



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 29, 2020 – 09:22 PM BST

PDB ID : 6AZV  
Title : IDO1/BMS-978587 crystal structure  
Authors : Lewis, H.A.  
Deposited on : 2017-09-13  
Resolution : 2.75 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	:	2.13
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)	:	2.13

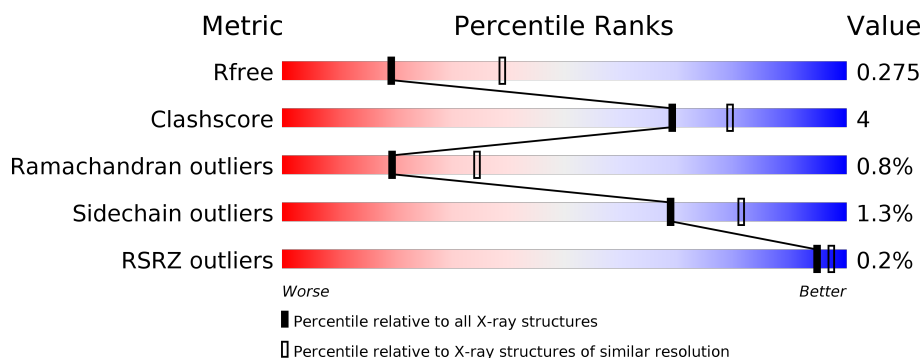
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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  $\leq 5\%$ . 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	402	
1	B	402	
1	C	402	
1	D	402	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22176 atoms, of which 10864 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.

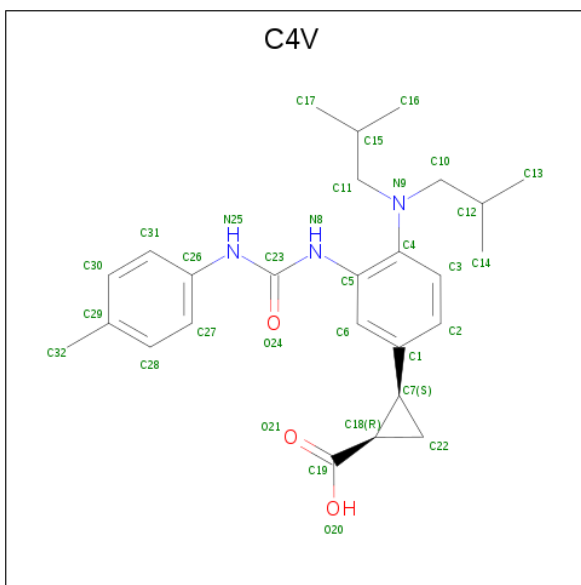
- Molecule 1 is a protein called Indoleamine 2,3-dioxygenase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	367	Total	C	H	N	O	S	0	0	0
			5399	1800	2630	466	486	17			
1	B	367	Total	C	H	N	O	S	0	0	0
			5446	1817	2661	467	484	17			
1	C	362	Total	C	H	N	O	S	0	0	0
			5400	1805	2631	461	487	16			
1	D	366	Total	C	H	N	O	S	0	0	0
			5345	1791	2590	466	481	17			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLY	-	expression tag	UNP P14902
A	3	SER	-	expression tag	UNP P14902
A	4	HIS	-	expression tag	UNP P14902
B	2	GLY	-	expression tag	UNP P14902
B	3	SER	-	expression tag	UNP P14902
B	4	HIS	-	expression tag	UNP P14902
C	2	GLY	-	expression tag	UNP P14902
C	3	SER	-	expression tag	UNP P14902
C	4	HIS	-	expression tag	UNP P14902
D	2	GLY	-	expression tag	UNP P14902
D	3	SER	-	expression tag	UNP P14902
D	4	HIS	-	expression tag	UNP P14902

- Molecule 2 is (1R,2S)-2-(4-[bis(2-methylpropyl)amino]-3-[[4-methylphenyl]carbamoyl]amino)phenyl)cyclopropane-1-carboxylic acid (three-letter code: C4V) (formula: C<sub>26</sub>H<sub>35</sub>N<sub>3</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	0	0
			67	26	35	3	3		
2	B	1	Total	C	H	N	O	0	0
			67	26	35	3	3		
2	C	1	Total	C	H	N	O	0	0
			67	26	35	3	3		
2	D	1	Total	C	H	N	O	0	0
			67	26	35	3	3		


- Molecule 3 is water.

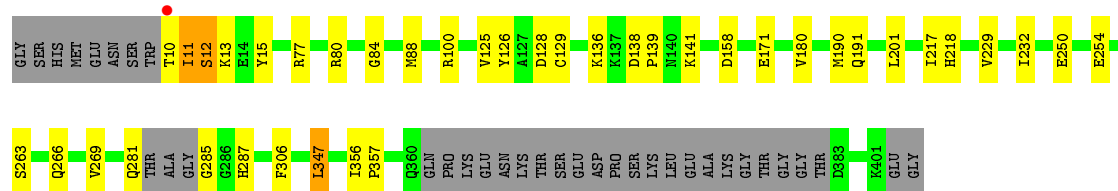
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	44	Total	H	O	0	0
			132	88	44		
3	B	31	Total	H	O	0	0
			93	62	31		
3	C	15	Total	H	O	0	0
			45	30	15		
3	D	16	Total	H	O	0	0
			48	32	16		

### 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.

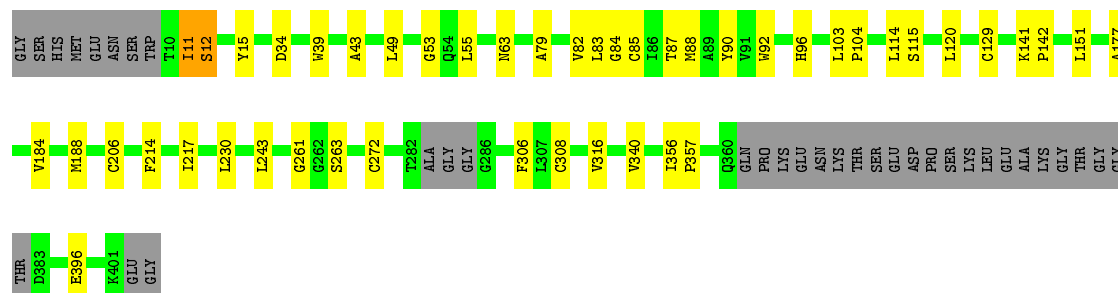
#### • Molecule 1: Indoleamine 2,3-dioxygenase 1

Chain A: 




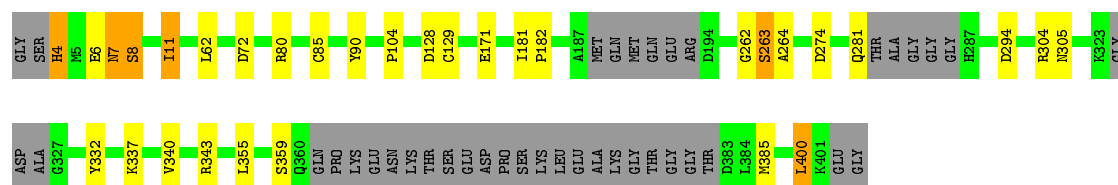
#### • Molecule 1: Indoleamine 2,3-dioxygenase 1

Chain B: 




#### • Molecule 1: Indoleamine 2,3-dioxygenase 1

Chain C: 



#### • Molecule 1: Indoleamine 2,3-dioxygenase 1

Chain D: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	203.39Å 120.87Å 101.53Å 90.00° 119.11° 90.00°	Depositor
Resolution (Å)	45.11 – 2.75 45.11 – 2.75	Depositor EDS
% Data completeness (in resolution range)	98.4 (45.11-2.75) 98.4 (45.11-2.75)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.52 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, $R_{free}$	0.195 , 0.272 0.198 , 0.275	Depositor DCC
$R_{free}$ test set	2771 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	55.0	Xtriage
Anisotropy	0.607	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 43.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.138 for -h-2*k,l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	22176	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: C4V

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	0.78	3/2835 (0.1%)	0.81	3/3858 (0.1%)
1	B	0.74	4/2851 (0.1%)	0.79	1/3879 (0.0%)
1	C	0.72	2/2836 (0.1%)	0.77	3/3861 (0.1%)
1	D	0.68	1/2821 (0.0%)	0.75	0/3842
All	All	0.73	10/11343 (0.1%)	0.78	7/15440 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	129	CYS	CB-SG	-10.05	1.65	1.82
1	C	85	CYS	CB-SG	-8.00	1.68	1.82
1	B	129	CYS	CB-SG	-7.57	1.69	1.82
1	C	129	CYS	CB-SG	-7.22	1.70	1.82
1	A	254	GLU	C-N	6.30	1.48	1.34
1	B	92	TRP	CB-CG	-5.64	1.40	1.50
1	B	85	CYS	CB-SG	-5.64	1.72	1.81
1	B	272	CYS	CB-SG	-5.57	1.72	1.81
1	A	269	VAL	CB-CG1	-5.51	1.41	1.52
1	D	121	PRO	C-N	5.00	1.43	1.34

All (7) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	77	ARG	NE-CZ-NH2	-7.16	116.72	120.30
1	C	304	ARG	NE-CZ-NH1	6.05	123.32	120.30
1	C	62	LEU	CA-CB-CG	5.88	128.83	115.30
1	A	158	ASP	CB-CG-OD1	5.60	123.34	118.30
1	B	243	LEU	CB-CG-CD2	-5.52	101.61	111.00
1	A	347	LEU	CA-CB-CG	5.17	127.19	115.30
1	C	294	ASP	CB-CG-OD1	5.03	122.82	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	12	SER	Peptide

## 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	2769	2630	2626	15	1
1	B	2785	2661	2655	23	0
1	C	2769	2631	2629	17	1
1	D	2755	2590	2588	24	0
2	A	32	35	0	1	0
2	B	32	35	0	0	0
2	C	32	35	0	2	0
2	D	32	35	0	1	0
3	A	44	88	0	2	0
3	B	31	62	0	2	0
3	C	15	30	0	1	0
3	D	16	32	0	0	0
All	All	11312	10864	10498	80	1

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 (80) 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:80:ARG:NH2	1:A:128:ASP:OD2	2.11	0.83
1:A:250:GLU:OE1	3:A:601:HOH:O	2.12	0.68
1:C:80:ARG:NH2	1:C:128:ASP:OD2	2.28	0.67
1:D:21:VAL:HG13	1:D:24:ALA:HB3	1.79	0.63
1:C:181:ILE:HG22	1:C:182:PRO:HD3	1.80	0.62
3:A:637:HOH:O	1:B:308:CYS:HB3	2.01	0.59
1:A:10:THR:O	1:A:11:ILE:CB	2.51	0.58
1:B:63:ASN:ND2	3:B:603:HOH:O	2.37	0.56
1:C:90:TYR:CE2	1:C:104:PRO:HD3	2.41	0.55
1:B:340:VAL:HG11	1:B:396:GLU:HG2	1.89	0.54
1:B:141:LYS:HB3	1:B:142:PRO:HD2	1.90	0.54
1:A:15:TYR:HB3	1:A:306:PHE:HB2	1.90	0.54
1:C:6:GLU:O	1:C:7:ASN:HB2	2.09	0.53
1:C:4:HIS:ND1	1:C:4:HIS:N	2.56	0.52
1:D:174:ALA:O	1:D:177:ALA:N	2.43	0.51
1:D:11:ILE:CB	1:D:182:PRO:HG3	2.40	0.51
1:C:4:HIS:N	1:C:4:HIS:HD1	2.08	0.51
1:A:201:LEU:HD13	1:C:359:SER:OG	2.11	0.51
2:C:501:C4V:N8	2:C:501:C4V:C10	2.74	0.51
1:B:53:GLY:HA3	1:D:71:THR:HB	1.94	0.50
1:D:275:VAL:CG2	1:D:310:LEU:HB3	2.41	0.50
1:B:261:GLY:O	3:B:601:HOH:O	2.18	0.50
1:D:21:VAL:CG1	1:D:24:ALA:HB3	2.43	0.49
1:C:171:GLU:OE2	3:C:601:HOH:O	2.20	0.49
2:D:501:C4V:N8	2:D:501:C4V:C10	2.76	0.49
1:B:90:TYR:CE2	1:B:104:PRO:HD3	2.48	0.49
1:C:343:ARG:HH11	1:C:343:ARG:HG3	1.78	0.49
1:A:84:GLY:O	1:A:88:MET:HG2	2.13	0.48
1:D:188:MET:HE3	1:D:319:PHE:CD2	2.48	0.47
1:B:184:VAL:HG12	1:B:188:MET:HE2	1.96	0.47
1:A:281:GLN:CB	1:A:285:GLY:N	2.77	0.47
1:B:188:MET:HE2	1:B:316:VAL:HG22	1.96	0.47
1:A:229:VAL:O	1:A:232:ILE:HG12	2.16	0.46
1:C:262:GLY:O	1:C:263:SER:CB	2.62	0.46
1:D:126:TYR:OH	1:D:171:GLU:OE1	2.26	0.46
1:C:355:LEU:HD11	1:C:385:MET:HG3	1.97	0.46
1:C:332:TYR:CD1	1:C:400:LEU:CD2	2.99	0.46
1:A:136:LYS:HD3	1:A:139:PRO:HA	1.98	0.46
1:B:39:TRP:CD2	1:B:83:LEU:HD21	2.51	0.46
1:B:177:ALA:HB2	1:B:206:CYS:HB2	1.98	0.45
1:B:356:ILE:N	1:B:357:PRO:CD	2.80	0.45
1:A:138:ASP:OD2	1:A:141:LYS:HG3	2.16	0.45

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:MET:CE	1:B:316:VAL:HG22	2.47	0.45
1:B:84:GLY:O	1:B:88:MET:HG2	2.16	0.45
1:D:12:SER:O	1:D:14:GLU:N	2.49	0.45
1:D:105:ARG:HG2	1:D:250:GLU:HG2	1.98	0.45
1:A:356:ILE:HB	1:A:357:PRO:HD3	1.99	0.45
1:C:264:ALA:N	2:C:501:C4V:O21	2.45	0.44
1:D:133:ASN:OD1	1:D:151:LEU:HB2	2.16	0.44
1:B:15:TYR:HB3	1:B:306:PHE:HB2	1.99	0.44
1:B:214:PHE:O	1:B:217:ILE:HG22	2.17	0.44
1:D:80:ARG:HH21	1:D:125:VAL:HG22	1.83	0.44
1:D:275:VAL:HG22	1:D:310:LEU:HD13	1.98	0.44
1:D:325:ASP:O	1:D:329:ARG:HG3	2.17	0.44
1:B:356:ILE:HB	1:B:357:PRO:HD3	2.00	0.43
1:A:126:TYR:HB3	1:A:266:GLN:HB3	2.01	0.43
1:C:11:ILE:HD12	1:C:182:PRO:HG3	2.00	0.43
1:D:337:LYS:O	1:D:340:VAL:HG22	2.19	0.43
1:C:274:ASP:OD2	1:C:281:GLN:NE2	2.52	0.43
1:D:24:ALA:HA	1:D:131:LEU:HB3	2.01	0.43
2:A:501:C4V:N8	2:A:501:C4V:C10	2.81	0.43
1:B:87:THR:HG23	1:B:103:LEU:HD13	2.00	0.43
1:D:181:ILE:O	1:D:181:ILE:HG12	2.19	0.43
1:D:181:ILE:HD13	1:D:181:ILE:C	2.40	0.43
1:A:190:MET:O	1:A:191:GLN:C	2.57	0.42
1:C:337:LYS:O	1:C:340:VAL:HG22	2.19	0.42
1:D:196:LEU:O	1:D:200:LEU:HD13	2.19	0.42
1:B:79:ALA:HB3	1:B:114:LEU:HD21	2.02	0.42
1:D:78:LEU:O	1:D:82:VAL:HG23	2.20	0.42
1:B:115:SER:HB3	1:B:120:LEU:O	2.19	0.42
1:D:28:PRO:HD3	1:D:134:TRP:CZ2	2.54	0.42
1:B:11:ILE:O	1:B:12:SER:CB	2.67	0.41
1:B:49:LEU:HB3	1:B:55:LEU:HB2	2.02	0.41
1:D:146:GLU:CD	1:D:146:GLU:N	2.74	0.41
1:A:217:ILE:HG23	1:A:218:HIS:N	2.35	0.41
1:D:79:ALA:HB3	1:D:114:LEU:HD21	2.03	0.41
1:C:7:ASN:O	1:C:8:SER:CB	2.69	0.41
1:B:43:ALA:HB2	1:B:82:VAL:HG13	2.03	0.41
1:A:180:VAL:HG12	1:A:180:VAL:O	2.21	0.41
1:D:356:ILE:HB	1:D:357:PRO:HD3	2.02	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ARG:NH2	1:C:72:ASP:OD1[1_554]	2.18	0.02

## 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	361/402 (90%)	344 (95%)	12 (3%)	5 (1%)	11	19
1	B	361/402 (90%)	348 (96%)	10 (3%)	3 (1%)	19	34
1	C	352/402 (88%)	335 (95%)	14 (4%)	3 (1%)	17	31
1	D	360/402 (90%)	342 (95%)	17 (5%)	1 (0%)	41	60
All	All	1434/1608 (89%)	1369 (96%)	53 (4%)	12 (1%)	19	34

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	ILE
1	A	287	HIS
1	B	11	ILE
1	C	7	ASN
1	C	8	SER
1	A	12	SER
1	A	13	LYS
1	C	263	SER
1	A	263	SER
1	B	12	SER
1	B	263	SER
1	D	11	ILE

### 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	265/348 (76%)	262 (99%)	3 (1%)	73	84
1	B	266/348 (76%)	262 (98%)	4 (2%)	65	78
1	C	271/348 (78%)	267 (98%)	4 (2%)	65	78
1	D	261/348 (75%)	258 (99%)	3 (1%)	73	84
All	All	1063/1392 (76%)	1049 (99%)	14 (1%)	69	81

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	125	VAL
1	A	171	GLU
1	A	347	LEU
1	B	34	ASP
1	B	96	HIS
1	B	151	LEU
1	B	230	LEU
1	C	4	HIS
1	C	11	ILE
1	C	305	ASN
1	C	400	LEU
1	D	181	ILE
1	D	255	ASP
1	D	355	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	303	HIS
1	B	113	GLN
1	B	220	HIS
1	C	305	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](#)

4 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	C4V	C	501	-	30,34,34	0.28	0	43,48,48	0.68	2 (4%)
2	C4V	D	501	-	30,34,34	0.43	0	43,48,48	0.79	1 (2%)
2	C4V	A	501	-	30,34,34	0.37	0	43,48,48	0.61	0
2	C4V	B	501	-	30,34,34	0.31	0	43,48,48	0.74	1 (2%)

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	C4V	C	501	-	-	11/24/33/33	0/3/3/3
2	C4V	D	501	-	-	11/24/33/33	0/3/3/3
2	C4V	A	501	-	-	11/24/33/33	0/3/3/3
2	C4V	B	501	-	-	8/24/33/33	0/3/3/3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	C4V	C10-N9-C11	2.77	123.12	117.23
2	C	501	C4V	C15-C11-N9	2.62	117.17	114.13
2	C	501	C4V	C10-N9-C11	2.39	122.31	117.23
2	B	501	C4V	C15-C11-N9	2.26	116.75	114.13

There are no chirality outliers.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	501	C4V	C15-C11-N9-C4
2	C	501	C4V	C15-C11-N9-C10
2	D	501	C4V	C15-C11-N9-C4
2	D	501	C4V	C15-C11-N9-C10
2	D	501	C4V	C5-C4-N9-C11
2	A	501	C4V	C15-C11-N9-C4
2	A	501	C4V	C15-C11-N9-C10
2	B	501	C4V	C15-C11-N9-C4
2	A	501	C4V	N9-C10-C12-C13
2	C	501	C4V	N9-C11-C15-C17
2	C	501	C4V	N9-C10-C12-C13
2	D	501	C4V	N9-C11-C15-C17
2	D	501	C4V	N9-C10-C12-C13
2	A	501	C4V	N9-C11-C15-C17
2	C	501	C4V	N9-C11-C15-C16
2	B	501	C4V	N9-C11-C15-C16
2	B	501	C4V	C15-C11-N9-C10
2	D	501	C4V	C31-C26-N25-C23
2	D	501	C4V	C27-C26-N25-C23
2	D	501	C4V	N9-C11-C15-C16
2	A	501	C4V	C31-C26-N25-C23
2	A	501	C4V	N9-C11-C15-C16
2	B	501	C4V	N9-C11-C15-C17
2	C	501	C4V	C5-C4-N9-C11
2	C	501	C4V	C31-C26-N25-C23
2	A	501	C4V	C27-C26-N25-C23
2	D	501	C4V	N9-C10-C12-C14
2	A	501	C4V	C5-C4-N9-C11
2	B	501	C4V	C5-C4-N9-C10
2	D	501	C4V	C3-C4-N9-C11
2	C	501	C4V	C27-C26-N25-C23
2	C	501	C4V	C12-C10-N9-C4
2	D	501	C4V	C12-C10-N9-C4
2	A	501	C4V	C12-C10-N9-C4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	B	501	C4V	C31-C26-N25-C23
2	A	501	C4V	N9-C10-C12-C14
2	C	501	C4V	N9-C10-C12-C14
2	C	501	C4V	C3-C4-N9-C11
2	B	501	C4V	C27-C26-N25-C23
2	A	501	C4V	C3-C4-N9-C11
2	B	501	C4V	C3-C4-N9-C10

There are no ring outliers.

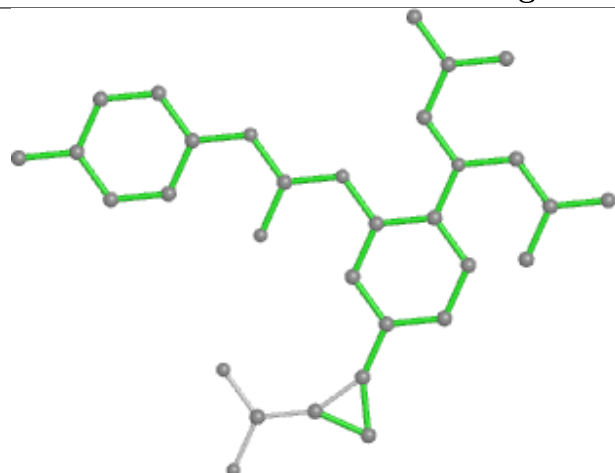
3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	C4V	2	0
2	D	501	C4V	1	0
2	A	501	C4V	1	0

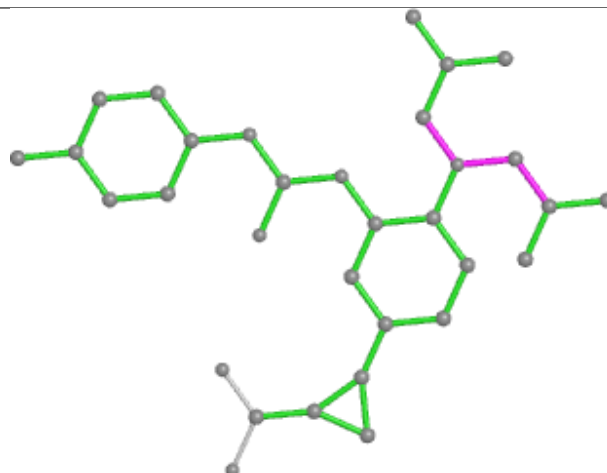
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



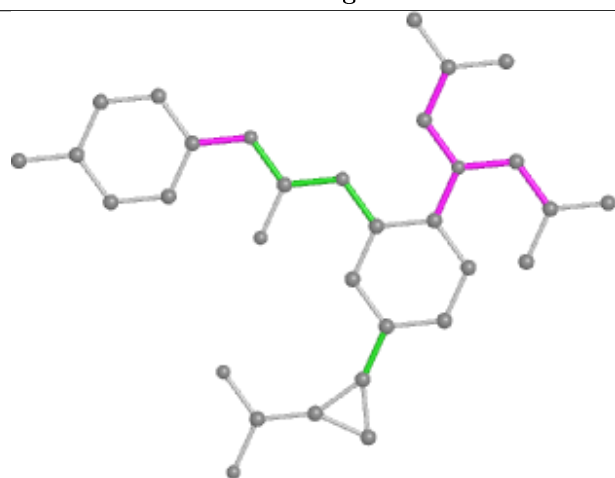
## Ligand C4V C 501



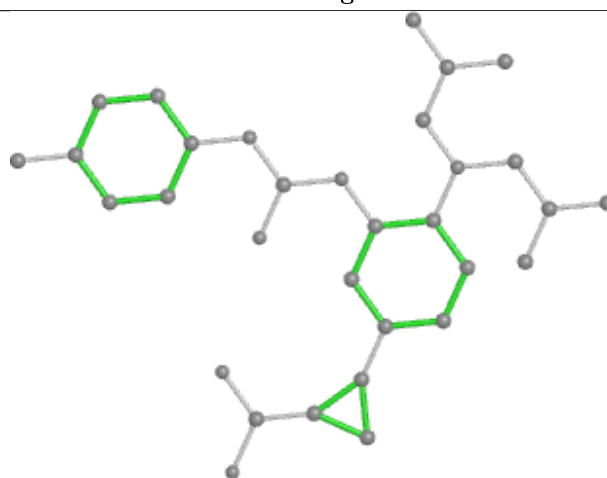
Bond lengths



Bond angles

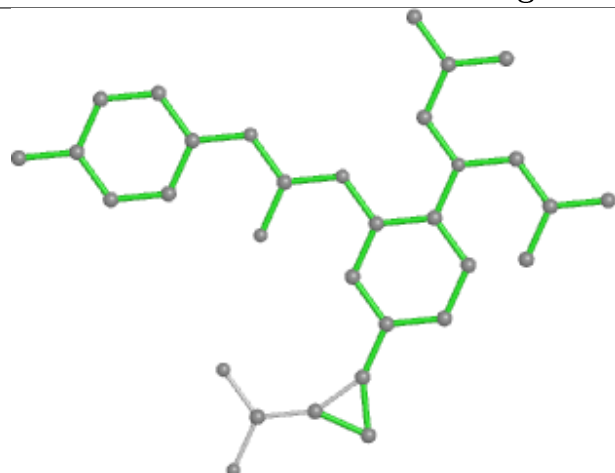


Torsions

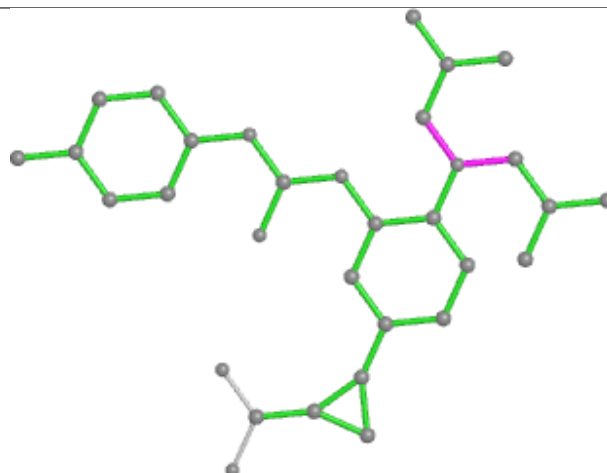


Rings

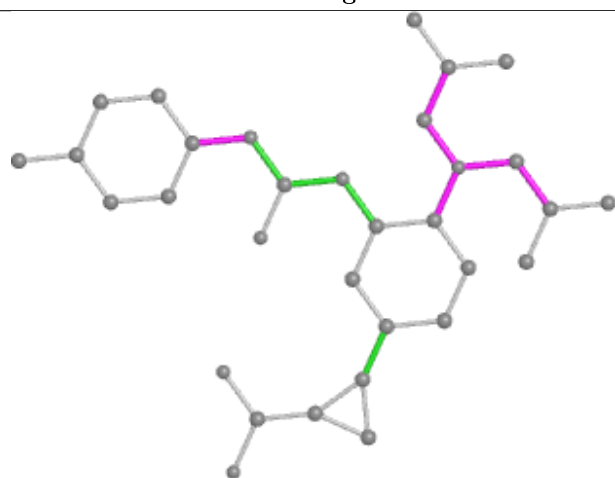
## Ligand C4V D 501



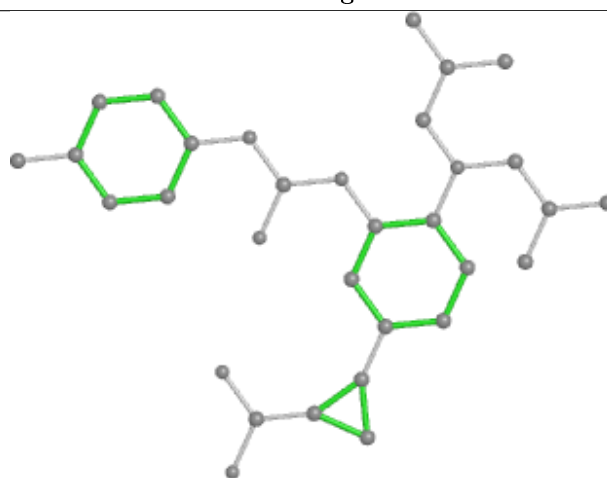
Bond lengths



Bond angles

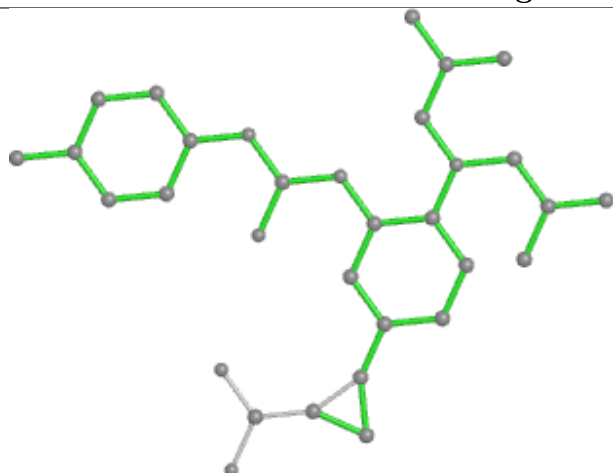


Torsions

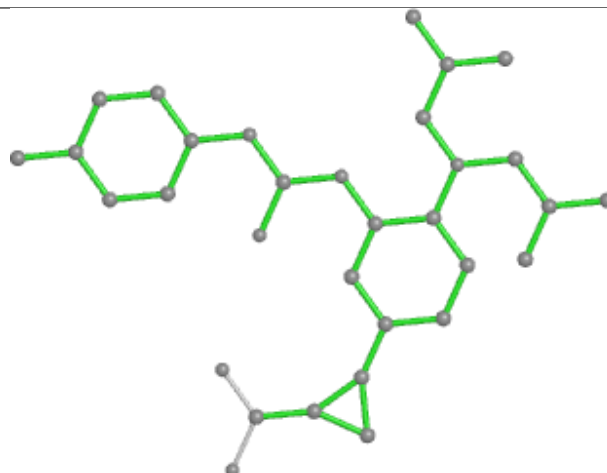


Rings

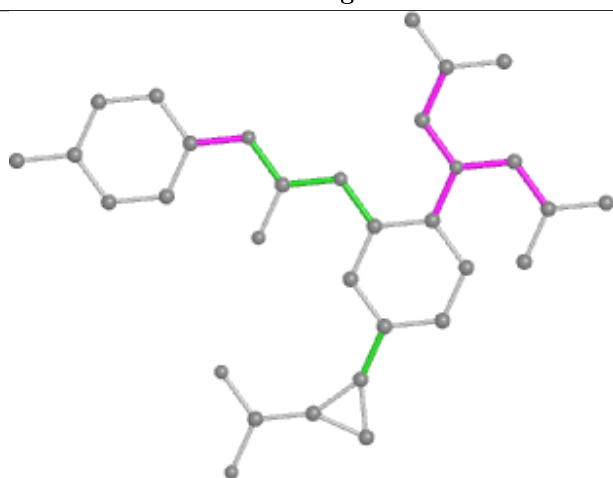
## Ligand C4V A 501



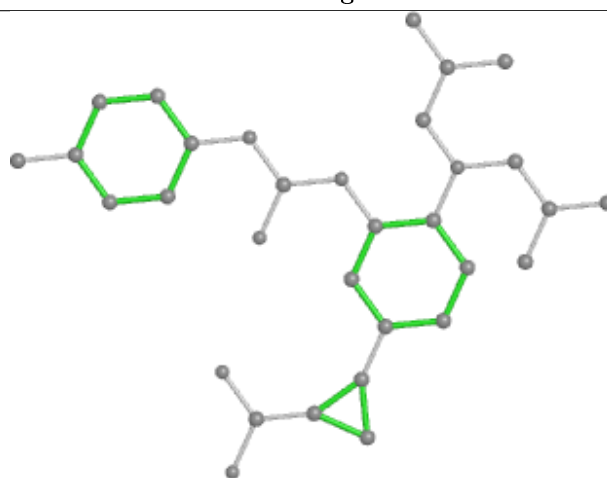
Bond lengths



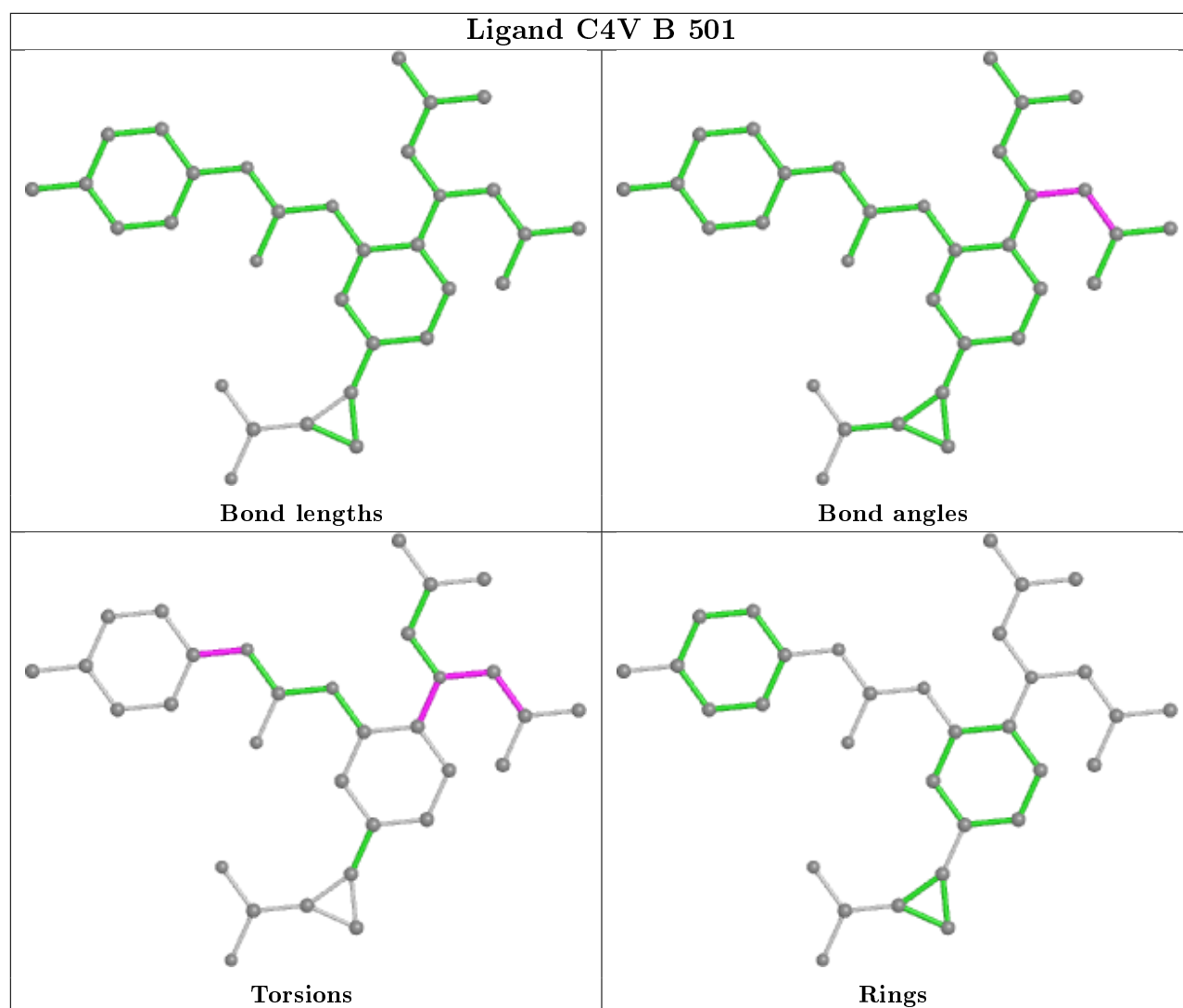
Bond angles



Torsions



Rings



## 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	367/402 (91%)	-0.14	1 (0%) 94 96	34, 57, 92, 179	0
1	B	367/402 (91%)	-0.17	0 100 100	32, 59, 92, 123	0
1	C	362/402 (90%)	-0.15	0 100 100	32, 60, 93, 124	0
1	D	366/402 (91%)	-0.13	2 (0%) 91 94	38, 62, 92, 138	0
All	All	1462/1608 (90%)	-0.15	3 (0%) 95 97	32, 59, 93, 179	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	11	ILE	2.2
1	A	10	THR	2.1
1	D	349	ILE	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](#)

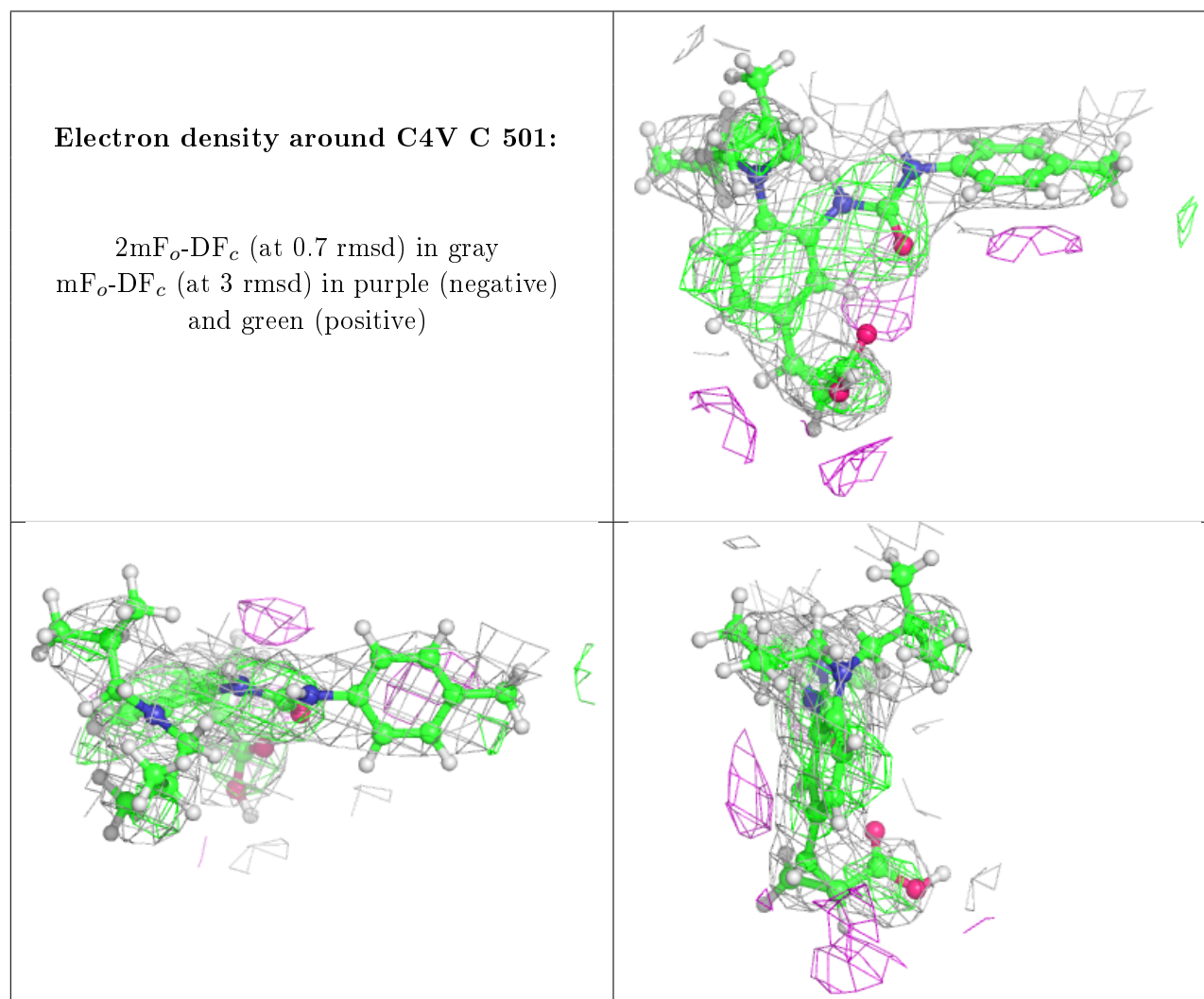
There are no monosaccharides in this entry.

### 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.

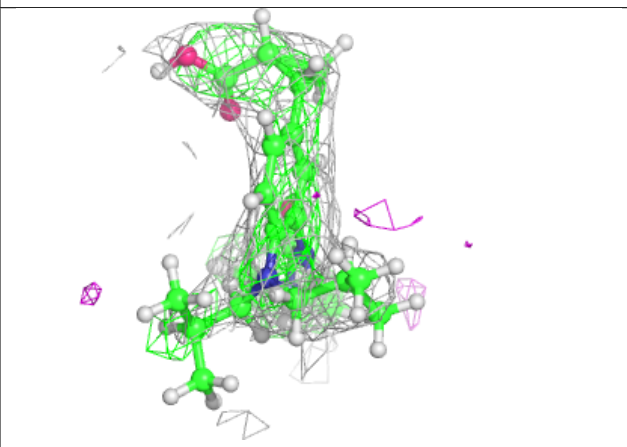
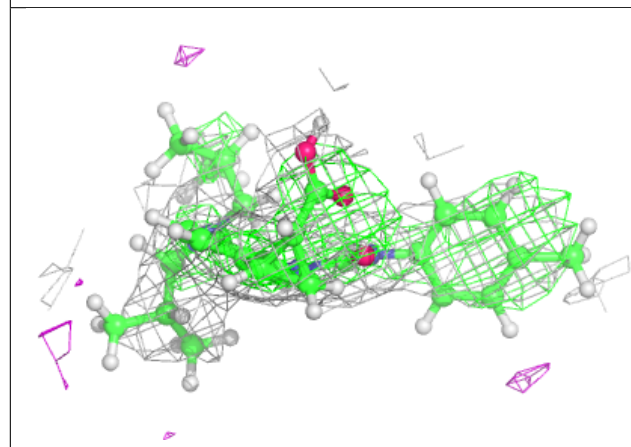
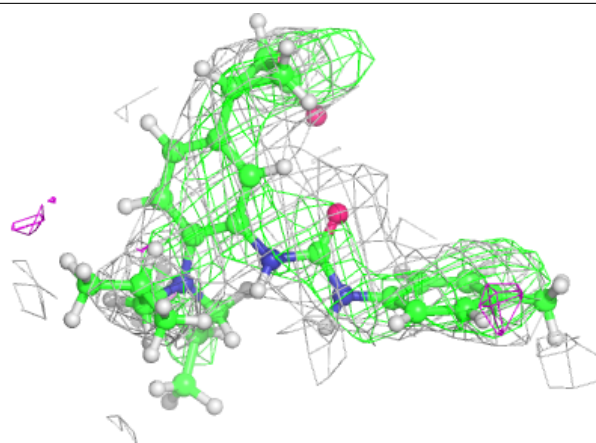
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	C4V	C	501	32/32	0.84	0.32	79,132,264,363	0
2	C4V	D	501	32/32	0.86	0.38	108,195,361,434	0
2	C4V	B	501	32/32	0.90	0.31	57,112,183,208	0
2	C4V	A	501	32/32	0.94	0.29	43,116,182,242	0

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.



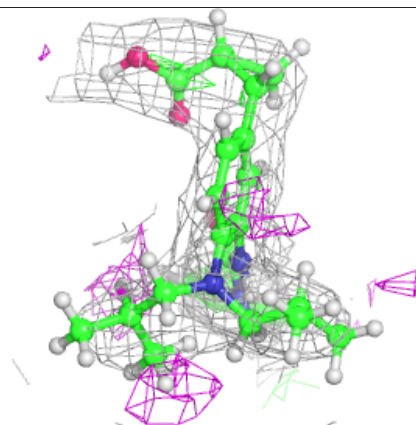
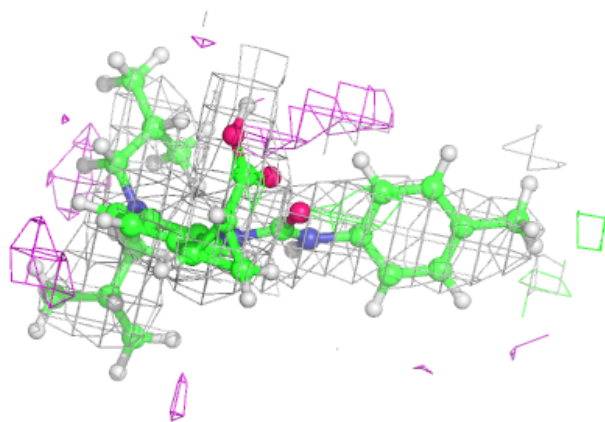
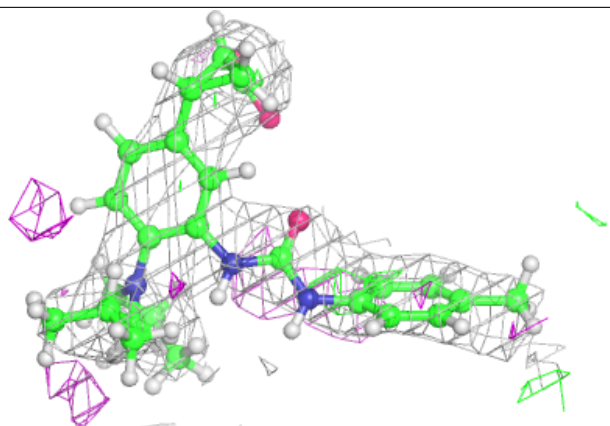
**Electron density around C4V D 501:**

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



**Electron density around C4V B 501:**

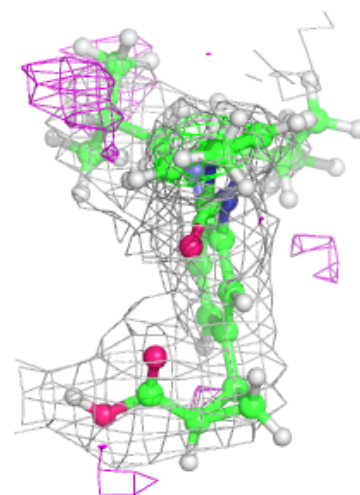
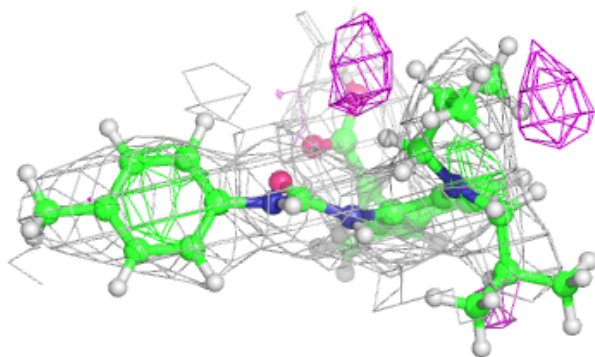
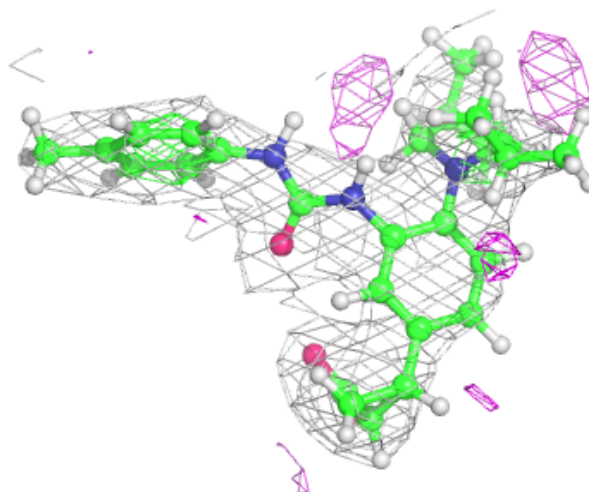
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around C4V A 501:**

$2mF_o-DF_c$  (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.