



# Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 10:20 pm BST

PDB ID : 2WXH  
Title : The crystal structure of the murine class IA PI 3-kinase p110delta in complex with SW14.  
Authors : Berndt, A.; Miller, S.; Williams, O.; Lee, D.D.; Houseman, B.T.; Pacold, J.I.; Gorrec, F.; Hon, W.-C.; Liu, Y.; Rommel, C.; Gaillard, P.; Ruckle, T.; Schwarz, M.K.; Shokat, K.M.; Shaw, J.P.; Williams, R.L.  
Deposited on : 2009-11-09  
Resolution : 1.90 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 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 : 2.11  
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) : 2.11

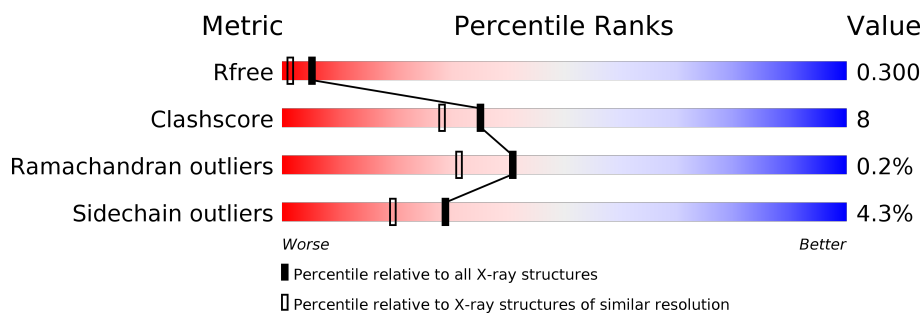
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 on 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	940	

## 2 Entry composition [i](#)

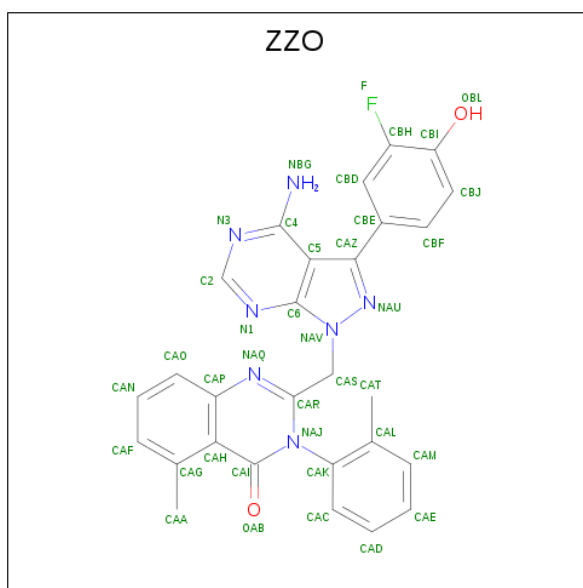
There are 3 unique types of molecules in this entry. The entry contains 6949 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE 3-KINASE CATALYTIC SUBUNIT DELTA ISOFORM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	822	Total	C	N	O	S	0	0	0
			6633	4254	1126	1199	54			

- Molecule 2 is 2-{[4-amino-3-(3-fluoro-4-hydroxyphenyl)-1H-pyrazolo[3,4-d]pyrimidin-1-yl]methyl}-5-methyl-3-(2-methylphenyl)quinazolin-4(3H)-one (three-letter code: ZZO) (formula: C<sub>28</sub>H<sub>22</sub>FN<sub>7</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			38	28	1	7	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	278	Total	O	0	0
			278	278		



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	142.87Å 65.01Å 117.08Å 90.00° 103.58° 90.00°	Depositor
Resolution (Å)	38.04 – 1.90 37.94 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.2 (38.04-1.90) 99.2 (37.94-1.90)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0053	Depositor
R, $R_{free}$	0.217 , 0.245 0.276 , 0.300	Depositor DCC
$R_{free}$ test set	2480 reflections (3.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.6	Xtriage
Anisotropy	0.328	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 45.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6949	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	7.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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: ZZO

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	0.54	0/6776	0.63	3/9142 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	902	ARG	NE-CZ-NH2	-7.45	116.58	120.30
1	A	902	ARG	NE-CZ-NH1	5.87	123.24	120.30
1	A	423	LEU	CA-CB-CG	5.13	127.10	115.30

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	6633	0	6615	109	0
2	A	38	0	21	1	0
3	A	278	0	0	2	0
All	All	6949	0	6636	109	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 8.

All (109) 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:367:SER:HB3	1:A:368:GLU:C	1.78	1.02
1:A:837:ILE:HD11	1:A:901:ILE:HD11	1.46	0.96
1:A:837:ILE:CD1	1:A:901:ILE:HD11	2.03	0.89
1:A:901:ILE:O	1:A:901:ILE:HD12	1.77	0.85
1:A:706:THR:OG1	1:A:710:GLN:OE1	1.98	0.81
1:A:846:ALA:HB1	3:A:2222:HOH:O	1.80	0.81
1:A:328:ILE:HB	1:A:472:VAL:HG23	1.66	0.76
1:A:699:VAL:HG21	1:A:715:MET:HE2	1.66	0.76
1:A:549:LEU:HG	1:A:564:MET:CE	2.16	0.75
1:A:715:MET:HE1	1:A:751:PHE:HB3	1.69	0.75
1:A:962:ARG:HG2	1:A:962:ARG:HH11	1.52	0.75
1:A:895:HIS:H	1:A:898:ASN:HD21	1.38	0.72
1:A:332:LYS:NZ	1:A:341:LEU:HD21	2.04	0.71
1:A:787:ASP:OD2	2:A:1500:ZZO:OBL	2.09	0.71
1:A:332:LYS:HZ2	1:A:341:LEU:HD21	1.57	0.70
1:A:858:TRP:CZ3	1:A:901:ILE:HD13	2.26	0.70
1:A:365:VAL:HG12	1:A:365:VAL:O	1.91	0.69
1:A:367:SER:HB3	1:A:368:GLU:CA	2.21	0.69
1:A:553:THR:HG21	1:A:564:MET:HE2	1.74	0.69
1:A:245:GLY:HA3	1:A:768:ALA:HB2	1.73	0.69
1:A:699:VAL:HG21	1:A:715:MET:CE	2.24	0.68
1:A:194:VAL:HG21	1:A:216:LEU:HD21	1.77	0.67
1:A:549:LEU:HG	1:A:564:MET:HE3	1.75	0.66
1:A:365:VAL:CG1	1:A:365:VAL:O	2.44	0.66
1:A:553:THR:CG2	1:A:564:MET:HE2	2.26	0.64
1:A:205:PHE:CE1	1:A:223:LYS:HG3	2.34	0.63
1:A:367:SER:HB3	1:A:368:GLU:O	1.99	0.62
1:A:435:GLY:HA2	1:A:475:LEU:O	2.01	0.60
1:A:329:GLU:HB2	1:A:369:PRO:O	2.02	0.60
1:A:834:ILE:HD11	1:A:901:ILE:HG23	1.83	0.60
1:A:929:ARG:HH22	1:A:1001:SER:HB3	1.67	0.59
1:A:549:LEU:HG	1:A:564:MET:HE1	1.83	0.59
1:A:870:ARG:NH2	1:A:874:GLU:OE2	2.34	0.59
1:A:929:ARG:HH22	1:A:1001:SER:CB	2.16	0.57
1:A:154:ARG:HG2	1:A:154:ARG:HH11	1.69	0.57
1:A:679:MET:O	1:A:683:MET:HG3	2.04	0.57
1:A:701:VAL:O	1:A:705:LYS:HD2	2.03	0.57
1:A:332:LYS:HE3	1:A:333:VAL:N	2.20	0.57
1:A:842:SER:O	1:A:844:MET:HG2	2.04	0.56
1:A:110:LYS:NZ	1:A:144:ARG:HH12	2.03	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:LYS:HD2	1:A:341:LEU:HD11	1.90	0.53
1:A:329:GLU:HG2	1:A:472:VAL:CG2	2.38	0.53
1:A:553:THR:HG21	1:A:564:MET:CE	2.37	0.53
1:A:984:ALA:HB3	1:A:986:LEU:HD13	1.90	0.53
1:A:110:LYS:HZ1	1:A:144:ARG:HH12	1.56	0.53
1:A:915:PHE:CD2	1:A:915:PHE:C	2.83	0.52
1:A:342:VAL:HG22	1:A:362:GLU:HG2	1.91	0.52
1:A:436:GLU:O	1:A:437:ARG:HD2	2.09	0.52
1:A:895:HIS:H	1:A:898:ASN:ND2	2.06	0.52
1:A:154:ARG:HD2	1:A:165:TYR:CE2	2.44	0.52
1:A:553:THR:CG2	1:A:564:MET:CE	2.88	0.52
1:A:512:ARG:O	1:A:516:GLU:HB2	2.10	0.51
1:A:246:ARG:NH1	1:A:248:GLU:OE1	2.44	0.51
1:A:583:LEU:HD11	1:A:600:LEU:HD11	1.92	0.51
1:A:693:LYS:HE2	1:A:780:ASN:ND2	2.27	0.49
1:A:1020:ASN:O	1:A:1024:ARG:HG3	2.13	0.49
1:A:860:LYS:HG2	1:A:868:LEU:HD22	1.96	0.47
1:A:213:PRO:O	1:A:217:MET:HG3	2.14	0.47
1:A:617:GLN:HE22	1:A:620:LYS:NZ	2.12	0.47
1:A:859:LEU:HD21	1:A:905:GLY:HA2	1.95	0.47
1:A:583:LEU:HD11	1:A:600:LEU:CD1	2.45	0.46
1:A:343:VAL:H	1:A:360:SER:HB2	1.78	0.46
1:A:187:ASN:N	1:A:210:LYS:HZ2	2.11	0.46
1:A:225:ALA:O	1:A:230:GLN:N	2.49	0.46
1:A:617:GLN:HE21	1:A:984:ALA:HA	1.80	0.46
1:A:205:PHE:HE1	1:A:223:LYS:HG3	1.78	0.46
1:A:194:VAL:HG21	1:A:216:LEU:CD2	2.45	0.46
1:A:216:LEU:HD12	1:A:256:LEU:HD11	1.98	0.45
1:A:437:ARG:O	1:A:472:VAL:HA	2.15	0.45
1:A:698:PHE:HZ	1:A:714:MET:HB3	1.81	0.45
1:A:348:PHE:HE2	1:A:453:LEU:HD23	1.81	0.45
1:A:617:GLN:HE22	1:A:620:LYS:HZ2	1.64	0.45
1:A:172:GLU:OE1	1:A:260:GLN:HG2	2.17	0.44
1:A:982:ARG:NH2	1:A:991:CYS:HA	2.33	0.44
1:A:194:VAL:CG2	1:A:216:LEU:HD21	2.45	0.43
1:A:386:ARG:HG3	1:A:387:MET:HE2	1.99	0.43
1:A:962:ARG:CG	1:A:962:ARG:HH11	2.28	0.43
1:A:137:ASN:O	1:A:141:THR:HG23	2.18	0.43
1:A:213:PRO:HD3	1:A:254:TYR:O	2.18	0.43
1:A:332:LYS:HZ3	1:A:341:LEU:HD21	1.82	0.43
1:A:285:MET:O	1:A:289:GLN:HG3	2.19	0.43

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:PRO:HG2	1:A:258:HIS:CD2	2.53	0.43
1:A:698:PHE:CZ	1:A:714:MET:HB3	2.54	0.42
1:A:475:LEU:HA	1:A:476:PRO:HD3	1.89	0.42
1:A:858:TRP:CH2	1:A:901:ILE:HD13	2.54	0.42
1:A:1006:LYS:HB3	1:A:1010:GLU:HB2	2.00	0.42
1:A:387:MET:HE2	1:A:590:CYS:SG	2.59	0.42
1:A:349:HIS:NE2	1:A:588:PRO:HG2	2.35	0.42
1:A:169:LEU:HD22	1:A:259:PHE:HE1	1.85	0.42
1:A:208:SER:OG	1:A:210:LYS:HG2	2.19	0.42
1:A:730:HIS:HD2	3:A:2139:HOH:O	2.03	0.42
1:A:348:PHE:CE2	1:A:453:LEU:HD23	2.54	0.41
1:A:637:ALA:HB1	1:A:644:GLY:HA2	2.02	0.41
1:A:693:LYS:HE2	1:A:780:ASN:HD21	1.85	0.41
1:A:139:PHE:CE2	1:A:666:LEU:HB3	2.54	0.41
1:A:209:THR:HB	1:A:257:CYS:HB3	2.02	0.41
1:A:386:ARG:HG3	1:A:387:MET:CE	2.51	0.41
1:A:610:GLN:HG2	1:A:796:LEU:HD13	2.02	0.41
1:A:713:GLU:O	1:A:717:MET:HG3	2.20	0.41
1:A:291:ASN:ND2	1:A:676:THR:H	2.19	0.41
1:A:191:LEU:O	1:A:271:THR:HG23	2.21	0.41
1:A:329:GLU:HG2	1:A:472:VAL:HG22	2.03	0.41
1:A:330:GLY:HA2	1:A:470:ALA:O	2.20	0.41
1:A:702:SER:O	1:A:706:THR:HG22	2.21	0.41
1:A:191:LEU:O	1:A:272:PRO:HD2	2.21	0.40
1:A:324:SER:HB3	1:A:376:GLU:HG3	2.03	0.40
1:A:700:LYS:HG2	1:A:757:LYS:HD2	2.04	0.40
1:A:154:ARG:HD2	1:A:165:TYR:CZ	2.56	0.40
1:A:638:LEU:HA	1:A:638:LEU:HD23	1.99	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	800/940 (85%)	775 (97%)	23 (3%)	2 (0%)	41 31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	365	VAL
1	A	913	GLY

### 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 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	728/827 (88%)	697 (96%)	31 (4%)	29 19

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	111	LYS
1	A	188	ARG
1	A	190	LEU
1	A	263	CYS
1	A	291	ASN
1	A	317	TRP
1	A	332	LYS
1	A	340	LYS
1	A	352	GLU
1	A	360	SER
1	A	394	LEU
1	A	415	ASP
1	A	423	LEU
1	A	467	SER
1	A	511	LEU
1	A	517	ARG
1	A	530	LEU
1	A	553	THR
1	A	560	ASP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	631	LYS
1	A	634	LEU
1	A	705	LYS
1	A	726	GLU
1	A	743	GLU
1	A	787	ASP
1	A	795	GLN
1	A	804	GLU
1	A	855	LEU
1	A	898	ASN
1	A	915	PHE
1	A	1004	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	GLN
1	A	126	HIS
1	A	156	GLN
1	A	273	HIS
1	A	278	HIS
1	A	291	ASN
1	A	334	ASN
1	A	344	GLN
1	A	617	GLN
1	A	730	HIS
1	A	780	ASN
1	A	851	ASN
1	A	895	HIS
1	A	898	ASN
1	A	976	HIS

### 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is 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	ZZO	A	1500	-	39,43,43	2.30	4 (10%)	36,64,64	1.89	7 (19%)

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	ZZO	A	1500	-	-	2/12/12/12	0/6/6/6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1500	ZZO	NAU-NAV	-10.98	1.25	1.37
2	A	1500	ZZO	CBE-CAZ	-6.06	1.40	1.49
2	A	1500	ZZO	CAK-NAJ	-3.45	1.41	1.45
2	A	1500	ZZO	CAA-CAG	2.29	1.55	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1500	ZZO	N1-C2-N3	-6.74	118.14	128.68
2	A	1500	ZZO	CBF-CBJ-CBI	-4.12	116.27	120.50
2	A	1500	ZZO	C2-N3-C4	3.62	124.95	118.75
2	A	1500	ZZO	CBE-CBD-CBH	-2.75	117.25	119.59
2	A	1500	ZZO	CBD-CBE-CAZ	-2.40	115.63	120.16

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1500	ZZO	CBF-CBE-CAZ	2.18	124.22	120.65
2	A	1500	ZZO	F-CBH-CBD	2.06	122.72	118.61

There are no chirality outliers.

All (2) torsion outliers are listed below:

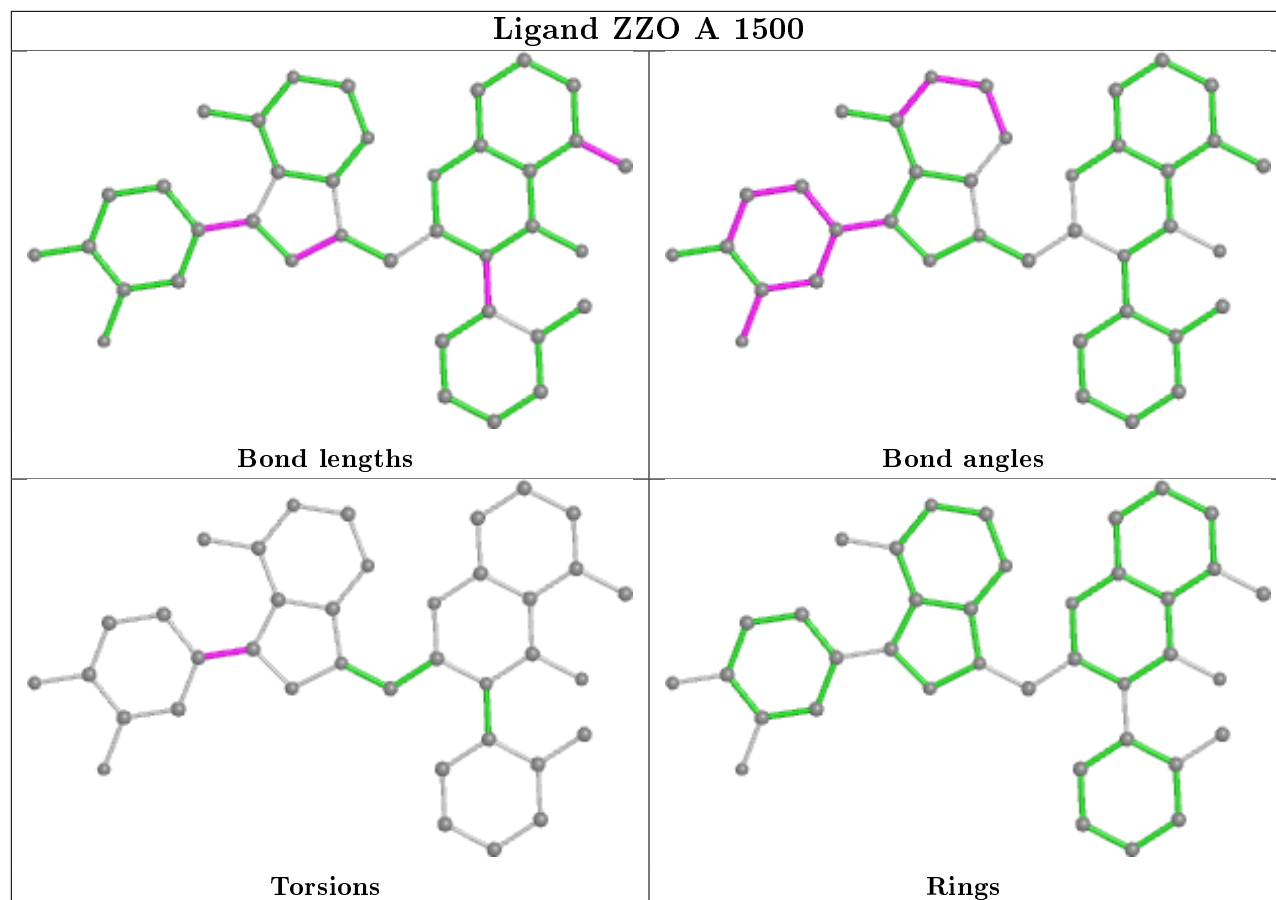
Mol	Chain	Res	Type	Atoms
2	A	1500	ZZO	NAU-CAZ-CBE-CBD
2	A	1500	ZZO	NAU-CAZ-CBE-CBF

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1500	ZZO	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 [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

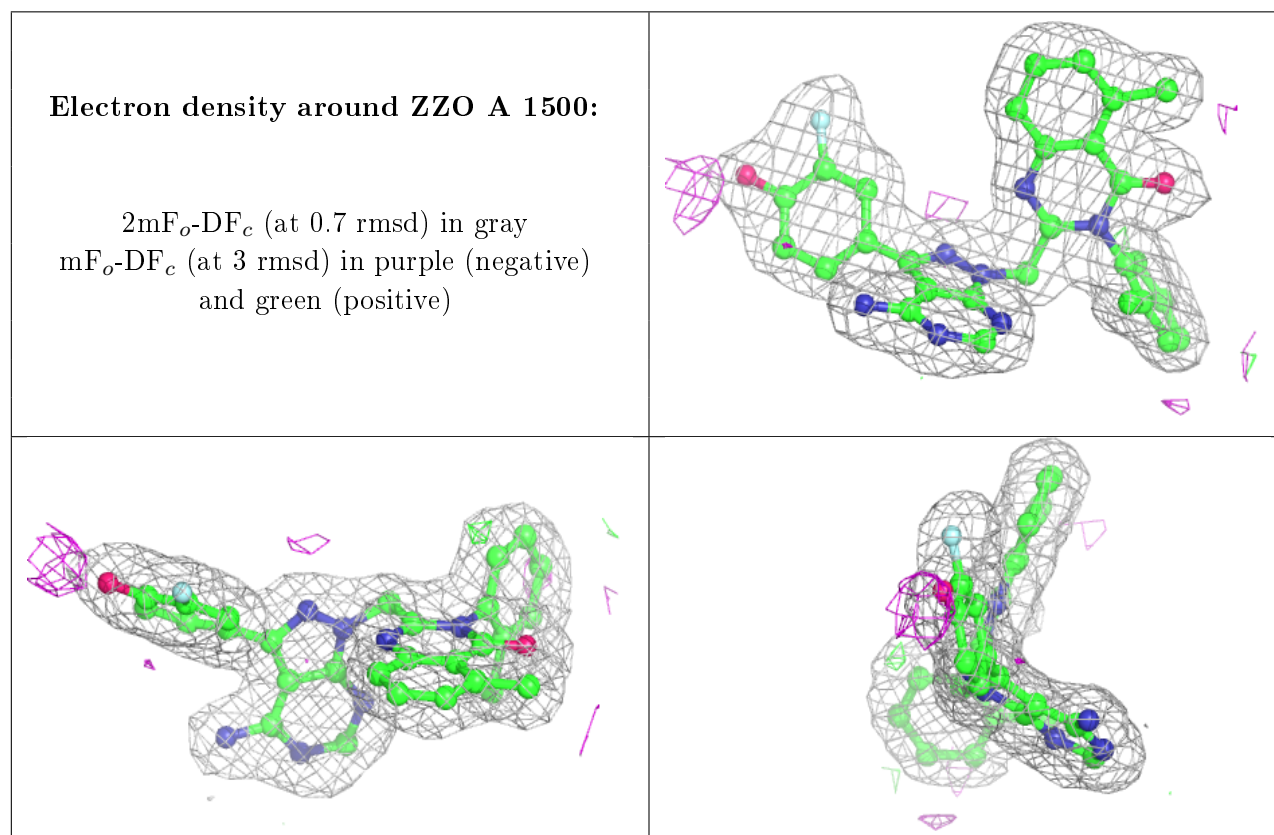
### 6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.