



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 5, 2023 – 10:59 PM EDT

PDB ID : 4D9P  
Title : Crystal structure of B. anthracis DHPS with compound 17  
Authors : Hammoudeh, D.; Lee, R.E.; White, S.W.  
Deposited on : 2012-01-11  
Resolution : 2.26 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/XrayValidationReportHelp>

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:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35

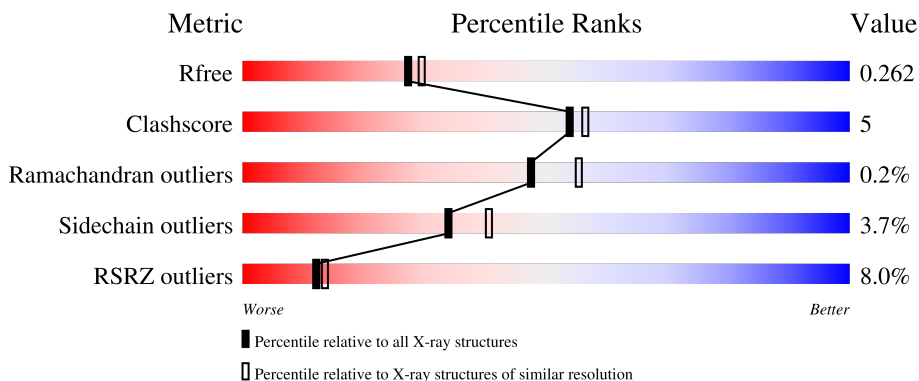
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.26 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	297	 5% 77% 10% • 11%
1	B	297	 9% 74% 12% • 12%

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
2	SO4	A	301	-	-	X	-

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 4203 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Dihydropteroate Synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	264	2041	1283	351	391	16	0	0	0
1	B	261	2022	1269	348	389	16	2	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP C3P9L8
A	-18	GLY	-	expression tag	UNP C3P9L8
A	-17	SER	-	expression tag	UNP C3P9L8
A	-16	SER	-	expression tag	UNP C3P9L8
A	-15	HIS	-	expression tag	UNP C3P9L8
A	-14	HIS	-	expression tag	UNP C3P9L8
A	-13	HIS	-	expression tag	UNP C3P9L8
A	-12	HIS	-	expression tag	UNP C3P9L8
A	-11	HIS	-	expression tag	UNP C3P9L8
A	-10	HIS	-	expression tag	UNP C3P9L8
A	-9	SER	-	expression tag	UNP C3P9L8
A	-8	SER	-	expression tag	UNP C3P9L8
A	-7	GLY	-	expression tag	UNP C3P9L8
A	-6	LEU	-	expression tag	UNP C3P9L8
A	-5	VAL	-	expression tag	UNP C3P9L8
A	-4	PRO	-	expression tag	UNP C3P9L8
A	-3	ARG	-	expression tag	UNP C3P9L8
A	-2	GLY	-	expression tag	UNP C3P9L8
A	-1	SER	-	expression tag	UNP C3P9L8
A	0	HIS	-	expression tag	UNP C3P9L8
B	-19	MET	-	expression tag	UNP C3P9L8
B	-18	GLY	-	expression tag	UNP C3P9L8
B	-17	SER	-	expression tag	UNP C3P9L8
B	-16	SER	-	expression tag	UNP C3P9L8
B	-15	HIS	-	expression tag	UNP C3P9L8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP C3P9L8
B	-13	HIS	-	expression tag	UNP C3P9L8
B	-12	HIS	-	expression tag	UNP C3P9L8
B	-11	HIS	-	expression tag	UNP C3P9L8
B	-10	HIS	-	expression tag	UNP C3P9L8
B	-9	SER	-	expression tag	UNP C3P9L8
B	-8	SER	-	expression tag	UNP C3P9L8
B	-7	GLY	-	expression tag	UNP C3P9L8
B	-6	LEU	-	expression tag	UNP C3P9L8
B	-5	VAL	-	expression tag	UNP C3P9L8
B	-4	PRO	-	expression tag	UNP C3P9L8
B	-3	ARG	-	expression tag	UNP C3P9L8
B	-2	GLY	-	expression tag	UNP C3P9L8
B	-1	SER	-	expression tag	UNP C3P9L8
B	0	HIS	-	expression tag	UNP C3P9L8

- Molecule 2 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



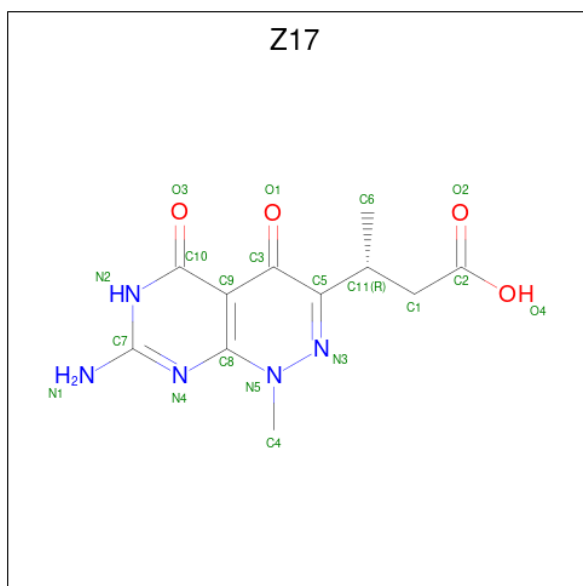
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is (3R)-3-(7-amino-1-methyl-4,5-dioxo-1,4,5,6-tetrahydropyrimido[4,5-c]pyridazin-3-yl)butanoic acid (three-letter code: Z17) (formula: C<sub>11</sub>H<sub>13</sub>N<sub>5</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			20	11	5	4		
3	B	1	Total	C	N	O	0	0
			20	11	5	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	27	Total	O	0	0
			27	27		

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	B	23	Total	O	0	0
			23	23		





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.67Å 99.67Å 261.08Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.26 29.18 – 2.26	Depositor EDS
% Data completeness (in resolution range)	83.1 (30.00-2.26) 83.1 (29.18-2.26)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.28 (at 2.26Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.234 , 0.269 0.227 , 0.262	Depositor DCC
$R_{free}$ test set	1554 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.3	Xtrriage
Anisotropy	0.724	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 31.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4203	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.06 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.1549e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, Z17

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	0.45	0/2071	0.60	0/2793
1	B	0.50	0/2049	0.60	0/2760
All	All	0.48	0/4120	0.60	0/5553

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	2041	0	2047	21	0
1	B	2022	0	2031	25	0
2	A	25	0	0	2	0
2	B	25	0	0	0	0
3	A	20	0	12	2	0
3	B	20	0	12	0	0
4	A	27	0	0	0	0
4	B	23	0	0	0	0
All	All	4203	0	4102	44	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 5.

All (44) 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:B:216:GLY:O	1:B:220:LYS:HE3	1.75	0.86
1:B:82:ARG:HH11	1:B:82:ARG:HG3	1.43	0.82
1:B:22:ILE:H	1:B:58:HIS:HD1	1.31	0.77
1:A:50:LYS:HE2	2:A:301:SO4:O1	1.93	0.69
1:A:185:PRO:HG3	1:A:203:LEU:HD21	1.75	0.69
1:B:267:MET:HA	1:B:267:MET:HE2	1.75	0.66
1:B:161:ILE:HG23	1:B:209:LEU:HD11	1.80	0.62
1:B:82:ARG:HH11	1:B:82:ARG:CG	2.12	0.61
1:A:189:PHE:CZ	3:A:306:Z17:H9	2.37	0.60
1:B:79:GLU:OE1	1:B:104:LYS:HE3	2.03	0.58
1:B:85:PRO:HA	1:B:88:GLN:HE21	1.70	0.56
1:B:2:LYS:C	1:B:2:LYS:CD	2.74	0.55
1:A:93:GLU:OE2	1:B:39:TYR:OH	2.23	0.54
1:B:145:MET:HA	1:B:184:ASP:HB3	1.90	0.54
1:B:155:ASN:HD22	1:B:155:ASN:C	2.11	0.54
1:A:189:PHE:HZ	3:A:306:Z17:H9	1.72	0.53
1:B:218:SER:HA	1:B:238:THR:HG23	1.90	0.53
1:A:244:LEU:HD11	1:A:248:LYS:HE2	1.93	0.51
1:A:50:LYS:CE	2:A:301:SO4:O1	2.60	0.49
1:A:218:SER:HA	1:A:238:THR:HG23	1.95	0.48
1:A:145:MET:HA	1:A:184:ASP:HB3	1.95	0.47
1:A:12:TYR:OH	1:A:95:LYS:HA	2.14	0.47
1:B:208:VAL:HG23	1:B:209:LEU:HD12	1.97	0.47
1:A:216:GLY:O	1:A:220:LYS:HE3	2.15	0.47
1:A:145:MET:HG3	1:A:184:ASP:CG	2.35	0.46
1:B:2:LYS:C	1:B:2:LYS:HD3	2.36	0.46
1:B:65:GLU:HB2	1:B:66:SER:H	1.70	0.45
1:B:244:LEU:HD11	1:B:248:LYS:HE2	1.99	0.45
1:B:35:ASP:HA	1:B:82:ARG:HH22	1.82	0.44
1:B:26:LEU:HD21	1:B:45:ALA:HB1	1.99	0.44
1:A:39:TYR:OH	1:B:93:GLU:OE2	2.33	0.43
1:A:155:ASN:HD22	1:A:158:ALA:H	1.66	0.42
1:B:82:ARG:CG	1:B:82:ARG:NH1	2.74	0.42
1:A:29:THR:HA	1:A:30:PRO:HD3	1.85	0.42
1:A:217:THR:HA	1:A:220:LYS:HD2	2.01	0.42
1:A:101:ASP:OD2	1:A:101:ASP:C	2.58	0.42
1:B:2:LYS:HD3	1:B:2:LYS:O	2.20	0.42
1:A:26:LEU:HD21	1:A:45:ALA:HB1	2.01	0.41
1:A:31:ASP:CG	1:A:41:GLU:HG3	2.41	0.41
1:B:43:ASP:OD2	1:B:47:ARG:NH1	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:242:VAL:HG13	1:B:253:VAL:HG11	2.02	0.41
1:A:156:LEU:O	1:A:160:MET:HG3	2.21	0.40
1:B:192:THR:HB	1:B:193:PRO:HD2	2.03	0.40
1:A:117:HIS:O	1:A:140:VAL:HB	2.22	0.40

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 X-ray entries followed by that with respect to entries of similar resolution.

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	260/297 (88%)	248 (95%)	11 (4%)	1 (0%)	34 37
1	B	255/297 (86%)	250 (98%)	5 (2%)	0	100 100
All	All	515/594 (87%)	498 (97%)	16 (3%)	1 (0%)	47 55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	10	GLY

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	218/247 (88%)	212 (97%)	6 (3%)	43 52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	216/247 (87%)	206 (95%)	10 (5%)	27	30
All	All	434/494 (88%)	418 (96%)	16 (4%)	34	40

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	47	ARG
1	A	95	LYS
1	A	101	ASP
1	A	151	MET
1	A	155	ASN
1	B	2	LYS
1	B	7	LEU
1	B	8	ARG
1	B	65	GLU
1	B	76	VAL
1	B	82	ARG
1	B	95	LYS
1	B	96	LEU
1	B	155	ASN
1	B	197	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	ASN
1	A	88	GLN
1	A	155	ASN
1	A	180	ASN
1	B	88	GLN
1	B	152	ASN
1	B	155	ASN
1	B	180	ASN

### 5.3.3 RNA

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

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
2	SO4	A	303	-	4,4,4	0.17	0	6,6,6	0.16	0
2	SO4	A	305	-	4,4,4	0.15	0	6,6,6	0.08	0
3	Z17	A	306	-	19,21,21	2.75	6 (31%)	17,31,31	2.27	8 (47%)
2	SO4	B	303	-	4,4,4	0.13	0	6,6,6	0.16	0
2	SO4	A	301	-	4,4,4	0.18	0	6,6,6	0.26	0
2	SO4	A	302	-	4,4,4	0.19	0	6,6,6	0.17	0
2	SO4	B	301	-	4,4,4	0.12	0	6,6,6	0.34	0
2	SO4	A	304	-	4,4,4	0.18	0	6,6,6	0.08	0
3	Z17	B	306	-	19,21,21	2.81	6 (31%)	17,31,31	1.98	5 (29%)
2	SO4	B	305	-	4,4,4	0.16	0	6,6,6	0.10	0
2	SO4	B	304	-	4,4,4	0.15	0	6,6,6	0.04	0
2	SO4	B	302	-	4,4,4	0.19	0	6,6,6	0.33	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	Z17	A	306	-	-	1/7/8/8	0/2/2/2
3	Z17	B	306	-	-	1/7/8/8	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	306	Z17	O3-C10	7.77	1.38	1.23
3	A	306	Z17	O3-C10	7.14	1.37	1.23
3	A	306	Z17	O1-C3	6.16	1.36	1.23
3	B	306	Z17	O1-C3	6.02	1.36	1.23
3	A	306	Z17	C7-N1	3.77	1.43	1.34
3	A	306	Z17	C8-N5	3.70	1.44	1.38
3	B	306	Z17	C8-N5	3.54	1.44	1.38
3	B	306	Z17	C7-N1	3.41	1.42	1.34
3	B	306	Z17	C7-N2	3.23	1.45	1.37
3	A	306	Z17	C7-N2	3.13	1.45	1.37
3	B	306	Z17	C7-N4	2.78	1.39	1.33
3	A	306	Z17	C7-N4	2.36	1.38	1.33

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	306	Z17	C7-N4-C8	4.95	121.12	112.30
3	B	306	Z17	C7-N4-C8	4.59	120.48	112.30
3	A	306	Z17	C6-C11-C1	-3.61	105.53	111.39
3	B	306	Z17	C9-C8-N5	-2.96	115.67	120.10
3	A	306	Z17	N2-C7-N4	-2.95	117.81	123.32
3	A	306	Z17	C9-C8-N5	-2.89	115.79	120.10
3	B	306	Z17	N2-C7-N4	-2.70	118.28	123.32
3	B	306	Z17	C7-N2-C10	-2.44	120.66	125.10
3	A	306	Z17	C7-N2-C10	-2.43	120.67	125.10
3	A	306	Z17	C10-C9-C3	2.36	123.89	120.49
3	A	306	Z17	N1-C7-N2	2.21	121.41	116.71
3	B	306	Z17	C10-C9-C3	2.17	123.62	120.49
3	A	306	Z17	O4-C2-C1	2.04	120.62	114.07

There are no chirality outliers.

All (2) torsion outliers are listed below:

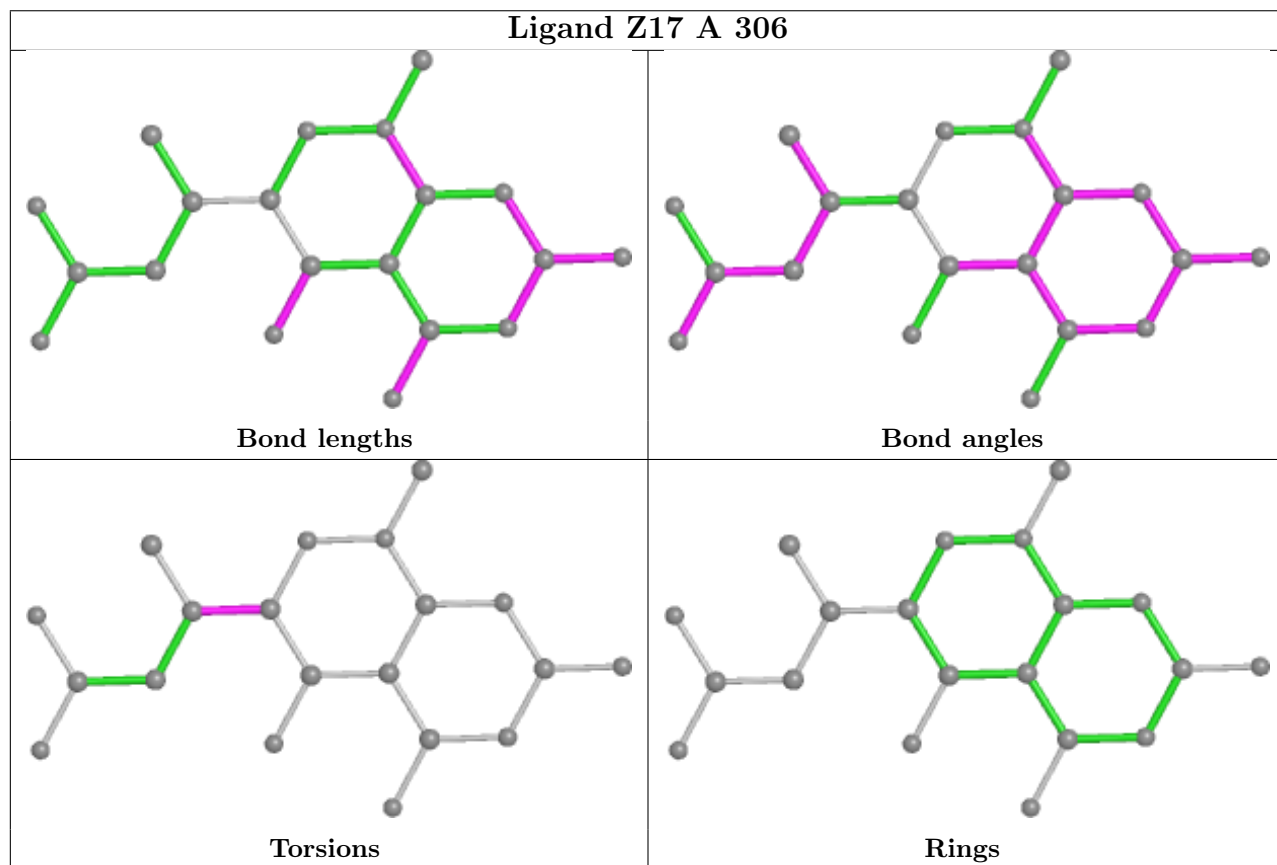
Mol	Chain	Res	Type	Atoms
3	A	306	Z17	C1-C11-C5-C3
3	B	306	Z17	C1-C11-C5-C3

There are no ring outliers.

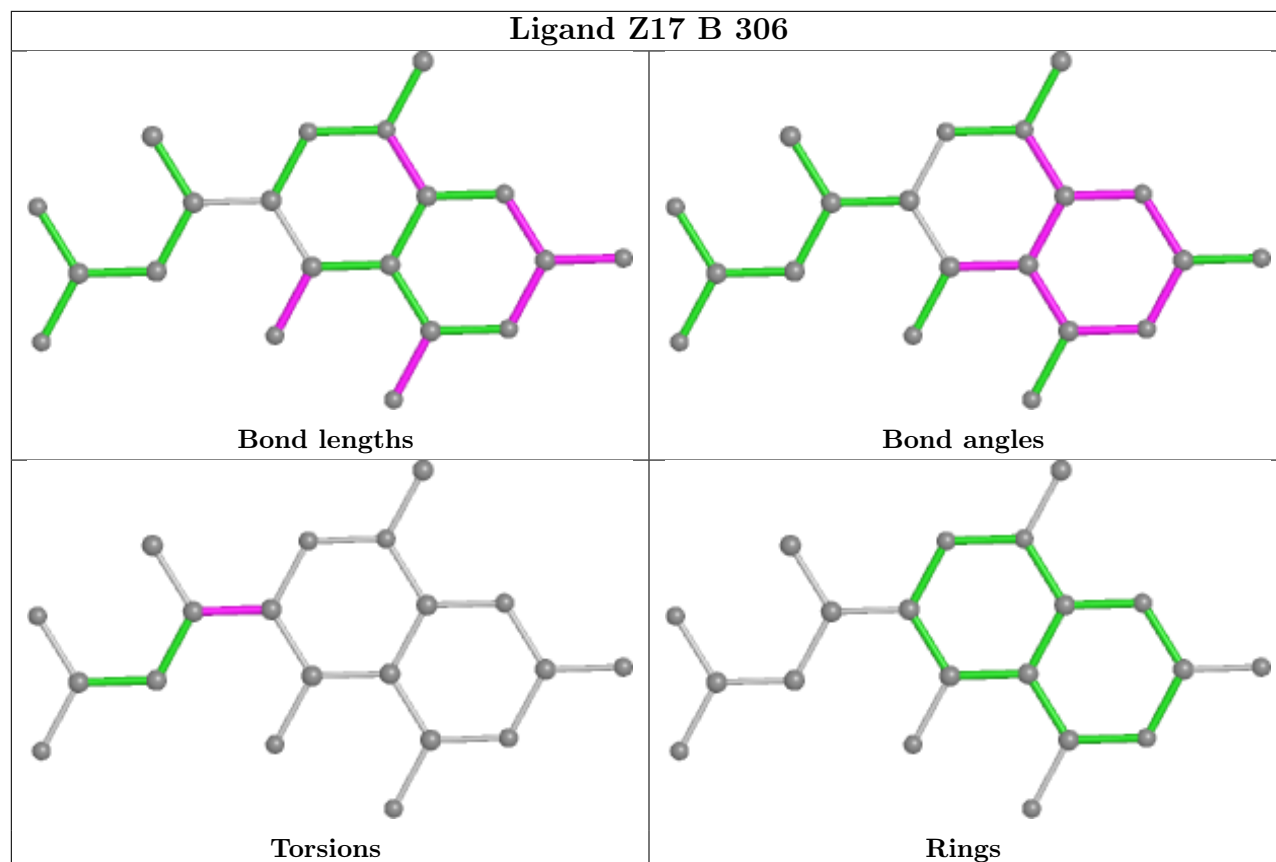
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	306	Z17	2	0
2	A	301	SO4	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	264/297 (88%)	0.26	16 (6%) 21 23	40, 56, 76, 104	0
1	B	261/297 (87%)	0.41	26 (9%) 7 7	36, 52, 74, 97	1 (0%)
All	All	525/594 (88%)	0.33	42 (8%) 12 13	36, 54, 76, 104	1 (0%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	214	LEU	5.0
1	B	215	LEU	4.3
1	A	35	ASP	4.3
1	B	23	MET	4.1
1	B	253	VAL	3.9
1	A	214	LEU	3.9
1	B	143	ILE	3.6
1	A	215	LEU	3.4
1	B	35	ASP	3.3
1	B	187	ILE	3.2
1	B	66	SER	3.2
1	A	151	MET	3.2
1	B	182	ILE	3.2
1	A	253	VAL	3.2
1	B	183	LEU	3.2
1	A	183	LEU	3.1
1	B	149	ASP	3.1
1	B	216	GLY	3.0
1	B	273	GLY	3.0
1	A	252	PHE	3.0
1	B	82	ARG	2.9
1	B	252	PHE	2.8
1	B	59	ILE	2.8
1	A	33	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	143	ILE	2.7
1	B	185	PRO	2.6
1	B	151	MET	2.6
1	B	254	ARG	2.4
1	B	61	ASP	2.3
1	A	74	VAL	2.3
1	A	231	VAL	2.3
1	B	190	ALA	2.3
1	A	23	MET	2.3
1	B	24	GLY	2.3
1	B	65	GLU	2.3
1	A	8	ARG	2.2
1	B	22	ILE	2.2
1	B	2	LYS	2.1
1	B	184	ASP	2.1
1	A	144	LEU	2.1
1	A	242	VAL	2.1
1	A	250	CYS	2.1

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

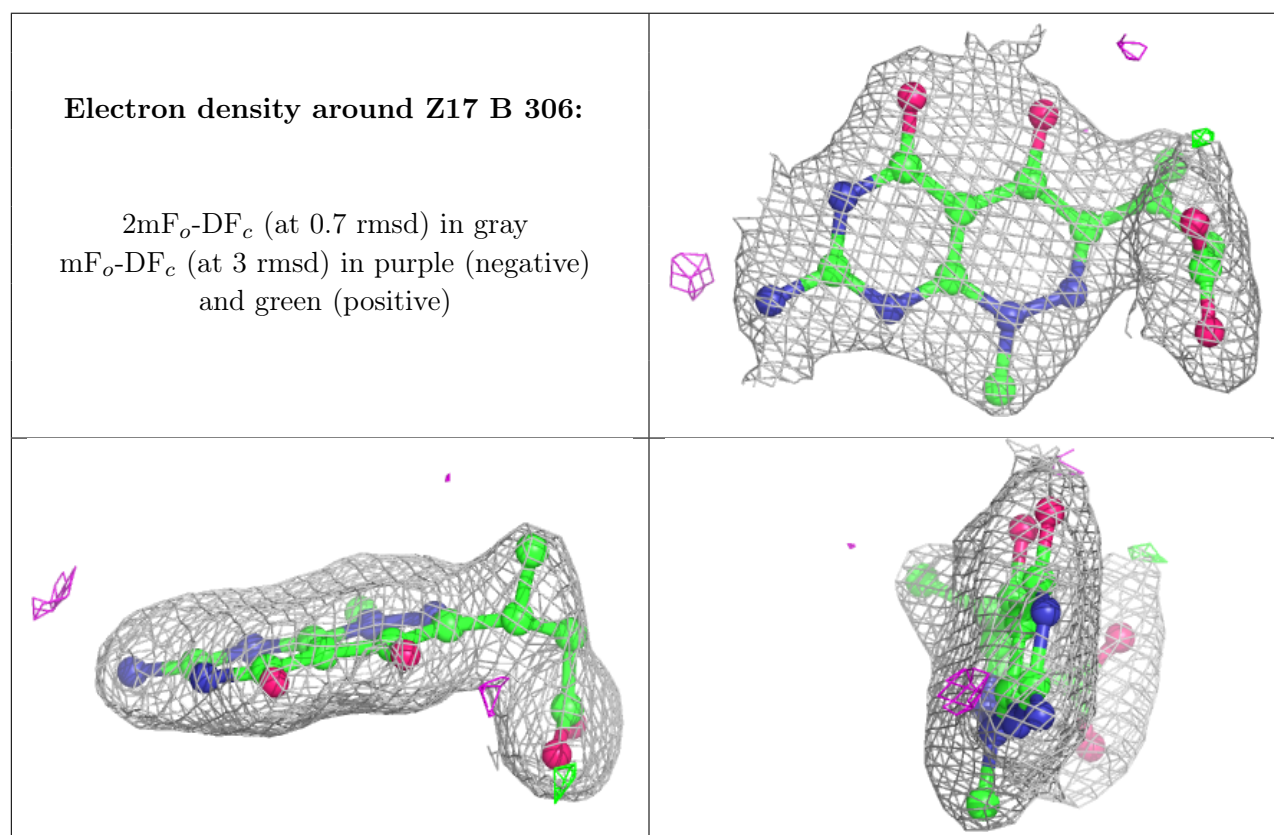
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	SO4	A	305	5/5	0.59	0.35	157,157,157,157	0
2	SO4	A	303	5/5	0.78	0.27	140,140,140,140	0
2	SO4	B	305	5/5	0.81	0.34	128,128,129,129	0
3	Z17	B	306	20/20	0.87	0.21	37,44,52,53	0
2	SO4	A	301	5/5	0.90	0.17	92,92,93,93	0

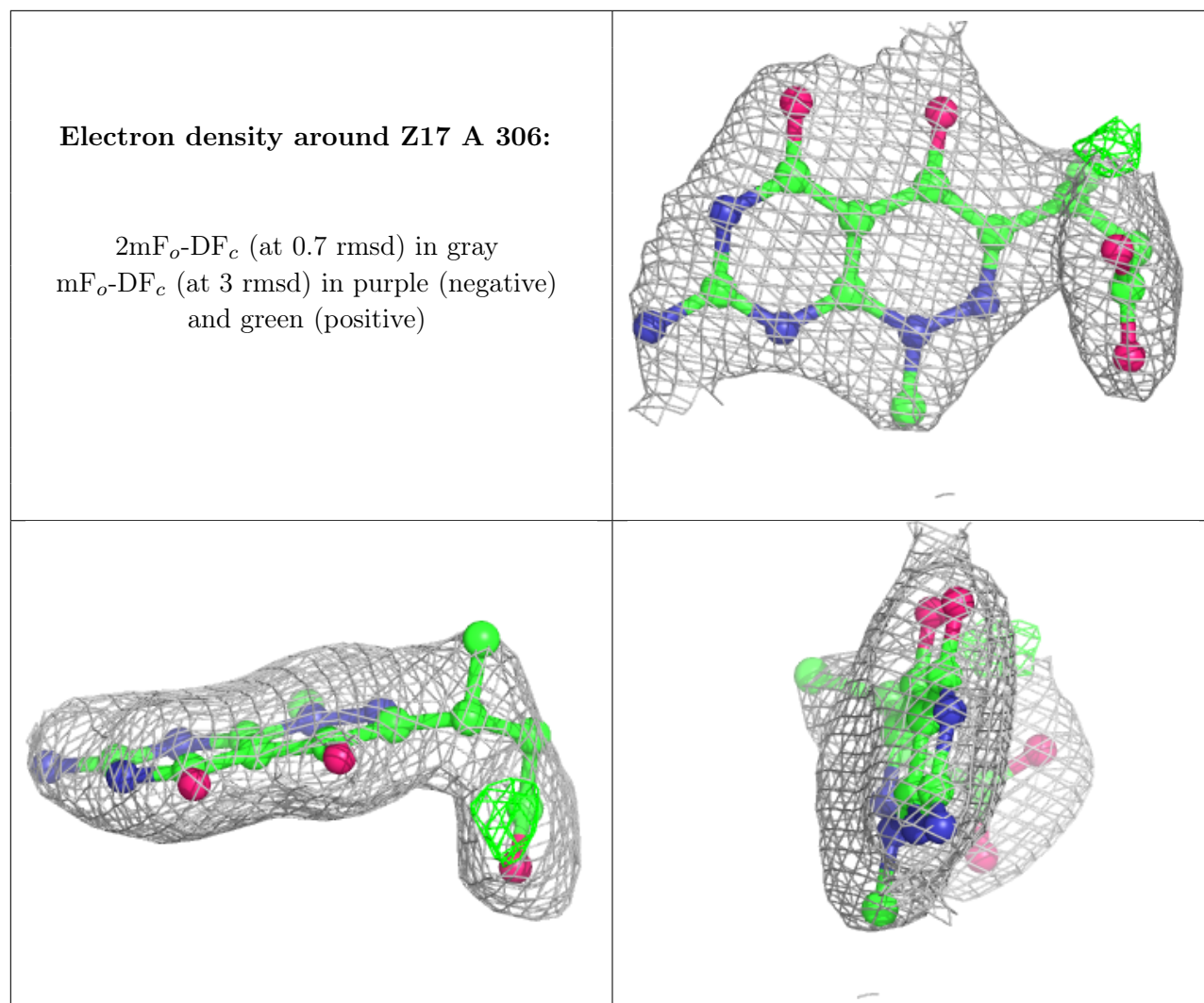
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	A	302	5/5	0.91	0.17	99,99,100,100	0
3	Z17	A	306	20/20	0.91	0.16	46,48,53,54	0
2	SO4	B	302	5/5	0.91	0.18	94,95,95,95	0
2	SO4	A	304	5/5	0.92	0.21	107,108,108,108	0
2	SO4	B	303	5/5	0.95	0.10	103,103,104,104	0
2	SO4	B	301	5/5	0.95	0.20	78,79,80,80	0
2	SO4	B	304	5/5	0.96	0.41	118,118,118,118	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.