



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 8, 2023 – 11:41 PM EDT

PDB ID : 6XQV  
Title : Crystal structure of the catalytic domain of PBP2 S310A from *Neisseria gonorrhoeae* in a pre-acylation complex with ceftriaxone  
Authors : Fenton, B.A.; Zhou, P.; Davies, C.  
Deposited on : 2020-07-10  
Resolution : 2.05 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)  
Xtrriage (Phenix) : 1.13  
EDS : 2.35.1  
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

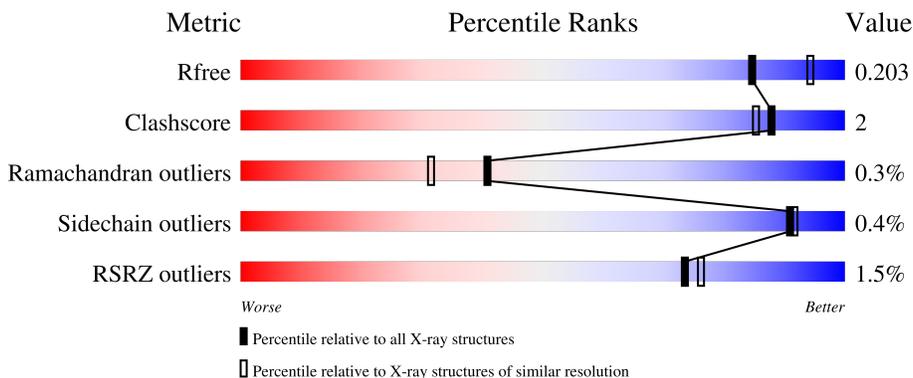
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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	327	 2% 94% 6%
1	B	327	 2% 93% 7%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5429 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.

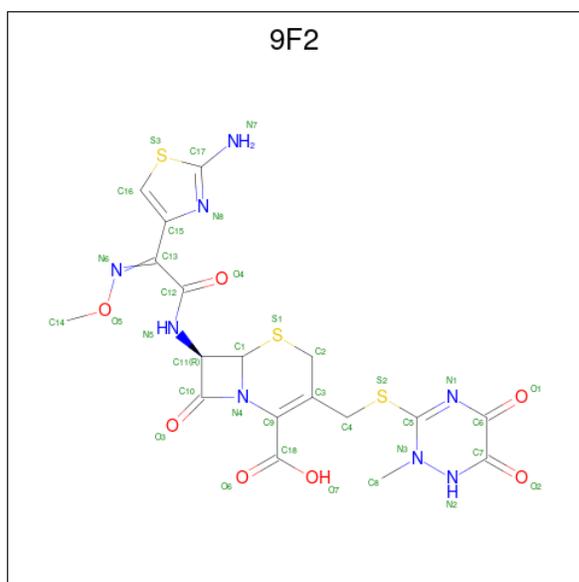
- Molecule 1 is a protein called Probable peptidoglycan D,D-transpeptidase PenA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	327	Total	C	N	O	S	0	8	0
			2560	1618	461	473	8			
1	B	327	Total	C	N	O	S	0	5	0
			2515	1591	448	468	8			

There are 10 discrepancies between the modelled and reference sequences:

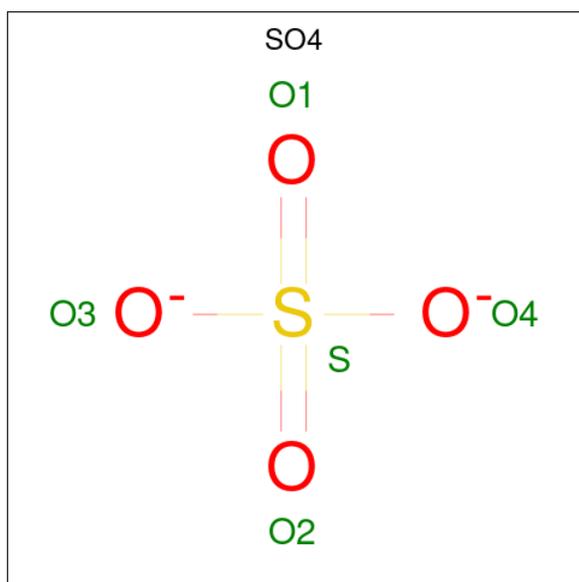
Chain	Residue	Modelled	Actual	Comment	Reference
A	235	ASP	-	expression tag	UNP P08149
A	236	MET	-	expression tag	UNP P08149
A	296	GLY	-	linker	UNP P08149
A	297	GLY	-	linker	UNP P08149
A	310	ALA	SER	engineered mutation	UNP P08149
B	235	ASP	-	expression tag	UNP P08149
B	236	MET	-	expression tag	UNP P08149
B	296	GLY	-	linker	UNP P08149
B	297	GLY	-	linker	UNP P08149
B	310	ALA	SER	engineered mutation	UNP P08149

- Molecule 2 is Ceftriaxone (three-letter code: 9F2) (formula:  $C_{18}H_{18}N_8O_7S_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	Total	C	N	O	S	0	0
			36	18	8	7	3		
2	B	1	Total	C	N	O	S	0	0
			36	18	8	7	3		
2	B	1	Total	C	N	O	S	0	0
			36	18	8	7	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	113	Total	O	0	0
			113	113		
5	B	117	Total	O	0	0
			117	117		

### 3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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: Probable peptidoglycan D,D-transpeptidase PenA

Chain A: 



- Molecule 1: Probable peptidoglycan D,D-transpeptidase PenA

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.60Å 77.99Å 87.69Å 90.00° 91.11° 90.00°	Depositor
Resolution (Å)	43.84 – 2.05 43.84 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.84-2.05) 99.5 (43.84-2.05)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.68 (at 2.05Å)	Xtrriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, $R_{free}$	0.168 , 0.203 0.168 , 0.203	Depositor DCC
$R_{free}$ test set	1795 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.6	Xtrriage
Anisotropy	0.330	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 52.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.035 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5429	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.46% of the height of the origin peak. No significant pseudotranslation is detected.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, SO4, 9F2

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	0.29	0/2612	0.51	0/3539
1	B	0.29	0/2573	0.49	0/3488
All	All	0.29	0/5185	0.50	0/7027

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 [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	2560	0	2588	11	0
1	B	2515	0	2540	12	0
2	A	36	0	0	0	0
2	B	72	0	0	0	0
3	A	10	0	0	0	0
3	B	5	0	0	0	0
4	A	1	0	0	0	0
5	A	113	0	0	0	0
5	B	117	0	0	0	0
All	All	5429	0	5128	21	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 2.

All (21) 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:459:LYS:HE3	1:A:461:ILE:HD11	1.81	0.63
1:B:391:ARG:HG3	1:B:401:ALA:HB2	1.81	0.61
1:A:264:THR:OG1	1:A:534[B]:THR:OG1	2.20	0.59
1:B:264[A]:THR:HG22	1:B:428:LEU:HD23	1.88	0.56
1:B:385:GLU:HG2	1:B:461:ILE:HD12	1.91	0.51
1:B:459:LYS:HE3	1:B:461:ILE:HD11	1.93	0.50
1:B:516:ALA:HB1	1:B:545:GLY:HA2	1.96	0.48
1:A:441:ASP:HB3	1:A:464:GLU:HG3	1.95	0.47
1:A:516:ALA:HB1	1:A:545:GLY:HA2	1.97	0.47
1:A:264:THR:CG2	1:A:300:ARG:HB2	2.45	0.47
1:A:433:ARG:HG3	1:A:447:LEU:HG	1.97	0.47
1:B:392:MET:HE1	1:B:447:LEU:HD12	1.99	0.44
1:B:459:LYS:CE	1:B:461:ILE:HD11	2.48	0.44
1:A:428:LEU:HD13	1:A:534[B]:THR:HG23	2.00	0.44
1:A:302[A]:VAL:HG12	1:A:429:LEU:HD22	2.01	0.42
1:A:446:PRO:HB3	1:B:407:TRP:HH2	1.85	0.42
1:B:287:GLU:OE2	1:B:451:LYS:HA	2.19	0.42
1:A:393:HIS:HE1	1:B:409:ARG:HH11	1.66	0.41
1:B:403:LEU:HB3	1:B:425:GLN:HB2	2.02	0.41
1:B:491:GLY:HA3	1:B:572:LEU:HD23	2.03	0.40
1:A:313:LYS:HG2	1:A:367:THR:HG21	2.03	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	334/327 (102%)	329 (98%)	4 (1%)	1 (0%)	41 31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	330/327 (101%)	323 (98%)	6 (2%)	1 (0%)	41	31
All	All	664/654 (102%)	652 (98%)	10 (2%)	2 (0%)	41	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	505	VAL
1	A	506	ASN

### 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	266/257 (104%)	266 (100%)	0	100	100
1	B	262/257 (102%)	260 (99%)	2 (1%)	81	82
All	All	528/514 (103%)	526 (100%)	2 (0%)	91	91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	424	LEU
1	B	426	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	384	HIS
1	A	512	ASN
1	B	440	HIS
1	B	506	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	SO4	A	603	-	4,4,4	0.12	0	6,6,6	0.08	0
2	9F2	B	602	-	34,39,39	1.49	2 (5%)	34,57,57	2.85	12 (35%)
2	9F2	B	601	-	34,39,39	0.93	2 (5%)	34,57,57	2.68	12 (35%)
3	SO4	A	602	-	4,4,4	0.14	0	6,6,6	0.10	0
3	SO4	B	603	-	4,4,4	0.14	0	6,6,6	0.06	0
2	9F2	A	601	-	34,39,39	0.87	1 (2%)	34,57,57	2.64	9 (26%)

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
2	9F2	B	601	-	-	6/19/53/53	0/3/4/4
2	9F2	B	602	-	-	5/19/53/53	0/3/4/4
2	9F2	A	601	-	-	10/19/53/53	0/3/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	602	9F2	C5-S2	6.88	1.85	1.74
2	B	602	9F2	C6-C7	-2.30	1.38	1.46
2	B	601	9F2	C6-C7	-2.18	1.38	1.46
2	B	601	9F2	C16-S3	2.11	1.73	1.70
2	A	601	9F2	C6-C7	-2.06	1.39	1.46

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	602	9F2	C4-S2-C5	7.56	114.88	99.09
2	A	601	9F2	C11-C1-S1	7.29	130.10	116.51
2	B	602	9F2	C11-C1-S1	6.94	129.43	116.51
2	B	601	9F2	C11-C1-S1	6.73	129.05	116.51
2	A	601	9F2	O5-N6-C13	6.07	117.95	111.28
2	B	602	9F2	C2-S1-C1	-5.59	83.50	94.47
2	B	602	9F2	C10-N4-C9	5.38	146.07	133.77
2	B	601	9F2	O4-C12-C13	5.35	126.52	120.35
2	B	601	9F2	C10-N4-C9	5.28	145.84	133.77
2	A	601	9F2	C10-N4-C9	5.11	145.46	133.77
2	B	601	9F2	C2-S1-C1	-5.04	84.58	94.47
2	B	601	9F2	O5-N6-C13	4.68	116.42	111.28
2	A	601	9F2	C2-S1-C1	-4.40	85.83	94.47
2	B	601	9F2	C8-N3-N2	4.39	121.08	113.89
2	A	601	9F2	O4-C12-C13	4.15	125.13	120.35
2	B	602	9F2	O5-N6-C13	4.08	115.76	111.28
2	B	602	9F2	C5-N1-C6	4.06	123.61	117.41
2	A	601	9F2	C4-S2-C5	3.66	106.74	99.09
2	B	601	9F2	C1-C11-N5	-3.63	110.34	118.27
2	B	602	9F2	C8-N3-C5	3.62	126.76	120.63
2	A	601	9F2	C8-N3-N2	3.61	119.80	113.89
2	A	601	9F2	C14-O5-N6	3.40	112.35	108.40
2	B	602	9F2	O7-C18-O6	-3.21	116.26	123.61
2	B	602	9F2	C14-O5-N6	3.19	112.11	108.40
2	B	601	9F2	C3-C2-S1	-2.81	109.87	115.08
2	B	601	9F2	C14-O5-N6	2.81	111.66	108.40
2	B	601	9F2	C13-C12-N5	-2.68	109.93	114.38
2	B	602	9F2	C1-C11-N5	-2.54	112.72	118.27
2	B	601	9F2	C4-S2-C5	2.37	104.05	99.09
2	B	602	9F2	C10-C11-N5	2.33	122.03	115.38
2	A	601	9F2	C1-C11-N5	-2.29	113.27	118.27
2	B	601	9F2	C5-N1-C6	2.22	120.80	117.41
2	B	602	9F2	C11-N5-C12	-2.20	116.96	121.56

There are no chirality outliers.

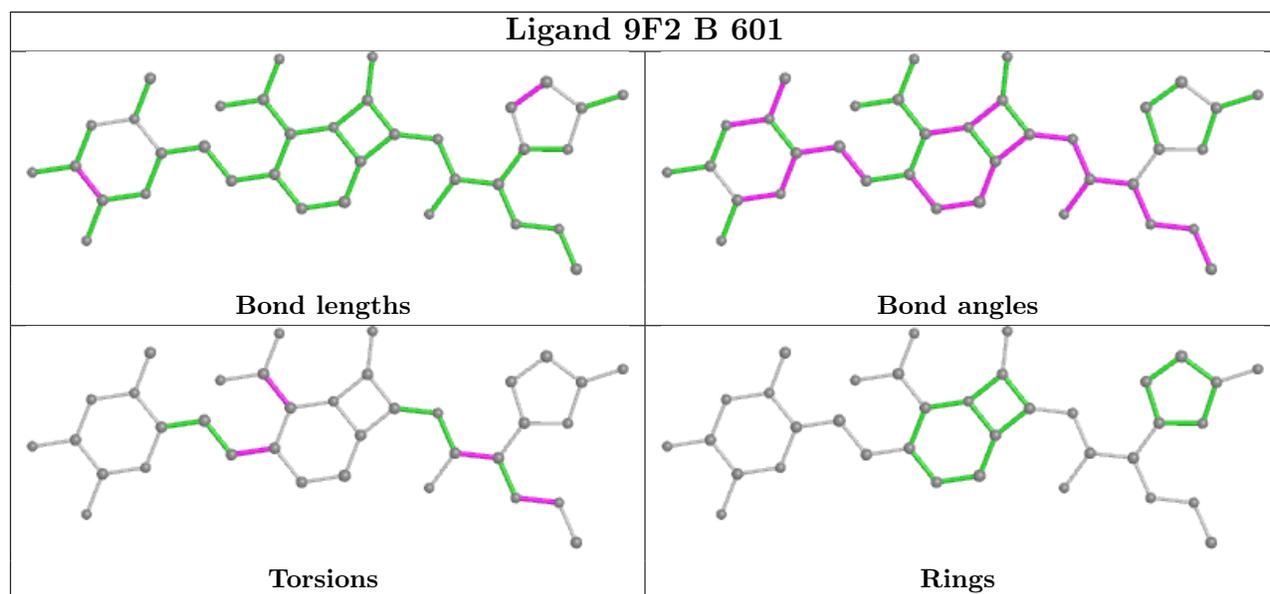
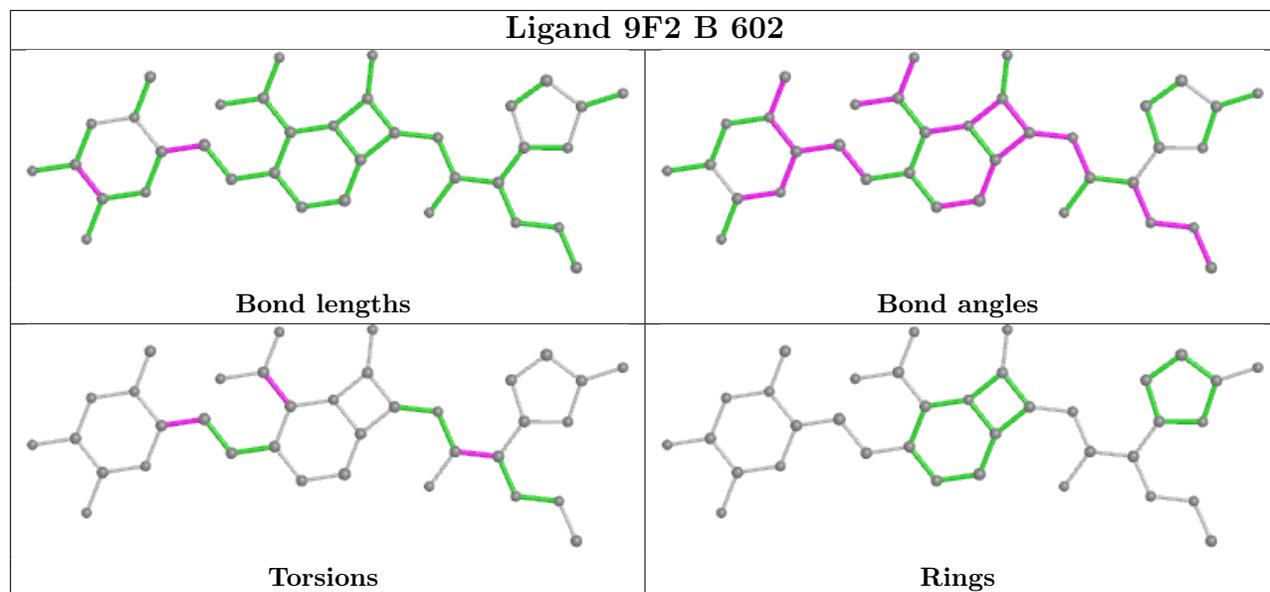
All (21) torsion outliers are listed below:

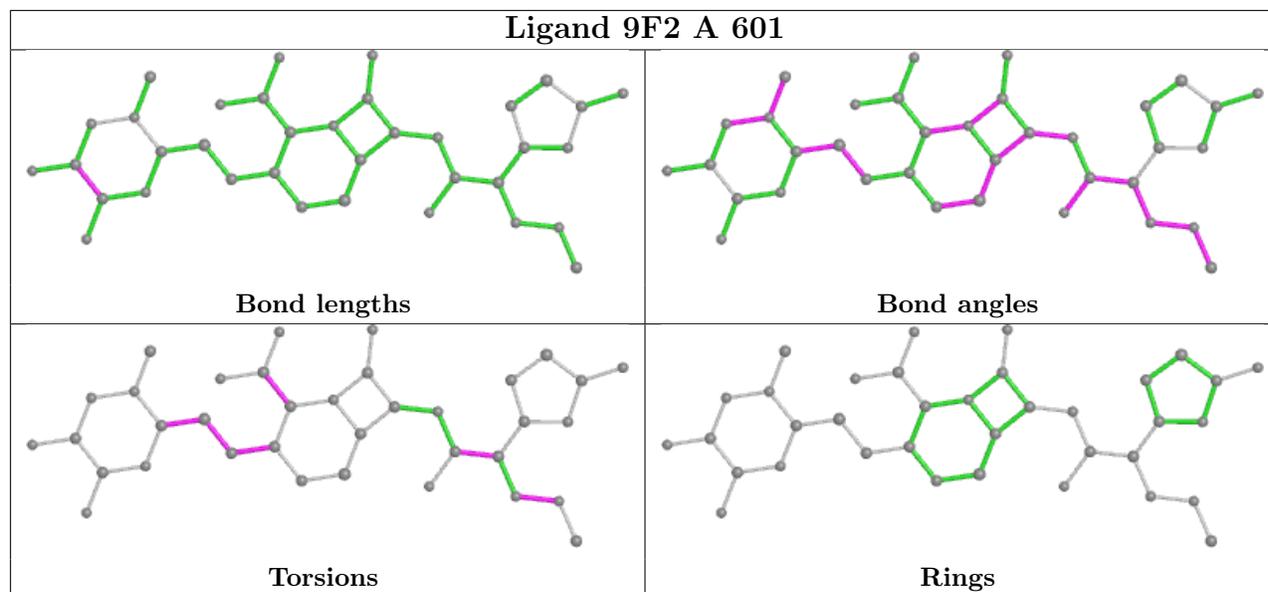
Mol	Chain	Res	Type	Atoms
2	A	601	9F2	C9-C3-C4-S2
2	A	601	9F2	N1-C5-S2-C4
2	A	601	9F2	C13-N6-O5-C14
2	B	601	9F2	C9-C3-C4-S2
2	B	601	9F2	O7-C18-C9-C3
2	B	601	9F2	C13-N6-O5-C14
2	B	602	9F2	N1-C5-S2-C4
2	B	602	9F2	N3-C5-S2-C4
2	A	601	9F2	N3-C5-S2-C4
2	B	601	9F2	O4-C12-C13-N6
2	B	602	9F2	O6-C18-C9-C3
2	B	602	9F2	O6-C18-C9-N4
2	A	601	9F2	O4-C12-C13-N6
2	B	601	9F2	N5-C12-C13-N6
2	A	601	9F2	O6-C18-C9-N4
2	A	601	9F2	C3-C4-S2-C5
2	A	601	9F2	O4-C12-C13-C15
2	A	601	9F2	O7-C18-C9-C3
2	B	602	9F2	O4-C12-C13-N6
2	A	601	9F2	O6-C18-C9-C3
2	B	601	9F2	O6-C18-C9-N4

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	327/327 (100%)	-0.31	5 (1%) 73 76	16, 29, 55, 108	0
1	B	327/327 (100%)	-0.35	5 (1%) 73 76	19, 28, 59, 117	0
All	All	654/654 (100%)	-0.33	10 (1%) 73 76	16, 28, 58, 117	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	297	GLY	6.6
1	B	505	VAL	4.6
1	A	506	ASN	3.5
1	A	507	GLY	3.4
1	A	508	ARG	2.8
1	B	508	ARG	2.8
1	A	504	PHE	2.5
1	A	512	ASN	2.3
1	B	504	PHE	2.1
1	B	454	VAL	2.0

### 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](#)

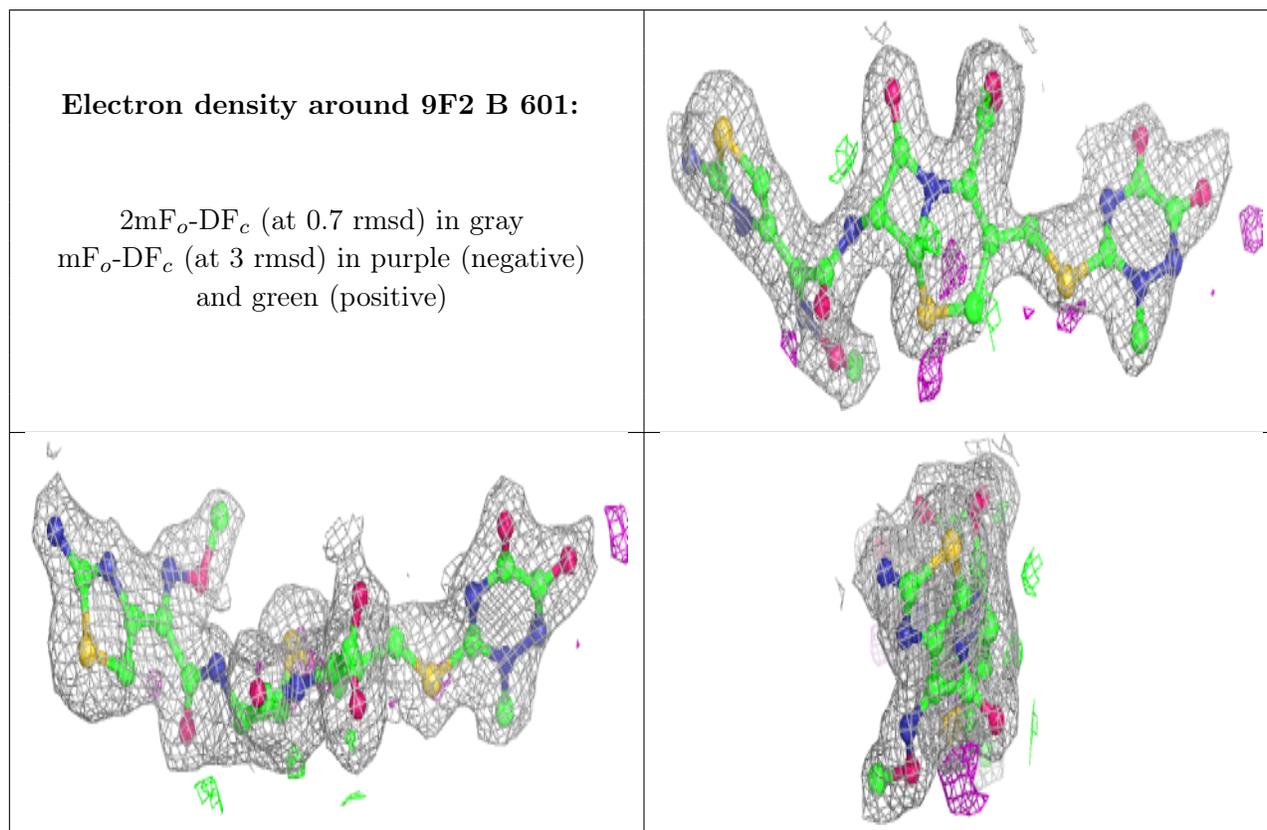
There are no monosaccharides in this entry.

## 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.

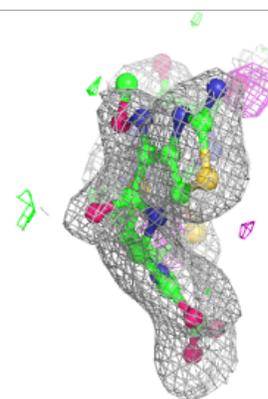
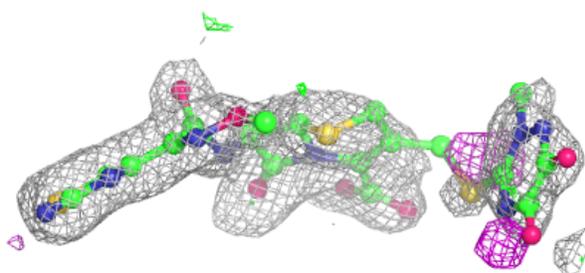
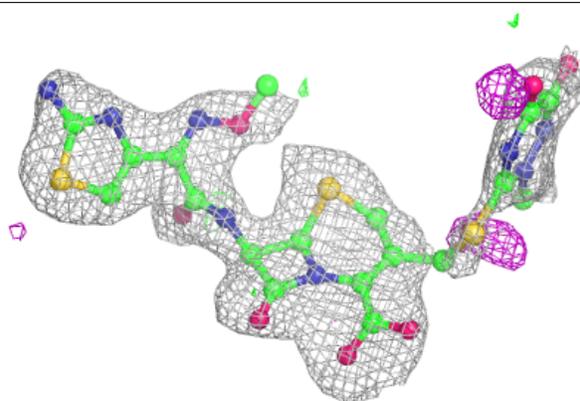
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	9F2	B	601	36/36	0.88	0.15	29,42,61,61	0
2	9F2	B	602	36/36	0.89	0.20	36,52,84,88	0
3	SO4	B	603	5/5	0.89	0.17	96,97,97,98	0
2	9F2	A	601	36/36	0.92	0.13	24,38,50,52	0
3	SO4	A	603	5/5	0.94	0.13	76,76,76,78	0
4	CL	A	604	1/1	0.97	0.10	55,55,55,55	0
3	SO4	A	602	5/5	0.99	0.08	49,51,52,53	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.

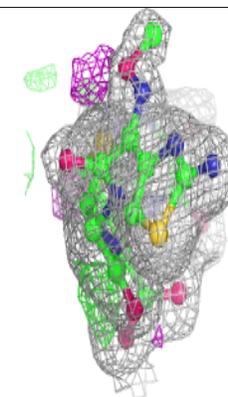
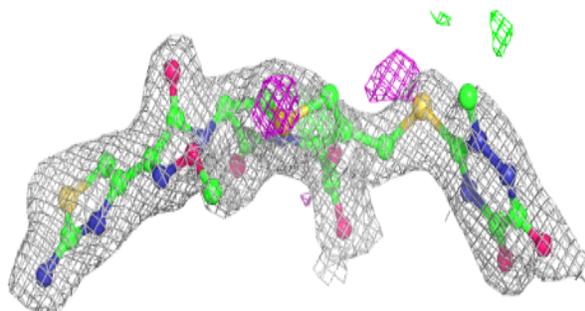
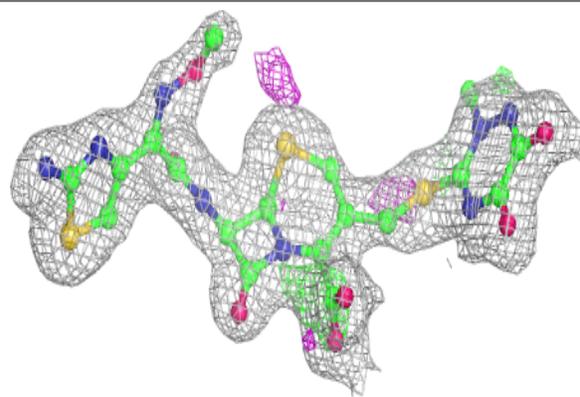


**Electron density around 9F2 B 602:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around 9F2 A 601:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.