



wwPDB EM Validation Summary Report ⓘ

May 27, 2024 – 02:42 PM JST

PDB ID : 8J0F
EMDB ID : EMD-35901
Title : GK tetramer with adjacent hooks at reaction state
Authors : Zhang, T.; Guo, C.J.; Liu, J.L.
Deposited on : 2023-04-10
Resolution : 3.30 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.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)	:	2.36.2

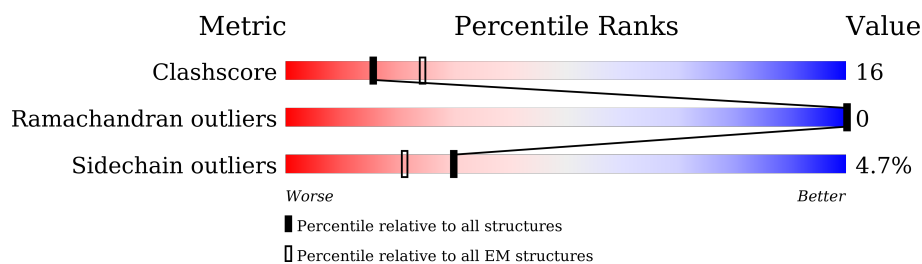
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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 $\leq 5\%$. 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	726	 25% 12% . 63%
1	B	726	 25% 11% . 63%
1	C	726	 25% 11% . 63%
1	D	726	 25% 12% . 63%
1	E	726	 .. 98%
1	F	726	 .. 98%
1	G	726	 .. 98%
1	H	726	 .. 98%

2 Entry composition

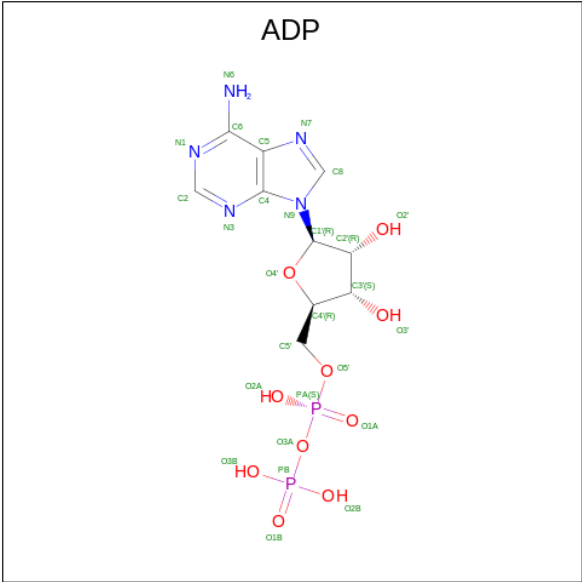
There are 4 unique types of molecules in this entry. The entry contains 8932 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Delta-1-pyrroline-5-carboxylate synthase B.

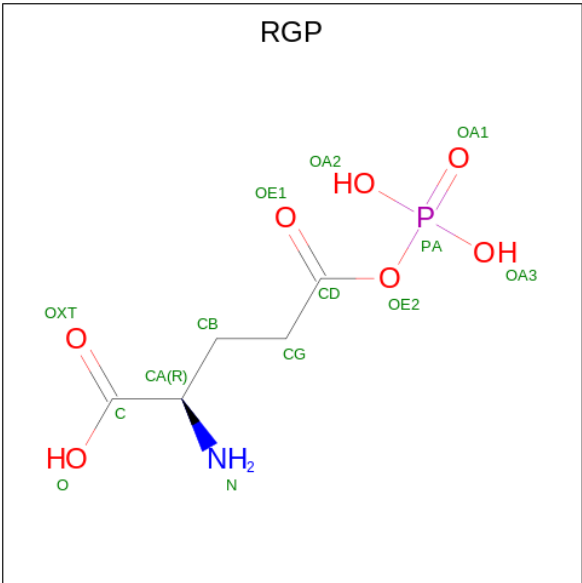
Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	270	Total 2067	C 1303	N 365	O 390	S 9	0	0
1	F	15	Total 124	C 79	N 22	O 23		0	0
1	A	270	Total 2067	C 1303	N 365	O 390	S 9	0	0
1	E	15	Total 124	C 79	N 22	O 23		0	0
1	B	270	Total 2067	C 1303	N 365	O 390	S 9	0	0
1	G	15	Total 124	C 79	N 22	O 23		0	0
1	D	270	Total 2067	C 1303	N 365	O 390	S 9	0	0
1	H	15	Total 124	C 79	N 22	O 23		0	0

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	C	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	D	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 3 is GAMMA-GLUTAMYL PHOSPHATE (three-letter code: RGP) (formula: C₅H₁₀NO₇P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	C	1	Total	C	N	O	P	0
			14	5	1	7	1	
3	A	1	Total	C	N	O	P	0
			14	5	1	7	1	
3	B	1	Total	C	N	O	P	0
			14	5	1	7	1	
3	D	1	Total	C	N	O	P	0
			14	5	1	7	1	

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	C	1	Total	Mg	0
			1	1	
4	A	1	Total	Mg	0
			1	1	
4	B	1	Total	Mg	0
			1	1	
4	D	1	Total	Mg	0
			1	1	

GLY ILE	GLY	GLU	ALA	ASP	LEU	LYS
ALA	GLU	ILE	MET	LEU	ALA	ILE
GLU	VAL	VAL	GLU	VAL	ILE	SER
VAL	GLY	GLU	THR	ILE	ARG	SER
ILE	VAL	VAL	LEU	PRO	SER	LEU
SER	THR	TYR	VAL	ARG	GLY	ALA
THR	GLY	GLY	HIS	SER	GLY	ALA
SER	ALA	ALA	HIS	ASN	GLY	SER
ARG	ILE	ILE	ASP	ASN	LEU	VAL
ILE	ASP	ASP	LYS	LYS	LEU	ARG
HIS	ASP	ASP	GLY	VAL	LEU	GLN
ALA	HIS	ILE	GLU	VAL	LYS	LEU
ARG	HIS	ILE	ASN	SER	GLY	ALA
GLY	GLN	GLN	PHE	VAL	GLY	GLU
PRO	VAL	GLY	LEU	ASN	ALA	ASP
VAL	GLY	SER	ASP	SER	PRO	ASP
VAL	ALA	HIS	ASP	THR	ARG	ILE
GLU	HIS	HIS	LEU	LYS	SER	GLY
GLY	THR	THR	ILE	ILE	ASN	GLY
LEU	ASP	ASP	TYR	PRO	ALA	VAL
LEU	CYS	VAL	VAL	VAL	ILE	LEU
THR	ILE	VAL	LEU	LEU	LEU	LYS
THR	VAL	VAL	GLN	GLY	HIS	LYS
ARG	THR	THR	THR	HIS	LYS	THR
TRP	GLU	GLU	LYS	ALA	VAL	GLN
ILE	ASP	ILE	GLY	ASP	ILE	VAL
MET	SER	SER	VAL	GLY	THR	ALA
ARG	GLU	GLU	THR	ILE	ASP	ASP
GLY	VAL	VAL	LEU	CYS	ALA	ASP
LYS	ALA	ALA	TYR	HIS	ILE	LEU
GLY	GLU	ILE	GLY	VAL	PRO	ILE
GLN	ILE	ILE	PRO	TYR	GLU	LEU
VAL	VAL	PHE	PRO	ASP	THR	GLU
VAL	LEU	LEU	ARG	VAL	VAL	LYS
ASP	ASP	ARG	ALA	LYS	GLY	THR
GLY	GLN	GLN	SER	SER	GLY	SER
ASP	VAL	VAL	ALA	GLY	LYS	SER
ASN	ASP	ASP	LYS	LEU	LEU	PRO
ILE	ILE	ALA	ASN	LEU	ILE	ILE
VAL	VAL	ALA	ILE	MET	GLY	VAL
TYR	TYR	VAL	PRO	ALA	VAL	LEU
HIS	THR	PHE	GLU	LYS	THR	LEU
THR	HIS	HIS	THR	ARG	SER	ILE
LYS	ASN	ASN	LYS	VAL	GLU	ARG
ASP	ASP	ALA	SER	VAL	ILE	PHE
LEU	LEU	SER	PHE	SER	GLY	GLY
PRO	PRO	THR	HIS	ASP	ILE	SER
VAL	VAL	ARG	HIS	ALA	PRO	ARG
GLN	PHE	PHE	GLU	ASP	ASP	ASP
ARG	SER	SER	TYR	LEU	LEU	ALA
THR	GLY	GLY	SER	TYR	LYS	LEU
ALA	ARG	PHE	LYS	PRO	LEU	VAL
VAL	PHE	PHE	ALA	ALA	ASP	GLN
GLU	GLU	GLY	CYS	ALA	ASP	ILE
ASN	ASN	LEU	THR	CYS	VAL	SER
			VAL	ASN	ILE	ASP

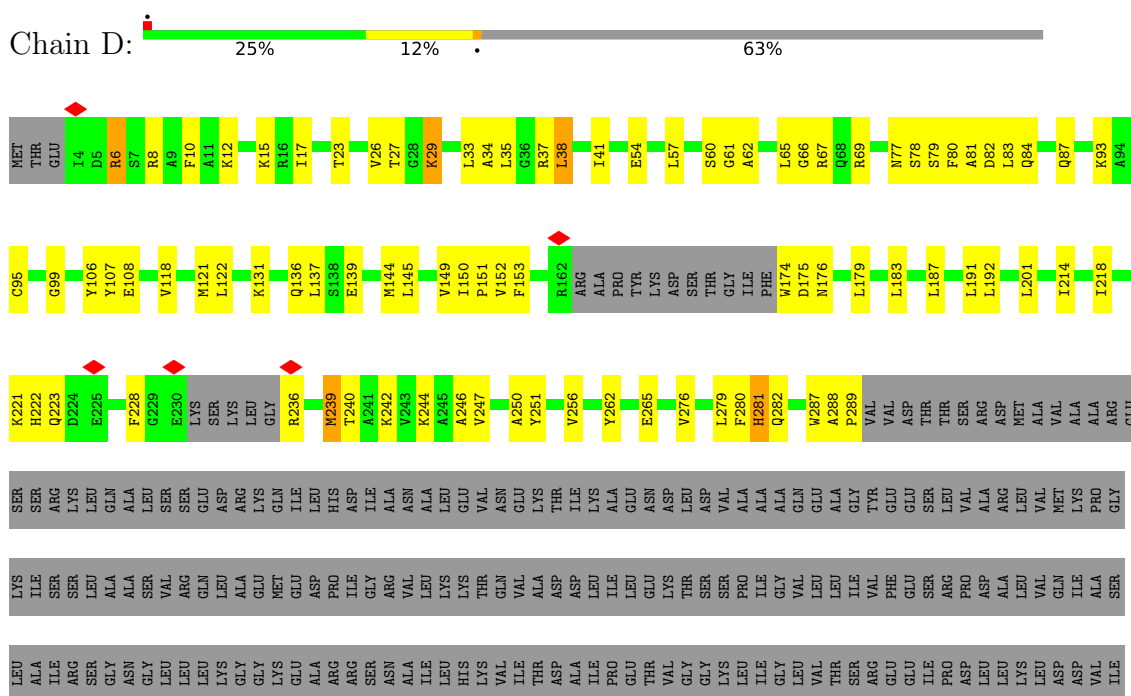
- Molecule 1: Delta-1-pyrroline-5-carboxylate synthase B

Chain E: 98%

[illegible]

[illegible]

- Molecule 1: Delta-1-pyrroline-5-carboxylate synthase B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	223041	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.022	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.005	Depositor
Map size (\AA)	254.4, 254.4, 254.4	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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: MG, ADP, RGP

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	0.39	0/2094	0.59	0/2821
1	B	0.39	0/2094	0.59	0/2821
1	C	0.39	0/2094	0.59	0/2821
1	D	0.39	0/2094	0.59	0/2821
1	E	0.40	0/126	0.42	0/169
1	F	0.40	0/126	0.42	0/169
1	G	0.40	0/126	0.42	0/169
1	H	0.40	0/126	0.42	0/169
All	All	0.39	0/8880	0.59	0/11960

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	2067	0	2110	69	0
1	B	2067	0	2110	67	0
1	C	2067	0	2110	67	0
1	D	2067	0	2110	68	0
1	E	124	0	122	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	124	0	122	12	0
1	G	124	0	122	12	0
1	H	124	0	122	12	0
2	A	27	0	12	2	0
2	B	27	0	12	2	0
2	C	27	0	12	2	0
2	D	27	0	12	1	0
3	A	14	0	7	2	0
3	B	14	0	7	2	0
3	C	14	0	7	2	0
3	D	14	0	7	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
All	All	8932	0	9004	293	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 16.

The worst 5 of 293 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:279:LEU:HD21	1:A:281:HIS:HB2	1.71	0.72
1:D:279:LEU:HD21	1:D:281:HIS:HB2	1.71	0.72
1:B:279:LEU:HD21	1:B:281:HIS:HB2	1.71	0.71
1:C:279:LEU:HD21	1:C:281:HIS:HB2	1.71	0.70
1:C:26:VAL:HG11	1:C:60:SER:O	1.96	0.66

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	264/726 (36%)	259 (98%)	5 (2%)	0	100	100
1	B	264/726 (36%)	259 (98%)	5 (2%)	0	100	100
1	C	264/726 (36%)	259 (98%)	5 (2%)	0	100	100
1	D	264/726 (36%)	259 (98%)	5 (2%)	0	100	100
1	E	13/726 (2%)	13 (100%)	0	0	100	100
1	F	13/726 (2%)	13 (100%)	0	0	100	100
1	G	13/726 (2%)	13 (100%)	0	0	100	100
1	H	13/726 (2%)	13 (100%)	0	0	100	100
All	All	1108/5808 (19%)	1088 (98%)	20 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	221/601 (37%)	211 (96%)	10 (4%)	27	58
1	B	221/601 (37%)	211 (96%)	10 (4%)	27	58
1	C	221/601 (37%)	211 (96%)	10 (4%)	27	58
1	D	221/601 (37%)	211 (96%)	10 (4%)	27	58
1	E	14/601 (2%)	13 (93%)	1 (7%)	14	42
1	F	14/601 (2%)	13 (93%)	1 (7%)	14	42
1	G	14/601 (2%)	13 (93%)	1 (7%)	14	42
1	H	14/601 (2%)	13 (93%)	1 (7%)	14	42
All	All	940/4808 (20%)	896 (95%)	44 (5%)	30	57

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

Mol	Chain	Res	Type
1	B	175	ASP
1	D	29	LYS

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Mol	Chain	Res	Type
1	B	223	GLN
1	G	84	GLN
1	D	107	TYR

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	D	222	HIS
1	D	281	HIS
1	A	281	HIS
1	B	113	GLN
1	B	281	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 for Mogul analysis.

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	RGP	B	802	-	11,13,13	0.88	0	14,18,18	1.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ADP	C	801	4	24,29,29	0.96	1 (4%)	29,45,45	1.43	4 (13%)
3	RGP	A	802	-	11,13,13	0.89	0	14,18,18	1.13	0
3	RGP	D	802	-	11,13,13	0.88	0	14,18,18	1.09	0
2	ADP	D	801	4	24,29,29	0.96	1 (4%)	29,45,45	1.43	4 (13%)
3	RGP	C	802	-	11,13,13	0.89	0	14,18,18	1.13	0
2	ADP	A	801	4	24,29,29	0.96	1 (4%)	29,45,45	1.43	4 (13%)
2	ADP	B	801	4	24,29,29	0.96	1 (4%)	29,45,45	1.43	4 (13%)

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	RGP	B	802	-	-	4/12/14/14	-
2	ADP	C	801	4	-	4/12/32/32	0/3/3/3
3	RGP	A	802	-	-	2/12/14/14	-
3	RGP	D	802	-	-	4/12/14/14	-
2	ADP	D	801	4	-	3/12/32/32	0/3/3/3
3	RGP	C	802	-	-	2/12/14/14	-
2	ADP	A	801	4	-	4/12/32/32	0/3/3/3
2	ADP	B	801	4	-	3/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	801	ADP	C5-C4	2.42	1.47	1.40
2	A	801	ADP	C5-C4	2.42	1.47	1.40
2	B	801	ADP	C5-C4	2.42	1.47	1.40
2	D	801	ADP	C5-C4	2.42	1.47	1.40

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	801	ADP	PA-O3A-PB	-3.52	120.76	132.83
2	A	801	ADP	PA-O3A-PB	-3.52	120.76	132.83
2	B	801	ADP	PA-O3A-PB	-3.52	120.76	132.83
2	D	801	ADP	PA-O3A-PB	-3.52	120.76	132.83
2	C	801	ADP	N3-C2-N1	-3.17	123.73	128.68

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

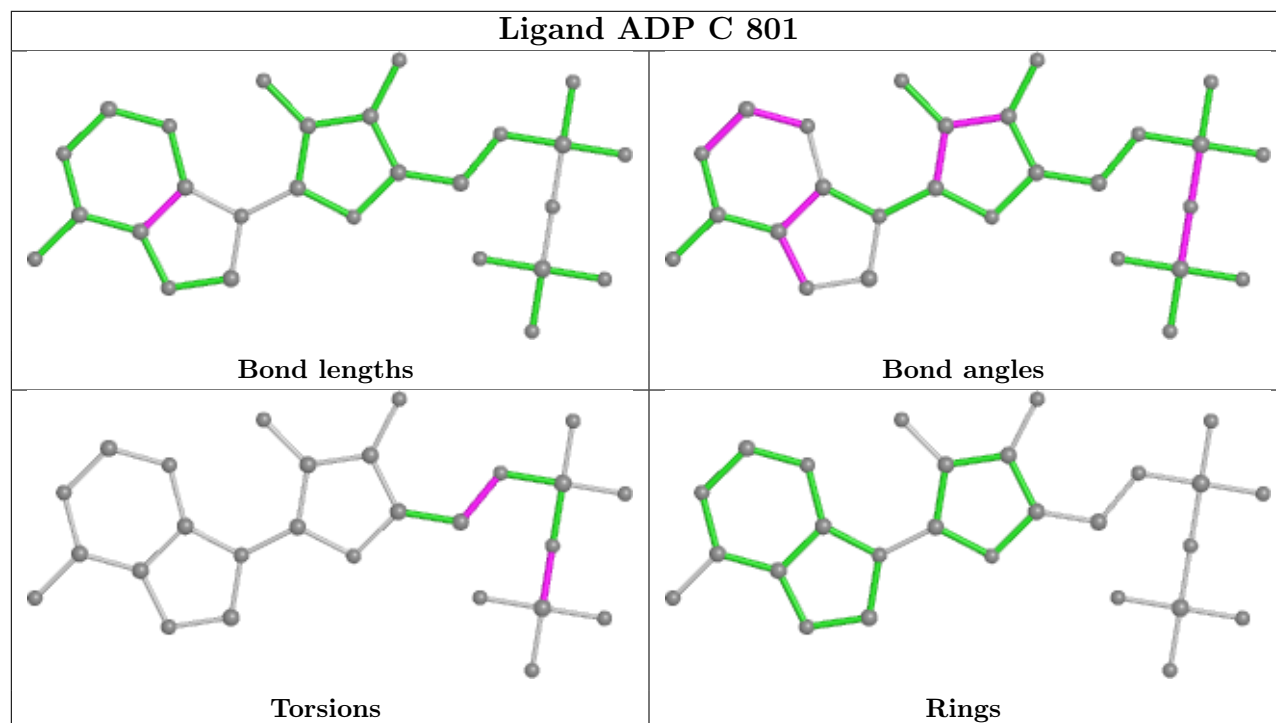
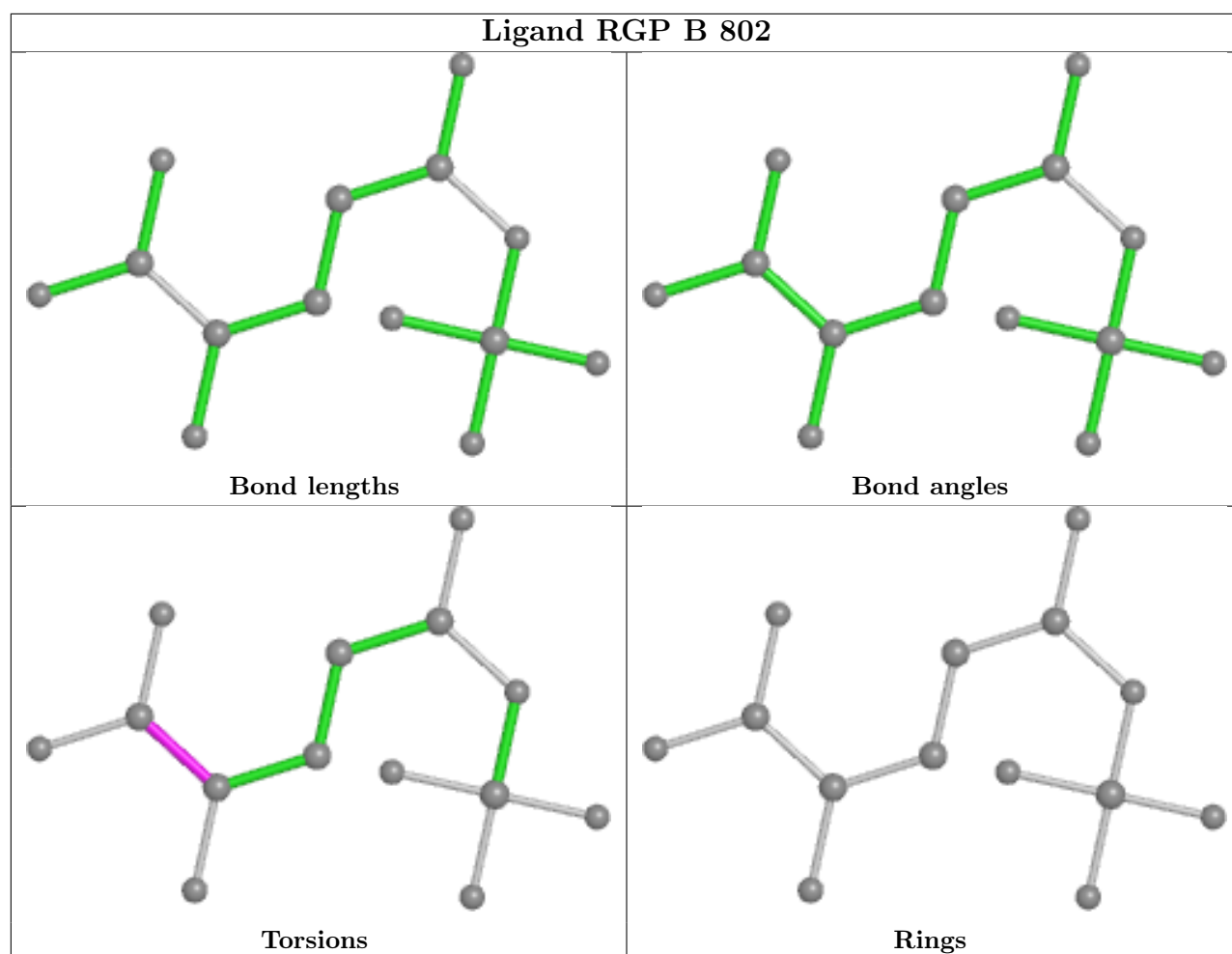
Mol	Chain	Res	Type	Atoms
2	C	801	ADP	PA-O3A-PB-O3B
2	A	801	ADP	PA-O3A-PB-O3B
3	C	802	RGP	OXT-C-CA-N
3	A	802	RGP	OXT-C-CA-N
3	B	802	RGP	OXT-C-CA-N

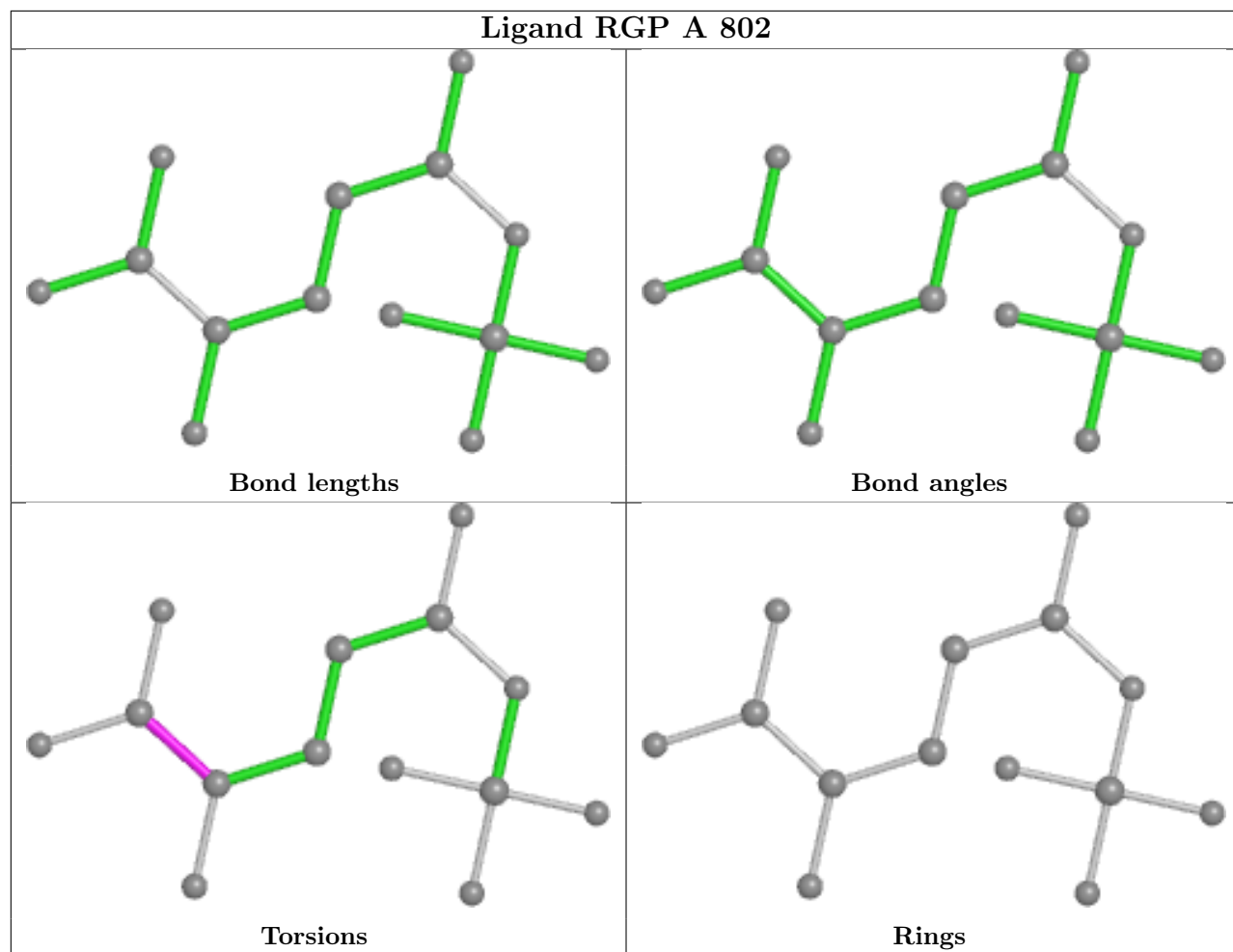
There are no ring outliers.

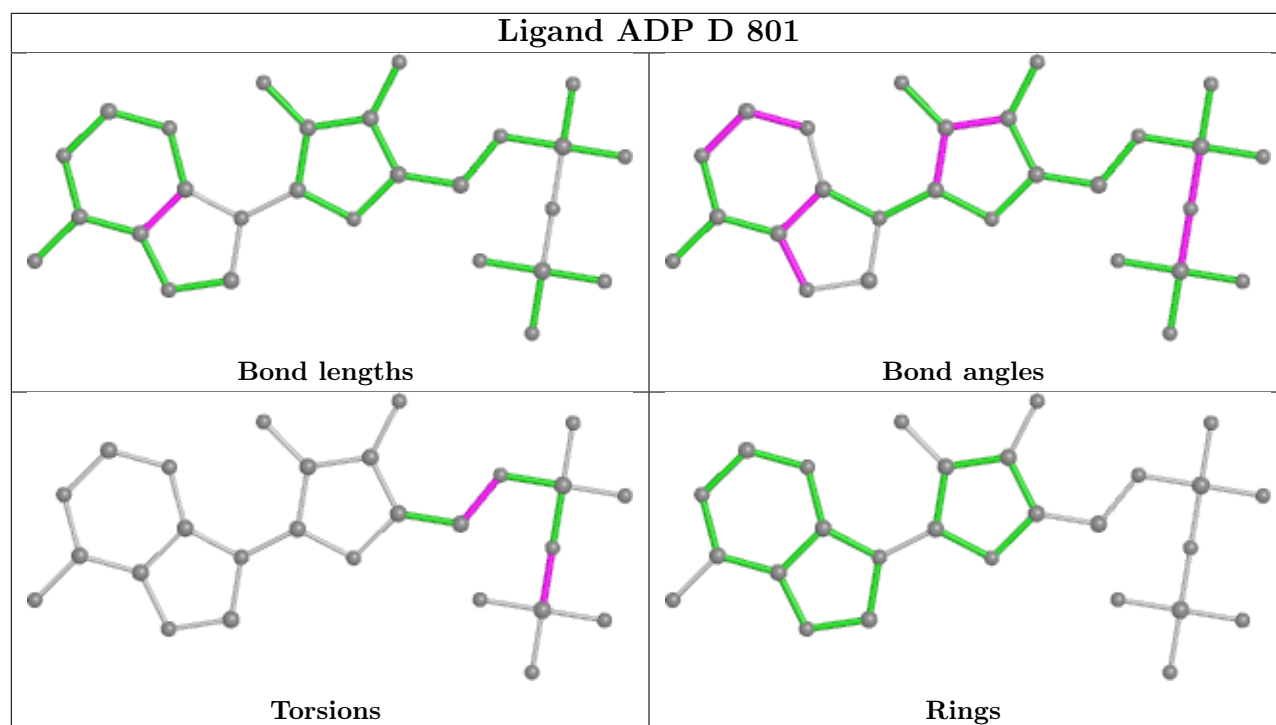
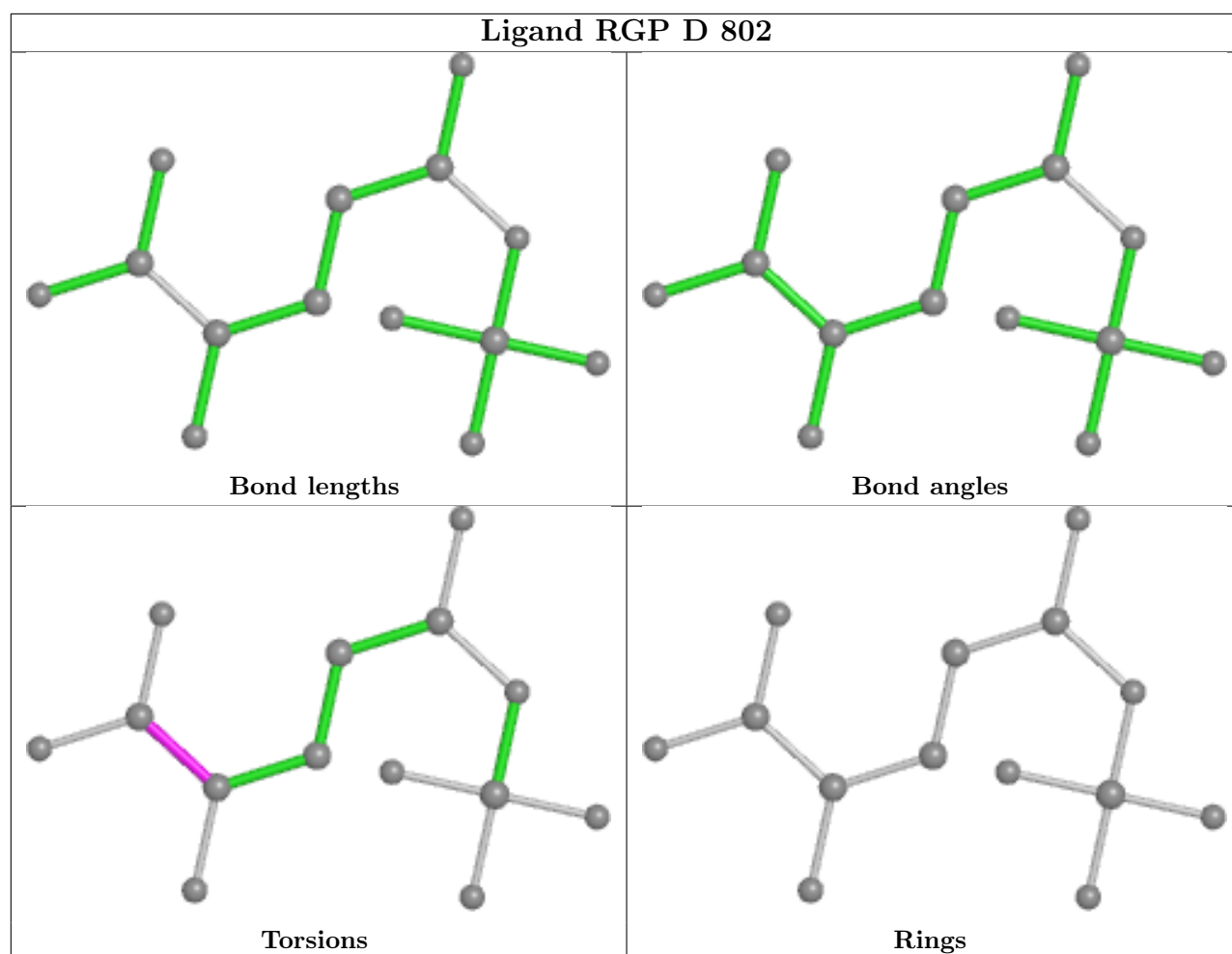
8 monomers are involved in 15 short contacts:

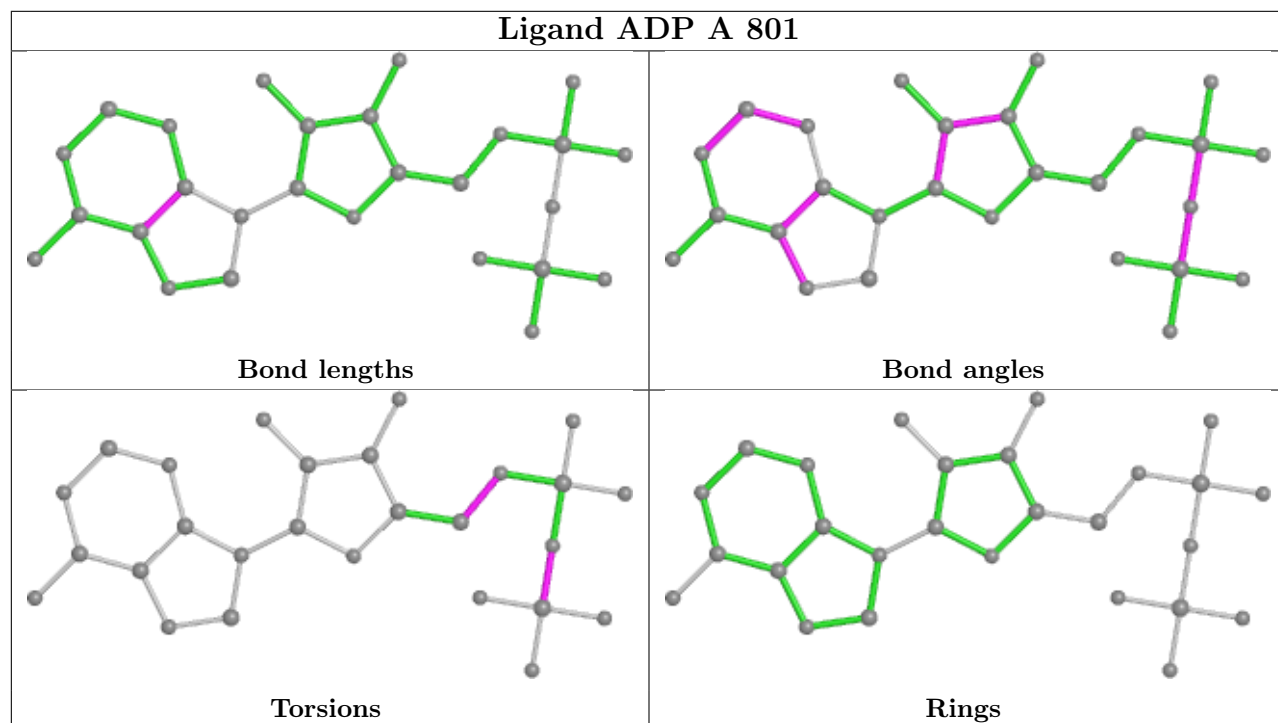
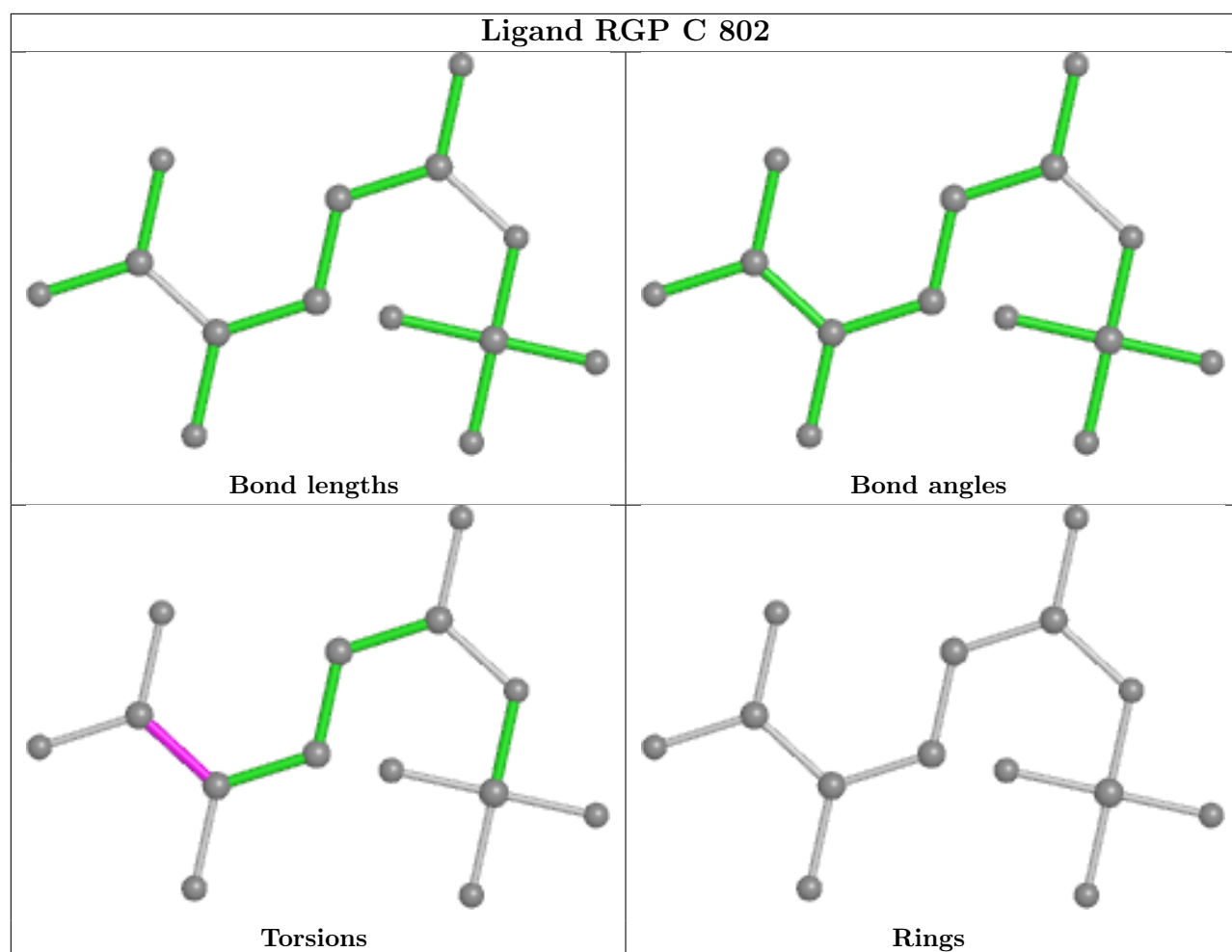
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	802	RGP	2	0
2	C	801	ADP	2	0
3	A	802	RGP	2	0
3	D	802	RGP	2	0
2	D	801	ADP	1	0
3	C	802	RGP	2	0
2	A	801	ADP	2	0
2	B	801	ADP	2	0

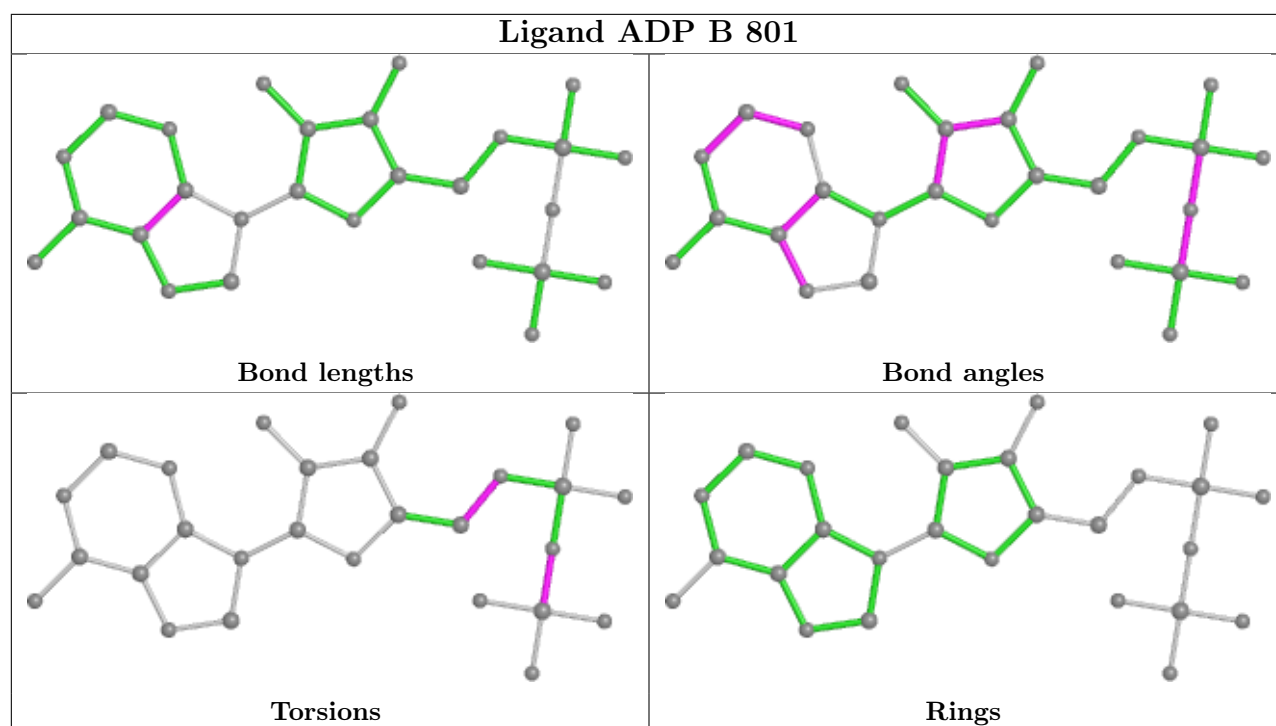
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











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.

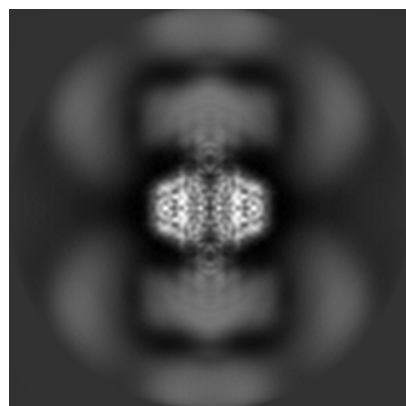
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35901. These allow visual inspection of the internal detail of the map and identification of artifacts.

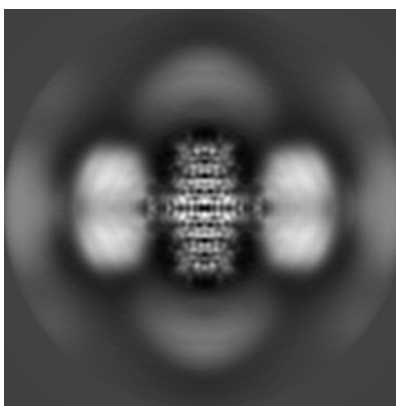
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

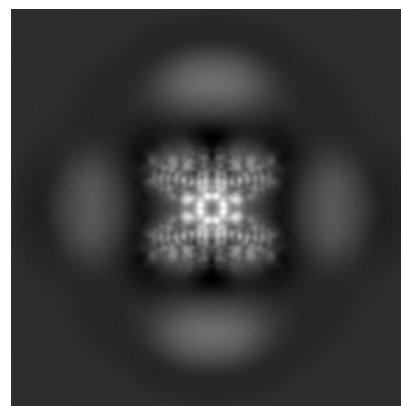
6.1.1 Primary map



X

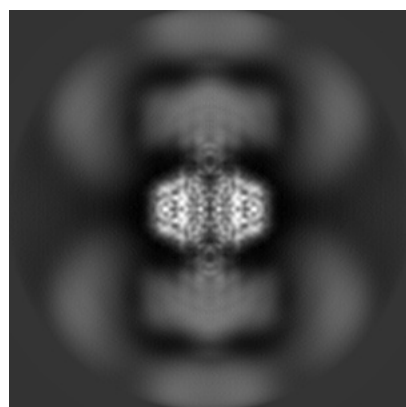


Y

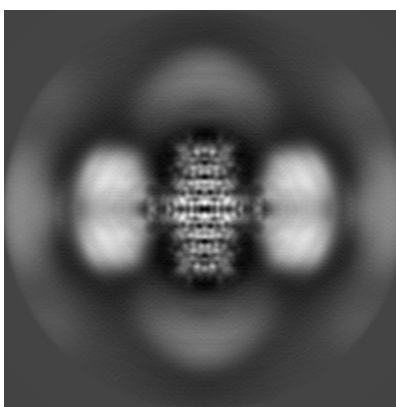


Z

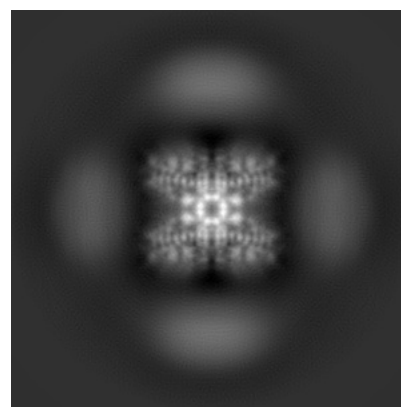
6.1.2 Raw map



X



Y

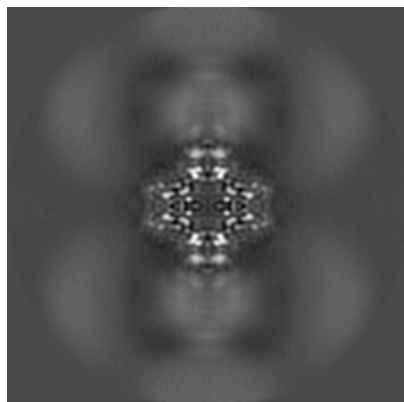


Z

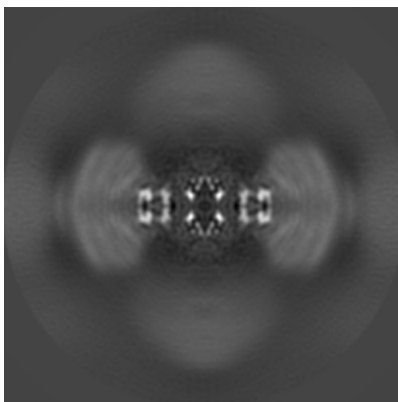
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

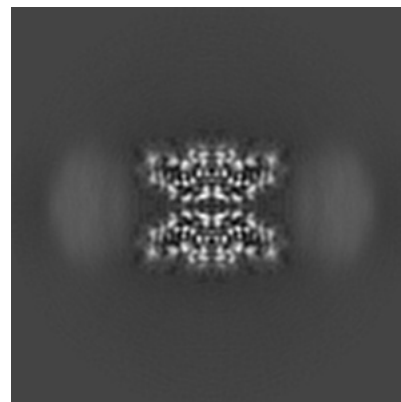
6.2.1 Primary map



X Index: 120

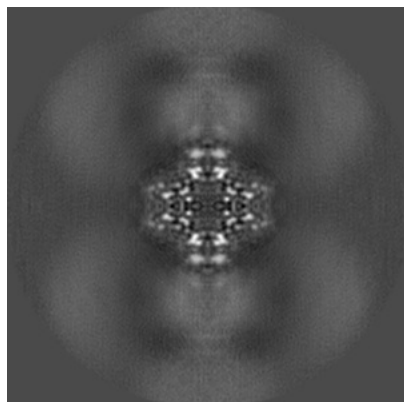


Y Index: 120

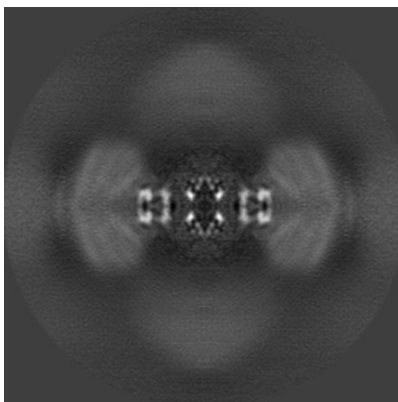


Z Index: 120

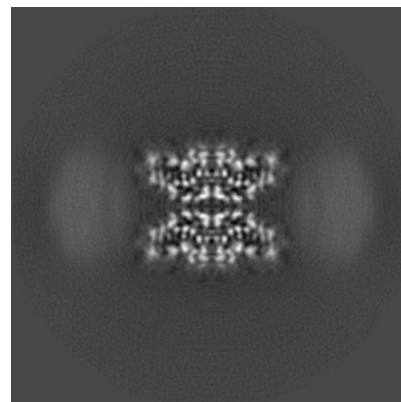
6.2.2 Raw map



X Index: 120



Y Index: 120

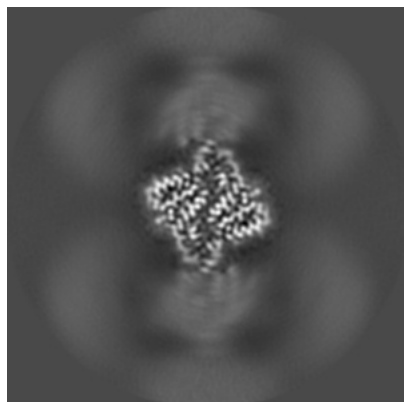


Z Index: 120

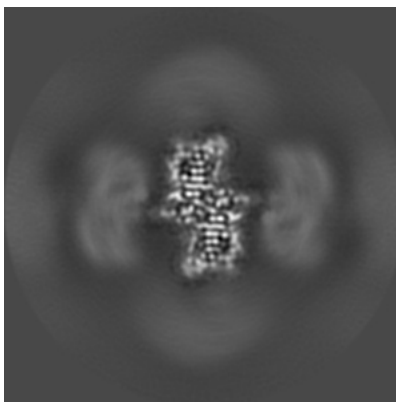
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

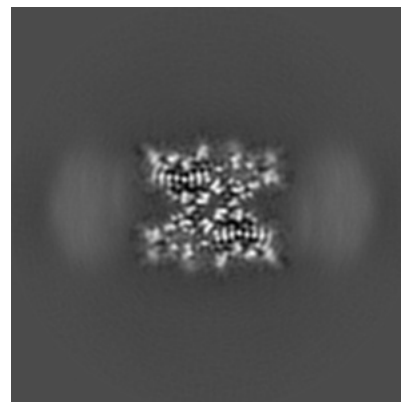
6.3.1 Primary map



X Index: 116

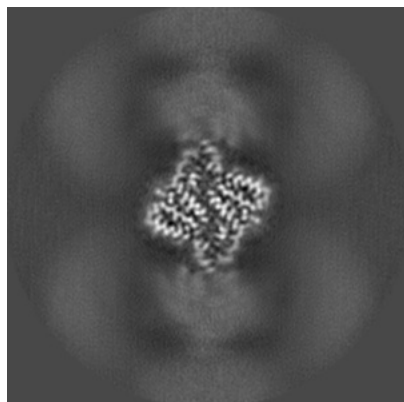


Y Index: 104

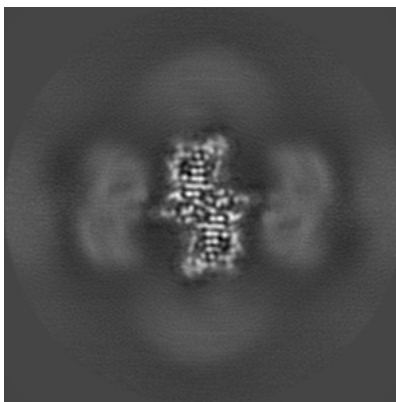


Z Index: 116

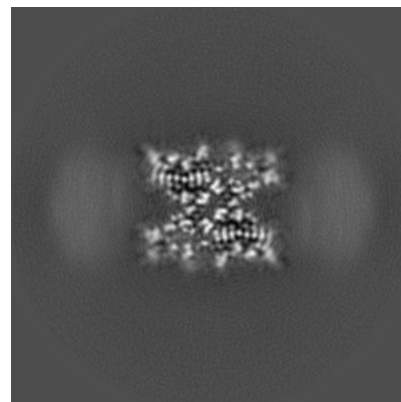
6.3.2 Raw map



X Index: 124



Y Index: 104

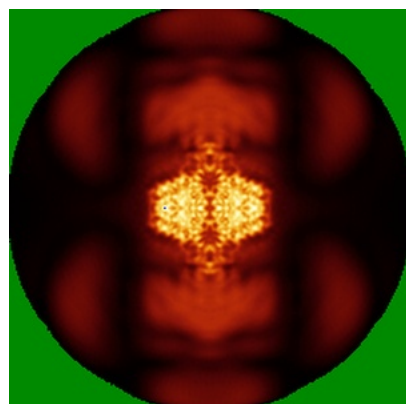


Z Index: 116

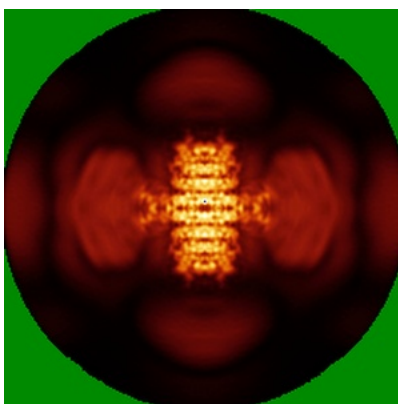
The images above show the largest variance slices of the map in three orthogonal directions.

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

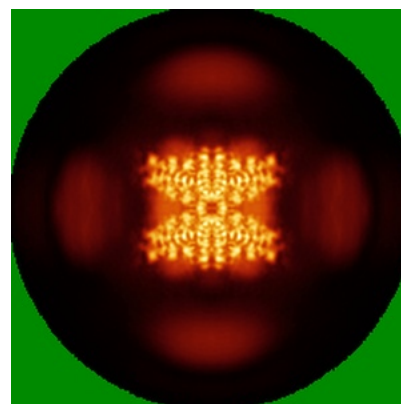
6.4.1 Primary map



X

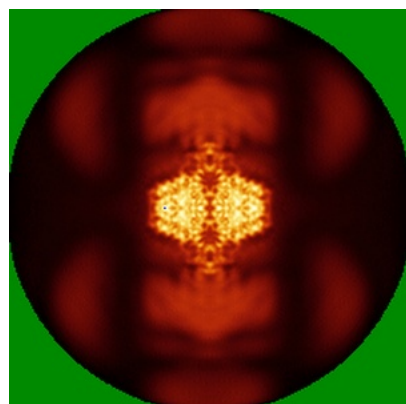


Y

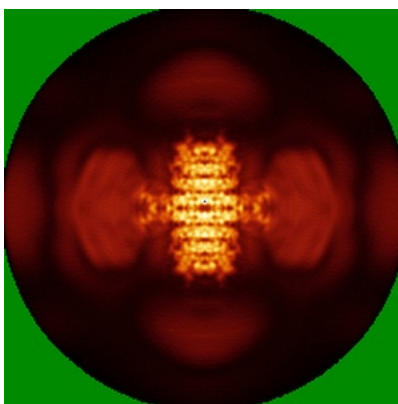


Z

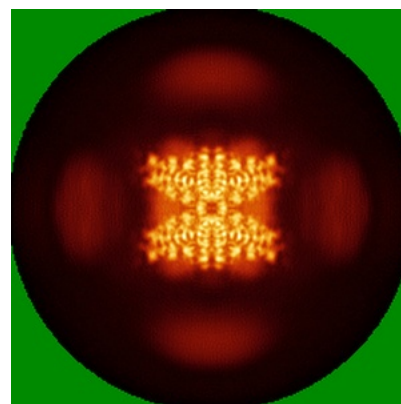
6.4.2 Raw map



X



Y

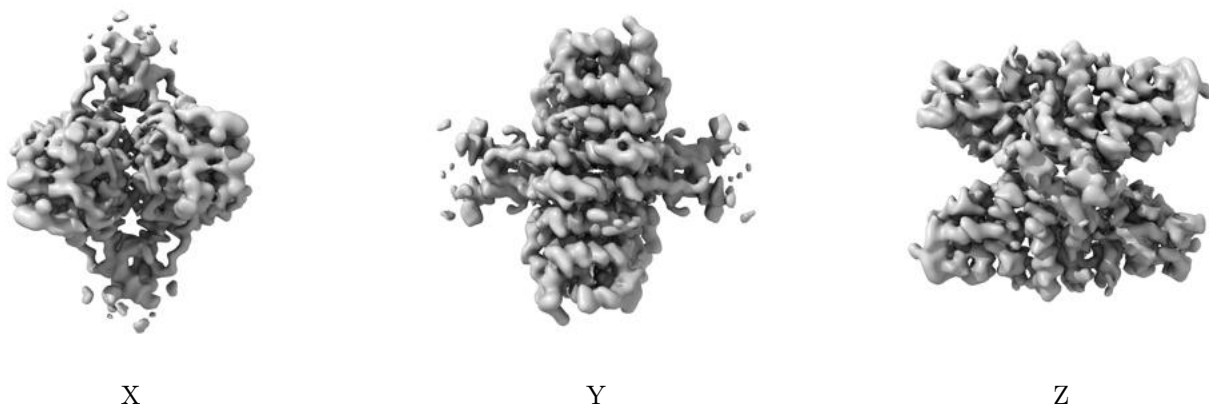


Z

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.

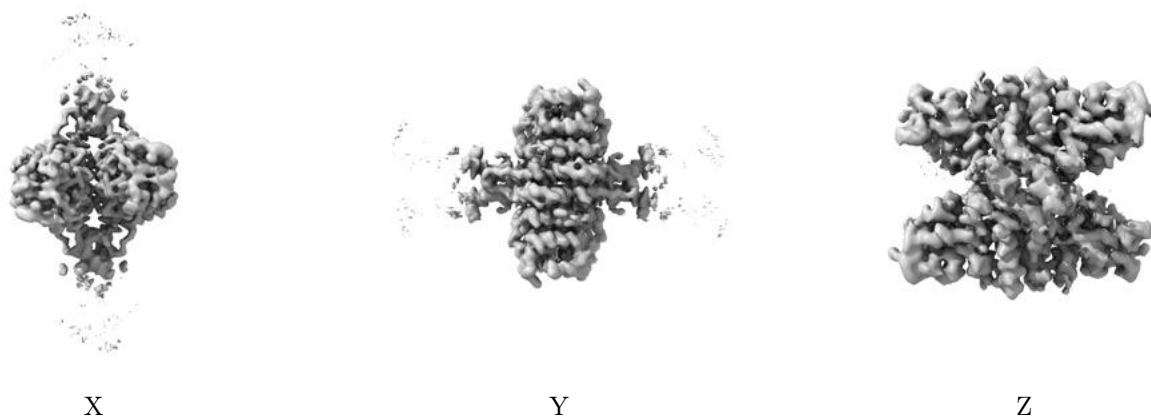
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. 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.

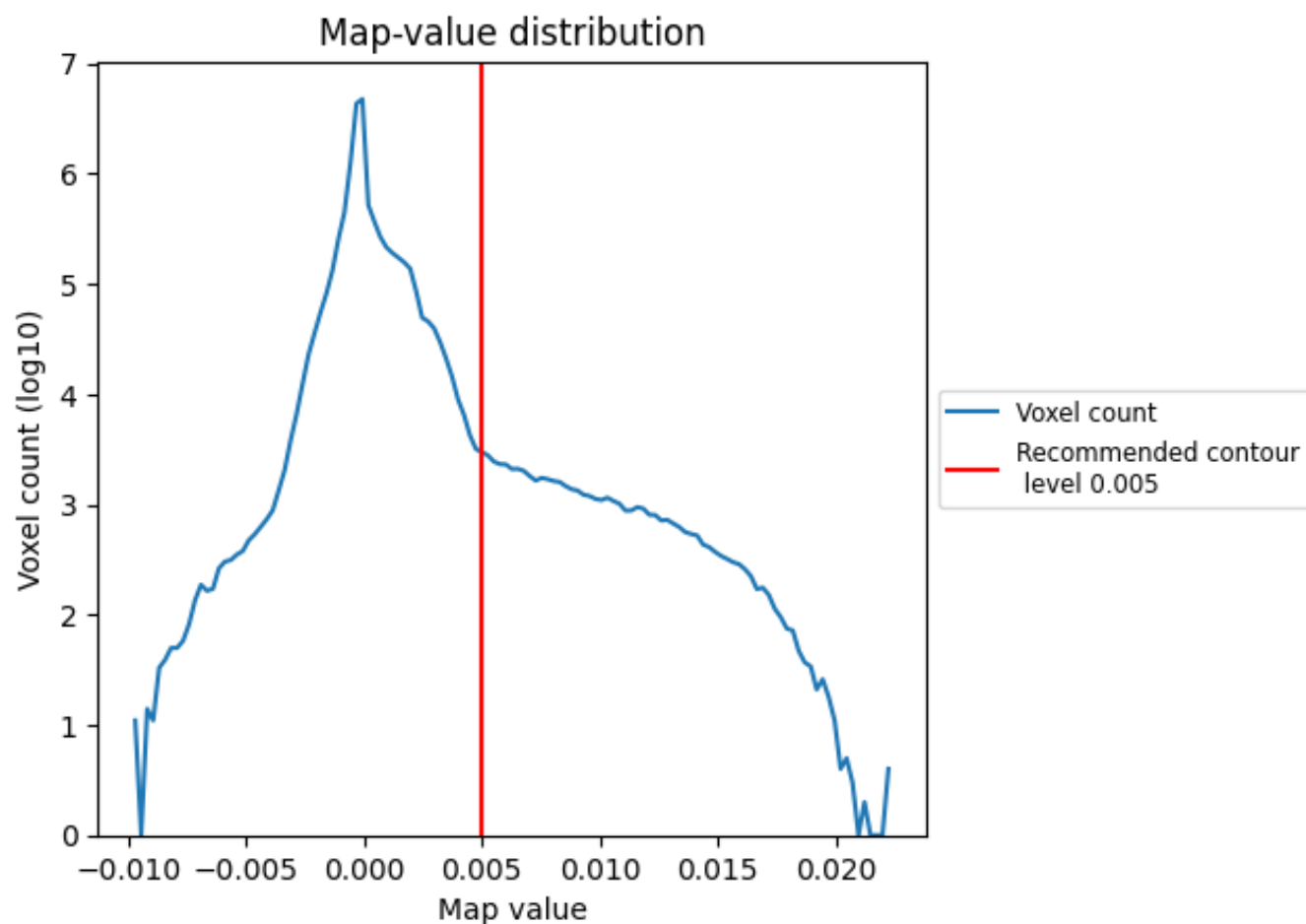
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

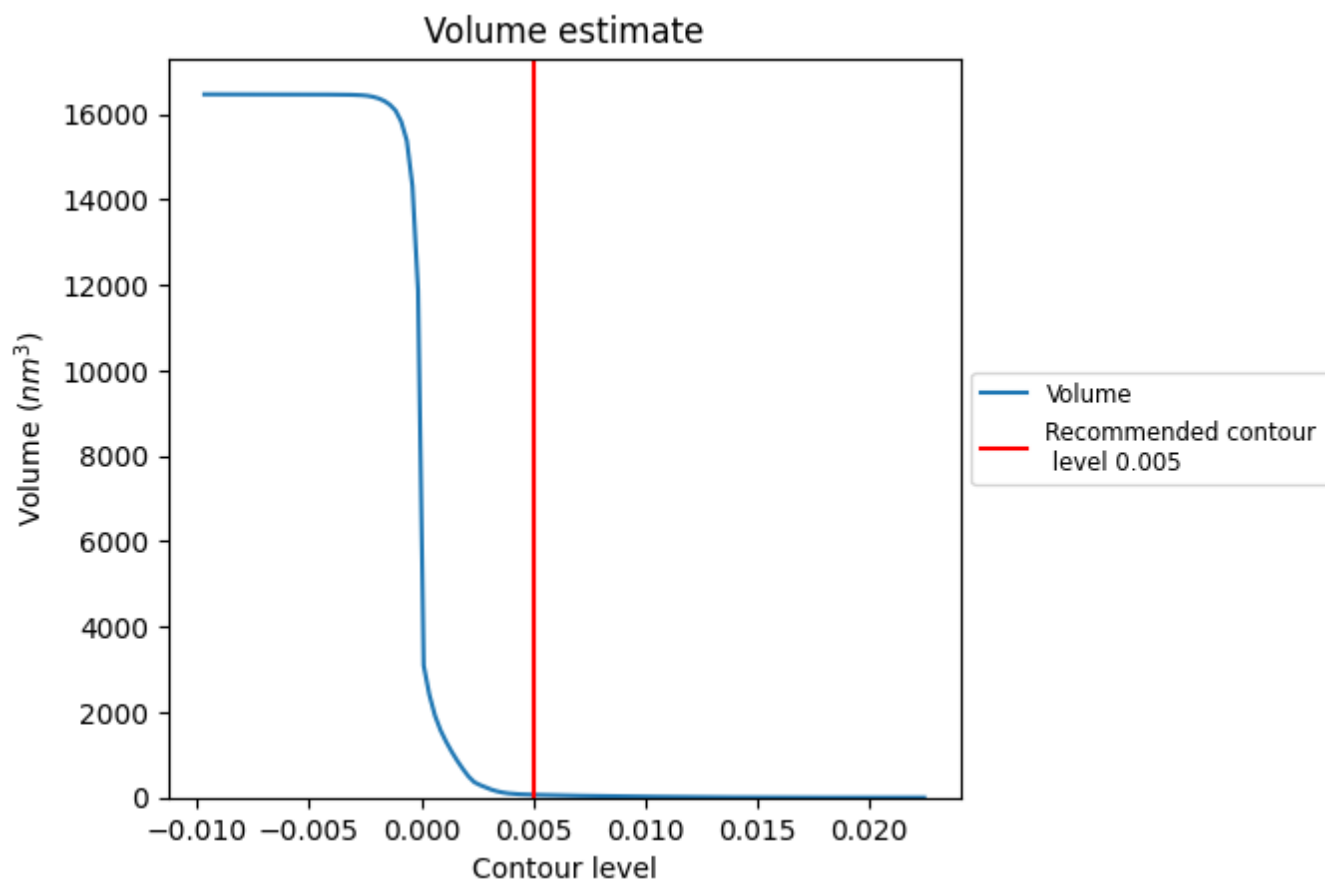
This section contains the results of statistical analysis of the map.

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.

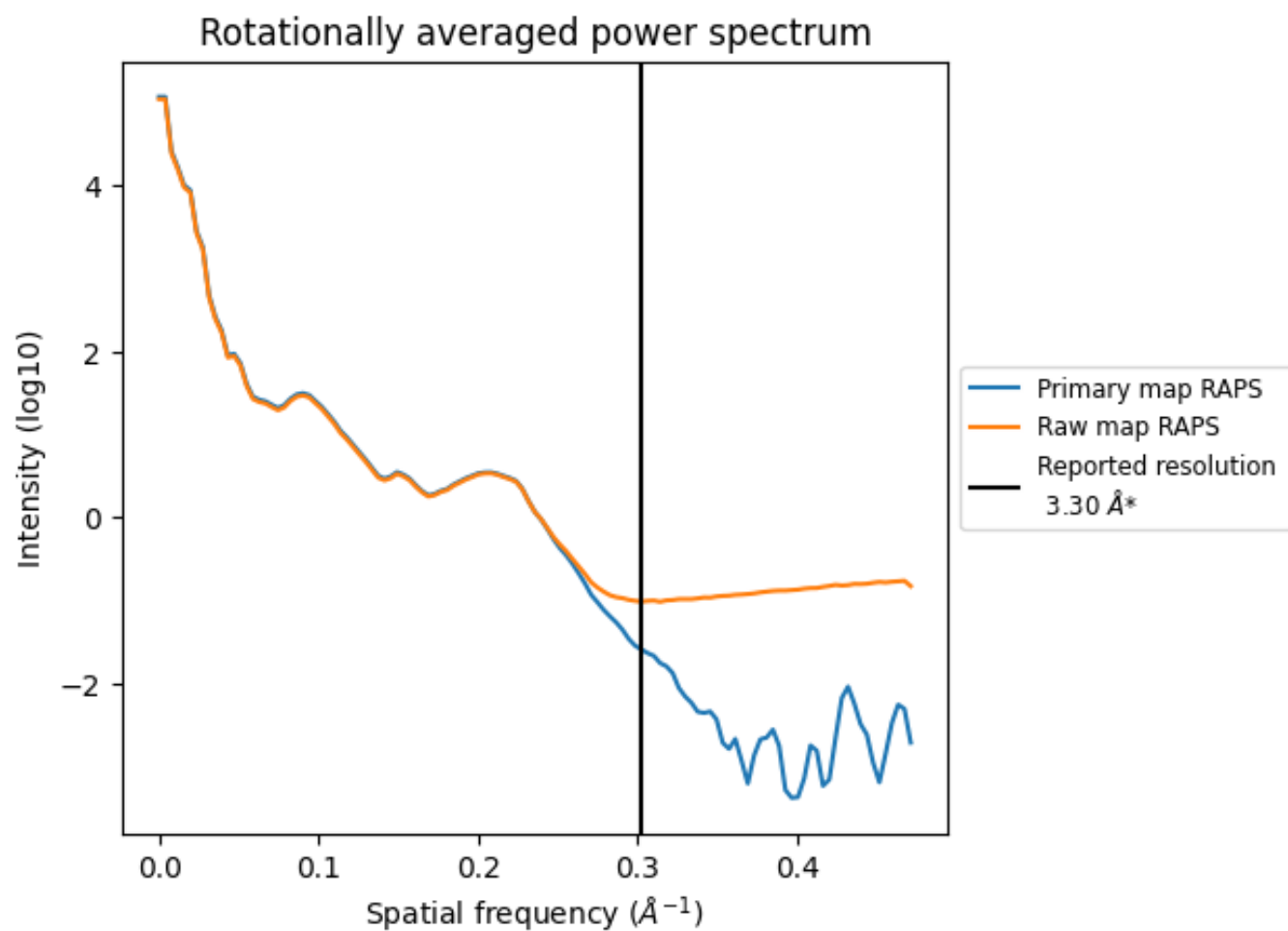
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 66 nm³; this corresponds to an approximate mass of 59 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 ⓘ

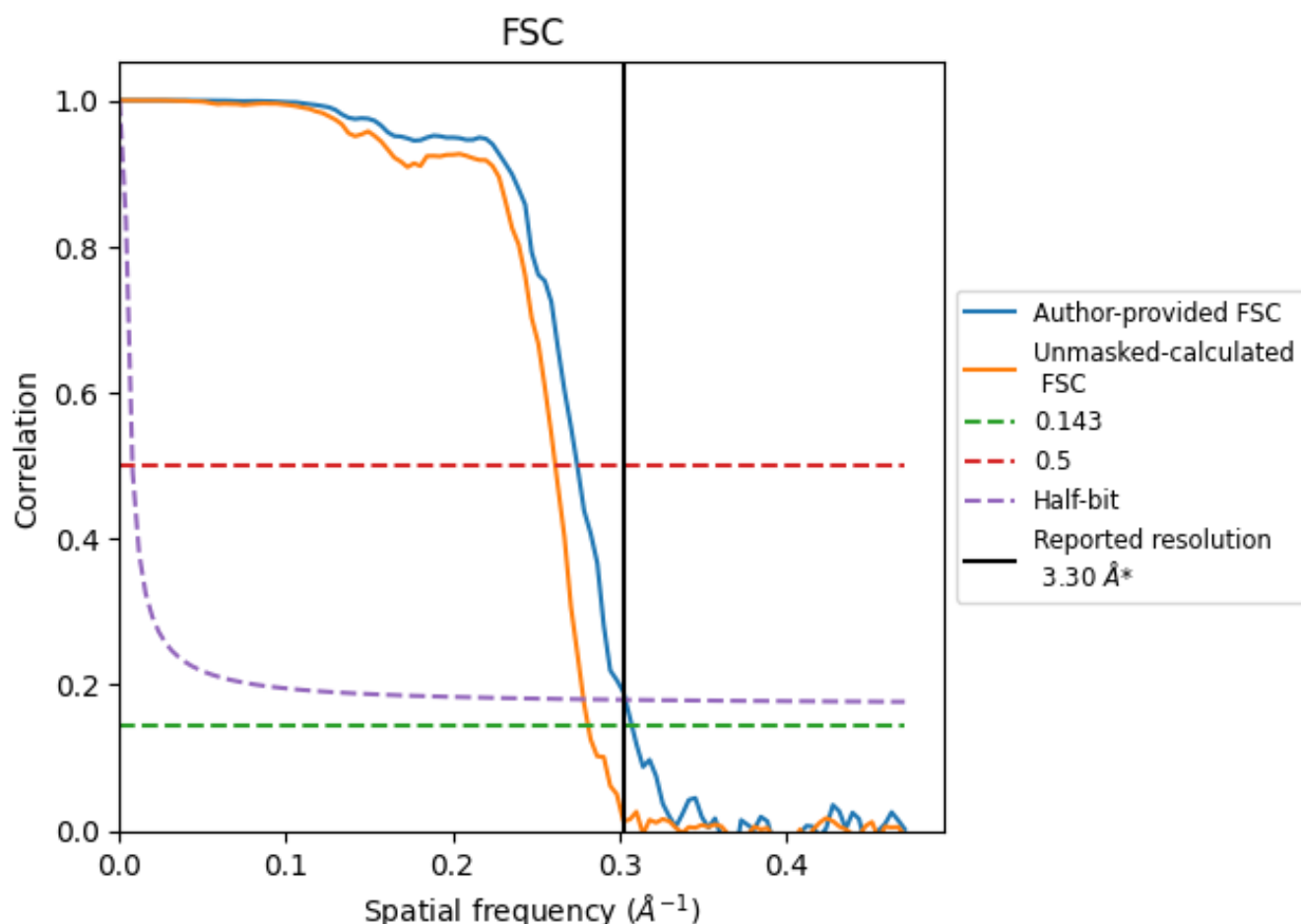


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 \AA^{-1}

8.2 Resolution estimates [i](#)

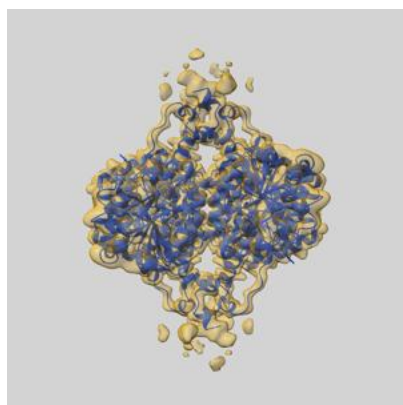
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.25	3.64	3.29
Unmasked-calculated*	3.55	3.82	3.59

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

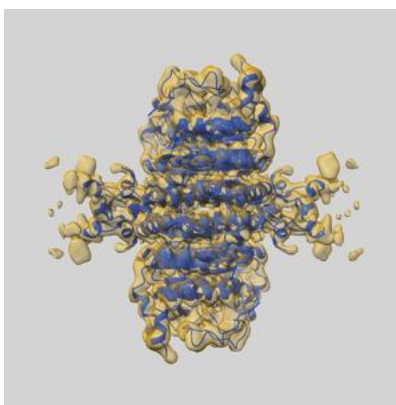
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35901 and PDB model 8J0F. Per-residue inclusion information can be found in section [3](#) on page [6](#).

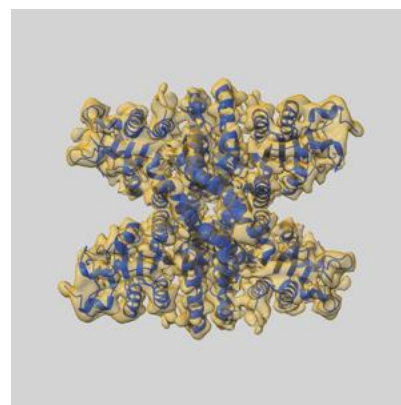
9.1 Map-model overlay [i](#)



X



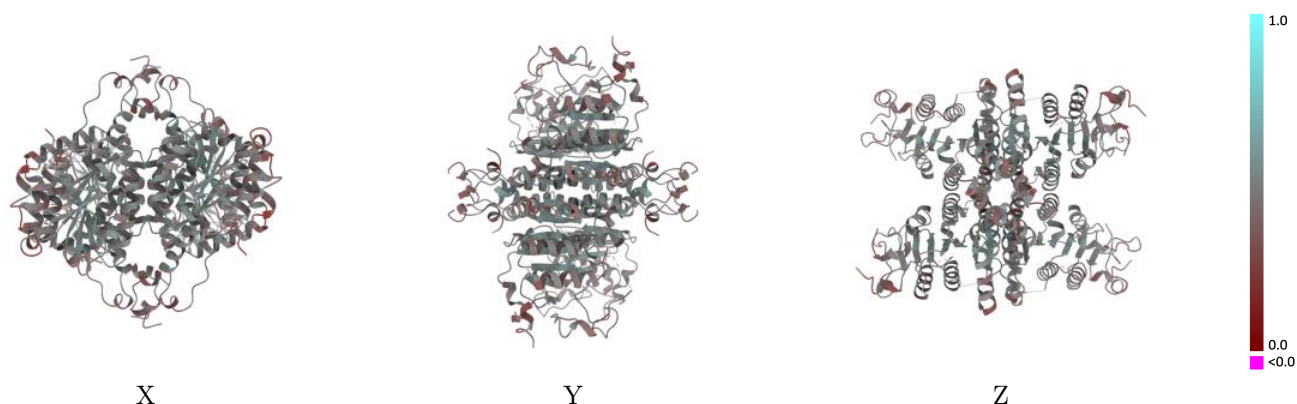
Y



Z

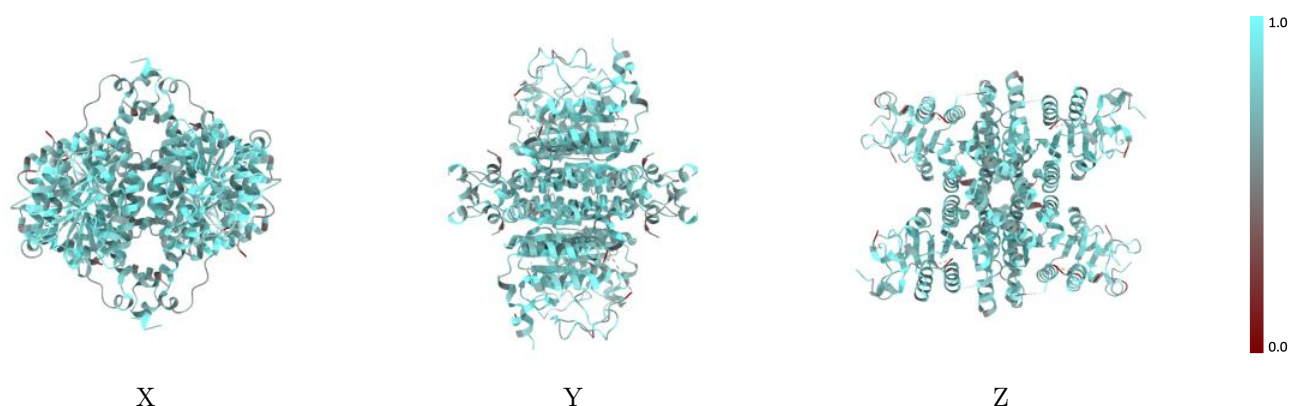
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



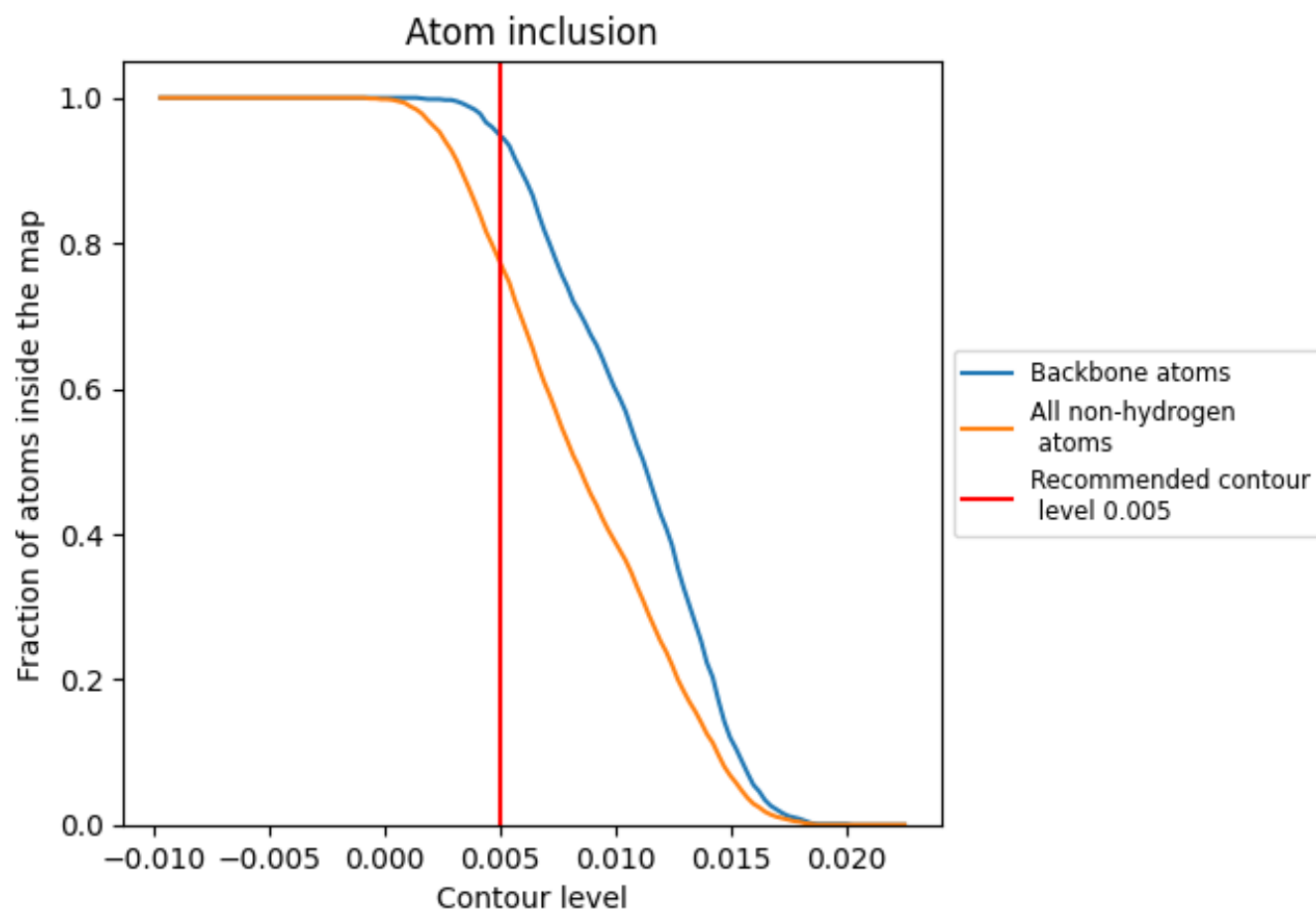
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 77% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.7730</div>	<div><div></div>0.4560</div>
A	<div><div></div>0.7750</div>	<div><div></div>0.4600</div>
B	<div><div></div>0.7810</div>	<div><div></div>0.4600</div>
C	<div><div></div>0.7790</div>	<div><div></div>0.4590</div>
D	<div><div></div>0.7790</div>	<div><div></div>0.4600</div>
E	<div><div></div>0.6860</div>	<div><div></div>0.3880</div>
F	<div><div></div>0.6860</div>	<div><div></div>0.3920</div>
G	<div><div></div>0.6860</div>	<div><div></div>0.3980</div>
H	<div><div></div>0.6780</div>	<div><div></div>0.3900</div>

1.0

0.0

<0.0