



Full wwPDB EM Validation Report ⓘ

Mar 19, 2026 – 07:52 PM UTC

PDB ID : 8U43 / pdb_00008u43
EMDB ID : EMD-41873
Title : TRPV1 in nanodisc bound with PIP2-Br4
Authors : Arnold, W.R.; Julius, D.; Cheng, Y.
Deposited on : 2023-09-08
Resolution : 2.40 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

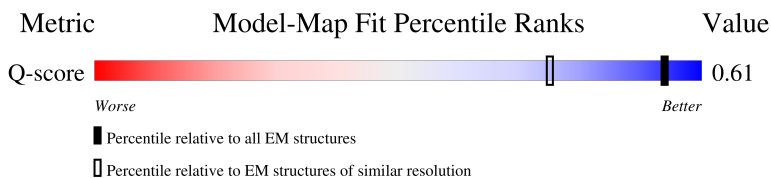
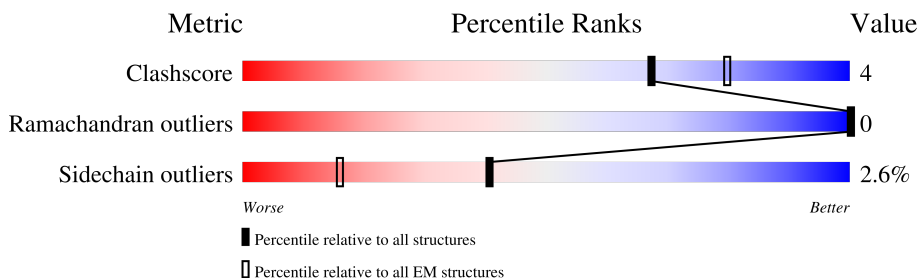
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 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	5628 (1.90 - 2.90)

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	635	7% 78% 9% 12%
1	B	635	7% 78% 9% 12%
1	C	635	7% 77% 9% 12%
1	D	635	7% 78% 9% 12%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 37207 atoms, of which 18616 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 Transient receptor potential cation channel subfamily V member 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	556	Total	C	H	N	O	S	0	0
			9019	2947	4514	730	803	25		
1	B	556	Total	C	H	N	O	S	0	0
			9019	2947	4514	730	803	25		
1	C	556	Total	C	H	N	O	S	0	0
			9019	2947	4514	730	803	25		
1	D	556	Total	C	H	N	O	S	0	0
			9019	2947	4514	730	803	25		

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	MET	-	initiating methionine	UNP O35433
A	108	GLY	-	expression tag	UNP O35433
A	109	SER	-	expression tag	UNP O35433
A	?	-	ASN	deletion	UNP O35433
A	?	-	ASN	deletion	UNP O35433
A	?	-	SER	deletion	UNP O35433
A	?	-	LEU	deletion	UNP O35433
A	?	-	PRO	deletion	UNP O35433
A	?	-	MET	deletion	UNP O35433
A	?	-	GLU	deletion	UNP O35433
A	?	-	SER	deletion	UNP O35433
A	?	-	THR	deletion	UNP O35433
A	?	-	PRO	deletion	UNP O35433
A	?	-	HIS	deletion	UNP O35433
A	?	-	LYS	deletion	UNP O35433
A	?	-	CYS	deletion	UNP O35433
A	?	-	ARG	deletion	UNP O35433
A	?	-	GLY	deletion	UNP O35433
A	?	-	SER	deletion	UNP O35433
A	?	-	ALA	deletion	UNP O35433
A	?	-	CYS	deletion	UNP O35433

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LYS	deletion	UNP O35433
A	?	-	PRO	deletion	UNP O35433
A	?	-	GLY	deletion	UNP O35433
A	?	-	ASN	deletion	UNP O35433
A	?	-	SER	deletion	UNP O35433
B	107	MET	-	initiating methionine	UNP O35433
B	108	GLY	-	expression tag	UNP O35433
B	109	SER	-	expression tag	UNP O35433
B	?	-	ASN	deletion	UNP O35433
B	?	-	ASN	deletion	UNP O35433
B	?	-	SER	deletion	UNP O35433
B	?	-	LEU	deletion	UNP O35433
B	?	-	PRO	deletion	UNP O35433
B	?	-	MET	deletion	UNP O35433
B	?	-	GLU	deletion	UNP O35433
B	?	-	SER	deletion	UNP O35433
B	?	-	THR	deletion	UNP O35433
B	?	-	PRO	deletion	UNP O35433
B	?	-	HIS	deletion	UNP O35433
B	?	-	LYS	deletion	UNP O35433
B	?	-	CYS	deletion	UNP O35433
B	?	-	ARG	deletion	UNP O35433
B	?	-	GLY	deletion	UNP O35433
B	?	-	SER	deletion	UNP O35433
B	?	-	ALA	deletion	UNP O35433
B	?	-	CYS	deletion	UNP O35433
B	?	-	LYS	deletion	UNP O35433
B	?	-	PRO	deletion	UNP O35433
B	?	-	GLY	deletion	UNP O35433
B	?	-	ASN	deletion	UNP O35433
B	?	-	SER	deletion	UNP O35433
C	107	MET	-	initiating methionine	UNP O35433
C	108	GLY	-	expression tag	UNP O35433
C	109	SER	-	expression tag	UNP O35433
C	?	-	ASN	deletion	UNP O35433
C	?	-	ASN	deletion	UNP O35433
C	?	-	SER	deletion	UNP O35433
C	?	-	LEU	deletion	UNP O35433
C	?	-	PRO	deletion	UNP O35433
C	?	-	MET	deletion	UNP O35433
C	?	-	GLU	deletion	UNP O35433
C	?	-	SER	deletion	UNP O35433

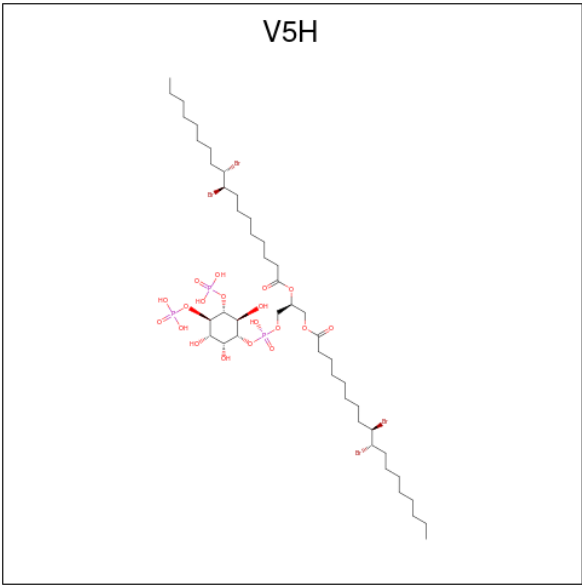
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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	THR	deletion	UNP O35433
C	?	-	PRO	deletion	UNP O35433
C	?	-	HIS	deletion	UNP O35433
C	?	-	LYS	deletion	UNP O35433
C	?	-	CYS	deletion	UNP O35433
C	?	-	ARG	deletion	UNP O35433
C	?	-	GLY	deletion	UNP O35433
C	?	-	SER	deletion	UNP O35433
C	?	-	ALA	deletion	UNP O35433
C	?	-	CYS	deletion	UNP O35433
C	?	-	LYS	deletion	UNP O35433
C	?	-	PRO	deletion	UNP O35433
C	?	-	GLY	deletion	UNP O35433
C	?	-	ASN	deletion	UNP O35433
C	?	-	SER	deletion	UNP O35433
D	107	MET	-	initiating methionine	UNP O35433
D	108	GLY	-	expression tag	UNP O35433
D	109	SER	-	expression tag	UNP O35433
D	?	-	ASN	deletion	UNP O35433
D	?	-	ASN	deletion	UNP O35433
D	?	-	SER	deletion	UNP O35433
D	?	-	LEU	deletion	UNP O35433
D	?	-	PRO	deletion	UNP O35433
D	?	-	MET	deletion	UNP O35433
D	?	-	GLU	deletion	UNP O35433
D	?	-	SER	deletion	UNP O35433
D	?	-	THR	deletion	UNP O35433
D	?	-	PRO	deletion	UNP O35433
D	?	-	HIS	deletion	UNP O35433
D	?	-	LYS	deletion	UNP O35433
D	?	-	CYS	deletion	UNP O35433
D	?	-	ARG	deletion	UNP O35433
D	?	-	GLY	deletion	UNP O35433
D	?	-	SER	deletion	UNP O35433
D	?	-	ALA	deletion	UNP O35433
D	?	-	CYS	deletion	UNP O35433
D	?	-	LYS	deletion	UNP O35433
D	?	-	PRO	deletion	UNP O35433
D	?	-	GLY	deletion	UNP O35433
D	?	-	ASN	deletion	UNP O35433
D	?	-	SER	deletion	UNP O35433

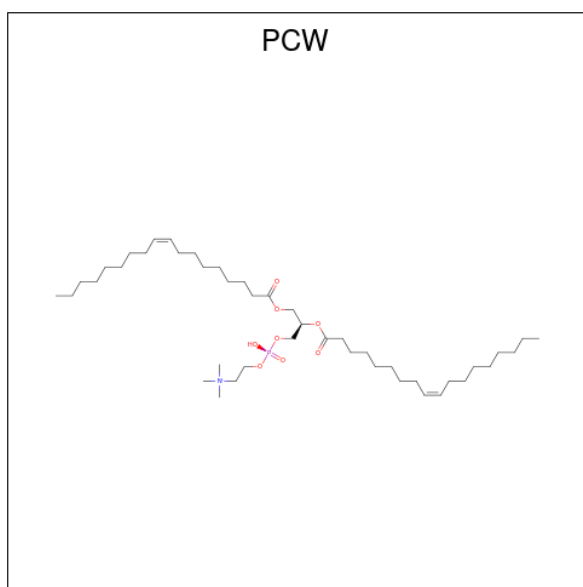
- Molecule 2 is (2S)-2-[(9,10-dibromooctadecanoyl)oxy]-3-[[[(S)-hydroxy{[(1R,2R,3S,4R,5R,6S

)-2,3,6-trihydroxy-4,5-bis(phosphonooxy)cyclohexyl]oxy}phosphoryl]oxy}propyl (9R,10S)-9,10-dibromooctadecanoate (CCD ID: V5H) (formula: C₄₅H₈₅Br₄O₁₉P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
			Total	Br	C	H	O	P	
2	A	1	Total	Br	C	H	O	P	0
			111	2	32	55	19	3	
2	B	1	Total	Br	C	H	O	P	0
			111	2	32	55	19	3	
2	C	1	Total	Br	C	H	O	P	0
			111	2	32	55	19	3	
2	D	1	Total	Br	C	H	O	P	0
			111	2	32	55	19	3	

- Molecule 3 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW) (formula: C₄₄H₈₅NO₈P).



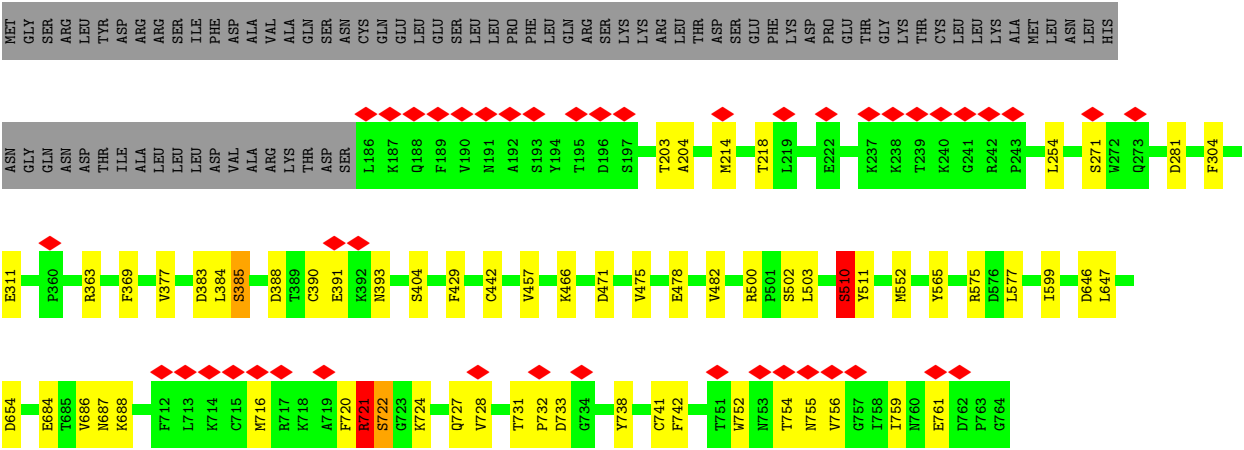
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	H	N	O	P
			138	44	84	1	8	1
3	B	1	Total	C	H	N	O	P
			138	44	84	1	8	1
3	C	1	Total	C	H	N	O	P
			138	44	84	1	8	1
3	D	1	Total	C	H	N	O	P
			138	44	84	1	8	1

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

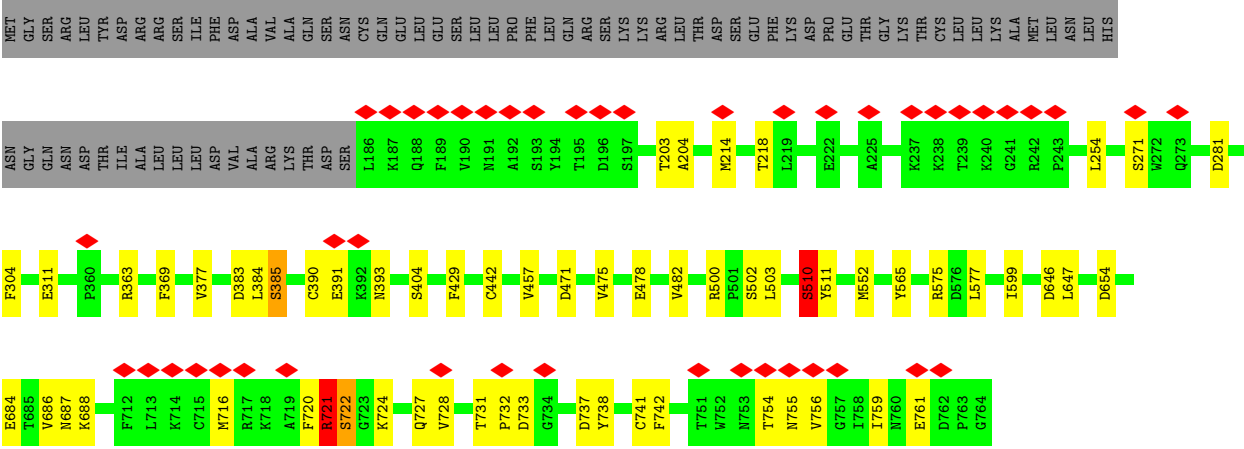
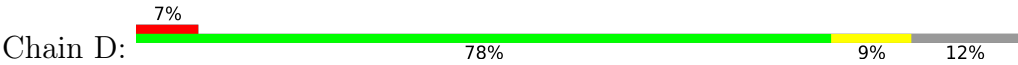
Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Na	
			1	1	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms			AltConf
5	A	33	Total	H	O	
			35	2	33	0
5	B	33	Total	H	O	
			35	2	33	0
5	C	32	Total	O		
			32	32		0
5	D	32	Total	O		
			32	32		0



● Molecule 1: Transient receptor potential cation channel subfamily V member 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1089955	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 ($e^-/\text{\AA}^2$)	45.8	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	10.471	Depositor
Minimum map value	-4.364	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.094	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	347.36, 347.36, 347.36	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.835, 0.835, 0.835	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: V5H, NA, PCW

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	0.30	2/4613 (0.0%)	0.53	7/6248 (0.1%)
1	B	0.30	2/4613 (0.0%)	0.53	7/6248 (0.1%)
1	C	0.30	2/4613 (0.0%)	0.53	8/6248 (0.1%)
1	D	0.30	2/4613 (0.0%)	0.53	7/6248 (0.1%)
All	All	0.30	8/18452 (0.0%)	0.53	29/24992 (0.1%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	722	SER	CA-CB	-7.05	1.44	1.54
1	A	722	SER	CA-CB	-7.01	1.44	1.54
1	B	722	SER	CA-CB	-7.01	1.44	1.54
1	C	722	SER	CA-CB	-7.01	1.44	1.54
1	A	577	LEU	C-O	-5.39	1.17	1.24
1	C	577	LEU	C-O	-5.39	1.17	1.24
1	D	577	LEU	C-O	-5.39	1.17	1.24
1	B	577	LEU	C-O	-5.32	1.17	1.24

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	761	GLU	CA-C-N	10.51	147.45	121.80
1	C	761	GLU	C-N-CA	10.51	147.45	121.80
1	A	761	GLU	CA-C-N	10.50	147.43	121.80
1	A	761	GLU	C-N-CA	10.50	147.43	121.80
1	B	761	GLU	CA-C-N	10.50	147.43	121.80
1	B	761	GLU	C-N-CA	10.50	147.43	121.80
1	D	761	GLU	CA-C-N	10.49	147.39	121.80
1	D	761	GLU	C-N-CA	10.49	147.39	121.80
1	B	721	ARG	CB-CA-C	-7.58	95.34	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	721	ARG	CB-CA-C	-7.56	95.37	110.42
1	C	721	ARG	CB-CA-C	-7.56	95.37	110.42
1	D	721	ARG	CB-CA-C	-7.55	95.39	110.42
1	A	510	SER	N-CA-CB	-7.48	100.34	111.71
1	B	510	SER	N-CA-CB	-7.48	100.34	111.71
1	C	510	SER	N-CA-CB	-7.48	100.34	111.71
1	D	510	SER	N-CA-CB	-7.48	100.34	111.71
1	C	752	TRP	N-CA-C	6.48	119.17	111.33
1	B	721	ARG	N-CA-C	6.35	124.33	110.80
1	A	721	ARG	N-CA-C	6.35	124.32	110.80
1	C	721	ARG	N-CA-C	6.35	124.32	110.80
1	D	721	ARG	N-CA-C	6.35	124.32	110.80
1	C	741	CYS	N-CA-C	5.25	117.45	110.53
1	A	741	CYS	N-CA-C	5.23	117.43	110.53
1	B	741	CYS	N-CA-C	5.23	117.43	110.53
1	D	741	CYS	N-CA-C	5.23	117.43	110.53
1	A	511	TYR	CA-C-O	-5.17	114.50	120.24
1	C	511	TYR	CA-C-O	-5.17	114.50	120.24
1	D	511	TYR	CA-C-O	-5.17	114.50	120.24
1	B	511	TYR	CA-C-O	-5.13	114.55	120.24

There are no chirality outliers.

There are no planarity outliers.

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	4505	4514	4535	34	0
1	B	4505	4514	4535	36	0
1	C	4505	4514	4535	37	0
1	D	4505	4514	4535	36	0
2	A	56	55	0	0	0
2	B	56	55	0	0	0
2	C	56	55	0	0	0
2	D	56	55	0	0	0
3	A	54	84	84	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	54	84	84	0	0
3	C	54	84	84	1	0
3	D	54	84	84	1	0
4	A	1	0	0	0	0
5	A	33	2	0	3	0
5	B	33	2	0	3	0
5	C	32	0	0	3	0
5	D	32	0	0	3	0
All	All	18591	18616	18476	139	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 4.

All (139) 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:646:ASP:O	5:C:901:HOH:O	2.04	0.76
1:A:646:ASP:O	5:A:901:HOH:O	2.04	0.76
1:B:646:ASP:O	5:B:901:HOH:O	2.04	0.76
1:D:646:ASP:O	5:D:901:HOH:O	2.04	0.75
1:A:599:ILE:O	5:A:902:HOH:O	2.16	0.62
1:D:565:TYR:OH	5:D:903:HOH:O	2.16	0.61
1:B:565:TYR:OH	5:B:903:HOH:O	2.16	0.61
1:C:599:ILE:O	5:C:902:HOH:O	2.16	0.61
1:B:599:ILE:O	5:B:902:HOH:O	2.16	0.60
1:D:599:ILE:O	5:D:902:HOH:O	2.16	0.60
1:B:457:VAL:O	1:B:457:VAL:HG23	2.04	0.58
1:A:457:VAL:O	1:A:457:VAL:HG23	2.04	0.58
1:C:565:TYR:OH	5:C:903:HOH:O	2.16	0.58
1:A:565:TYR:OH	5:A:903:HOH:O	2.16	0.58
1:C:457:VAL:HG23	1:C:457:VAL:O	2.04	0.58
1:D:457:VAL:HG23	1:D:457:VAL:O	2.04	0.57
1:B:442:CYS:HA	1:B:552:MET:HE1	1.91	0.53
1:C:442:CYS:HA	1:C:552:MET:HE1	1.91	0.53
1:D:442:CYS:HA	1:D:552:MET:HE1	1.91	0.52
1:A:442:CYS:HA	1:A:552:MET:HE1	1.91	0.51
1:A:363:ARG:HH11	1:A:728:VAL:HG23	1.76	0.51
1:D:363:ARG:HH11	1:D:728:VAL:HG23	1.76	0.51
1:C:363:ARG:HH11	1:C:728:VAL:HG23	1.76	0.50
1:B:363:ARG:NH1	1:B:728:VAL:HG23	2.27	0.50
1:C:214:MET:O	1:C:218:THR:HG23	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:MET:O	1:A:218:THR:HG23	2.12	0.50
1:B:214:MET:O	1:B:218:THR:HG23	2.12	0.50
1:B:363:ARG:HH11	1:B:728:VAL:HG23	1.76	0.50
1:C:363:ARG:NH1	1:C:728:VAL:HG23	2.27	0.49
1:D:214:MET:O	1:D:218:THR:HG23	2.12	0.49
1:D:363:ARG:NH1	1:D:728:VAL:HG23	2.27	0.49
1:D:754:THR:CG2	1:D:756:VAL:HG13	2.43	0.49
1:B:755:ASN:HD22	1:B:755:ASN:N	2.10	0.49
1:A:363:ARG:NH1	1:A:728:VAL:HG23	2.27	0.49
1:A:755:ASN:HD22	1:A:755:ASN:N	2.10	0.49
1:C:369:PHE:HB3	1:C:759:ILE:HD11	1.95	0.49
1:C:754:THR:CG2	1:C:756:VAL:HG13	2.43	0.49
1:C:755:ASN:N	1:C:755:ASN:HD22	2.10	0.48
1:D:755:ASN:HD22	1:D:755:ASN:N	2.10	0.48
1:B:369:PHE:HB3	1:B:759:ILE:HD11	1.95	0.48
1:B:754:THR:CG2	1:B:756:VAL:HG13	2.43	0.48
1:D:369:PHE:HB3	1:D:759:ILE:HD11	1.95	0.48
1:A:369:PHE:HB3	1:A:759:ILE:HD11	1.95	0.48
1:A:754:THR:CG2	1:A:756:VAL:HG13	2.43	0.48
1:B:478:GLU:O	1:B:482:VAL:HG23	2.15	0.47
1:C:478:GLU:O	1:C:482:VAL:HG23	2.15	0.47
1:D:478:GLU:O	1:D:482:VAL:HG23	2.15	0.47
1:A:478:GLU:O	1:A:482:VAL:HG23	2.15	0.47
1:B:724:LYS:HD2	1:B:738:TYR:HB3	1.98	0.46
1:B:311:GLU:HA	1:B:311:GLU:OE1	2.16	0.46
1:C:724:LYS:HD2	1:C:738:TYR:HB3	1.98	0.46
1:A:311:GLU:HA	1:A:311:GLU:OE1	2.16	0.46
1:A:384:LEU:HD11	1:A:742:PHE:HB2	1.98	0.46
1:D:384:LEU:HD11	1:D:742:PHE:HB2	1.98	0.46
1:B:384:LEU:HD11	1:B:742:PHE:HB2	1.98	0.45
1:B:687:ASN:OD1	1:B:688:LYS:NZ	2.49	0.45
1:C:311:GLU:OE1	1:C:311:GLU:HA	2.16	0.45
1:A:724:LYS:HD2	1:A:738:TYR:HB3	1.98	0.45
1:D:311:GLU:HA	1:D:311:GLU:OE1	2.16	0.45
1:D:724:LYS:HD2	1:D:738:TYR:HB3	1.98	0.45
1:C:203:THR:HG22	1:C:204:ALA:N	2.32	0.45
1:C:384:LEU:HD11	1:C:742:PHE:HB2	1.98	0.45
1:D:203:THR:HG22	1:D:204:ALA:N	2.32	0.45
1:A:687:ASN:OD1	1:A:688:LYS:NZ	2.49	0.45
1:B:754:THR:HG22	1:B:756:VAL:HG13	1.99	0.44
1:A:203:THR:HG22	1:A:204:ALA:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:471:ASP:O	1:A:475:VAL:HG23	2.18	0.44
1:A:500:ARG:NH1	1:A:500:ARG:HA	2.33	0.44
1:B:203:THR:HG22	1:B:204:ALA:N	2.32	0.44
1:B:471:ASP:O	1:B:475:VAL:HG23	2.18	0.44
1:D:754:THR:HG22	1:D:756:VAL:HG13	1.99	0.44
1:B:383:ASP:CG	1:B:385:SER:HG	2.26	0.44
1:A:754:THR:HG22	1:A:756:VAL:HG13	1.99	0.44
1:C:754:THR:HG22	1:C:756:VAL:HG13	1.99	0.44
1:C:500:ARG:HA	1:C:500:ARG:NH1	2.33	0.44
1:D:383:ASP:CG	1:D:385:SER:HG	2.26	0.44
1:D:500:ARG:HH11	1:D:500:ARG:HA	1.83	0.44
1:B:500:ARG:HA	1:B:500:ARG:HH11	1.83	0.44
1:D:500:ARG:HA	1:D:500:ARG:NH1	2.33	0.43
1:B:724:LYS:HD2	1:B:738:TYR:CB	2.49	0.43
1:C:510:SER:O	1:C:510:SER:OG	2.35	0.43
1:A:383:ASP:CG	1:A:385:SER:HG	2.26	0.43
1:B:500:ARG:HA	1:B:500:ARG:NH1	2.33	0.43
1:C:724:LYS:HD2	1:C:738:TYR:CB	2.49	0.43
1:A:731:THR:HB	1:A:732:PRO:HD2	2.00	0.43
1:C:466:LYS:N	1:C:471:ASP:OD2	2.48	0.43
1:D:471:ASP:O	1:D:475:VAL:HG23	2.18	0.43
1:C:383:ASP:CG	1:C:385:SER:HG	2.27	0.43
1:C:731:THR:HB	1:C:732:PRO:HD2	2.00	0.43
1:A:724:LYS:HD2	1:A:738:TYR:CB	2.49	0.43
1:D:731:THR:HB	1:D:732:PRO:HD2	2.00	0.43
1:A:500:ARG:HA	1:A:500:ARG:HH11	1.83	0.42
1:C:471:ASP:O	1:C:475:VAL:HG23	2.18	0.42
1:D:510:SER:O	1:D:510:SER:OG	2.35	0.42
1:B:466:LYS:N	1:B:471:ASP:OD2	2.48	0.42
1:D:724:LYS:HD2	1:D:738:TYR:CB	2.49	0.42
1:C:500:ARG:HA	1:C:500:ARG:HH11	1.83	0.42
1:B:731:THR:HB	1:B:732:PRO:HD2	2.00	0.42
1:C:281:ASP:OD1	1:C:281:ASP:C	2.63	0.42
1:A:502:SER:O	1:A:503:LEU:HB2	2.20	0.42
1:A:281:ASP:OD1	1:A:281:ASP:C	2.63	0.42
1:D:502:SER:O	1:D:503:LEU:HB2	2.20	0.42
1:C:388:ASP:OD1	1:C:388:ASP:N	2.53	0.41
1:C:721:ARG:CG	1:C:722:SER:H	2.34	0.41
1:D:281:ASP:OD1	1:D:281:ASP:C	2.63	0.41
1:D:390:CYS:O	1:D:391:GLU:HB3	2.20	0.41
1:B:281:ASP:OD1	1:B:281:ASP:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:721:ARG:CG	1:B:722:SER:H	2.34	0.41
1:A:388:ASP:OD1	1:A:388:ASP:N	2.53	0.41
1:B:254:LEU:HD12	1:B:254:LEU:O	2.21	0.41
1:B:429:PHE:CD1	1:B:429:PHE:N	2.88	0.41
1:C:684:GLU:HG3	1:D:686:VAL:HG12	2.03	0.41
1:A:254:LEU:HD12	1:A:254:LEU:O	2.21	0.41
1:D:429:PHE:N	1:D:429:PHE:CD1	2.88	0.41
1:D:721:ARG:CG	1:D:722:SER:H	2.34	0.41
1:C:646:ASP:O	1:C:647:LEU:HB2	2.21	0.41
1:A:390:CYS:O	1:A:391:GLU:HB3	2.20	0.41
1:A:429:PHE:CD1	1:A:429:PHE:N	2.88	0.41
1:B:737:ASP:N	1:B:737:ASP:OD1	2.54	0.41
1:A:466:LYS:N	1:A:471:ASP:OD2	2.48	0.41
1:B:502:SER:O	1:B:503:LEU:HB2	2.20	0.41
1:B:684:GLU:HG3	1:C:686:VAL:HG12	2.03	0.41
1:C:254:LEU:HD12	1:C:254:LEU:O	2.21	0.41
1:C:429:PHE:CD1	1:C:429:PHE:N	2.88	0.41
1:D:254:LEU:HD12	1:D:254:LEU:O	2.21	0.41
1:A:686:VAL:HG12	1:D:684:GLU:HG3	2.03	0.41
1:C:687:ASN:OD1	1:C:688:LYS:NZ	2.49	0.41
1:C:390:CYS:O	1:C:391:GLU:HB3	2.20	0.40
1:C:502:SER:O	1:C:503:LEU:HB2	2.20	0.40
1:D:737:ASP:N	1:D:737:ASP:OD1	2.54	0.40
1:B:388:ASP:OD1	1:B:388:ASP:N	2.53	0.40
1:A:684:GLU:HG3	1:B:686:VAL:HG12	2.02	0.40
1:B:646:ASP:O	1:B:647:LEU:HB2	2.21	0.40
1:D:687:ASN:OD1	1:D:688:LYS:NZ	2.49	0.40
1:A:575:ARG:HH21	3:A:802:PCW:C7	2.34	0.40
1:B:390:CYS:O	1:B:391:GLU:HB3	2.21	0.40
1:D:575:ARG:HH21	3:D:802:PCW:H72	1.87	0.40
1:D:646:ASP:O	1:D:647:LEU:HB2	2.21	0.40
1:C:575:ARG:HH21	3:C:802:PCW:C7	2.34	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	554/635 (87%)	519 (94%)	35 (6%)	0	100	100
1	B	554/635 (87%)	519 (94%)	35 (6%)	0	100	100
1	C	554/635 (87%)	518 (94%)	36 (6%)	0	100	100
1	D	554/635 (87%)	519 (94%)	35 (6%)	0	100	100
All	All	2216/2540 (87%)	2075 (94%)	141 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	491/562 (87%)	478 (97%)	13 (3%)	40	63
1	B	491/562 (87%)	478 (97%)	13 (3%)	40	63
1	C	491/562 (87%)	478 (97%)	13 (3%)	40	63
1	D	491/562 (87%)	478 (97%)	13 (3%)	40	63
All	All	1964/2248 (87%)	1912 (97%)	52 (3%)	41	63

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	271	SER
1	A	304	PHE
1	A	377	VAL
1	A	385	SER
1	A	393	ASN
1	A	404	SER
1	A	510	SER
1	A	654	ASP

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Mol	Chain	Res	Type
1	A	716	MET
1	A	720	PHE
1	A	721	ARG
1	A	727	GLN
1	A	733	ASP
1	B	271	SER
1	B	304	PHE
1	B	377	VAL
1	B	385	SER
1	B	393	ASN
1	B	404	SER
1	B	510	SER
1	B	654	ASP
1	B	716	MET
1	B	720	PHE
1	B	721	ARG
1	B	727	GLN
1	B	733	ASP
1	C	271	SER
1	C	304	PHE
1	C	377	VAL
1	C	385	SER
1	C	393	ASN
1	C	404	SER
1	C	510	SER
1	C	654	ASP
1	C	716	MET
1	C	720	PHE
1	C	721	ARG
1	C	727	GLN
1	C	733	ASP
1	D	271	SER
1	D	304	PHE
1	D	377	VAL
1	D	385	SER
1	D	393	ASN
1	D	404	SER
1	D	510	SER
1	D	654	ASP
1	D	716	MET
1	D	720	PHE
1	D	721	ARG

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Mol	Chain	Res	Type
1	D	727	GLN
1	D	733	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	354	GLN
1	A	358	HIS
1	A	408	ASN
1	A	498	GLN
1	A	755	ASN
1	B	354	GLN
1	B	358	HIS
1	B	408	ASN
1	B	755	ASN
1	C	354	GLN
1	C	358	HIS
1	C	408	ASN
1	C	498	GLN
1	C	755	ASN
1	D	354	GLN
1	D	358	HIS
1	D	408	ASN
1	D	498	GLN
1	D	755	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PCW	B	802	-	53,53,53	1.30	6 (11%)	59,61,61	0.94	3 (5%)
3	PCW	D	802	-	53,53,53	1.30	6 (11%)	59,61,61	0.94	3 (5%)
2	V5H	A	801	-	56,56,71	1.96	15 (26%)	71,76,93	2.81	26 (36%)
3	PCW	C	802	-	53,53,53	1.30	6 (11%)	59,61,61	0.94	3 (5%)
2	V5H	C	801	-	56,56,71	1.97	15 (26%)	71,76,93	2.81	26 (36%)
3	PCW	A	802	-	53,53,53	1.30	6 (11%)	59,61,61	0.94	3 (5%)
2	V5H	B	801	-	56,56,71	1.96	15 (26%)	71,76,93	2.81	26 (36%)
2	V5H	D	801	-	56,56,71	1.96	15 (26%)	71,76,93	2.81	26 (36%)

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	PCW	B	802	-	-	30/57/57/57	-
3	PCW	D	802	-	-	30/57/57/57	-
2	V5H	A	801	-	-	21/56/80/98	0/1/1/1
3	PCW	C	802	-	-	30/57/57/57	-
2	V5H	C	801	-	-	21/56/80/98	0/1/1/1
3	PCW	A	802	-	-	30/57/57/57	-
2	V5H	B	801	-	-	21/56/80/98	0/1/1/1
2	V5H	D	801	-	-	21/56/80/98	0/1/1/1

All (84) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	V5H	P44-O43	5.84	1.69	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	V5H	P44-O43	5.84	1.69	1.59
2	C	801	V5H	P44-O43	5.82	1.69	1.59
2	D	801	V5H	P44-O43	5.78	1.69	1.59
2	C	801	V5H	P38-O37	5.28	1.68	1.59
2	A	801	V5H	P38-O37	5.25	1.68	1.59
2	D	801	V5H	P38-O37	5.25	1.68	1.59
2	B	801	V5H	P38-O37	5.23	1.68	1.59
2	B	801	V5H	P27-O28	-4.28	1.36	1.50
2	C	801	V5H	P27-O28	-4.28	1.36	1.50
2	A	801	V5H	P27-O28	-4.28	1.36	1.50
2	D	801	V5H	P27-O28	-4.28	1.36	1.50
2	A	801	V5H	O50-C24	-4.25	1.36	1.46
2	C	801	V5H	O50-C24	-4.25	1.36	1.46
2	B	801	V5H	O50-C24	-4.24	1.36	1.46
2	D	801	V5H	O50-C24	-4.24	1.36	1.46
2	A	801	V5H	P27-O29	-3.98	1.36	1.55
2	B	801	V5H	P27-O29	-3.98	1.36	1.55
2	C	801	V5H	P27-O29	-3.98	1.36	1.55
2	D	801	V5H	P27-O29	-3.98	1.36	1.55
3	D	802	PCW	O2-C31	3.67	1.44	1.34
3	A	802	PCW	O2-C31	3.64	1.44	1.34
3	B	802	PCW	O2-C31	3.64	1.44	1.34
3	C	802	PCW	O2-C31	3.64	1.44	1.34
2	A	801	V5H	O22-C23	-3.14	1.38	1.45
2	B	801	V5H	O22-C23	-3.14	1.38	1.45
2	C	801	V5H	O22-C23	-3.14	1.38	1.45
2	D	801	V5H	O22-C23	-3.13	1.38	1.45
3	A	802	PCW	O3-C11	3.04	1.42	1.33
3	B	802	PCW	O3-C11	3.04	1.42	1.33
3	C	802	PCW	O3-C11	3.04	1.42	1.33
3	D	802	PCW	O3-C11	3.04	1.42	1.33
2	C	801	V5H	P38-O40	-3.04	1.43	1.54
2	B	801	V5H	P38-O40	-3.02	1.43	1.54
2	A	801	V5H	P38-O40	-3.01	1.43	1.54
2	D	801	V5H	P38-O40	-3.01	1.43	1.54
2	A	801	V5H	BR12-C11	-2.99	1.90	1.97
2	B	801	V5H	BR12-C11	-2.96	1.90	1.97
2	C	801	V5H	BR12-C11	-2.96	1.90	1.97
2	D	801	V5H	BR12-C11	-2.94	1.90	1.97
2	A	801	V5H	P44-O47	-2.93	1.43	1.54
2	C	801	V5H	P44-O47	-2.93	1.43	1.54
2	D	801	V5H	P44-O47	-2.93	1.43	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	V5H	P44-O47	-2.92	1.44	1.54
3	A	802	PCW	C7-N	-2.87	1.41	1.50
3	B	802	PCW	C7-N	-2.87	1.41	1.50
3	C	802	PCW	C7-N	-2.87	1.41	1.50
3	D	802	PCW	C7-N	-2.87	1.41	1.50
2	B	801	V5H	O22-C20	2.79	1.41	1.33
2	C	801	V5H	O22-C20	2.79	1.41	1.33
2	A	801	V5H	O22-C20	2.79	1.41	1.33
2	B	801	V5H	O35-C34	-2.78	1.36	1.43
2	C	801	V5H	O35-C34	-2.78	1.36	1.43
2	D	801	V5H	O35-C34	-2.78	1.36	1.43
2	A	801	V5H	O35-C34	-2.78	1.36	1.43
2	D	801	V5H	O22-C20	2.76	1.41	1.33
3	D	802	PCW	C8-N	-2.63	1.42	1.50
2	B	801	V5H	P44-O46	-2.62	1.45	1.54
2	C	801	V5H	P44-O46	-2.62	1.45	1.54
2	D	801	V5H	P44-O46	-2.62	1.45	1.54
2	A	801	V5H	P44-O46	-2.62	1.45	1.54
3	A	802	PCW	C8-N	-2.61	1.42	1.50
3	B	802	PCW	C8-N	-2.61	1.42	1.50
3	C	802	PCW	C8-N	-2.61	1.42	1.50
2	C	801	V5H	P38-O39	-2.41	1.45	1.54
2	A	801	V5H	P38-O39	-2.40	1.45	1.54
2	D	801	V5H	P38-O39	-2.40	1.45	1.54
2	B	801	V5H	P38-O39	-2.37	1.46	1.54
2	D	801	V5H	O52-C51	-2.27	1.15	1.22
2	A	801	V5H	O52-C51	-2.25	1.15	1.22
2	B	801	V5H	O52-C51	-2.25	1.15	1.22
2	C	801	V5H	O52-C51	-2.25	1.15	1.22
3	C	802	PCW	C5-N	-2.19	1.44	1.51
3	A	802	PCW	C5-N	-2.18	1.44	1.51
3	B	802	PCW	C5-N	-2.18	1.44	1.51
3	D	802	PCW	C5-N	-2.15	1.44	1.51
2	D	801	V5H	O30-C31	-2.12	1.36	1.44
2	A	801	V5H	O30-C31	-2.10	1.36	1.44
3	B	802	PCW	O3-C3	-2.09	1.40	1.45
2	C	801	V5H	O30-C31	-2.08	1.37	1.44
3	A	802	PCW	O3-C3	-2.08	1.40	1.45
3	C	802	PCW	O3-C3	-2.08	1.40	1.45
3	D	802	PCW	O3-C3	-2.08	1.40	1.45
2	B	801	V5H	O30-C31	-2.08	1.37	1.44

All (116) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	V5H	BR12-C11-C13	-7.76	95.39	108.87
2	C	801	V5H	BR12-C11-C13	-7.75	95.41	108.87
2	A	801	V5H	BR12-C11-C13	-7.74	95.42	108.87
2	B	801	V5H	BR12-C11-C13	-7.74	95.42	108.87
2	A	801	V5H	O50-C51-C53	7.36	127.39	111.48
2	D	801	V5H	O50-C51-C53	7.34	127.36	111.48
2	C	801	V5H	O50-C51-C53	7.33	127.34	111.48
2	B	801	V5H	O50-C51-C53	7.33	127.34	111.48
2	D	801	V5H	C42-C48-C31	6.66	122.61	109.11
2	B	801	V5H	C42-C48-C31	6.64	122.58	109.11
2	A	801	V5H	C42-C48-C31	6.64	122.56	109.11
2	C	801	V5H	C42-C48-C31	6.62	122.54	109.11
2	C	801	V5H	C32-C34-C36	5.75	122.73	109.68
2	D	801	V5H	C32-C34-C36	5.75	122.72	109.68
2	A	801	V5H	C32-C34-C36	5.73	122.69	109.68
2	B	801	V5H	C32-C34-C36	5.73	122.69	109.68
2	B	801	V5H	O49-C48-C31	-5.71	95.31	109.94
2	C	801	V5H	O49-C48-C31	-5.70	95.33	109.94
2	D	801	V5H	O49-C48-C31	-5.68	95.38	109.94
2	A	801	V5H	O49-C48-C31	-5.68	95.38	109.94
2	B	801	V5H	O29-P27-O28	-5.55	86.64	112.44
2	C	801	V5H	O29-P27-O28	-5.55	86.64	112.44
2	C	801	V5H	O47-P44-O43	5.54	127.45	105.85
2	A	801	V5H	O29-P27-O28	-5.54	86.68	112.44
2	D	801	V5H	O29-P27-O28	-5.54	86.68	112.44
2	A	801	V5H	O47-P44-O43	5.53	127.42	105.85
2	D	801	V5H	O47-P44-O43	5.53	127.41	105.85
2	B	801	V5H	O47-P44-O43	5.53	127.39	105.85
2	A	801	V5H	O40-P38-O41	-5.05	91.17	110.83
2	D	801	V5H	O40-P38-O41	-5.05	91.17	110.83
2	B	801	V5H	O40-P38-O41	-5.03	91.23	110.83
2	C	801	V5H	O40-P38-O41	-5.03	91.24	110.83
2	B	801	V5H	O40-P38-O37	4.87	124.84	105.85
2	C	801	V5H	O40-P38-O37	4.87	124.83	105.85
2	A	801	V5H	O40-P38-O37	4.86	124.81	105.85
2	D	801	V5H	O40-P38-O37	4.86	124.80	105.85
2	B	801	V5H	C48-C31-C32	4.64	117.30	110.86
2	A	801	V5H	C48-C31-C32	4.63	117.28	110.86
2	C	801	V5H	C48-C31-C32	4.62	117.27	110.86
2	D	801	V5H	C48-C31-C32	4.57	117.20	110.86
2	A	801	V5H	O47-P44-O46	-4.19	92.08	107.80
2	C	801	V5H	O47-P44-O46	-4.19	92.11	107.80
2	D	801	V5H	O47-P44-O46	-4.19	92.11	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	V5H	O47-P44-O46	-4.18	92.11	107.80
3	A	802	PCW	O2-C31-C32	3.99	120.11	111.48
3	B	802	PCW	O2-C31-C32	3.99	120.11	111.48
3	C	802	PCW	O2-C31-C32	3.99	120.11	111.48
3	D	802	PCW	O2-C31-C32	3.99	120.10	111.48
2	D	801	V5H	O50-C51-O52	-3.95	114.47	123.70
2	C	801	V5H	O50-C51-O52	-3.92	114.53	123.70
2	A	801	V5H	O50-C51-O52	-3.92	114.53	123.70
2	B	801	V5H	O50-C51-O52	-3.92	114.53	123.70
2	A	801	V5H	O35-C34-C32	-3.90	101.17	110.38
2	C	801	V5H	O35-C34-C32	-3.89	101.20	110.38
2	B	801	V5H	O35-C34-C32	-3.89	101.20	110.38
2	D	801	V5H	O35-C34-C32	-3.88	101.24	110.38
2	C	801	V5H	O30-P27-O28	3.65	121.47	109.81
2	A	801	V5H	O30-P27-O28	3.64	121.45	109.81
2	B	801	V5H	O30-P27-O28	3.64	121.44	109.81
2	D	801	V5H	O30-P27-O28	3.64	121.43	109.81
2	A	801	V5H	O30-C31-C32	3.36	115.85	108.73
2	D	801	V5H	O30-C31-C32	3.36	115.85	108.73
2	C	801	V5H	O30-C31-C32	3.34	115.81	108.73
2	B	801	V5H	O30-C31-C32	3.33	115.78	108.73
2	D	801	V5H	O30-C31-C48	3.28	115.68	108.73
2	B	801	V5H	O30-C31-C48	3.27	115.65	108.73
2	C	801	V5H	O30-C31-C48	3.26	115.64	108.73
2	A	801	V5H	O30-C31-C48	3.26	115.63	108.73
2	D	801	V5H	C34-C32-C31	3.26	117.07	109.68
2	C	801	V5H	C34-C32-C31	3.25	117.05	109.68
2	A	801	V5H	C34-C32-C31	3.23	117.02	109.68
2	B	801	V5H	C34-C32-C31	3.23	117.02	109.68
2	D	801	V5H	O47-P44-O45	-3.16	98.50	110.83
2	C	801	V5H	O47-P44-O45	-3.16	98.52	110.83
2	A	801	V5H	O47-P44-O45	-3.15	98.57	110.83
2	B	801	V5H	O47-P44-O45	-3.15	98.58	110.83
2	C	801	V5H	C13-C11-C09	2.98	123.16	115.61
2	D	801	V5H	C13-C11-C09	2.97	123.13	115.61
2	A	801	V5H	C13-C11-C09	2.97	123.12	115.61
2	B	801	V5H	C13-C11-C09	2.97	123.12	115.61
3	A	802	PCW	O3-C11-C12	2.90	120.69	111.83
3	C	802	PCW	O3-C11-C12	2.90	120.69	111.83
3	D	802	PCW	O3-C11-C12	2.90	120.69	111.83
3	B	802	PCW	O3-C11-C12	2.90	120.67	111.83
2	D	801	V5H	O37-C36-C42	-2.56	103.31	108.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	V5H	C34-C36-C42	2.55	117.45	111.72
2	A	801	V5H	C34-C36-C42	2.55	117.45	111.72
2	B	801	V5H	C34-C36-C42	2.55	117.45	111.72
2	B	801	V5H	O37-C36-C42	-2.54	103.36	108.76
2	A	801	V5H	O37-C36-C42	-2.53	103.38	108.76
2	C	801	V5H	O37-C36-C42	-2.53	103.38	108.76
2	C	801	V5H	C34-C36-C42	2.53	117.41	111.72
2	C	801	V5H	O43-C42-C48	2.47	113.97	108.73
2	D	801	V5H	O43-C42-C48	2.47	113.96	108.73
2	A	801	V5H	O43-C42-C48	2.46	113.95	108.73
2	B	801	V5H	O43-C42-C48	2.46	113.95	108.73
3	C	802	PCW	C3-C2-C1	-2.38	106.24	111.78
3	A	802	PCW	C3-C2-C1	-2.37	106.26	111.78
3	B	802	PCW	C3-C2-C1	-2.37	106.26	111.78
3	D	802	PCW	C3-C2-C1	-2.36	106.29	111.78
2	A	801	V5H	P38-O37-C36	2.30	129.59	123.43
2	C	801	V5H	P38-O37-C36	2.30	129.56	123.43
2	B	801	V5H	P38-O37-C36	2.29	129.55	123.43
2	A	801	V5H	O22-C20-C19	2.29	118.81	111.83
2	D	801	V5H	P38-O37-C36	2.29	129.53	123.43
2	D	801	V5H	O22-C20-C19	2.27	118.76	111.83
2	B	801	V5H	O22-C20-C19	2.26	118.73	111.83
2	C	801	V5H	O22-C20-C19	2.26	118.73	111.83
2	C	801	V5H	BR10-C09-C11	-2.15	106.11	110.27
2	C	801	V5H	C48-C42-C36	2.15	116.55	111.72
2	A	801	V5H	BR10-C09-C11	-2.14	106.11	110.27
2	A	801	V5H	C48-C42-C36	2.14	116.54	111.72
2	B	801	V5H	C48-C42-C36	2.14	116.54	111.72
2	D	801	V5H	BR10-C09-C11	-2.14	106.13	110.27
2	B	801	V5H	BR10-C09-C11	-2.14	106.13	110.27
2	D	801	V5H	C48-C42-C36	2.12	116.48	111.72

There are no chirality outliers.

All (204) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	V5H	C08-C09-C11-C13
2	A	801	V5H	BR10-C09-C11-C13
2	A	801	V5H	C08-C09-C11-BR12
2	A	801	V5H	BR10-C09-C11-BR12
2	A	801	V5H	C06-C07-C08-C09
2	A	801	V5H	C53-C51-O50-C24

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Mol	Chain	Res	Type	Atoms
2	A	801	V5H	O52-C51-O50-C24
2	A	801	V5H	C25-O26-P27-O28
2	A	801	V5H	C25-O26-P27-O29
2	A	801	V5H	C25-O26-P27-O30
2	B	801	V5H	C08-C09-C11-C13
2	B	801	V5H	BR10-C09-C11-C13
2	B	801	V5H	C08-C09-C11-BR12
2	B	801	V5H	BR10-C09-C11-BR12
2	B	801	V5H	C06-C07-C08-C09
2	B	801	V5H	C53-C51-O50-C24
2	B	801	V5H	O52-C51-O50-C24
2	B	801	V5H	C25-O26-P27-O28
2	B	801	V5H	C25-O26-P27-O29
2	B	801	V5H	C25-O26-P27-O30
2	C	801	V5H	C08-C09-C11-C13
2	C	801	V5H	BR10-C09-C11-C13
2	C	801	V5H	C08-C09-C11-BR12
2	C	801	V5H	BR10-C09-C11-BR12
2	C	801	V5H	C06-C07-C08-C09
2	C	801	V5H	C53-C51-O50-C24
2	C	801	V5H	O52-C51-O50-C24
2	C	801	V5H	C25-O26-P27-O28
2	C	801	V5H	C25-O26-P27-O29
2	C	801	V5H	C25-O26-P27-O30
2	D	801	V5H	C08-C09-C11-C13
2	D	801	V5H	BR10-C09-C11-C13
2	D	801	V5H	C08-C09-C11-BR12
2	D	801	V5H	BR10-C09-C11-BR12
2	D	801	V5H	C06-C07-C08-C09
2	D	801	V5H	C53-C51-O50-C24
2	D	801	V5H	O52-C51-O50-C24
2	D	801	V5H	C25-O26-P27-O28
2	D	801	V5H	C25-O26-P27-O29
2	D	801	V5H	C25-O26-P27-O30
3	A	802	PCW	C2-C1-O3P-P
3	A	802	PCW	O4P-C4-C5-N
3	A	802	PCW	C32-C31-O2-C2
3	A	802	PCW	O31-C31-O2-C2
3	A	802	PCW	C1-O3P-P-O1P
3	A	802	PCW	C1-O3P-P-O2P
3	A	802	PCW	C1-O3P-P-O4P
3	A	802	PCW	C4-O4P-P-O1P

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Mol	Chain	Res	Type	Atoms
3	A	802	PCW	C4-O4P-P-O2P
3	A	802	PCW	C4-O4P-P-O3P
3	B	802	PCW	C2-C1-O3P-P
3	B	802	PCW	O4P-C4-C5-N
3	B	802	PCW	C32-C31-O2-C2
3	B	802	PCW	O31-C31-O2-C2
3	B	802	PCW	C1-O3P-P-O1P
3	B	802	PCW	C1-O3P-P-O2P
3	B	802	PCW	C1-O3P-P-O4P
3	B	802	PCW	C4-O4P-P-O1P
3	B	802	PCW	C4-O4P-P-O2P
3	B	802	PCW	C4-O4P-P-O3P
3	C	802	PCW	C2-C1-O3P-P
3	C	802	PCW	O4P-C4-C5-N
3	C	802	PCW	C32-C31-O2-C2
3	C	802	PCW	O31-C31-O2-C2
3	C	802	PCW	C1-O3P-P-O1P
3	C	802	PCW	C1-O3P-P-O2P
3	C	802	PCW	C1-O3P-P-O4P
3	C	802	PCW	C4-O4P-P-O1P
3	C	802	PCW	C4-O4P-P-O2P
3	C	802	PCW	C4-O4P-P-O3P
3	D	802	PCW	C2-C1-O3P-P
3	D	802	PCW	O4P-C4-C5-N
3	D	802	PCW	C32-C31-O2-C2
3	D	802	PCW	O31-C31-O2-C2
3	D	802	PCW	C1-O3P-P-O1P
3	D	802	PCW	C1-O3P-P-O2P
3	D	802	PCW	C1-O3P-P-O4P
3	D	802	PCW	C4-O4P-P-O1P
3	D	802	PCW	C4-O4P-P-O2P
3	D	802	PCW	C4-O4P-P-O3P
2	A	801	V5H	C19-C20-O22-C23
2	B	801	V5H	C19-C20-O22-C23
2	C	801	V5H	C19-C20-O22-C23
2	D	801	V5H	C19-C20-O22-C23
3	A	802	PCW	C32-C33-C34-C35
3	B	802	PCW	C32-C33-C34-C35
3	C	802	PCW	C32-C33-C34-C35
3	D	802	PCW	C32-C33-C34-C35
3	A	802	PCW	C4-C5-N-C6
3	B	802	PCW	C4-C5-N-C6

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Mol	Chain	Res	Type	Atoms
3	C	802	PCW	C4-C5-N-C6
3	D	802	PCW	C4-C5-N-C6
2	A	801	V5H	O21-C20-O22-C23
2	B	801	V5H	O21-C20-O22-C23
2	C	801	V5H	O21-C20-O22-C23
2	D	801	V5H	O21-C20-O22-C23
2	A	801	V5H	C17-C18-C19-C20
2	B	801	V5H	C17-C18-C19-C20
2	C	801	V5H	C17-C18-C19-C20
2	D	801	V5H	C17-C18-C19-C20
3	A	802	PCW	C4-C5-N-C7
3	B	802	PCW	C4-C5-N-C7
3	C	802	PCW	C4-C5-N-C7
3	D	802	PCW	C4-C5-N-C7
3	A	802	PCW	C35-C36-C37-C38
3	B	802	PCW	C35-C36-C37-C38
3	C	802	PCW	C35-C36-C37-C38
3	D	802	PCW	C35-C36-C37-C38
3	A	802	PCW	C24-C25-C26-C27
3	B	802	PCW	C24-C25-C26-C27
3	C	802	PCW	C24-C25-C26-C27
3	D	802	PCW	C24-C25-C26-C27
3	C	802	PCW	C14-C15-C16-C17
3	D	802	PCW	C14-C15-C16-C17
3	A	802	PCW	C14-C15-C16-C17
3	A	802	PCW	C22-C23-C24-C25
3	B	802	PCW	C14-C15-C16-C17
3	B	802	PCW	C22-C23-C24-C25
3	C	802	PCW	C22-C23-C24-C25
3	D	802	PCW	C22-C23-C24-C25
3	A	802	PCW	C4-C5-N-C8
3	B	802	PCW	C4-C5-N-C8
3	C	802	PCW	C4-C5-N-C8
3	D	802	PCW	C4-C5-N-C8
2	A	801	V5H	C03-C04-C05-C06
2	B	801	V5H	C03-C04-C05-C06
2	C	801	V5H	C03-C04-C05-C06
2	D	801	V5H	C03-C04-C05-C06
3	A	802	PCW	C20-C21-C22-C23
3	B	802	PCW	C20-C21-C22-C23
3	C	802	PCW	C20-C21-C22-C23
3	D	802	PCW	C20-C21-C22-C23

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Mol	Chain	Res	Type	Atoms
2	A	801	V5H	C16-C17-C18-C19
2	B	801	V5H	C16-C17-C18-C19
2	C	801	V5H	C16-C17-C18-C19
2	D	801	V5H	C16-C17-C18-C19
2	A	801	V5H	C53-C54-C55-C56
2	B	801	V5H	C53-C54-C55-C56
2	C	801	V5H	C53-C54-C55-C56
2	D	801	V5H	C53-C54-C55-C56
3	B	802	PCW	C15-C16-C17-C18
3	A	802	PCW	C15-C16-C17-C18
3	C	802	PCW	C15-C16-C17-C18
3	D	802	PCW	C15-C16-C17-C18
2	A	801	V5H	C23-C24-C25-O26
2	B	801	V5H	C23-C24-C25-O26
2	C	801	V5H	C23-C24-C25-O26
2	D	801	V5H	C23-C24-C25-O26
3	A	802	PCW	O3P-C1-C2-C3
3	B	802	PCW	O3P-C1-C2-C3
3	C	802	PCW	O3P-C1-C2-C3
3	D	802	PCW	O3P-C1-C2-C3
3	A	802	PCW	C34-C35-C36-C37
3	B	802	PCW	C34-C35-C36-C37
3	C	802	PCW	C34-C35-C36-C37
3	D	802	PCW	C34-C35-C36-C37
2	A	801	V5H	O50-C24-C25-O26
2	B	801	V5H	O50-C24-C25-O26
2	C	801	V5H	O50-C24-C25-O26
2	D	801	V5H	O50-C24-C25-O26
3	A	802	PCW	O3P-C1-C2-O2
3	B	802	PCW	O3P-C1-C2-O2
3	C	802	PCW	O3P-C1-C2-O2
3	D	802	PCW	O3P-C1-C2-O2
3	A	802	PCW	C5-C4-O4P-P
3	B	802	PCW	C5-C4-O4P-P
3	C	802	PCW	C5-C4-O4P-P
3	D	802	PCW	C5-C4-O4P-P
2	B	801	V5H	C02-C03-C04-C05
2	A	801	V5H	C02-C03-C04-C05
2	C	801	V5H	C02-C03-C04-C05
2	D	801	V5H	C02-C03-C04-C05
2	C	801	V5H	C42-O43-P44-O45
2	D	801	V5H	C42-O43-P44-O45

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Mol	Chain	Res	Type	Atoms
3	A	802	PCW	C43-C44-C45-C46
3	B	802	PCW	C43-C44-C45-C46
3	D	802	PCW	C43-C44-C45-C46
3	C	802	PCW	C43-C44-C45-C46
3	A	802	PCW	C1-C2-C3-O3
3	B	802	PCW	C1-C2-C3-O3
3	C	802	PCW	C1-C2-C3-O3
3	D	802	PCW	C1-C2-C3-O3
3	A	802	PCW	O2-C2-C3-O3
3	B	802	PCW	O2-C2-C3-O3
3	C	802	PCW	O2-C2-C3-O3
3	D	802	PCW	O2-C2-C3-O3
2	A	801	V5H	C36-O37-P38-O40
2	B	801	V5H	C36-O37-P38-O40
2	C	801	V5H	C36-O37-P38-O40
2	D	801	V5H	C36-O37-P38-O40
3	A	802	PCW	O2-C31-C32-C33
3	B	802	PCW	O2-C31-C32-C33
3	C	802	PCW	O2-C31-C32-C33
3	D	802	PCW	O2-C31-C32-C33
2	A	801	V5H	C42-O43-P44-O45
2	B	801	V5H	C42-O43-P44-O45
3	B	802	PCW	O31-C31-C32-C33
3	C	802	PCW	O31-C31-C32-C33
3	A	802	PCW	O31-C31-C32-C33
3	D	802	PCW	O31-C31-C32-C33
3	A	802	PCW	C17-C18-C19-C20
3	B	802	PCW	C17-C18-C19-C20
3	C	802	PCW	C17-C18-C19-C20
3	D	802	PCW	C17-C18-C19-C20

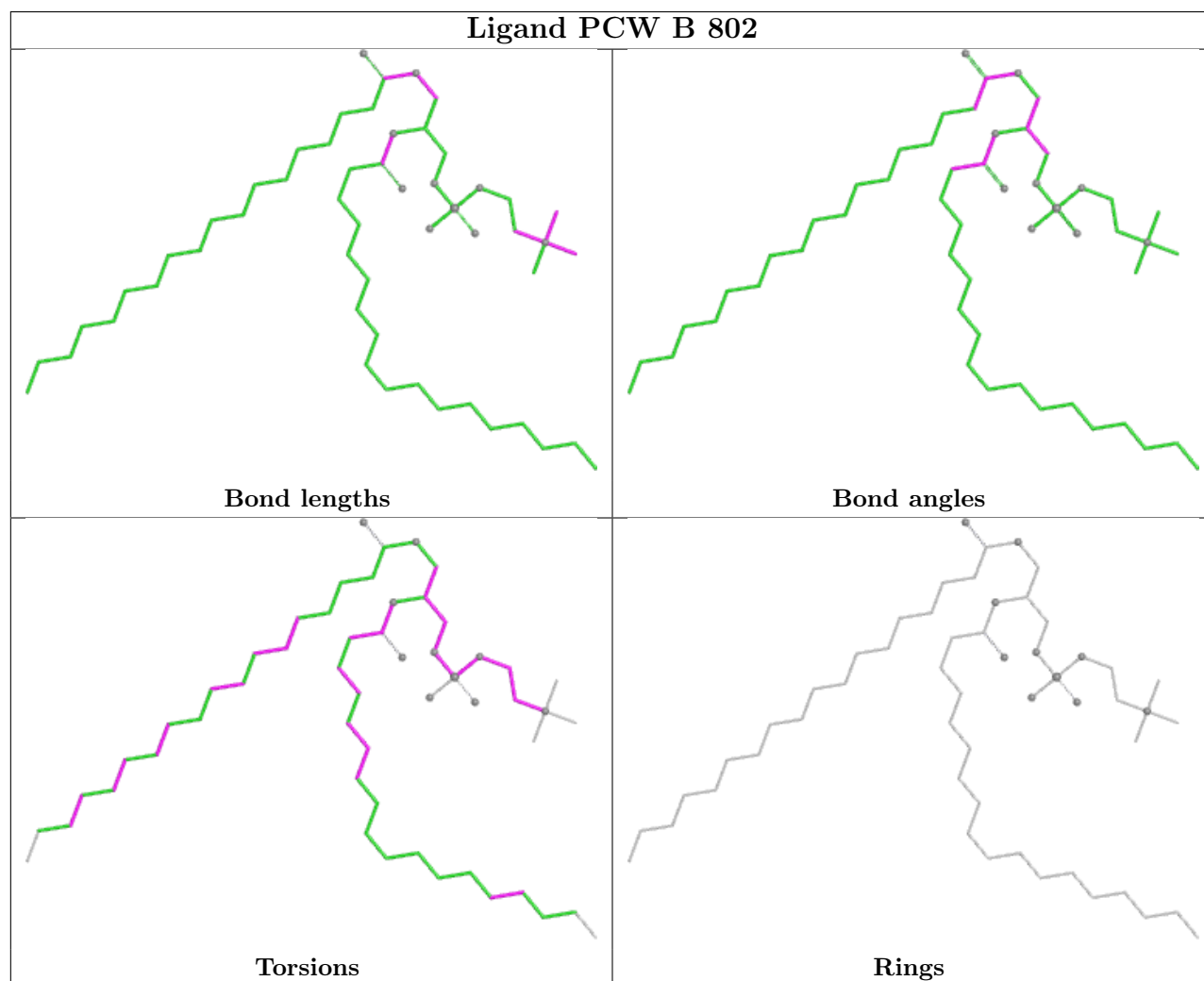
There are no ring outliers.

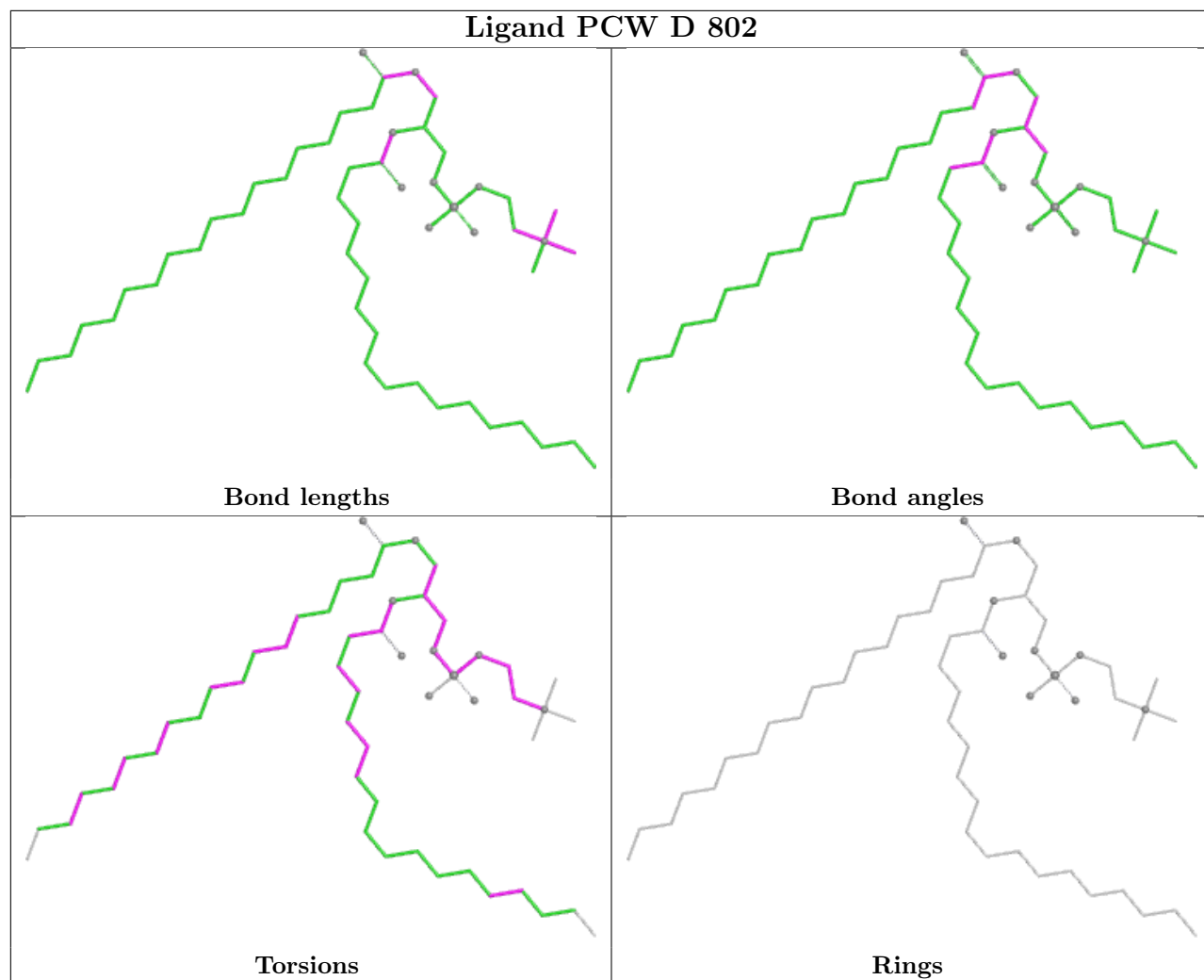
3 monomers are involved in 3 short contacts:

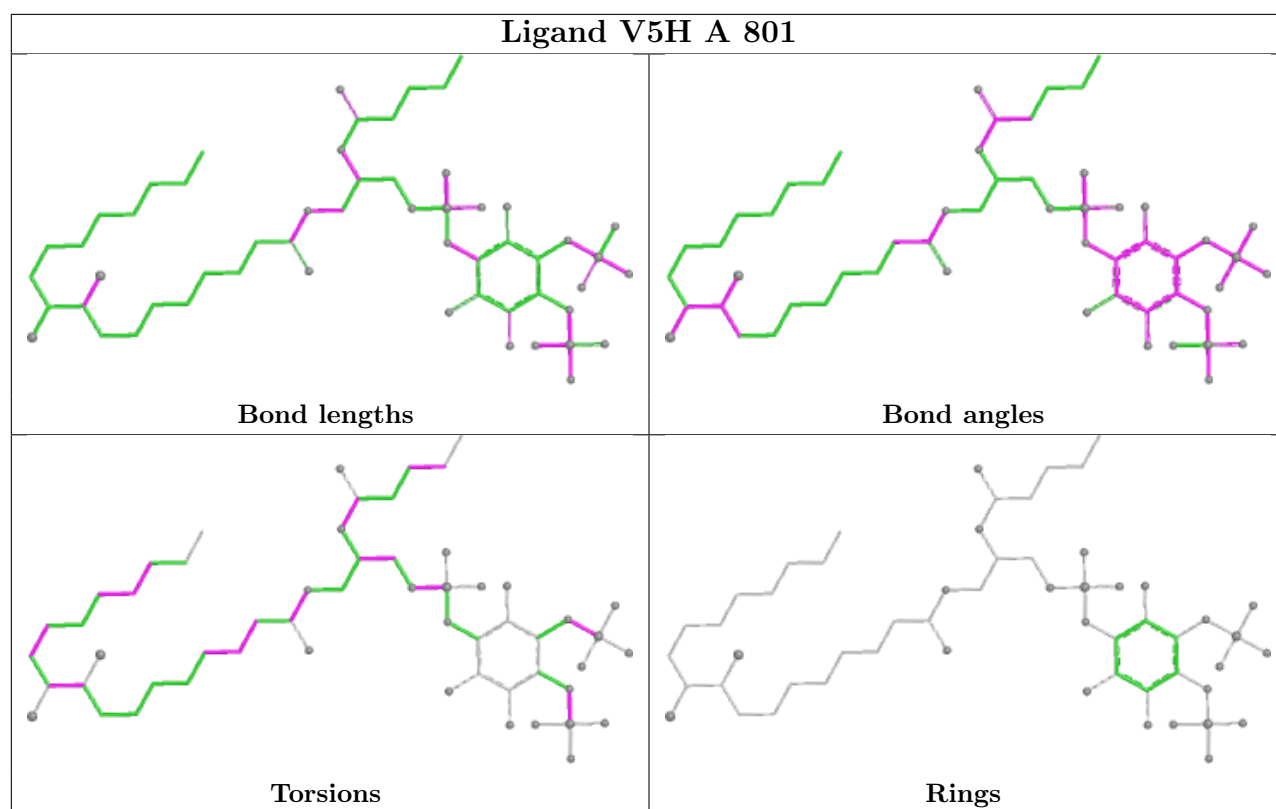
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	802	PCW	1	0
3	C	802	PCW	1	0
3	A	802	PCW	1	0

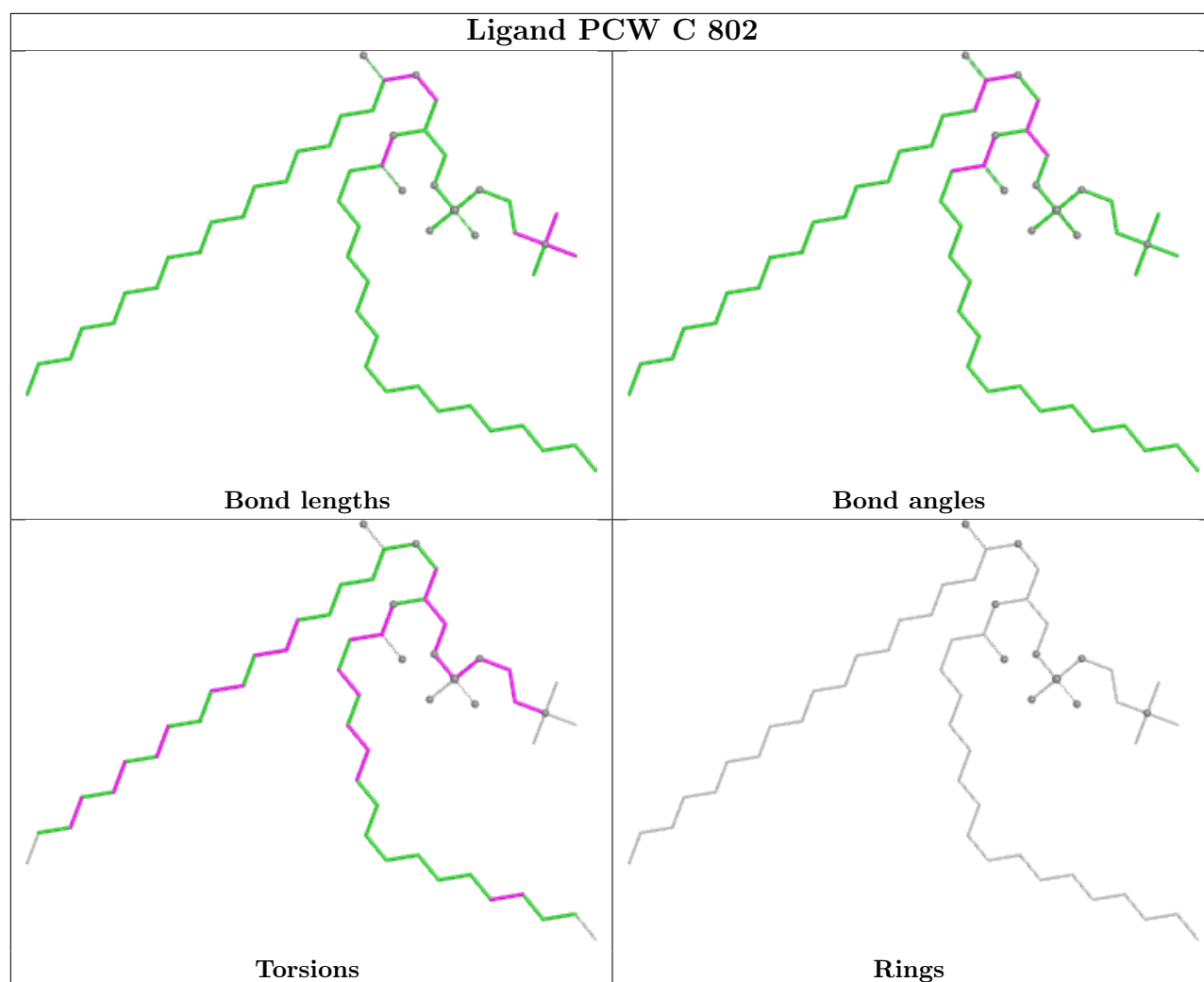
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

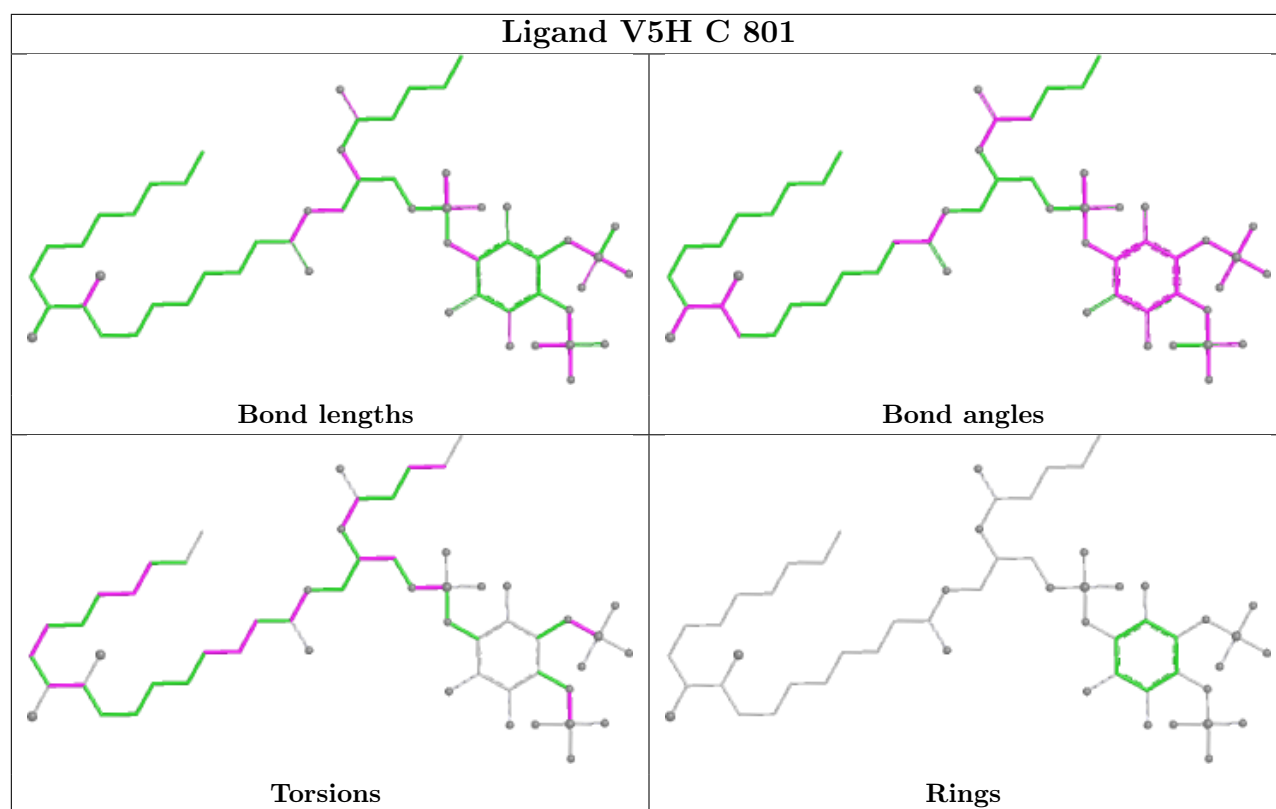
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.

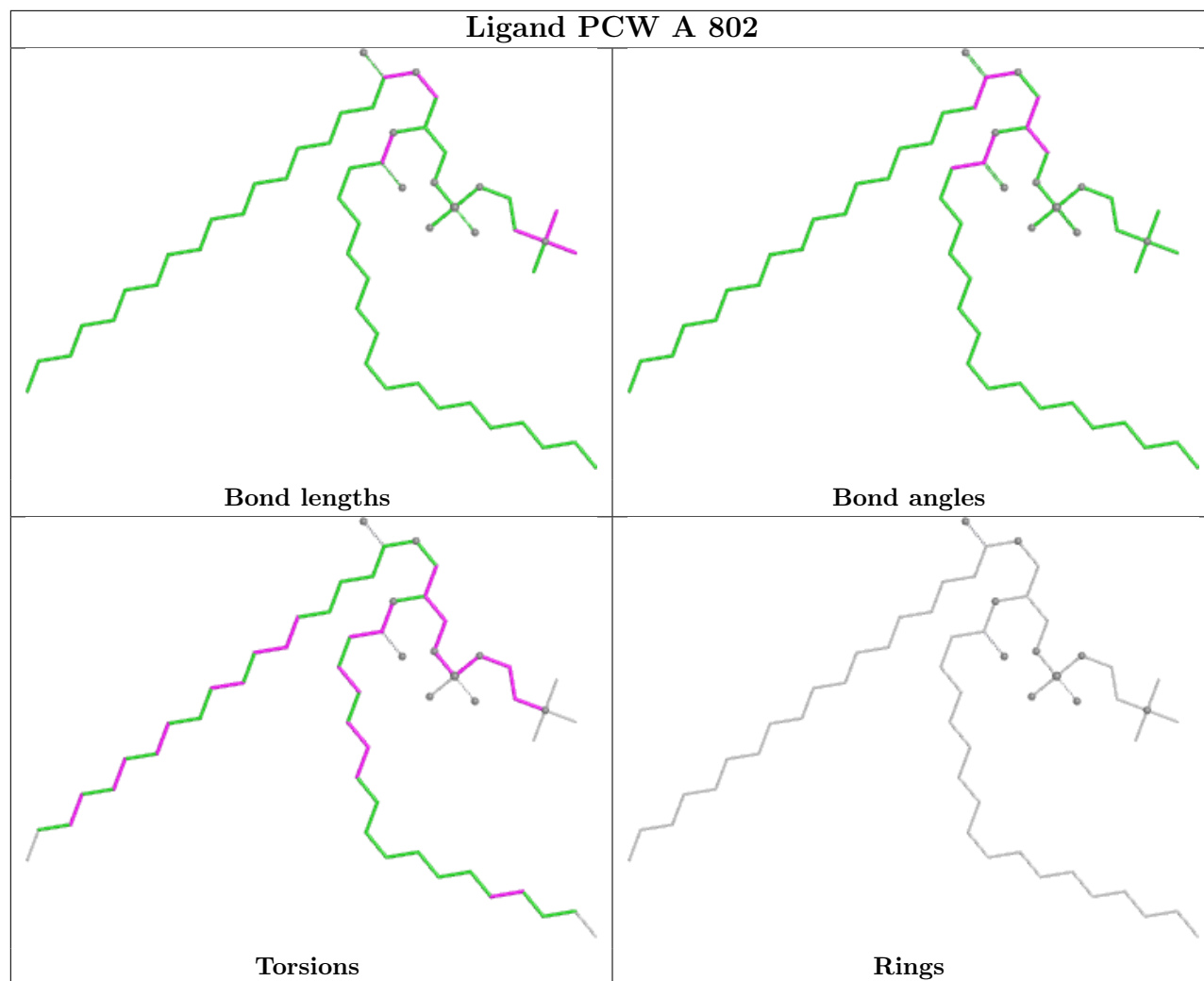


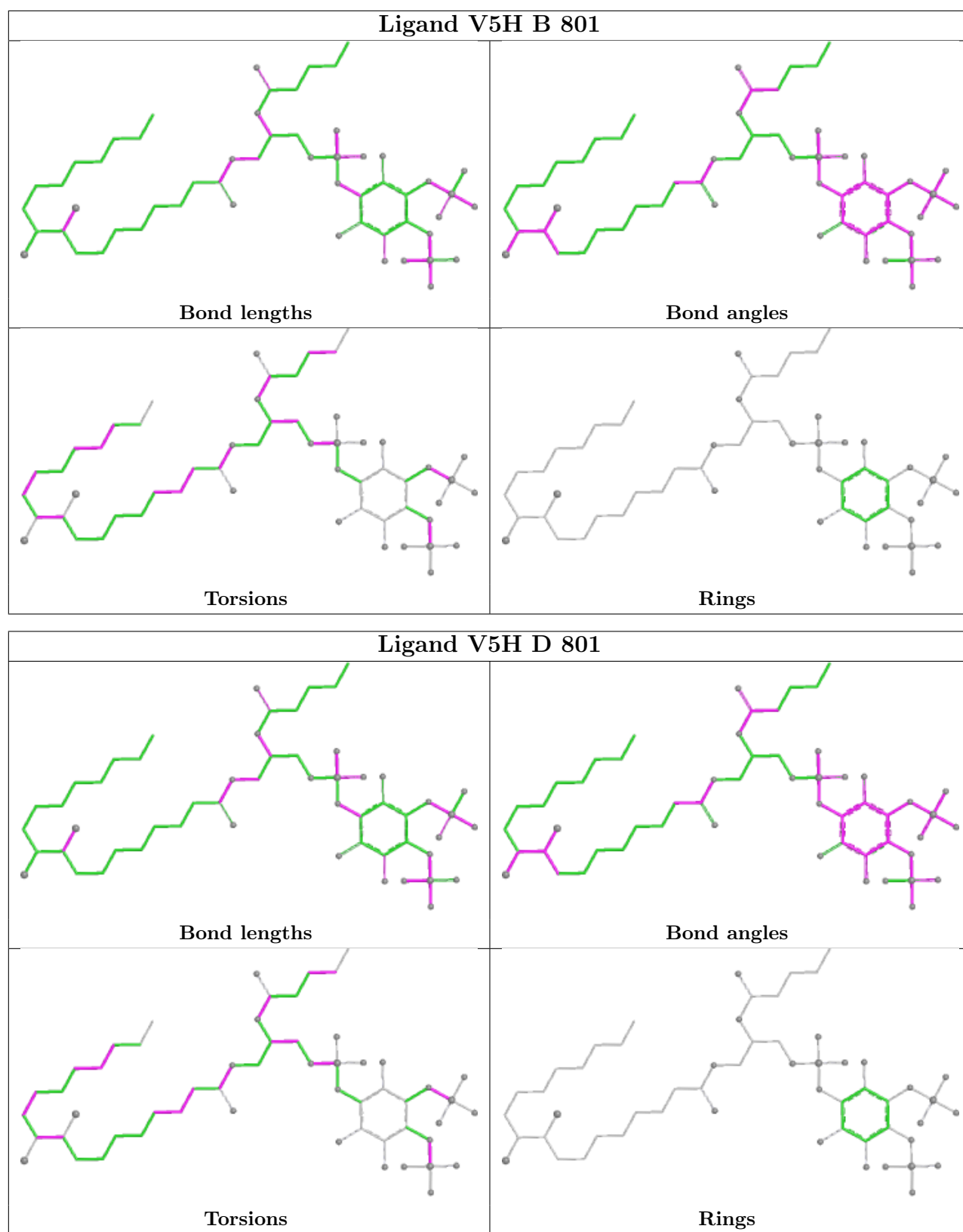












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

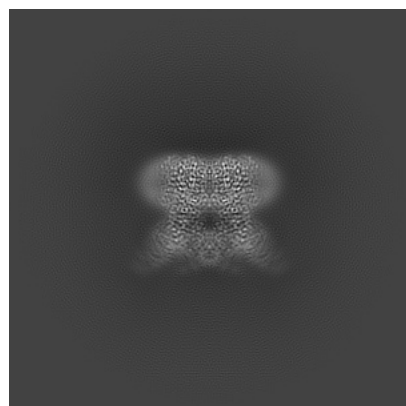
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41873. These allow visual inspection of the internal detail of the map and identification of artifacts.

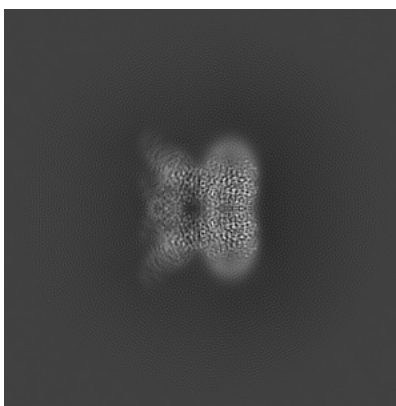
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

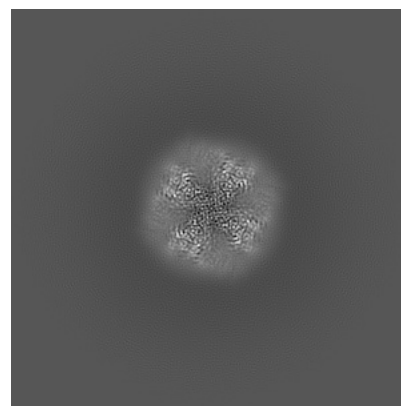
6.1.1 Primary map



X

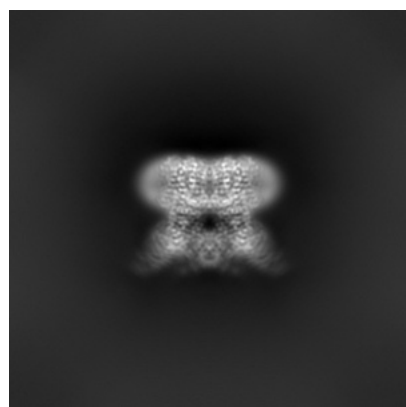


Y

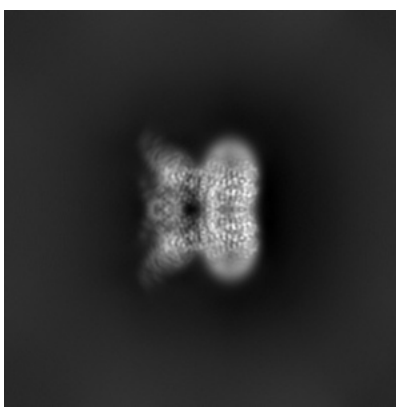


Z

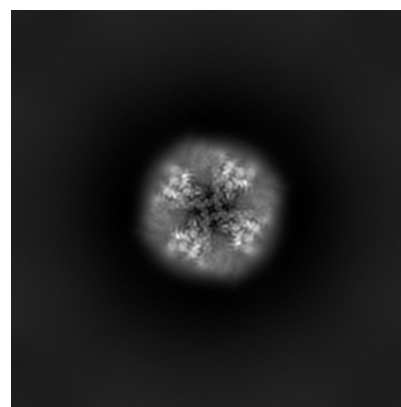
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

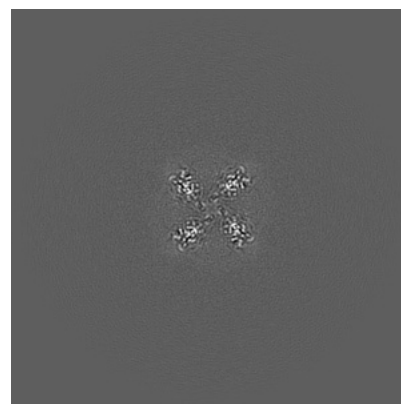
6.2.1 Primary map



X Index: 208

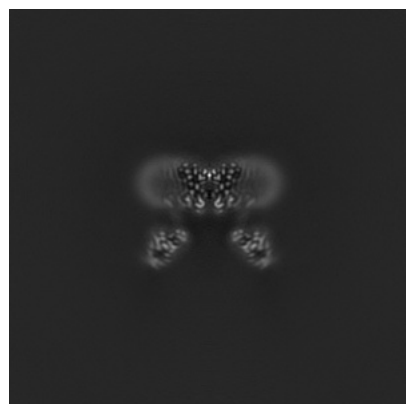


Y Index: 208

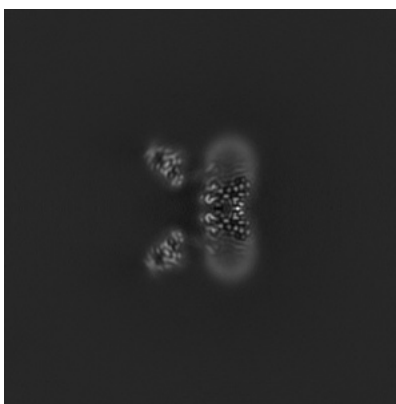


Z Index: 208

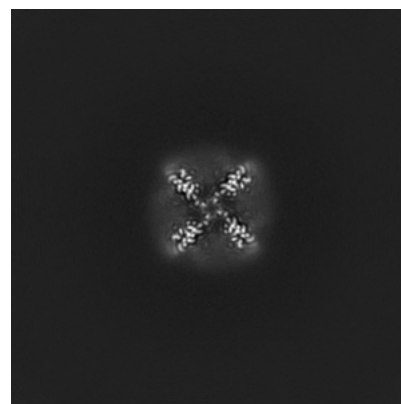
6.2.2 Raw map



X Index: 208



Y Index: 208

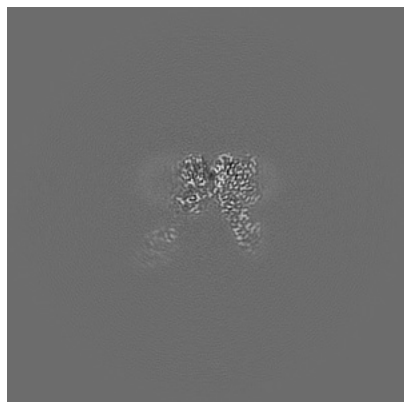


Z Index: 208

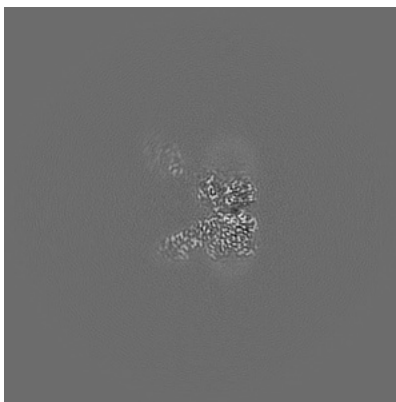
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

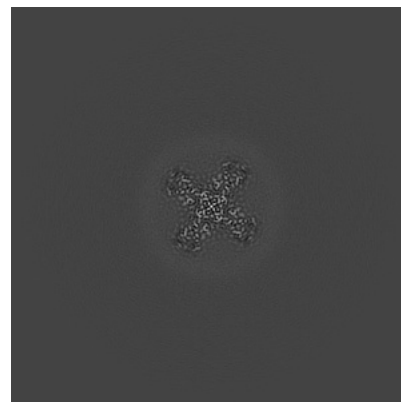
6.3.1 Primary map



X Index: 225

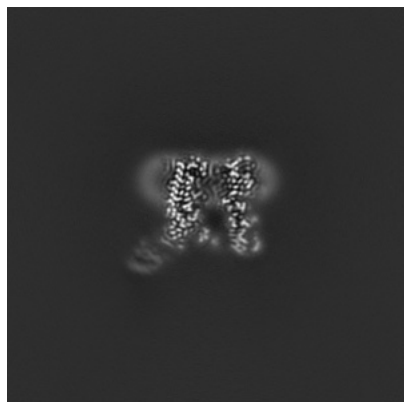


Y Index: 225

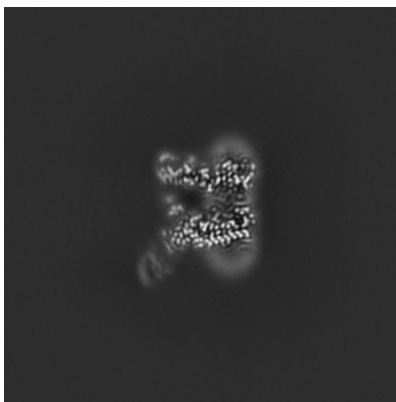


Z Index: 242

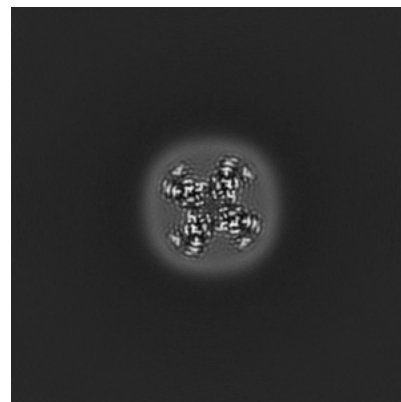
6.3.2 Raw map



X Index: 235



Y Index: 181

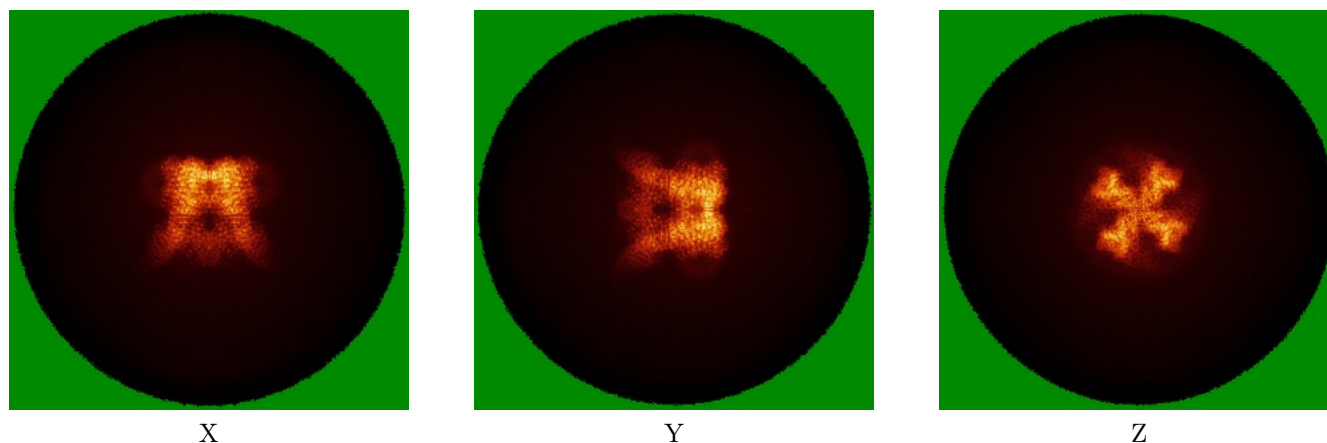


Z Index: 250

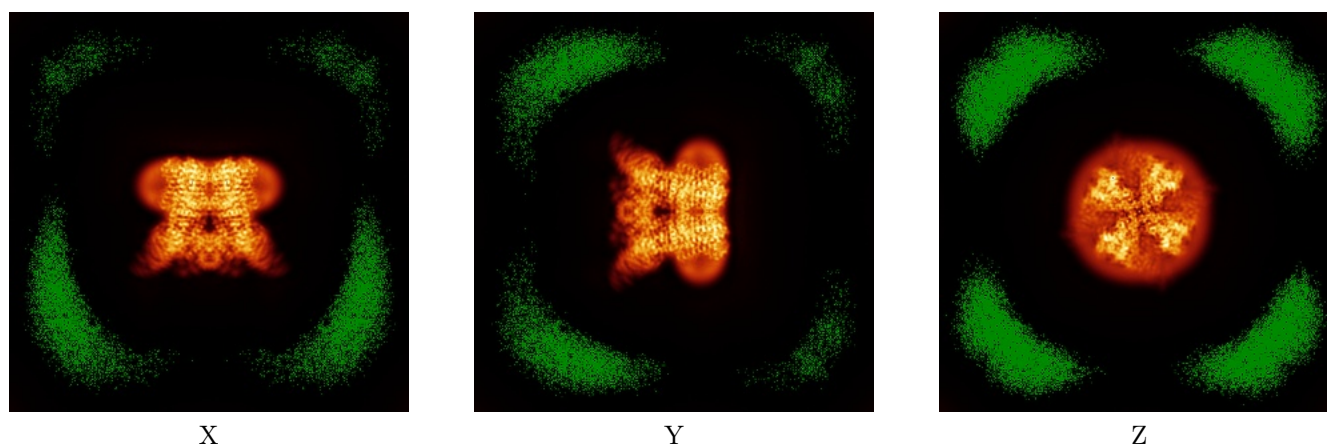
The images above show the largest variance slices of the map in three orthogonal directions.

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.

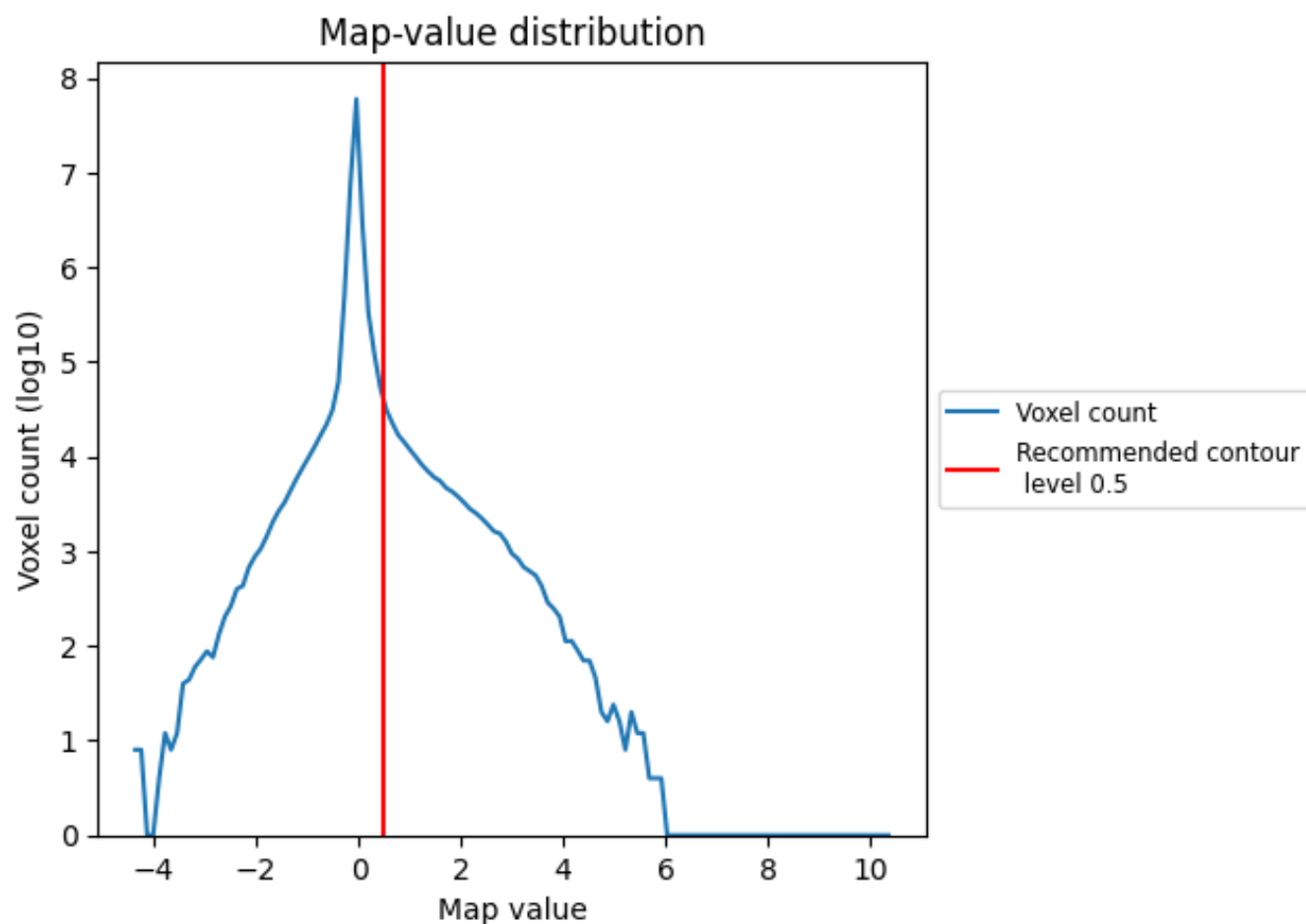
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

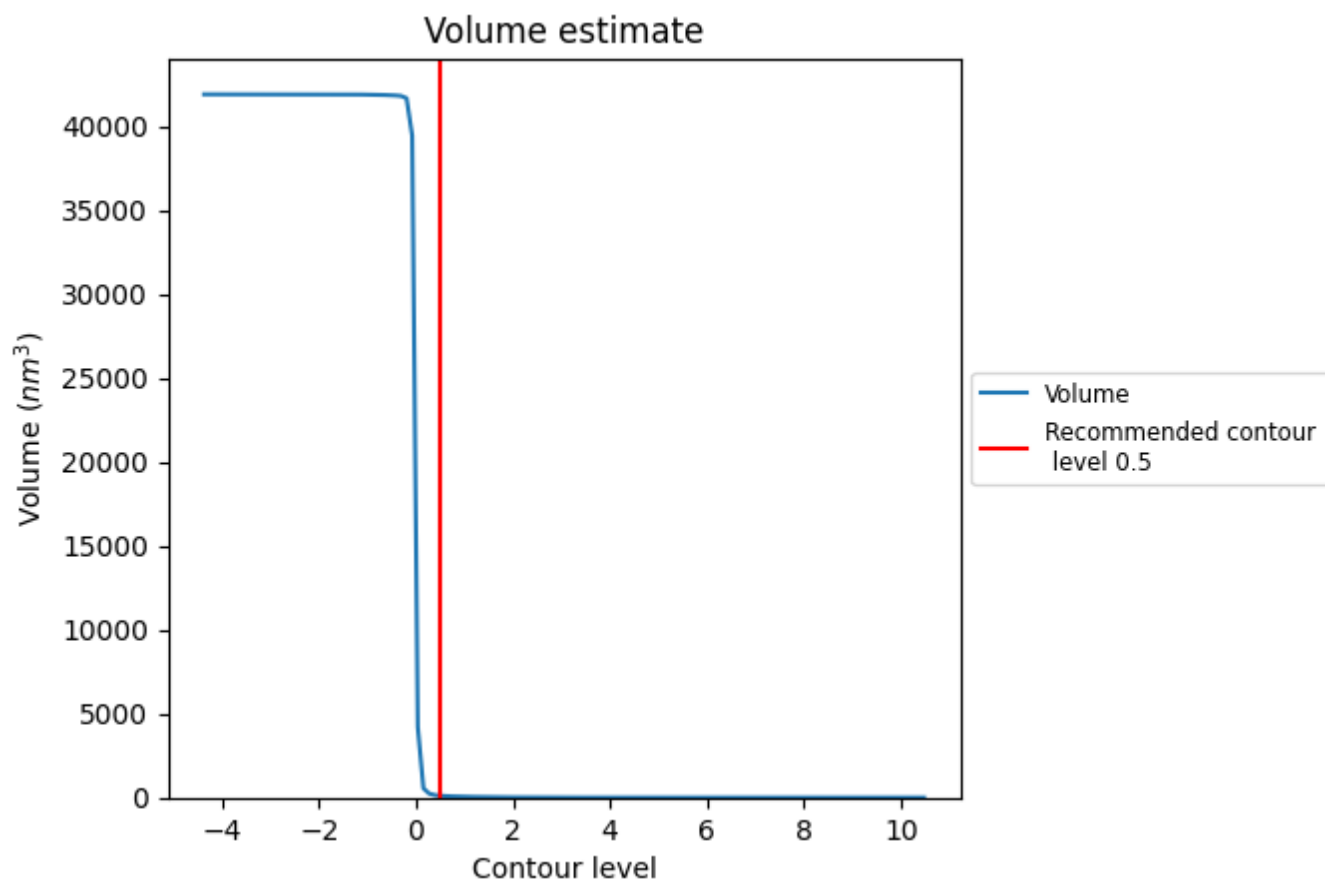
This section contains the results of statistical analysis of the map.

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.

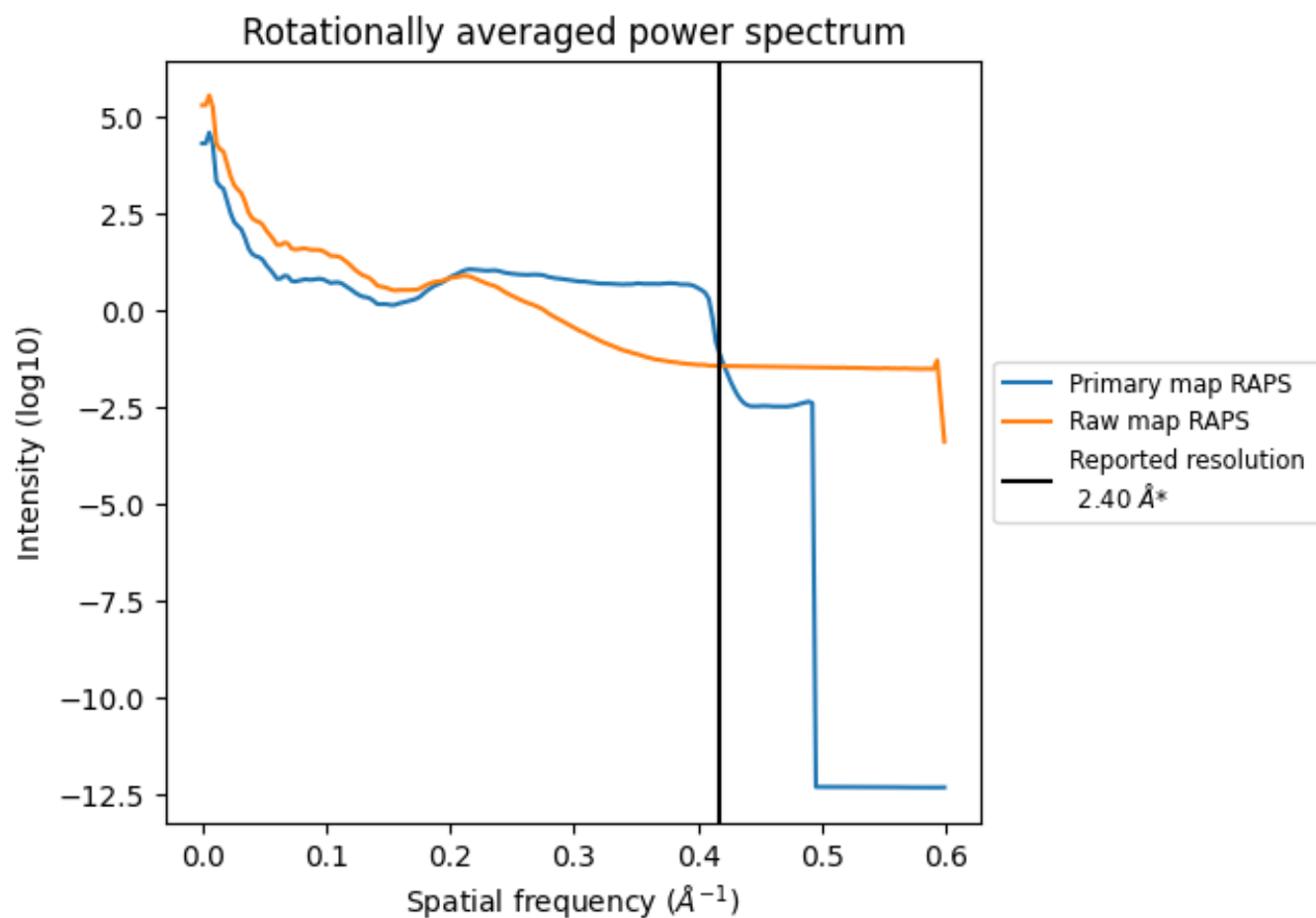
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 108 nm^3 ; this corresponds to an approximate mass of 97 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 ⓘ

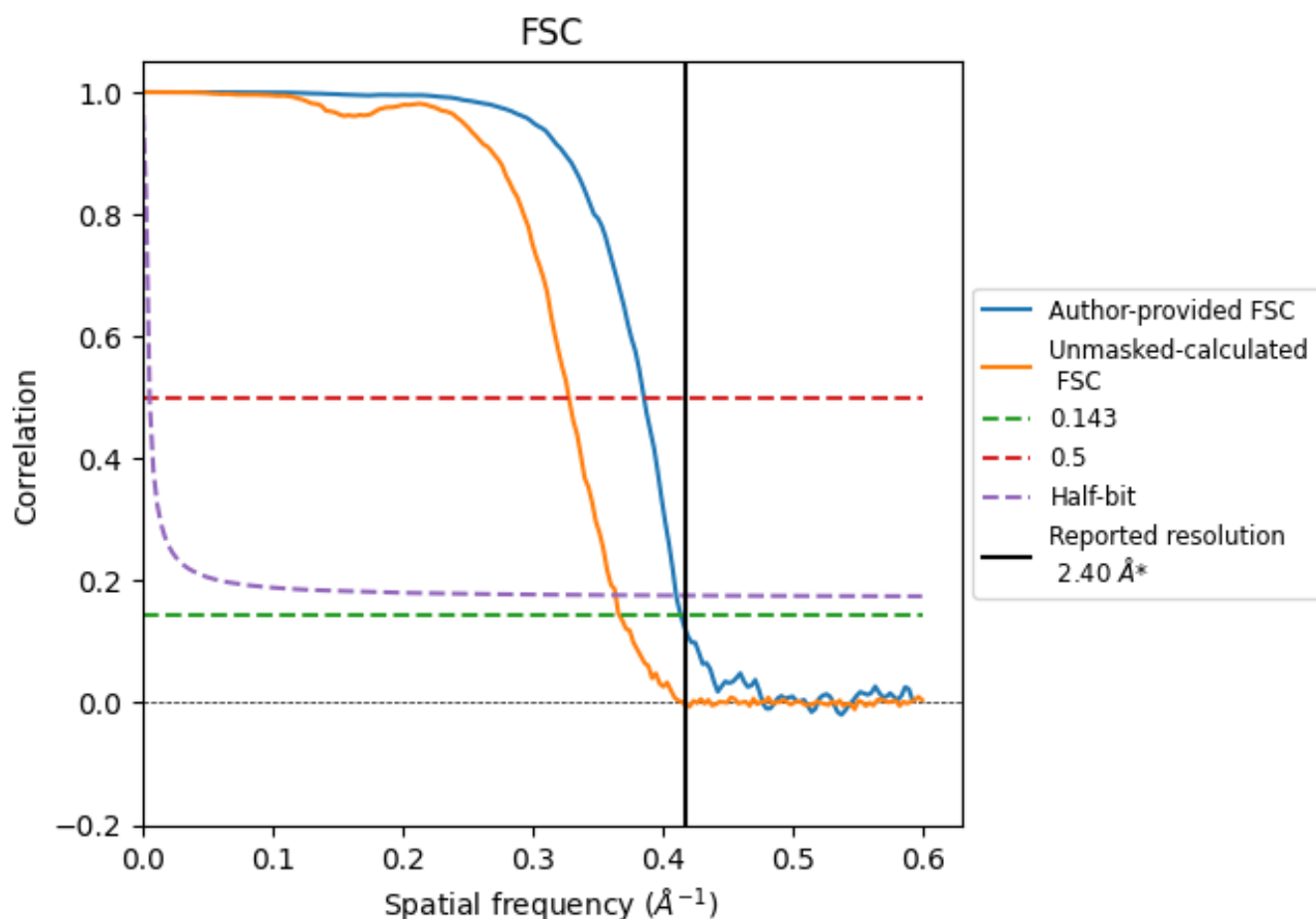


*Reported resolution corresponds to spatial frequency of 0.417 $\text{\AA}^{-1}$

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 $0.417 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

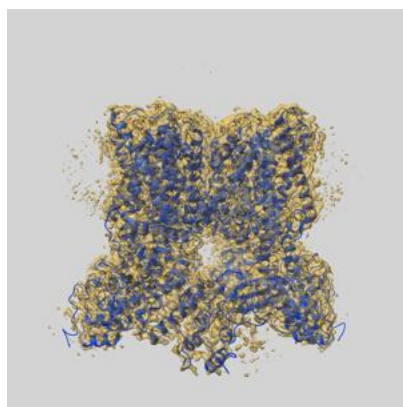
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.42	2.60	2.44
Unmasked-calculated*	2.73	3.05	2.75

*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 2.73 differs from the reported value 2.4 by more than 10 %

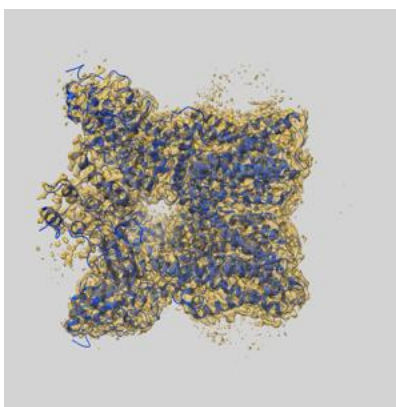
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41873 and PDB model 8U43. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

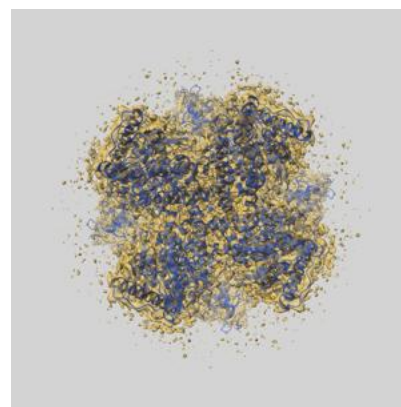
9.1 Map-model overlay [i](#)



X



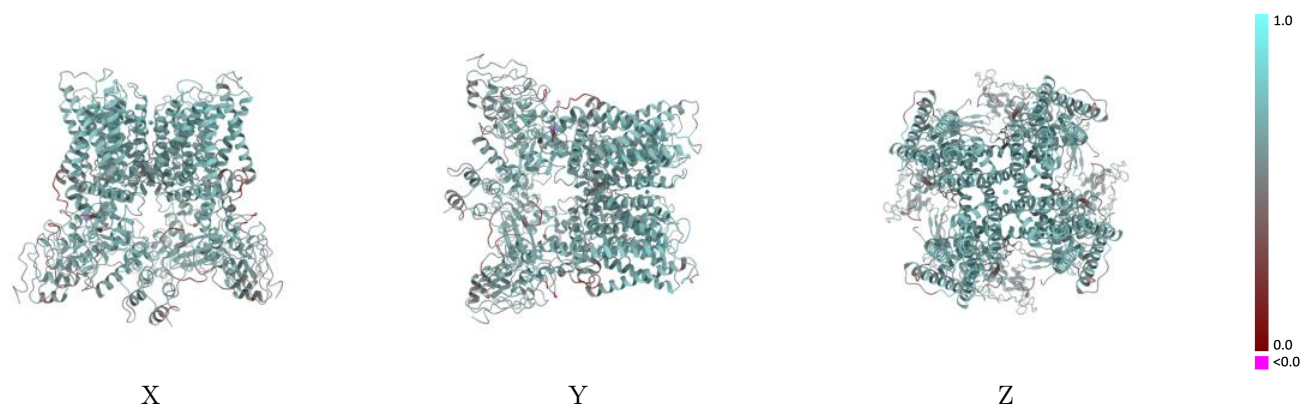
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5 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](#)

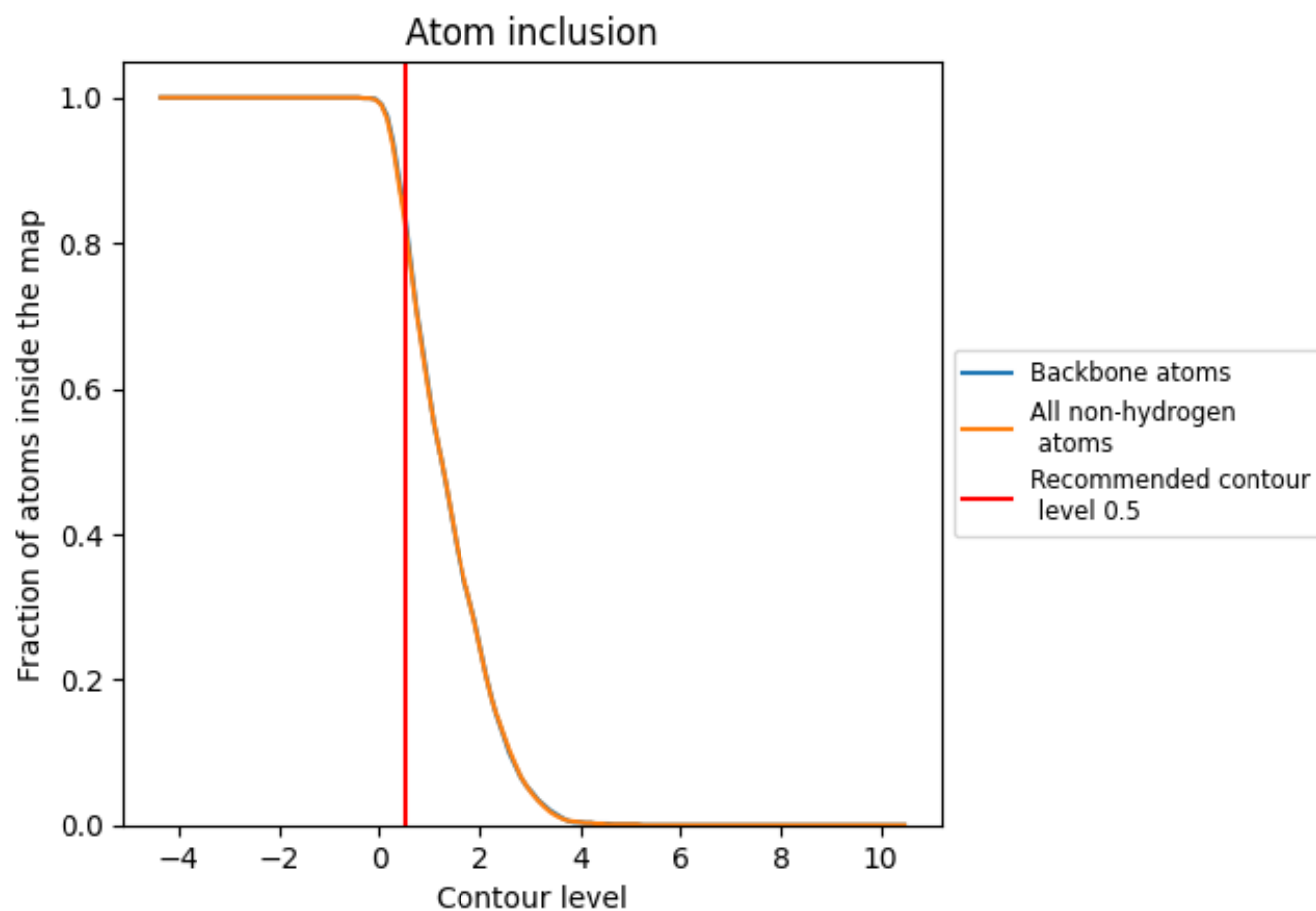


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 83% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8320	0.6100
A	0.8370	0.6100
B	0.8380	0.6100
C	0.8380	0.6090
D	0.8380	0.6100

