



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 06:56 AM UTC

PDB ID : 9IZ2 / pdb_00009iz2
EMDB ID : EMD-61009
Title : Focus refinement dmCTPS bound with dATP dUTP dGTP and DON
Authors : Guo, C.J.; Liu, J.L.
Deposited on : 2024-07-31
Resolution : 2.79 Å(reported)

This is a Full wwPDB EM Validation 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.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

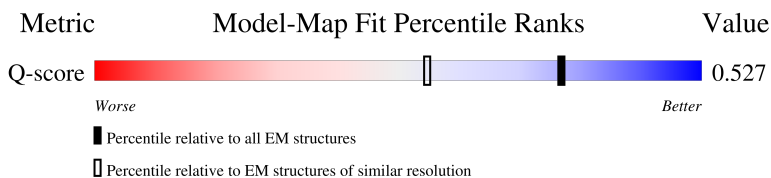
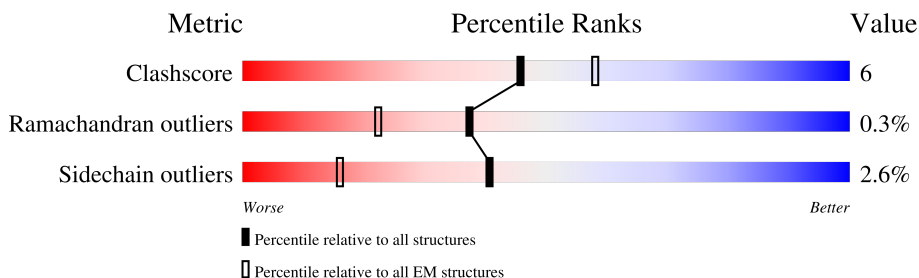
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.79 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	10811 (2.29 - 3.29)

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	556	 8% 82% 17% .
1	B	556	 10% . 89%
1	C	556	 5% . 93%

2 Entry composition [i](#)

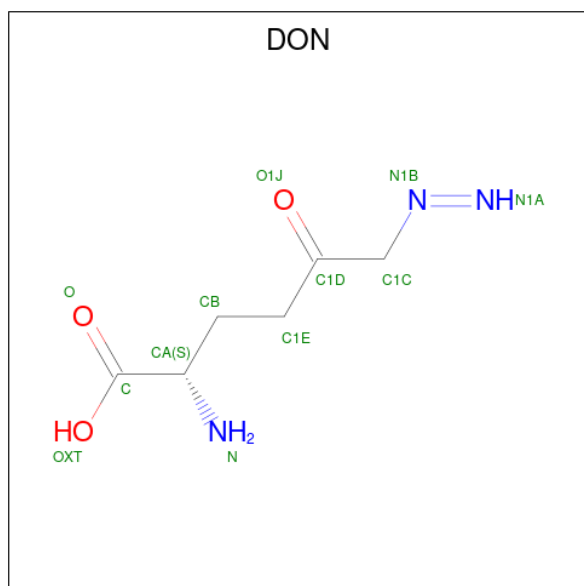
There are 6 unique types of molecules in this entry. The entry contains 5274 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 CTP synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	556	Total	C	N	O	S	0	0
			4384	2779	770	813	22		
1	B	60	Total	C	N	O	S	0	0
			454	282	81	87	4		
1	C	41	Total	C	N	O		0	0
			333	214	57	62			

- Molecule 2 is 6-DIAZENYL-5-OXO-L-NORLEUCINE (CCD ID: DON) (formula: $C_6H_{11}N_3O_3$) (labeled as "Ligand of Interest" by depositor).

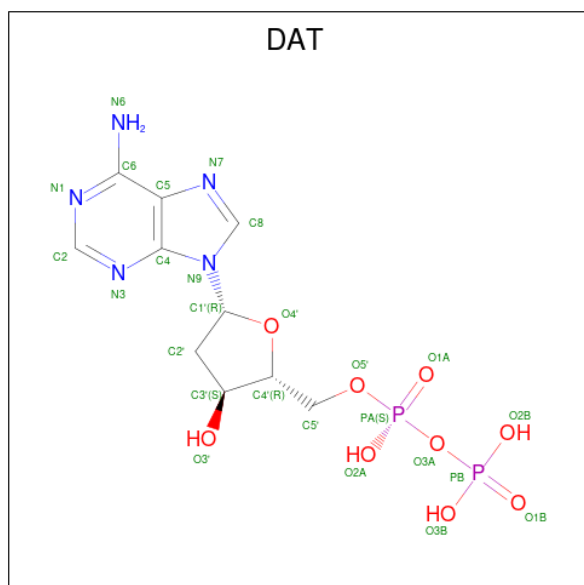


Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			10	6	1	3	

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

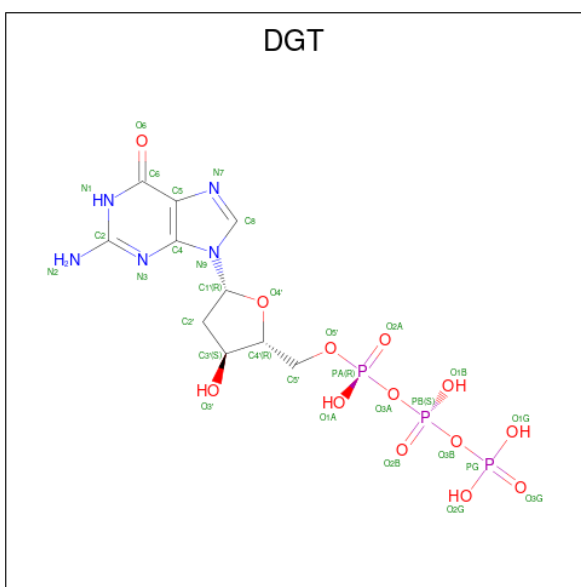
Mol	Chain	Residues	Atoms		AltConf
3	A	3	Total	Mg	0
			3	3	
3	B	1	Total	Mg	0
			1	1	

- Molecule 4 is 2'-DEOXYADENOSINE-5'-DIPHOSPHATE (CCD ID: DAT) (formula: $C_{10}H_{15}N_5O_9P_2$) (labeled as "Ligand of Interest" by depositor).



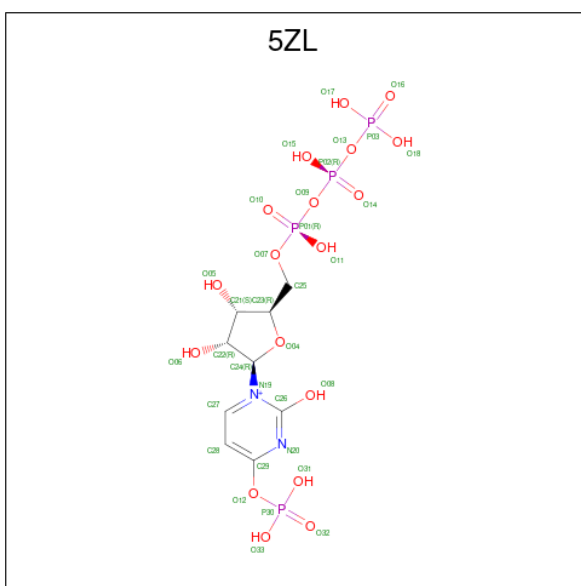
Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			26	10	5	9	2	

- Molecule 5 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (CCD ID: DGT) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 6 is [[(2 {R},3 {S},4 {R},5 {R})-3,4-bis(oxidanyl)-5-(2-oxidanyl-4-phosphonooxy-pyrimidin-1-yl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl] phosphono hydrogen phosphate (CCD ID: 5ZL) (formula: C₉H₁₇N₂O₁₈P₄) (labeled as "Ligand of Interest" by depositor).

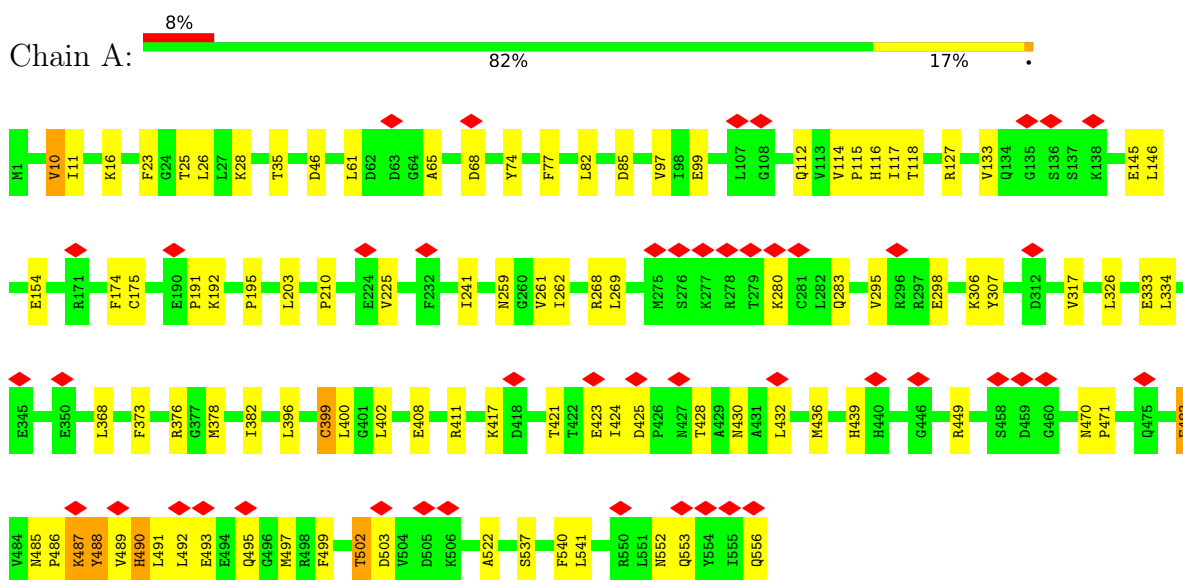


Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	N	O	P	0
			32	9	2	17	4	

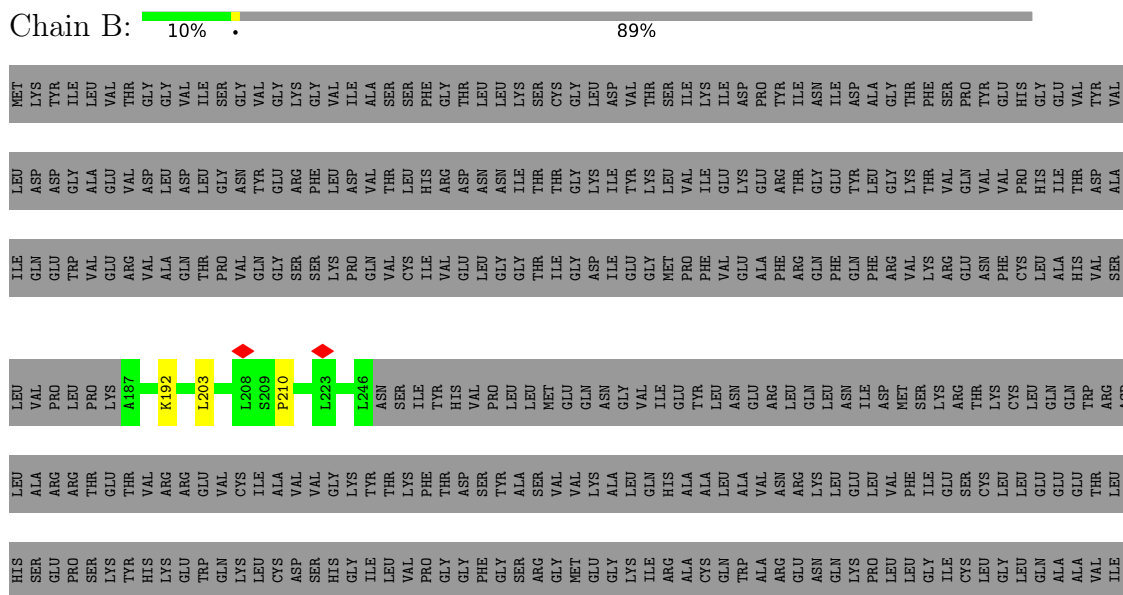
3 Residue-property plots

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: CTP synthase



• Molecule 1: CTP synthase



GLU TYR LEU SER ARG PRO LEU LYS PRO PRO PRO PHE LEU GLY LEU ILE LEU ALA SER VAL ASP ARG LEU LEU ASN GLN TYR ILE GLN

- Molecule 1: CTP synthase

Chain C: 5% . 93%

MET	LYS	TYR	ILE	LEU	VAL	THR	GLY	GLY	VAL	VAL	ILE	SER	GLY	VAL	GLY	LYS	LYS	SER	SER	PHE	GLY	THR	LEU	LEU	LYS	CYS	GLY	ASP	ASP	VAL	THR	SER	SER	ILE	ILE	LYS	ASN	PRO	TYR	ILE	ILE	ASP	ALA	THR	GLY	THR	SER	PRO	TYR	GLU	HIS	GLY	GLU	VAL	VAL	TYR	VAL
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LEU	ASP	GLY	ALA	GLU	VAL	ASP	LEU	LEU	GLY	ASN	TTR	GLU	ARG	PHE	LEU	ASP	VAL	THR	THR	E96	V97	R102	T103	G104	E105	T106	L107	Q112	V113	V114	P115	H116	L117	T118	Q122	E126	A129	Q130	THR	PRO	VAL	GLN	GLY
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SER	LYS	PRO	GLN	VAL	CYS	ILE	VAL	GLU	LEU	GLY	GLY	THR	ILE	GLY	ASP	ILE	GLU	GLY	MET	PRO	PHE	VAL	GLU	ALA	PHE	ARG	GLN	GLN	PHE	PHE	GLN	ASN	GLU	ARG	VAL	LYS	VAL	LEU	ALA	HIS	VAL	SER	LEU	VAL	PRO	LEU	PRO	PRO	THR	LYS	LYS	PRO	THR
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GLN SER SER SER VAL ARG GLU LEU LEU ARG GLY CYS GLY LEU SER SER PRO ASP ASP LEU LEU VAL CYS ARG SER SER GLU GLU LYS PRO PRO ILE GLY LEU GLU VAL VAL LYS GLU LYS ILE ILE SER ASN PHE CYS HIS VAL VAL GLY GLY PRO PRO ASP GLN VAL VAL ILE ILE ILE ILE HIS ASP LEU LEU SER SER ILE TYR HIS VAL PRO PRO LEU LEU LEU LEU MET

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

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	832381	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	59.5	Depositor
Minimum defocus (nm)	5000	Depositor
Maximum defocus (nm)	20000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.276	Depositor
Minimum map value	-0.119	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	262.4, 262.4, 262.4	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.025, 1.025, 1.025	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: DAT, DGT, 5ZL, DON, MG

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	0.16	0/4473	0.32	1/6055 (0.0%)
1	B	0.12	0/461	0.26	0/622
1	C	0.13	0/338	0.30	0/457
All	All	0.16	0/5272	0.31	1/7134 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	488	TYR	N-CA-C	-6.10	104.63	111.28

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	4384	0	4430	58	0
1	B	454	0	466	2	0
1	C	333	0	344	8	0
2	A	10	0	7	0	0
3	A	3	0	0	0	0
3	B	1	0	0	0	0
4	A	26	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	31	0	12	2	0
6	A	32	0	0	0	0
All	All	5274	0	5271	65	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 6.

All (65) 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:493:GLU:HG2	1:A:499:PHE:HD1	1.46	0.80
1:A:114:VAL:O	1:A:118:THR:OG1	2.06	0.71
1:C:114:VAL:O	1:C:118:THR:OG1	2.10	0.68
1:A:241:ILE:HG23	1:A:259:ASN:HD22	1.59	0.68
1:A:421:THR:HG22	1:A:423:GLU:H	1.59	0.67
1:A:203:LEU:HD23	1:A:210:PRO:HG3	1.78	0.65
1:A:306:LYS:O	1:A:376:ARG:NH2	2.30	0.65
1:A:425:ASP:O	1:A:428:THR:OG1	2.15	0.64
1:A:487:LYS:H	1:A:487:LYS:HD2	1.64	0.63
1:A:10:VAL:HG23	1:A:11:ILE:HG23	1.82	0.62
1:A:552:ASN:O	1:A:556:GLN:NE2	2.36	0.59
1:A:488:TYR:HA	1:A:491:LEU:HD12	1.85	0.59
1:A:85:ASP:OD2	1:A:127:ARG:NH1	2.39	0.56
1:C:103:THR:OG1	1:C:105:GLU:OE1	2.22	0.56
1:A:82:LEU:HD23	1:A:133:VAL:HG21	1.88	0.55
1:A:74:TYR:OH	1:A:145:GLU:OE1	2.21	0.55
1:A:486:PRO:O	1:A:489:VAL:HB	2.07	0.55
1:A:378:MET:HG3	1:A:424:ILE:HD11	1.89	0.54
1:B:203:LEU:HD23	1:B:210:PRO:HG3	1.90	0.54
1:A:432:LEU:HD13	1:A:488:TYR:HB3	1.90	0.54
1:A:26:LEU:HD22	1:A:262:ILE:HD11	1.90	0.53
1:A:61:LEU:HD12	1:A:65:ALA:HB3	1.92	0.52
1:A:411:ARG:HG3	1:A:417:LYS:HA	1.92	0.51
1:A:97:VAL:HG21	1:A:117:ILE:HD13	1.93	0.50
1:A:112:GLN:HB2	1:A:115:PRO:HD2	1.93	0.49
1:A:368:LEU:HD12	1:A:396:LEU:HB3	1.93	0.48
1:A:10:VAL:HG11	1:A:195:PRO:HB3	1.96	0.48
1:A:432:LEU:CD1	1:A:488:TYR:HB3	2.44	0.48
1:A:382:ILE:HG23	1:A:408:GLU:HB2	1.97	0.47
1:A:553:GLN:N	1:A:553:GLN:OE1	2.46	0.47
1:A:439:HIS:CE1	1:A:449:ARG:HG3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:97:VAL:HG21	1:C:117:ILE:HD13	1.96	0.46
1:C:122:GLN:O	1:C:126:GLU:HG2	2.16	0.46
1:A:432:LEU:HD13	1:A:488:TYR:CB	2.45	0.46
1:A:436:MET:HG2	1:A:483:GLU:HG2	1.98	0.46
1:A:485:ASN:O	1:A:489:VAL:HG23	2.15	0.46
1:A:402:LEU:HA	1:A:522:ALA:HB1	1.98	0.46
1:A:306:LYS:NZ	1:A:373:PHE:O	2.34	0.45
1:A:430:ASN:HA	1:A:488:TYR:OH	2.15	0.45
1:A:46:ASP:OD1	1:C:102:ARG:NH2	2.44	0.45
1:A:490:HIS:CG	1:A:491:LEU:N	2.82	0.45
1:A:241:ILE:HG23	1:A:259:ASN:ND2	2.31	0.45
1:A:307:TYR:OH	5:A:606:DGT:O2B	2.19	0.44
1:A:192:LYS:HA	1:A:192:LYS:HD2	1.72	0.44
1:A:502:THR:OG1	1:A:503:ASP:N	2.50	0.43
1:C:112:GLN:HB2	1:C:115:PRO:HD2	2.00	0.43
1:A:11:ILE:HB	1:B:192:LYS:HE2	2.00	0.43
1:A:493:GLU:HA	1:A:497:MET:O	2.18	0.43
1:A:174:PHE:O	1:A:268:ARG:NH2	2.51	0.43
1:A:23:PHE:HE1	1:A:261:VAL:HG11	1.83	0.42
1:A:154:GLU:HG3	1:C:113:VAL:HG23	2.02	0.42
1:A:334:LEU:HD12	1:A:334:LEU:HA	1.86	0.42
1:A:280:LYS:HG2	1:A:283:GLN:HB2	2.02	0.42
1:A:112:GLN:O	1:A:116:HIS:HB2	2.20	0.41
1:A:492:LEU:HB3	1:A:497:MET:HE2	2.02	0.41
1:A:470:ASN:N	1:A:471:PRO:HD3	2.35	0.41
1:A:488:TYR:O	1:A:489:VAL:C	2.63	0.41
1:A:537:SER:HB3	1:A:540:PHE:HD2	1.86	0.41
1:A:28:LYS:HE3	1:A:28:LYS:HB2	1.94	0.41
1:A:175:CYS:HB2	1:A:269:LEU:HD21	2.03	0.41
1:A:298:GLU:OE2	1:A:333:GLU:HB2	2.21	0.41
5:A:606:DGT:H5'A	1:C:107:LEU:HG	2.03	0.40
1:A:16:LYS:HB2	1:A:16:LYS:HE2	1.89	0.40
1:A:191:PRO:HB2	1:A:225:VAL:HG21	2.02	0.40
1:A:399:CYS:HB3	1:A:400:LEU:H	1.76	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	554/556 (100%)	538 (97%)	14 (2%)	2 (0%)	30	60
1	B	58/556 (10%)	57 (98%)	1 (2%)	0	100	100
1	C	39/556 (7%)	39 (100%)	0	0	100	100
All	All	651/1668 (39%)	634 (97%)	15 (2%)	2 (0%)	37	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	495	GLN
1	A	399	CYS

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	486/486 (100%)	471 (97%)	15 (3%)	35	70
1	B	54/486 (11%)	54 (100%)	0	100	100
1	C	36/486 (7%)	36 (100%)	0	100	100
All	All	576/1458 (40%)	561 (97%)	15 (3%)	41	75

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	VAL

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Mol	Chain	Res	Type
1	A	25	THR
1	A	35	THR
1	A	68	ASP
1	A	77	PHE
1	A	99	GLU
1	A	146	LEU
1	A	295	VAL
1	A	317	VAL
1	A	326	LEU
1	A	483	GLU
1	A	487	LYS
1	A	490	HIS
1	A	502	THR
1	A	541	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	173	ASN
1	A	259	ASN
1	A	524	GLN
1	A	556	GLN

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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\# Z > 2$
6	5ZL	A	607	3	29,33,34	3.26	9 (31%)	43,52,54	1.54	1 (2%)
5	DGT	A	606	3	32,33,33	3.45	17 (53%)	48,52,52	2.09	12 (25%)
4	DAT	A	605	3	27,28,28	1.42	4 (14%)	41,43,43	1.86	8 (19%)
2	DON	A	601	1	8,9,11	0.78	0	8,11,13	1.34	1 (12%)

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
6	5ZL	A	607	3	-	14/24/39/43	0/2/2/2
5	DGT	A	606	3	-	4/22/34/34	0/3/3/3
4	DAT	A	605	3	-	3/16/28/28	0/3/3/3
2	DON	A	601	1	-	2/9/9/12	-

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	607	5ZL	P02-O13	9.12	1.69	1.59
5	A	606	DGT	C2'-C3'	-7.85	1.32	1.52
6	A	607	5ZL	P02-O09	7.03	1.67	1.59
6	A	607	5ZL	O04-C23	6.93	1.60	1.45
5	A	606	DGT	C4-N3	6.81	1.49	1.34
6	A	607	5ZL	C21-C23	-6.27	1.36	1.53
5	A	606	DGT	C2-N3	5.52	1.46	1.33
6	A	607	5ZL	O04-C24	-5.47	1.30	1.42
5	A	606	DGT	PB-O3B	5.24	1.65	1.59
5	A	606	DGT	O4'-C1'	-5.19	1.30	1.42
5	A	606	DGT	O4'-C4'	5.18	1.56	1.45
5	A	606	DGT	PA-O3A	4.95	1.64	1.59
5	A	606	DGT	PB-O3A	4.90	1.64	1.59
5	A	606	DGT	C2-N2	4.76	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	605	DAT	C5-C4	4.49	1.47	1.39
5	A	606	DGT	C2'-C1'	4.17	1.63	1.52
5	A	606	DGT	C5'-C4'	-4.10	1.39	1.51
6	A	607	5ZL	C27-N19	-3.56	1.31	1.36
5	A	606	DGT	C5-N7	-3.21	1.32	1.39
6	A	607	5ZL	P01-O09	2.95	1.62	1.59
6	A	607	5ZL	O05-C21	2.73	1.49	1.43
4	A	605	DAT	C5-C6	2.72	1.48	1.41
5	A	606	DGT	C2-N1	2.69	1.44	1.37
5	A	606	DGT	O3'-C3'	2.64	1.48	1.43
5	A	606	DGT	C5-C6	2.56	1.54	1.44
5	A	606	DGT	O6-C6	-2.55	1.18	1.23
4	A	605	DAT	C5-N7	-2.38	1.34	1.39
5	A	606	DGT	C6-N1	2.34	1.43	1.38
6	A	607	5ZL	C22-C24	2.27	1.58	1.52
4	A	605	DAT	C8-N7	2.23	1.36	1.31

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	607	5ZL	C26-N20-C29	8.28	120.00	114.49
5	A	606	DGT	C5-C4-N3	-6.36	118.27	128.39
4	A	605	DAT	C5-C4-N3	-5.80	118.73	126.72
5	A	606	DGT	C1'-N9-C8	5.33	139.87	127.91
5	A	606	DGT	C2-N3-C4	5.25	121.34	112.30
5	A	606	DGT	C1'-N9-C4	-4.66	112.92	125.50
4	A	605	DAT	N3-C4-N9	4.45	134.74	127.17
5	A	606	DGT	N9-C4-N3	4.03	134.01	125.95
4	A	605	DAT	C2-N3-C4	3.68	120.82	111.83
4	A	605	DAT	C4-C5-N7	-3.63	106.43	110.58
5	A	606	DGT	C2-N1-C6	-3.32	119.09	125.11
4	A	605	DAT	N3-C2-N1	-3.18	123.77	128.58
2	A	601	DON	OXT-C-O	-3.08	117.08	124.08
5	A	606	DGT	C5-C6-N1	2.74	120.23	113.25
4	A	605	DAT	C5-N7-C8	2.61	107.55	103.45
4	A	605	DAT	C4-N9-C8	2.50	108.36	105.74
5	A	606	DGT	O6-C6-C5	-2.48	119.99	126.53
5	A	606	DGT	N9-C8-N7	-2.42	108.92	113.40
5	A	606	DGT	C3'-C2'-C1'	2.18	107.93	102.60
4	A	605	DAT	C6-C5-N7	2.18	136.29	132.09
5	A	606	DGT	C2'-C3'-C4'	2.16	107.19	102.80
5	A	606	DGT	C8-N7-C5	2.10	107.99	104.26

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	607	5ZL	O04-C23-C25-O07
6	A	607	5ZL	P02-O13-P03-O17
6	A	607	5ZL	P02-O13-P03-O18
5	A	606	DGT	O4'-C4'-C5'-O5'
5	A	606	DGT	C3'-C4'-C5'-O5'
6	A	607	5ZL	C21-C23-C25-O07
4	A	605	DAT	O4'-C4'-C5'-O5'
5	A	606	DGT	PG-O3B-PB-O2B
2	A	601	DON	O1J-C1D-C1E-CB
2	A	601	DON	C1C-C1D-C1E-CB
6	A	607	5ZL	P02-O09-P01-O10
6	A	607	5ZL	C25-O07-P01-O09
6	A	607	5ZL	C25-O07-P01-O10
6	A	607	5ZL	C25-O07-P01-O11
6	A	607	5ZL	N20-C29-O12-P30
6	A	607	5ZL	P01-O09-P02-O14
4	A	605	DAT	PB-O3A-PA-O1A
5	A	606	DGT	PG-O3B-PB-O1B
6	A	607	5ZL	C28-C29-O12-P30
4	A	605	DAT	PB-O3A-PA-O2A
6	A	607	5ZL	P01-O09-P02-O15
6	A	607	5ZL	P02-O13-P03-O16
6	A	607	5ZL	P02-O09-P01-O11

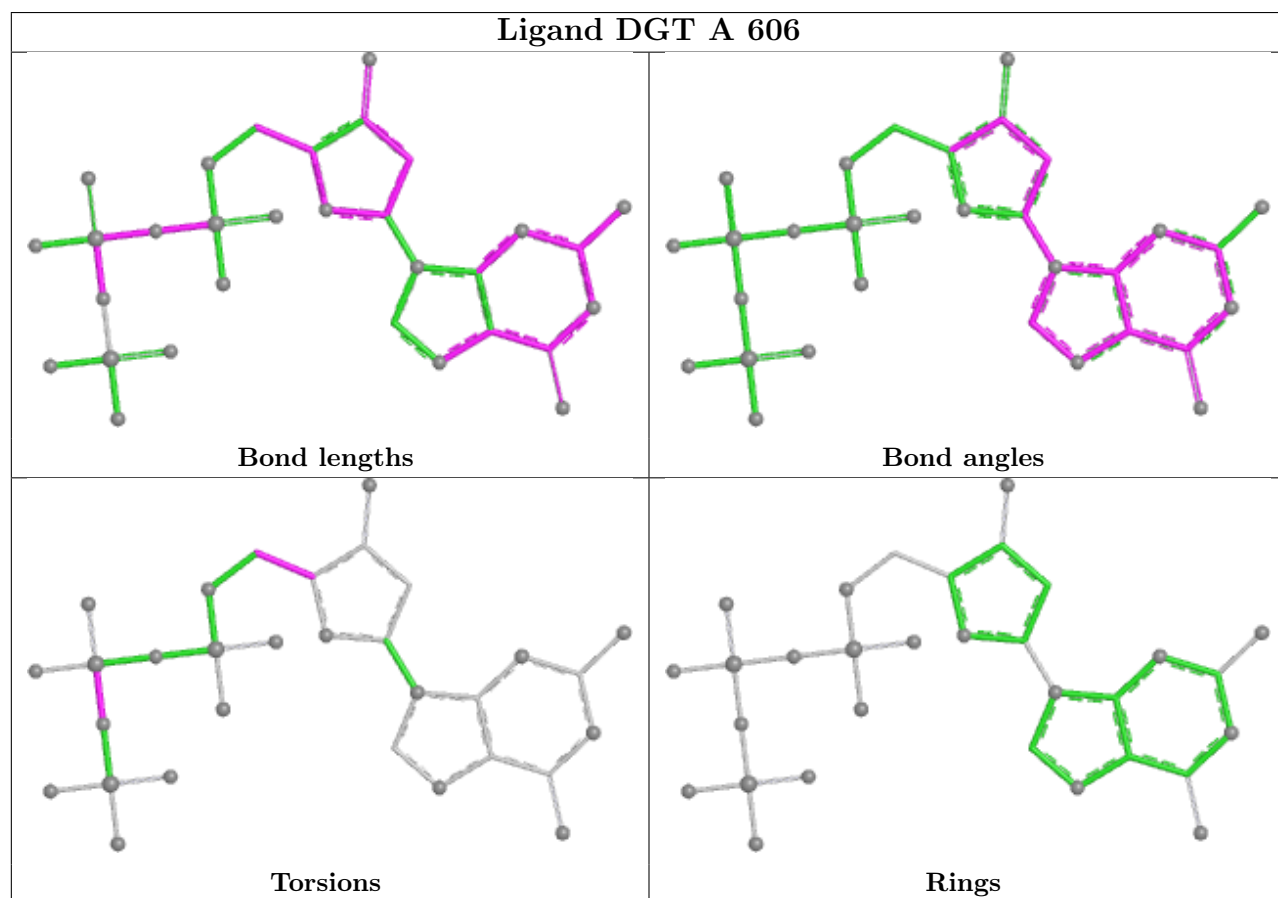
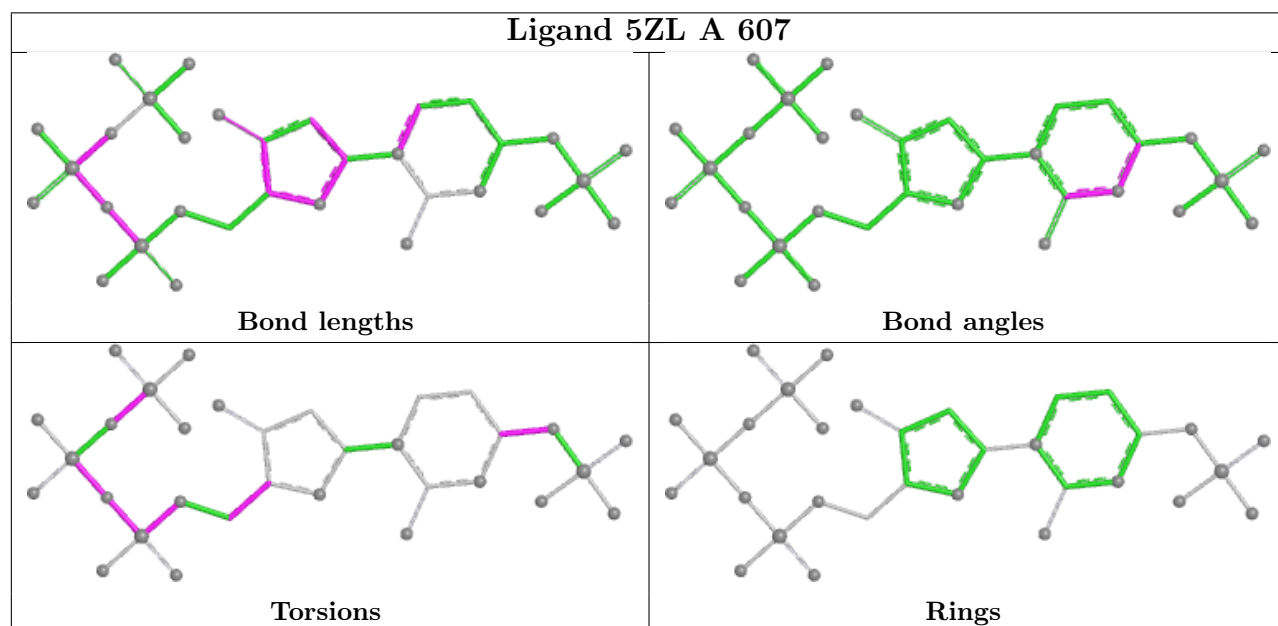
There are no ring outliers.

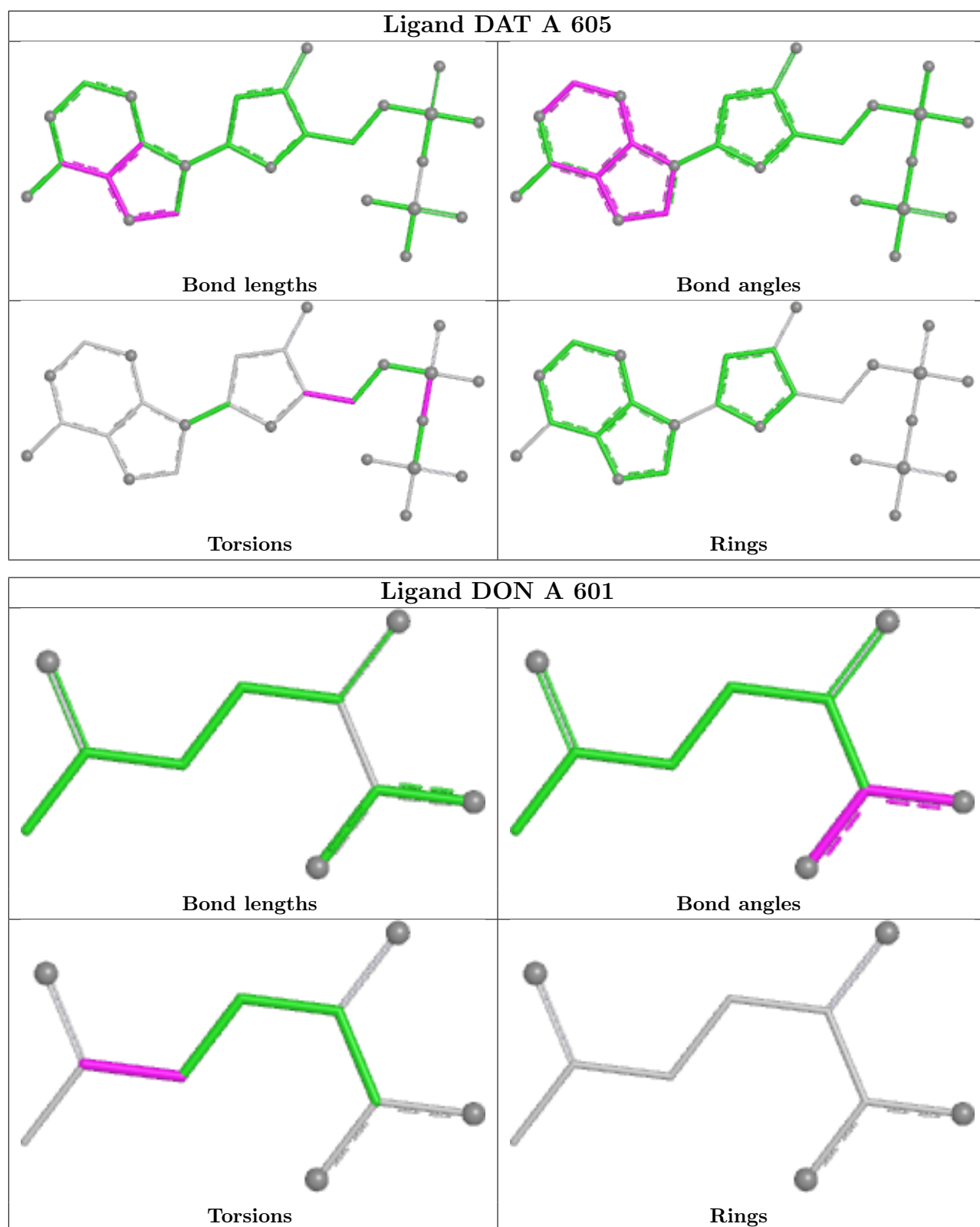
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	606	DGT	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

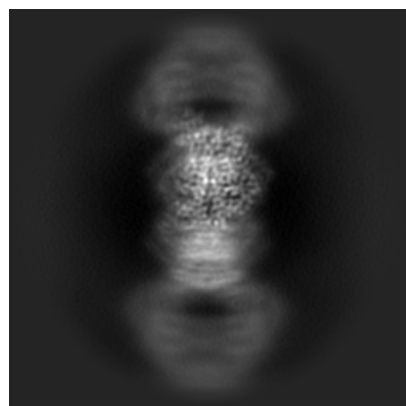
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61009. These allow visual inspection of the internal detail of the map and identification of artifacts.

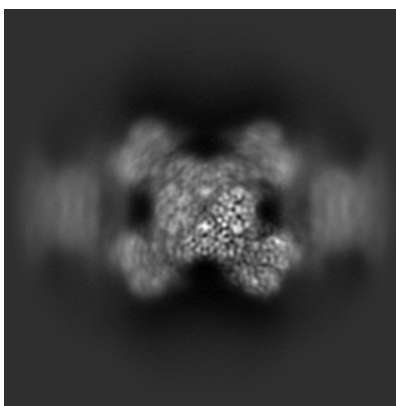
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

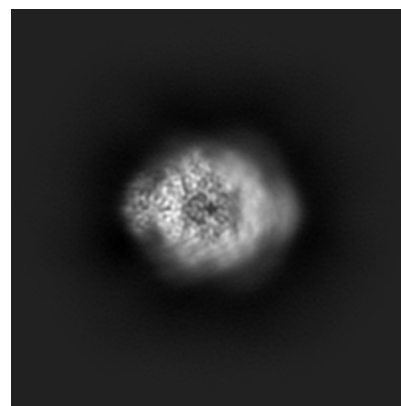
6.1.1 Primary map



X

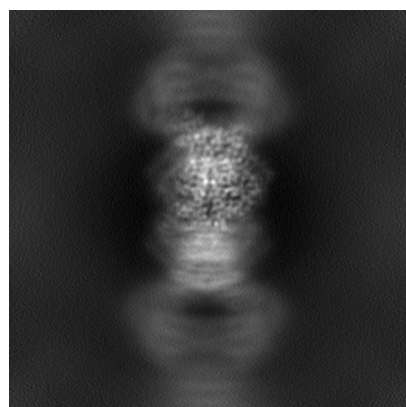


Y

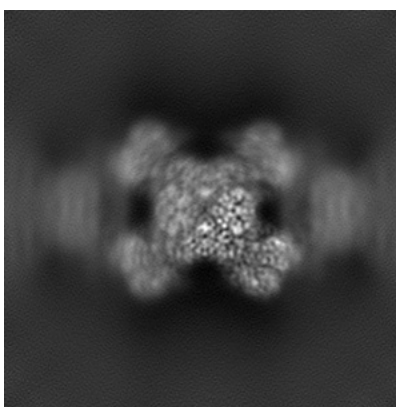


Z

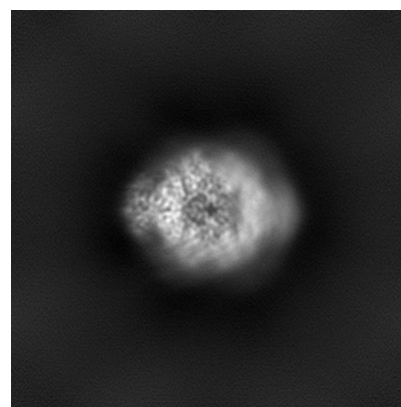
6.1.2 Raw map



X



Y

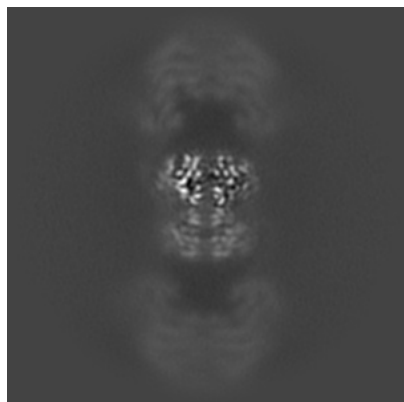


Z

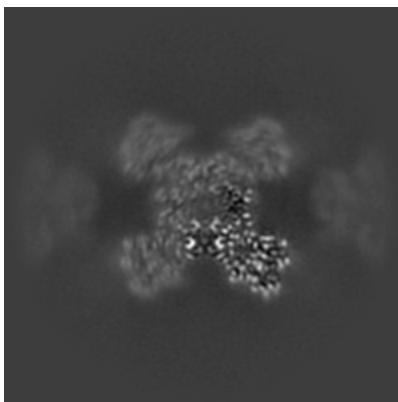
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

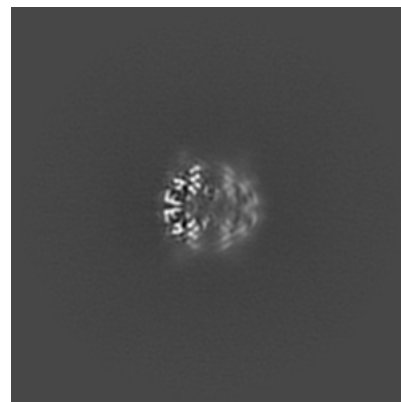
6.2.1 Primary map



X Index: 128

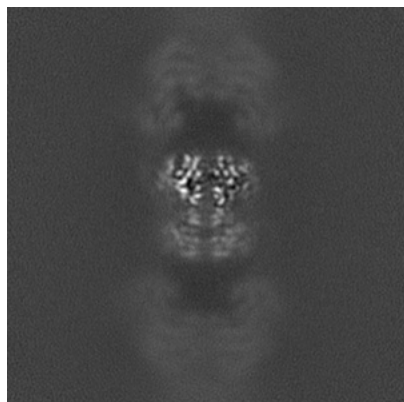


Y Index: 128

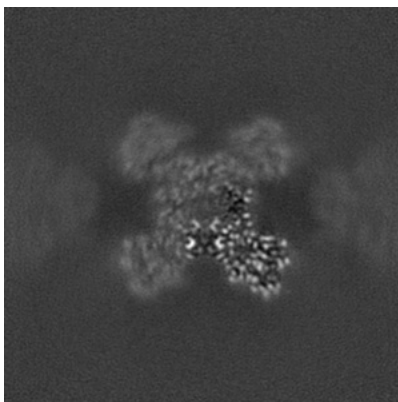


Z Index: 128

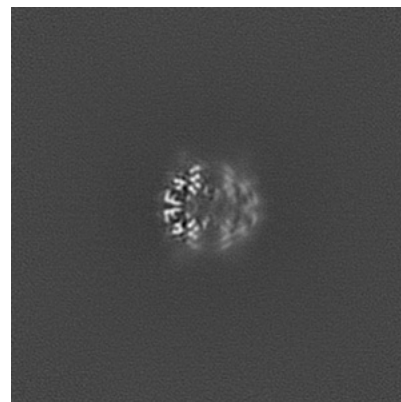
6.2.2 Raw map



X Index: 128



Y Index: 128

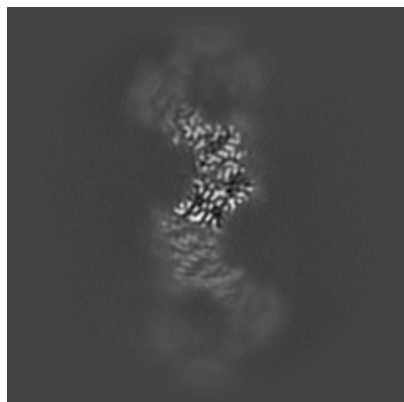


Z Index: 128

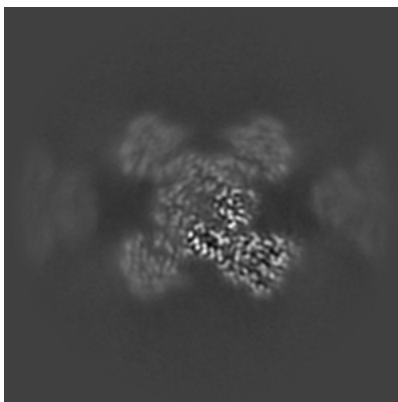
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

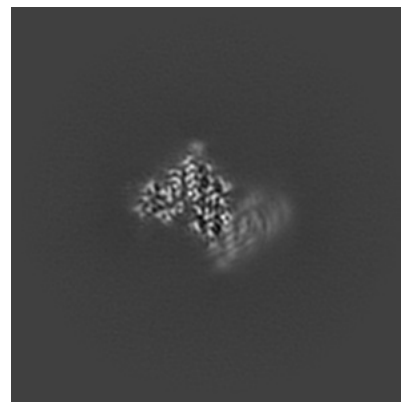
6.3.1 Primary map



X Index: 105

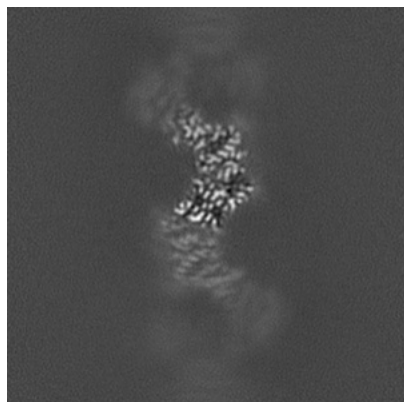


Y Index: 124

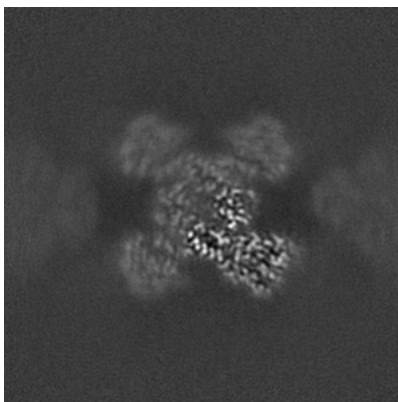


Z Index: 150

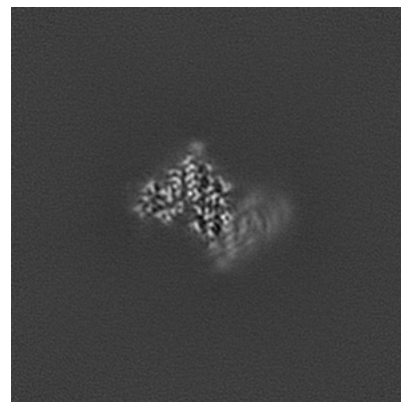
6.3.2 Raw map



X Index: 105



Y Index: 124

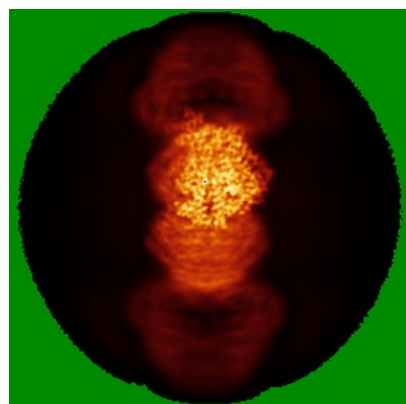


Z Index: 150

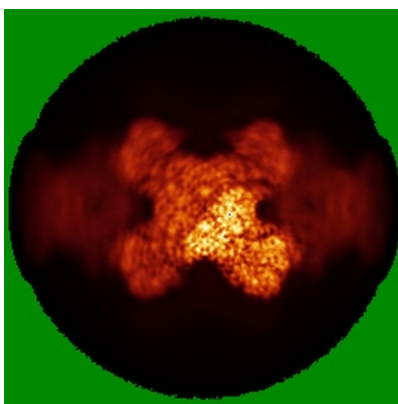
The images above show the largest variance slices of the map in three orthogonal directions.

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

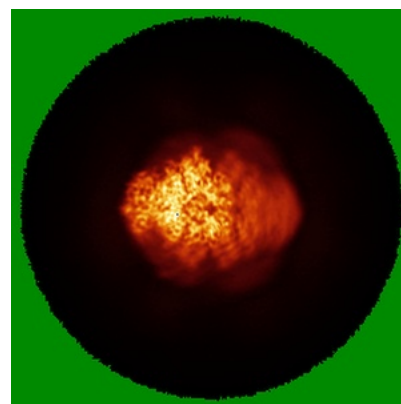
6.4.1 Primary map



X

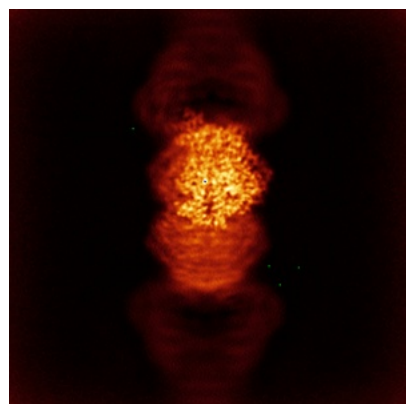


Y

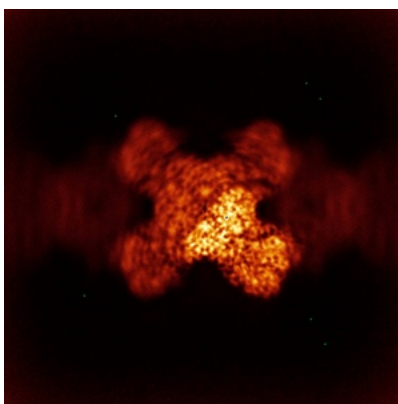


Z

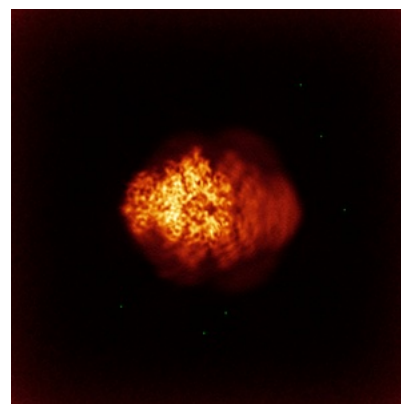
6.4.2 Raw map



X



Y

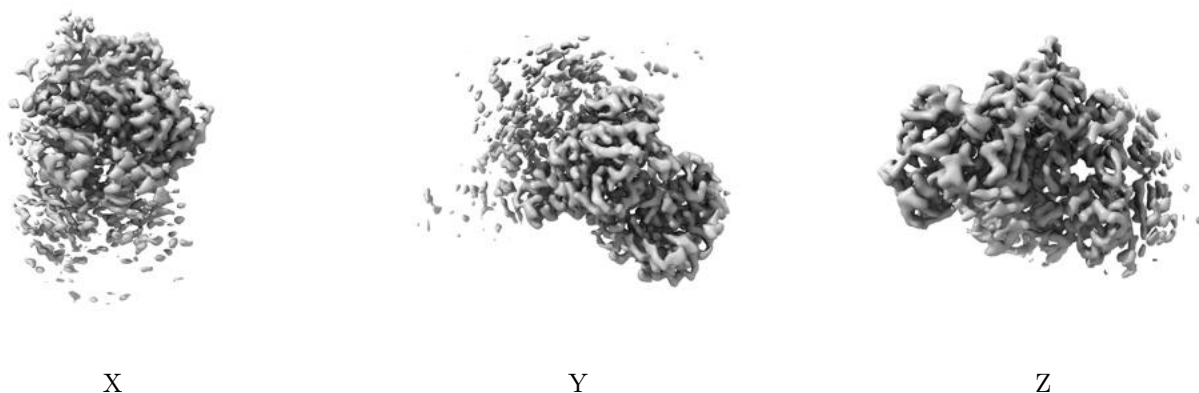


Z

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

6.5.2 Raw map



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

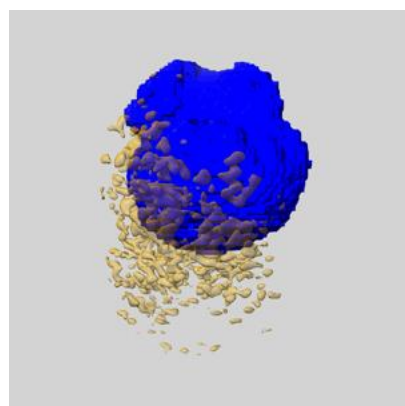
6.6 Mask visualisation [i](#)

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

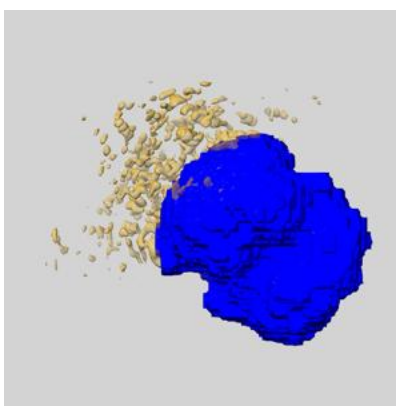
A mask typically either:

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

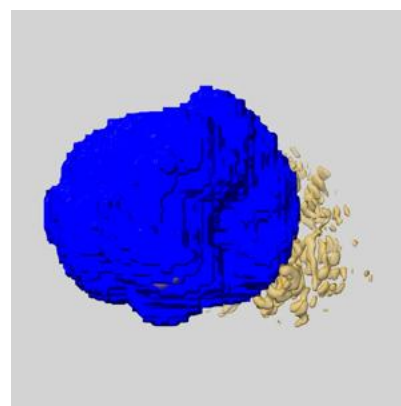
6.6.1 emd_61009_msk_1.map [i](#)



X



Y

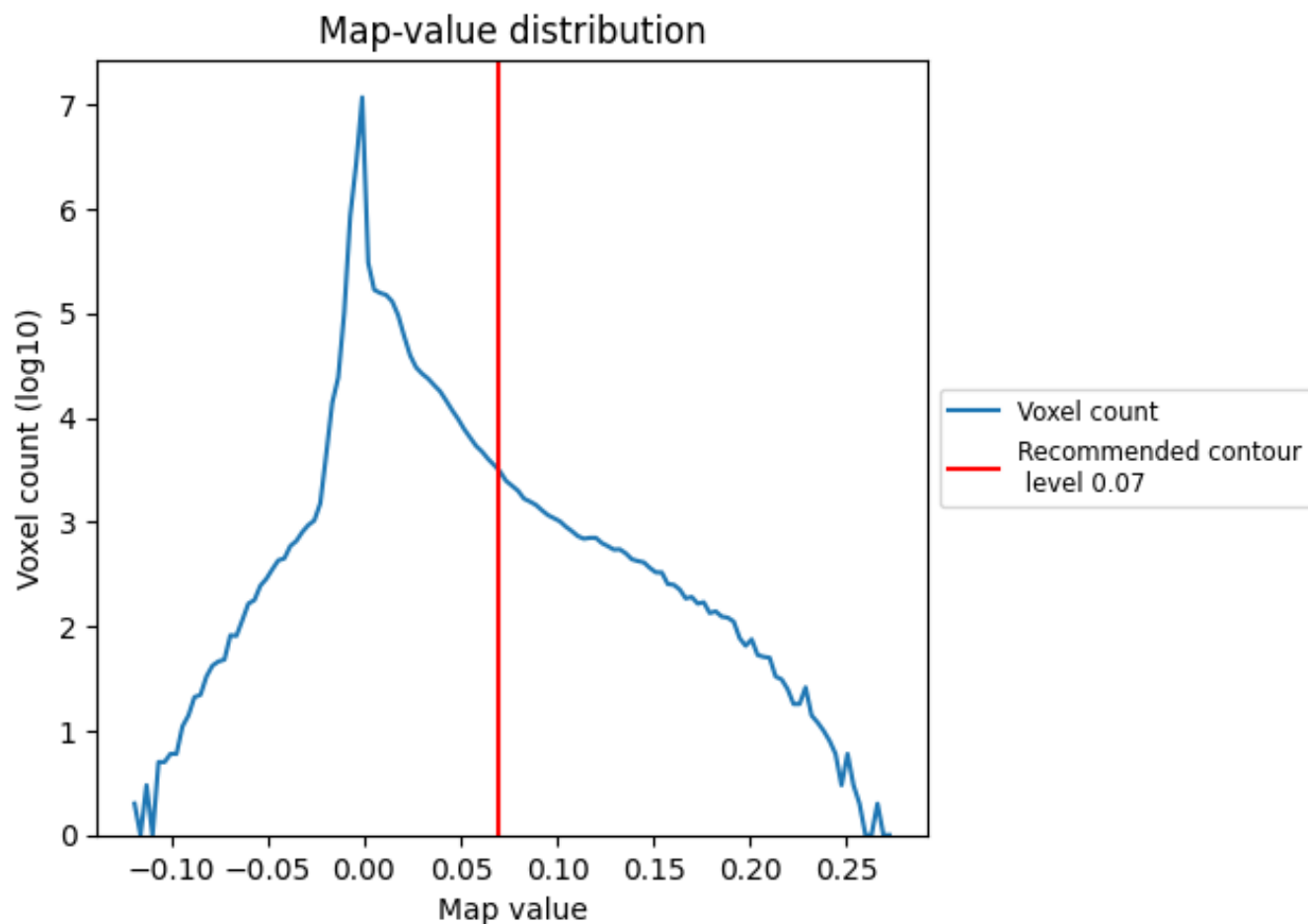


Z

7 Map analysis [i](#)

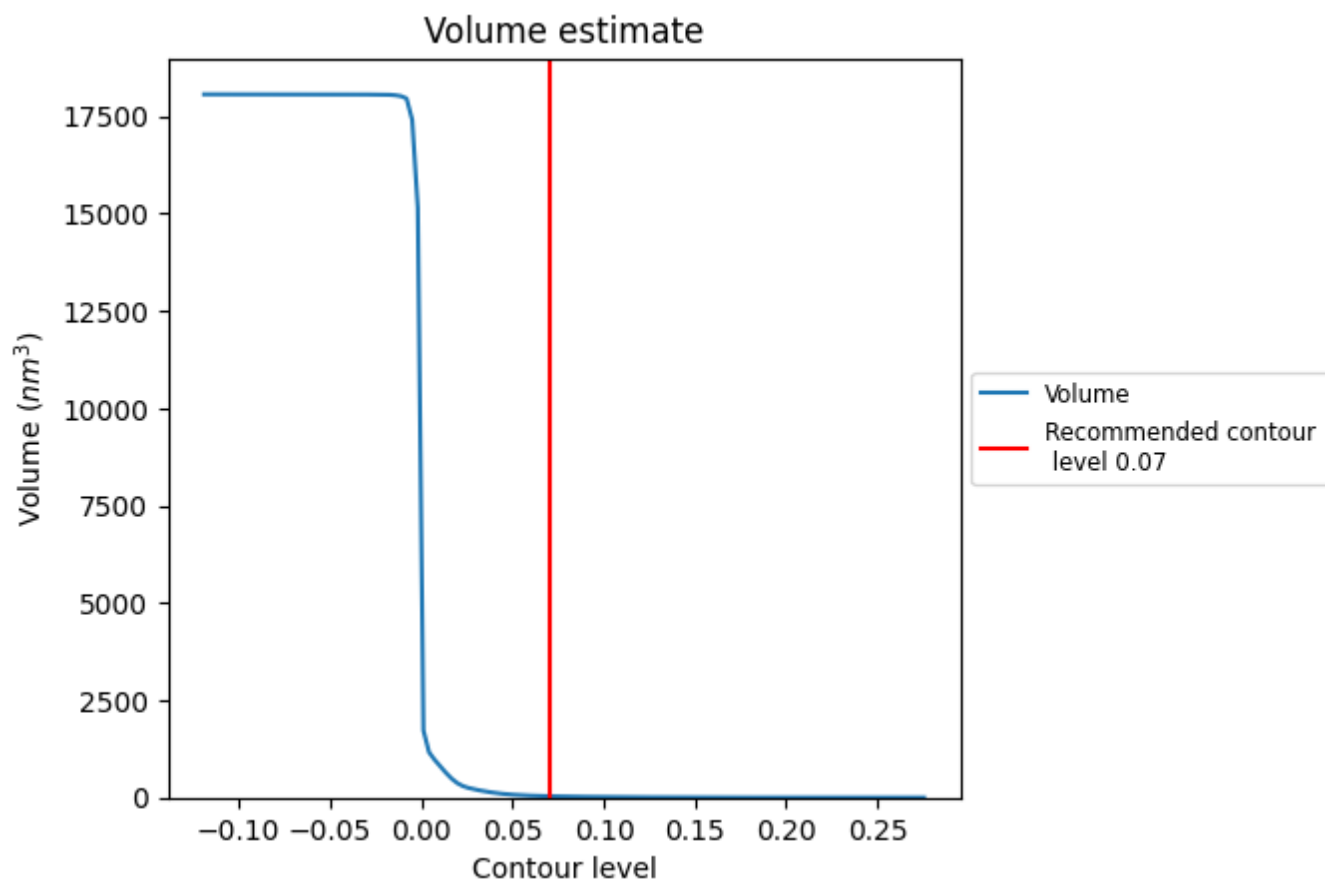
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

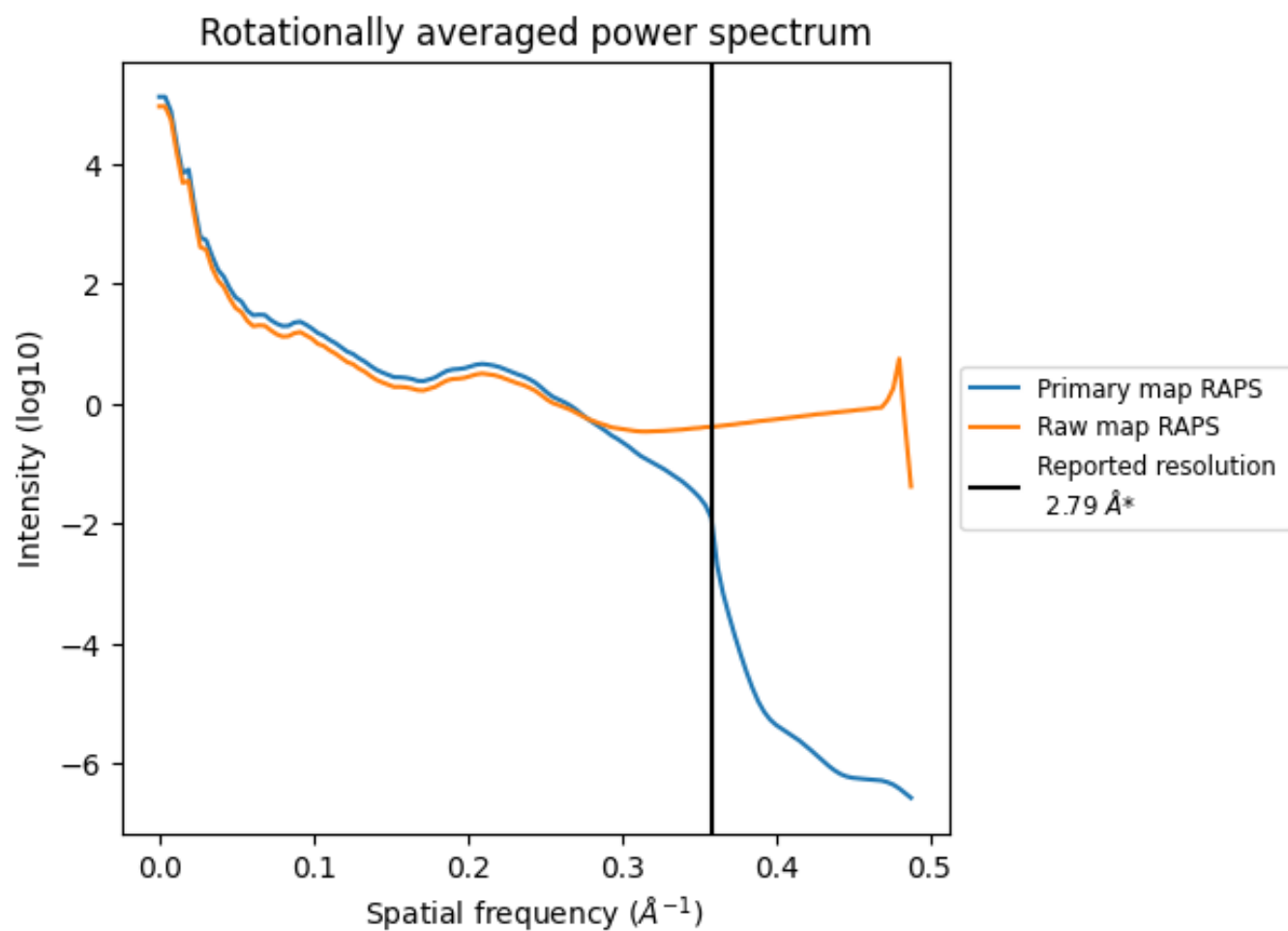
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 34 nm³; this corresponds to an approximate mass of 31 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 ⓘ

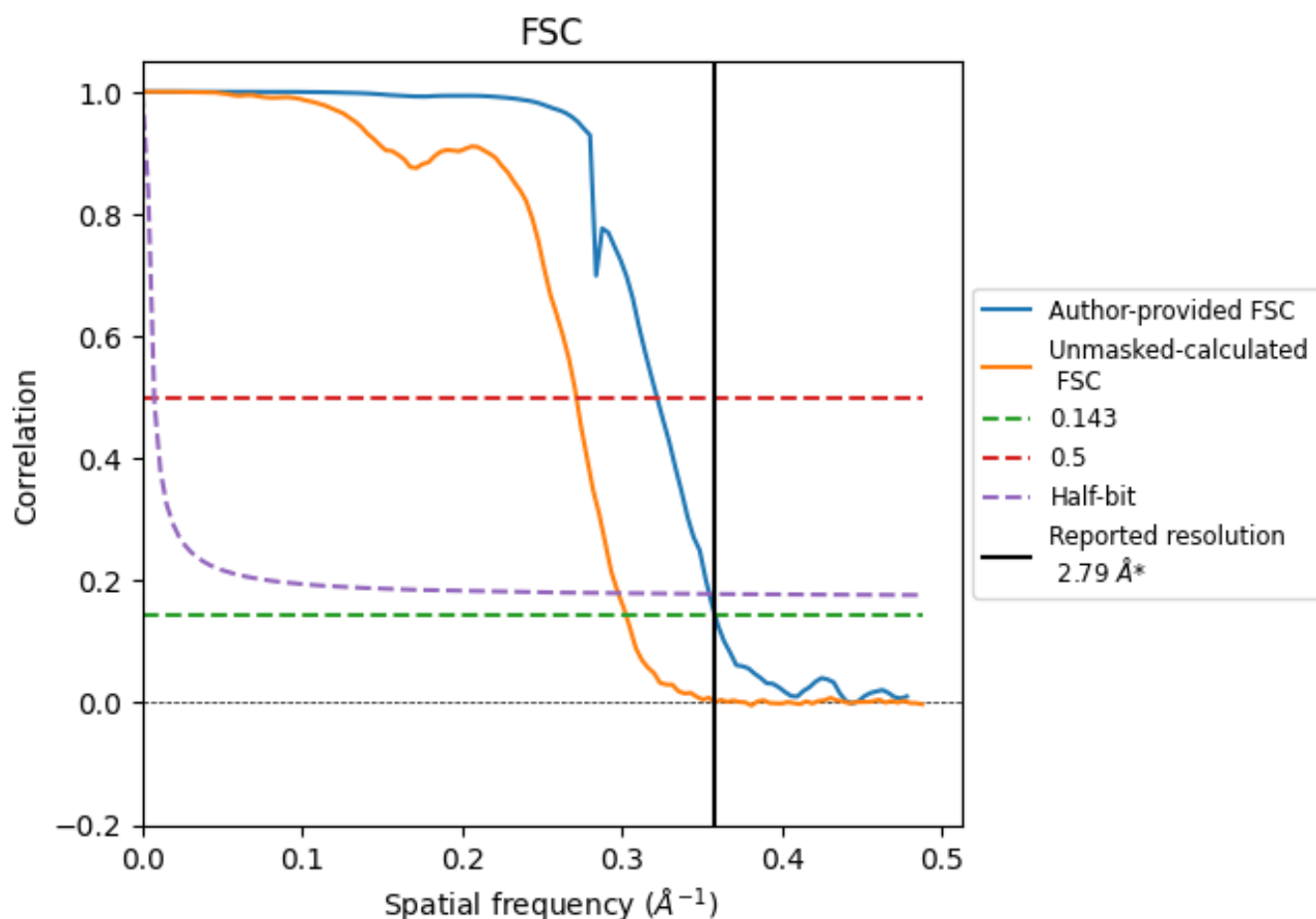


*Reported resolution corresponds to spatial frequency of 0.358 Å⁻¹

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 0.358 $\text{\AA}^{-1}$

8.2 Resolution estimates

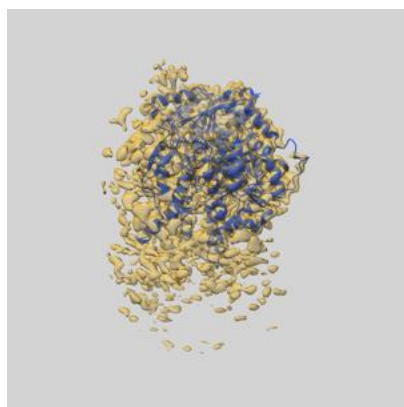
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.79	-	-
Author-provided FSC curve	2.79	3.11	2.82
Unmasked-calculated*	3.30	3.68	3.36

*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 3.30 differs from the reported value 2.79 by more than 10 %

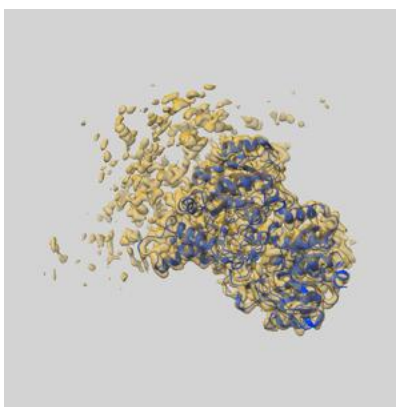
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61009 and PDB model 9IZ2. Per-residue inclusion information can be found in section [3](#) on page [6](#).

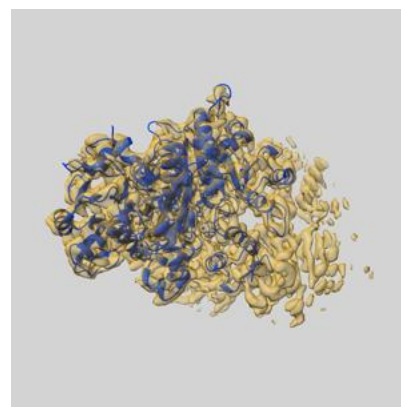
9.1 Map-model overlay [i](#)



X



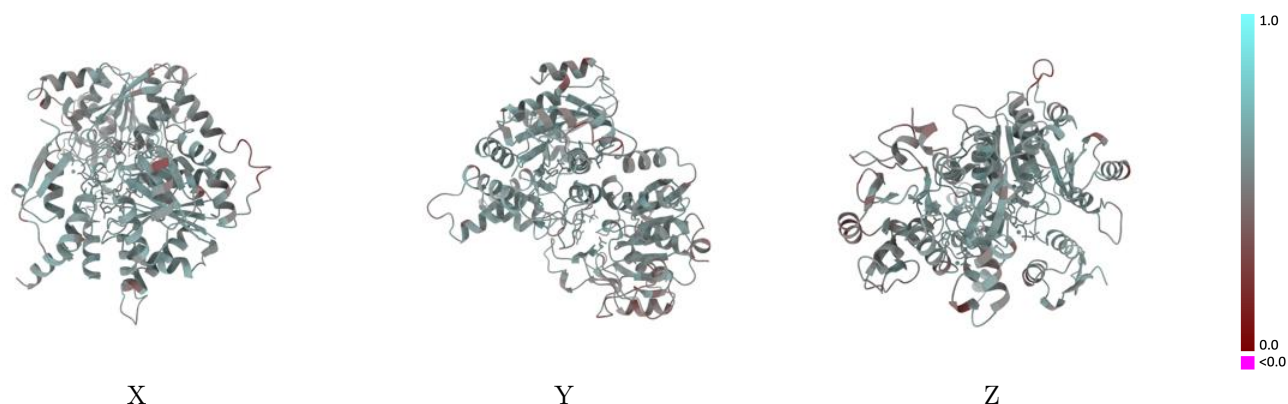
Y



Z

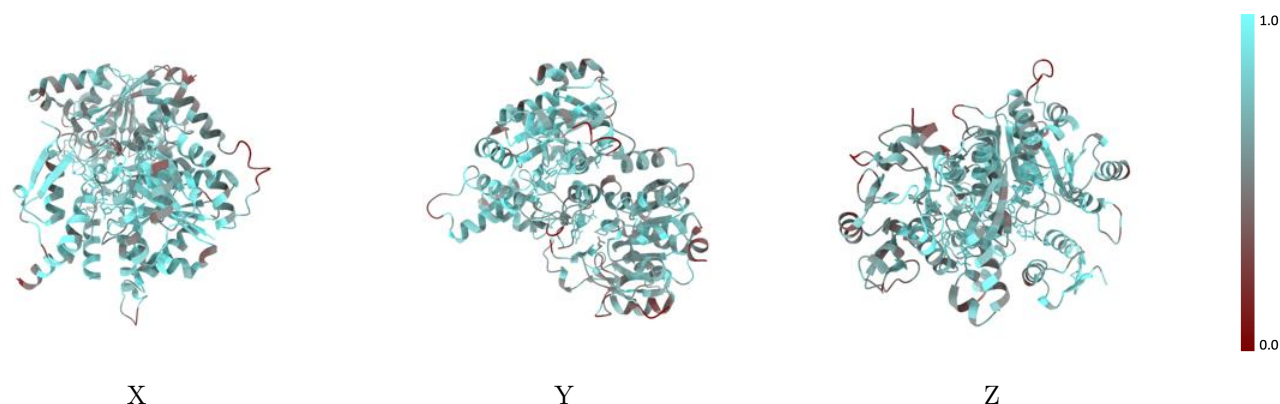
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



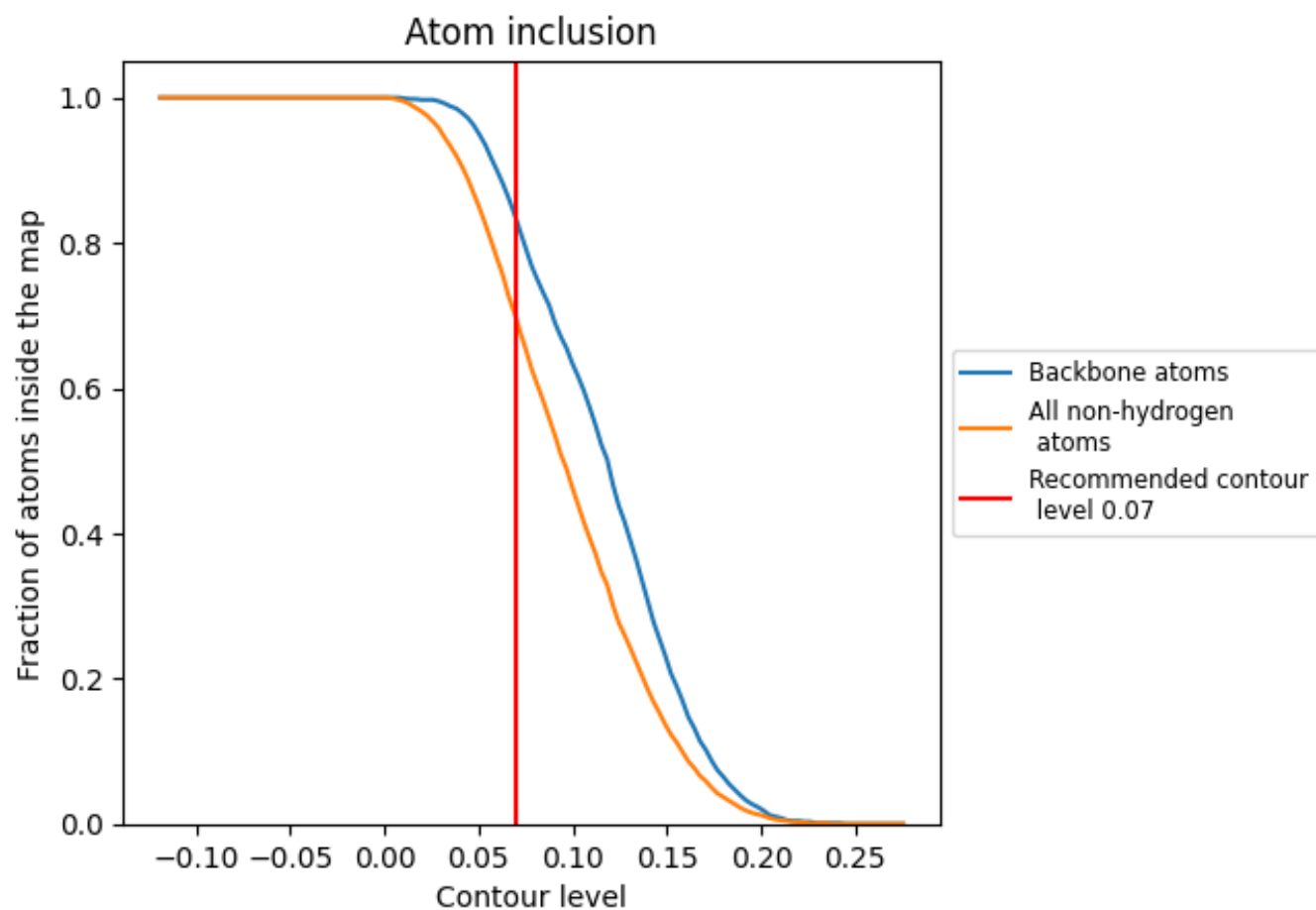
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 70% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6960	0.5270
A	0.6890	0.5250
B	0.7280	0.5370
C	0.7580	0.5500

