



# Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 10:40 pm BST

PDB ID : 2V5X  
Title : Crystal structure of HDAC8-inhibitor complex  
Authors : Di Marco, S.; Vannini, A.; Volpari, C.; Gallinari, P.; Jones, P.; Mattu, M.; Carfi, A.; Defrancesco, R.; Steinkuhler, C.  
Deposited on : 2007-07-10  
Resolution : 2.25 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

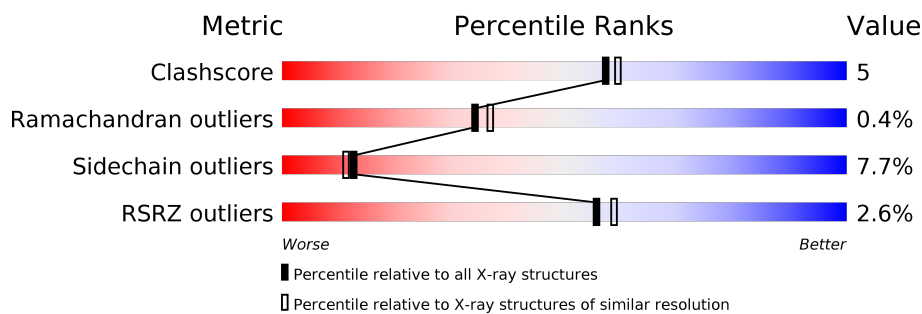
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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))
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	388	 3% 78% 13% • 6%
1	B	388	 2% 78% 11% • 8%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6038 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 HISTONE DEACETYLASE 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	1	0
			2837	1817	472	529	19			
1	B	356	Total	C	N	O	S	0	1	0
			2782	1787	462	513	20			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	ASP	SER	engineered mutation	UNP Q9BY41
B	39	ASP	SER	engineered mutation	UNP Q9BY41

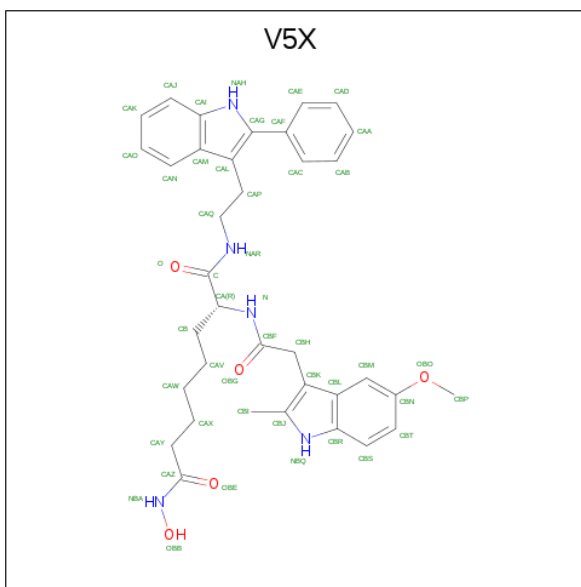
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	K	0	0
			2	2		
3	A	2	Total	K	0	0
			2	2		

- Molecule 4 is (2R)-N 8 -HYDROXY-2-([(5-METHOXY-2-METHYL-1H-INDOL-3-YL) ACETYL]AMINO)-N 1 -[2-(2-PHENYL-1H-INDOL-3-YL)ETHYL]OCTANEDIAMIDE (three-letter code: V5X) (formula: C<sub>36</sub>H<sub>41</sub>N<sub>5</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 46	C 36	N 5	O 5	0	0
4	B	1	Total 46	C 36	N 5	O 5	0	0

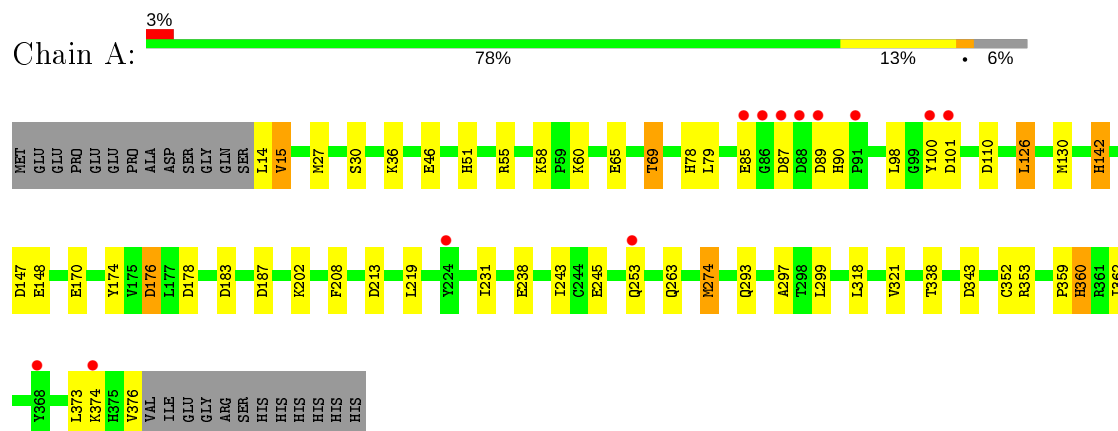
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	153	Total O 153 153	0	0
5	B	168	Total O 168 168	0	0

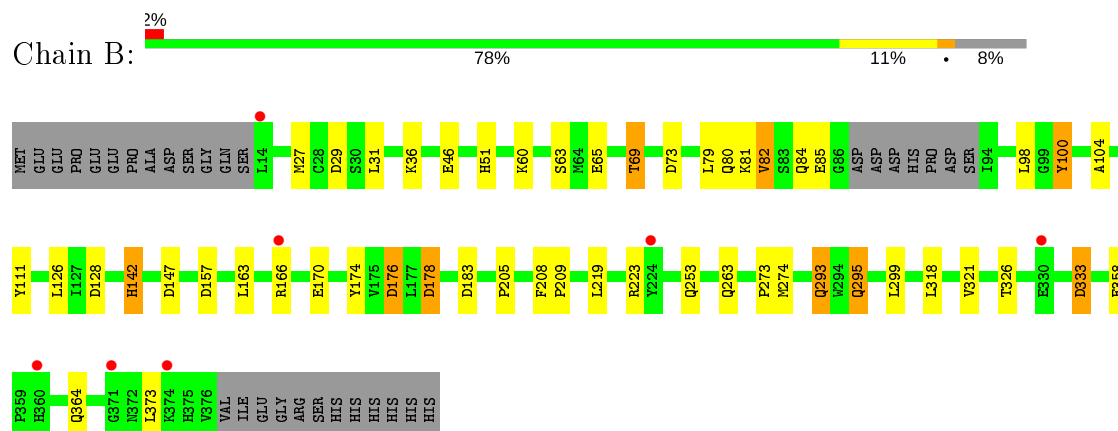
### 3 Residue-property plots [i](#)

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 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: HISTONE DEACETYLASE 8



#### • Molecule 1: HISTONE DEACETYLASE 8



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	84.30 Å 98.69 Å 110.47 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.25 48.20 – 2.25	Depositor EDS
% Data completeness (in resolution range)	98.5 (50.00-2.25) 98.5 (48.20-2.25)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.98 (at 2.24 Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.196 , 0.240 0.203 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.7	Xtriage
Anisotropy	0.657	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 38.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6038	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% 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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, K, V5X

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	0.61	0/2914	0.83	9/3953 (0.2%)
1	B	0.60	0/2855	0.80	7/3870 (0.2%)
All	All	0.60	0/5769	0.81	16/7823 (0.2%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	187	ASP	CB-CG-OD2	8.28	125.75	118.30
1	B	147	ASP	CB-CG-OD2	7.50	125.05	118.30
1	A	147	ASP	CB-CG-OD2	7.22	124.80	118.30
1	B	183	ASP	CB-CG-OD2	6.92	124.53	118.30
1	B	178	ASP	CB-CG-OD2	6.80	124.42	118.30
1	A	183	ASP	CB-CG-OD2	6.55	124.20	118.30
1	A	89	ASP	CB-CG-OD2	6.40	124.06	118.30
1	B	333	ASP	CB-CG-OD2	6.31	123.98	118.30
1	A	213	ASP	CB-CG-OD2	6.28	123.95	118.30
1	B	176	ASP	CB-CG-OD2	6.11	123.80	118.30
1	A	343	ASP	CB-CG-OD2	5.91	123.62	118.30
1	A	176	ASP	CB-CG-OD2	5.76	123.49	118.30
1	A	101	ASP	CB-CG-OD2	5.73	123.46	118.30
1	B	128	ASP	CB-CG-OD2	5.54	123.29	118.30
1	A	110	ASP	CB-CG-OD2	5.24	123.02	118.30
1	B	157	ASP	CB-CG-OD2	5.08	122.87	118.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2837	0	2782	23	0
1	B	2782	0	2746	27	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	46	0	40	7	0
4	B	46	0	40	5	0
5	A	153	0	0	8	0
5	B	168	0	0	5	0
All	All	6038	0	5608	56	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (56) 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)
4:B:1380:V5X:HAQ2	4:B:1380:V5X:HAN	1.51	0.90
4:A:1380:V5X:HAP1	4:A:1380:V5X:HAC	1.63	0.78
4:A:1380:V5X:HAQ1	4:A:1380:V5X:HAN	1.67	0.75
1:A:376:VAL:C	5:A:2150:HOH:O	2.24	0.75
1:B:274:MET:HE1	5:B:2066:HOH:O	1.87	0.74
4:A:1380:V5X:HAQ1	4:A:1380:V5X:CAN	2.20	0.71
1:B:208:PHE:CG	4:B:1380:V5X:HBC1	2.34	0.62
1:B:293:GLN:O	1:B:295:GLN:NE2	2.35	0.59
4:B:1380:V5X:HAQ2	4:B:1380:V5X:CAN	2.24	0.59
1:B:31:LEU:HB2	1:B:111:TYR:CZ	2.38	0.58
4:A:1380:V5X:HAP2	1:B:273:PRO:HB2	1.87	0.56
1:A:142:HIS:CD2	1:A:142:HIS:H	2.24	0.56
1:B:82:VAL:HG13	1:B:104:ALA:HB1	1.88	0.56
1:B:81:LYS:O	1:B:85:GLU:HG2	2.05	0.56
1:A:274:MET:HE1	5:A:2061:HOH:O	2.05	0.55
1:B:100:TYR:N	5:B:2040:HOH:O	2.42	0.52
4:A:1380:V5X:HAP1	4:A:1380:V5X:CAC	2.38	0.52

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:PHE:CG	4:A:1380:V5X:HBC2	2.44	0.51
1:A:69:THR:HG21	5:A:2055:HOH:O	2.11	0.50
1:B:142:HIS:CD2	1:B:142:HIS:H	2.30	0.50
1:B:333:ASP:CG	5:B:2131:HOH:O	2.49	0.49
1:B:69:THR:HG23	1:B:163:LEU:HD13	1.93	0.49
1:B:80:GLN:O	1:B:84:GLN:HG3	2.13	0.49
1:B:63:SER:OG	1:B:65:GLU:HG2	2.14	0.47
1:B:174:TYR:CE2	1:B:176:ASP:HB2	2.50	0.47
1:B:178:ASP:HB2	1:B:263:GLN:OE1	2.14	0.46
4:B:1380:V5X:CAN	4:B:1380:V5X:CAQ	2.93	0.46
1:B:208:PHE:CD1	4:B:1380:V5X:HAW2	2.51	0.46
1:B:46:GLU:HA	1:B:51:HIS:CD2	2.52	0.45
1:A:27:MET:HA	1:A:27:MET:HE2	1.98	0.45
1:A:360:HIS:CE1	5:A:2146:HOH:O	2.70	0.45
1:A:178:ASP:HB2	1:A:263:GLN:OE1	2.18	0.44
1:B:318:LEU:HA	1:B:321:VAL:HG13	1.99	0.44
1:A:243:ILE:HD11	1:A:362:ILE:HG21	2.00	0.43
1:B:208:PHE:HA	1:B:209:PRO:HA	1.83	0.43
1:A:202:LYS:HA	1:A:231:ILE:O	2.19	0.43
1:A:100:TYR:O	5:A:2034:HOH:O	2.21	0.43
1:A:174:TYR:CE2	1:A:176:ASP:HB2	2.53	0.43
1:B:166:ARG:HD3	5:B:2063:HOH:O	2.18	0.43
1:A:142:HIS:H	1:A:142:HIS:HD2	1.63	0.43
1:A:78:HIS:HE1	1:A:90:HIS:CD2	2.36	0.43
1:A:360:HIS:NE2	5:A:2146:HOH:O	2.36	0.43
1:B:163:LEU:HA	1:B:166:ARG:HG3	2.01	0.43
1:A:126:LEU:HG	1:A:297:ALA:HB1	2.00	0.42
1:A:46:GLU:HA	1:A:51:HIS:CD2	2.54	0.42
1:A:55:ARG:HD3	1:A:130:MET:HE2	2.01	0.42
1:A:243:ILE:N	1:A:243:ILE:HD13	2.35	0.42
4:A:1380:V5X:HAP2	1:B:273:PRO:CB	2.49	0.41
1:A:318:LEU:HA	1:A:321:VAL:HG13	2.02	0.41
1:A:359:PRO:HD2	5:A:2146:HOH:O	2.20	0.41
1:B:142:HIS:ND1	1:B:176:ASP:OD2	2.53	0.41
1:B:31:LEU:HB2	1:B:111:TYR:OH	2.20	0.41
1:B:29:ASP:OD2	1:B:36:LYS:HA	2.20	0.41
1:B:333:ASP:OD1	5:B:2131:HOH:O	2.22	0.41
1:A:352:CYS:O	1:B:205:PRO:HG2	2.21	0.41
1:A:353:ARG:HG2	5:A:2142:HOH:O	2.21	0.41

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	362/388 (93%)	349 (96%)	11 (3%)	2 (1%)	25	25
1	B	353/388 (91%)	341 (97%)	11 (3%)	1 (0%)	41	46
All	All	715/776 (92%)	690 (96%)	22 (3%)	3 (0%)	34	37

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	100	TYR
1	A	87	ASP
1	A	15	VAL

### 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	305/326 (94%)	278 (91%)	27 (9%)	9	8
1	B	298/326 (91%)	277 (93%)	21 (7%)	15	13
All	All	603/652 (92%)	555 (92%)	48 (8%)	13	10

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LEU
1	A	15	VAL
1	A	30	SER

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	36[A]	LYS
1	A	36[B]	LYS
1	A	58	LYS
1	A	60	LYS
1	A	65	GLU
1	A	69	THR
1	A	79	LEU
1	A	85	GLU
1	A	98	LEU
1	A	126	LEU
1	A	142	HIS
1	A	148	GLU
1	A	170	GLU
1	A	219	LEU
1	A	238	GLU
1	A	245	GLU
1	A	253	GLN
1	A	274	MET
1	A	293	GLN
1	A	299	LEU
1	A	338	THR
1	A	360	HIS
1	A	373	LEU
1	A	374	LYS
1	B	27[A]	MET
1	B	27[B]	MET
1	B	60	LYS
1	B	69	THR
1	B	73	ASP
1	B	79	LEU
1	B	82	VAL
1	B	98	LEU
1	B	126	LEU
1	B	142	HIS
1	B	170	GLU
1	B	219	LEU
1	B	223	ARG
1	B	253	GLN
1	B	293	GLN
1	B	295	GLN
1	B	299	LEU
1	B	326	THR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	358	GLU
1	B	364	GLN
1	B	373	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	HIS
1	A	78	HIS
1	A	90	HIS
1	A	136	ASN
1	A	232	GLN
1	A	256	ASN
1	B	51	HIS
1	B	78	HIS
1	B	136	ASN
1	B	372	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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	$\# Z  > 2$
4	V5X	B	1380	2	46,50,50	1.47	3 (6%)	56,68,68	1.61	10 (17%)
4	V5X	A	1380	2	46,50,50	1.48	3 (6%)	56,68,68	1.65	13 (23%)

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
4	V5X	B	1380	2	-	13/34/34/34	0/5/5/5
4	V5X	A	1380	2	-	11/34/34/34	0/5/5/5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1380	V5X	CAF-CAG	-6.72	1.41	1.49
4	B	1380	V5X	CAF-CAG	-6.71	1.41	1.49
4	B	1380	V5X	CAY-CAZ	3.24	1.57	1.51
4	A	1380	V5X	CBI-CBJ	3.01	1.55	1.50
4	B	1380	V5X	CA-N	2.23	1.50	1.45
4	A	1380	V5X	CA-N	2.11	1.50	1.45

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1380	V5X	CB-CA-N	5.36	121.71	110.88
4	A	1380	V5X	CAQ-CAP-CAL	-4.45	103.54	113.07
4	A	1380	V5X	CAP-CAL-CAG	3.95	131.78	127.48
4	B	1380	V5X	CBP-OBO-CBN	-3.69	109.50	117.51
4	A	1380	V5X	CA-N-CBF	3.59	130.88	121.65
4	B	1380	V5X	CA-C-NAR	-3.13	110.24	116.54
4	B	1380	V5X	CAG-NAH-CAI	3.01	110.08	103.90
4	B	1380	V5X	CBI-CBJ-CBK	-2.95	123.04	129.47
4	B	1380	V5X	CAQ-CAP-CAL	-2.88	106.90	113.07
4	A	1380	V5X	CAN-CAM-CAI	2.83	121.92	118.17
4	A	1380	V5X	CAG-NAH-CAI	2.80	109.66	103.90
4	A	1380	V5X	C-CA-N	2.79	118.76	111.16
4	B	1380	V5X	OBO-CBN-CBM	-2.77	116.87	124.43

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1380	V5X	CBM-CBL-CBR	2.60	121.81	118.26
4	B	1380	V5X	CBH-CBK-CBJ	2.52	128.63	126.41
4	B	1380	V5X	CBM-CBL-CBK	-2.37	130.08	134.17
4	A	1380	V5X	CBI-CBJ-CBK	-2.36	124.33	129.47
4	A	1380	V5X	OBO-CBN-CBM	-2.36	118.01	124.43
4	A	1380	V5X	O-C-CA	2.27	125.23	120.45
4	A	1380	V5X	CAK-CAO-CAN	-2.27	117.26	120.44
4	A	1380	V5X	CBP-OBO-CBN	-2.26	112.60	117.51
4	A	1380	V5X	CAP-CAQ-NAR	2.23	118.73	111.99
4	A	1380	V5X	CBH-CBF-N	-2.23	112.29	115.88

There are no chirality outliers.

All (24) torsion outliers are listed below:

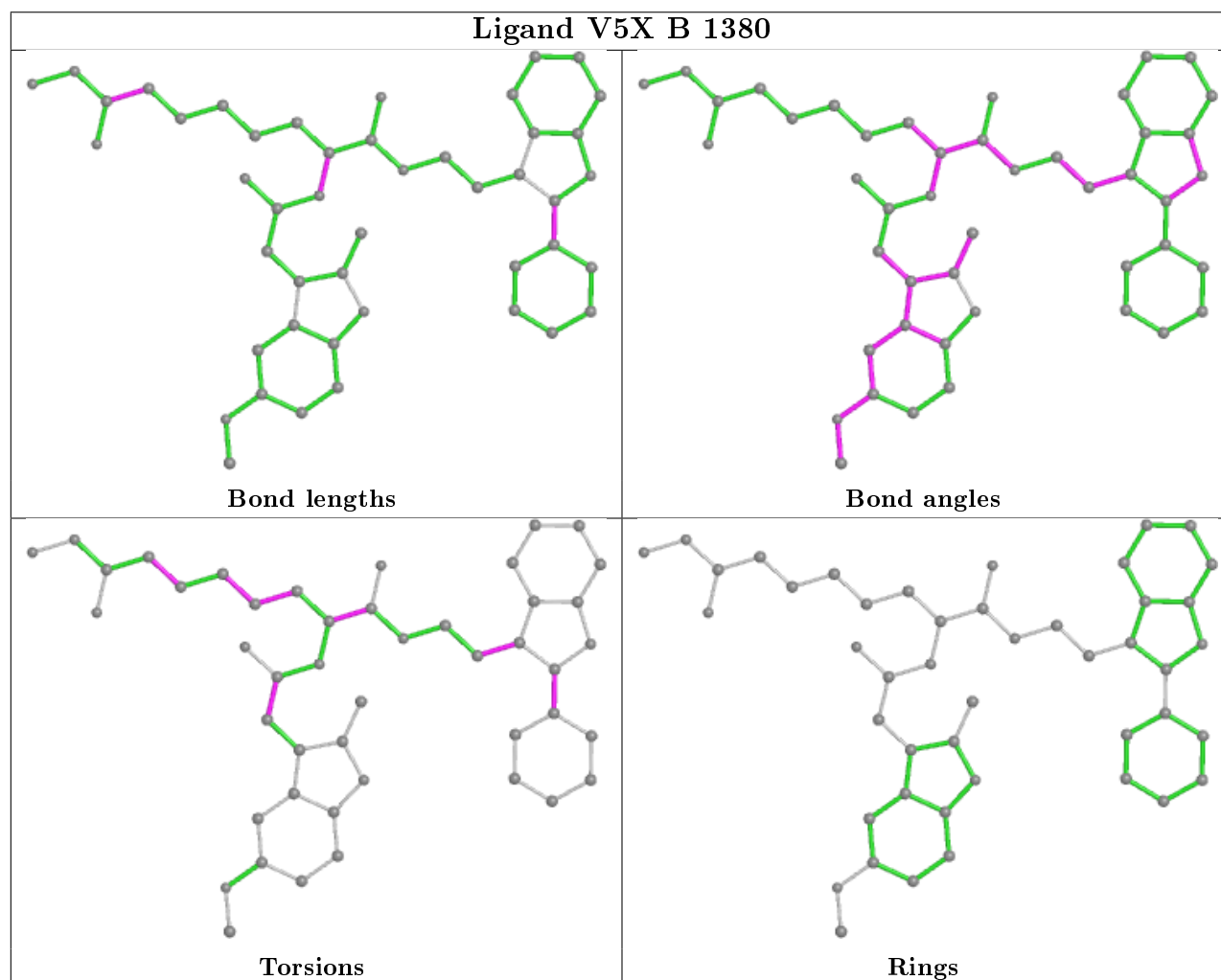
Mol	Chain	Res	Type	Atoms
4	B	1380	V5X	CAM-CAL-CAP-CAQ
4	B	1380	V5X	CAG-CAL-CAP-CAQ
4	B	1380	V5X	CAE-CAF-CAG-NAH
4	B	1380	V5X	CAC-CAF-CAG-NAH
4	A	1380	V5X	CAM-CAL-CAP-CAQ
4	A	1380	V5X	CBM-CBN-OBO-CBP
4	A	1380	V5X	CBT-CBN-OBO-CBP
4	B	1380	V5X	CAW-CAX-CAY-CAZ
4	A	1380	V5X	CAP-CAQ-NAR-C
4	B	1380	V5X	CAW-CAV-CB-CA
4	A	1380	V5X	CAW-CAV-CB-CA
4	A	1380	V5X	O-C-CA-N
4	A	1380	V5X	C-CA-CB-CAV
4	B	1380	V5X	OBG-CBF-CBH-CBK
4	A	1380	V5X	NAR-C-CA-N
4	A	1380	V5X	CAW-CAX-CAY-CAZ
4	A	1380	V5X	CAG-CAL-CAP-CAQ
4	B	1380	V5X	N-CBF-CBH-CBK
4	B	1380	V5X	CB-CAV-CAW-CAX
4	B	1380	V5X	NAR-C-CA-N
4	B	1380	V5X	O-C-CA-N
4	B	1380	V5X	O-C-CA-CB
4	A	1380	V5X	CAC-CAF-CAG-CAL
4	B	1380	V5X	NAR-C-CA-CB

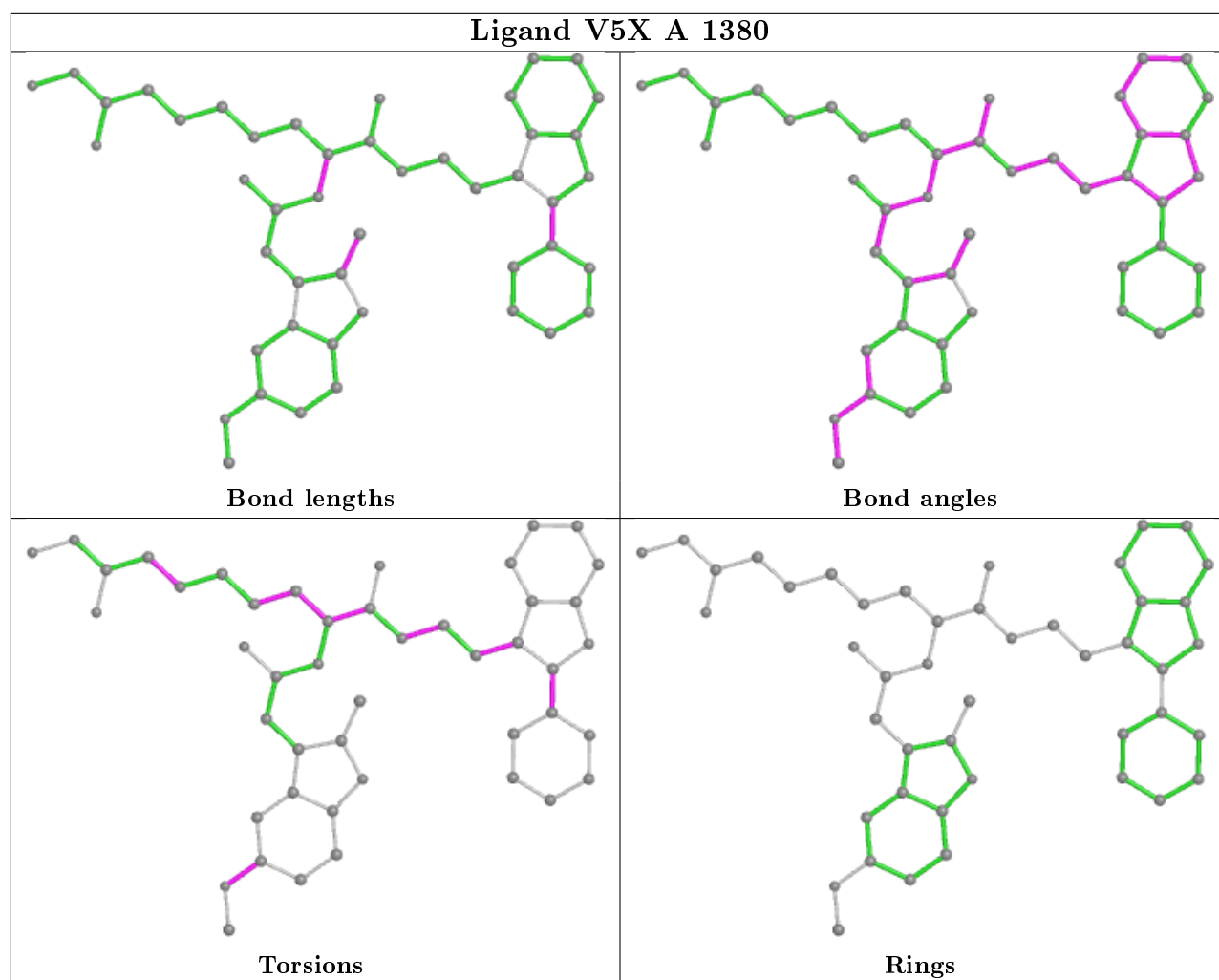
There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1380	V5X	5	0
4	A	1380	V5X	7	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](#)

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	363/388 (93%)	0.00	12 (3%) 46 48	23, 36, 64, 85	0
1	B	356/388 (91%)	-0.02	7 (1%) 65 68	24, 38, 57, 66	0
All	All	719/776 (92%)	-0.01	19 (2%) 56 59	23, 37, 58, 85	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	86	GLY	7.2
1	A	88	ASP	3.8
1	A	100	TYR	3.6
1	A	89	ASP	3.6
1	A	101	ASP	3.0
1	B	360	HIS	2.9
1	A	91	PRO	2.7
1	A	374	LYS	2.7
1	B	166	ARG	2.7
1	B	224	TYR	2.7
1	A	87	ASP	2.6
1	A	224	TYR	2.6
1	B	374	LYS	2.5
1	A	368	TYR	2.5
1	B	330	GLU	2.4
1	B	371	GLY	2.2
1	B	14	LEU	2.1
1	A	253	GLN	2.1
1	A	85	GLU	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

There are no carbohydrates in this entry.

### 6.4 Ligands

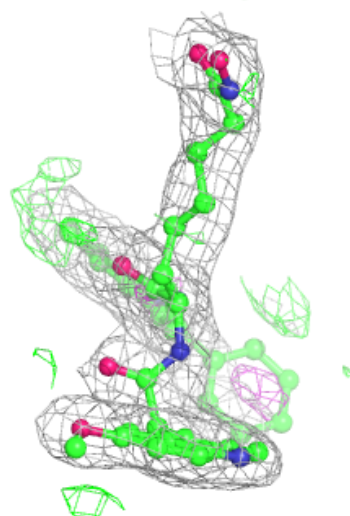
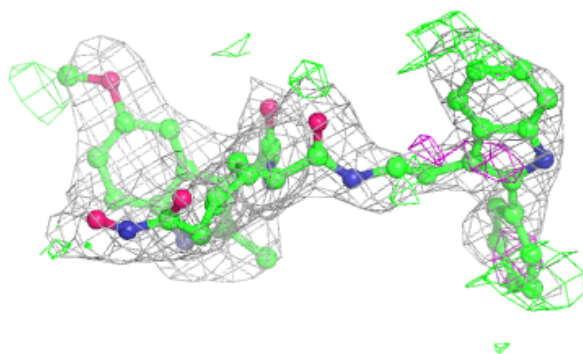
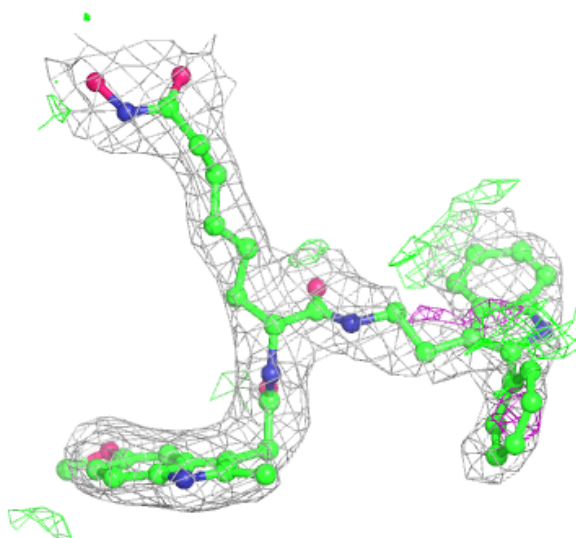
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
4	V5X	B	1380	46/46	0.90	0.21	27,45,66,68	0
4	V5X	A	1380	46/46	0.90	0.22	28,46,61,61	0
3	K	A	1378	1/1	0.99	0.12	24,24,24,24	0
3	K	B	1379	1/1	0.99	0.08	32,32,32,32	0
3	K	A	1379	1/1	0.99	0.05	28,28,28,28	0
3	K	B	1378	1/1	0.99	0.08	25,25,25,25	0
2	ZN	A	1377	1/1	1.00	0.13	24,24,24,24	0
2	ZN	B	1377	1/1	1.00	0.14	24,24,24,24	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.

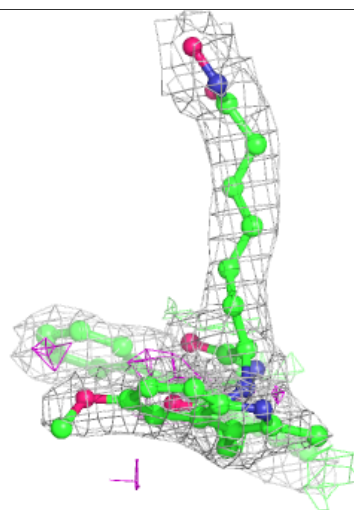
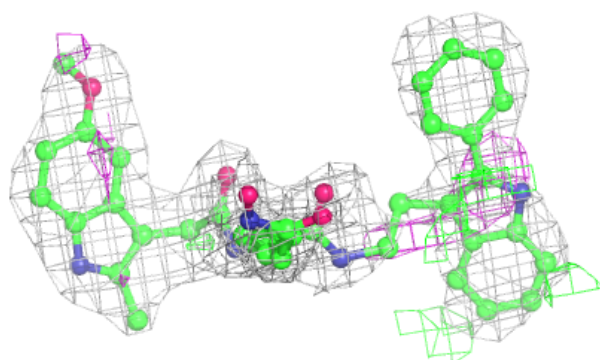
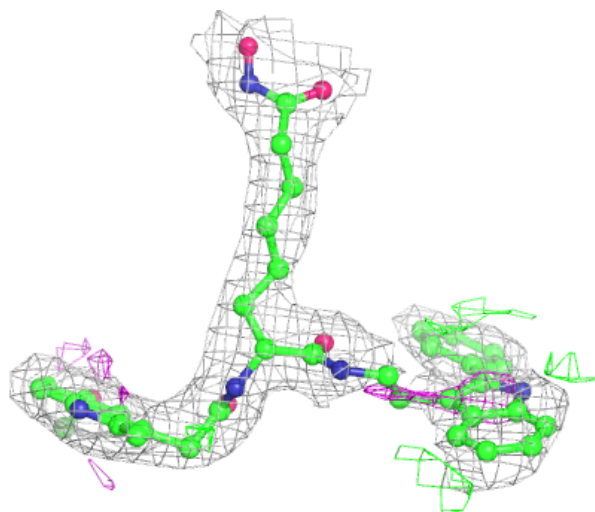
**Electron density around V5X B 1380:**

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



**Electron density around V5X A 1380:**

$2mF_o-DF_c$  (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.