



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 11:09 pm BST

PDB ID : 3PDC  
Title : Crystal structure of hydrolase domain of human soluble epoxide hydrolase complexed with a benzoxazole inhibitor  
Authors : Kurumbail, R.G.; Williams, J.M.  
Deposited on : 2010-10-22  
Resolution : 2.60 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.

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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	:	2.11
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

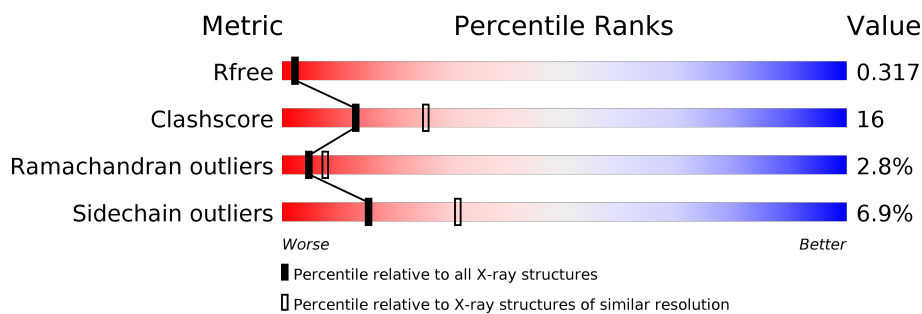
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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	344	
1	B	344	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5425 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 Epoxide hydrolase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	0	0	0
			2598	1668	437	470	23			
1	B	323	Total	C	N	O	S	0	0	0
			2598	1668	437	470	23			

There are 42 discrepancies between the modelled and reference sequences:

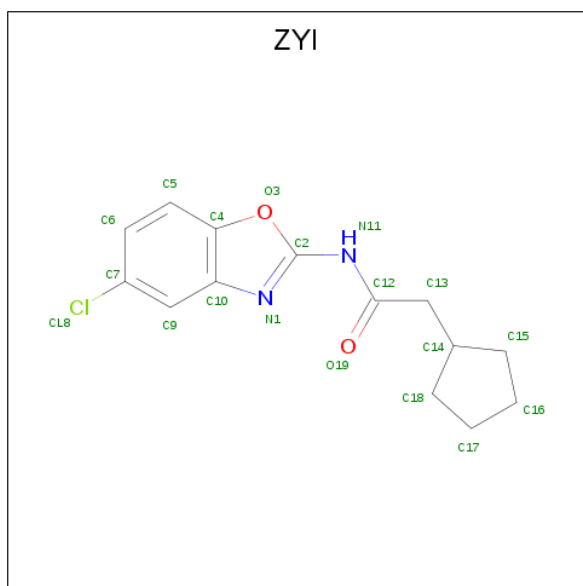
Chain	Residue	Modelled	Actual	Comment	Reference
A	203	MET	-	EXPRESSION TAG	UNP P34913
A	204	GLY	-	EXPRESSION TAG	UNP P34913
A	205	SER	-	EXPRESSION TAG	UNP P34913
A	206	SER	-	EXPRESSION TAG	UNP P34913
A	207	HIS	-	EXPRESSION TAG	UNP P34913
A	208	HIS	-	EXPRESSION TAG	UNP P34913
A	209	HIS	-	EXPRESSION TAG	UNP P34913
A	210	HIS	-	EXPRESSION TAG	UNP P34913
A	211	HIS	-	EXPRESSION TAG	UNP P34913
A	212	HIS	-	EXPRESSION TAG	UNP P34913
A	213	SER	-	EXPRESSION TAG	UNP P34913
A	214	SER	-	EXPRESSION TAG	UNP P34913
A	215	GLY	-	EXPRESSION TAG	UNP P34913
A	216	LEU	-	EXPRESSION TAG	UNP P34913
A	217	VAL	-	EXPRESSION TAG	UNP P34913
A	218	PRO	-	EXPRESSION TAG	UNP P34913
A	219	ARG	-	EXPRESSION TAG	UNP P34913
A	220	GLY	-	EXPRESSION TAG	UNP P34913
A	221	SER	-	EXPRESSION TAG	UNP P34913
A	222	HIS	-	EXPRESSION TAG	UNP P34913
A	223	MET	-	EXPRESSION TAG	UNP P34913
B	203	MET	-	EXPRESSION TAG	UNP P34913
B	204	GLY	-	EXPRESSION TAG	UNP P34913
B	205	SER	-	EXPRESSION TAG	UNP P34913
B	206	SER	-	EXPRESSION TAG	UNP P34913

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Chain	Residue	Modelled	Actual	Comment	Reference
B	207	HIS	-	EXPRESSION TAG	UNP P34913
B	208	HIS	-	EXPRESSION TAG	UNP P34913
B	209	HIS	-	EXPRESSION TAG	UNP P34913
B	210	HIS	-	EXPRESSION TAG	UNP P34913
B	211	HIS	-	EXPRESSION TAG	UNP P34913
B	212	HIS	-	EXPRESSION TAG	UNP P34913
B	213	SER	-	EXPRESSION TAG	UNP P34913
B	214	SER	-	EXPRESSION TAG	UNP P34913
B	215	GLY	-	EXPRESSION TAG	UNP P34913
B	216	LEU	-	EXPRESSION TAG	UNP P34913
B	217	VAL	-	EXPRESSION TAG	UNP P34913
B	218	PRO	-	EXPRESSION TAG	UNP P34913
B	219	ARG	-	EXPRESSION TAG	UNP P34913
B	220	GLY	-	EXPRESSION TAG	UNP P34913
B	221	SER	-	EXPRESSION TAG	UNP P34913
B	222	HIS	-	EXPRESSION TAG	UNP P34913
B	223	MET	-	EXPRESSION TAG	UNP P34913

- Molecule 2 is N-(5-chloro-1,3-benzoxazol-2-yl)-2-cyclopentylacetamide (three-letter code: ZYI) (formula: C<sub>14</sub>H<sub>15</sub>ClN<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			19	14	1	2	2		
2	B	1	Total	C	Cl	N	O	0	0
			19	14	1	2	2		

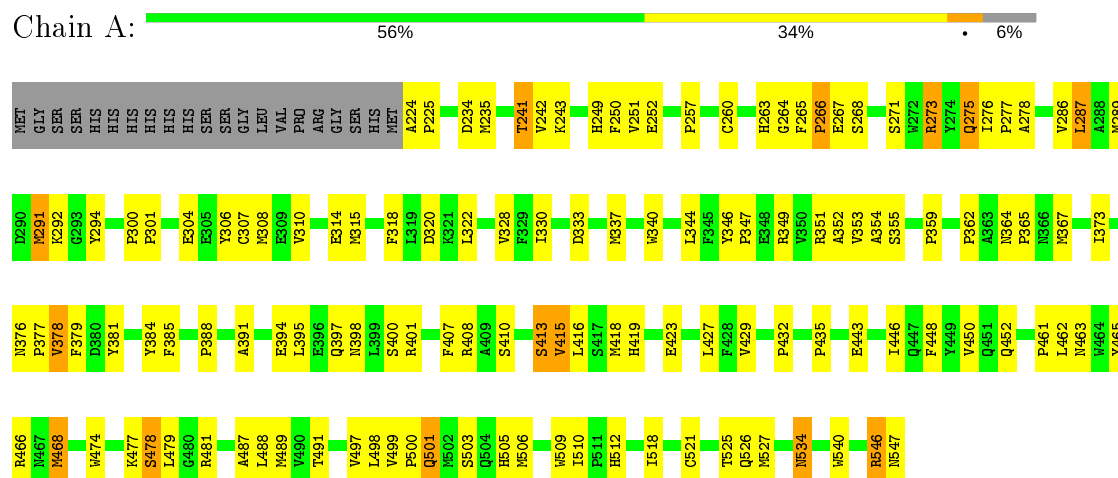
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	93	Total 93	O 93	0	0
3	B	98	Total 98	O 98	0	0

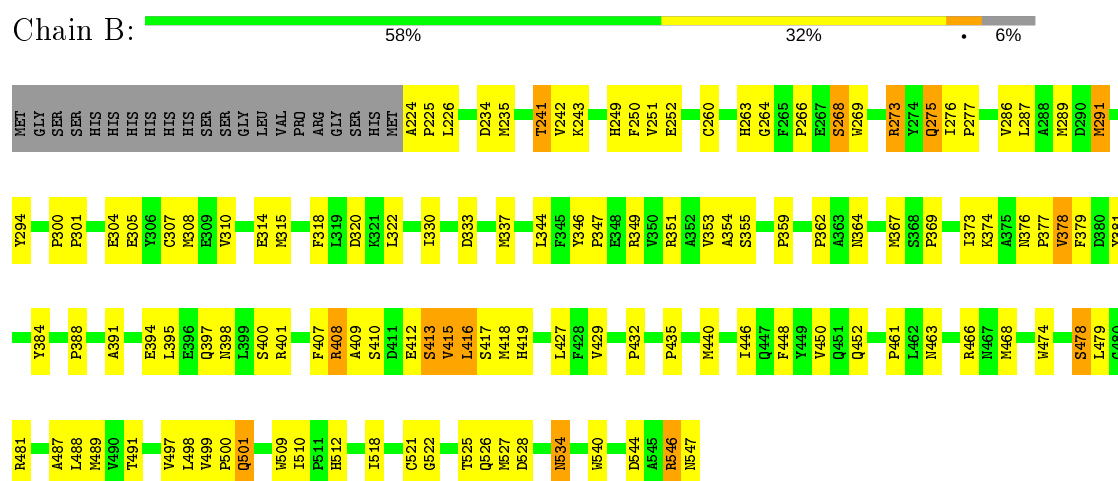
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. 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: Epoxide hydrolase 2



#### • Molecule 1: Epoxide hydrolase 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.52Å 79.90Å 89.32Å 90.00° 90.22° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60 19.85 – 2.60	Depositor EDS
% Data completeness (in resolution range)	90.0 (20.00-2.60) 88.3 (19.85-2.60)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.84 (at 2.59Å)	Xtriage
Refinement program	CNS, X-PLOR	Depositor
R, $R_{free}$	0.279 , 0.333 0.265 , 0.317	Depositor DCC
$R_{free}$ test set	897 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.0	Xtriage
Anisotropy	0.589	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 7.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.399 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	5425	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.38% 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: ZYI

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	0.34	0/2676	0.74	4/3631 (0.1%)
1	B	0.34	0/2676	0.73	4/3631 (0.1%)
All	All	0.34	0/5352	0.73	8/7262 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	408	ARG	NE-CZ-NH2	-14.92	112.84	120.30
1	A	408	ARG	NE-CZ-NH1	14.44	127.52	120.30
1	B	408	ARG	NE-CZ-NH1	-14.40	113.10	120.30
1	B	408	ARG	NE-CZ-NH2	12.93	126.77	120.30
1	A	408	ARG	CD-NE-CZ	7.17	133.64	123.60
1	B	408	ARG	CD-NE-CZ	6.73	133.02	123.60
1	A	488	LEU	CA-CB-CG	6.08	129.29	115.30
1	B	488	LEU	CA-CB-CG	6.05	129.21	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	2598	0	2527	87	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2598	0	2527	82	0
2	A	19	0	15	1	0
2	B	19	0	15	2	0
3	A	93	0	0	13	0
3	B	98	0	0	14	0
All	All	5425	0	5084	169	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 16.

All (169) 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:388:PRO:HA	1:B:466:ARG:NH2	1.90	0.86
1:A:388:PRO:HA	1:A:466:ARG:NH2	1.91	0.84
1:A:432:PRO:HG2	1:A:435:PRO:HG3	1.64	0.80
1:B:264:GLY:HA3	1:B:333:ASP:HB3	1.67	0.77
1:A:264:GLY:HA3	1:A:333:ASP:HB3	1.66	0.76
1:B:376:ASN:ND2	1:B:378:VAL:HG12	2.02	0.74
1:B:432:PRO:HG2	1:B:435:PRO:HG3	1.69	0.74
1:A:376:ASN:ND2	1:A:378:VAL:HG12	2.02	0.74
1:B:276:ILE:HB	1:B:277:PRO:HD3	1.72	0.72
1:B:330:ILE:HG12	1:B:354:ALA:HB3	1.74	0.70
1:A:276:ILE:HB	1:A:277:PRO:HD3	1.72	0.69
1:A:330:ILE:HG12	1:A:354:ALA:HB3	1.73	0.69
1:B:417:SER:HA	3:B:1150:HOH:O	1.92	0.68
1:B:518:ILE:HG22	1:B:521:CYS:HB2	1.76	0.66
1:A:518:ILE:HG22	1:A:521:CYS:HB2	1.78	0.66
1:B:463:ASN:HA	1:B:466:ARG:HD2	1.78	0.64
1:A:463:ASN:HA	1:A:466:ARG:HD2	1.80	0.63
1:A:534:ASN:N	1:A:534:ASN:HD22	1.95	0.63
1:A:364:ASN:HD22	1:A:367:MET:H	1.47	0.63
1:B:534:ASN:N	1:B:534:ASN:HD22	1.96	0.62
1:A:462:LEU:HB3	3:A:1064:HOH:O	1.98	0.62
1:B:364:ASN:HD22	1:B:367:MET:H	1.47	0.62
1:A:241:THR:HG22	1:A:243:LYS:O	2.00	0.61
1:A:362:PRO:HG3	1:A:509:TRP:CE2	2.37	0.60
1:A:446:ILE:O	1:A:450:VAL:HG23	2.02	0.60
1:B:241:THR:HG22	1:B:243:LYS:O	2.00	0.60
1:B:362:PRO:HG3	1:B:509:TRP:CE2	2.36	0.59
1:A:278:ALA:HA	3:A:1163:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:ARG:HH21	1:A:547:ASN:HB2	1.68	0.58
1:A:477:LYS:HE2	3:A:1060:HOH:O	2.04	0.57
1:B:497:VAL:HG13	1:B:498:LEU:HG	1.85	0.57
1:A:497:VAL:HG13	1:A:498:LEU:HG	1.86	0.57
1:A:364:ASN:HA	3:A:1076:HOH:O	2.05	0.57
1:B:351:ARG:HH21	1:B:547:ASN:HB2	1.70	0.56
1:B:481:ARG:HG2	3:B:1026:HOH:O	2.04	0.56
1:B:446:ILE:O	1:B:450:VAL:HG23	2.05	0.56
1:B:418:MET:SD	1:B:427:LEU:HD11	2.46	0.56
1:A:310:VAL:O	1:A:314:GLU:HG3	2.06	0.55
1:B:308:MET:HG3	1:B:474:TRP:HZ3	1.71	0.55
1:A:264:GLY:HA2	3:A:1013:HOH:O	2.06	0.55
1:B:242:VAL:O	1:B:243:LYS:HG3	2.07	0.55
1:B:249:HIS:CG	1:B:250:PHE:N	2.74	0.55
1:B:397:GLN:HG3	3:B:1083:HOH:O	2.06	0.55
1:B:544:ASP:HA	3:B:1157:HOH:O	2.06	0.55
1:A:505:HIS:HB2	3:A:1140:HOH:O	2.07	0.55
1:B:310:VAL:O	1:B:314:GLU:HG3	2.07	0.54
1:B:307:CYS:SG	1:B:310:VAL:HG23	2.48	0.53
1:B:333:ASP:OD2	2:B:2:ZYT:H13A	2.08	0.53
1:A:242:VAL:O	1:A:243:LYS:HG3	2.08	0.53
1:B:394:GLU:HG3	3:B:1154:HOH:O	2.09	0.53
1:A:418:MET:SD	1:A:427:LEU:HD11	2.49	0.53
1:A:308:MET:HG3	1:A:474:TRP:HZ3	1.75	0.52
1:A:249:HIS:CG	1:A:250:PHE:N	2.76	0.52
1:B:359:PRO:HA	1:B:489:MET:SD	2.50	0.51
1:A:423:GLU:HB2	3:A:1152:HOH:O	2.10	0.51
1:A:355:SER:O	1:A:489:MET:HE3	2.10	0.51
1:B:394:GLU:O	1:B:397:GLN:HB3	2.11	0.51
1:A:478:SER:HA	1:A:481:ARG:HH21	1.76	0.50
1:B:499:VAL:HG12	1:B:501:GLN:H	1.76	0.50
1:B:518:ILE:HB	3:B:1030:HOH:O	2.10	0.50
1:B:260:CYS:SG	1:B:289:MET:HG2	2.51	0.50
1:B:347:PRO:HG2	3:B:1018:HOH:O	2.11	0.50
1:A:307:CYS:SG	1:A:310:VAL:HG23	2.51	0.50
1:B:491:THR:HB	1:B:500:PRO:HB3	1.92	0.50
1:A:394:GLU:O	1:A:397:GLN:HB3	2.12	0.50
1:A:359:PRO:HA	1:A:489:MET:SD	2.52	0.49
1:B:273:ARG:NH2	1:B:527:MET:HG2	2.26	0.49
1:A:391:ALA:O	1:A:395:LEU:HD12	2.13	0.49
1:A:235:MET:HE3	1:A:251:VAL:CG1	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:499:VAL:HG12	1:A:501:GLN:H	1.78	0.49
1:B:381:TYR:O	1:B:384:TYR:HB3	2.13	0.49
1:B:376:ASN:ND2	1:B:378:VAL:H	2.11	0.49
1:B:522:GLY:HA3	3:B:1031:HOH:O	2.13	0.49
1:A:491:THR:HB	1:A:500:PRO:HB3	1.95	0.49
1:A:376:ASN:ND2	1:A:378:VAL:H	2.12	0.48
1:A:364:ASN:HD22	1:A:367:MET:N	2.11	0.48
1:A:443:GLU:HB2	3:A:1058:HOH:O	2.13	0.48
1:A:427:LEU:HD21	2:A:1:ZYL:CL8	2.50	0.48
1:B:373:ILE:HG23	1:B:379:PHE:HB3	1.96	0.48
1:A:346:TYR:N	1:A:347:PRO:HD3	2.29	0.48
1:A:273:ARG:NH2	1:A:527:MET:HG2	2.29	0.48
1:B:249:HIS:CD2	1:B:250:PHE:H	2.32	0.48
1:B:355:SER:O	1:B:489:MET:HE3	2.13	0.47
1:B:409:ALA:HB1	3:B:1051:HOH:O	2.13	0.47
1:A:373:ILE:HG23	1:A:379:PHE:HB3	1.95	0.47
1:A:491:THR:HG22	3:A:1038:HOH:O	2.14	0.47
1:B:478:SER:O	1:B:481:ARG:HB2	2.13	0.47
1:A:252:GLU:HA	1:A:286:VAL:O	2.15	0.47
1:A:407:PHE:CD1	1:A:407:PHE:N	2.82	0.47
1:A:381:TYR:O	1:A:384:TYR:HB3	2.14	0.47
1:B:300:PRO:HA	1:B:301:PRO:HD2	1.78	0.47
1:B:346:TYR:N	1:B:347:PRO:HD3	2.29	0.47
1:B:448:PHE:O	1:B:452:GLN:HG2	2.15	0.47
1:B:252:GLU:HA	1:B:286:VAL:O	2.14	0.47
1:A:235:MET:HE3	1:A:251:VAL:HG11	1.97	0.46
1:B:391:ALA:O	1:B:395:LEU:HD12	2.14	0.46
1:B:276:ILE:CB	1:B:277:PRO:HD3	2.44	0.46
1:A:249:HIS:CD2	1:A:250:PHE:H	2.33	0.46
1:A:546:ARG:O	1:A:547:ASN:HB3	2.16	0.46
1:A:260:CYS:SG	1:A:289:MET:HG2	2.56	0.46
1:A:385:PHE:HB3	3:A:1133:HOH:O	2.16	0.46
1:B:305:GLU:HG2	3:B:1066:HOH:O	2.15	0.46
1:B:373:ILE:HB	3:B:1174:HOH:O	2.16	0.46
1:A:365:PRO:HD3	3:A:1076:HOH:O	2.15	0.45
1:B:546:ARG:O	1:B:547:ASN:HB3	2.16	0.45
1:A:478:SER:O	1:A:481:ARG:HB2	2.15	0.45
1:A:353:VAL:O	1:A:487:ALA:HA	2.17	0.45
1:B:364:ASN:HD22	1:B:367:MET:N	2.13	0.45
1:A:413:SER:O	1:A:415:VAL:HG13	2.16	0.45
1:A:304:GLU:CD	1:A:304:GLU:H	2.20	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:374:LYS:HG3	3:B:1174:HOH:O	2.18	0.44
1:A:294:TYR:CE2	1:A:461:PRO:HB3	2.52	0.44
1:B:498:LEU:HD21	2:B:2:ZYT:H13	1.98	0.44
1:B:304:GLU:CD	1:B:304:GLU:H	2.21	0.44
1:B:364:ASN:ND2	1:B:367:MET:H	2.14	0.44
1:A:448:PHE:O	1:A:452:GLN:HG2	2.17	0.44
1:B:353:VAL:O	1:B:487:ALA:HA	2.17	0.44
1:B:407:PHE:N	1:B:407:PHE:CD1	2.82	0.44
1:B:378:VAL:O	1:B:381:TYR:HD2	2.01	0.44
1:A:468:MET:HB2	3:A:1032:HOH:O	2.18	0.43
1:A:364:ASN:ND2	1:A:367:MET:H	2.14	0.43
1:B:294:TYR:CE2	1:B:461:PRO:HB3	2.54	0.43
1:B:487:ALA:HB3	1:B:510:ILE:HG21	2.00	0.43
1:A:292:LYS:HG2	1:A:306:TYR:CE2	2.54	0.43
1:A:378:VAL:O	1:A:381:TYR:HD2	2.01	0.43
1:A:376:ASN:HA	1:A:377:PRO:HD3	1.79	0.43
1:B:235:MET:HE3	1:B:251:VAL:CG1	2.48	0.43
1:B:413:SER:O	1:B:415:VAL:HG13	2.17	0.43
1:B:408:ARG:HD3	1:B:412:GLU:O	2.19	0.43
1:B:330:ILE:HA	1:B:354:ALA:O	2.19	0.43
1:B:376:ASN:HA	1:B:377:PRO:HD3	1.80	0.43
1:A:465:TYR:HB2	3:A:1133:HOH:O	2.18	0.43
1:A:265:PHE:HA	1:A:266:PRO:HA	1.86	0.43
1:A:503:SER:HB2	1:A:506:MET:SD	2.59	0.43
1:A:359:PRO:HB3	1:A:503:SER:HB3	2.02	0.42
1:B:263:HIS:CE1	1:B:291:MET:HB2	2.53	0.42
1:A:263:HIS:CE1	1:A:291:MET:HB2	2.54	0.42
1:B:315:MET:O	1:B:318:PHE:HB3	2.19	0.42
1:B:308:MET:HG3	1:B:474:TRP:CZ3	2.53	0.42
1:A:224:ALA:N	1:A:225:PRO:HD3	2.34	0.42
1:A:499:VAL:HA	1:A:500:PRO:HD3	1.94	0.42
1:A:330:ILE:HA	1:A:354:ALA:O	2.19	0.42
1:A:487:ALA:HB3	1:A:510:ILE:HG21	2.02	0.42
1:B:354:ALA:HB2	1:B:540:TRP:CH2	2.55	0.41
1:B:224:ALA:N	1:B:225:PRO:HD3	2.34	0.41
1:B:226:LEU:HG	3:B:1183:HOH:O	2.19	0.41
1:B:478:SER:HA	1:B:481:ARG:HH21	1.85	0.41
1:B:534:ASN:N	1:B:534:ASN:ND2	2.66	0.41
1:A:354:ALA:HB2	1:A:540:TRP:CH2	2.55	0.41
1:B:275:GLN:NE2	1:B:534:ASN:HD21	2.18	0.41
1:A:398:ASN:HB3	1:A:401:ARG:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:GLU:HB3	1:A:271:SER:OG	2.20	0.41
1:A:250:PHE:CE2	1:A:287:LEU:HD13	2.55	0.41
1:A:376:ASN:HD22	1:A:378:VAL:HG12	1.83	0.41
1:B:416:LEU:HD12	1:B:427:LEU:O	2.21	0.41
1:A:275:GLN:NE2	1:A:534:ASN:HD21	2.19	0.41
1:A:300:PRO:HA	1:A:301:PRO:HD2	1.80	0.41
1:A:340:TRP:CE3	1:A:340:TRP:HA	2.55	0.41
1:B:268:SER:OG	1:B:269:TRP:N	2.52	0.41
1:A:328:VAL:HG13	1:A:352:ALA:O	2.21	0.40
1:A:376:ASN:HD21	1:A:378:VAL:HG12	1.85	0.40
1:A:275:GLN:CD	1:A:275:GLN:H	2.24	0.40
1:A:364:ASN:HA	1:A:365:PRO:HD3	1.93	0.40
1:B:320:ASP:OD1	1:B:349:ARG:NH2	2.55	0.40
1:A:320:ASP:OD1	1:A:349:ARG:NH2	2.54	0.40
1:B:369:PRO:HB2	3:B:1048:HOH:O	2.21	0.40
1:B:440:MET:SD	1:B:528:ASP:HA	2.62	0.40
1:A:315:MET:O	1:A:318:PHE:HB3	2.22	0.40
1:B:398:ASN:HB3	1:B:401:ARG:HB3	2.02	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 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	321/344 (93%)	282 (88%)	30 (9%)	9 (3%)	5	7
1	B	321/344 (93%)	280 (87%)	32 (10%)	9 (3%)	5	7
All	All	642/688 (93%)	562 (88%)	62 (10%)	18 (3%)	5	7

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	291	MET
1	A	413	SER
1	B	291	MET
1	B	413	SER
1	A	273	ARG
1	A	415	VAL
1	A	478	SER
1	A	479	LEU
1	B	273	ARG
1	B	415	VAL
1	B	478	SER
1	B	479	LEU
1	A	525	THR
1	A	546	ARG
1	B	525	THR
1	B	546	ARG
1	B	266	PRO
1	A	266	PRO

### 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	283/301 (94%)	263 (93%)	20 (7%)	14	29
1	B	283/301 (94%)	264 (93%)	19 (7%)	16	33
All	All	566/602 (94%)	527 (93%)	39 (7%)	15	31

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	234	ASP
1	A	241	THR
1	A	257	PRO
1	A	268	SER
1	A	275	GLN
1	A	287	LEU

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Mol	Chain	Res	Type
1	A	322	LEU
1	A	337	MET
1	A	344	LEU
1	A	378	VAL
1	A	400	SER
1	A	410	SER
1	A	416	LEU
1	A	419	HIS
1	A	429	VAL
1	A	468	MET
1	A	501	GLN
1	A	512	HIS
1	A	526	GLN
1	A	534	ASN
1	B	234	ASP
1	B	241	THR
1	B	268	SER
1	B	275	GLN
1	B	287	LEU
1	B	322	LEU
1	B	337	MET
1	B	344	LEU
1	B	378	VAL
1	B	400	SER
1	B	410	SER
1	B	416	LEU
1	B	419	HIS
1	B	429	VAL
1	B	468	MET
1	B	501	GLN
1	B	512	HIS
1	B	526	GLN
1	B	534	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	364	ASN
1	A	376	ASN
1	A	382	GLN
1	A	504	GLN
1	A	534	ASN

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Mol	Chain	Res	Type
1	B	364	ASN
1	B	376	ASN
1	B	382	GLN
1	B	419	HIS
1	B	504	GLN
1	B	534	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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

2 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	ZYI	A	1	-	18,21,21	1.31	4 (22%)	19,29,29	1.33	4 (21%)
2	ZYI	B	2	-	18,21,21	1.29	4 (22%)	19,29,29	1.35	4 (21%)

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	ZYI	A	1	-	-	2/6/15/15	0/3/3/3
2	ZYI	B	2	-	-	0/6/15/15	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	ZYI	C2-N1	-2.45	1.31	1.35
2	B	2	ZYI	C12-N11	2.43	1.41	1.35
2	A	1	ZYI	C5-C6	2.42	1.41	1.36
2	A	1	ZYI	C2-N11	2.32	1.40	1.36
2	B	2	ZYI	C5-C6	2.32	1.41	1.36
2	A	1	ZYI	C9-C7	2.21	1.40	1.36
2	B	2	ZYI	C9-C7	2.10	1.40	1.36
2	A	1	ZYI	C12-N11	2.03	1.40	1.35

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	ZYI	C2-N11-C12	-3.16	121.00	129.54
2	A	1	ZYI	C13-C12-N11	-2.95	110.44	114.50
2	A	1	ZYI	C2-N11-C12	-2.33	123.26	129.54
2	B	2	ZYI	C13-C12-N11	-2.32	111.31	114.50
2	B	2	ZYI	C9-C10-C4	-2.31	118.80	121.12
2	B	2	ZYI	C5-C4-C10	2.25	124.45	120.35
2	A	1	ZYI	C5-C4-C10	2.21	124.37	120.35
2	A	1	ZYI	C9-C10-C4	-2.13	118.97	121.12

There are no chirality outliers.

All (2) torsion outliers are listed below:

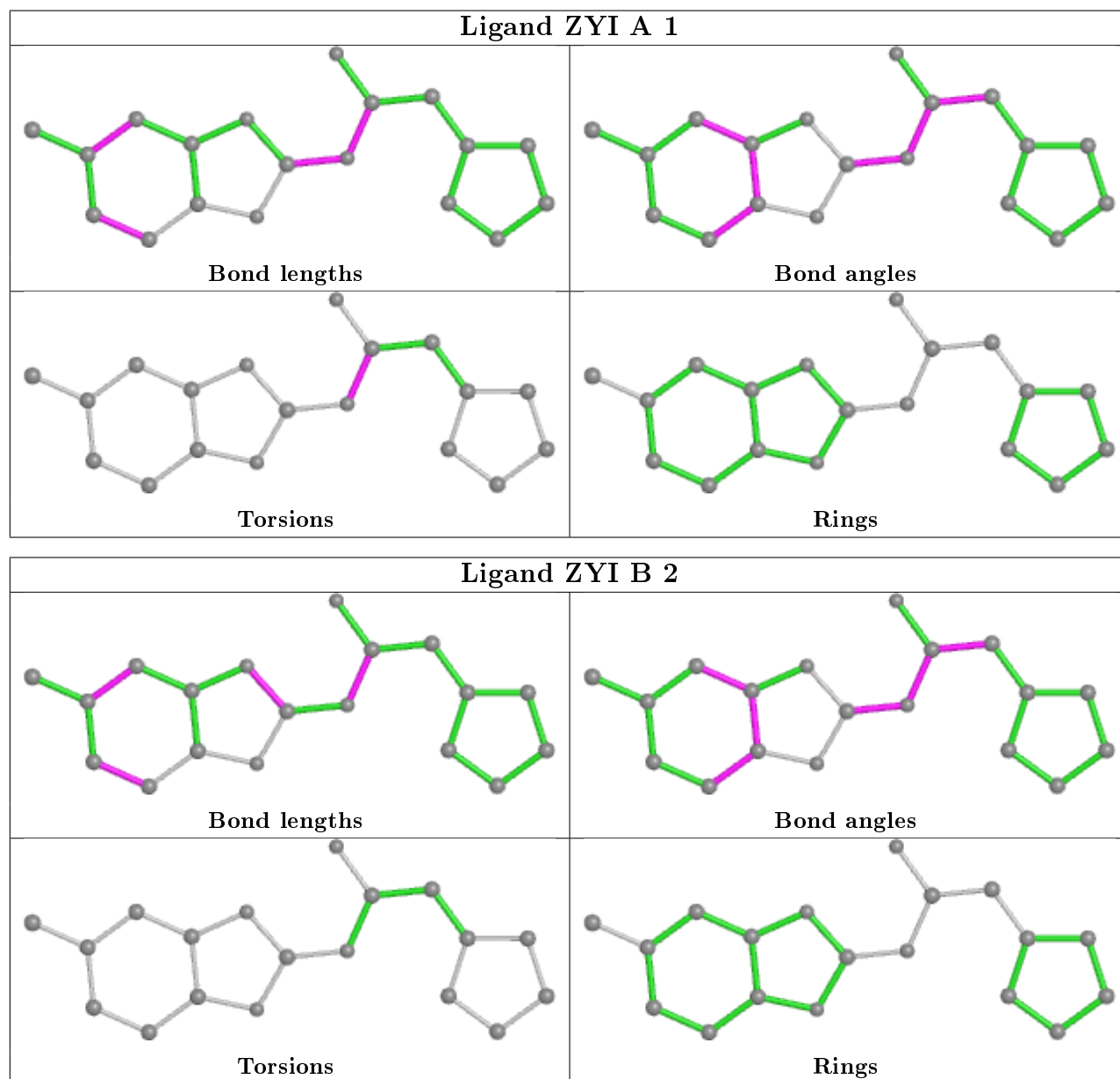
Mol	Chain	Res	Type	Atoms
2	A	1	ZYI	C13-C12-N11-C2
2	A	1	ZYI	O19-C12-N11-C2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	ZYI	1	0
2	B	2	ZYI	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 ⓘ

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

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

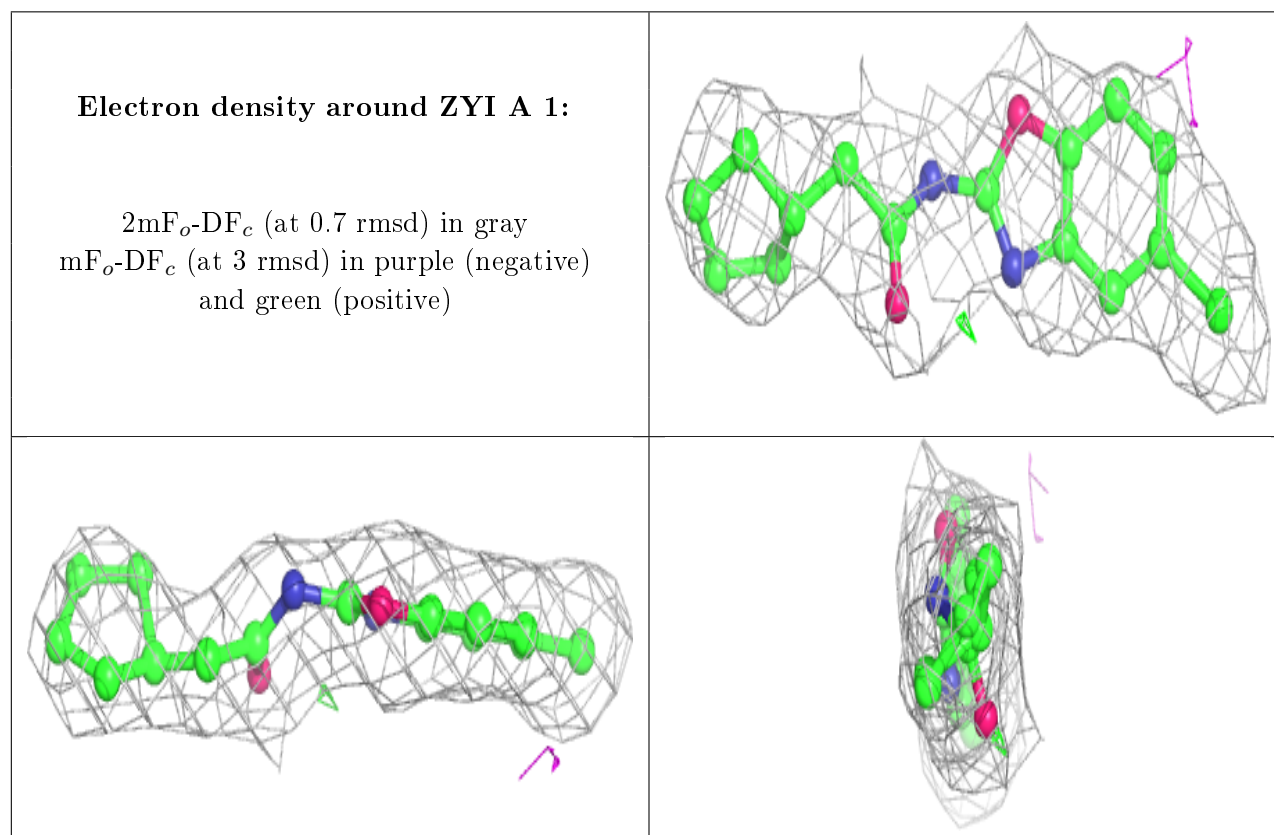
### 6.3 Carbohydrates ⓘ

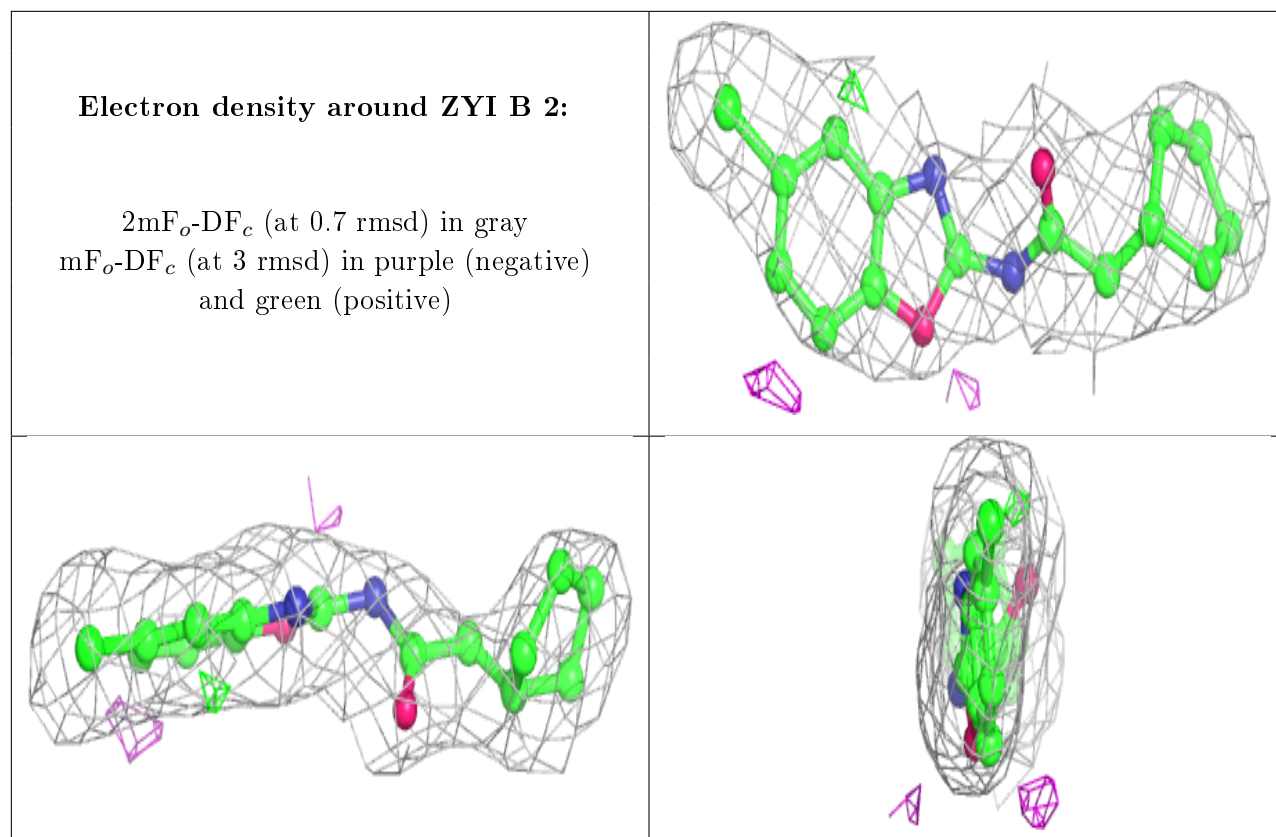
Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands ⓘ

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 [i](#)

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