	F294
	V717	K570	P434	G306
			L435	V315
			Q436	A316
D725	K579	K437	N322	
TYR		S438	F325	
SER	F594	L448	Q326	
THR	I595	M451	I329	
LYS	D599	F455	C343	
PHE	T600	R460	I346	
ASN	I601	K464	V349	
PRO	K602	D465		
SER	D603	K466	S362	
GLN	S604	Y467	L363	
GLU	L608	D468	K364	
LYS	D609	F478	Y365	
ASP	N610	V481	D366	
GLY	N611	L482	Y367	
LYS	Q612	G483	P368	
ASP	P619	L484	L369	
GLY	D624	L488	D370	
LYS	I629	Q495	G371	
ILE	D633	T498	N372	
ASN	D634	F501	Q373	
THR	L635	R502	E374	
ASN	P636	T503	C385	
GLY	E640	N513	G386	
GLY	V641	I514	V387	
LEU	P642	T517	F388	
ARG	H647		R389	
ARG	S648		S394	
VAL	L649		R399	
TYR			Q403	
GLU				

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	218752	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 ( $e^-/\text{\AA}^2$ )	50.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.688	Depositor
Minimum map value	-1.637	Depositor
Average map value	0.019	Depositor
Map value standard deviation	0.089	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	233.19998, 233.19998, 233.19998	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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: Y01, A1LZR

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	0.15	0/5605	0.31	0/7608
1	B	0.15	0/5605	0.31	0/7608
All	All	0.15	0/11210	0.31	0/15216

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	5486	0	5698	130	0
1	B	5486	0	5698	127	0
2	A	140	0	196	7	0
2	B	140	0	196	6	0
3	A	26	0	0	1	0
3	B	26	0	0	1	0
All	All	11304	0	11788	248	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 11.

The worst 5 of 248 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:264:THR:HG21	1:B:436:GLN:HE21	1.36	0.89
1:A:275:VAL:HG11	1:A:292:ILE:HG12	1.58	0.84
1:B:326:GLN:HB3	1:B:389:ARG:HH11	1.47	0.79
1:A:60:ILE:HD11	1:A:64:LEU:HD22	1.64	0.79
1:B:85:ILE:HG21	1:B:294:PHE:HB2	1.66	0.78

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	699/764 (92%)	654 (94%)	45 (6%)	0	100	100
1	B	699/764 (92%)	652 (93%)	47 (7%)	0	100	100
All	All	1398/1528 (92%)	1306 (93%)	92 (7%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	606/661 (92%)	603 (100%)	3 (0%)	86	91
1	B	606/661 (92%)	606 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1212/1322 (92%)	1209 (100%)	3 (0%)	91	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	170	ASP
1	A	424	VAL
1	A	679	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	618	GLN
1	B	695	ASN
1	A	695	ASN
1	B	25	HIS
1	B	237	HIS

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

10 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	Y01	A	803	-	38,38,38	0.56	0	57,57,57	0.66	0
2	Y01	A	802	-	38,38,38	0.54	0	57,57,57	0.55	0
2	Y01	B	801	-	38,38,38	0.53	0	57,57,57	0.57	0
2	Y01	A	801	-	38,38,38	0.55	0	57,57,57	0.62	0
2	Y01	B	803	-	38,38,38	0.56	0	57,57,57	0.71	0
2	Y01	B	804	-	38,38,38	0.56	0	57,57,57	0.69	0
3	A1LZR	B	805	-	28,28,28	3.35	8 (28%)	35,40,40	1.48	7 (20%)
2	Y01	B	802	-	38,38,38	0.55	0	57,57,57	0.63	0
2	Y01	A	804	-	38,38,38	0.57	0	57,57,57	0.76	0
3	A1LZR	A	805	-	28,28,28	3.35	8 (28%)	35,40,40	1.61	7 (20%)

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	Y01	A	803	-	-	11/19/77/77	0/4/4/4
2	Y01	A	802	-	-	6/19/77/77	0/4/4/4
2	Y01	B	801	-	-	6/19/77/77	0/4/4/4
2	Y01	A	801	-	-	9/19/77/77	0/4/4/4
2	Y01	B	803	-	-	7/19/77/77	0/4/4/4
2	Y01	B	804	-	-	14/19/77/77	0/4/4/4
3	A1LZR	B	805	-	-	5/9/9/9	0/3/3/3
2	Y01	B	802	-	-	6/19/77/77	0/4/4/4
2	Y01	A	804	-	-	13/19/77/77	0/4/4/4
3	A1LZR	A	805	-	-	6/9/9/9	0/3/3/3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	805	A1LZR	O3-C4	9.01	1.40	1.21
3	B	805	A1LZR	O3-C4	9.00	1.40	1.21
3	A	805	A1LZR	C18-C13	8.16	1.53	1.39
3	B	805	A1LZR	C18-C13	8.06	1.53	1.39
3	A	805	A1LZR	C16-C17	6.96	1.52	1.38

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	805	A1LZR	O5-C11-C9	4.91	120.40	115.33
3	B	805	A1LZR	O5-C11-C9	4.15	119.61	115.33
3	B	805	A1LZR	C6-C5-C3	-3.13	119.23	124.29
3	A	805	A1LZR	C6-C5-C3	-3.02	119.41	124.29
3	B	805	A1LZR	O4-C4-O3	2.87	120.00	116.22

There are no chirality outliers.

5 of 83 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	803	Y01	CAR-CBC-OAW-CAY
2	A	804	Y01	OAG-CAY-OAW-CBC
2	A	804	Y01	CAM-CAY-OAW-CBC
2	B	802	Y01	CAM-CAY-OAW-CBC
2	B	804	Y01	CAM-CAY-OAW-CBC

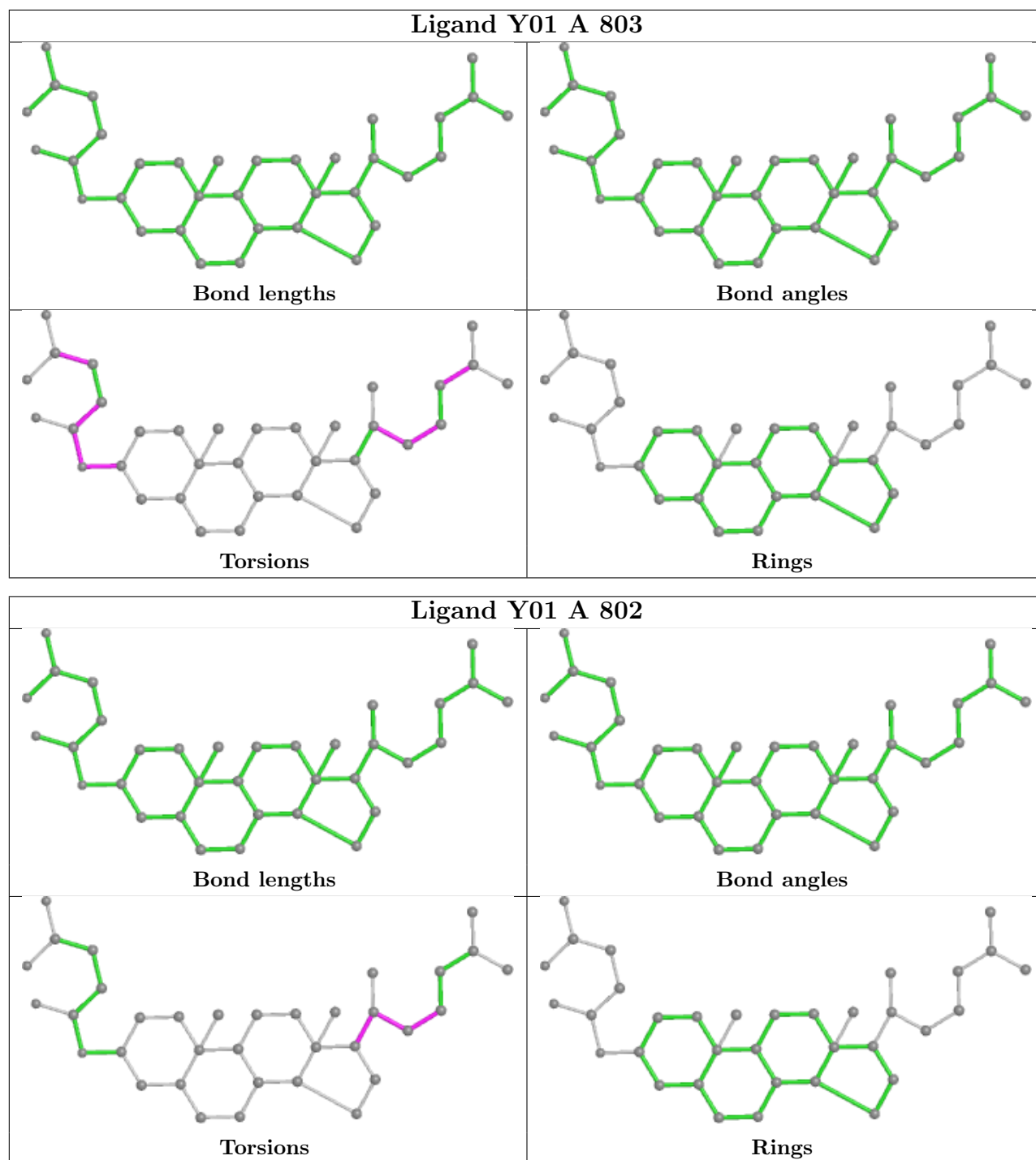
There are no ring outliers.

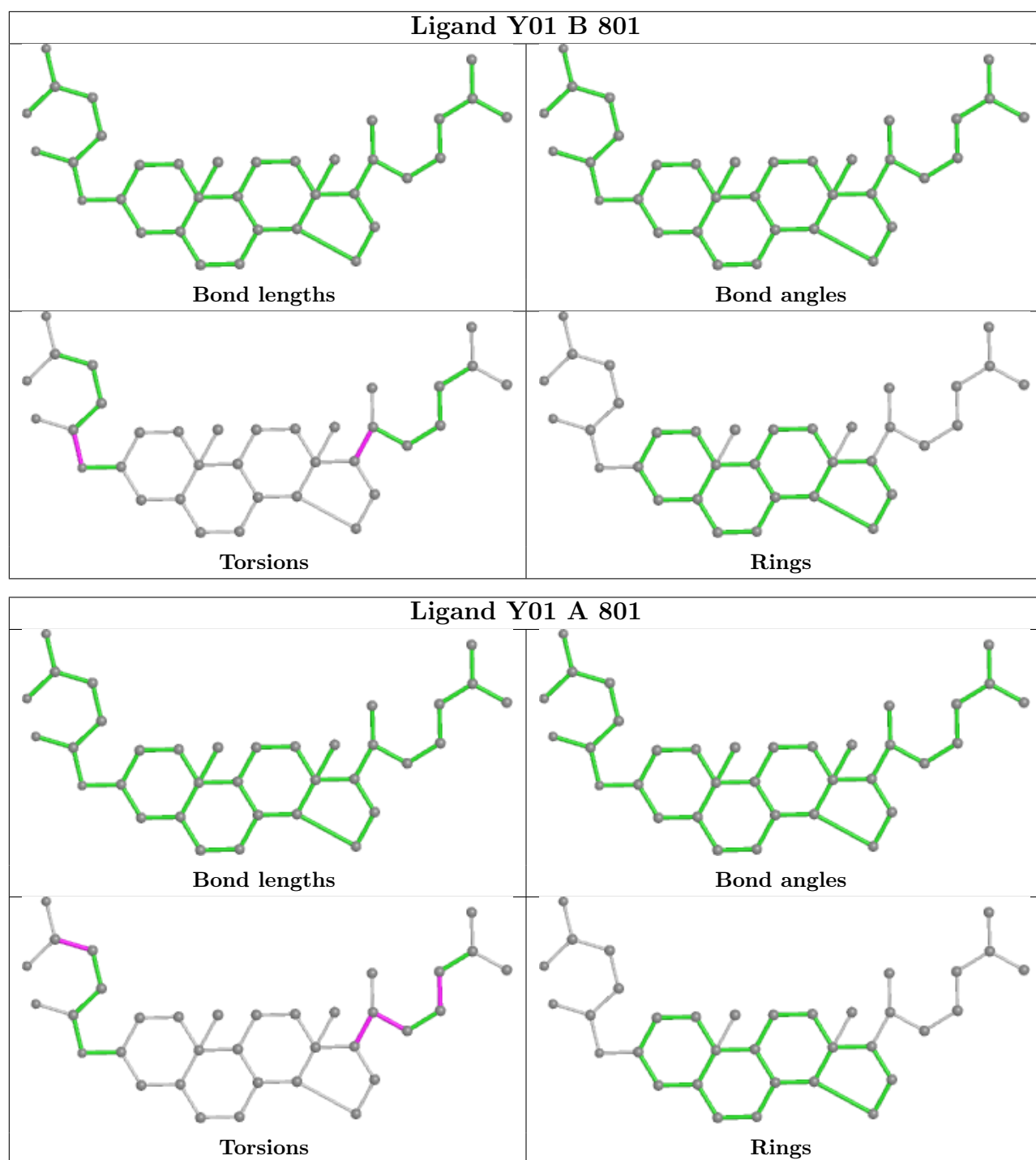
9 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	803	Y01	2	0
2	A	802	Y01	4	0
2	B	801	Y01	1	0
2	A	801	Y01	2	0
2	B	803	Y01	1	0
2	B	804	Y01	1	0
3	B	805	A1LZR	1	0
2	B	802	Y01	4	0
3	A	805	A1LZR	1	0

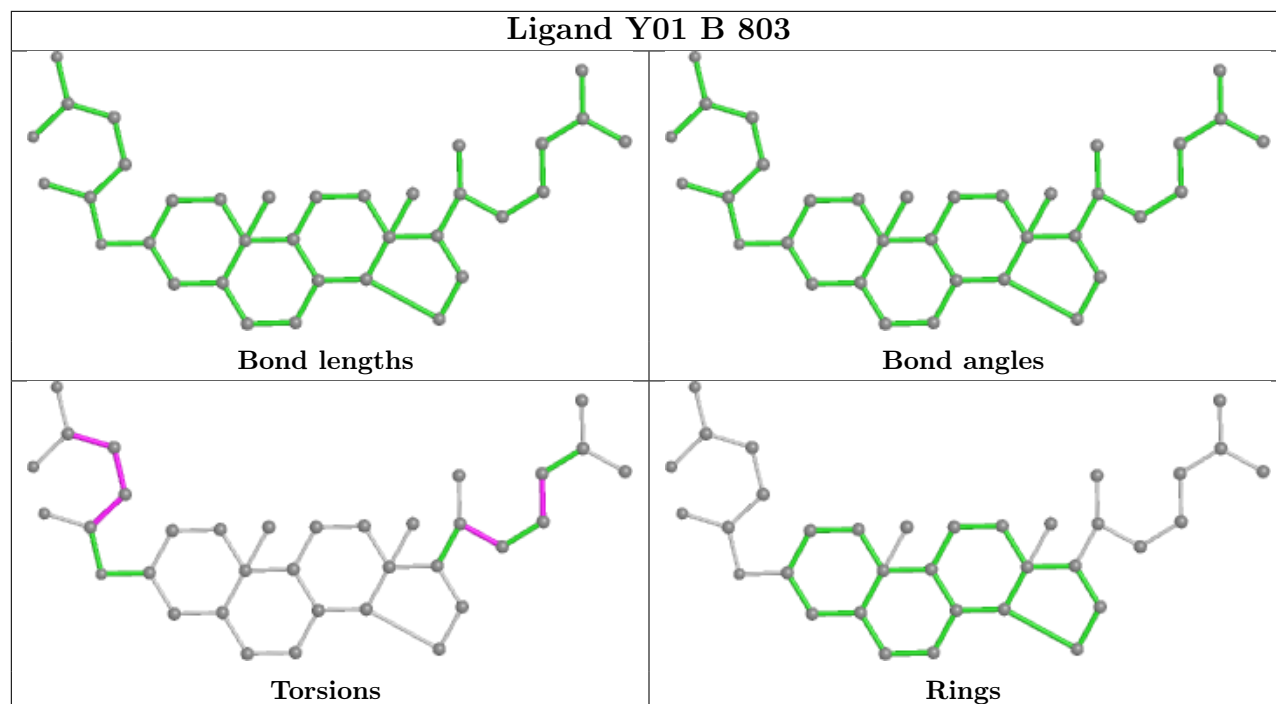
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

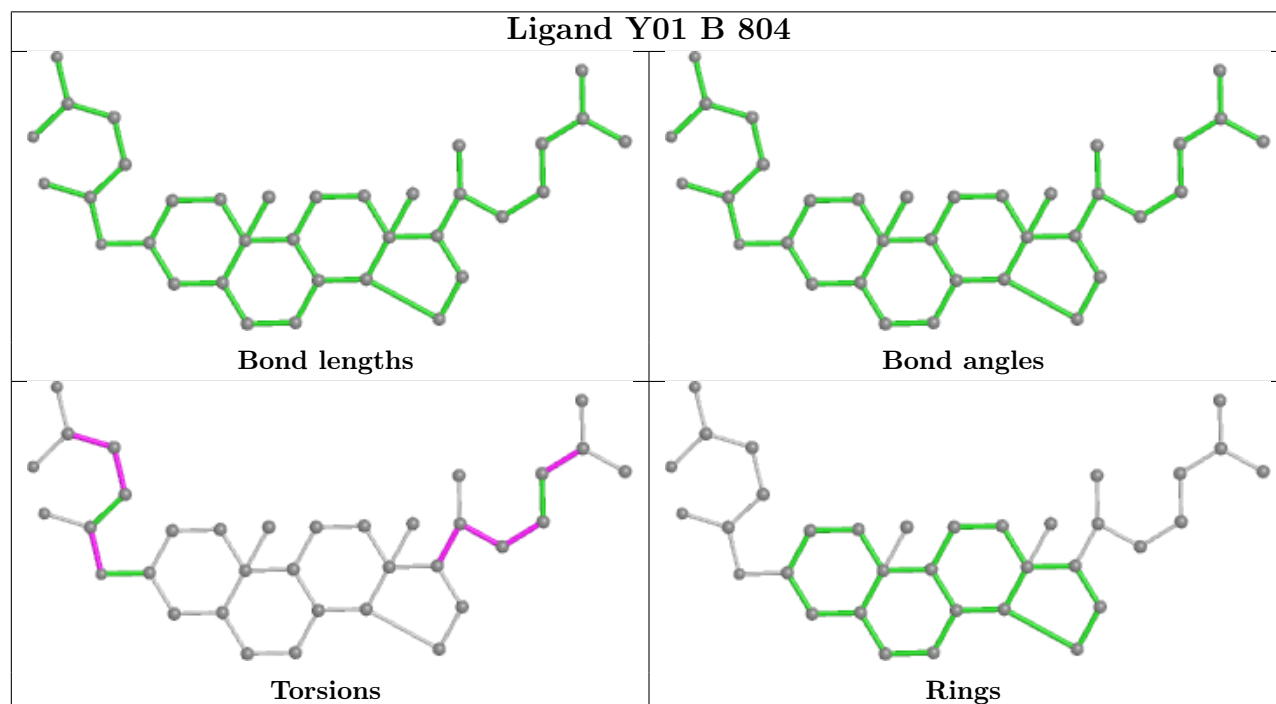


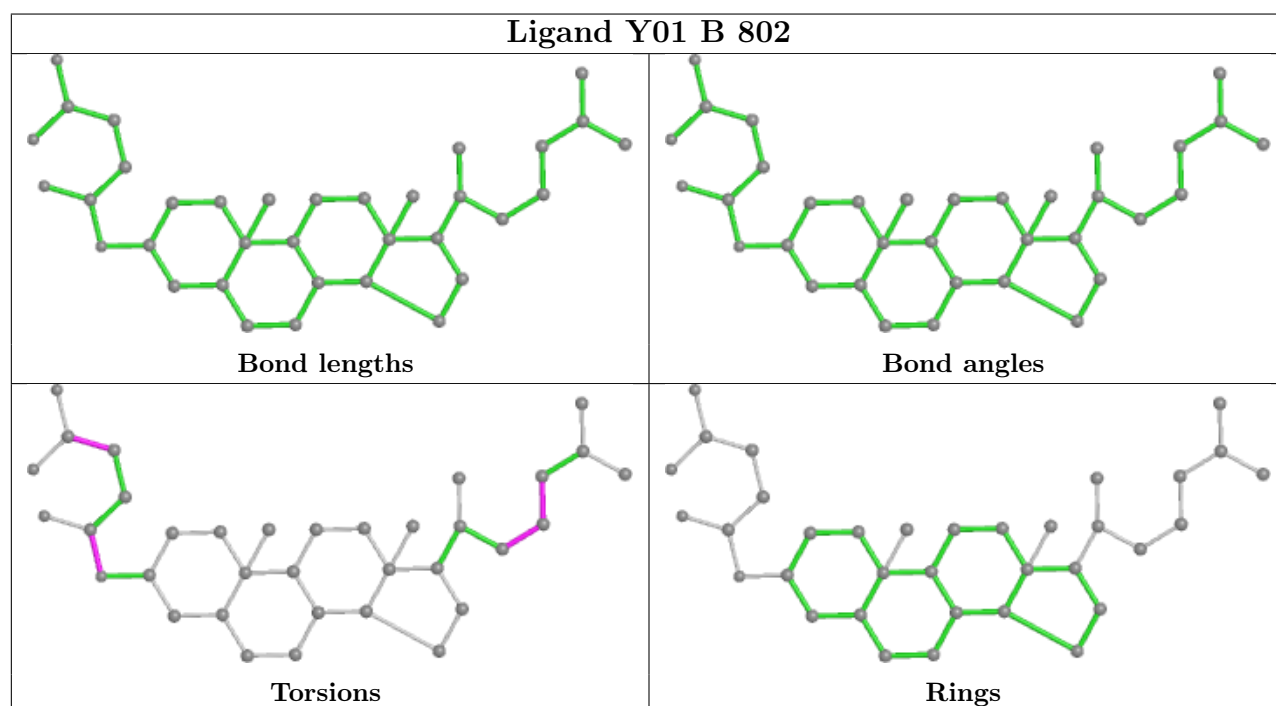
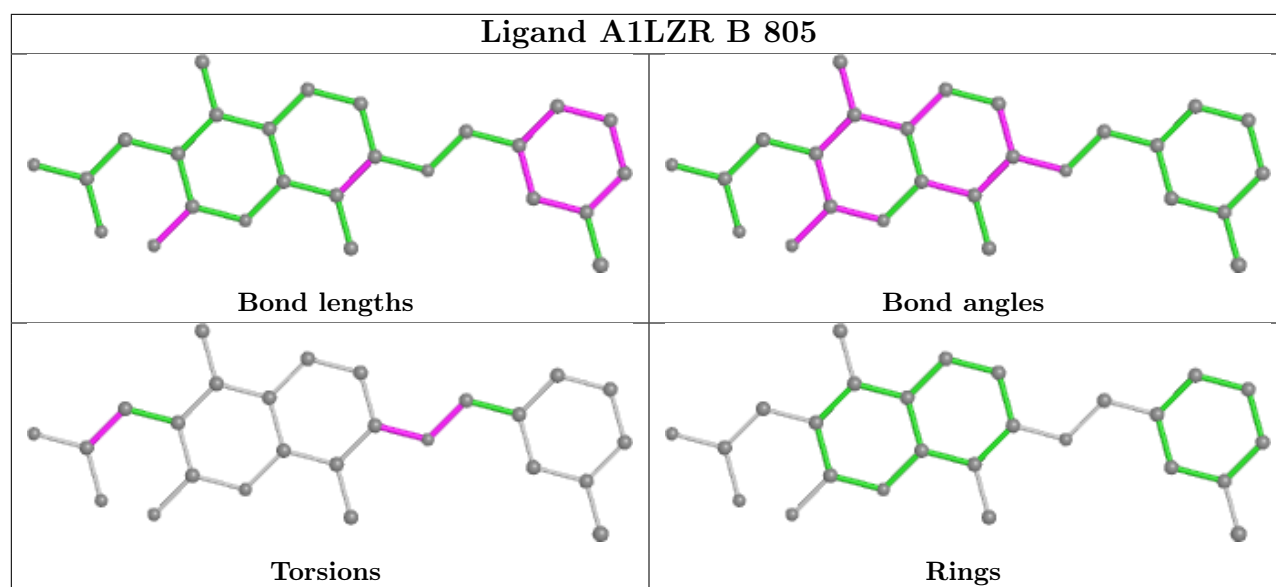


## Ligand Y01 B 803

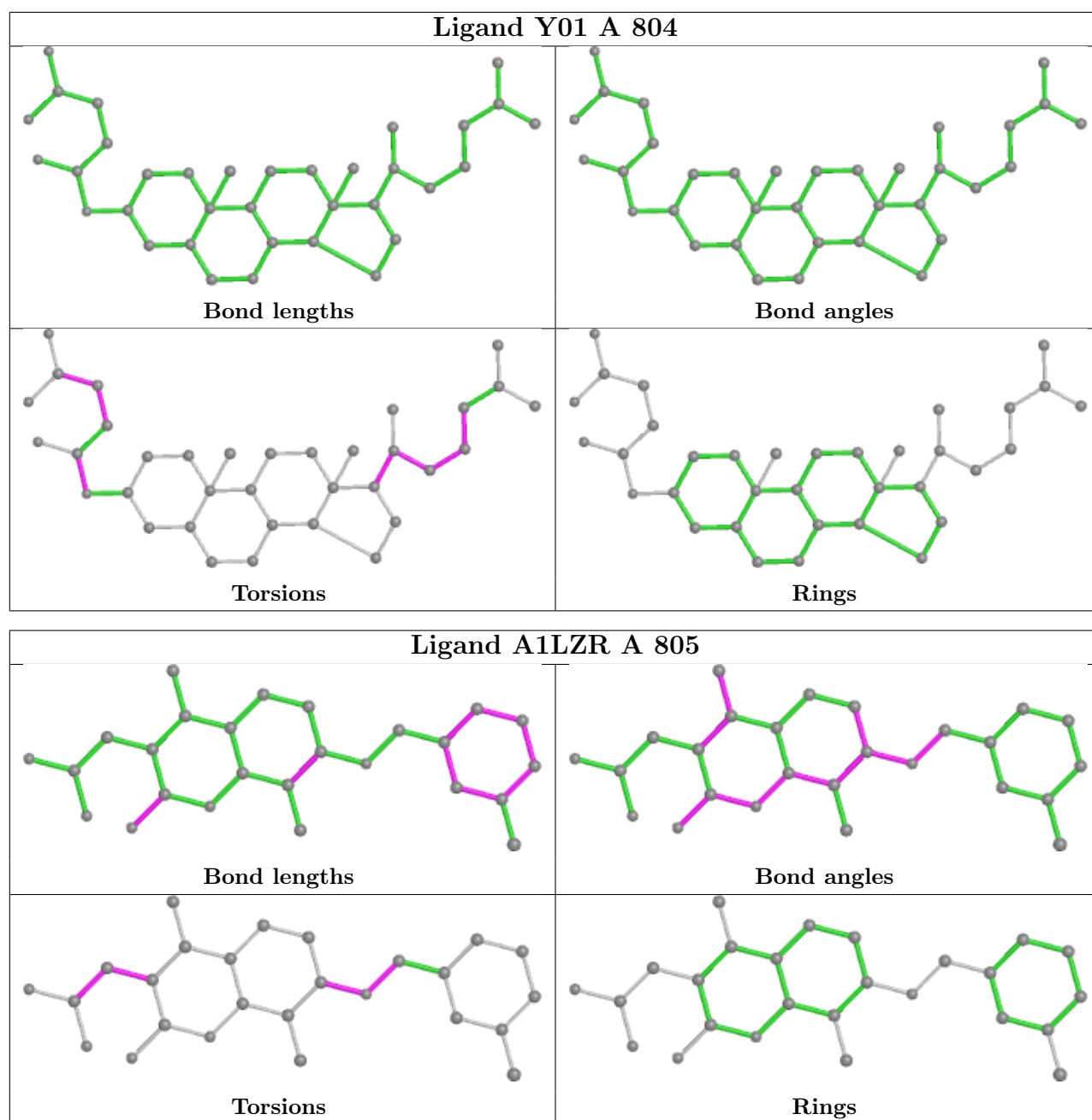


## Ligand Y01 B 804









## 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.

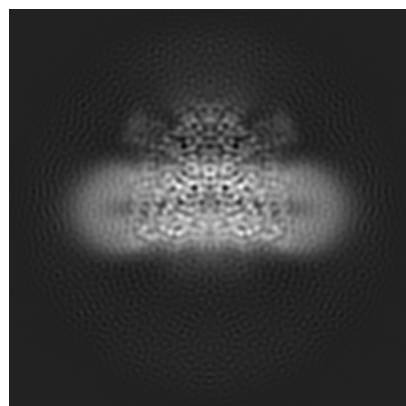
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39539. These allow visual inspection of the internal detail of the map and identification of artifacts.

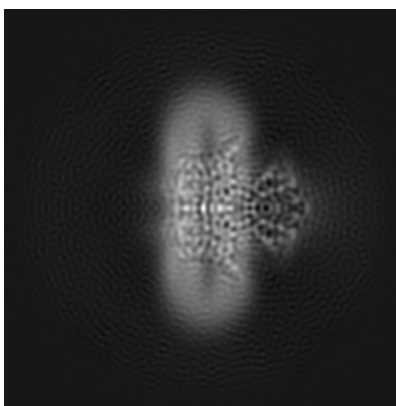
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

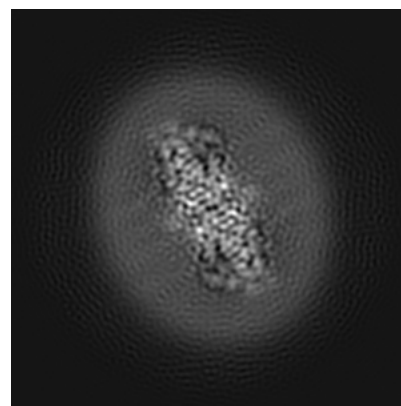
#### 6.1.1 Primary map



X

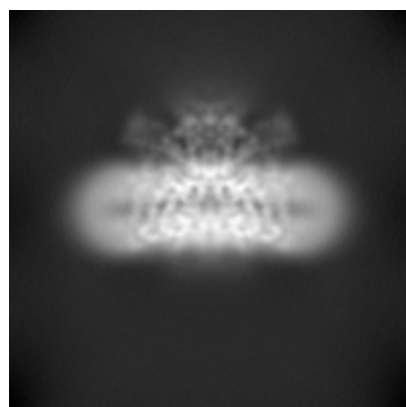


Y

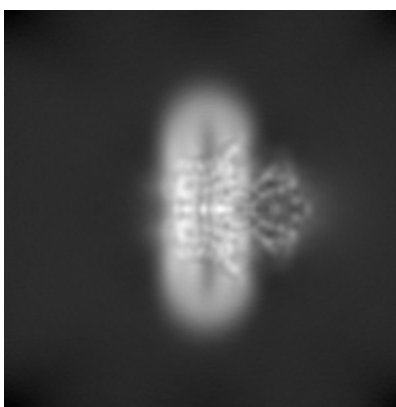


Z

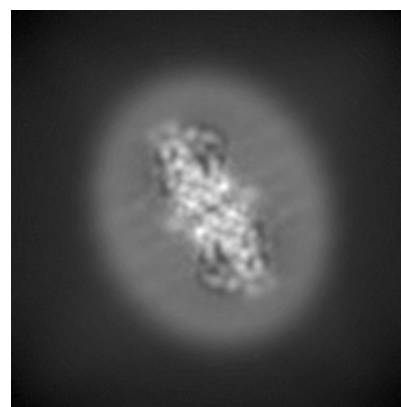
#### 6.1.2 Raw map



X



Y

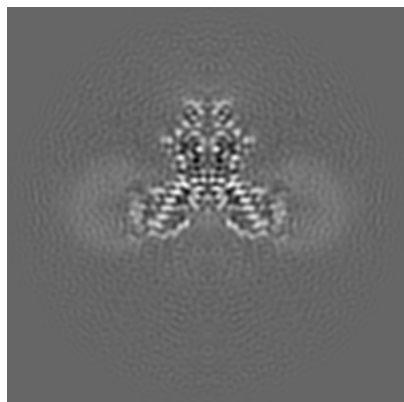


Z

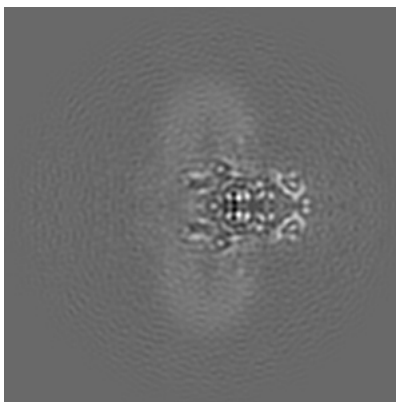
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

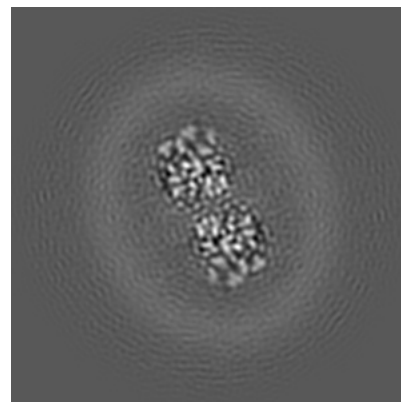
### 6.2.1 Primary map



X Index: 110

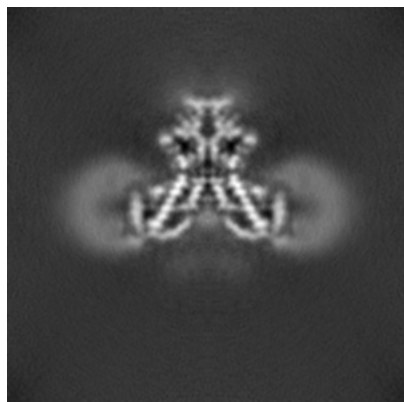


Y Index: 110

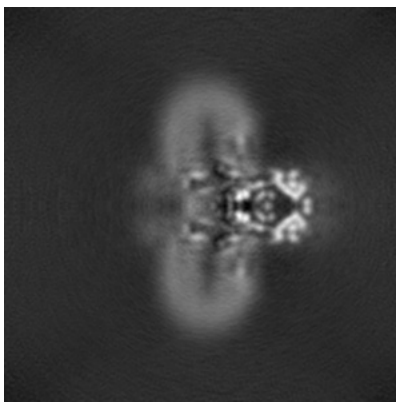


Z Index: 110

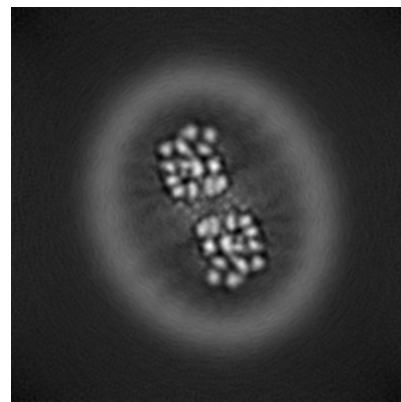
### 6.2.2 Raw map



X Index: 110



Y Index: 110

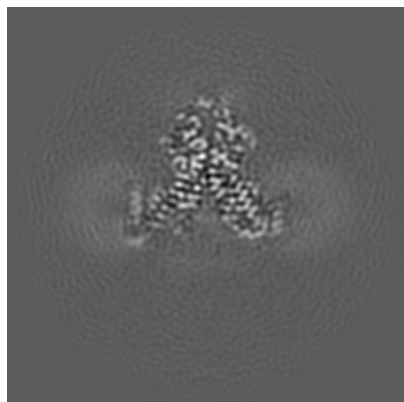


Z Index: 110

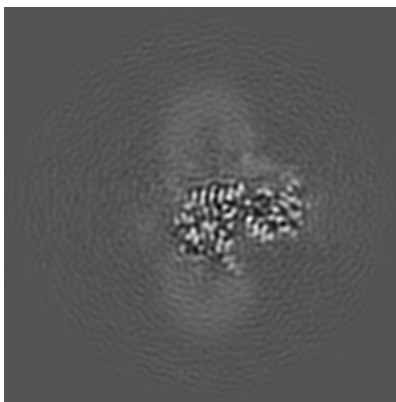
The images above show central slices of the map in three orthogonal directions.

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

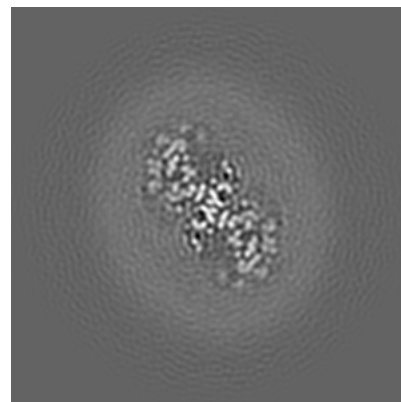
### 6.3.1 Primary map



X Index: 112

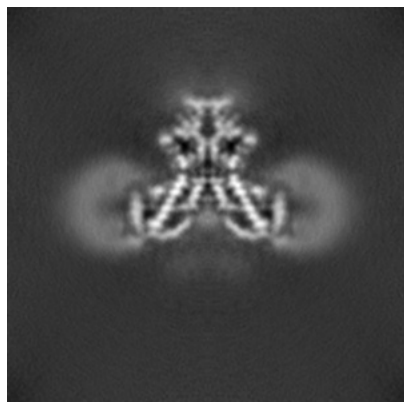


Y Index: 121

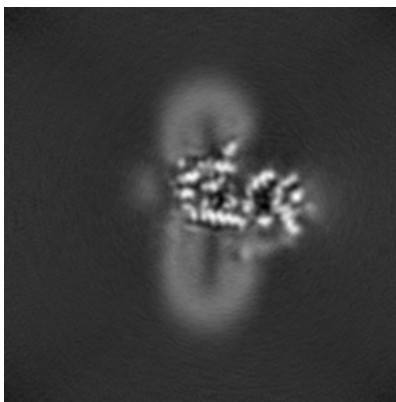


Z Index: 124

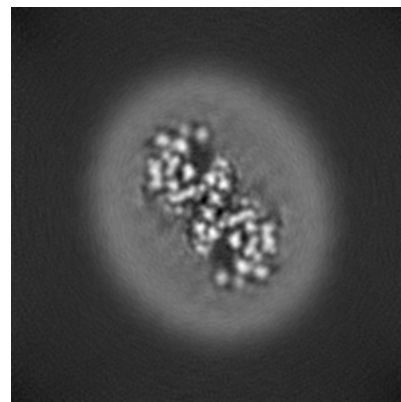
### 6.3.2 Raw map



X Index: 110



Y Index: 98

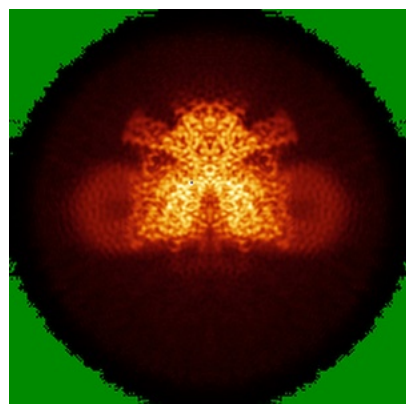


Z Index: 123

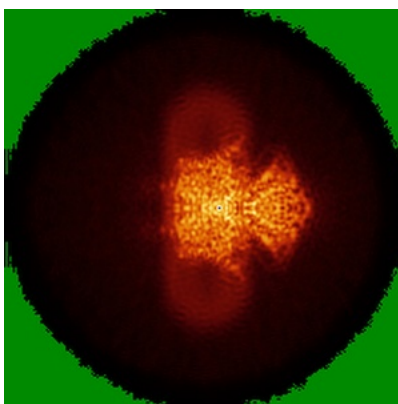
The images above show the largest variance slices of the map in three orthogonal directions.

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

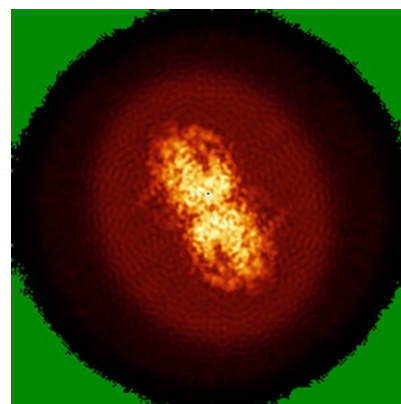
### 6.4.1 Primary map



X

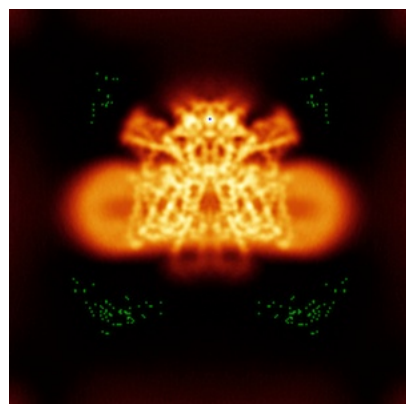


Y

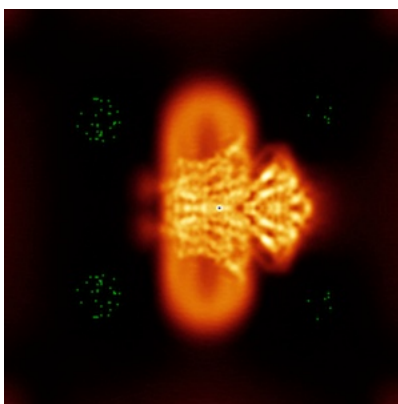


Z

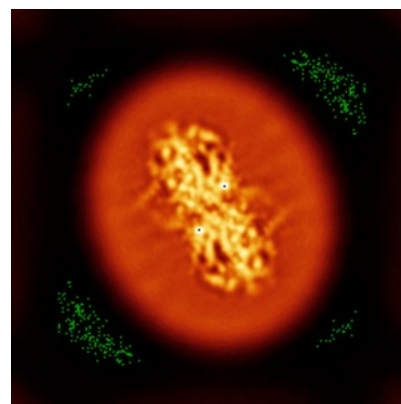
### 6.4.2 Raw map



X



Y

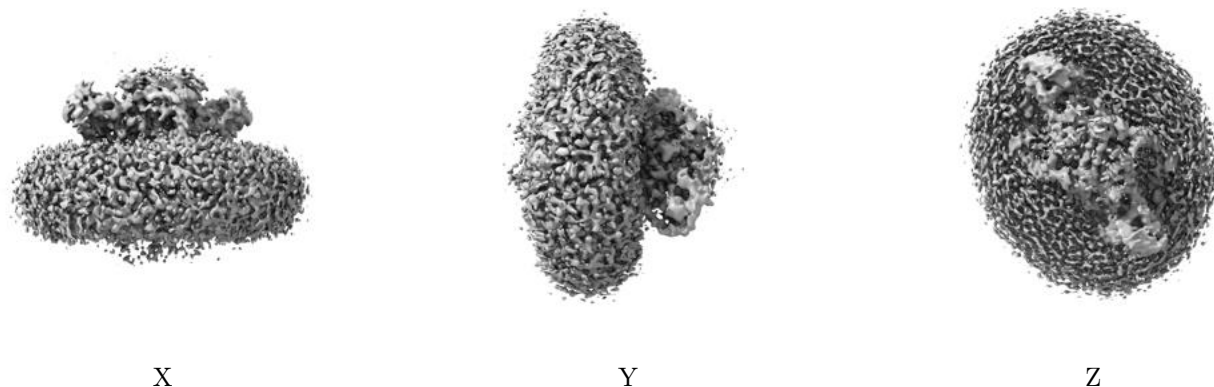


Z

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 0.25. 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.

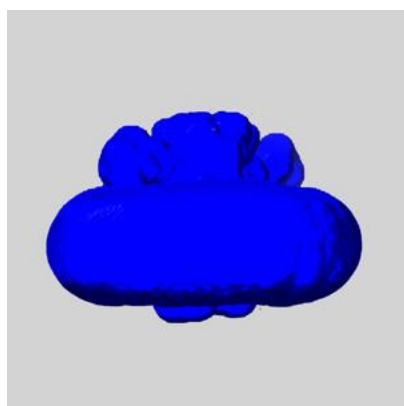
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

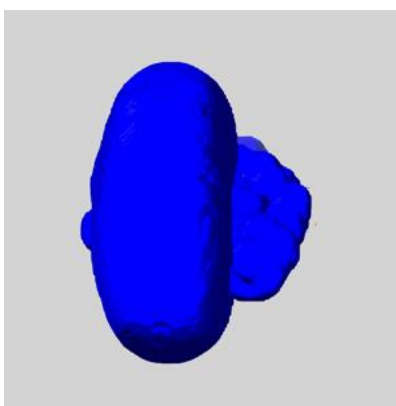
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

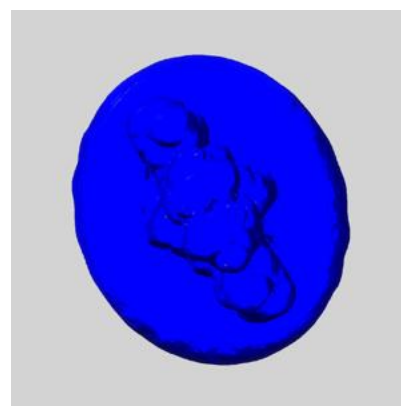
### 6.6.1 emd\_39539\_msk\_1.map [i](#)



X



Y



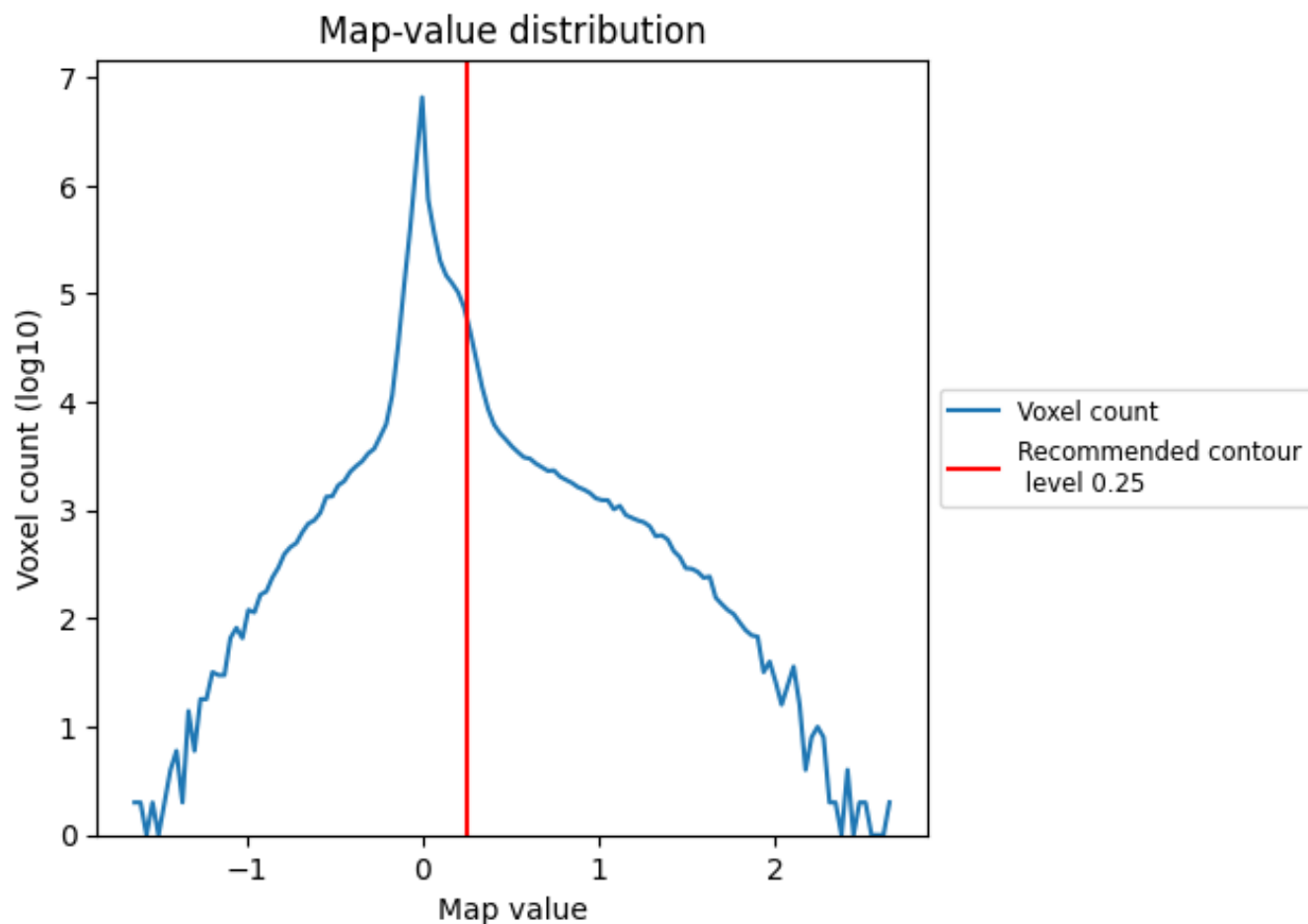
Z



## 7 Map analysis [i](#)

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

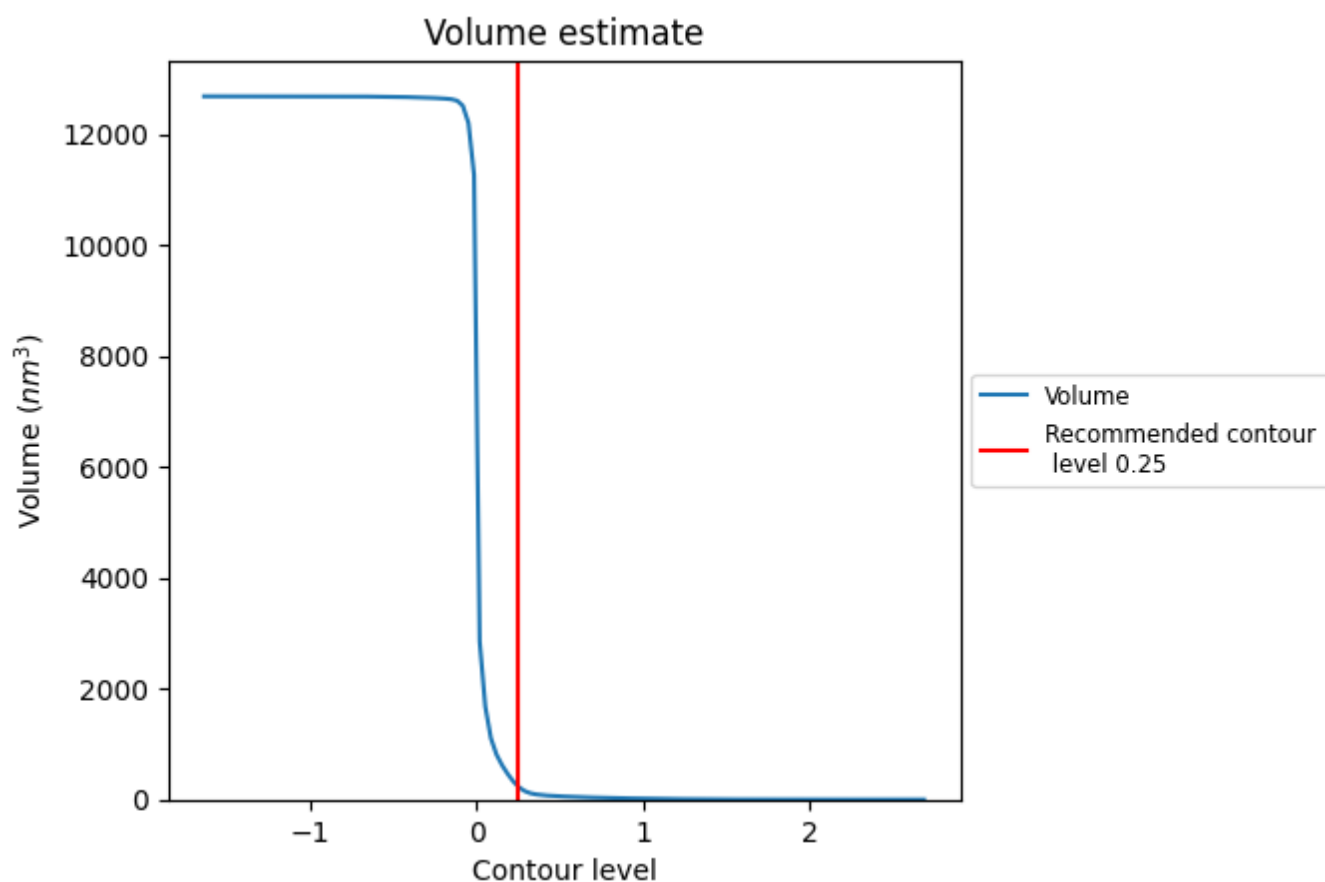
### 7.1 Map-value distribution [i](#)



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.



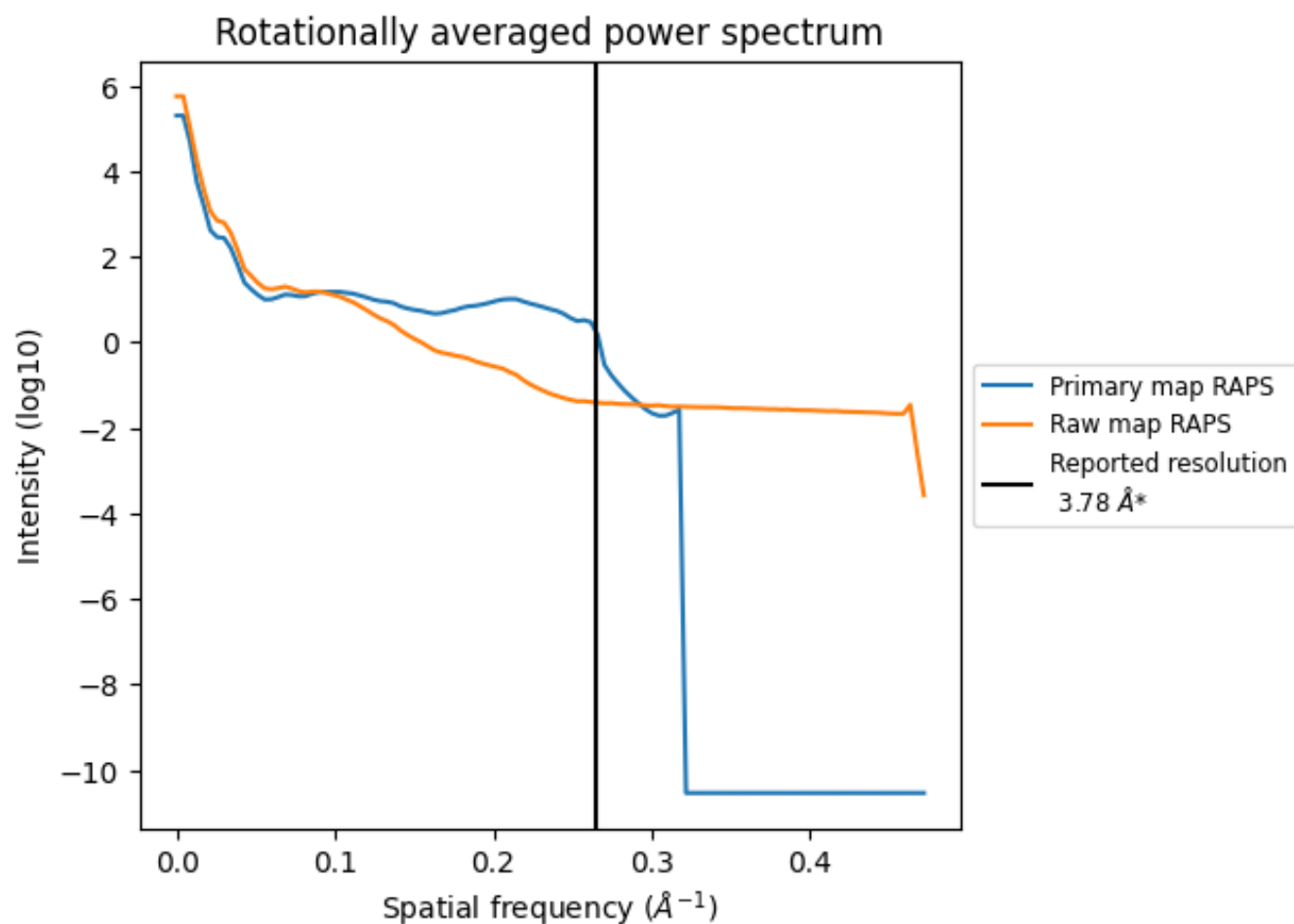
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 237  $\text{nm}^3$ ; this corresponds to an approximate mass of 214 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 ⓘ

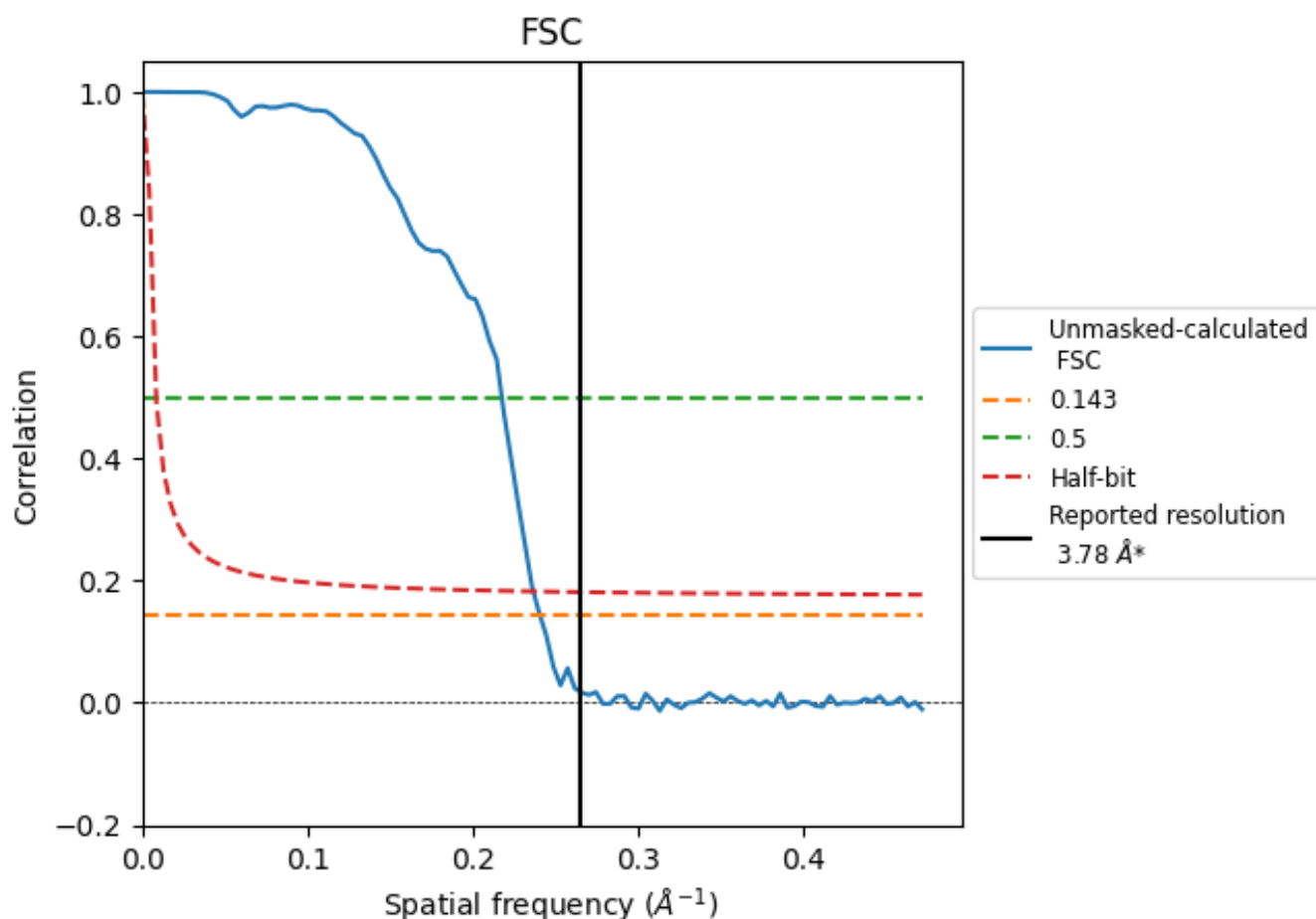


\*Reported resolution corresponds to spatial frequency of 0.265 Å<sup>-1</sup>

## 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 0.265 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

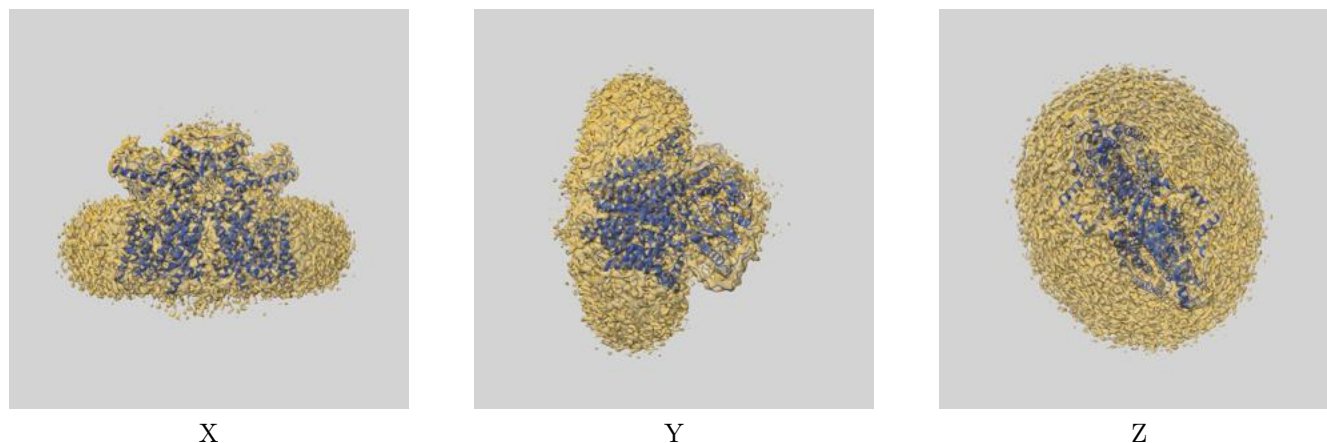
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.78	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.16	4.60	4.23

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.16 differs from the reported value 3.78 by more than 10 %

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

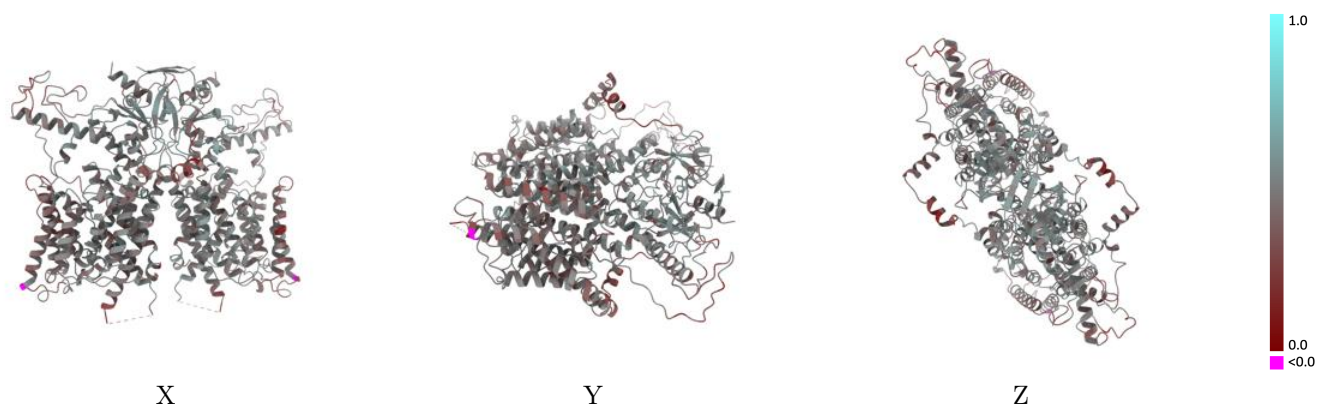
This section contains information regarding the fit between EMDB map EMD-39539 and PDB model 8YRA. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

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



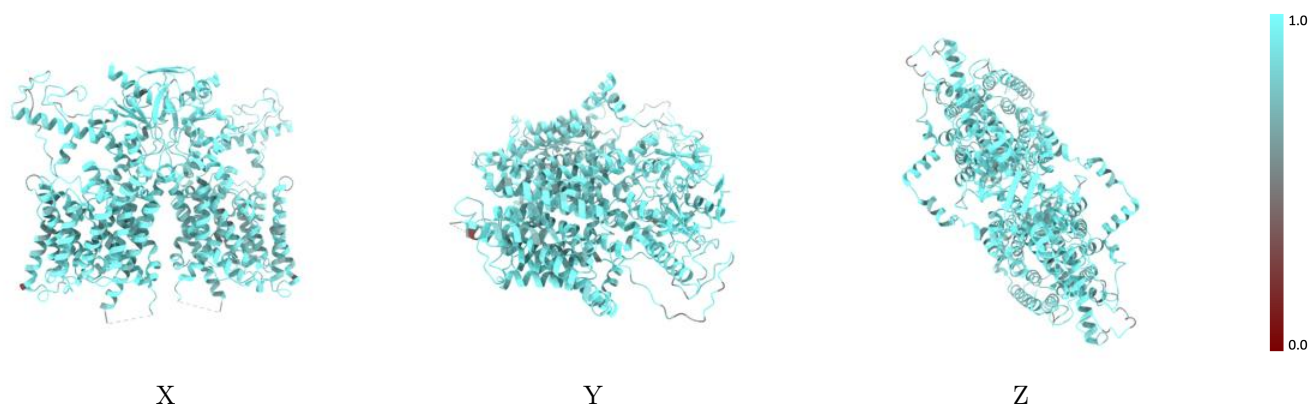
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



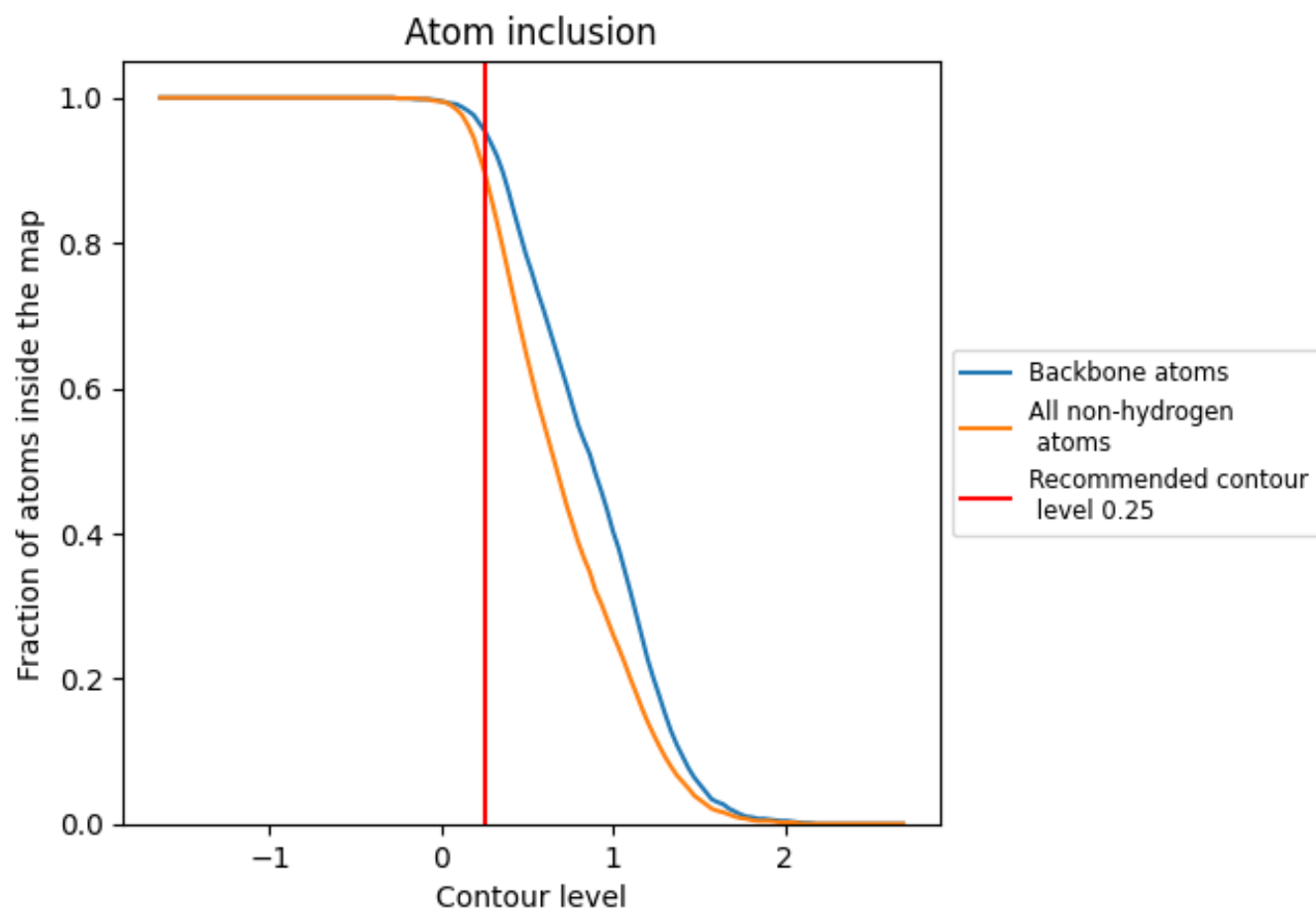
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.25).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8980	<div></div> 0.4520
A	<div></div> 0.8990	<div></div> 0.4520
B	<div></div> 0.8970	<div></div> 0.4520

