



## wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:25 AM UTC

PDB ID : 8UCL / pdb\_00008ucl  
EMDB ID : EMD-42130  
Title : Komagataella pastoris Cytochrome c oxidase in complex with human VMAT2 and Tetrabenazine  
Authors : Ye, J.; Liu, B.; Li, W.  
Deposited on : 2023-09-26  
Resolution : 3.18 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:

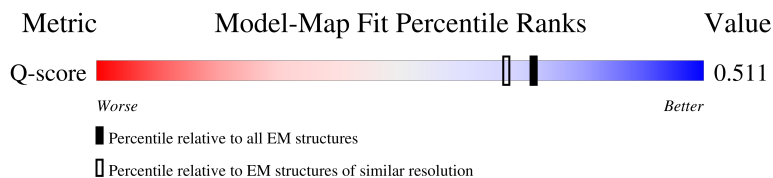
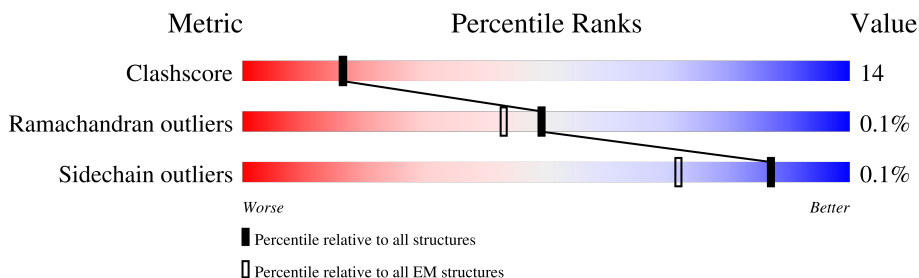
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.18 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14470 ( 2.68 - 3.68 )

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	514	
2	a	535	
3	b	236	
4	c	268	

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Mol	Chain	Length	Quality of chain
5	d	117	 64% 36%
6	e	124	 81% 19%
7	f	100	 81% 19%
8	g	58	 79% 19%
9	h	48	 81% 19%
10	i	56	 91% 9%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	EBZ	A	601	-	X	-	-

## 2 Entry composition i

There are 16 unique types of molecules in this entry. The entry contains 15439 atoms, of which 27 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 Synaptic vesicular amine transporter.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	374	2807	1876	436	471	24	0	0

- Molecule 2 is a protein called Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	a	535	4169	2788	646	717	18	0	0

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	4	ILE	MET	conflict	UNP F2R0K8
a	16	ILE	MET	conflict	UNP F2R0K8
a	22	ILE	MET	conflict	UNP F2R0K8
a	33	ILE	MET	conflict	UNP F2R0K8
a	37	ILE	MET	conflict	UNP F2R0K8
a	49	ILE	MET	conflict	UNP F2R0K8
a	78	ILE	MET	conflict	UNP F2R0K8
a	85	LEU	THR	conflict	UNP F2R0K8
a	90	ILE	MET	conflict	UNP F2R0K8
a	121	ILE	MET	conflict	UNP F2R0K8
a	150	ILE	MET	conflict	UNP F2R0K8
a	158	ILE	MET	conflict	UNP F2R0K8
a	165	ILE	MET	conflict	UNP F2R0K8
a	168	ILE	MET	conflict	UNP F2R0K8
a	177	ILE	MET	conflict	UNP F2R0K8
a	232	ILE	MET	conflict	UNP F2R0K8
a	237	LEU	THR	conflict	UNP F2R0K8
a	250	ILE	MET	conflict	UNP F2R0K8
a	256	ILE	MET	conflict	UNP F2R0K8
a	260	ILE	MET	conflict	UNP F2R0K8
a	273	ILE	MET	conflict	UNP F2R0K8

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Chain	Residue	Modelled	Actual	Comment	Reference
a	314	ILE	MET	conflict	UNP F2R0K8
a	320	ILE	MET	conflict	UNP F2R0K8
a	322	ILE	MET	conflict	UNP F2R0K8
a	334	ILE	MET	conflict	UNP F2R0K8
a	367	ILE	MET	conflict	UNP F2R0K8
a	401	LEU	THR	conflict	UNP F2R0K8
a	402	ILE	MET	conflict	UNP F2R0K8
a	421	ILE	MET	conflict	UNP F2R0K8
a	442	ILE	MET	conflict	UNP F2R0K8
a	455	ILE	MET	conflict	UNP F2R0K8
a	462	ILE	MET	conflict	UNP F2R0K8
a	464	ILE	MET	conflict	UNP F2R0K8
a	465	ILE	MET	conflict	UNP F2R0K8
a	510	ILE	MET	conflict	UNP F2R0K8
a	515	ILE	MET	conflict	UNP F2R0K8
a	524	LEU	THR	conflict	UNP F2R0K8

- Molecule 3 is a protein called Cytochrome c oxidase subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	b	236	1896	1247	287	352	10	0	0

- Molecule 4 is a protein called Cytochrome c oxidase subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	c	268	2163	1460	337	354	12	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	45	ILE	MET	conflict	UNP F2R0J6
c	55	ILE	MET	conflict	UNP F2R0J6
c	62	ILE	MET	conflict	UNP F2R0J6
c	81	ILE	MET	conflict	UNP F2R0J6
c	89	ILE	MET	conflict	UNP F2R0J6
c	101	ILE	MET	conflict	UNP F2R0J6
c	120	ILE	MET	conflict	UNP F2R0J6
c	129	ILE	MET	conflict	UNP F2R0J6
c	132	ILE	MET	conflict	UNP F2R0J6
c	143	ILE	MET	conflict	UNP F2R0J6

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Chain	Residue	Modelled	Actual	Comment	Reference
c	247	ILE	MET	conflict	UNP F2R0J6
c	248	LEU	THR	conflict	UNP F2R0J6

- Molecule 5 is a protein called Cytochrome c oxidase subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	d	117	910	576	147	183	4	0	0

- Molecule 6 is a protein called Cytochrome c oxidase subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	e	124	1027	659	176	191	1	0	0

- Molecule 7 is a protein called Cytochrome c oxidase subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	f	100	835	531	134	168	2	0	0

- Molecule 8 is a protein called Cytochrome c oxidase subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	g	58	465	309	74	81	1	0	0

- Molecule 9 is a protein called Cytochrome c oxidase subunit 8.

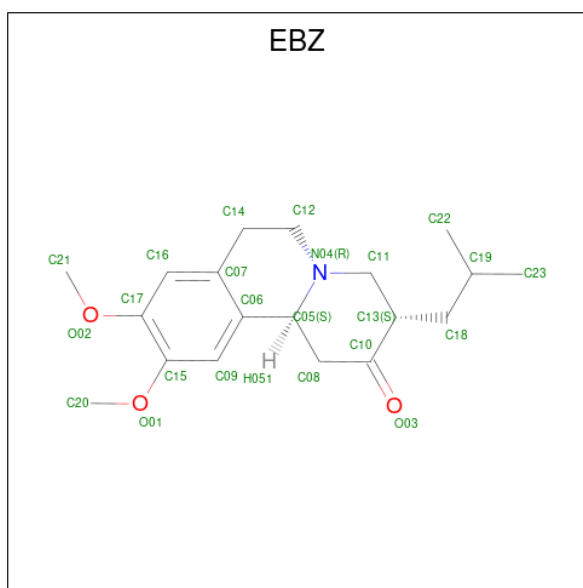
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	h	48	386	260	65	59	2	0	0

- Molecule 10 is a protein called Cytochrome c oxidase subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	i	56	460	302	83	75	0	0

- Molecule 11 is (3S,5R,11bS)-9,10-dimethoxy-3-(2-methylpropyl)-1,3,4,6,7,11b-hexahydro-2H-pyrido[2,1-a]isoquinolin-2-one (CCD ID: EBZ) (formula: C<sub>19</sub>H<sub>27</sub>NO<sub>3</sub>) (labeled as "Ligand

of Interest" by depositor).

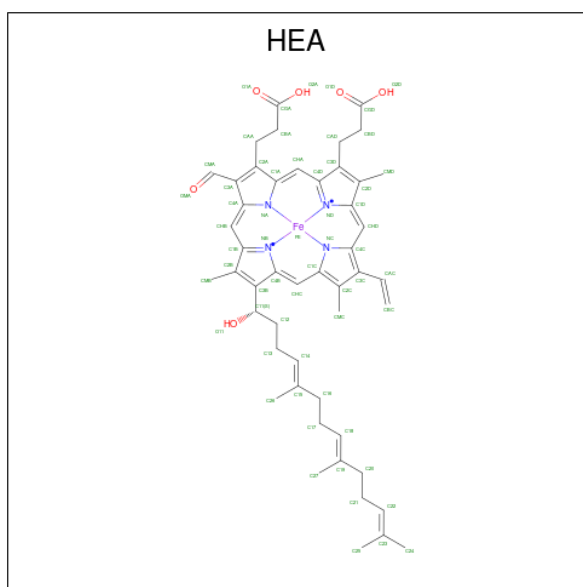


Mol	Chain	Residues	Atoms				AltConf	
			Total	C	H	N		O
11	A	1	50	19	27	1	3	0

- Molecule 12 is COPPER (II) ION (CCD ID: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

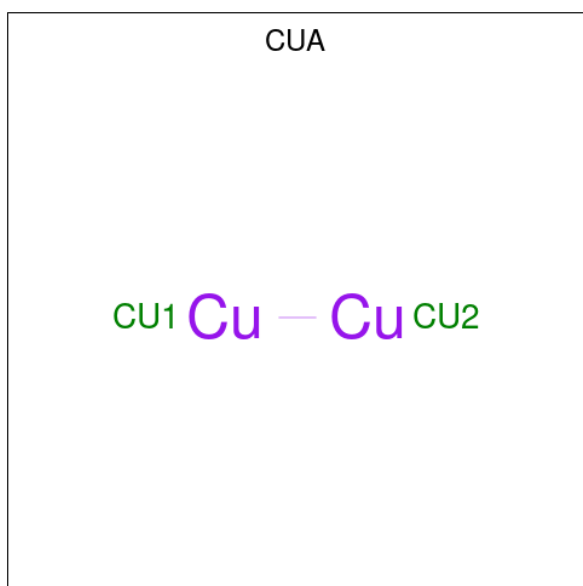
Mol	Chain	Residues	Atoms		AltConf
			Total	Cu	
12	a	1	1	1	0

- Molecule 13 is HEME-A (CCD ID: HEA) (formula: C<sub>49</sub>H<sub>56</sub>FeN<sub>4</sub>O<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).



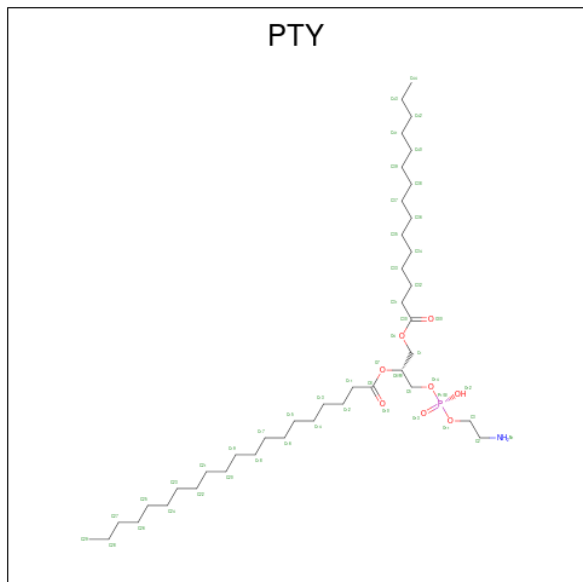
Mol	Chain	Residues	Atoms				AltConf	
			Total	C	Fe	N		O
13	a	1	60	49	1	4	6	0
13	a	1	60	49	1	4	6	0

- Molecule 14 is DINUCLEAR COPPER ION (CCD ID: CUA) (formula:  $\text{Cu}_2$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		AltConf
			Total	Cu	
14	b	1	2	2	0

- Molecule 15 is PHOSPHATIDYLETHANOLAMINE (CCD ID: PTY) (formula:  $C_{40}H_{80}NO_8P$ ) (labeled as "Ligand of Interest" by depositor).

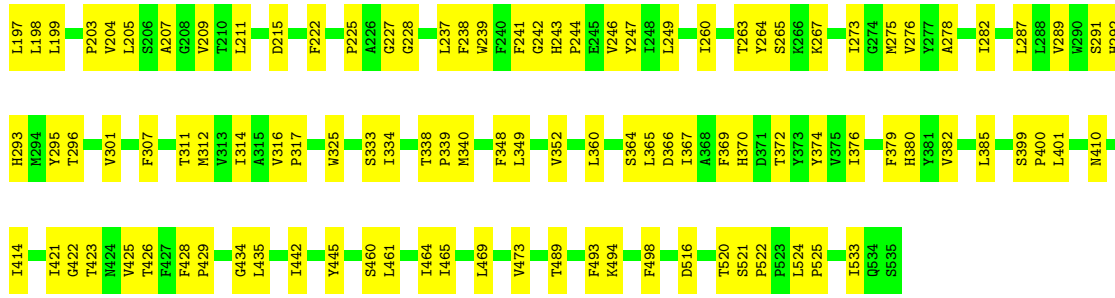


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
15	b	1	40	30	1	8	1	0
15	c	1	34	24	1	8	1	0
15	c	1	40	30	1	8	1	0
15	e	1	33	23	1	8	1	0

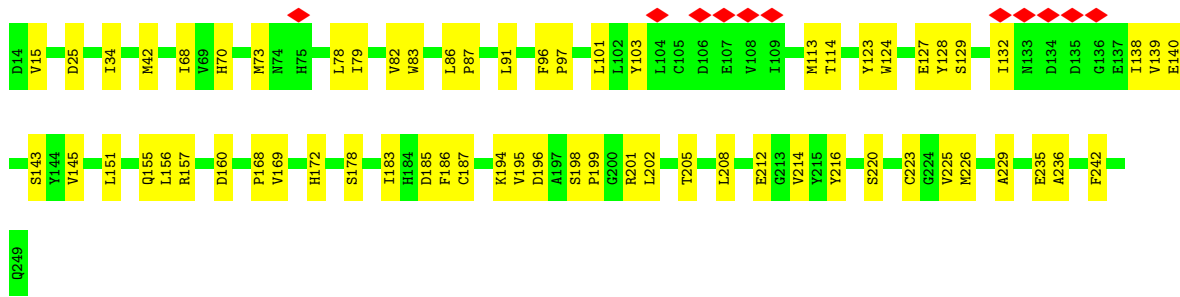
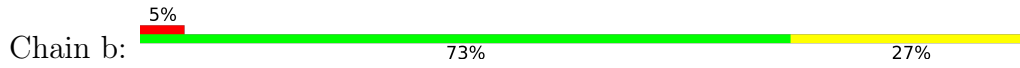
- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
16	d	1	1	1	0

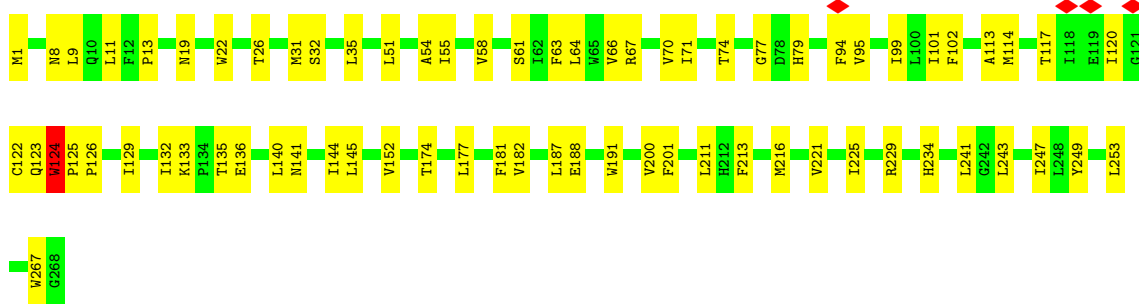




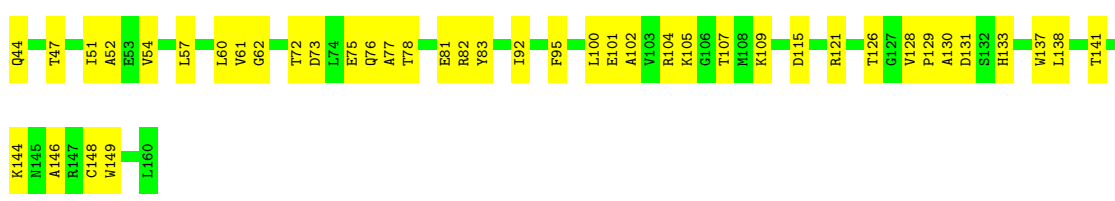
• Molecule 3: Cytochrome c oxidase subunit 2



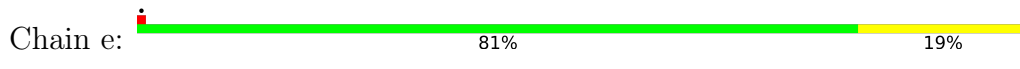
• Molecule 4: Cytochrome c oxidase subunit 3

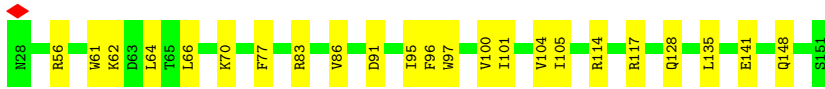


• Molecule 5: Cytochrome c oxidase subunit 4



• Molecule 6: Cytochrome c oxidase subunit 5





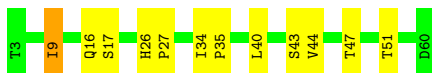
- Molecule 7: Cytochrome c oxidase subunit 6

Chain f: 81% 19%



- Molecule 8: Cytochrome c oxidase subunit 7

Chain g: 79% 19%



- Molecule 9: Cytochrome c oxidase subunit 8

Chain h: 81% 19%



- Molecule 10: Cytochrome c oxidase subunit 9

Chain i: 91% 9%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	116216	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	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.959	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	281.6, 281.6, 281.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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: CUA, CU, EBZ, HEA, ZN, PTY

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	0.18	0/2875	0.39	0/3911
2	a	0.21	0/4300	0.45	0/5878
3	b	0.20	0/1947	0.45	0/2664
4	c	0.23	0/2234	0.49	1/3057 (0.0%)
5	d	0.22	0/928	0.58	1/1260 (0.1%)
6	e	0.17	0/1055	0.41	0/1430
7	f	0.18	0/851	0.43	0/1148
8	g	0.18	0/478	0.46	1/647 (0.2%)
9	h	0.18	0/400	0.43	0/541
10	i	0.16	0/473	0.44	0/638
All	All	0.20	0/15541	0.45	3/21174 (0.0%)

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
4	c	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	g	9	ILE	N-CA-C	-5.76	106.87	112.29
4	c	124	TRP	CA-CB-CG	-5.65	102.86	113.60
5	d	52	ALA	N-CA-C	-5.07	106.93	114.64

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	c	124	TRP	Peptide

## 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	2807	0	2949	117	0
2	a	4169	0	4191	152	0
3	b	1896	0	1865	53	0
4	c	2163	0	2198	64	0
5	d	910	0	887	31	0
6	e	1027	0	1007	18	0
7	f	835	0	794	18	0
8	g	465	0	471	8	0
9	h	386	0	391	9	0
10	i	460	0	473	5	0
11	A	23	27	0	1	0
12	a	1	0	0	0	0
13	a	120	0	108	14	0
14	b	2	0	0	0	0
15	b	40	0	53	0	0
15	c	74	0	94	11	0
15	e	33	0	39	0	0
16	d	1	0	0	0	0
All	All	15412	27	15520	437	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 14.

The worst 5 of 437 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)
4:c:126:PRO:HG2	4:c:129:ILE:HD12	1.42	0.99
1:A:142:GLN:HG3	1:A:197:SER:HB3	1.49	0.94
2:a:349:LEU:HD13	2:a:385:LEU:HD23	1.55	0.88
2:a:367:ILE:HD11	3:b:34:ILE:HD11	1.56	0.88
2:a:360:LEU:HB2	13:a:603:HEA:HMA	1.60	0.83

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	368/514 (72%)	350 (95%)	18 (5%)	0	100	100
2	a	533/535 (100%)	506 (95%)	27 (5%)	0	100	100
3	b	234/236 (99%)	221 (94%)	13 (6%)	0	100	100
4	c	266/268 (99%)	246 (92%)	19 (7%)	1 (0%)	30	60
5	d	115/117 (98%)	101 (88%)	14 (12%)	0	100	100
6	e	122/124 (98%)	117 (96%)	5 (4%)	0	100	100
7	f	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
8	g	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
9	h	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
10	i	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
All	All	1892/2056 (92%)	1784 (94%)	107 (6%)	1 (0%)	49	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	c	125	PRO

### 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	299/427 (70%)	299 (100%)	0	100	100
2	a	452/452 (100%)	452 (100%)	0	100	100
3	b	212/212 (100%)	211 (100%)	1 (0%)	81	83
4	c	234/234 (100%)	234 (100%)	0	100	100
5	d	99/99 (100%)	99 (100%)	0	100	100
6	e	110/110 (100%)	110 (100%)	0	100	100
7	f	90/90 (100%)	90 (100%)	0	100	100
8	g	48/48 (100%)	48 (100%)	0	100	100
9	h	41/41 (100%)	41 (100%)	0	100	100
10	i	47/47 (100%)	47 (100%)	0	100	100
All	All	1632/1760 (93%)	1631 (100%)	1 (0%)	87	90

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	b	223	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
7	f	71	ASN
6	e	128	GLN
4	c	19	ASN
3	b	172	HIS
4	c	212	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](#)

Of 10 ligands modelled in this entry, 2 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
14	CUA	b	301	3	0,1,1	-	-	-		
13	HEA	a	602	-	67,67,67	1.04	5 (7%)	81,103,103	1.95	22 (27%)
15	PTY	c	301	-	33,33,49	0.47	0	36,38,54	1.34	4 (11%)
11	EBZ	A	601	-	25,25,25	6.58	15 (60%)	34,36,36	3.99	18 (52%)
15	PTY	e	201	-	32,32,49	0.48	0	35,37,54	1.33	4 (11%)
13	HEA	a	603	-	67,67,67	1.01	5 (7%)	81,103,103	2.24	28 (34%)
15	PTY	c	302	-	39,39,49	0.46	0	42,44,54	1.22	4 (9%)
15	PTY	b	302	-	39,39,49	0.46	0	42,44,54	1.29	4 (9%)

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
13	HEA	a	602	-	-	13/36/76/76	-
15	PTY	c	301	-	-	11/37/37/53	-
11	EBZ	A	601	-	-	6/8/33/33	0/3/3/3
15	PTY	e	201	-	-	9/36/36/53	-
13	HEA	a	603	-	-	12/36/76/76	-
15	PTY	c	302	-	-	10/43/43/53	-
15	PTY	b	302	-	-	17/43/43/53	-

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	601	EBZ	C14-C07	-17.07	1.22	1.51
11	A	601	EBZ	C12-C14	-14.14	1.25	1.51
11	A	601	EBZ	C16-C07	12.35	1.58	1.39
11	A	601	EBZ	C09-C15	-10.83	1.20	1.38
11	A	601	EBZ	C08-C05	-8.41	1.42	1.53

The worst 5 of 84 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	601	EBZ	C12-N04-C11	12.19	133.76	110.32
11	A	601	EBZ	C12-C14-C07	9.37	127.52	111.34
11	A	601	EBZ	C09-C15-C17	7.74	129.76	119.83
13	a	603	HEA	CHA-C1A-NA	-6.83	117.02	124.45
11	A	601	EBZ	C14-C12-N04	6.39	127.33	110.57

There are no chirality outliers.

5 of 78 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	a	602	HEA	C12-C11-C3B-C2B
13	a	602	HEA	C12-C11-C3B-C4B
13	a	602	HEA	C3B-C11-C12-C13
13	a	602	HEA	O11-C11-C12-C13
13	a	603	HEA	C4A-C3A-CMA-OMA

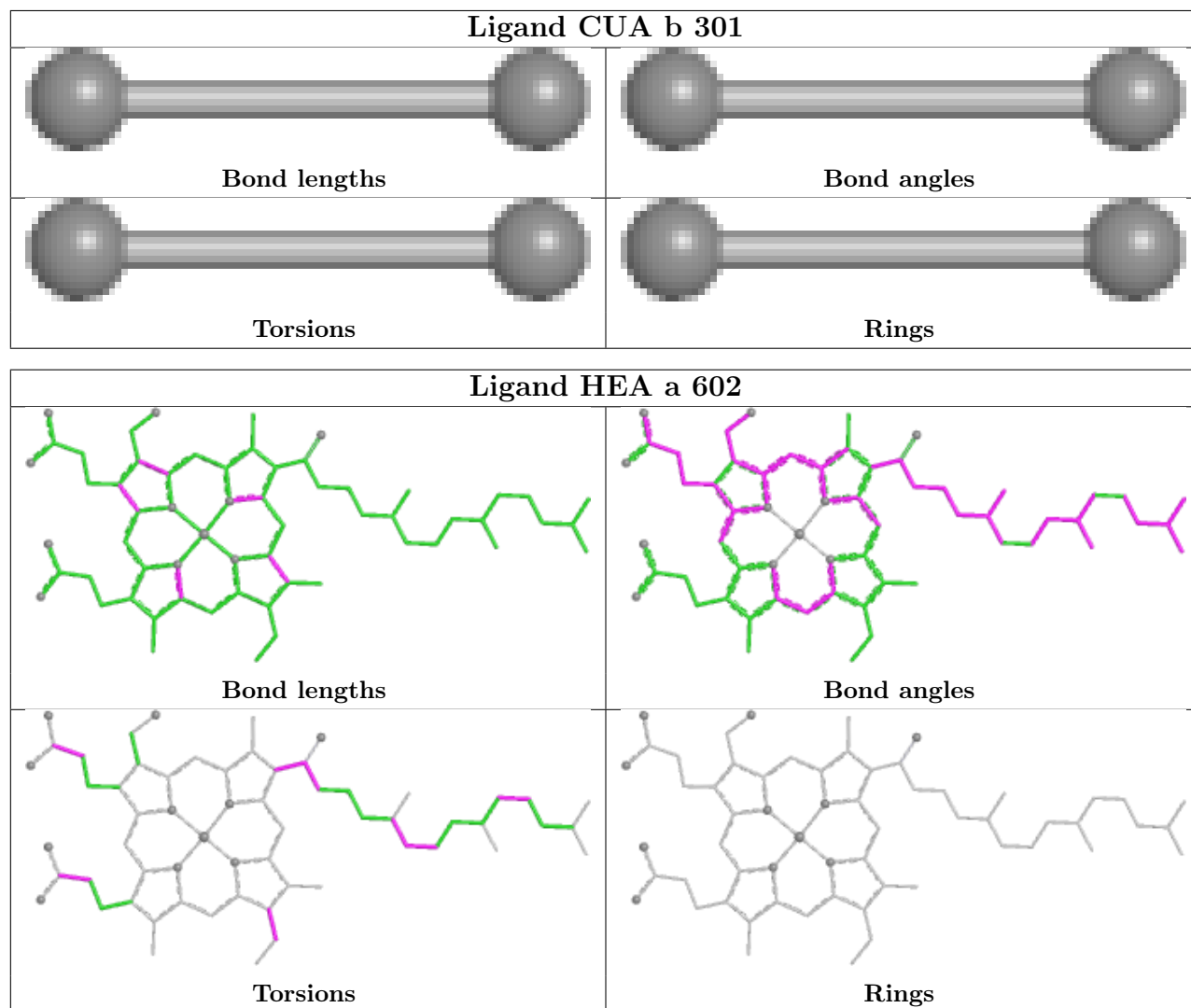
There are no ring outliers.

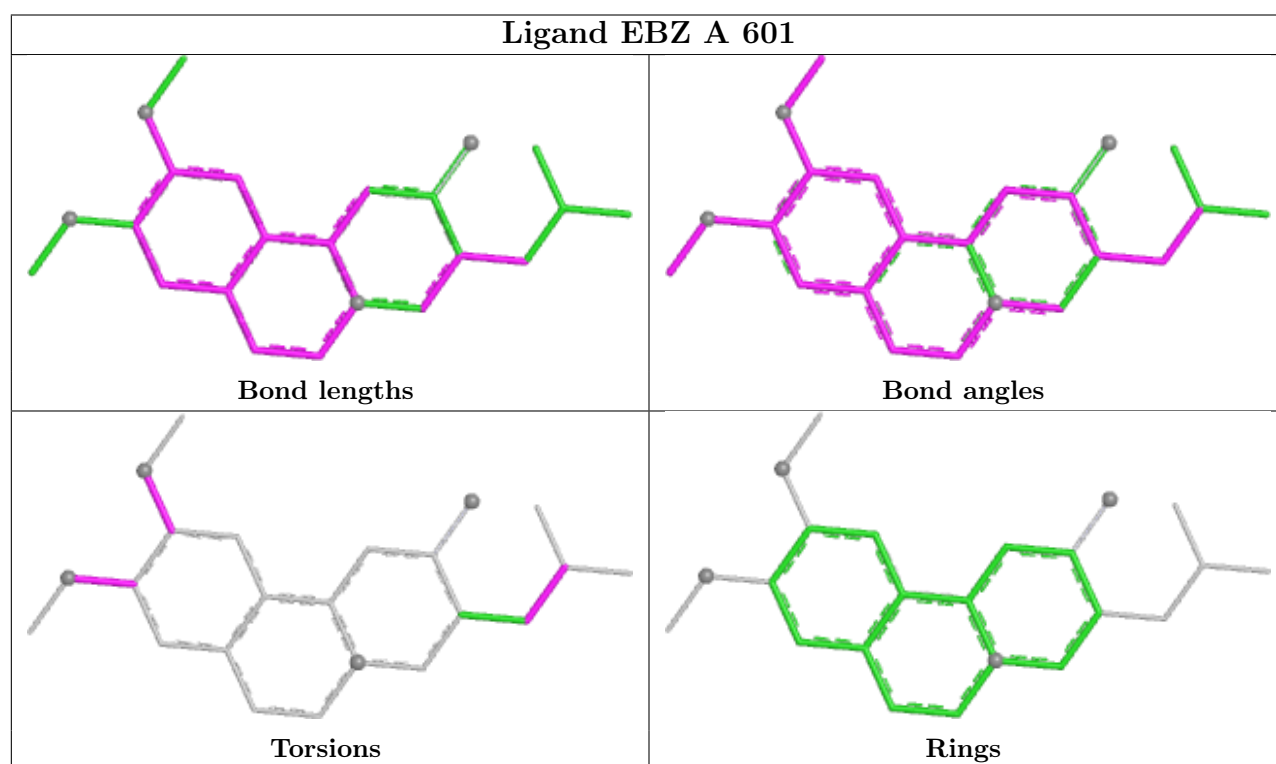
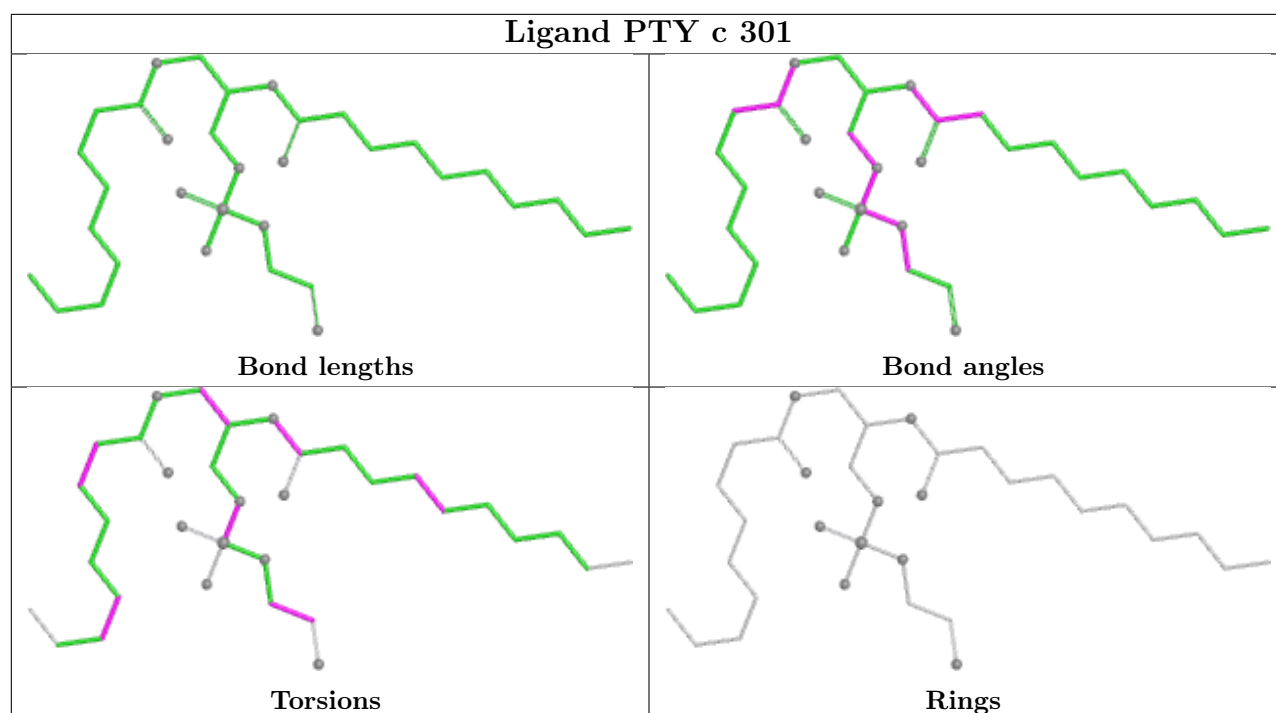
5 monomers are involved in 26 short contacts:

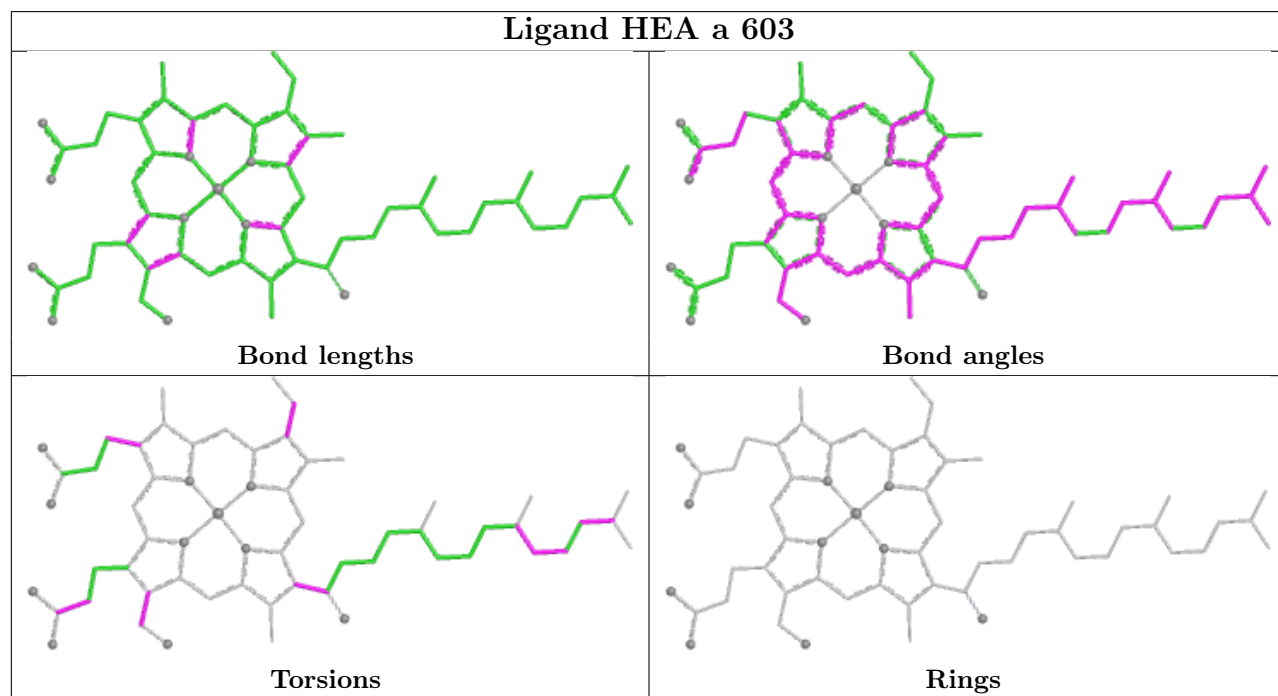
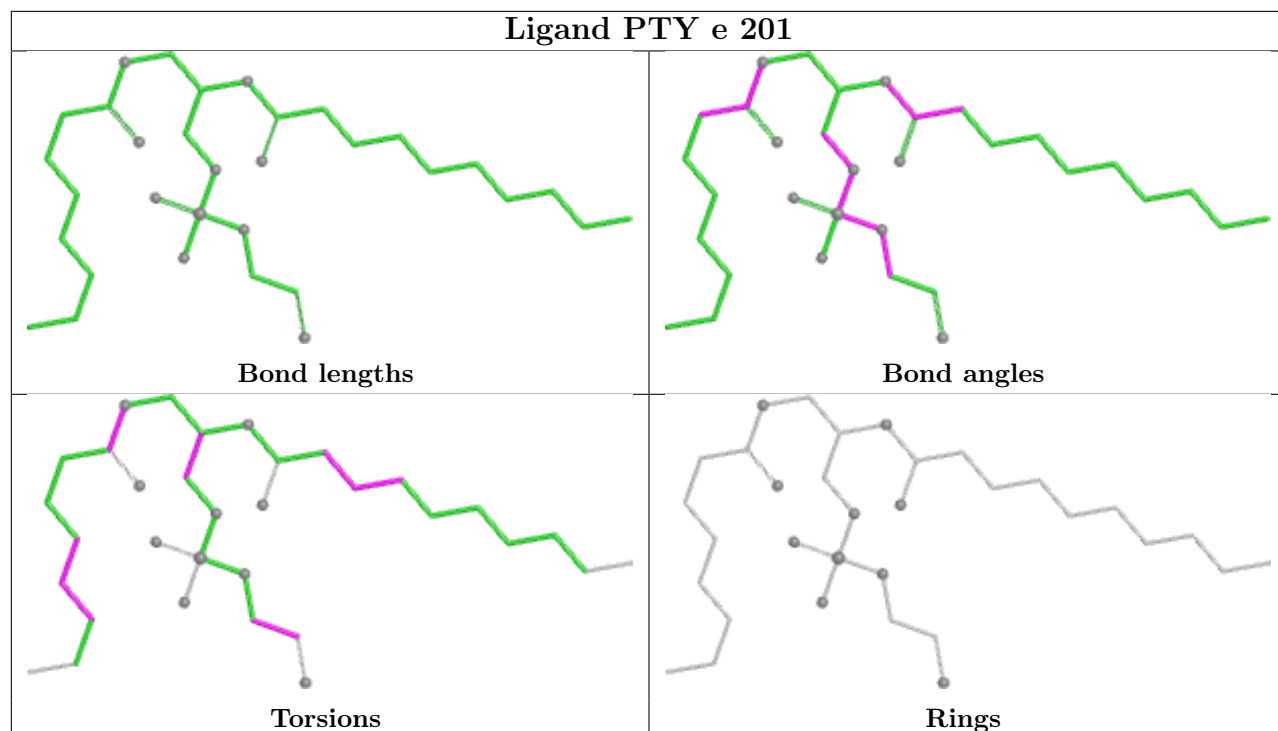
Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	a	602	HEA	5	0
15	c	301	PTY	8	0
11	A	601	EBZ	1	0
13	a	603	HEA	9	0
15	c	302	PTY	5	0

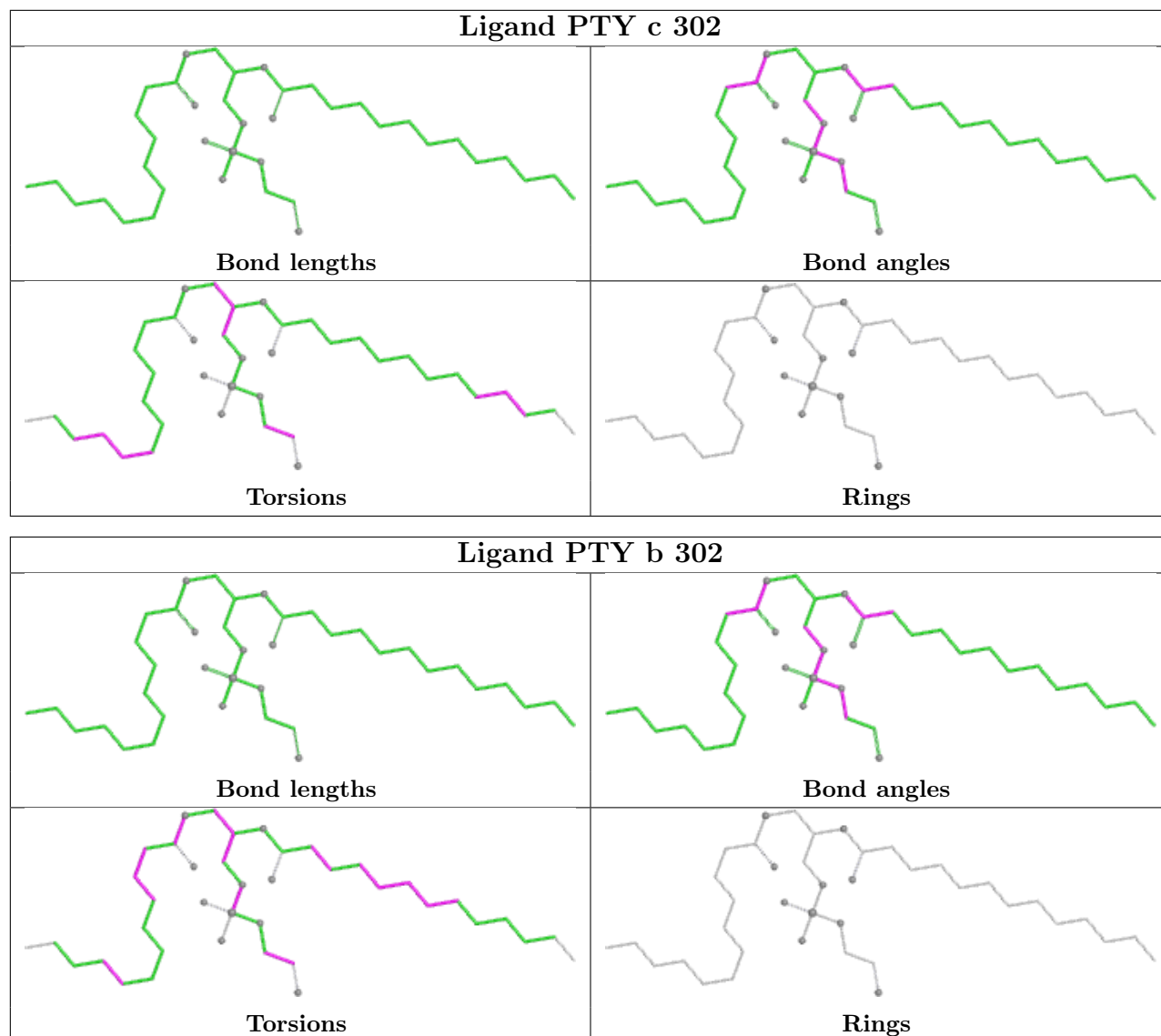
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

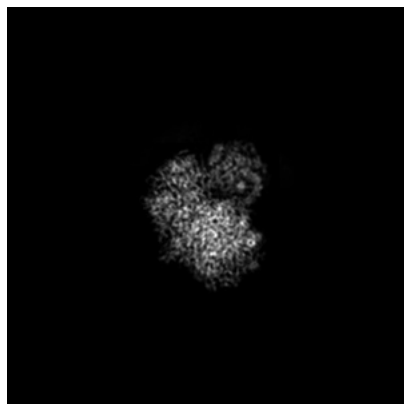
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42130. These allow visual inspection of the internal detail of the map and identification of artifacts.

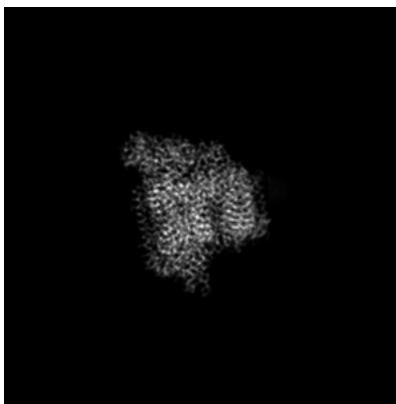
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

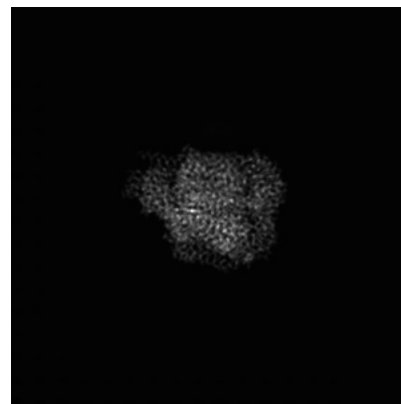
#### 6.1.1 Primary map



X

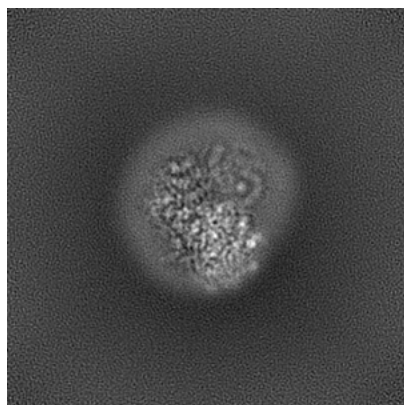


Y

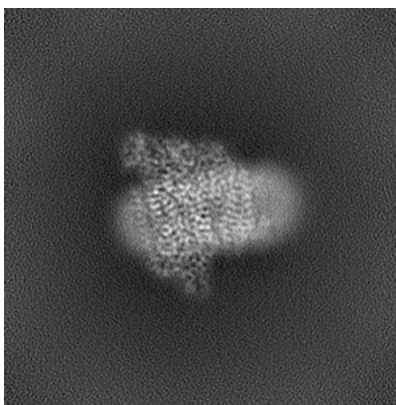


Z

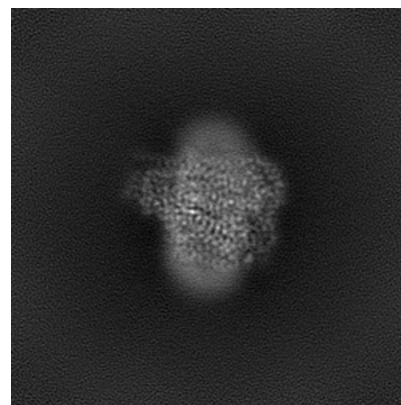
#### 6.1.2 Raw map



X



Y

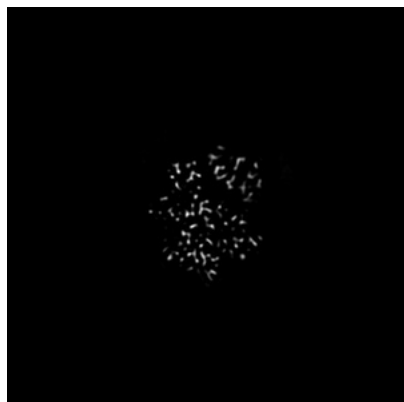


Z

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

## 6.2 Central slices [i](#)

### 6.2.1 Primary map



X Index: 128

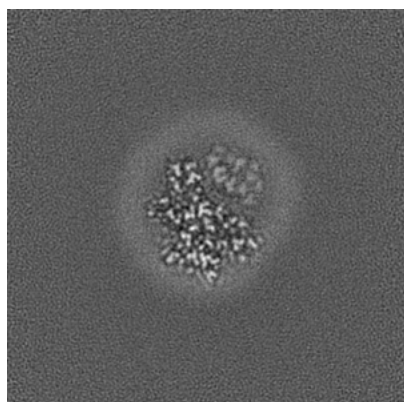


Y Index: 128

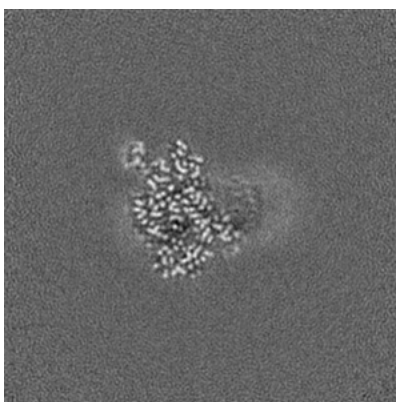


Z Index: 128

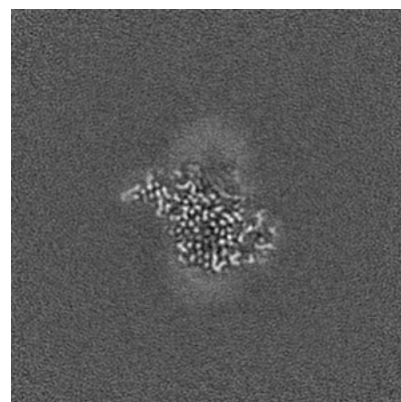
### 6.2.2 Raw map



X Index: 128



Y Index: 128

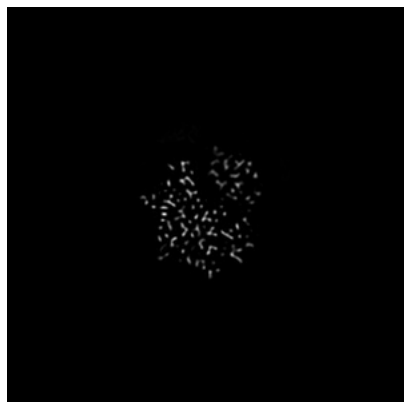


Z Index: 128

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: 136

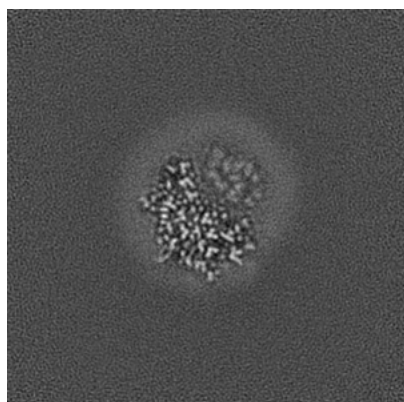


Y Index: 129

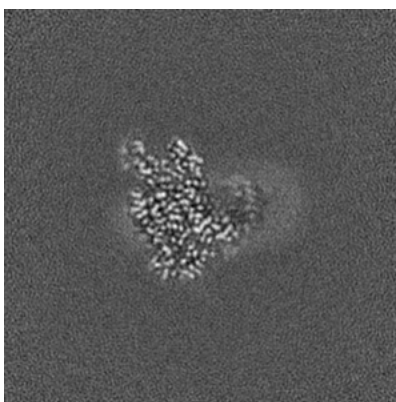


Z Index: 117

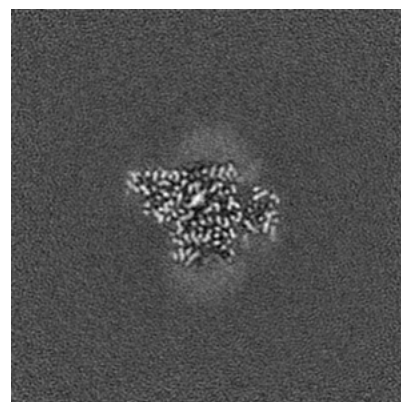
### 6.3.2 Raw map



X Index: 136



Y Index: 129

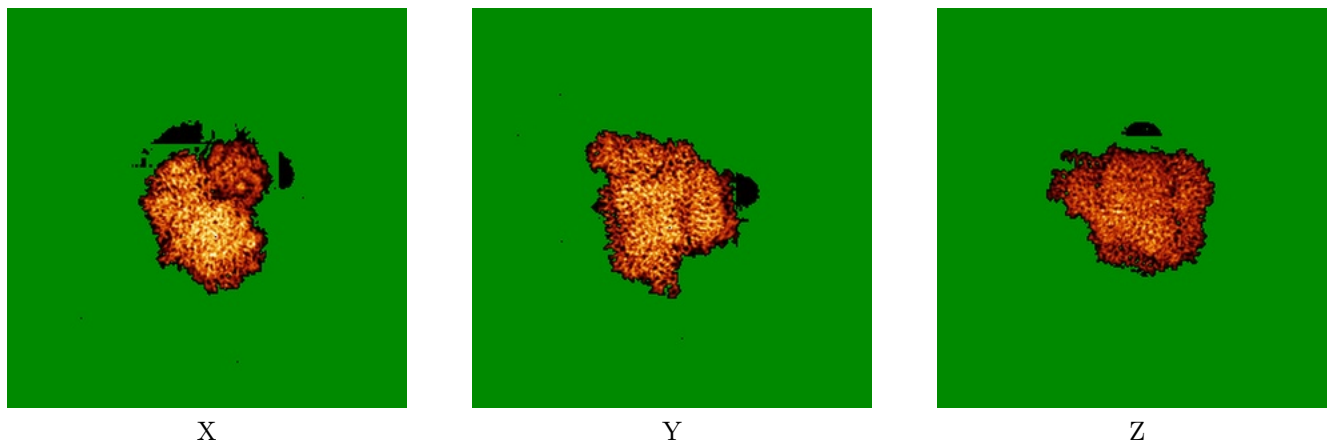


Z Index: 117

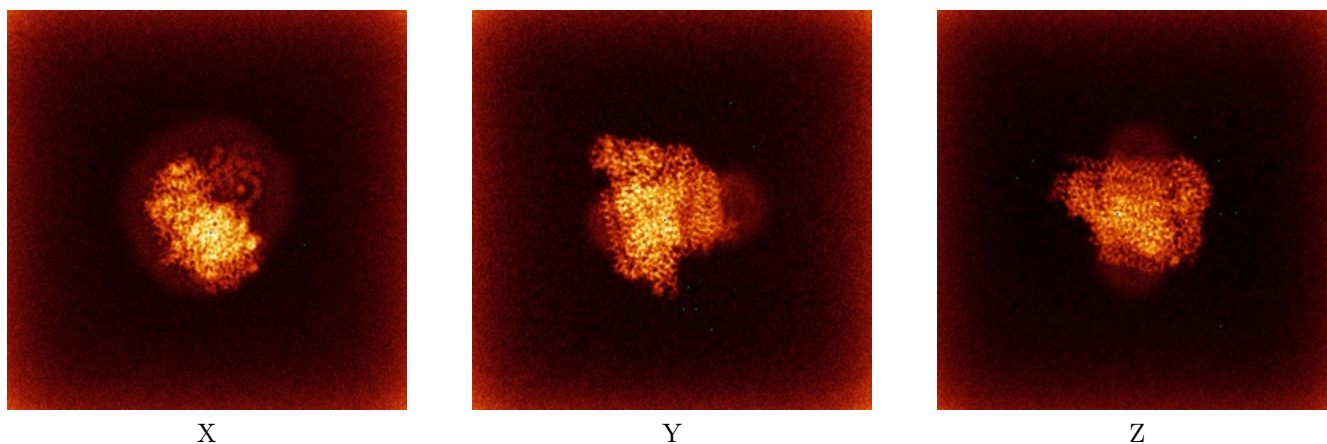
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



### 6.4.2 Raw map



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](#)

This section was not generated.

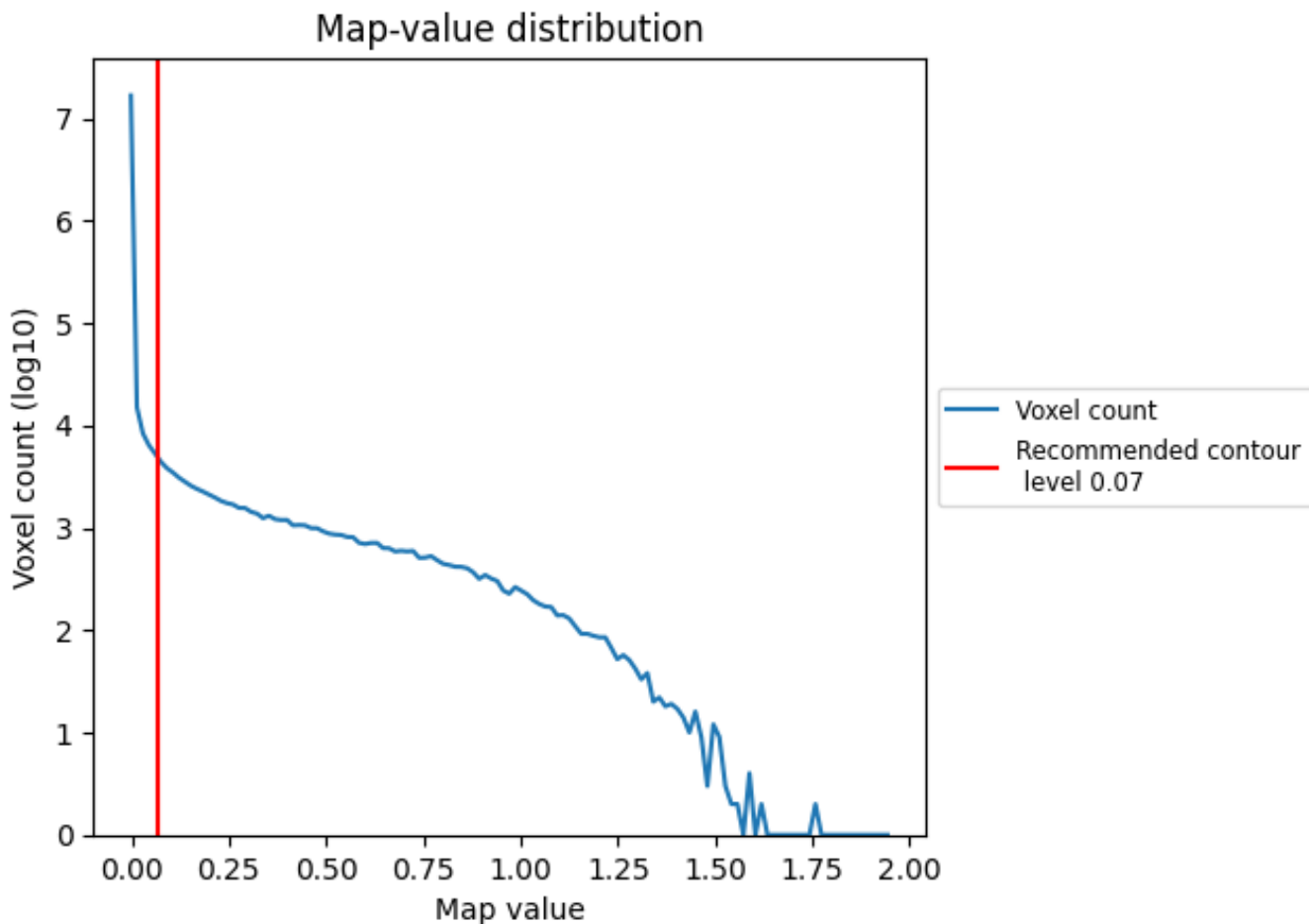
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

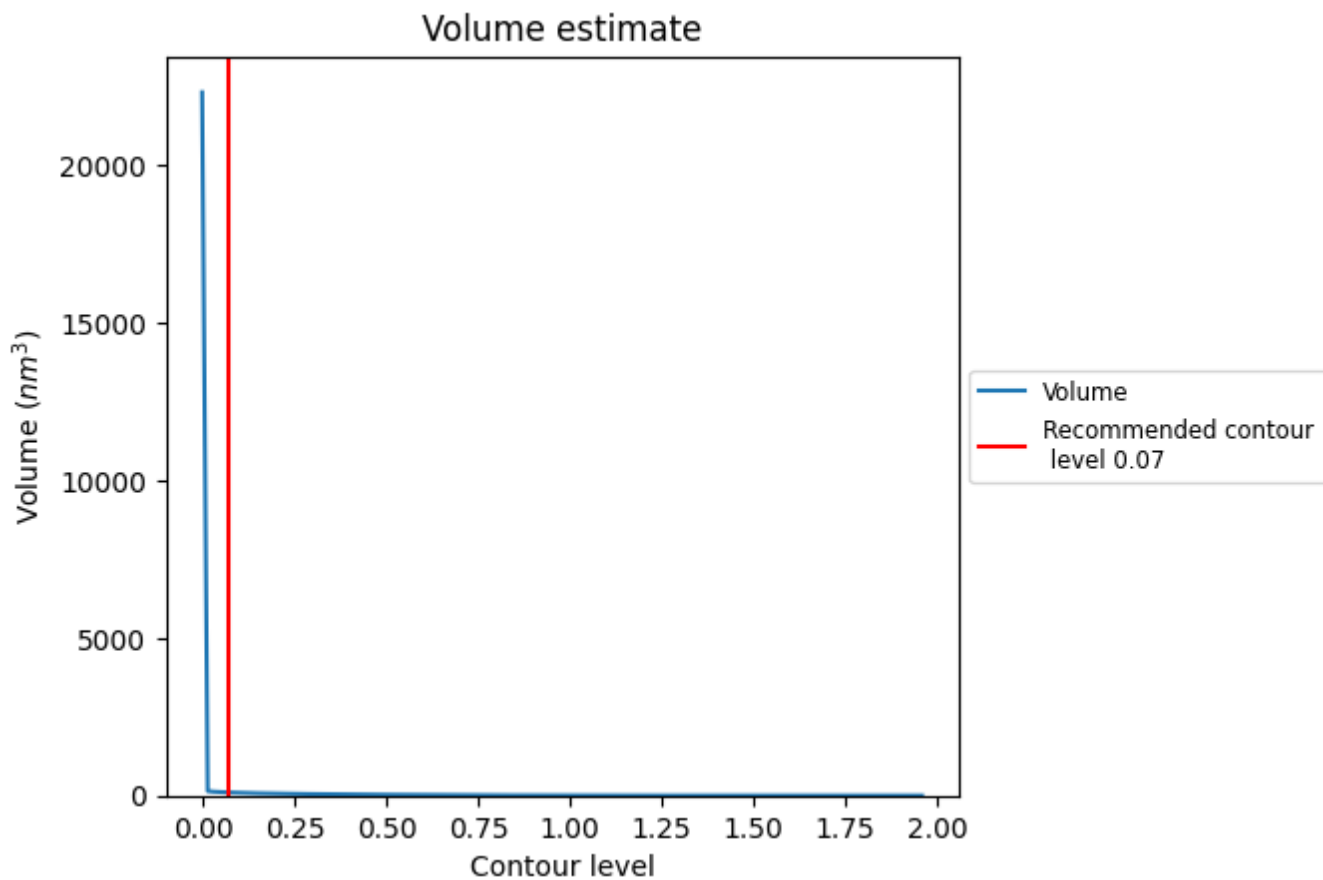
This section contains the results of statistical analysis of the map.

### 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.

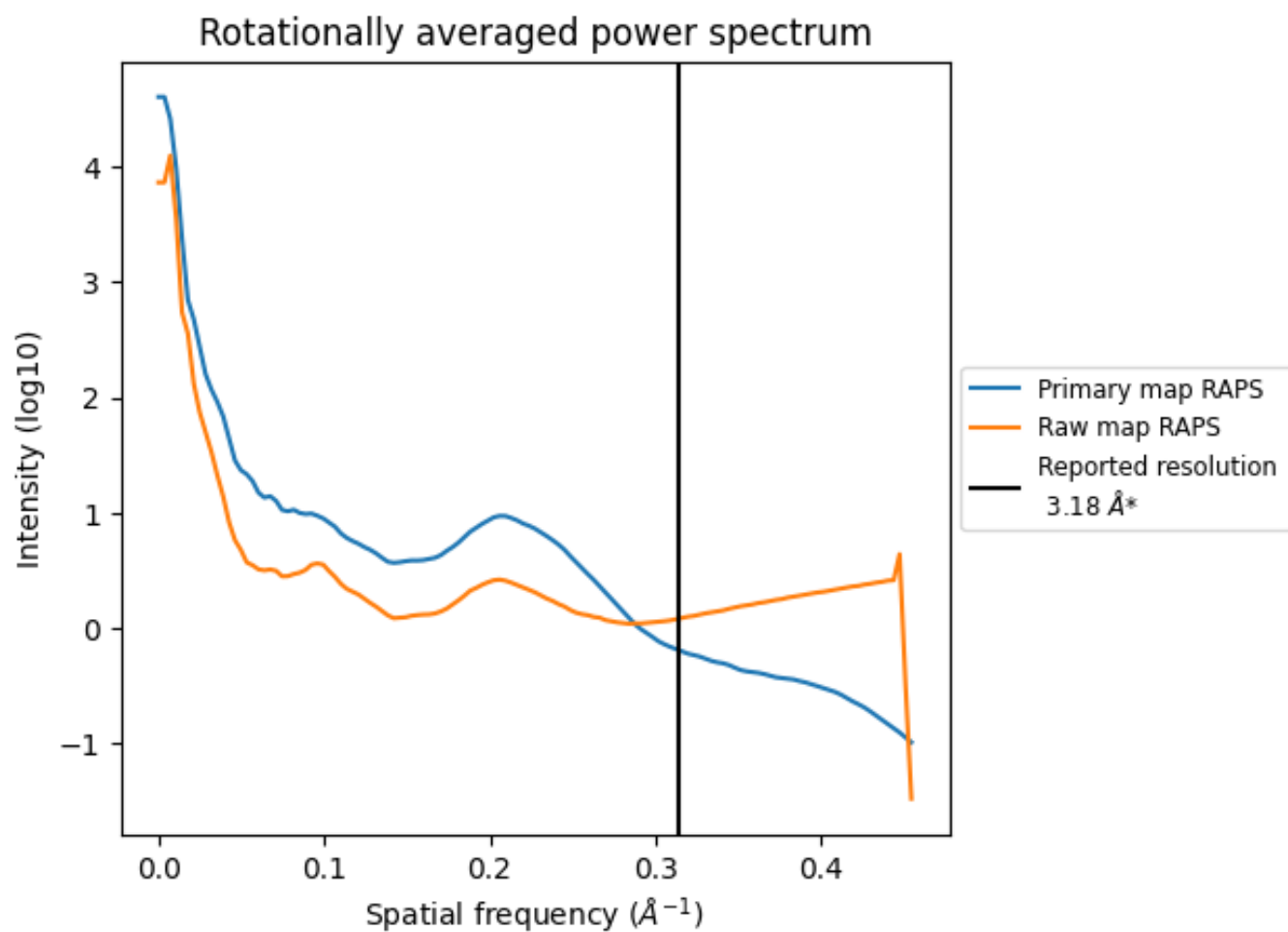
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 98  $\text{nm}^3$ ; this corresponds to an approximate mass of 89 kDa.

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

### 7.3 Rotationally averaged power spectrum i

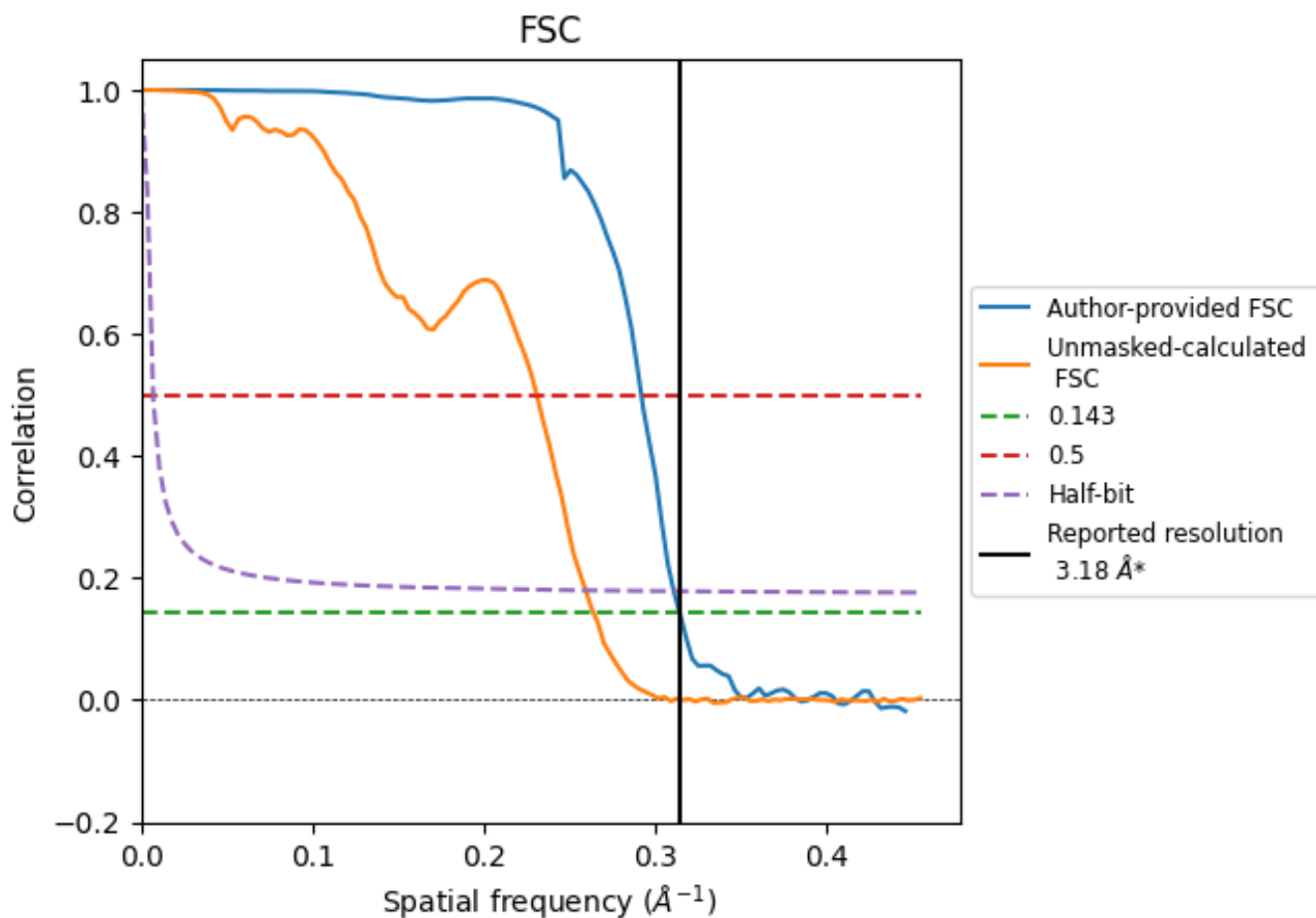


\*Reported resolution corresponds to spatial frequency of  $0.314 \text{ \AA}^{-1}$

## 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 0.314 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	3.18	-	-
Author-provided FSC curve	3.18	3.43	3.22
Unmasked-calculated*	3.79	4.33	3.86

\*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 3.79 differs from the reported value 3.18 by more than 10 %

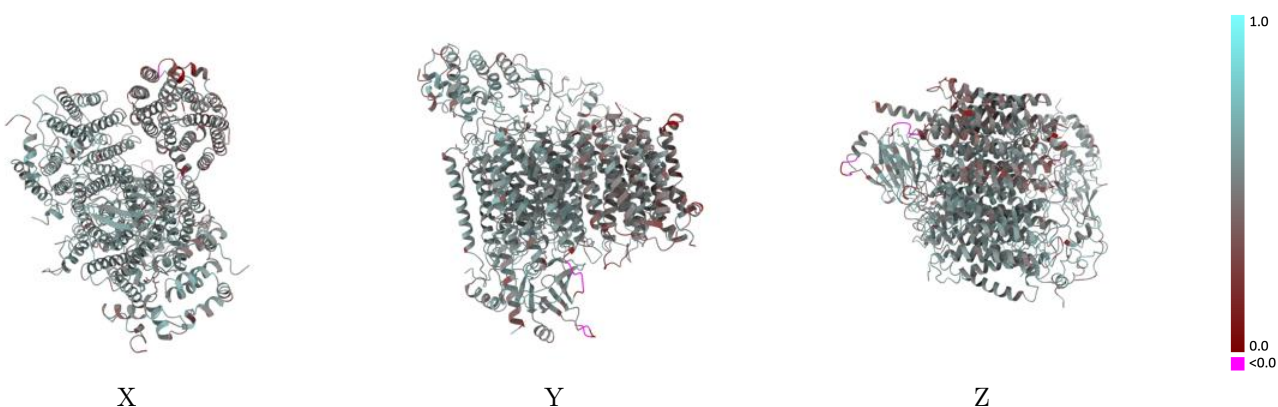
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42130 and PDB model 8UCL. Per-residue inclusion information can be found in section 3 on page 10.

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

This section was not generated.

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

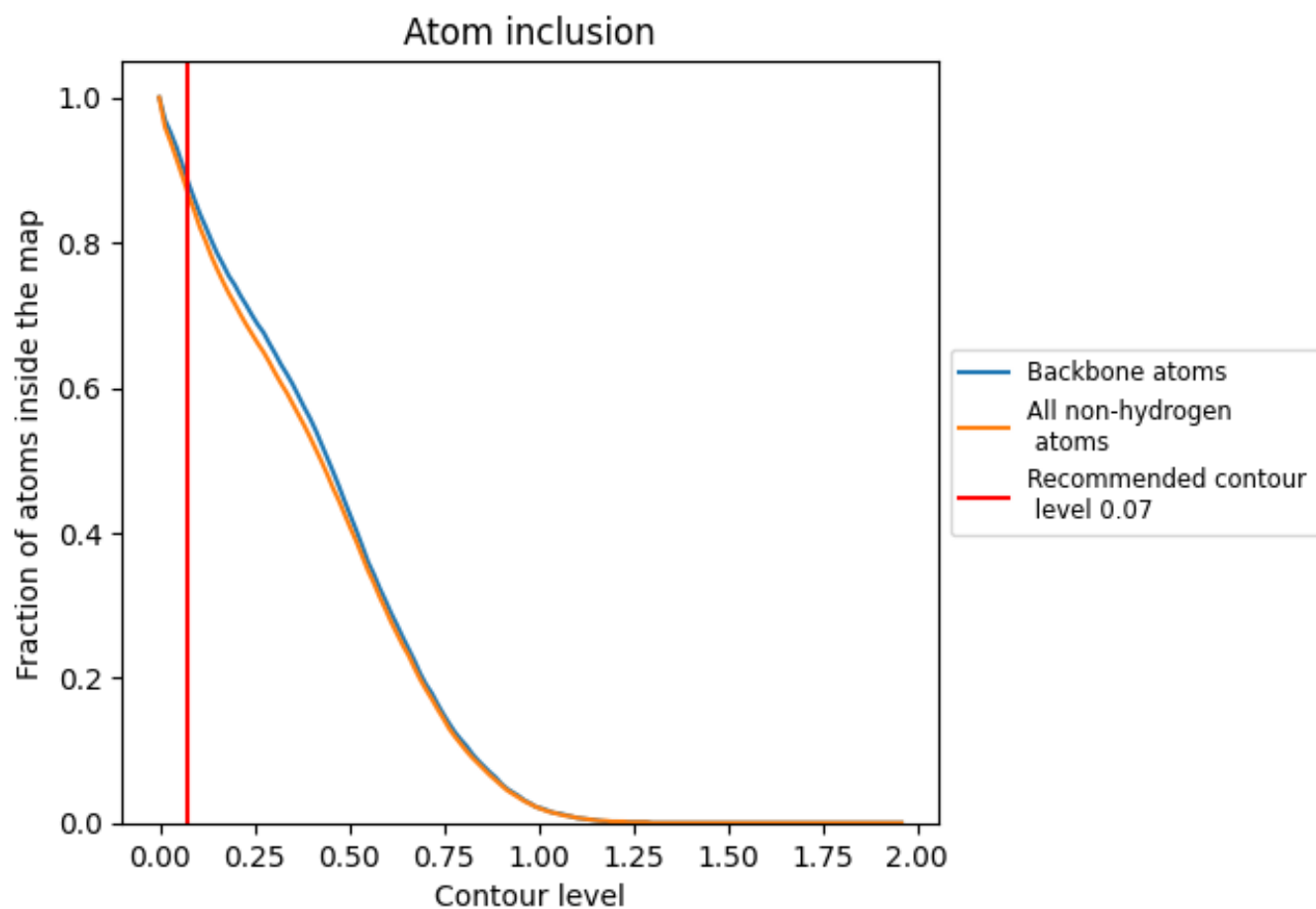


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.























## 9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8750	 0.5110
A	 0.8020	 0.4410
a	 0.9310	 0.5450
b	 0.8630	 0.5050
c	 0.8870	 0.5200
d	 0.8840	 0.5260
e	 0.8490	 0.5100
f	 0.8680	 0.5210
g	 0.9140	 0.5390
h	 0.8890	 0.5380
i	 0.8360	 0.5040

