



wwPDB EM Validation Summary Report ⓘ

Feb 20, 2025 – 02:28 PM EST

PDB ID : 8EUM
EMDB ID : EMD-28615
Title : MicroED structure of an Aeropyrum pernix protoglobin mutant
Authors : Danelius, E.; Gonen, T.; Unge, J.T.
Deposited on : 2022-10-18
Resolution : 2.10 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.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
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) : 2.41.4

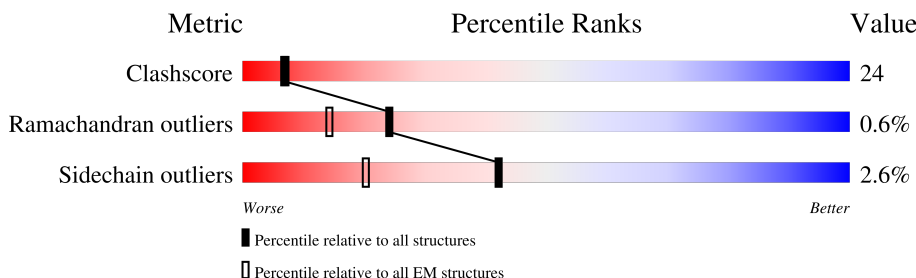
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON CRYSTALLOGRAPHY

The reported resolution of this entry is 2.10 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 ≥ 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	190	<div> <div>7%</div> <div>61%</div> <div>35%</div> <div>...</div> </div>
1	B	190	<div> <div>7%</div> <div>63%</div> <div>32%</div> <div>...</div> </div>
1	C	190	<div> <div>7%</div> <div>62%</div> <div>34%</div> <div>...</div> </div>
1	D	190	<div> <div>65%</div> <div>28%</div> <div>5%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6745 atoms, of which 55 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 Protogloblin ApPgb.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	187	Total	C	N	O	S	0	0
			1552	1008	260	281	3		
1	B	187	Total	C	N	O	S	0	0
			1551	1008	260	280	3		
1	C	187	Total	C	N	O	S	0	0
			1552	1008	260	281	3		
1	D	180	Total	C	N	O	S	0	0
			1476	961	242	270	3		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	45	GLY	CYS	engineered mutation	UNP Q9YFF4
A	59	LEU	TRP	engineered mutation	UNP Q9YFF4
A	60	VAL	TYR	engineered mutation	UNP Q9YFF4
A	63	ARG	VAL	engineered mutation	UNP Q9YFF4
A	102	SER	CYS	engineered mutation	UNP Q9YFF4
A	145	GLN	PHE	engineered mutation	UNP Q9YFF4
A	149	LEU	ILE	engineered mutation	UNP Q9YFF4
B	45	GLY	CYS	engineered mutation	UNP Q9YFF4
B	59	LEU	TRP	engineered mutation	UNP Q9YFF4
B	60	VAL	TYR	engineered mutation	UNP Q9YFF4
B	63	ARG	VAL	engineered mutation	UNP Q9YFF4
B	102	SER	CYS	engineered mutation	UNP Q9YFF4
B	145	GLN	PHE	engineered mutation	UNP Q9YFF4
B	149	LEU	ILE	engineered mutation	UNP Q9YFF4
C	45	GLY	CYS	engineered mutation	UNP Q9YFF4
C	59	LEU	TRP	engineered mutation	UNP Q9YFF4
C	60	VAL	TYR	engineered mutation	UNP Q9YFF4
C	63	ARG	VAL	engineered mutation	UNP Q9YFF4
C	102	SER	CYS	engineered mutation	UNP Q9YFF4
C	145	GLN	PHE	engineered mutation	UNP Q9YFF4
C	149	LEU	ILE	engineered mutation	UNP Q9YFF4
D	45	GLY	CYS	engineered mutation	UNP Q9YFF4

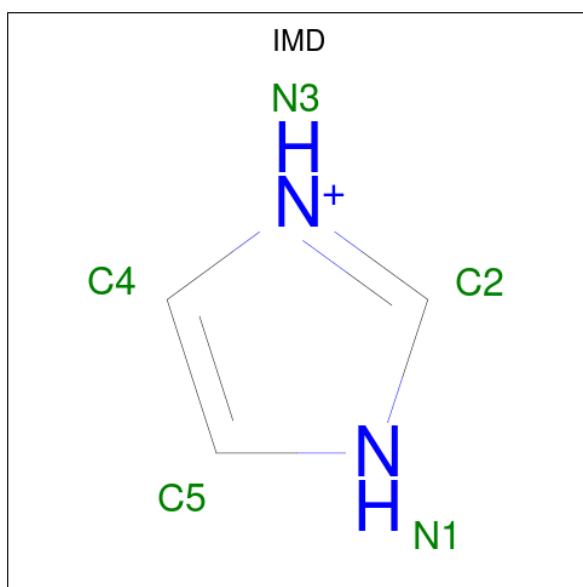
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Chain	Residue	Modelled	Actual	Comment	Reference
D	59	LEU	TRP	engineered mutation	UNP Q9YFF4
D	60	VAL	TYR	engineered mutation	UNP Q9YFF4
D	63	ARG	VAL	engineered mutation	UNP Q9YFF4
D	102	SER	CYS	engineered mutation	UNP Q9YFF4
D	145	GLN	PHE	engineered mutation	UNP Q9YFF4
D	149	LEU	ILE	engineered mutation	UNP Q9YFF4

- # HEM

Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0

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Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total 5	C 3	N 2	0	
3	A	1	Total 10	C 3	H 5 N 2	0	
3	A	1	Total 10	C 3	H 5 N 2	0	
3	A	1	Total 10	C 3	H 5 N 2	0	
3	A	1	Total 10	C 3	H 5 N 2	0	
3	B	1	Total 5	C 3	N 2	0	
3	B	1	Total 10	C 3	H 5 N 2	0	
3	C	1	Total 10	C 3	H 5 N 2	0	
3	C	1	Total 10	C 3	H 5 N 2	0	
3	C	1	Total 5	C 3	N 2	0	
3	C	1	Total 10	C 3	H 5 N 2	0	
3	C	1	Total 10	C 3	H 5 N 2	0	
3	C	1	Total 10	C 3	H 5 N 2	0	
3	D	1	Total 5	C 3	N 2	0	

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Mol	Chain	Residues	Atoms				AltConf
3	D	1	Total	C	H	N	0
			10	3	5	2	

- Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe).

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

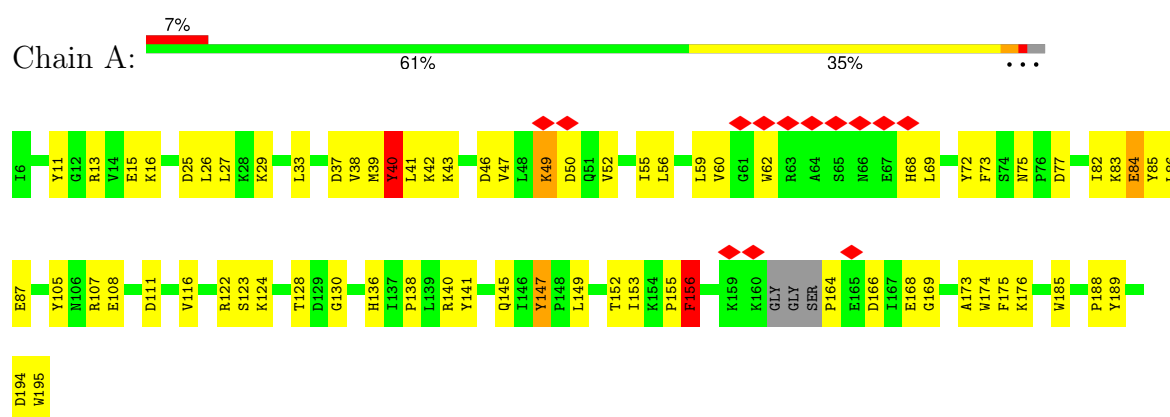
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		AltConf
5	A	68	Total	O	0
			68	68	
5	B	69	Total	O	0
			69	69	
5	C	81	Total	O	0
			81	81	
5	D	90	Total	O	0
			90	90	

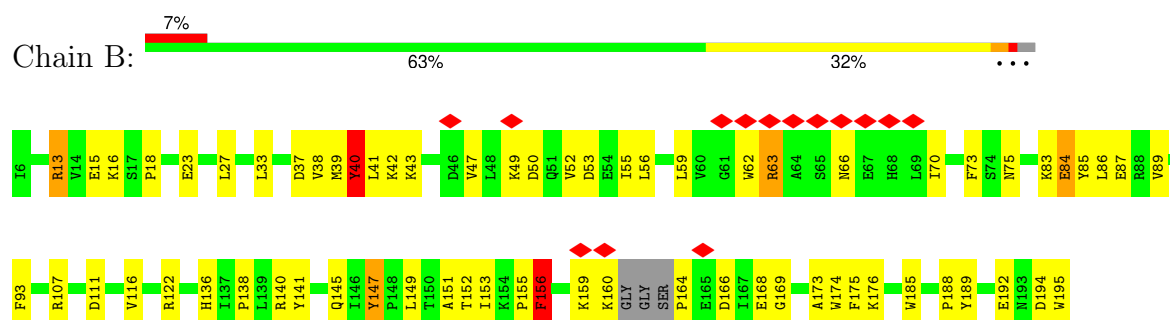
3 Residue-property plots

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.

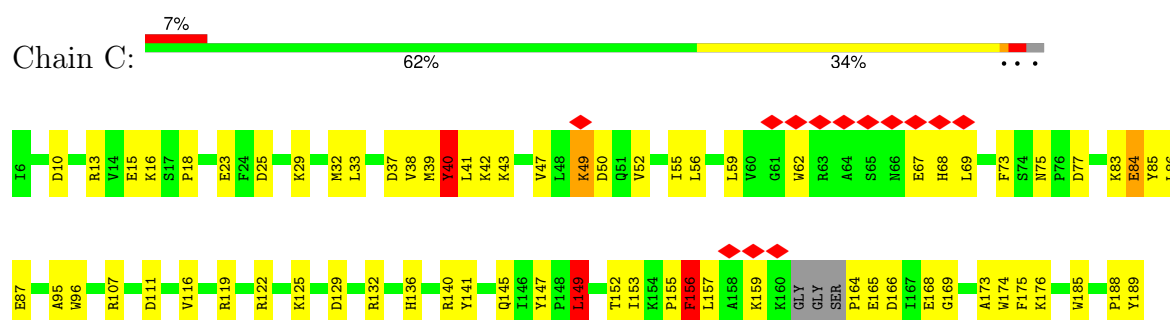
• Molecule 1: Protogloblin ApPgb



• Molecule 1: Protogloblin ApPgb

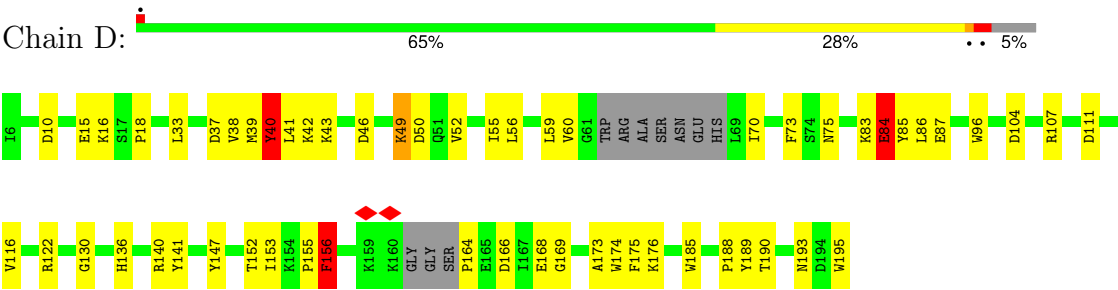


• Molecule 1: Protogloblin ApPgb





● Molecule 1: Protogloblin ApPgb



4 Experimental information

Property	Value	Source
EM reconstruction method	CRYSTALLOGRAPHY	Depositor
Imposed symmetry	3D CRYSTAL, $a=46.2$ Å, $b=58.3$ Å, $c=80.7$ Å, $\alpha=104.1^\circ$, $\beta=98.6^\circ$, $\gamma=90.1^\circ$, space group=P1	Depositor
Number of images used	Not provided	
Resolution determination method	DIFFRACTION PATTERN/LAYERLINES	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	0.00025	Depositor
Minimum defocus (nm)	0	Depositor
Maximum defocus (nm)	0	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	9.949	Depositor
Minimum map value	-3.492	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.948	Depositor
Recommended contour level	1.41858	Depositor
Map size (Å)	97.60764, 86.918076, 98.899025	wwPDB
Map dimensions	196, 179, 190	wwPDB
Map angles ($^\circ$)	104.095, 98.5833, 90.109	wwPDB
Pixel spacing (Å)	0.51372445, 0.48557585, 0.5045869	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE, HEM, IMD

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	0.61	0/1595	0.97	8/2163 (0.4%)
1	B	0.60	0/1594	0.95	8/2161 (0.4%)
1	C	0.61	0/1595	0.96	9/2163 (0.4%)
1	D	0.61	0/1515	0.96	9/2055 (0.4%)
All	All	0.61	0/6299	0.96	34/8542 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

There are no bond length outliers.

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	156	PHE	CB-CG-CD1	-14.24	110.83	120.80
1	B	156	PHE	CB-CG-CD1	-14.18	110.88	120.80
1	A	156	PHE	CB-CG-CD1	-14.15	110.89	120.80
1	D	156	PHE	CB-CG-CD1	-14.14	110.90	120.80
1	B	166	ASP	CB-CG-OD1	-10.94	108.45	118.30

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	156	PHE	Sidechain
1	A	40	TYR	Sidechain
1	B	156	PHE	Sidechain
1	B	40	TYR	Sidechain
1	C	40	TYR	Sidechain

5.2 Too-close contacts

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	1552	0	1537	89	1
1	B	1551	0	1537	79	1
1	C	1552	0	1537	78	1
1	D	1476	0	1453	54	1
2	A	43	0	30	15	0
2	B	43	0	30	9	0
2	C	43	0	30	11	0
2	D	43	0	30	8	0
3	A	25	20	24	2	0
3	B	10	5	9	1	0
3	C	30	25	28	1	0
3	D	10	5	9	1	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
5	A	68	0	0	9	0
5	B	69	0	0	19	0
5	C	81	0	0	18	2
5	D	90	0	0	9	2
All	All	6690	55	6254	303	4

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 24.

The worst 5 of 303 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:C:145:GLN:HG3	1:C:149:LEU:CD1	1.76	1.15
1:C:145:GLN:HG3	1:C:149:LEU:HD11	1.07	1.07
1:A:145:GLN:HG3	1:A:149:LEU:HD12	1.28	1.06
1:C:13:ARG:NH2	5:C:304:HOH:O	1.96	0.96
1:C:165:GLU:OE2	5:C:301:HOH:O	1.83	0.94

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:380:HOH:O	5:D:367:HOH:O[1_445]	1.92	0.28
5:C:380:HOH:O	5:D:373:HOH:O[1_445]	2.03	0.17
1:A:15:GLU:OE2	1:D:75:ASN:ND2[1_455]	2.15	0.05
1:B:75:ASN:ND2	1:C:15:GLU:OE2[1_455]	2.15	0.05

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	183/190 (96%)	175 (96%)	7 (4%)	1 (0%)	25	23
1	B	183/190 (96%)	175 (96%)	7 (4%)	1 (0%)	25	23
1	C	183/190 (96%)	174 (95%)	8 (4%)	1 (0%)	25	23
1	D	174/190 (92%)	168 (97%)	5 (3%)	1 (1%)	22	19
All	All	723/760 (95%)	692 (96%)	27 (4%)	4 (1%)	24	19

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	LYS
1	B	49	LYS
1	C	49	LYS

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Mol	Chain	Res	Type
1	D	49	LYS

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	166/168 (99%)	162 (98%)	4 (2%)	44	49
1	B	166/168 (99%)	161 (97%)	5 (3%)	36	40
1	C	166/168 (99%)	162 (98%)	4 (2%)	44	49
1	D	157/168 (94%)	153 (98%)	4 (2%)	42	47
All	All	655/672 (98%)	638 (97%)	17 (3%)	42	46

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	50	ASP
1	D	175	PHE
1	B	63	ARG
1	B	175	PHE
1	C	39	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	66	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 23 ligands modelled in this entry, 4 are monoatomic - leaving 19 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	IMD	D	203	4	3,5,5	0.51	0	4,5,5	0.54	0
3	IMD	C	206	4	3,5,5	0.34	0	4,5,5	0.52	0
3	IMD	C	201	-	3,5,5	0.43	0	4,5,5	0.47	0
2	HEM	D	201	1,3	42,50,50	1.46	7 (16%)	46,82,82	2.10	8 (17%)
3	IMD	A	205	-	3,5,5	0.30	0	4,5,5	0.40	0
3	IMD	A	204	4	3,5,5	0.52	0	4,5,5	0.59	0
2	HEM	C	203	1,3	42,50,50	1.64	9 (21%)	46,82,82	2.10	13 (28%)
2	HEM	B	201	1,3	42,50,50	1.47	8 (19%)	46,82,82	1.83	11 (23%)
3	IMD	C	204	2	3,5,5	0.42	0	4,5,5	0.74	0
3	IMD	B	202	2	3,5,5	0.43	0	4,5,5	0.74	0
2	HEM	A	201	1,3	42,50,50	1.46	6 (14%)	46,82,82	1.72	12 (26%)
3	IMD	A	203	4	3,5,5	0.39	0	4,5,5	0.53	0
3	IMD	A	202	2	3,5,5	0.43	0	4,5,5	0.75	0
3	IMD	A	206	-	3,5,5	0.37	0	4,5,5	0.58	0
3	IMD	C	205	4	3,5,5	0.33	0	4,5,5	0.57	0
3	IMD	C	207	4	3,5,5	0.43	0	4,5,5	0.66	0
3	IMD	B	203	4	3,5,5	0.48	0	4,5,5	0.60	0
3	IMD	C	202	-	3,5,5	0.40	0	4,5,5	0.57	0
3	IMD	D	202	2	3,5,5	0.43	0	4,5,5	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
3	IMD	D	203	4	-	-	0/1/1/1
3	IMD	C	206	4	-	-	0/1/1/1
3	IMD	C	201	-	-	-	0/1/1/1
2	HEM	D	201	1,3	-	4/12/54/54	-
3	IMD	A	205	-	-	-	0/1/1/1
3	IMD	A	204	4	-	-	0/1/1/1
2	HEM	C	203	1,3	-	4/12/54/54	-
2	HEM	B	201	1,3	-	4/12/54/54	-
3	IMD	C	204	2	-	-	0/1/1/1
3	IMD	B	202	2	-	-	0/1/1/1
2	HEM	A	201	1,3	-	4/12/54/54	-
3	IMD	A	203	4	-	-	0/1/1/1
3	IMD	A	202	2	-	-	0/1/1/1
3	IMD	A	206	-	-	-	0/1/1/1
3	IMD	C	205	4	-	-	0/1/1/1
3	IMD	C	207	4	-	-	0/1/1/1
3	IMD	B	203	4	-	-	0/1/1/1
3	IMD	C	202	-	-	-	0/1/1/1
3	IMD	D	202	2	-	-	0/1/1/1

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	203	HEM	C3C-C2C	-4.05	1.34	1.40
2	D	201	HEM	C3C-C2C	-4.05	1.34	1.40
2	A	201	HEM	C3C-C2C	-3.89	1.35	1.40
2	A	201	HEM	CAB-C3B	3.26	1.56	1.47
2	B	201	HEM	C3C-C2C	-3.17	1.36	1.40

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	201	HEM	CBA-CAA-C2A	-9.05	97.32	112.54
2	B	201	HEM	CBA-CAA-C2A	-5.84	102.71	112.54
2	C	203	HEM	C3B-C4B-NB	-5.68	105.39	109.47
2	C	203	HEM	C2C-C3C-C4C	5.48	110.72	106.90
2	C	203	HEM	CBA-CAA-C2A	-4.87	104.35	112.54

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

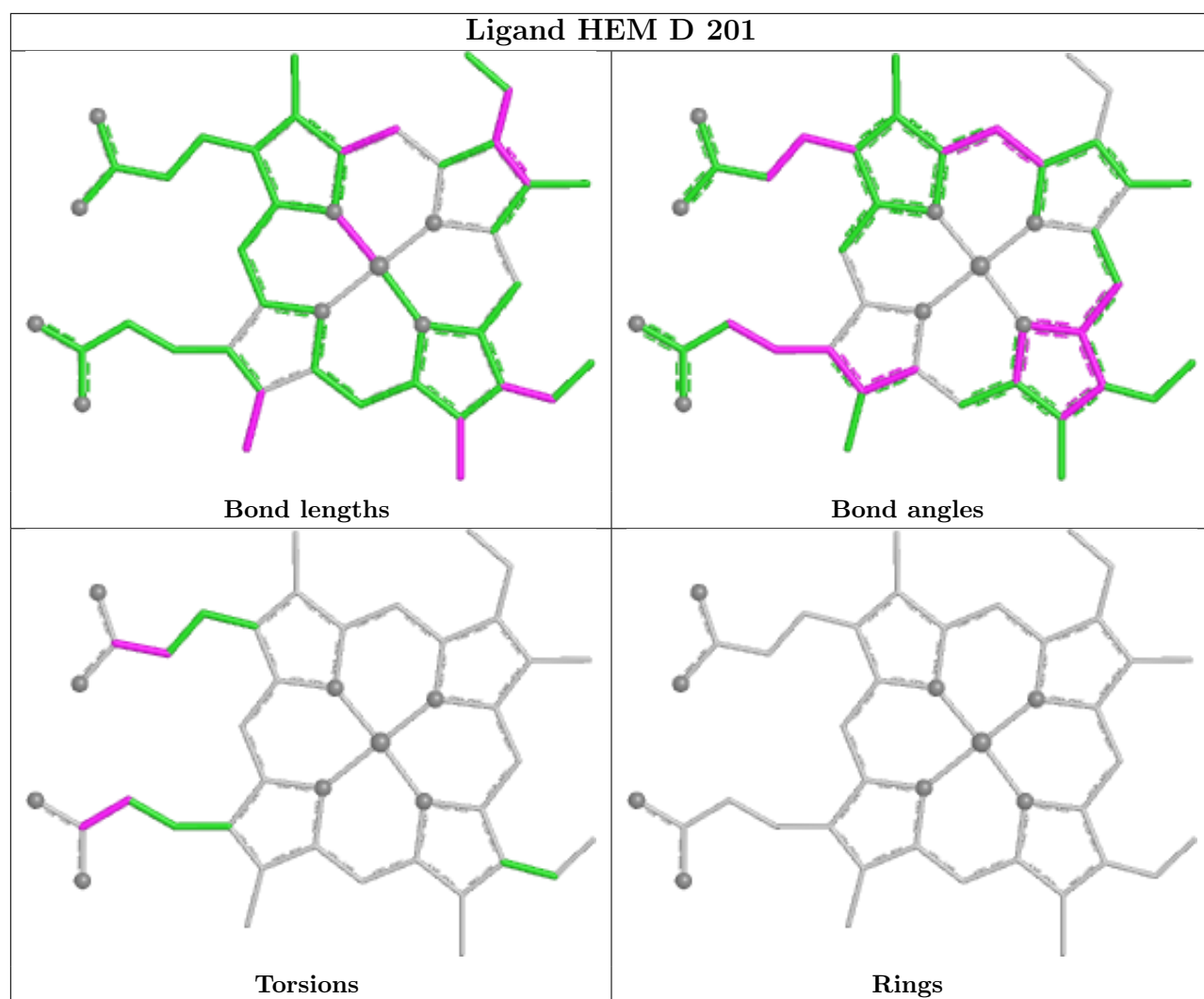
Mol	Chain	Res	Type	Atoms
2	B	201	HEM	CAD-CBD-CGD-O2D
2	D	201	HEM	CAA-CBA-CGA-O1A
2	D	201	HEM	CAD-CBD-CGD-O1D
2	B	201	HEM	CAD-CBD-CGD-O1D
2	D	201	HEM	CAD-CBD-CGD-O2D

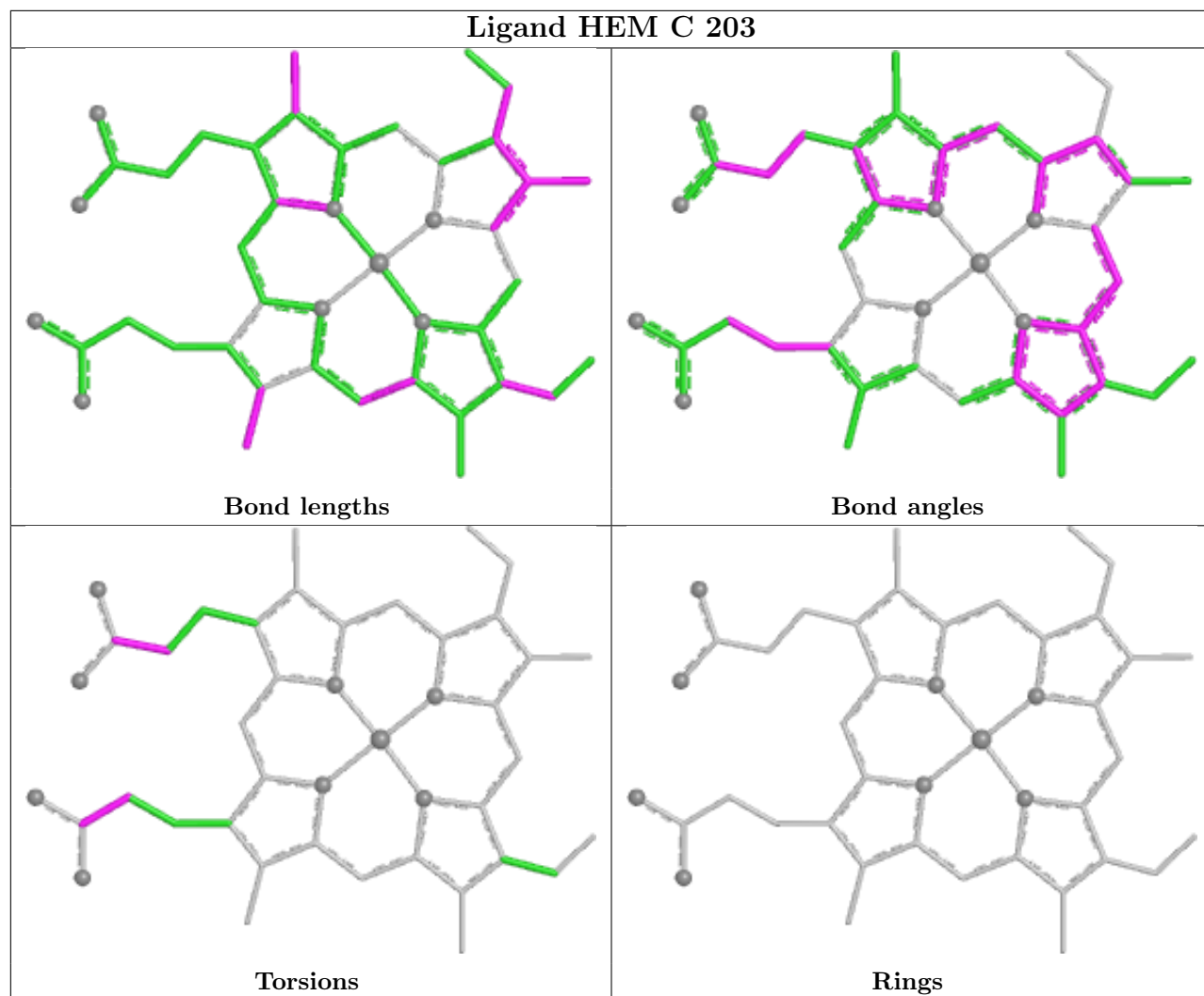
There are no ring outliers.

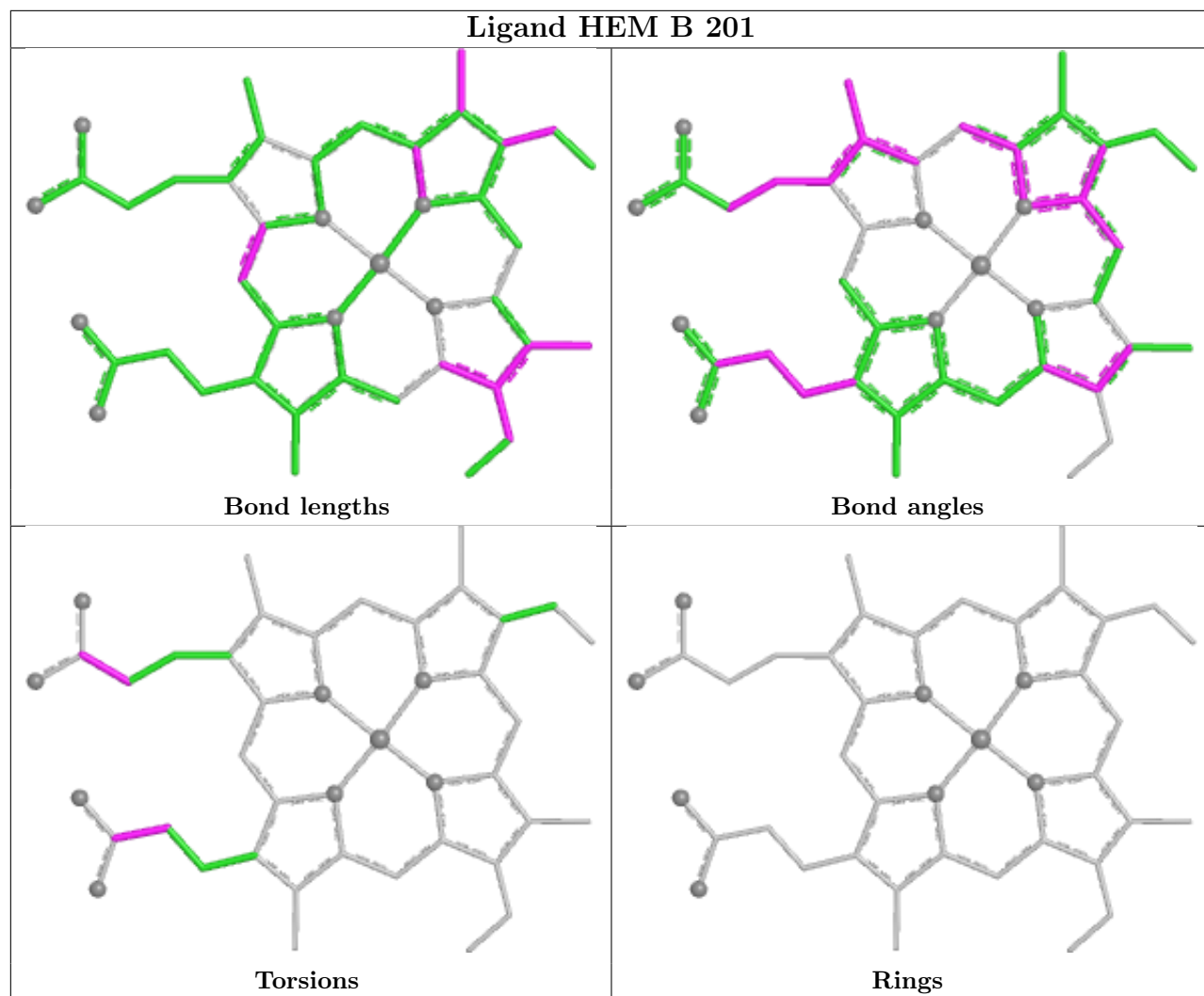
9 monomers are involved in 48 short contacts:

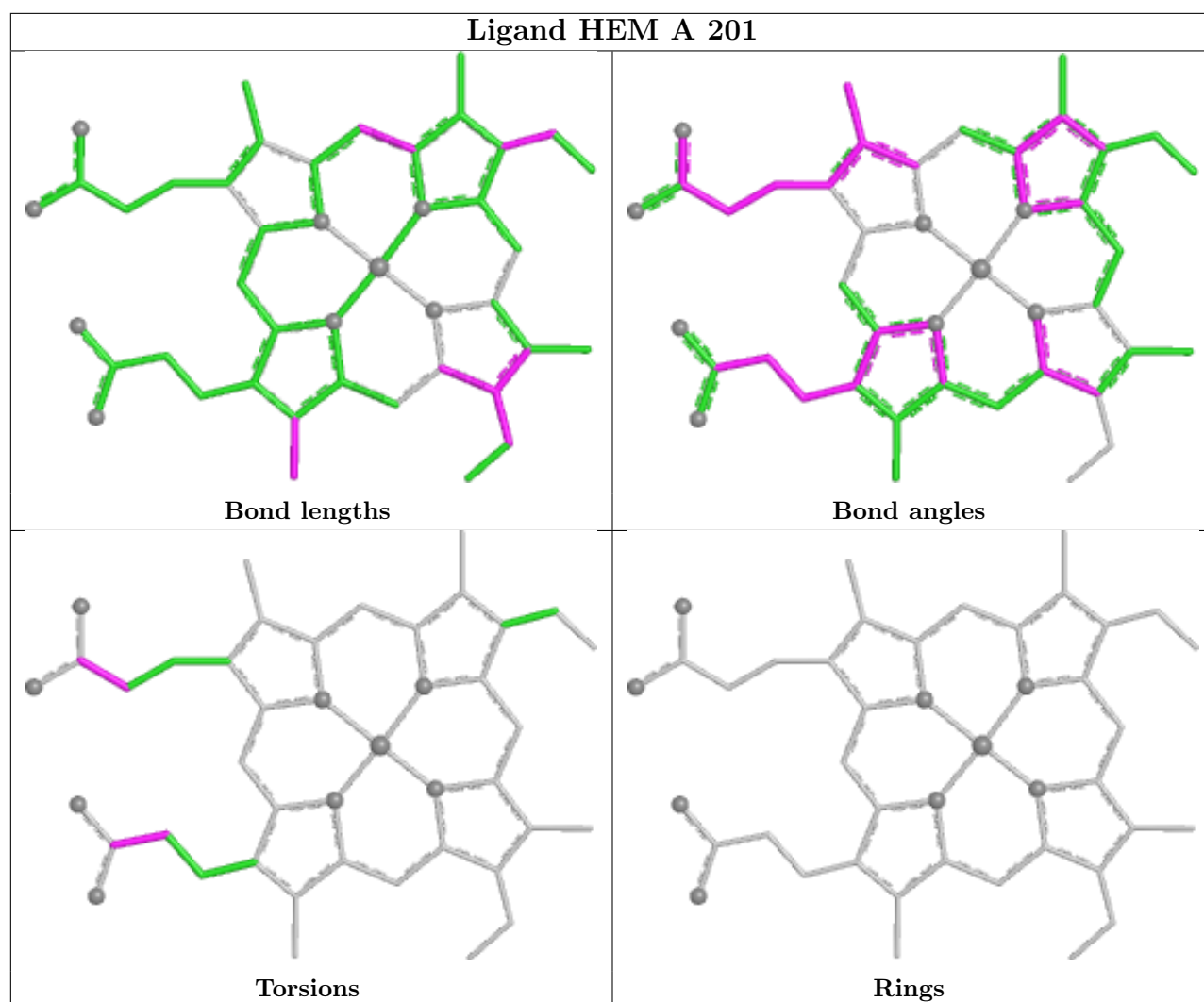
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	201	HEM	8	0
2	C	203	HEM	11	0
2	B	201	HEM	9	0
2	A	201	HEM	15	0
3	A	202	IMD	1	0
3	A	206	IMD	1	0
3	C	207	IMD	1	0
3	B	203	IMD	1	0
3	D	202	IMD	1	0

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.









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.

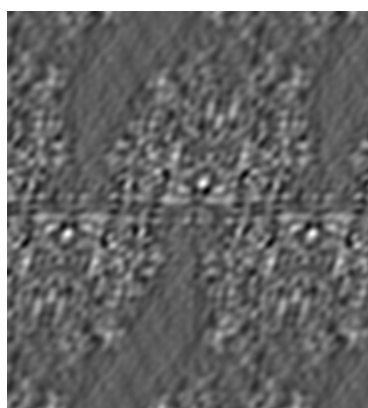
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28615. These allow visual inspection of the internal detail of the map and identification of artifacts.

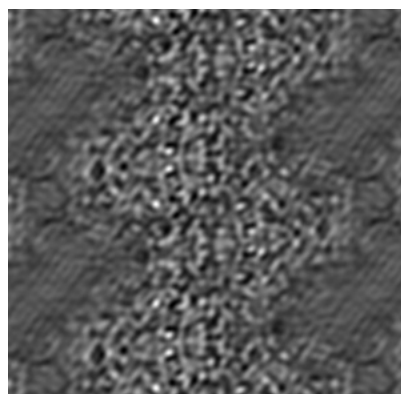
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

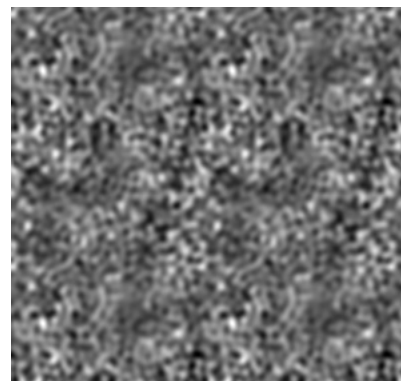
6.1.1 Primary map



X



Y

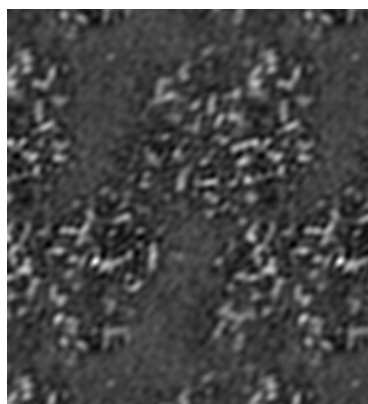


Z

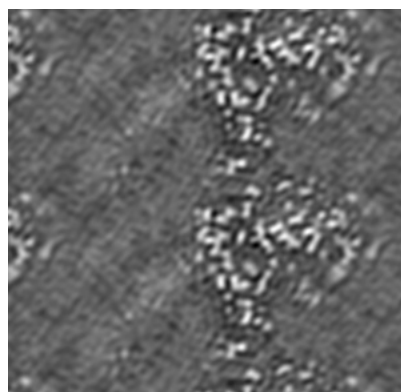
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

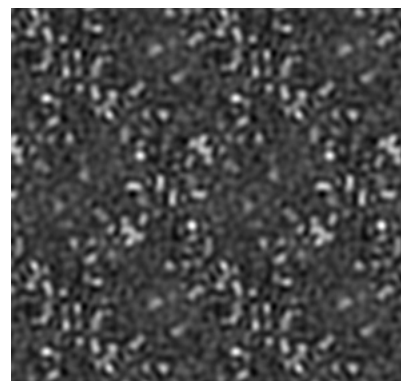
6.2.1 Primary map



X Index: 95



Y Index: 89

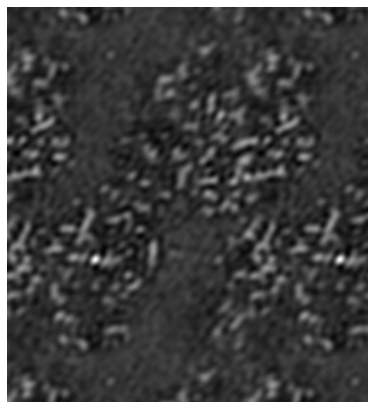


Z Index: 98

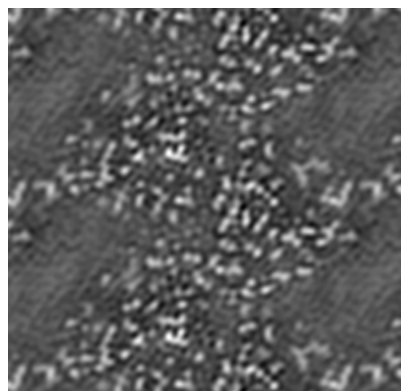
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

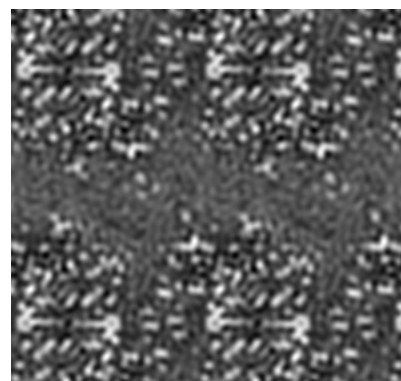
6.3.1 Primary map



X Index: 4



Y Index: 0

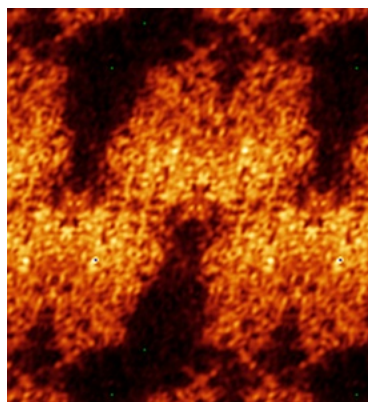


Z Index: 87

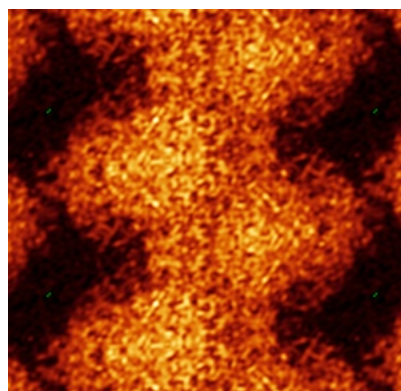
The images above show the largest variance slices of the map in three orthogonal directions.

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

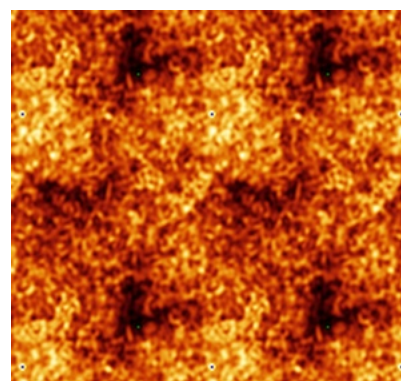
6.4.1 Primary map



X



Y



Z

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 1.41858. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

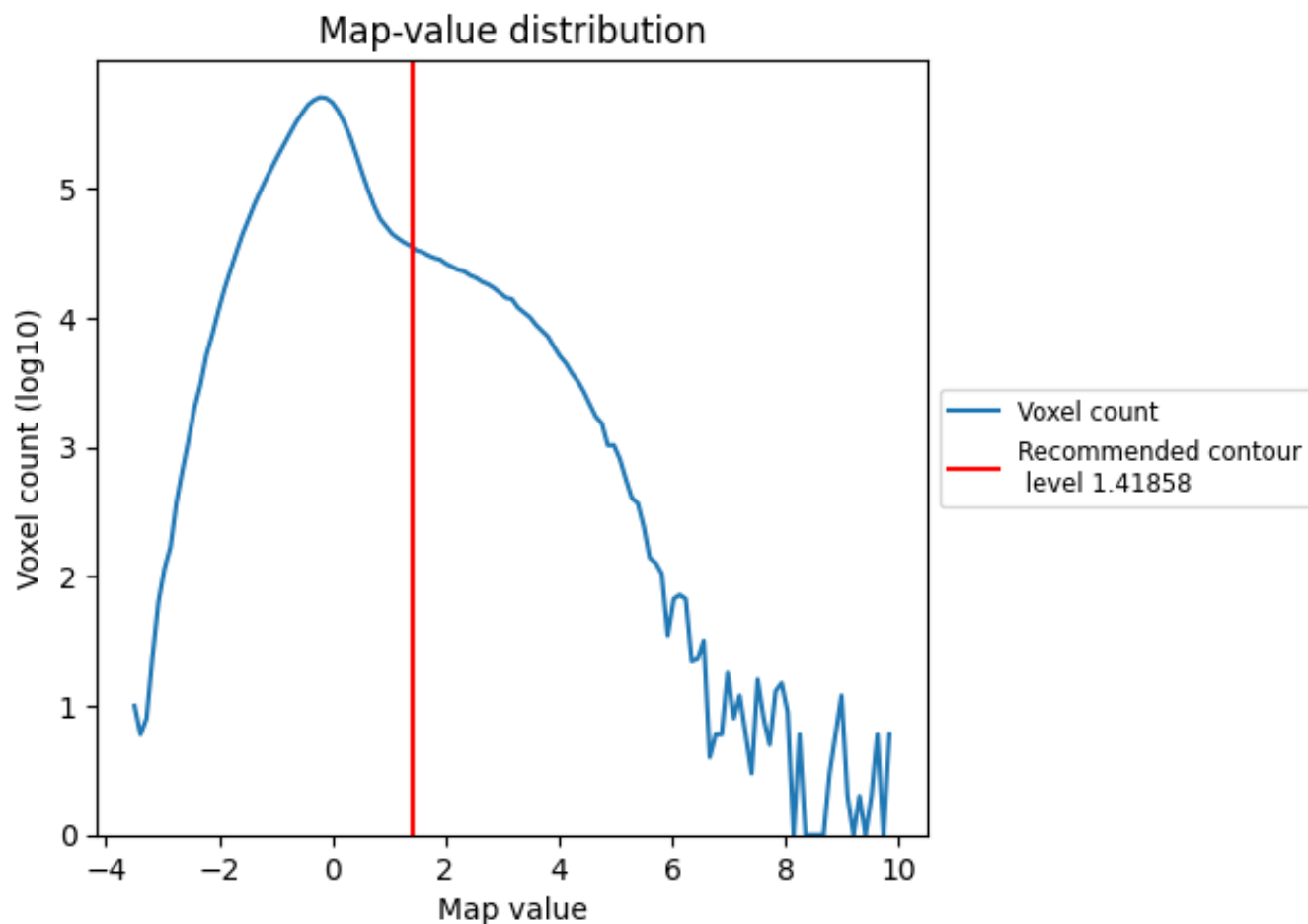
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

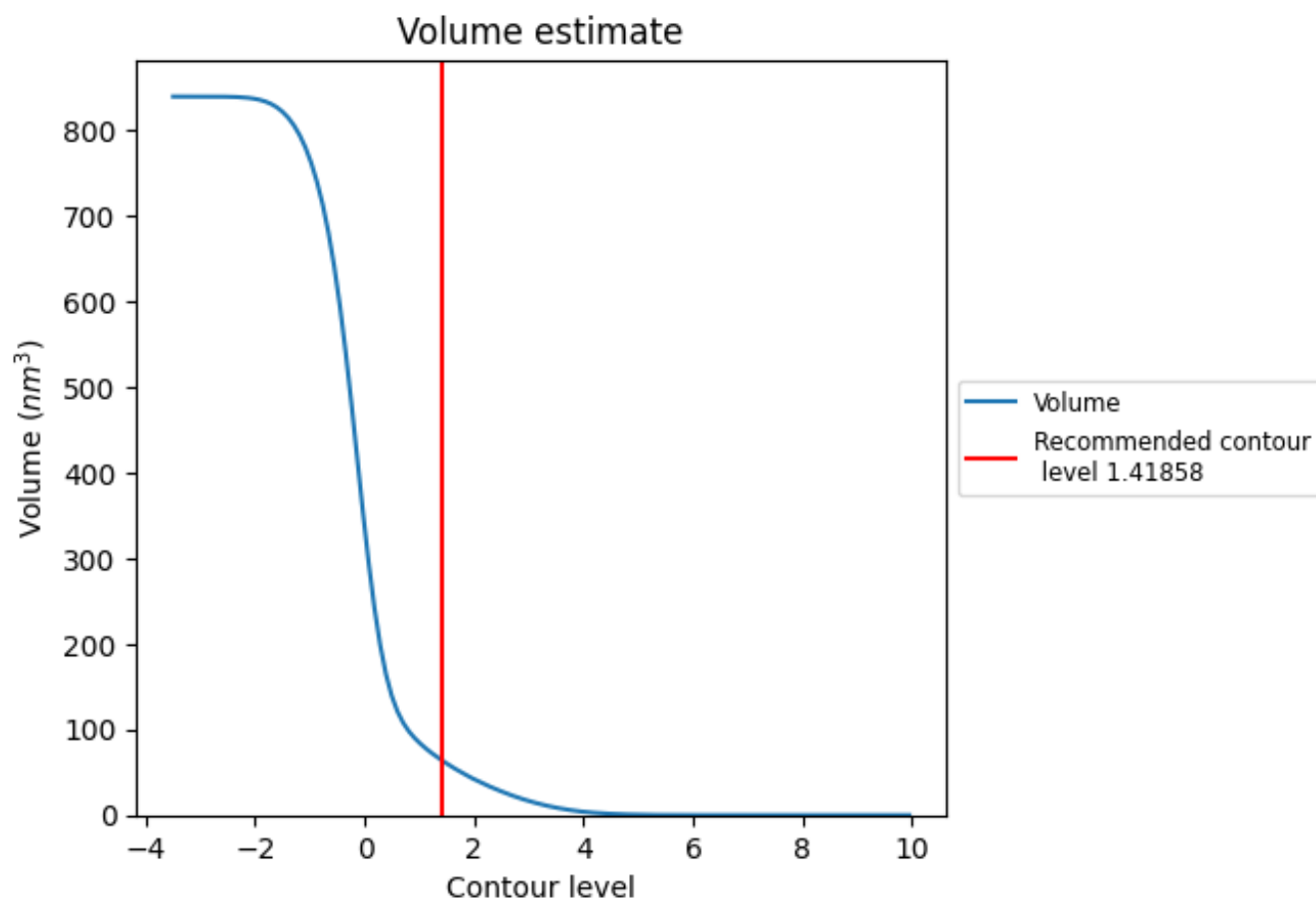
This section contains the results of statistical analysis of the map.

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 64 nm^3 ; this corresponds to an approximate mass of 58 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

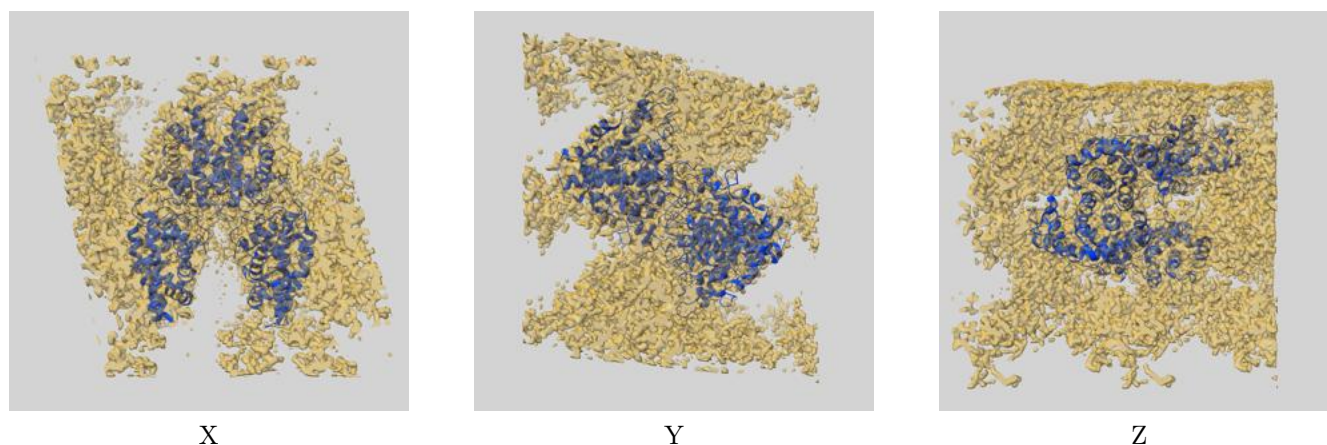
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

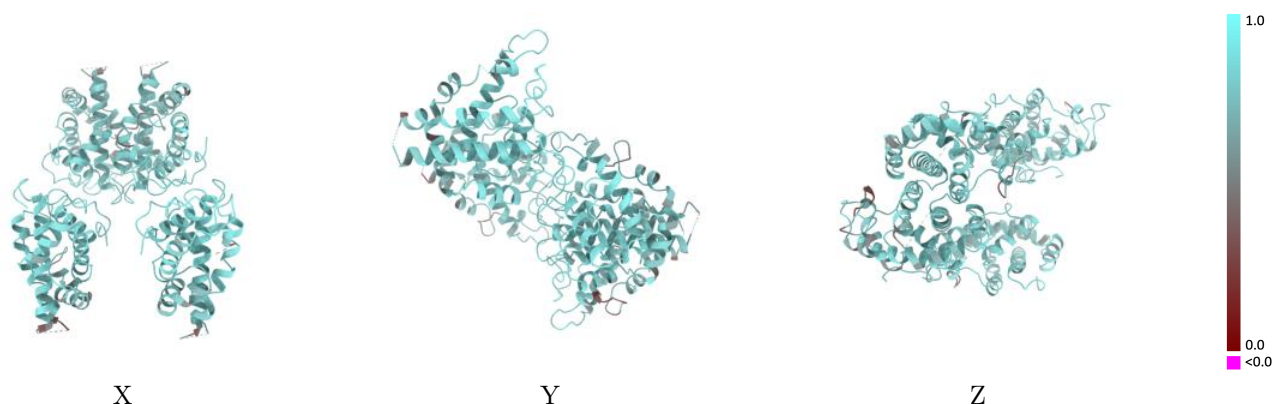
This section contains information regarding the fit between EMDB map EMD-28615 and PDB model 8EUM. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



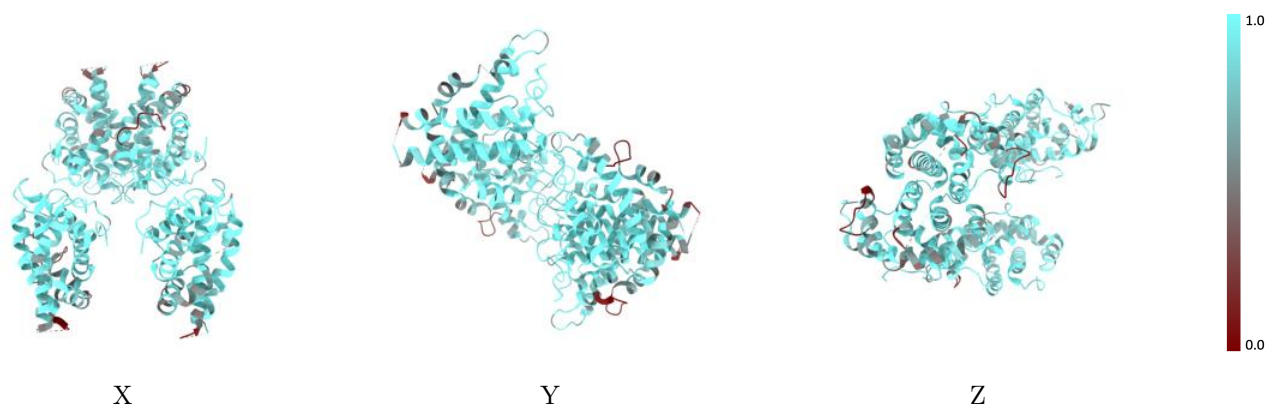
The images above show the 3D surface view of the map at the recommended contour level 1.41858 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



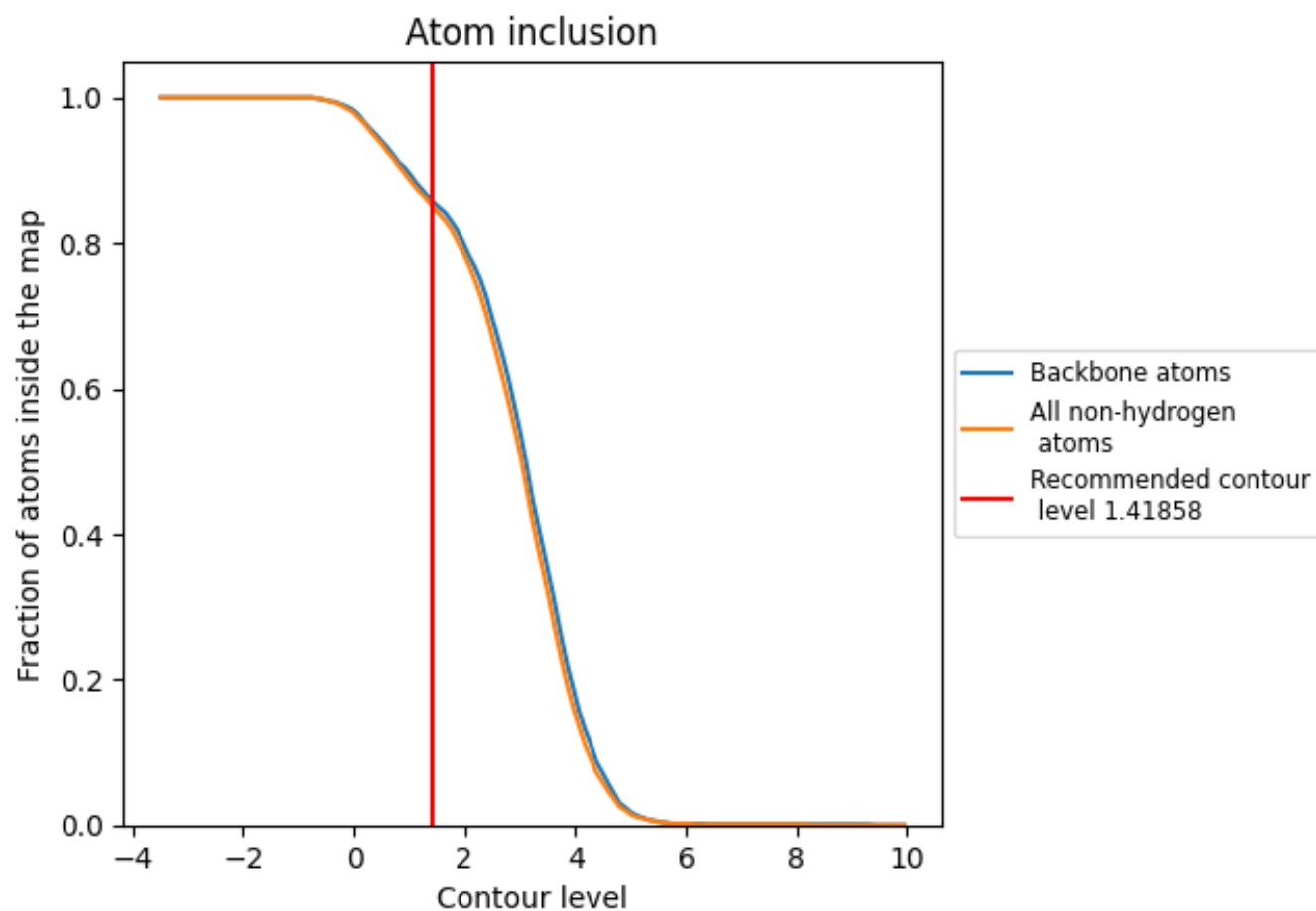
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.41858).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 85% 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 (1.41858) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8500	<div></div> 0.7420
A	<div></div> 0.8500	<div></div> 0.7420
B	<div></div> 0.8430	<div></div> 0.7340
C	<div></div> 0.8320	<div></div> 0.7330
D	<div></div> 0.8870	<div></div> 0.7580

